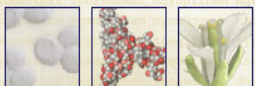
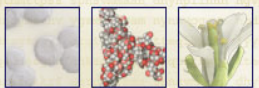
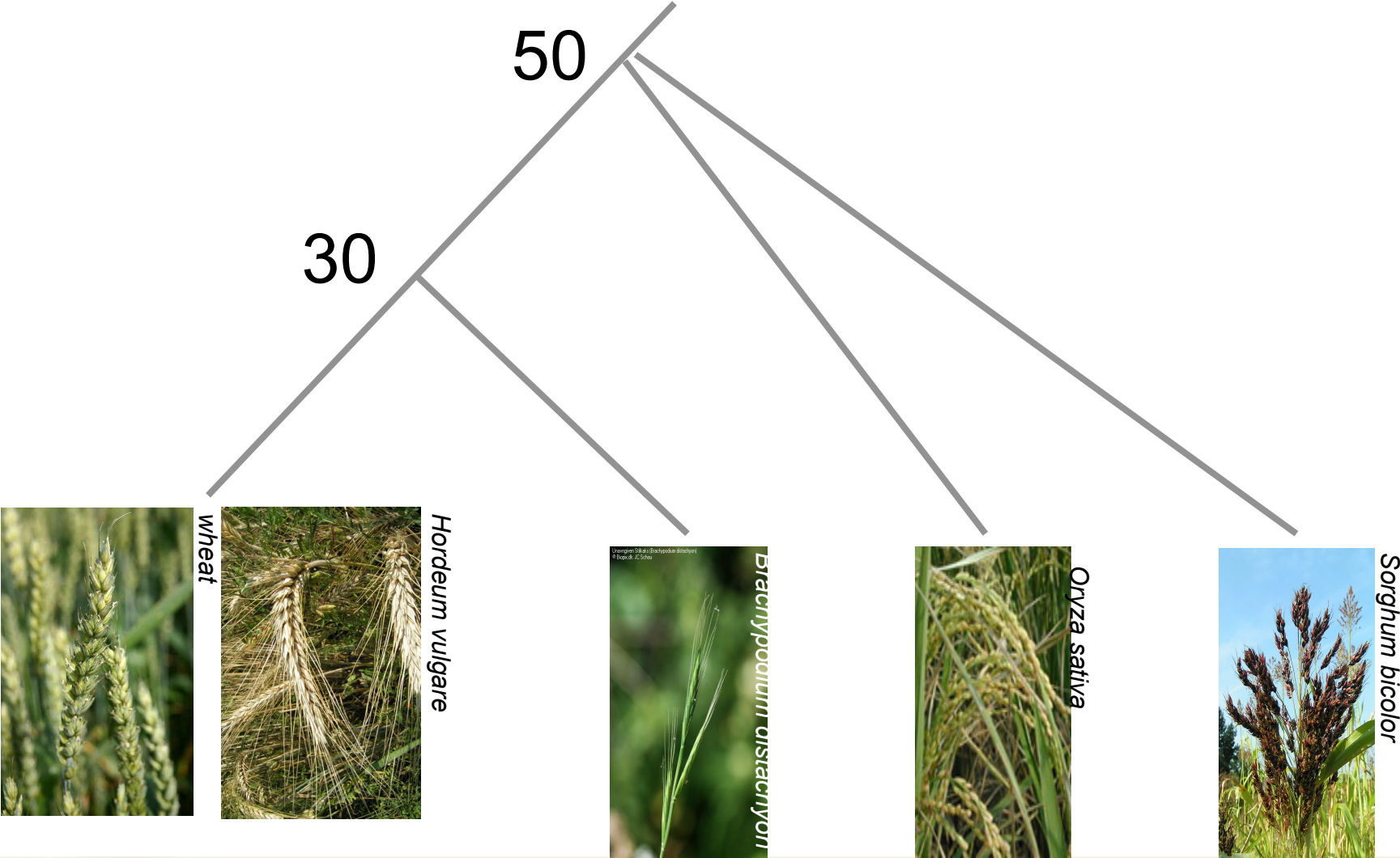


A poor mans approach to unlock cereal genomes

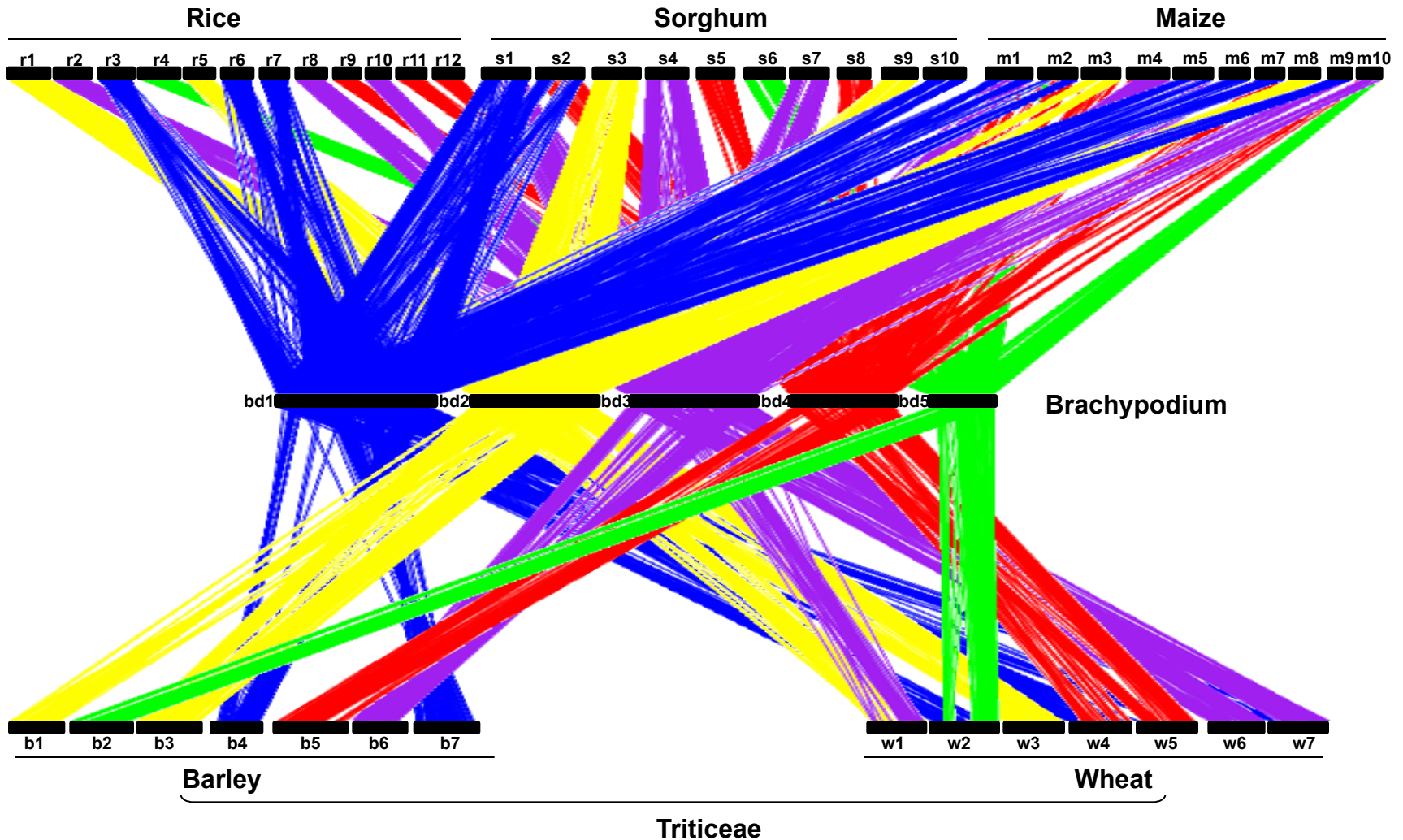
Klaus Mayer
MIPS, Helmholtz Center Munich



