Zipping the Three Nephews

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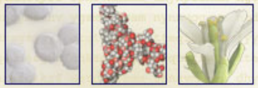
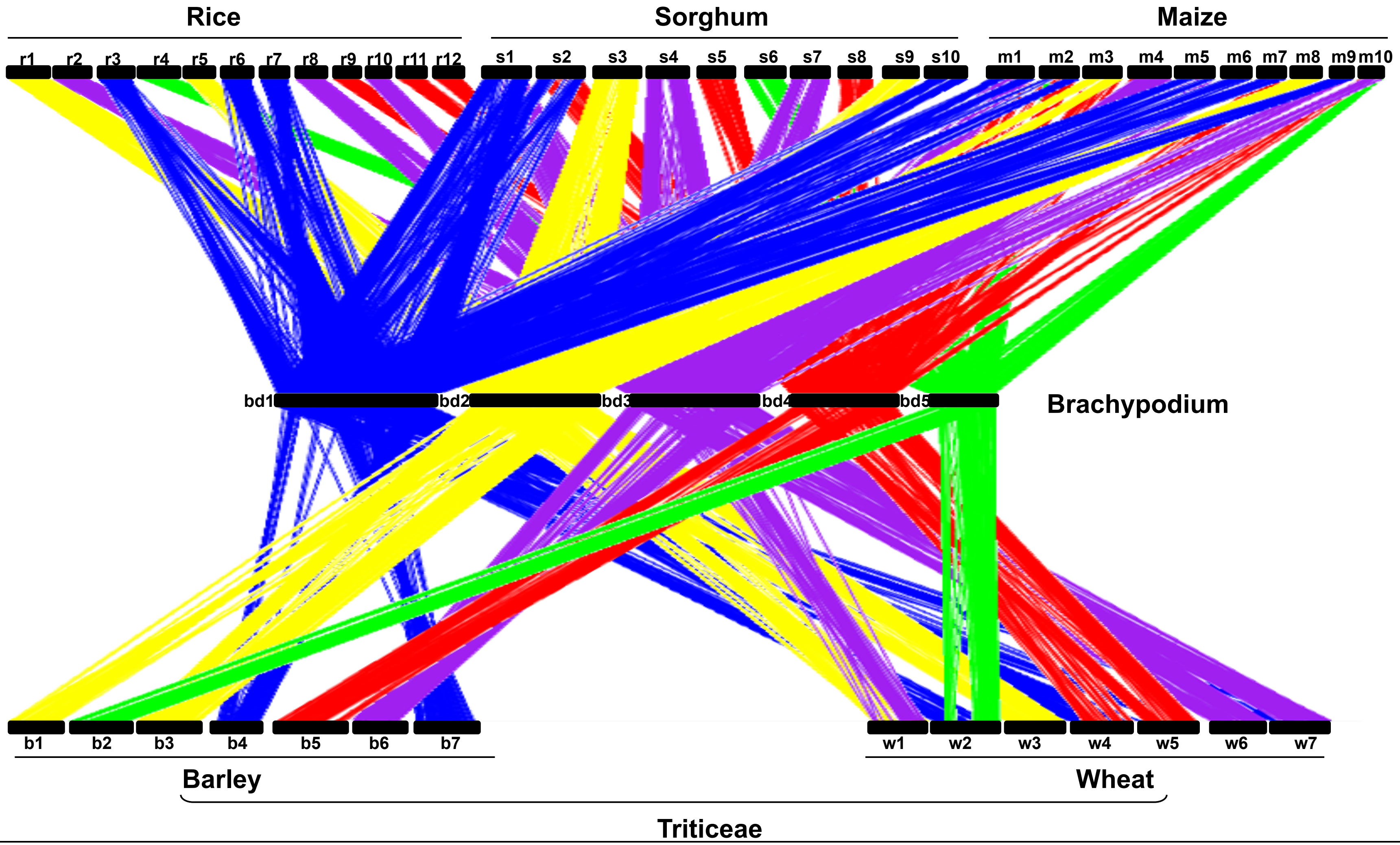
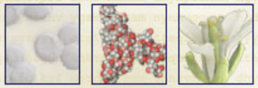


