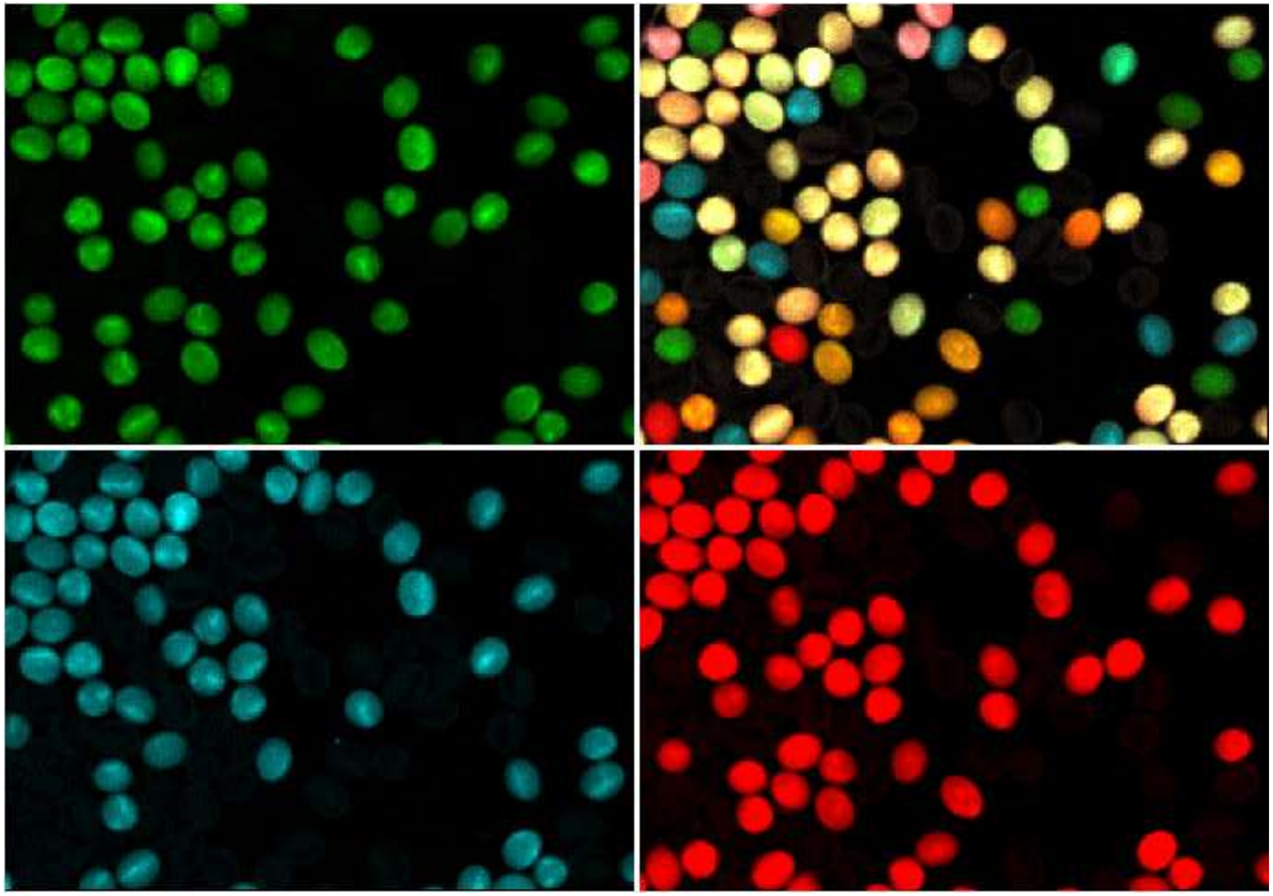
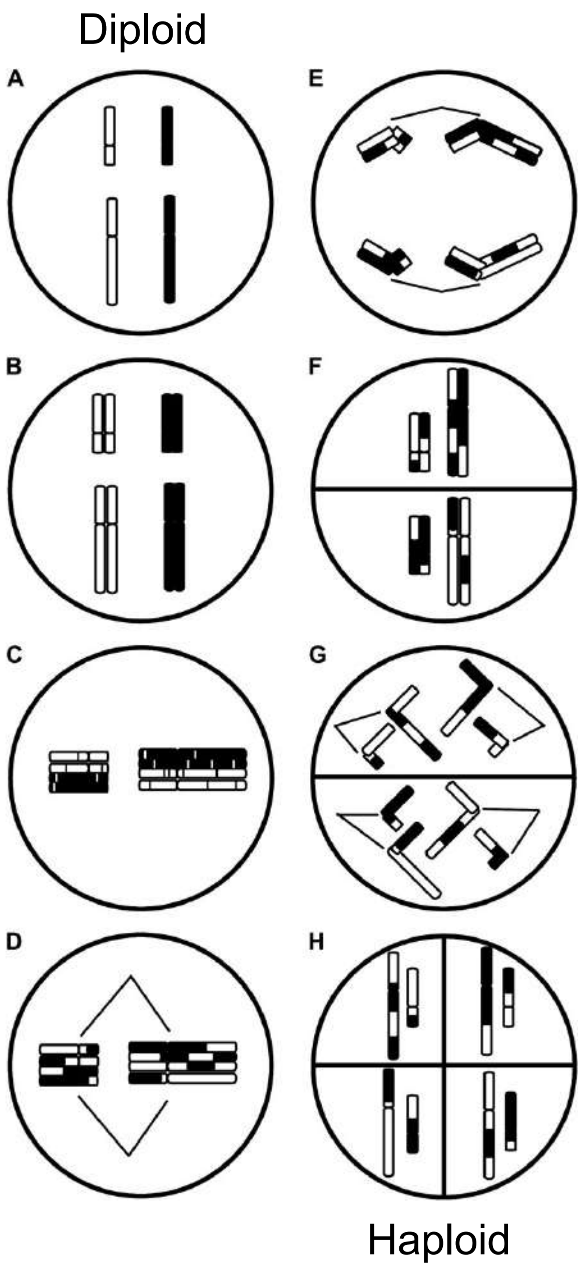
Recombination and chromatin landscapes in the wheat genome