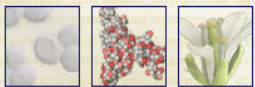
Grass Genomes and Evolutionary Relationships



Brachypodium Genome Synteny



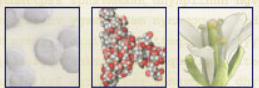
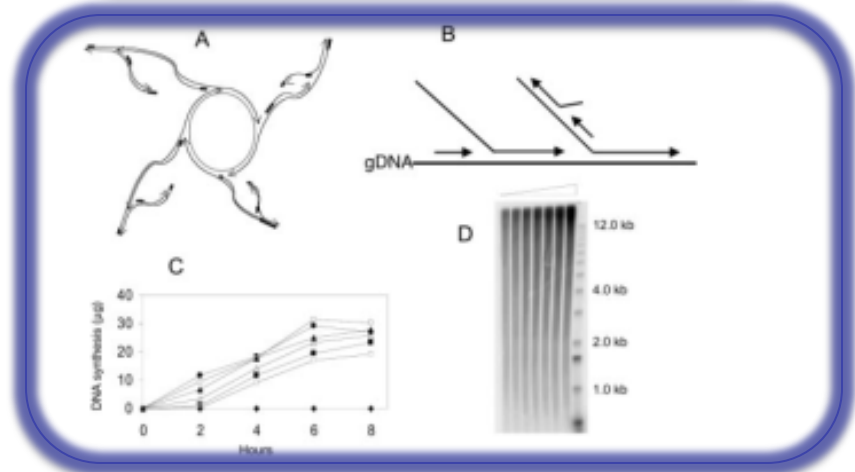
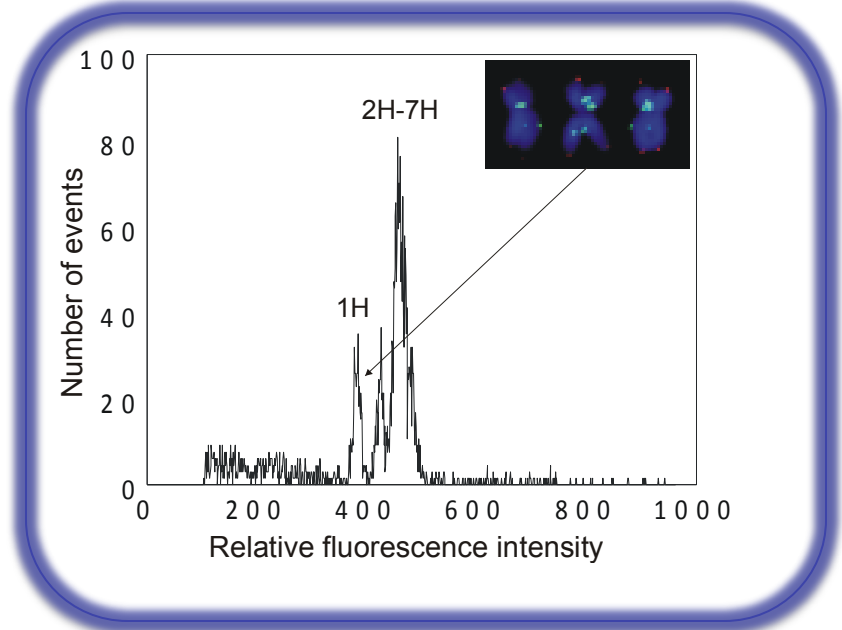
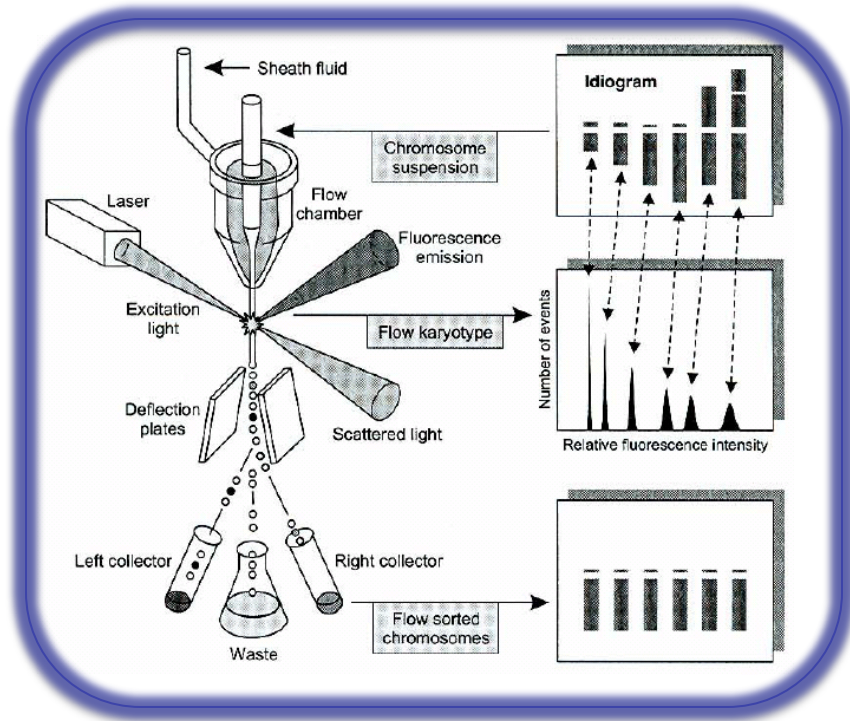
J. Salse



HelmholtzZentrum münchen
German Research Center for Environmental Health

mips
munich information center
for protein sequences

Reduction of complexity via chromosome sorting



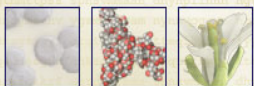
454 sequencing all barley chromosome arms

Chr/ Chr arm	Size (Mbp)	sequences (Mbp)	high quality sequences (Mbp)	high quality sequences (x-fold)
1H (MoBe)	622	1611	1244	2
2HS	362	528	377	1,04
2HL	428	924	670	1,57
3HS	336	657	470	1,40
3HL	419	1155	744	1,78
4HS	336	653	452	1,35
4HL	393	911	605	1,54
5HS	301	760	546	1,81
5HL	459	949	651	1,42
6HS	332	830	570	1,72
6HL	357	981	587	1,64
7HS	382	640	505	1,32
7HL	373	636	468	1,25
	5100	11235	7889	1,55

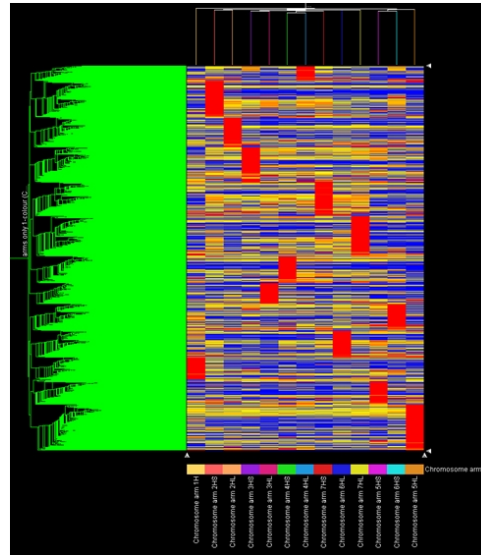


Sensitivity and Specificity

Chr./ Chr.-arm	expected Lander Waterman of high quality sequences	observed marker detection rate (sensitivity) of high quality sequences	specificity
1H (MoBe)	86,46%	98,19	88%
2HS	64,65%	82,35	97,9
2HL	79,20%	86,24	97,1
3HS	75,34%	80,58	98
3HL	83,14%	85,95	96,5
4HS	74,08%	80,55	97,9
4HL	78,56%	83,01	93,6
5HS	83,63%	90,29	97,9
5HL	75,83%	83,03	97,6
6HS	82,09%	86,29	97,8
6HL	80,60%	86,38	97,8
7HS	73,29%	80,97	97
7HL	71,35%	84,89	98