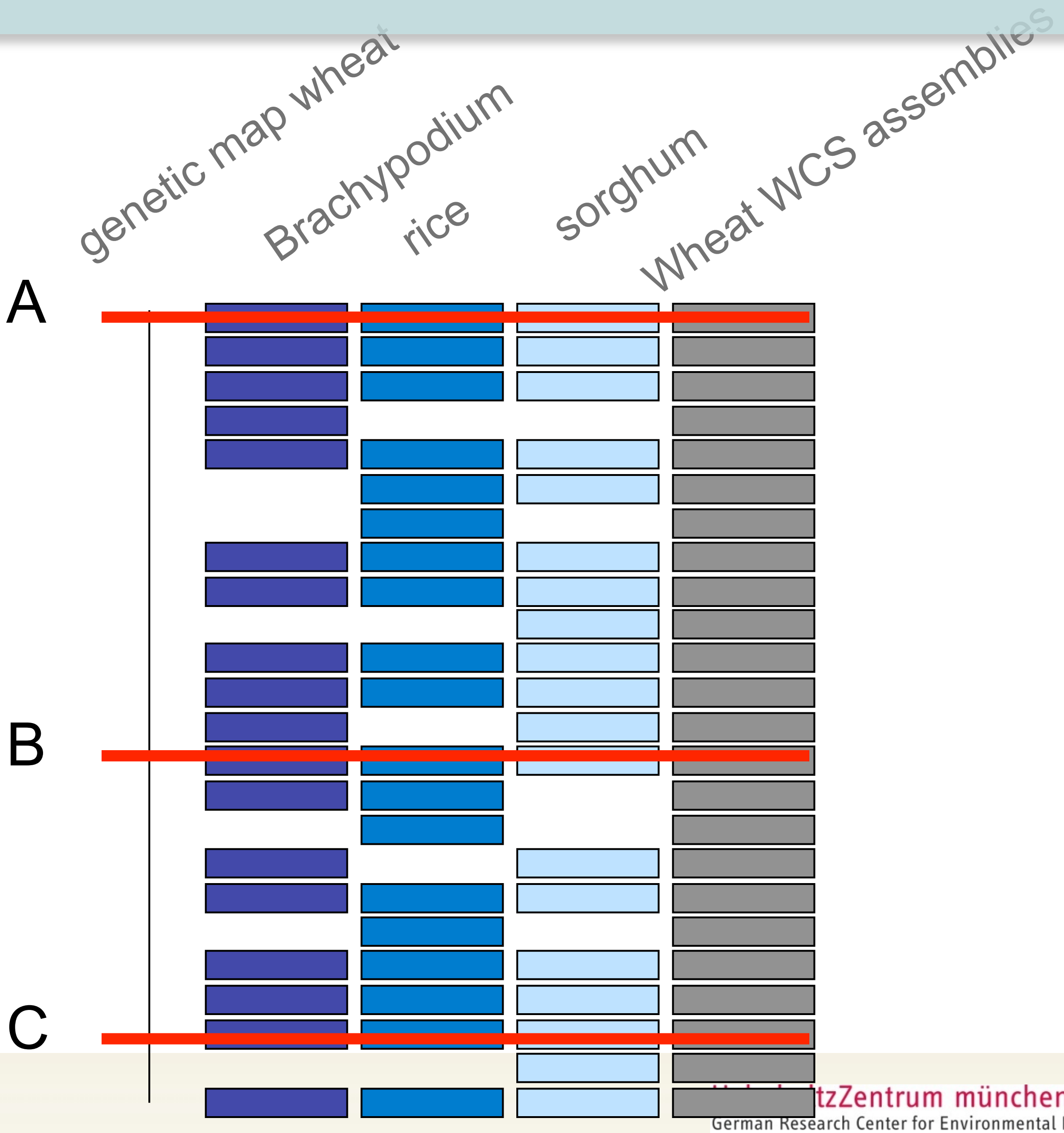
Brachypodium Genome Synteny



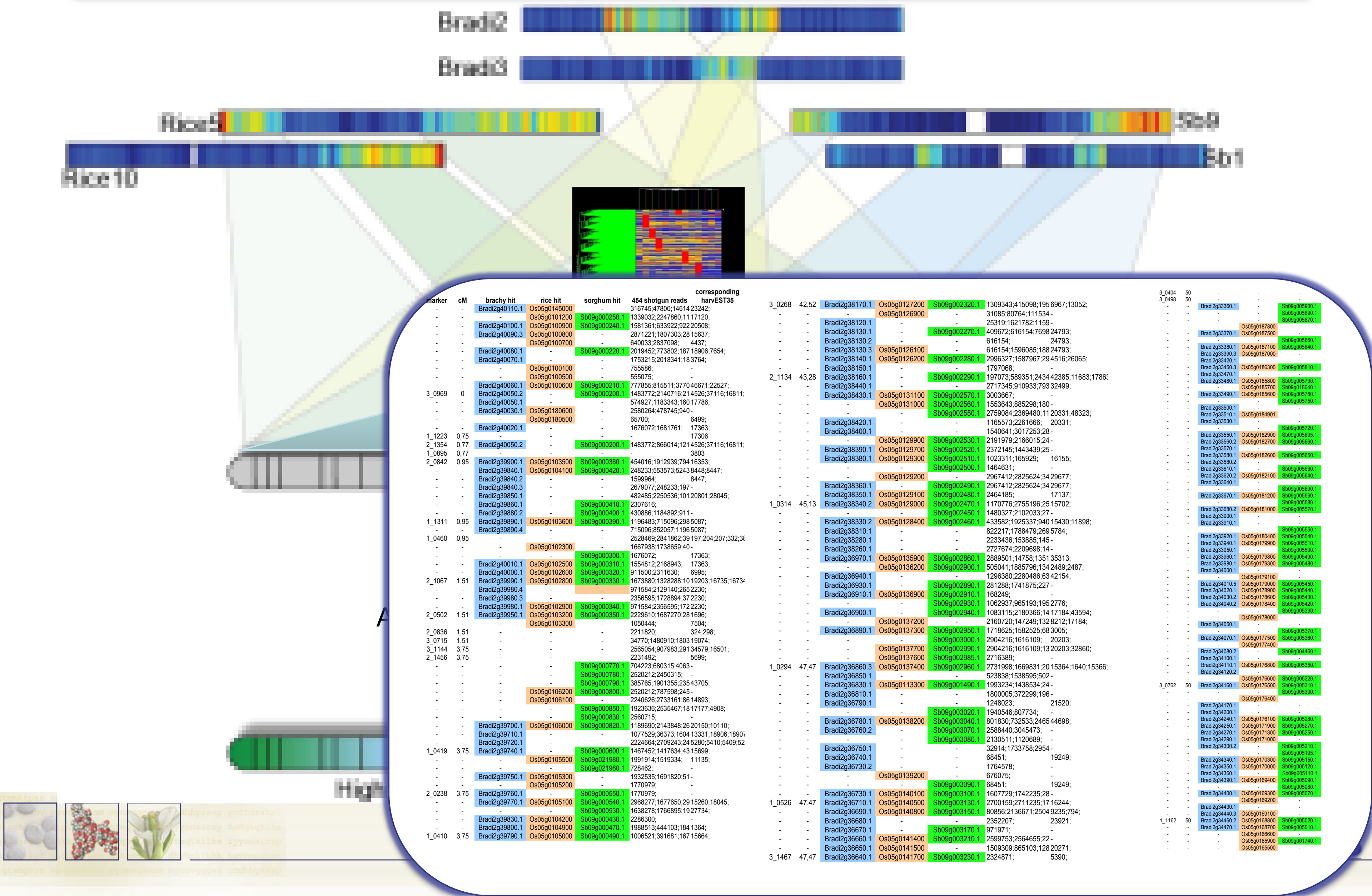
J. Salse



Syntenic integration aka „Genome Zipper“



Syntenic integration aka „Genome Zipper“



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-	-	-	Os05g0101200	Sb09g000250.1	1339032;2247860;11	17120;
-	-	Bradi2g40100.1	Os05g0100900	Sb09g000240.1	1581361;633922;922	20508;
-	-	Bradi2g40090.3	Os05g0100800	-	2871221;1807303;28	15637;
-	-	-	Os05g0100700	-	640033;2837098;	4437;
-	-	Bradi2g40080.1	-	Sb09g000220.1	2019452;773802;187	18906;7654;
-	-	Bradi2g40070.1	-	-	1753215;2018341;18	3764;
-	-	-	Os05g0100100	-	755586;	-
-	-	-	Os05g0100500	-	555075;	-
-	-	Bradi2g40060.1	Os05g0100600	Sb09g000210.1	777855;815511;3770	46671;22527;
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-	-	Bradi2g40050.1	-	-	574927;1183343;160	17786;
-	-	Bradi2g40030.1	Os05g0180600	-	2580264;478745;940	-
-	-	-	Os05g0180500	-	65700;	6499;
-	-	Bradi2g40020.1	-	-	1676072;1681761;	17363;
1_1223	0,75	-	-	-	-	17306
2_1354	0,77	Bradi2g40050.2	-	Sb09g000200.1	1483772;866014;121	4526;37116;16811;
1_0895	0,77	-	-	-	-	3803
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-	-	Bradi2g39840.1	Os05g0104100	Sb09g000420.1	248233;553573;5243	8448;8447;
-	-	Bradi2g39840.2	-	-	1599964;	8447;
-	-	Bradi2g39840.3	-	-	2679077;248233;197	-
-	-	Bradi2g39850.1	-	-	482485;2250536;101	20801;28045;
-	-	Bradi2g39860.1	-	Sb09g000410.1	2307616;	-
-	-	Bradi2g39880.2	-	Sb09g000400.1	430886;1184892;911	-
1_1311	0,95	Bradi2g39890.1	Os05g0103600	Sb09g000390.1	1196483;715096;298	5087;
-	-	Bradi2g39890.4	-	-	715096;852057;1196	5087;
1_0460	0,95	-	-	-	2528469;2841862;39	197;204;207;332;3
-	-	-	Os05g0102300	-	1667938;1738659;40	-
-	-	-	-	Sb09g000300.1	1676072;	17363;
-	-	Bradi2g40010.1	Os05g0102500	Sb09g000310.1	1554812;2168943;	17363;
-	-	Bradi2g40000.1	Os05g0102600	Sb09g000320.1	911500;2311630;	6995;
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-	-	Bradi2g39980.4	-	-	971584;2129140;265	2230;
-	-	Bradi2g39980.3	-	-	2356595;1728894;37	2230;
-	-	Bradi2g39980.1	Os05g0102900	Sb09g000340.1	971584;2356595;172	2230;
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-	-	-	Os05g0103300	-	1050444;	7504;
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3_0715	1,51	-	-	-	34770;1480910;1803	19074;
3_1144	3,75	-	-	-	2565054;907983;291	34579;16501;
2_1456	3,75	-	-	-	2231492;	5699;
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-	-	-	-	Sb09g000790.1	385765;1901355;235	43705;
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-	-	-	Os05g0106100	-	2240626;2733161;86	14893;
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-	-	-	-	Sb09g000830.1	2560715;	-
-	-	Bradi2g39700.1	Os05g0106000	Sb09g000820.1	1189690;2143848;26	20150;10110;
-	-	Bradi2g39710.1	-	-	1077529;36373;1604	13331;18906;1890
-	-	Bradi2g39720.1	-	-	2224664;2709243;24	5280;5410;5409;52
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-	-	-	-	Sb09g000530.1	1638278;1766895;19	27734;
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-	-	Bradi2g38120.1	-	-	25319;1621782;1159	-
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-	-	Bradi2g38150.1	-	-	1797068;	-
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-	-	Bradi2g38440.1	-	-	2717345;910933;793	32499;
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-	-	-	-	Sb09g002550.1	2759084;2369480;11	20331;48323;
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-	-	Bradi2g38400.1	-	-	1540641;3017253;28	-
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-	-	-	-	Sb09g002500.1	1464631;	-
-	-	-	Os05g0129200	-	2967412;2825624;34	29677;
-	-	Bradi2g38360.1	-	Sb09g002490.1	2967412;2825624;34	29677;
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-	-	Bradi2g38280.1	-	-	2233436;153885;145	-
-	-	Bradi2g38260.1	-	-	2727674;2209698;14	-
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-	-	-	-	Sb09g003000.1	2904216;1616109;	20203;
-	-	-	Os05g0137700	Sb09g002990.1	2904216;1616109;13	20203;32860;
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-	-	Bradi2g36810.1	-	-	1800005;372299;196	-
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-	-	Bradi2g36760.2	-	Sb09g003070.1	2588440;3045473;	-
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-	-	Bradi2g36750.1	-	-	32914;1733758;2954	-
-	-	Bradi2g36740.1	-	-	68451;	19249;
-	-	Bradi2g36730.2	-	-	1764578;	-
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-	-	-	-	Sb09g005870.1		
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-	-	Bradi2g33370.1	Os05g0187500	-		
-	-	-	-	Sb09g005860.1		
-	-	Bradi2g33380.1	Os05g0187100	Sb09g005840.1		
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-	-	Bradi2g33490.1	Os05g0185600	Sb09g005780.1		
-	-	-	-	Sb09g005750.1		
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-	-	Bradi2g33530.1	-	-		
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-	-	Bradi2g33570.1	-	-		
-	-	Bradi2g33580.1	Os05g0182600	Sb09g005650.1		
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-	-	Bradi2g33610.1	-	Sb09g005630.1		
-	-	Bradi2g33620.2	Os05g0182100	Sb09g005640.1		
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-	-	-	-	Sb09g005580.1		
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-	-	Bradi2g33900.1	-	-		
-	-	Bradi2g33910.1	-	-		
-	-	-	-	Sb09g005550.1		
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-	-	Bradi2g33950.1	-	Sb09g005500.1		
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-	-	-	Os05g0179100	-		
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-	-	-	-	Sb09g005390.1		
-	-	-	Os05g0178000	-		
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-	-	-	Os05g0177400	-		
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-	-	-	Os05g0176400	-		
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-	-	Bradi2g34200.1	-	-		
-	-	Bradi2g34240.1	Os05g0176100	Sb09g005280.1		
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-	-	Bradi2g34290.1	Os05g0171000	-		
-	-	Bradi2g34300.2	-	Sb09g005210.1		
-	-	-	-	Sb09g005195.1		
-	-	Bradi2g34340.1	Os05g0170300	Sb09g005150.1		
-	-	Bradi2g34350.1	Os05g0170000	Sb09g005120.1		
-	-	Bradi2g34360.1	-	Sb09g005110.1		
-	-	Bradi2g34390.1	Os05g0169400	Sb09g005090.1		
-	-	-	-	Sb09g005080.1		
-	-	Bradi2g34400.1	Os05g0169300	Sb09g005070.1		
-	-	-	Os05g0169200	-		
-	-	Bradi2g34430.1	-	-		
-	-	Bradi2g34440.3	Os05g0169100	-		
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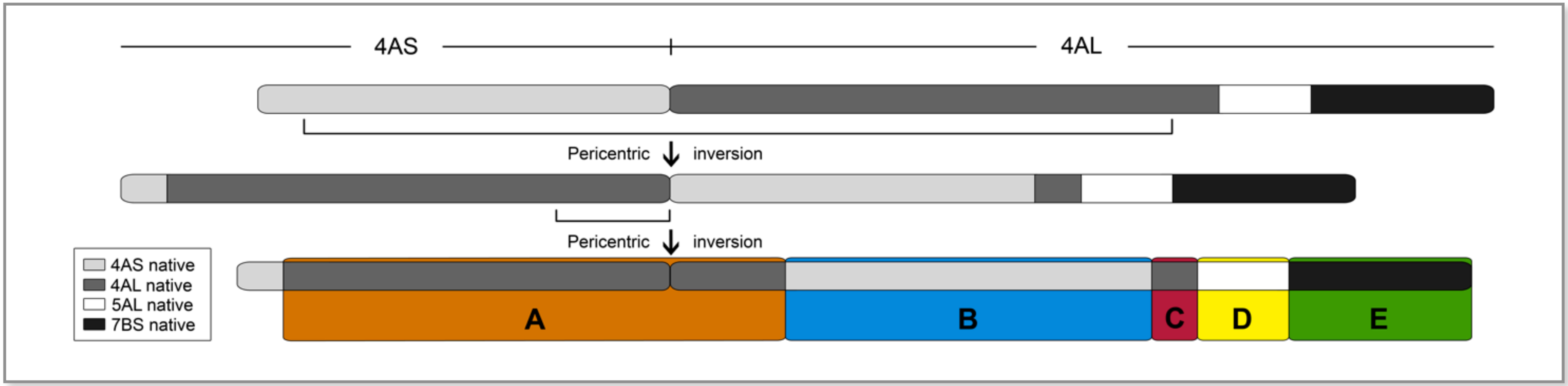
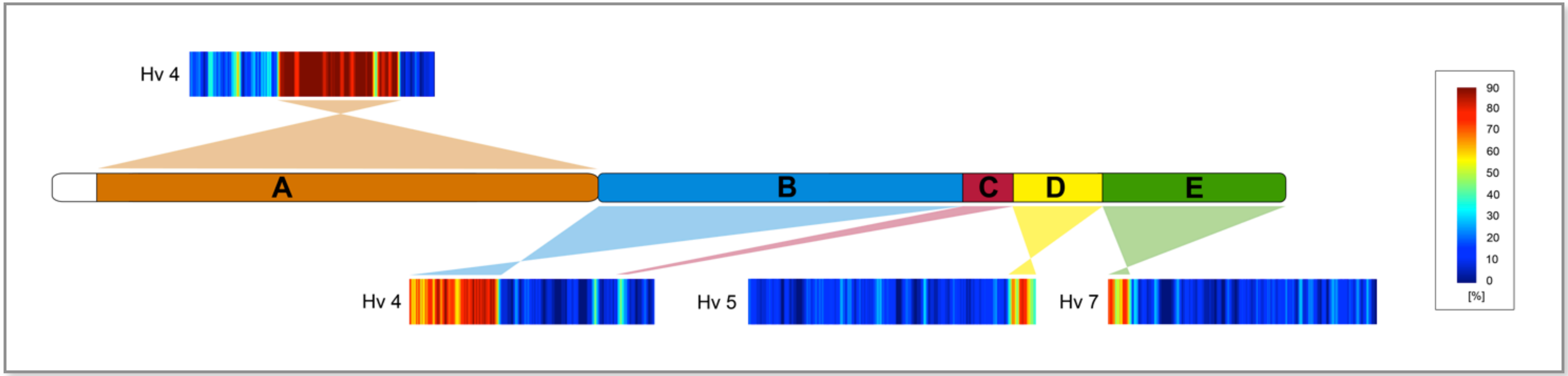
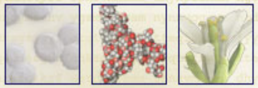
-	-	Bradi2g34470.1	Os05g0168700	Sb09g005010.1		
-	-	-	Os05g0166600	-		
-	-	-	Os05g0165900	Sb09g001740.1		
-	-	-	Os05g0165500	-		