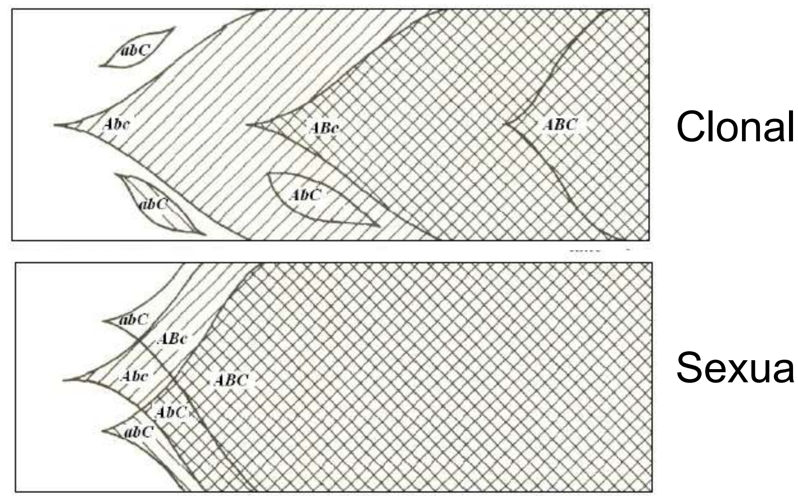


Ian Henderson, University of Cambridge

IWGSC webinar, Jan 2022

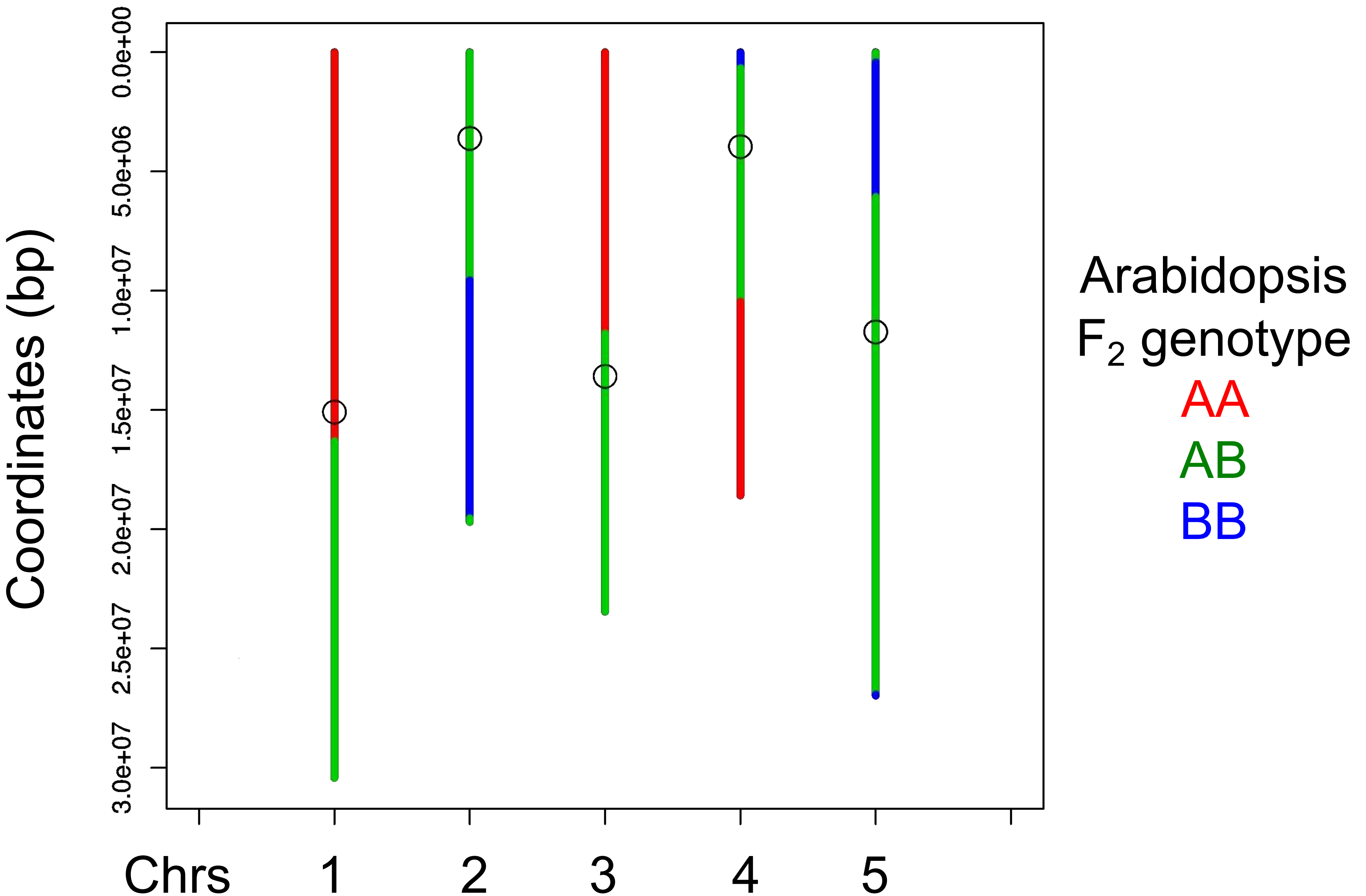
Meiosis, recombination and evolution





Fisher (1930) *The Genetical Theory of Natural Selection*
Muller (1932) *American Naturalist*