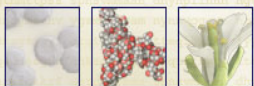


custom microarray vs. sorted chromosome arms



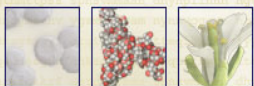
Info on chromosome arm
specific localisation of 17k
barley genes

SCRI
Pete Hedley & Robbie Waugh



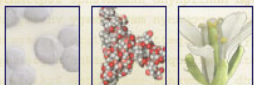
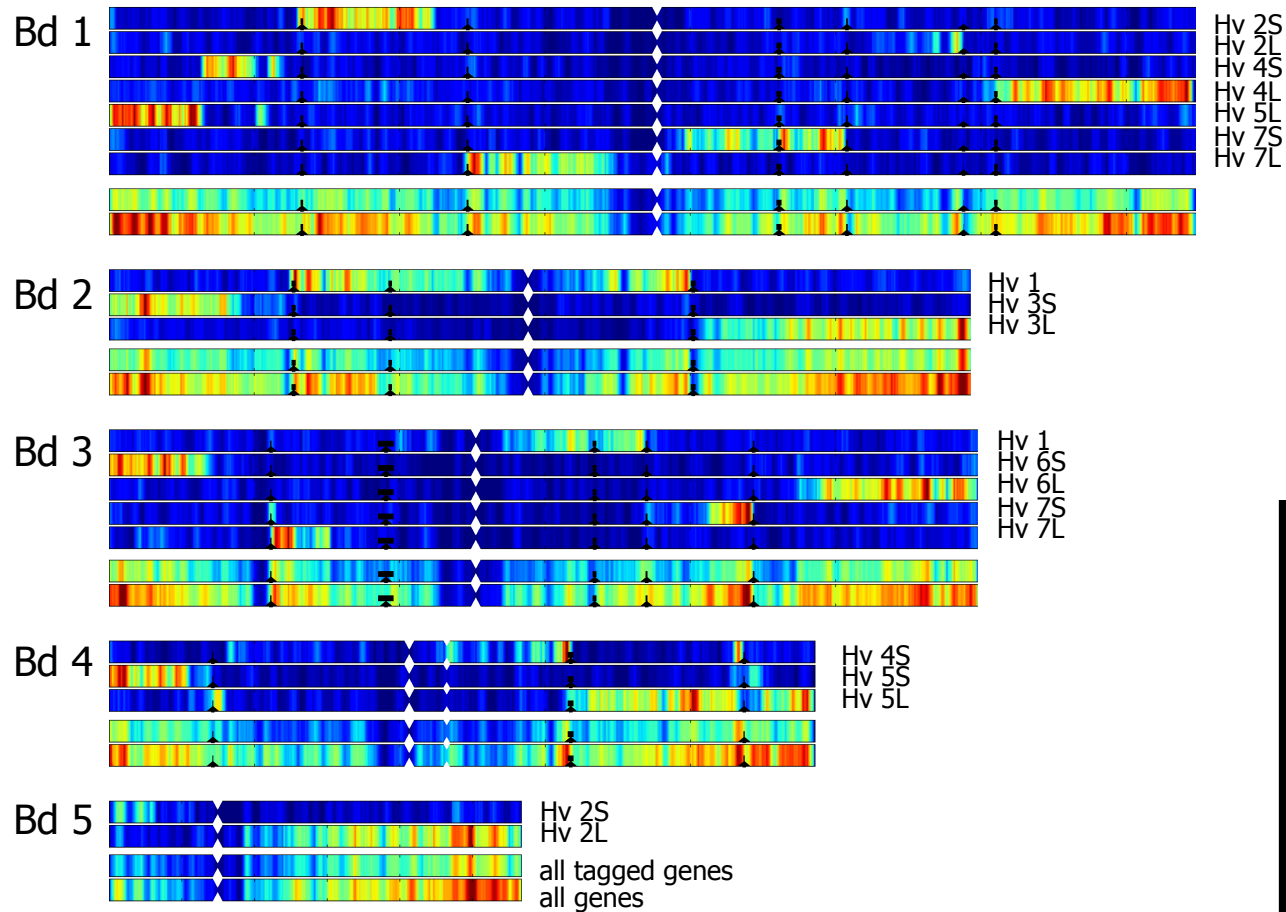
Gene counts...

	non redundant genes			Non- redundant genes (cumulative)
	<i>Brachypodium</i>	Rice	<i>Sorghum</i>	
Genes detected with 2GS data	19,289 (73%)	17,290 (61%)	18,340 (66%)	21,240
Expected hits with complete genome from 2GS data (sensitivity 0,86)	22,429 (85%)	20,104 (71%)	21,325 (77%)	24,698
number of matching non red. fl-cDNA against reference genomes (out of 23,588)	17,622 (75%)	15,340 (65%)	15,419 (65%)	18,204 (77%)
Array probes against reference genomes (out of 16,804)	12,382 (74%)	10,617 (63%)	10,915 (65%)	12,755 (76%)
Array probes not overlapping with 2GS dataset against reference genomes (out of 5196)	3,908 (75%)	3,357 (65%)	3,438 (66%)	4,046 (78%)
Genes detected from 2GS data and array hybridization	23,197	20,647	21,778	25,286
Barley genes detected from 2GS, array hybridization and fl-cDNA data	29,163	28,895	29,947	30,670