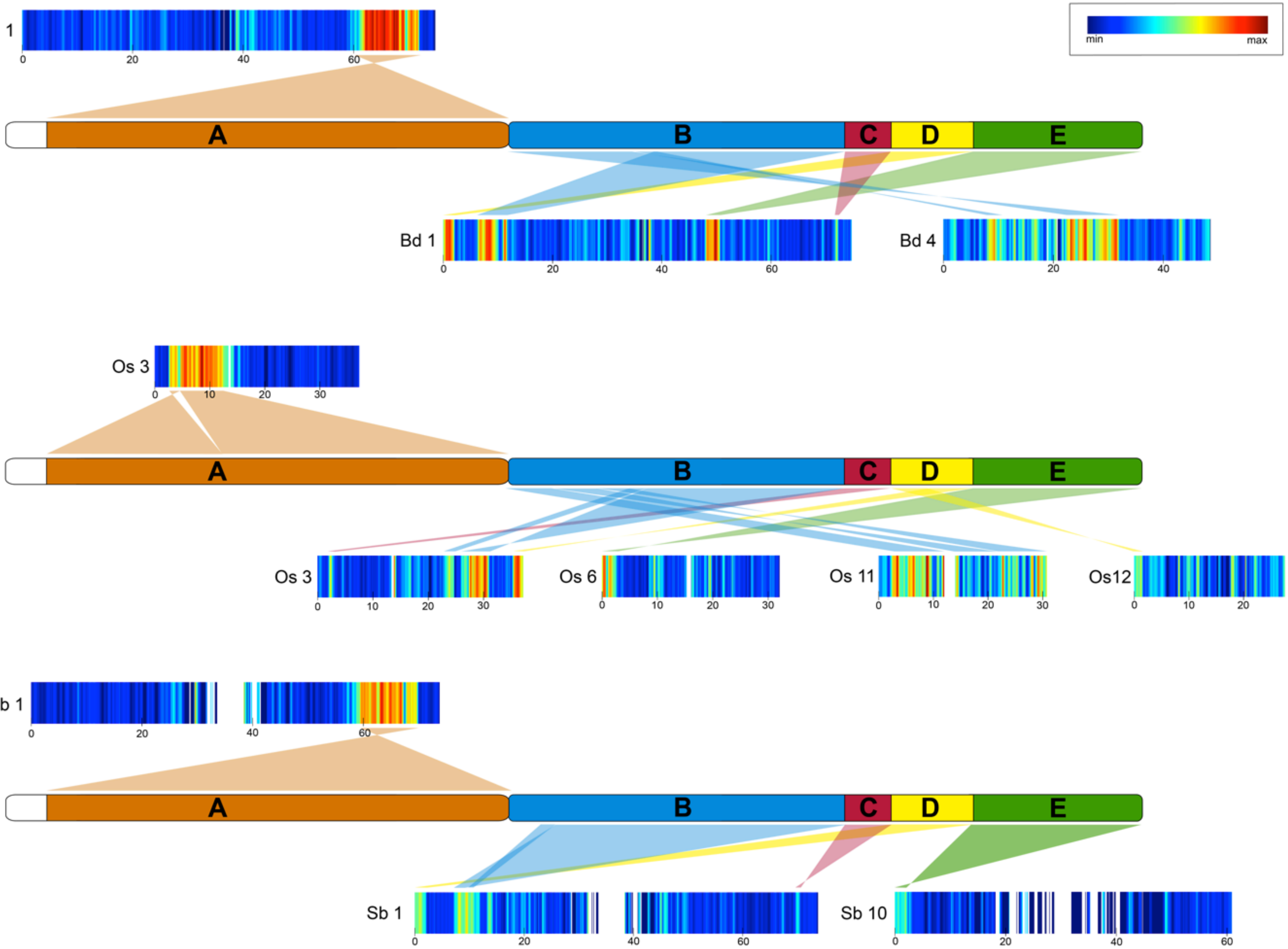
Wheat 4A is the most rearranges wheat chromosome

Hernandez and Dolezel labs





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20
40
60
A
B
C
D
E
Bd 1
Bd 4
Os 3
10
30
Os 6
Os 11
Os12
b 1
Sb 1
Sb 10