Meiosis generates genetic diversity



Trends in
Plant Science

CellPress
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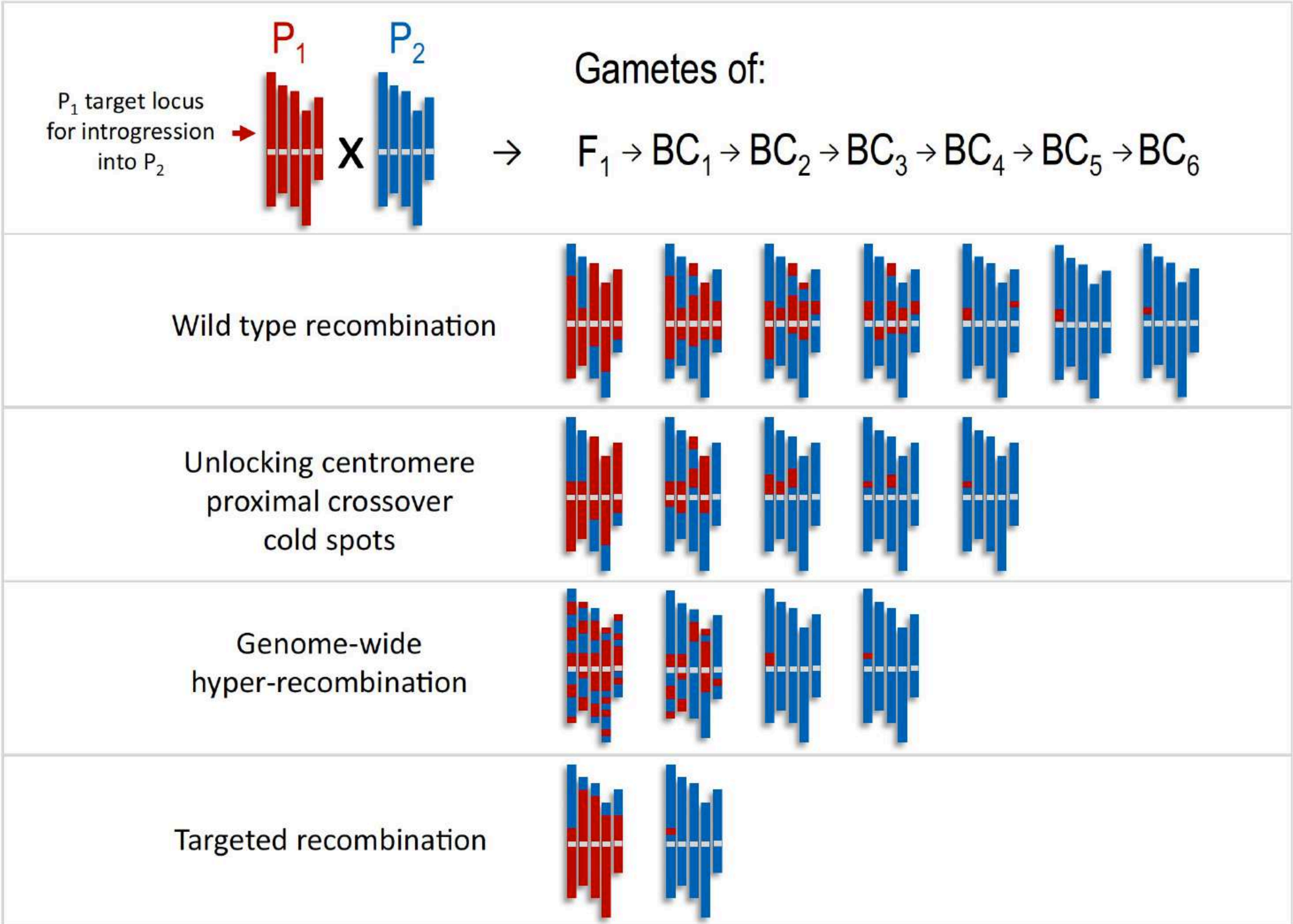
Special Issue: Feeding the World: The Future of Plant Breeding