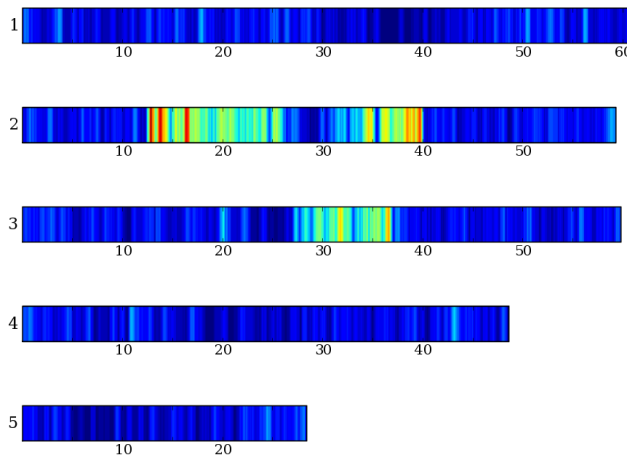
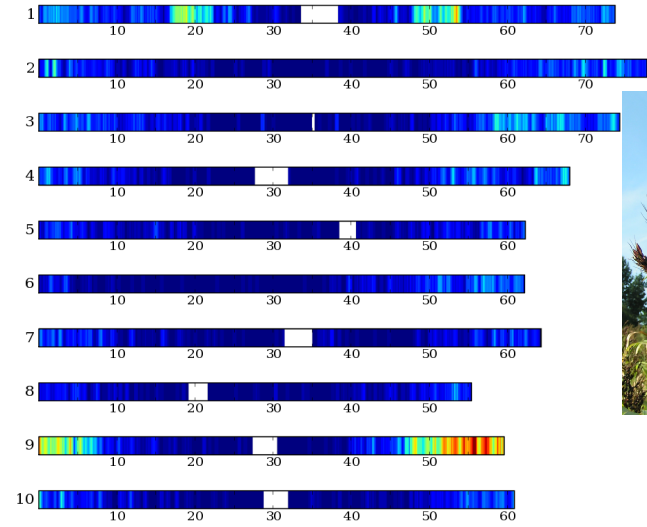
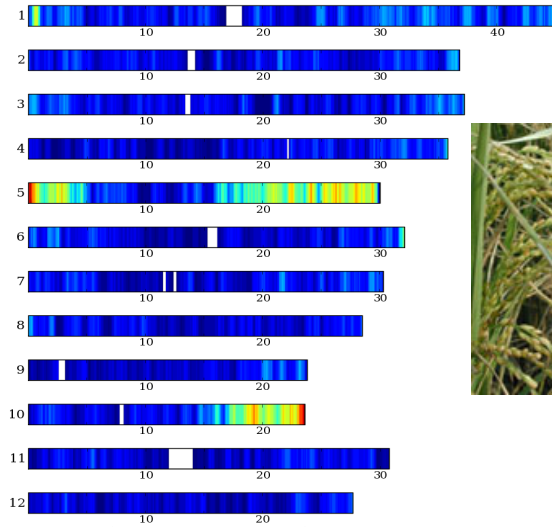
Brachypodium genes tagged by barley read

-Synteny on a per gene resolution-

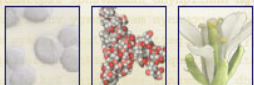


Barley 1H vs Rice/Sorghum and Brachypodium

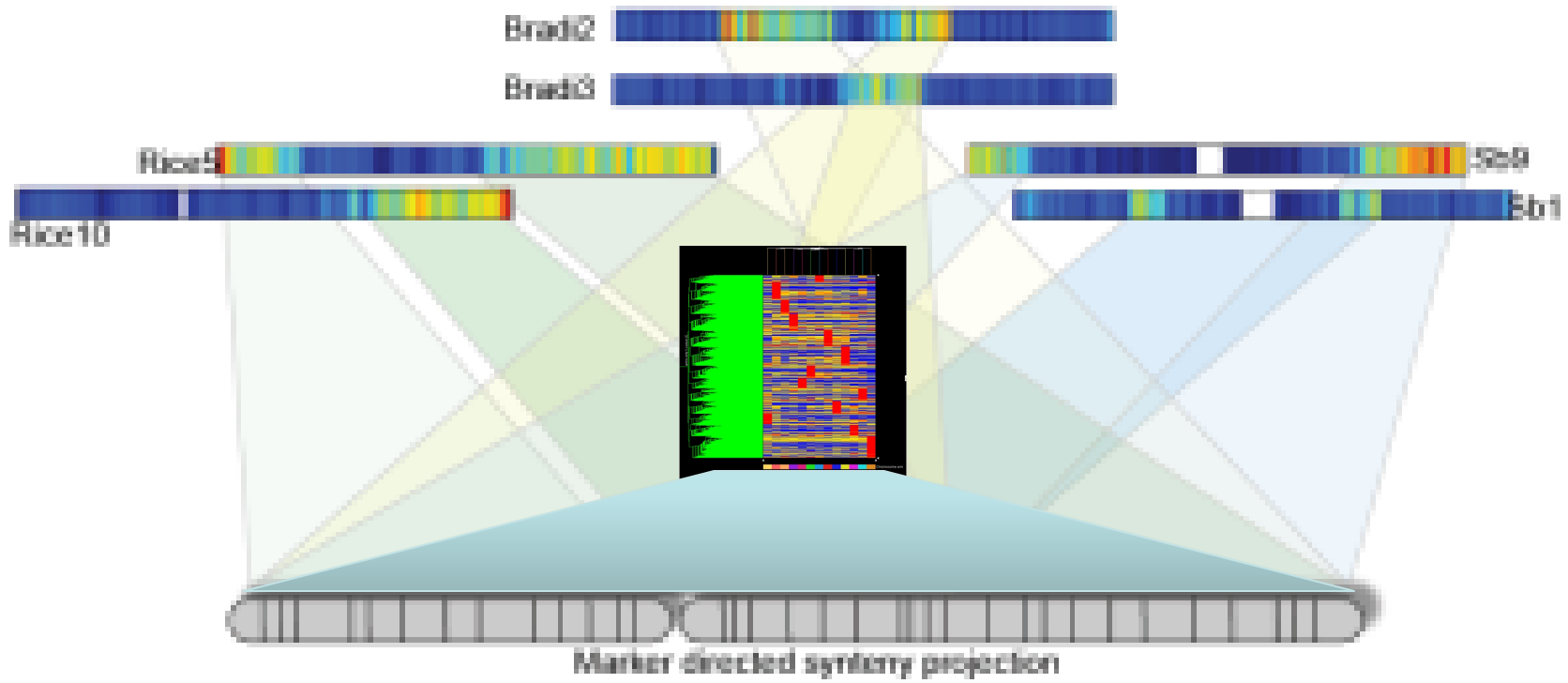
- Synteny on a per gene resolution -



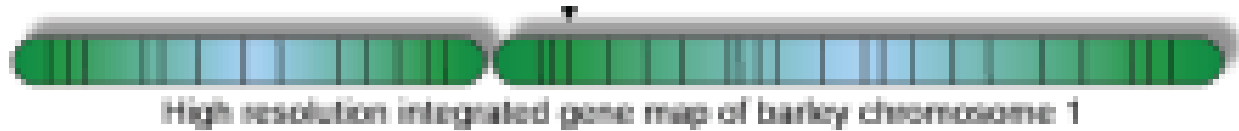
[Mb] (window size 0.5 Mb, shift 0.1 Mb)