Intervalls and breakpoints can be precisly identified

Block	Brachypodium	Oryza sativa	Sorghum
A	Bradi1g72080.1	Os03g0187500	Sb01g044730.1
	Bradi1g72086.1	Os03g0187400	Sb01g044740.1
	Bradi1g72092.1	Os03g0187300	Sb01g044750.1
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	Bradi1g65190.1	Os03g0296700	Sb01g038210.1
	Bradi1g65197.1	Os03g0296600	Sb01g038220.1
	Bradi1g65210.1	Os03g0296400	Sb01g038230.1
B	Bradi4g26690.1	Os11g0150450	Sb01g013770.1
	Bradi4g26670.3	Os11g0151600	Sb01g013780.1
	Bradi4g26640.1	Os11g0152700	Sb01g013830.1
	...	...	...
	Bradi1g13777.1	Os03g0652100	Sb01g013490.1
	Bradi1g13850.1	Os03g0648200	Sb01g013540.1
	Bradi1g13870.1	Os03g0645100	Sb01g013650.1
C	Bradi1g75740.1	Os03g0138200	Sb01g047640.1
	Bradi1g75720.1	Os03g0140100	Sb01g047630.1
	Bradi1g75707.1	Os03g0141100	Sb01g047610.1
	...	...	...
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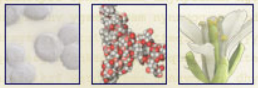
	Bradi1g75970.1	Os03g0147700	Sb01g047850.1
	Bradi1g76227.1	Os03g0136900	Sb01g047860.1
D	Bradi1g00227.1	Os03g0861800	Sb01g000210.1
	Bradi1g00237.1	Os03g0860900	Sb01g000220.1
	Bradi1g00247.1	Os03g0860700	Sb01g000300.1
	...	...	...
	Bradi1g02940.1	Os03g0823800	Sb01g002280.1
	Bradi1g02950.1	Os03g0822100	Sb01g002300.1
	Bradi1g02980.1	Os03g0821633	Sb01g002410.1
E	Bradi1g49450.1	Os06g0122200	Sb10g001470.1
	Bradi1g49460.1	Os06g0125000	Sb10g001520.1
	Bradi1g49470.1	Os06g0125300	Sb10g001530.1
	...	...	...
	Bradi1g52060.1	Os06g0103300	Sb10g000300.1
	Bradi1g52090.1	Os06g0102900	Sb10g000270.1
	Bradi1g52110.1	Os06g0102700	Sb10g000260.1



19,720 GBS-SNP marker (obtained from Jesse Poland)

Group A: 1A … 7A

Group B: 1B … 7B

Group D: 1D … 7D

	same cM	cM
same sequence	7,619	46
different sequence	12,101	ø

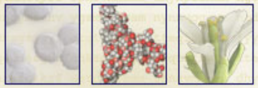
→ $\sum 15,308$

🟦 hold 1 copy => 4366 removed from data set

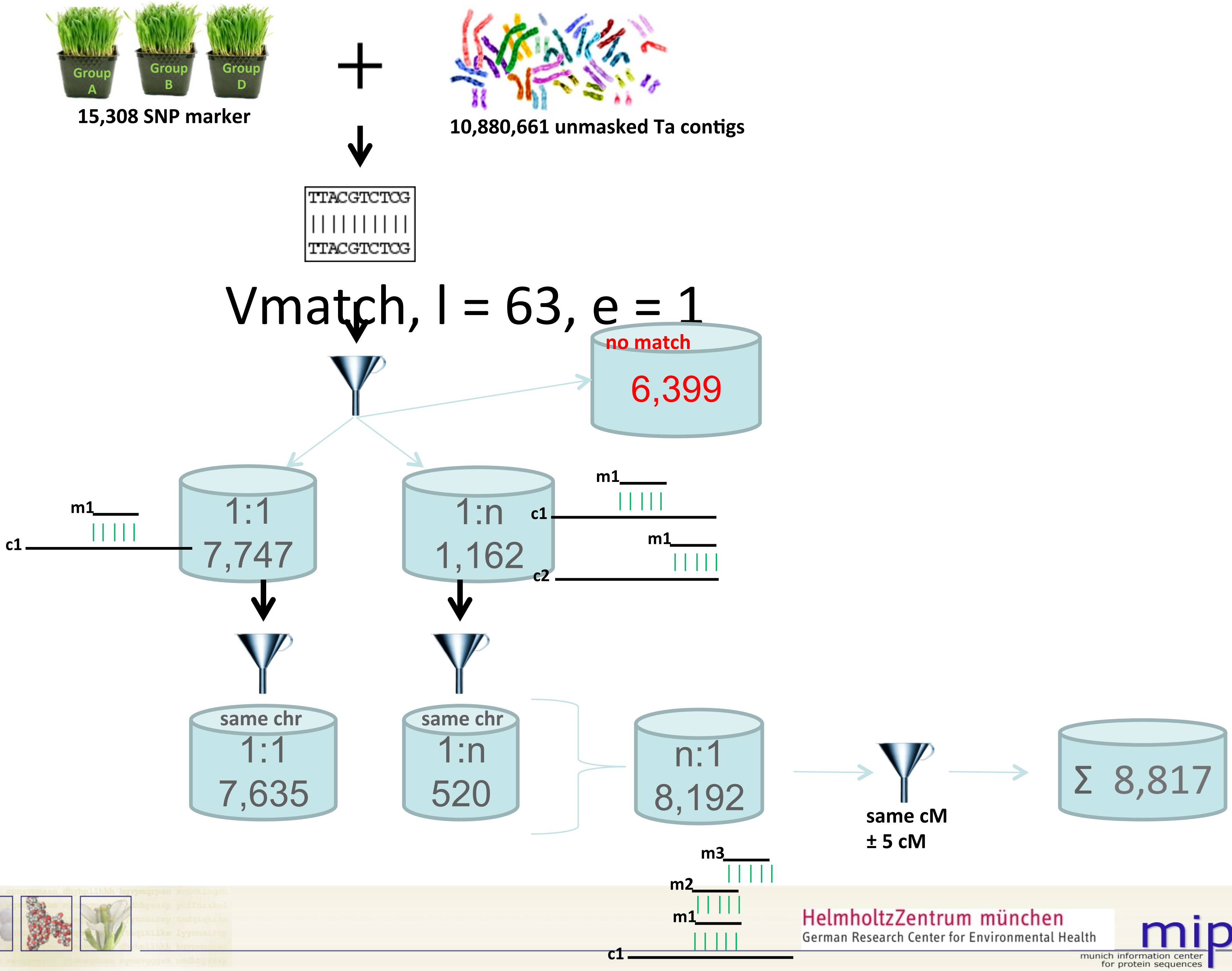
🟥 removed from data set

	# SNP marker per chromosome (unfiltered) = 19,720							
	1	2	3	4	5	6	7	Σ
A	697	661	936	925	658	775	1285	5937
B	1291	1363	1676	825	1110	1215	1436	8916
D	362	796	998	225	735	767	984	4867

	# SNP marker per chromosome (filtered) = 15,308							
	1	2	3	4	5	6	7	Σ
A	556	499	719	725	542	601	992	4634
B	988	1063	1260	647	852	910	1105	6825
D	291	652	771	194	580	587	774	3849

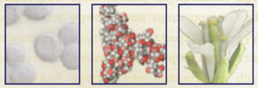


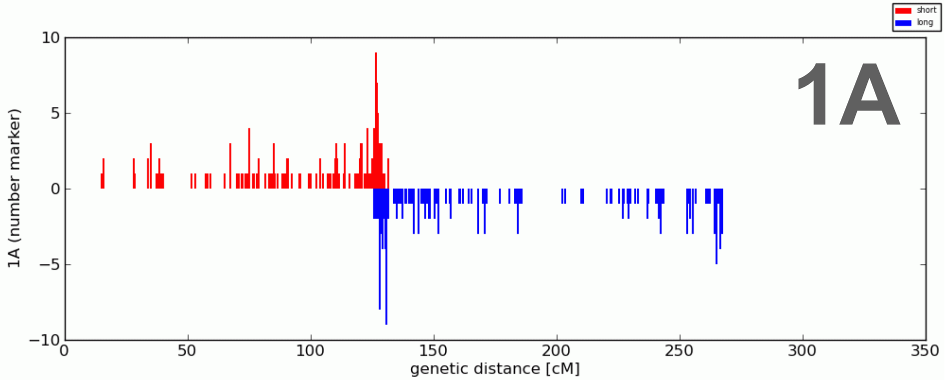
Vmatch, l = 63, e = 1

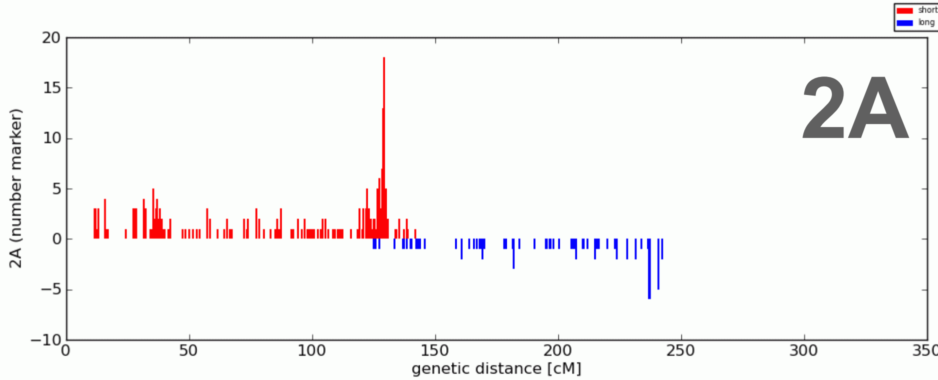


	# contig marker per chromosome arm (filtered) = 8,817														
	1S	**1L**	**2S**	**2L**	**3S**	**3L**	**4S**	**4L**	**5S**	**5L**	**6S**	**6L**	**7S**	**7L**	**Σ**
A	146	168	228	82	127	227	105	375	0	283	200	176	286	237	2640
B	268	285	338	402	766		229	164	123	465	229	181	163	347	3954
D	85	99	192	198	97	209	30	115	106	253	151	172	286	230	2223