Feature Review

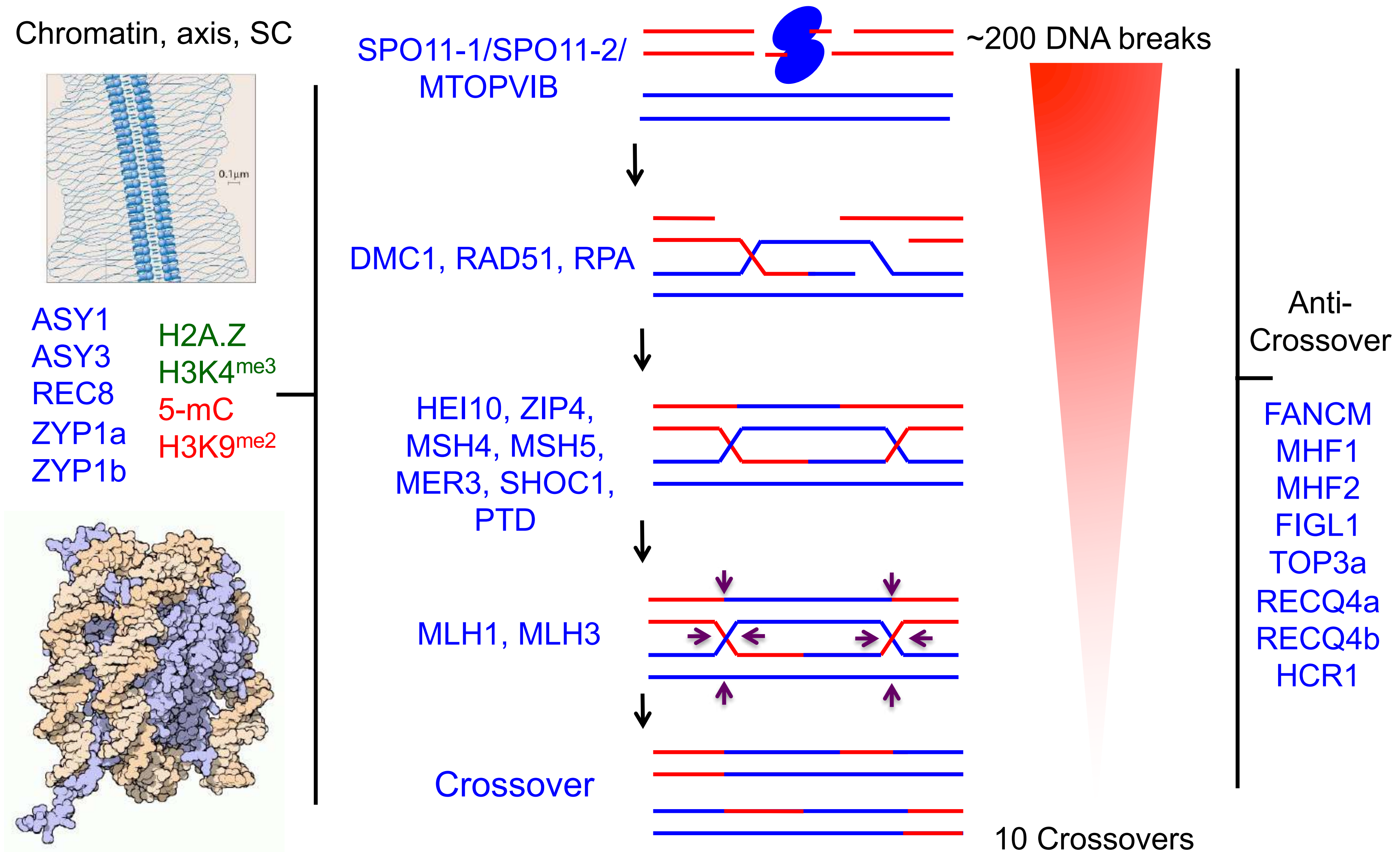
Addressing Research Bottlenecks to Crop Productivity

Matthew Reynolds[1,*] Owen K. Atkin[2,*,@] Malcolm Bennett[3,*] Mark Cooper[4] Ian C. Dodd,[5] M. John Foulkes,[3] Claus Frohberg,[6] Graeme Hammer[4] Ian R. Henderson,[7] Bingru Huang,[8,*] Viktor Korzun[9] Susan R. McCouch[10,*] Carlos D. Messina[11,*] Barry J. Pogson[2,@] Gustavo A. Slafer[12,13,*] Nicolas L. Taylor[14,@] and Peter E. Wittich[15,*]