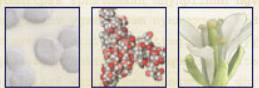
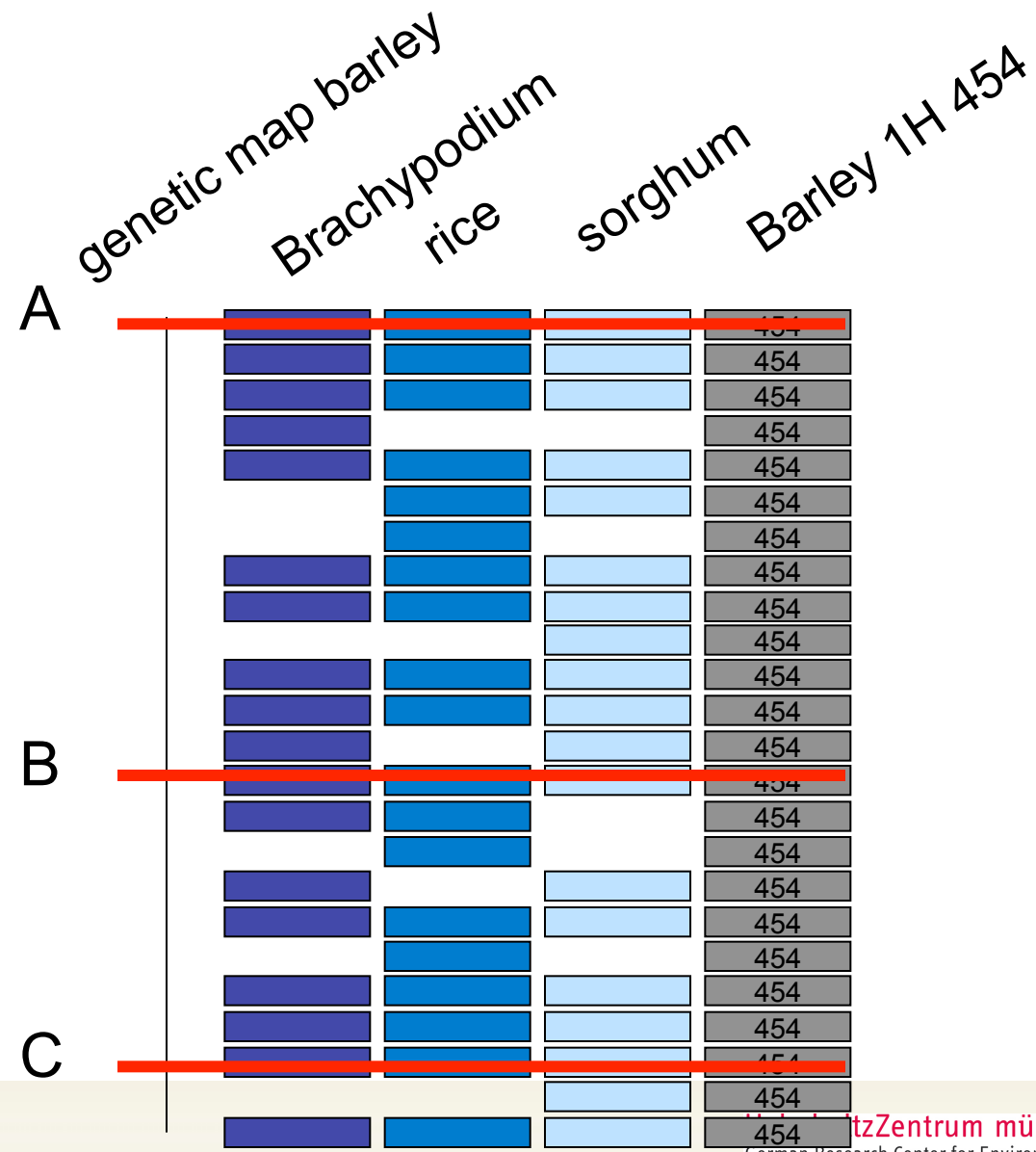
Syntenic integration – „genome zipper“



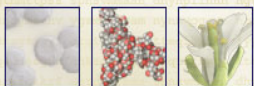
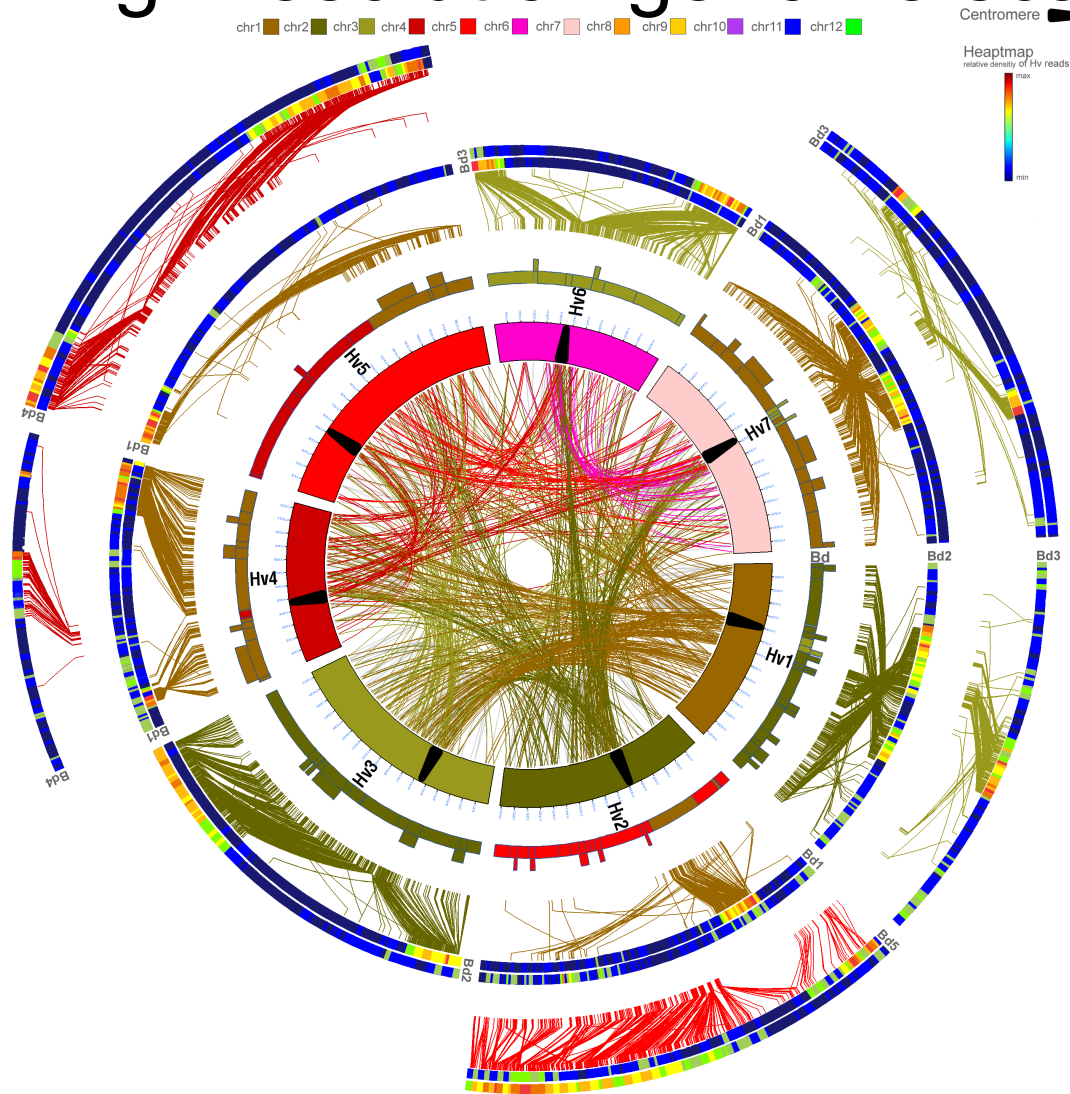
Associate syntenic genes and accessory information