	centromere positions (cM)						
	1	**2**	**3**	**4**	**5**	**6**	**7**
A	127	142	136	43	-	101	187
B	149	129	-	113	89	127	116
D	75	105	144	38	92	141	188




short
long
1A
1A (number marker)
10
5
0
−5
−10
0
50
100
150
200
250
300
350
genetic distance [cM]


short
long
2A
2A (number marker)
20
15
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5
0
−5
−10
0
50
100
150
200
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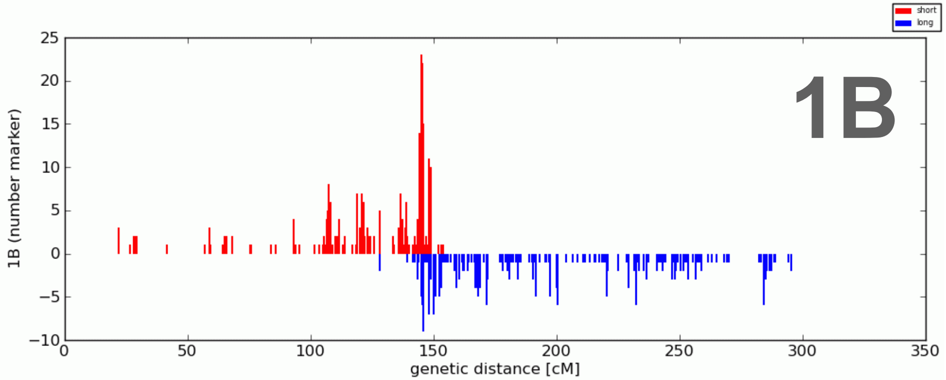
300
350
genetic distance [cM]


short
long
1B
1B (number marker)
25
20
15
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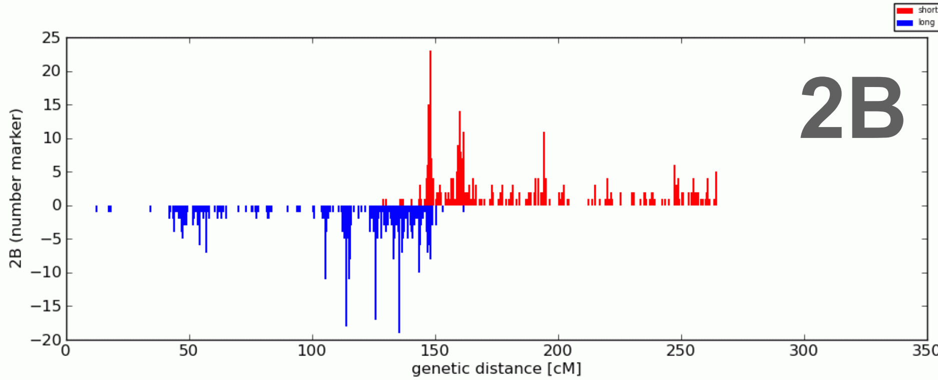
5
0
−5
−10
0
50
100
150
200
250
300
350
genetic distance [cM]


short
long
2B
2B (number marker)
25
20
15
10
5
0
−5
−10
−15
−20
0
50
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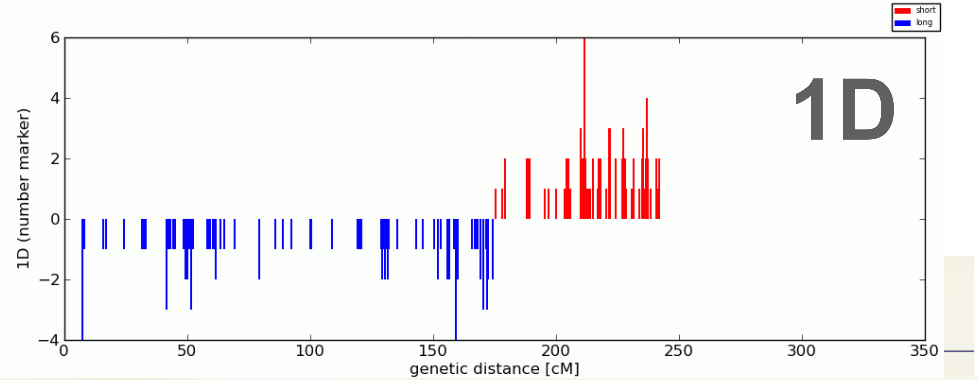
250
300
350
genetic distance [cM]


short
long
1D
1D (number marker)
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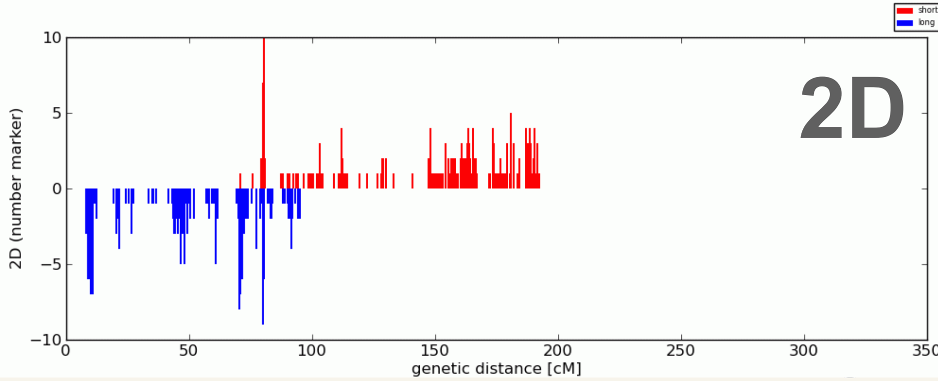
genetic distance [cM]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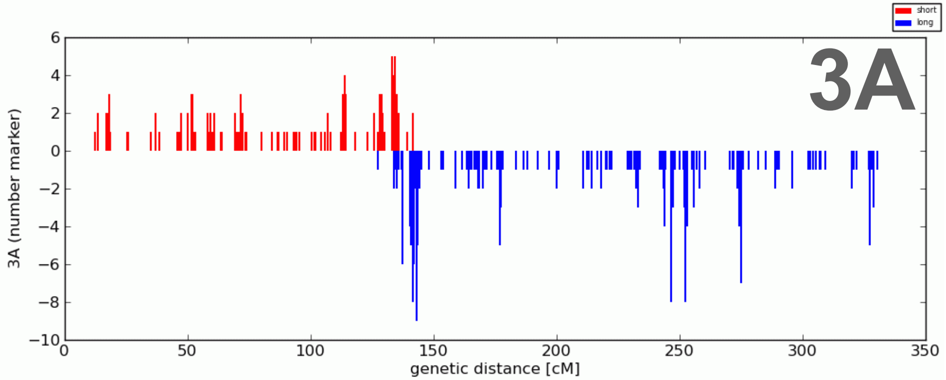
0
−5
−10
0
50
100
150
200
250
300
350
genetic distance [cM]


3A
short
long
3A (number marker)
6
4
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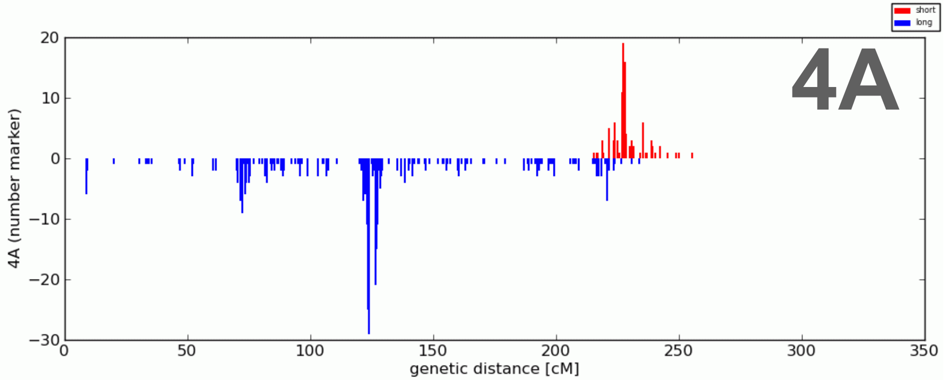
0
−2
−4
−6
−8
−10
0
50
100
150
200
250
300
350
genetic distance [cM]