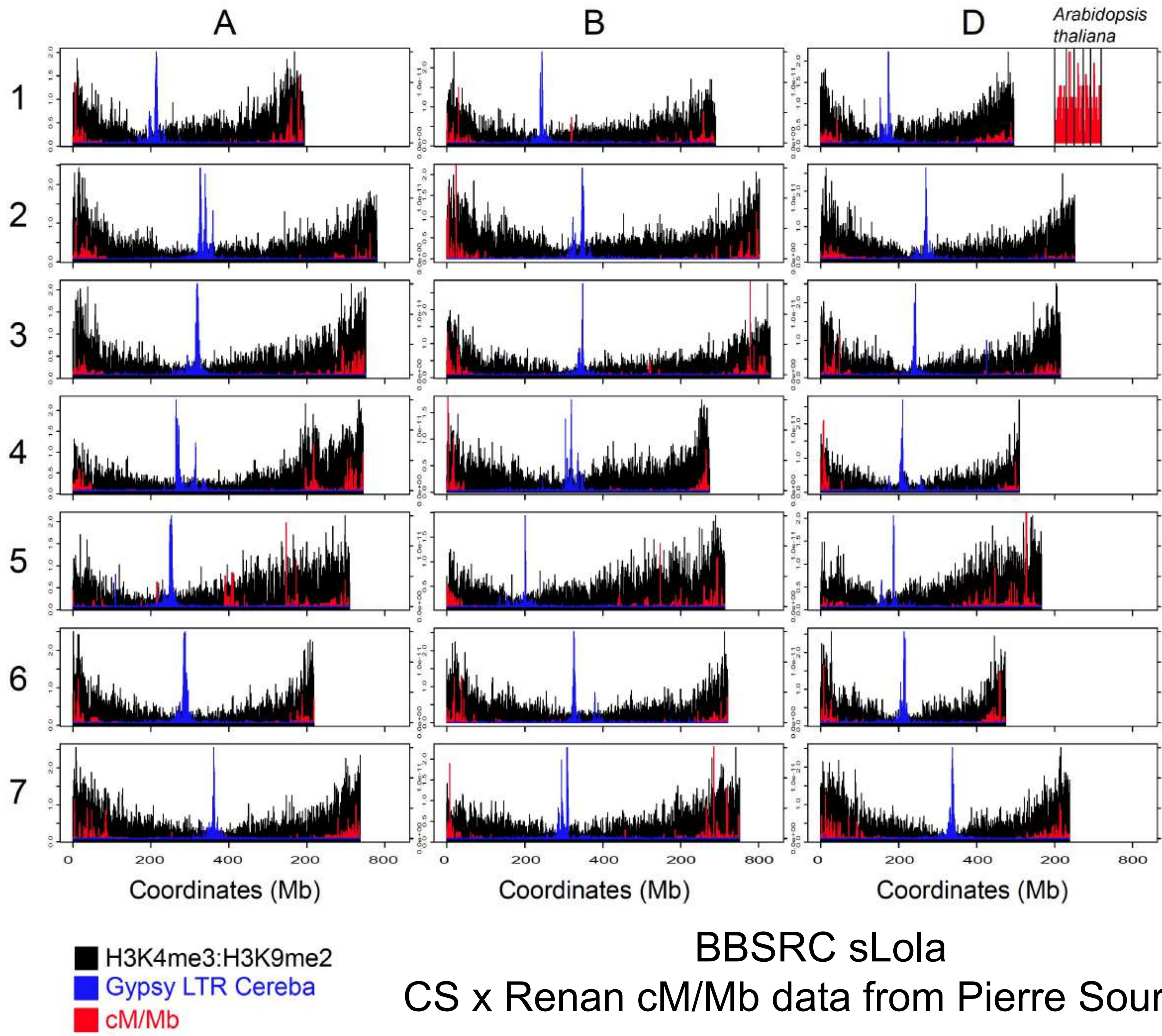


P1
P2
P1 target locus for introgression into P2
X
→
Gametes of:
F1 → BC1 → BC2 → BC3 → BC4 → BC5 → BC6
Wild type recombination
Unlocking centromere proximal crossover cold spots
Genome-wide hyper-recombination
Targeted recombination