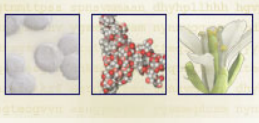
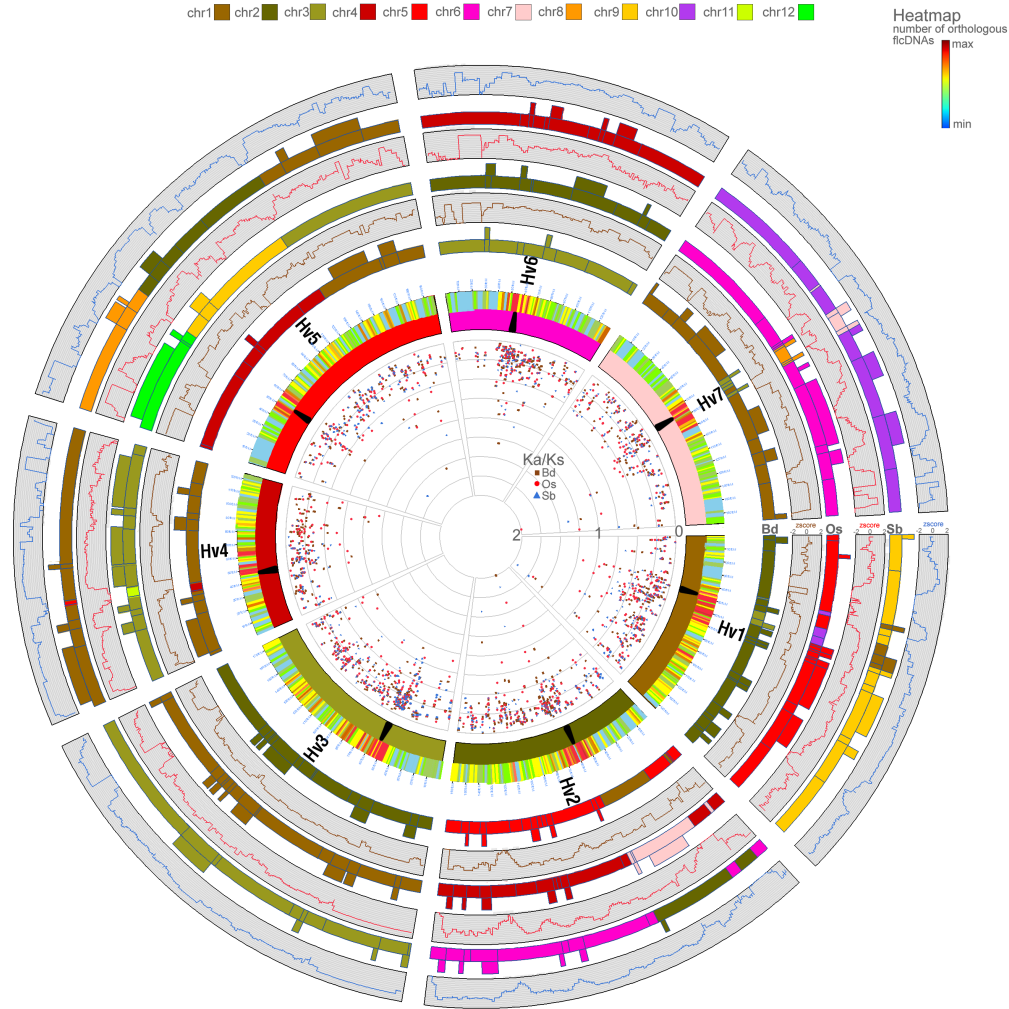
Syntenic integration – „genome zipper“



A high resolution genome scaffold



A high resolution genome scaffold



Barley Genome Zipper summary

- **22k barley genes** sequence tagged **positionally ordered and** in part associated with flcDNA & EST
- **Additional 6k genes with chromosome arm assignment**
- Resolution of appr. 0,05 (0,1) cM; 20 loci (9,3 fl-cDNAs) per cM
- >3000 (14%) genes are located in low/non-recombining regions
- All but 9 ordered and assigned to short and long arm respectively

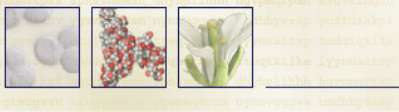
Shortcomings:

- Can't resolve small local rearrangements
- Can't position genes that are out of syntenic context
- Pseudogenes, tandem duplicates, ...

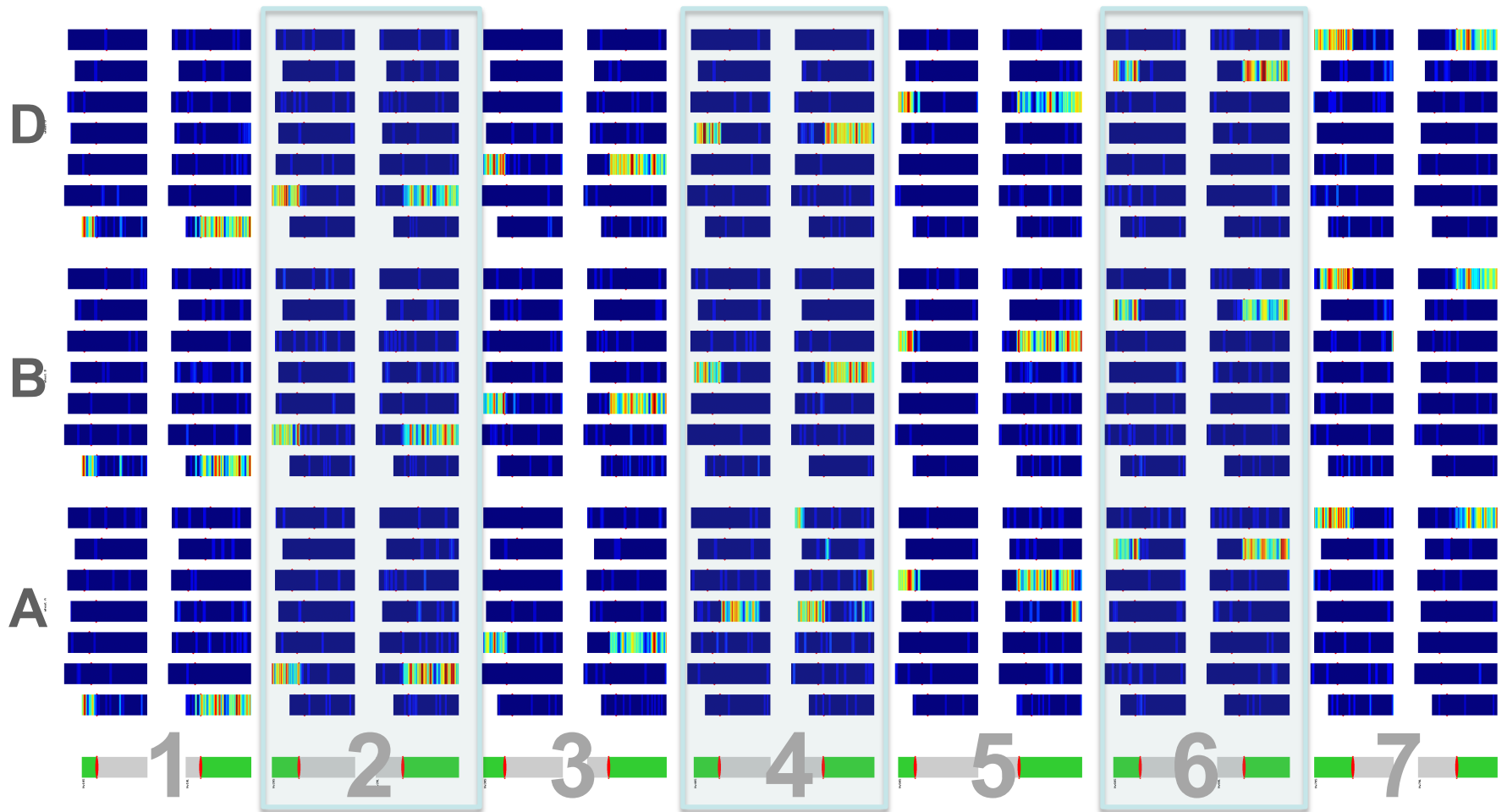


Case study chromosome 2HL (Nils & Naser @ IPK)