4A
short
long
4A (number marker)
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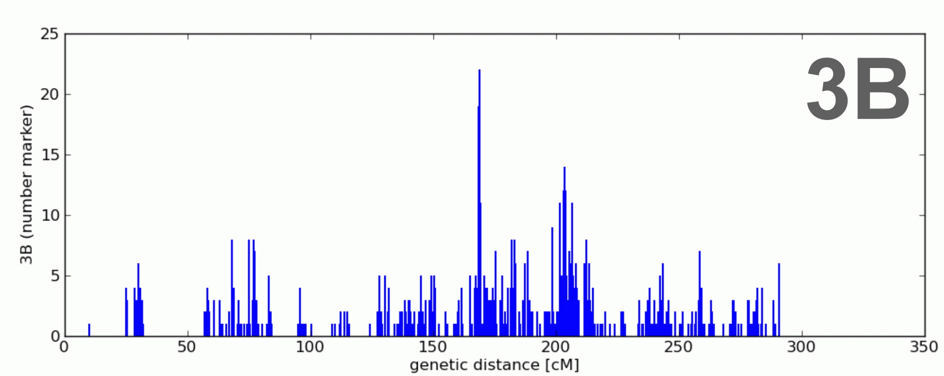
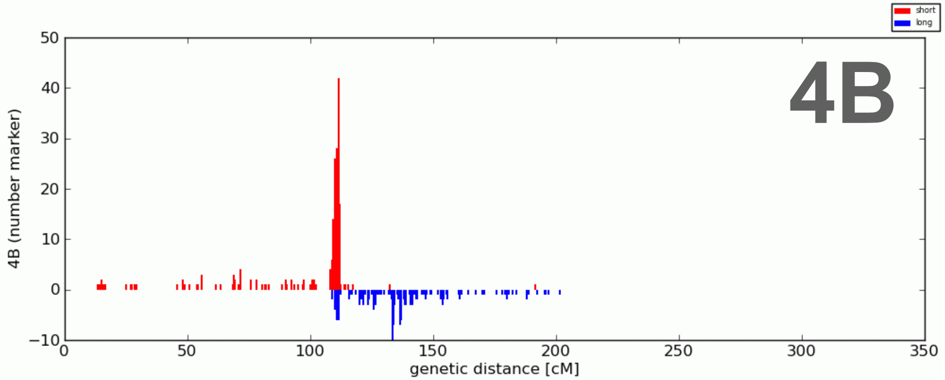
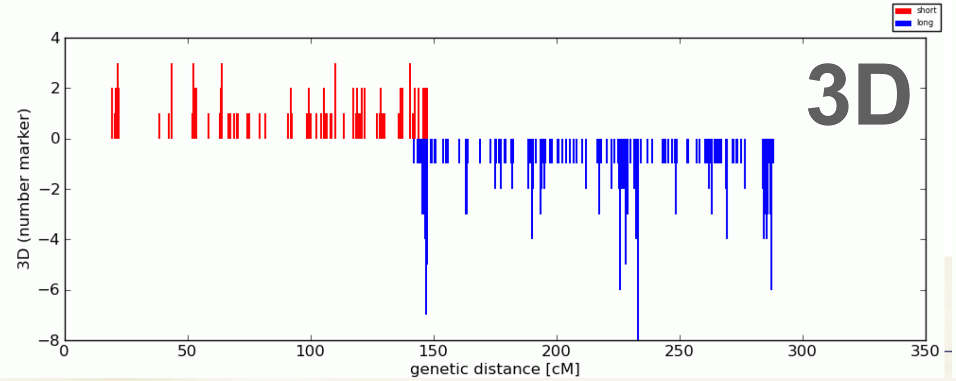
10
0
−10
−20
−30
0
50
100
150
200
250
300
350
genetic distance [cM]


3B
3B (number marker)
25
20
15
10
5
0
0
50
100
150
200
250
300
350
genetic distance [cM]


4B
short
long
4B (number marker)
50
40
30
20
10
0
−10
0
50
100
150
200
250
300
350
genetic distance [cM]


3D
short
long
3D (number marker)
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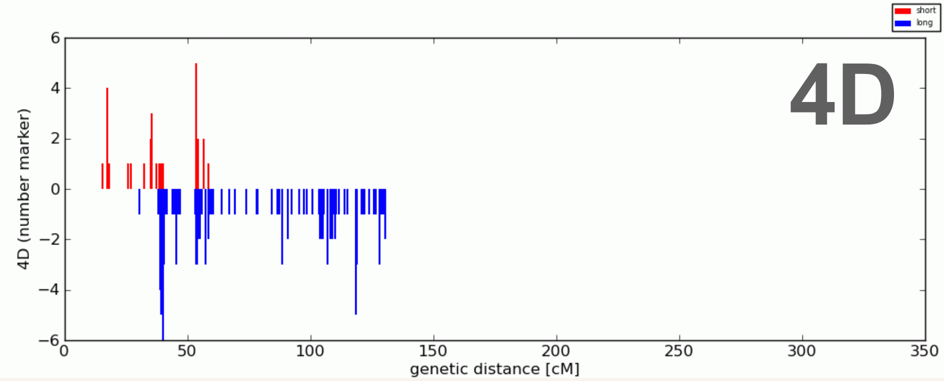
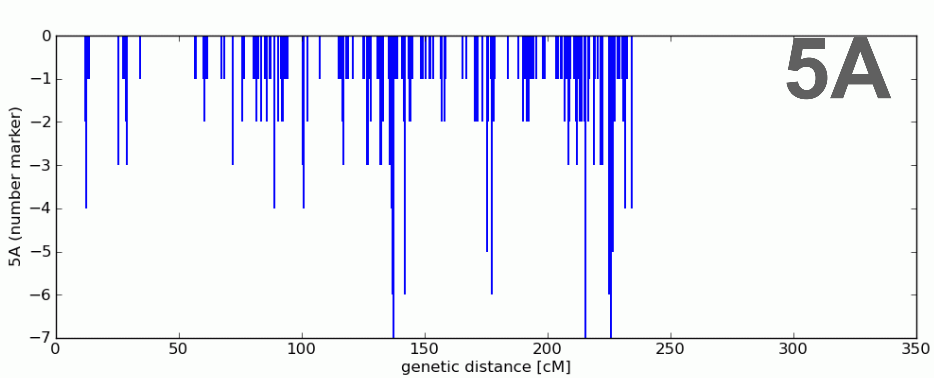
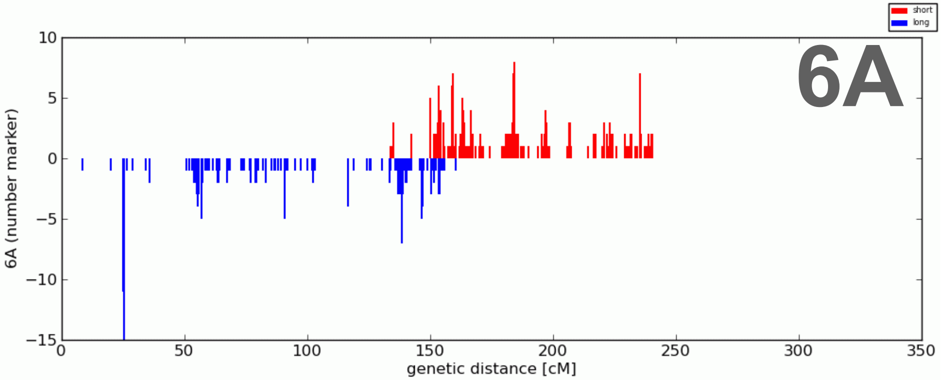
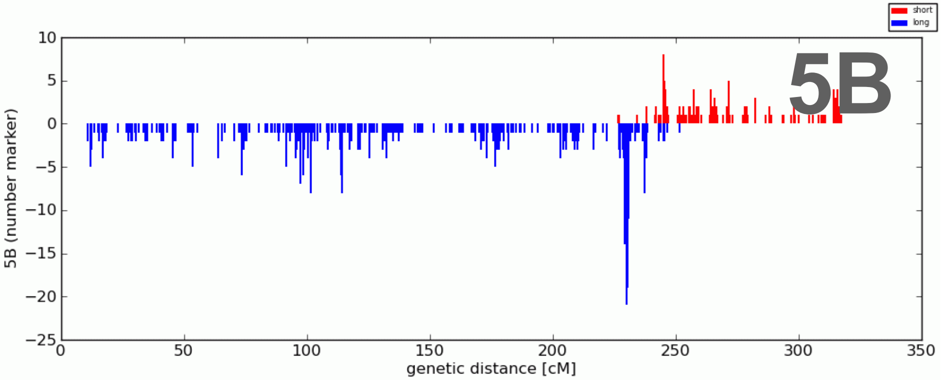
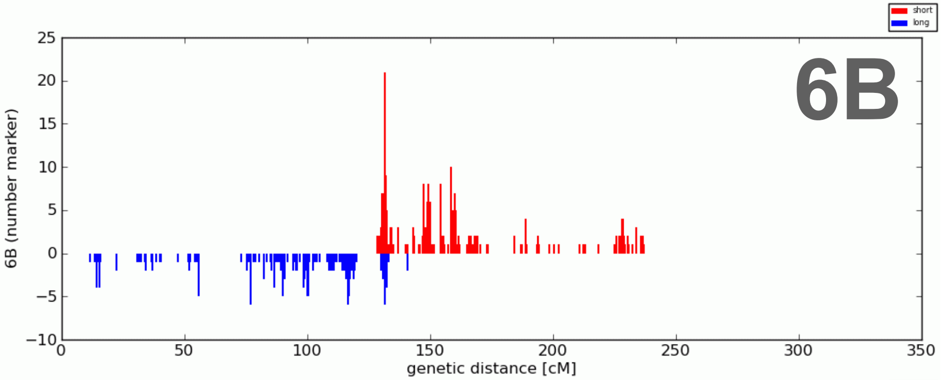
2
0
−2
−4
−6
−8
0
50
100
150
200
250
300
350
genetic distance [cM]