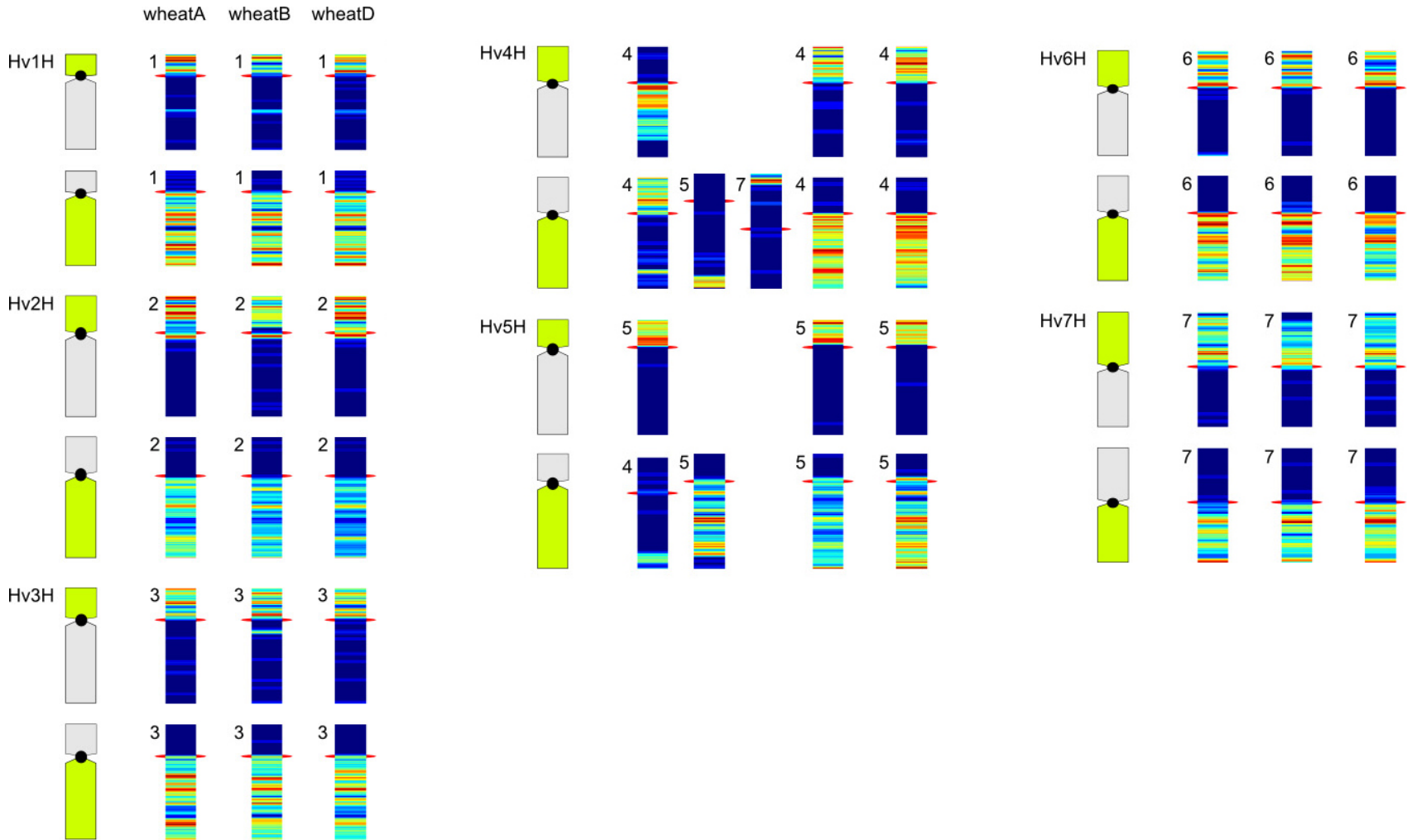
- 162 primers designed based on 454 read info
- 136 (83%) work under uniform PCR setup
- 96 assigned to 2HL (mapping and ditelo addition lines)
- 1 assigned to 2HS
- ~90 % of the genetically mapped markers follow the proposed model



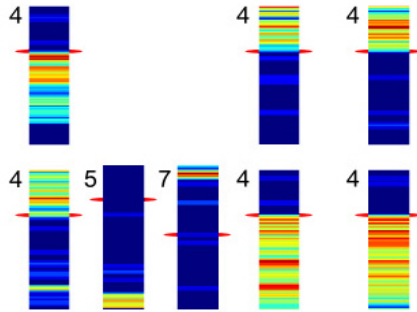
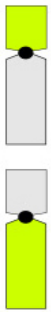
Artificial barley chromosomes form a stepping stone for other Triticeae



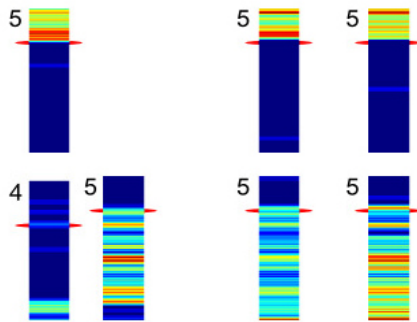
Wheat EST bin map vs artificial barley chromosomes