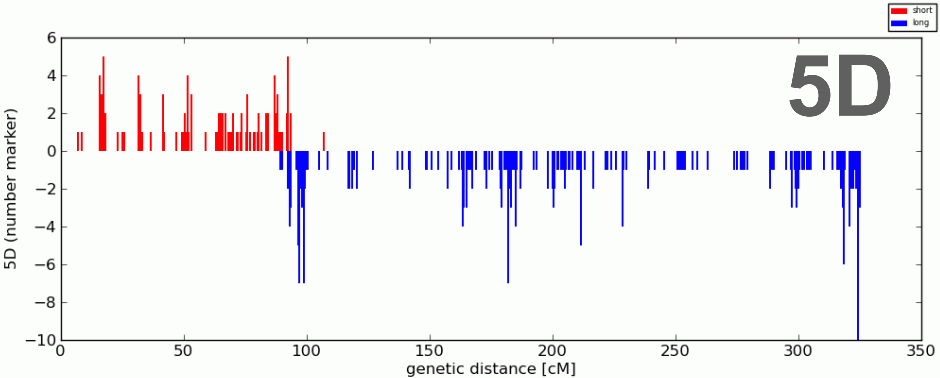

4D
short
long
4D (number marker)
6
4
2
0
−2
−4
−6
0
50
100
150
200
250
300
350
genetic distance [cM]

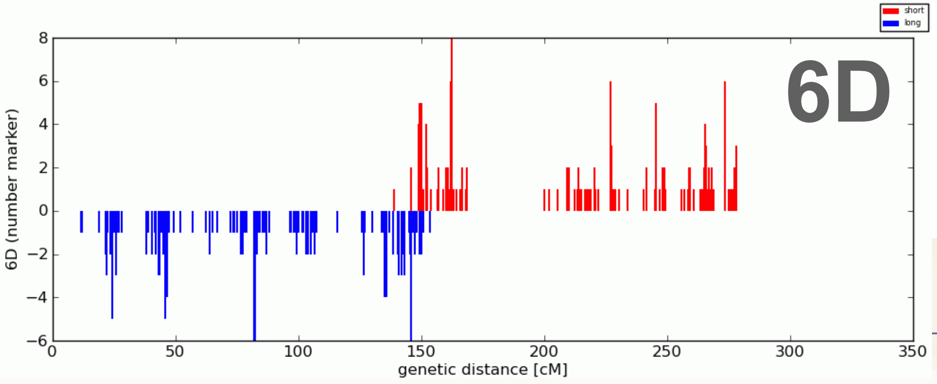

5A
5A (number marker)
0
−1
−2
−3
−4
−5
−6
−7
0
50
100
150
200
250
300
350
genetic distance [cM]

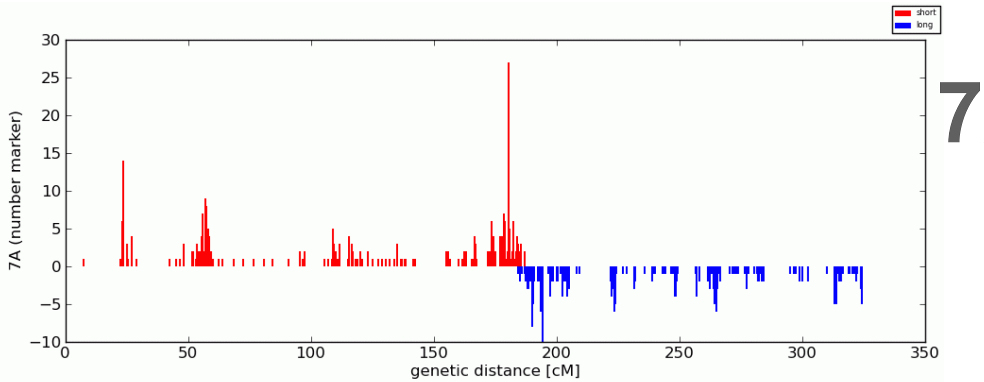

6A
short
long
6A (number marker)
10
5
0
−5
−10
−15
0
50
100
150
200
250
300
350
genetic distance [cM]


5B
short
long
5B (number marker)
10
5
0
−5
−10
−15
−20
−25
0
50
100
150
200
250
300
350
genetic distance [cM]

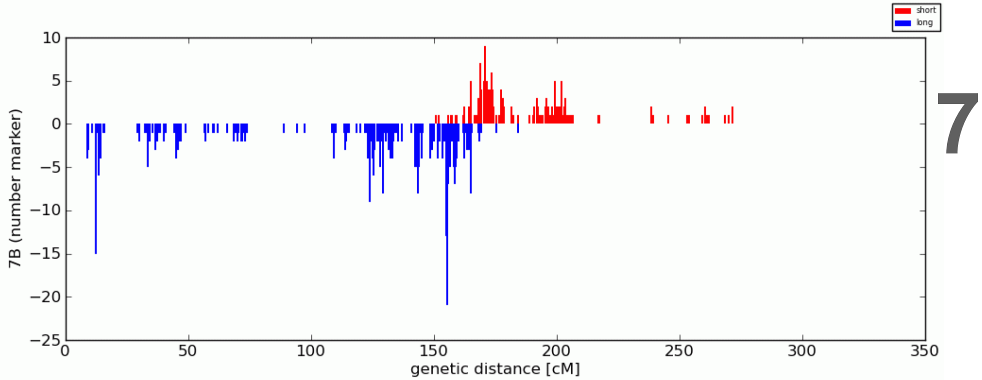

6B
short
long
6B (number marker)
25
20
15
10
5
0
−5
−10
0
50
100
150
200
250
300
350
genetic distance [cM]


5D
short
long
5D (number marker)
6
4
2
0
−2
−4
−6
−8
−10
0
50
100
150
200
250
300
350
genetic distance [cM]

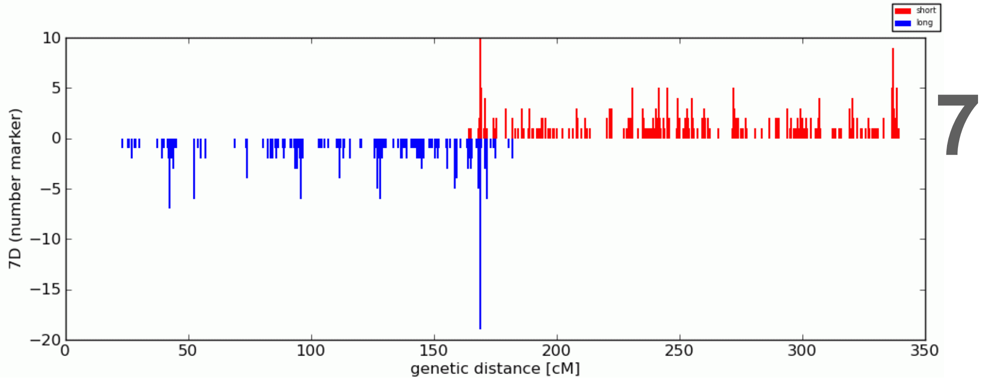

6D
short
long
6D (number marker)
8
6
4
2
0
−2
−4
−6
0
50
100
150
200
250
300
350
genetic distance [cM]


short
long
30
25
20
15
10
5
0
−5
−10
7A (number marker)
0
50
100
150
200
250
300
350
genetic distance [cM]

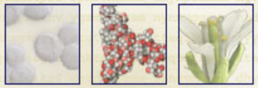
7A


short
long
10
5
0
−5
−10
−15
−20
−25
7B (number marker)
0
50
100
150
200
250
300
350
genetic distance [cM]

7B


short
long
10
5
0
−5
−10
−15
−20
7D (number marker)
0
50
100
150
200
250
300
350
genetic distance [cM]

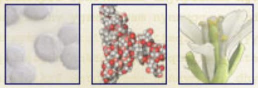
7D



Eduard Akhunov’s GBS collection

- 241,180 marker = 25,153 SNP + 216,027 PA
  - SNP = SNP polymorphism between the parent of SynOp populations
  - PA = presence/absence variation

	# GBS tags (EA) per chromosome (unfiltered) = 241,180							
	1	**2**	**3**	**4**	**5**	**6**	**7**	**Σ**
A	9,385	10,549	10,051	12,294	12,971	10,234	13,899	79,383
B	14,992	17,933	18,610	8,636	13,903	12,702	16,964	103,740
D	6,785	13,763	9,805	4,071	6,978	7,704	8,951	58,057