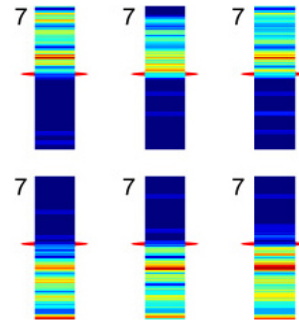
Hv4H



Hv5H



Hv7H



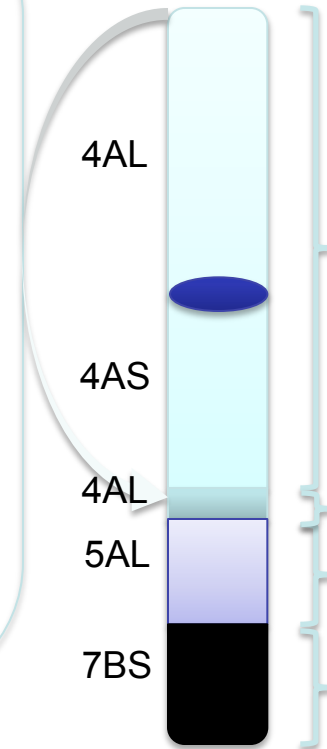
4AL

4AS

4AL

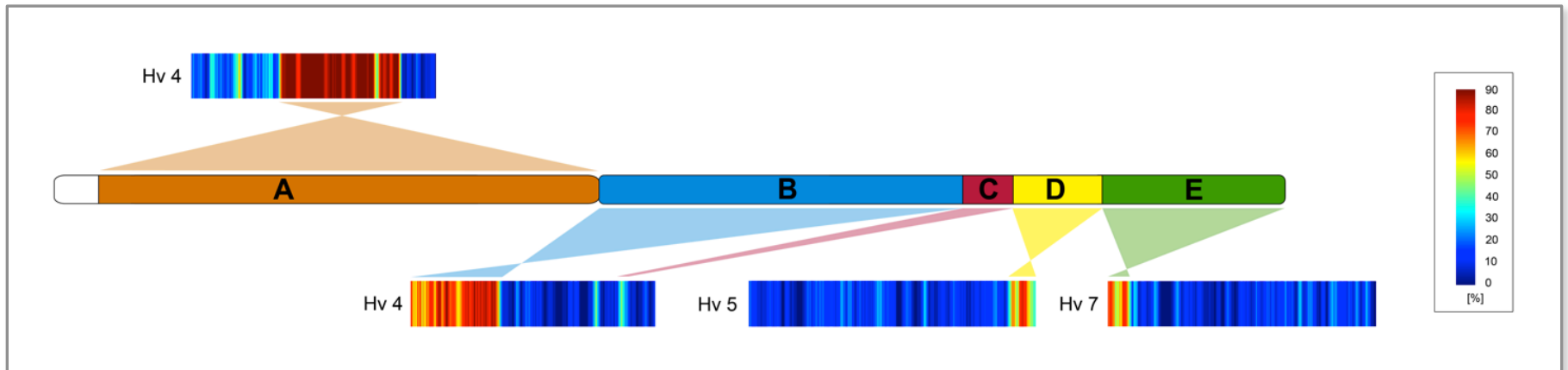
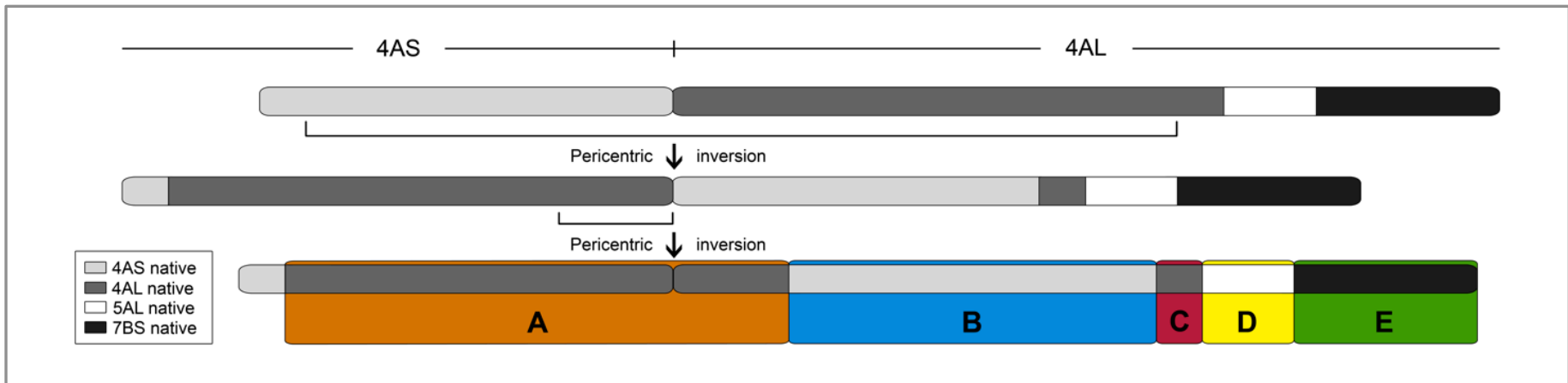
5AL

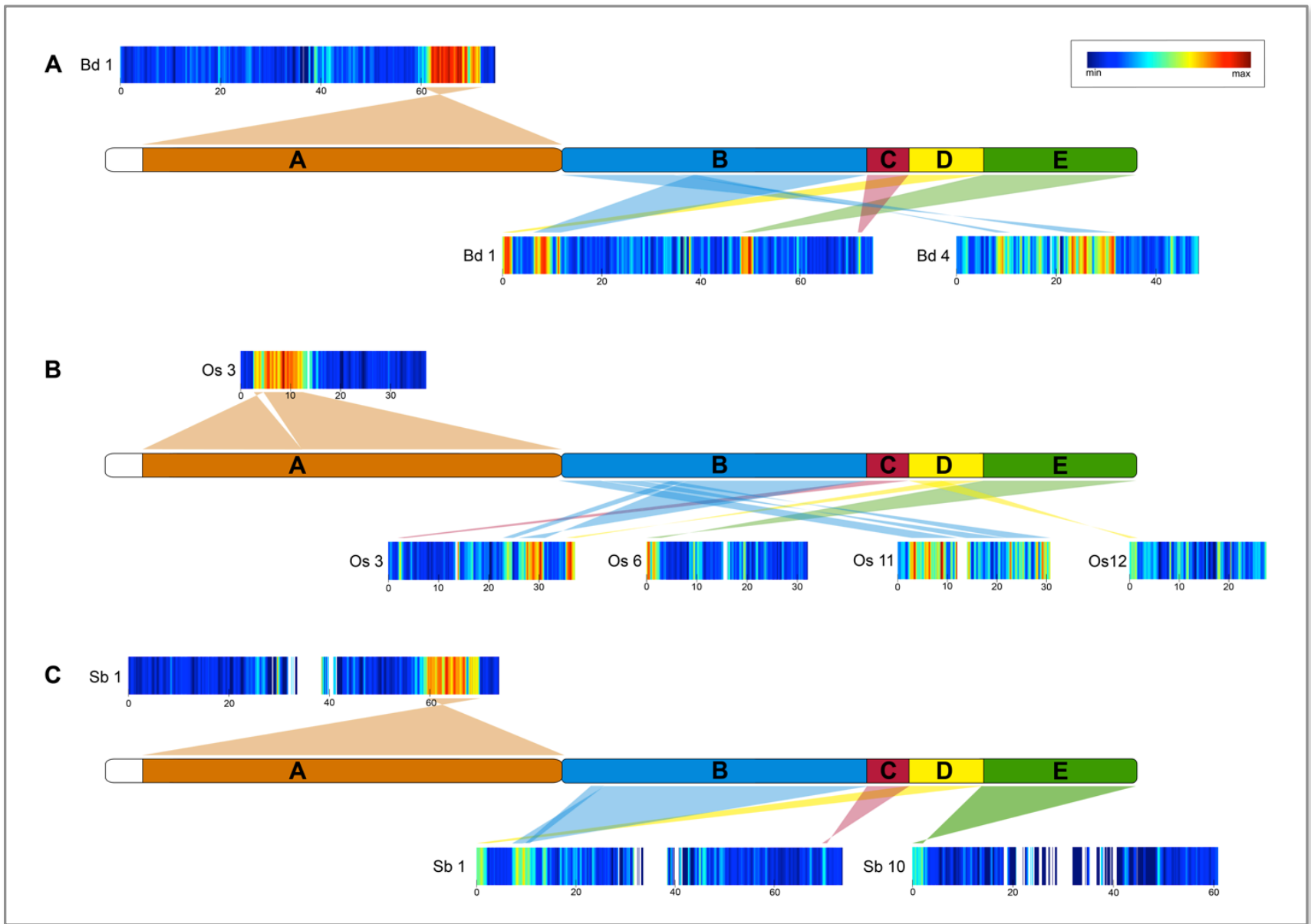
7BS



4A

(done by Jaroslav and Pilar)





Breakpoints

Block	Brachypodium	Oryza sativa	Sorghum
A	Bradi1g72080.1	Os03g0187500	Sb01g044730.1
	Bradi1g72086.1	Os03g0187400	Sb01g044740.1
	Bradi1g72092.1	Os03g0187300	Sb01g044750.1

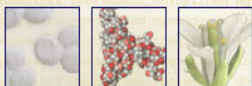
	Bradi1g65190.1	Os03g0296700	Sb01g038210.1
	Bradi1g65197.1	Os03g0296600	Sb01g038220.1
	Bradi1g65210.1	Os03g0296400	Sb01g038230.1
B	Bradi4g26690.1	Os11g0150450	Sb01g013770.1
	Bradi4g26670.3	Os11g0151600	Sb01g013780.1
	Bradi4g26640.1	Os11g0152700	Sb01g013830.1

	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

	Bradi1g75960.1	Os03g0147900	Sb01g047070.1
	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



acknowledgements

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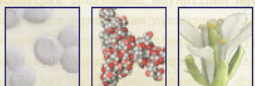
SCRI

Pete Hedley
Hui Liu
Robbie Waugh

NIAS/Okayama

Takashi Matsumoto
Tsuyoshi Tanaka
Takeshi Itoh

Kaz Sato et al.



A black and white photograph of a field with the text "THE END" overlaid in large white letters. The background shows a field of tall grass in the foreground, a line of trees in the middle ground, and a cloudy sky above. The text is centered horizontally and spans across the middle of the image.

THE END