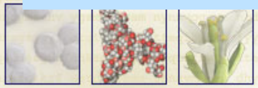


wheat chromosome arms: group A

	raw data				repeat masked data		
chr/ chr arm	**size (Mbp)**	**sequences (Mbp)**	**coverage (x-fold)**	**L50**	**% repeat content**	**# contigs**	**L50**
1AS	275	178.1	0.65	2,242	77.03	34,792	4,769
1AL	523	250.0	0.48	2,639	77.11	26,745	6,369
2AS	391	255.2	0.65	2,398	78.83	34,721	6,678
2AL	508	328.2	0.65	2,688	76.25	45,892	6,677
3AS	360	201.8	0.56	1,404	80.49	33,942	3,846
3AL	468	247.2	0.53	1,346	78.42	43,822	3,789
4AS	317	282.3	0.89	2,782	82.42	32,078	7,499
4AL	539	362.0	0.67	3,053	70.94	64,363	6,601
5AS	295	198.8	0.67	3,509	86.4	19,718	8,713
5AL	532	318.1	0.60	2,078	78.94	47,571	5,355
6AS	336	219.2	0.65	2,669	77.87	28,040	7,091
6AL	369	214.4	0.58	2,154	77.25	34,029	6,589
7AS	407	198.0	0.49	1,470	71.88	44,174	4,397
7AL	407	252.4	0.62	2,271	75.61	35,585	5,849
	5,727	**3,505.7**	**0.62**		77.82	500,236	

wheat chromosome arms: group B

		raw data			repeat masked data		
chr/ chr arm	**size (Mbp)**	**sequences (Mbp)**	**coverage (x-fold)**	**L50**	**% repeat content**	**# contigs**	**L50**
1BS	314	212.8	0.68	3,287	77.55	26,049	7,413
1BL	535	299.4	0.56	3,120	75.89	29,782	7,151
2BS	422	292	0.69	3,711	75.93	35,742	8,069
2BL	506	404.5	0.80	2,941	74.01	75,878	6,890
3B	993	638.6	0.64	2,655	77.69	75,021	6,855
4BS	319	308.2	0.97	3,463	80.43	38,514	8,755
4BL	430	248.7	0.58	1,974	77.01	46,575	5,883
5BS	290	174.5	0.60	3,315	80.74	18,000	7,365
5BL	580	415.2	0.72	2,924	73.31	75,886	7,537
6BS	415	210.2	0.51	2,366	77.17	29,565	4,972
6BL	498	257.4	0.52	2,031	79.62	35,726	4,824
7BS	360	206.1	0.57	2,428	80.53	24,118	6,435
7BL	540	259.6	0.48	1,556	73.03	58,553	4,144
	6,202	3,927	**0.63**		77.15	569,409	



wheat chromosome arms: group D

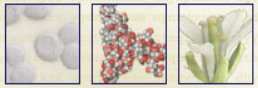
		raw data			repeat masked data		
chr/ chr arm	**Size (Mbp)**	**sequences (Mbp)**	**coverage (x-fold)**	**L50**	**% repeat content**	**# contigs**	**L50**
1DS	224	128.2	0.57	2,850	73.34	17,724	6,622
1DL	381	254.4	0.67	2,561	78.14	35,769	6,297
2DS	316	166	0.53	1,241	70.96	43,043	4,635
2DL	411	261.6	0.64	701	69.42	110,445	3,247
3DS	321	145.4	0.45	515	77.46	46,794	1,697
3DL	449	186.5	0.42	967	67.91	69,258	2,941
4DS	231	142,1	0.62	3,278	76.43	18,244	7,428
4DL	416	347.6	0.84	1,013	52.84	197,397	1,855
5DS	258	148.1	0.57	2,353	76.76	22,448	5,945
5DL	490	236.8	0.48	2,647	68.92	34,621	7,049
6DS	324	156.6	0.48	4,297	77.42	16,076	8,904
6DL	389	199.8	0.51	2,077	77.11	26,235	6,821
7DS	381	209.1	0.55	1,967	71.75	36,700	5,031
7DL	346	222.9	0.64	3,638	70.2	26,736	7,399
	4,937	**2,805.1**	**0.57**		72.05	701,490	

Sensitivity

chr/ chr arm	observed marker detection rate (sensitivity)
1AS	79,10
1AL	80,34
2AS	81,14
2AL	89,04
3AS	83,08
3AL	88,18
4AS	73,47
4AL	83,11
5AS	-
5AL	85,16
6AS	80,86
6AL	85,99
7AS	88,70
7AL	83,12

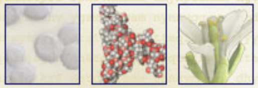
chr/ chr arm	Observed marker detection rate (sensitivity)
1BS	73,31
1BL	81,40
2BS	74,52
2BL	71,39
3B	79,77
4BS	64,63
4BL	81,12
5BS	82,20
5BL	80,04
6BS	76,40
6BL	78,48
7BS	83,66
7BL	83,89

chr/ chr arm	Observed marker detection rate (sensitivity)
1DS	76,47
1DL	86,60
2DS	87,04
2DL	85,35
3DS	89,01
3DL	89,86
4DS	68,75
4DL	78,63
5DS	80,61
5DL	85,27
6DS	81,82
6DL	83,03
7DS	89,23
7DL	76,09

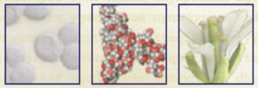


Gene counts...

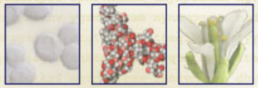
Genes detected with:	**non redundant genes**		
	Brachypodium	rice	sorghum
1AS	3,372	3,489	3,543
1AL	2,031	2,087	2,081
2AS	4,096	4,268	4,349
2AL	2,934	3,054	3,098
3AS	3,309	3,437	3,489
3AL	2,229	2,357	2,362
4AS	4,308	4,494	4,591
4AL	2,414	2,520	2,487
5AS	3,963	4,093	4,122
5AL	1,558	1,620	1,584
6AS	2,783	2,965	2,938
6AL	2,425	2,490	2,504
7AS	2,929	3,052	3,062
7AL	3,032	3,117	3,195



Genes detected with:	**non redundant genes**		
	Brachypodium	rice	sorghum
1BS	3,303	3,494	3,557
1BL	2,092	2,218	2,211
2BS	4,503	4,693	4,796
2BL	3,185	3,359	3,430
3B_cov88x	6,127	6,323	6,456
4BS	3,182	3,278	3,434
4BL	2,914	3,094	3,096
5BS	5,837	6,074	6,222
5BL	1,677	1,745	1,755
6BS	2,681	2,764	2,813
6BL	2,297	2,359	2,350
7BS	3,256	3,324	3,389
7BL	2,105	2,175	2,240



Genes detected with:	non redundant genes		
	Brachypodium	rice	sorghum
1DS	3,290	3,364	3,451
1DL	1,695	1,782	1,772
2DS	5,098	5,214	5,349
2DL	2,847	2,992	3,042
3DS	3,676	3,749	3,870
3DL	2,022	2,104	2,054
4DS	4,882	5,464	5,569
4DL	2,164	2,362	2,302
5DS	4,353	4,508	4,604
5DL	1,608	1,659	1,632
6DS	2,862	2,980	3,023
7DL	1,832	1,962	1,923
7DS	2,989	3,189	3,173
7DL	3,072	3,243	3,290



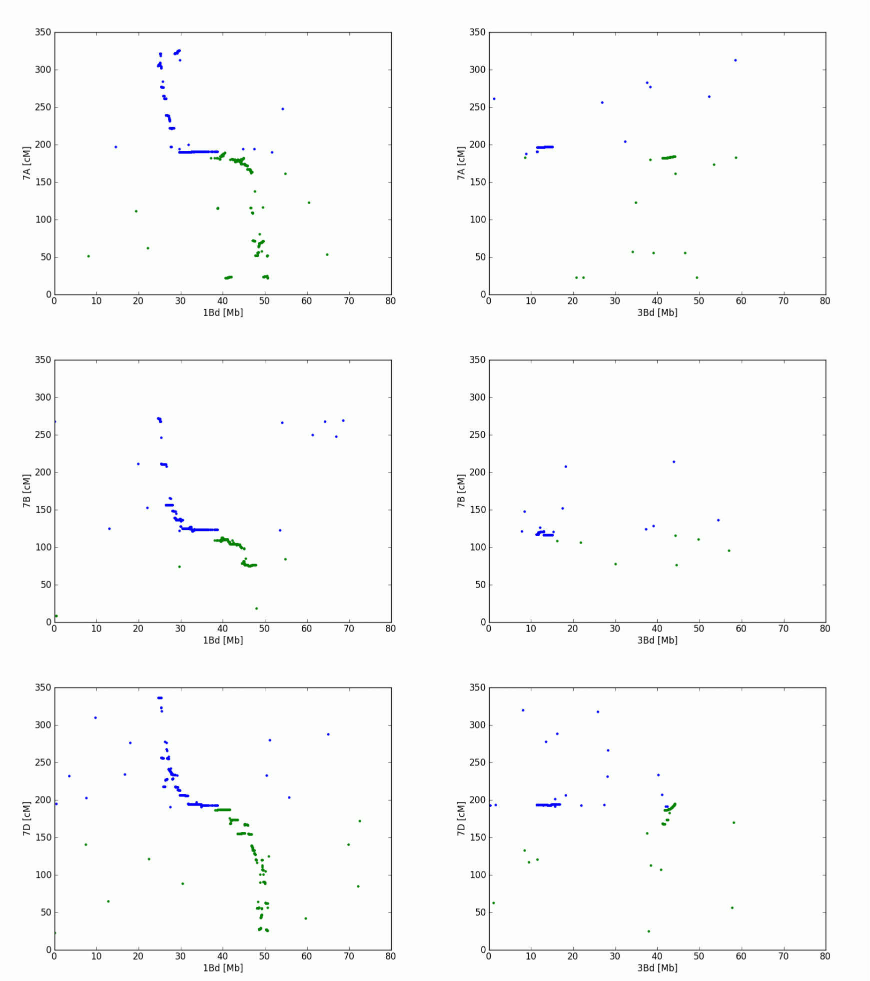
Bd1

Bd3

7A

7B

7D



THE END