Meiotic recombination pathways



Recombination in the wheat genome vs Arabidopsis



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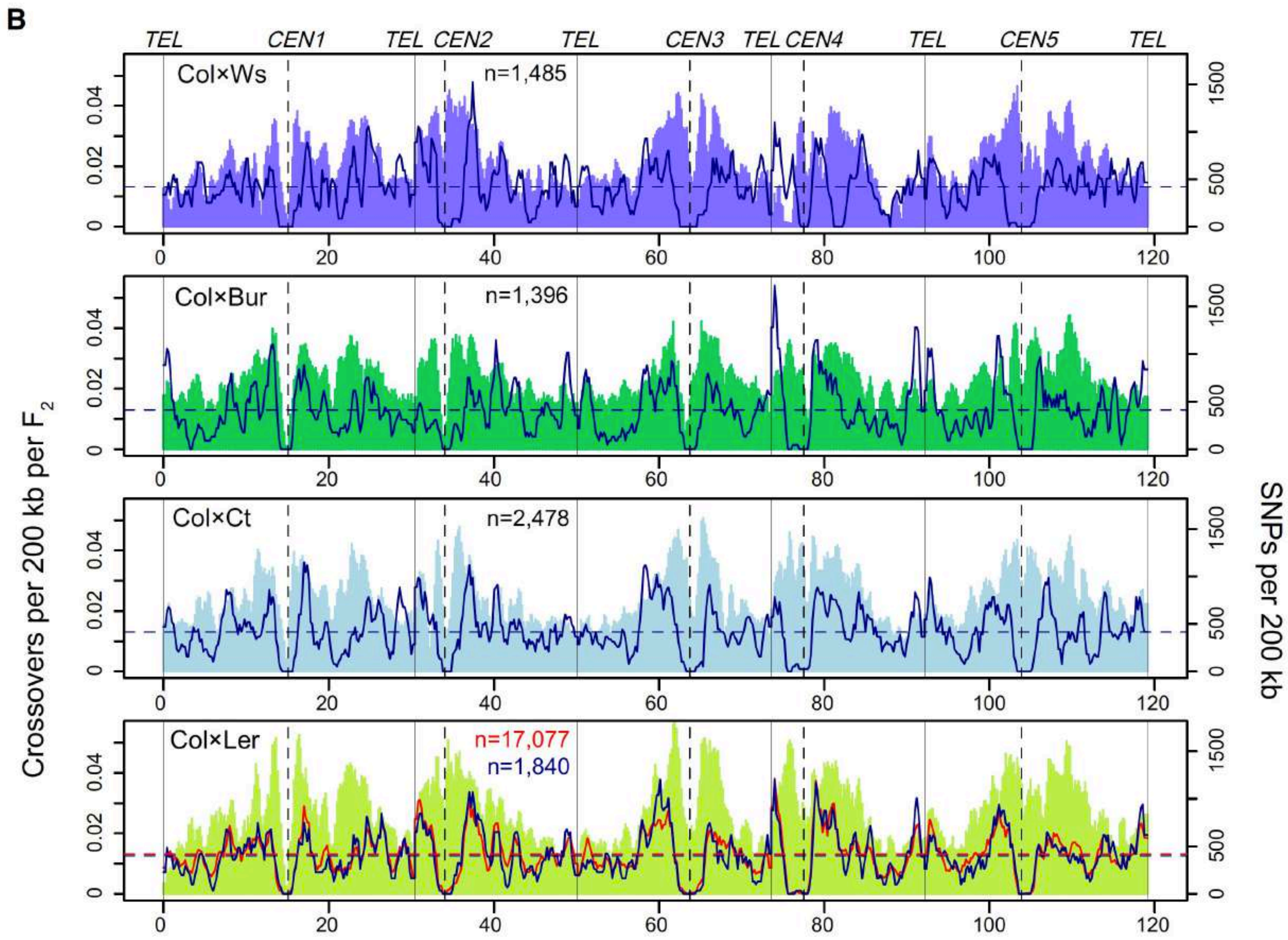
CS x Renan cM/Mb data from Pierre Sourdille

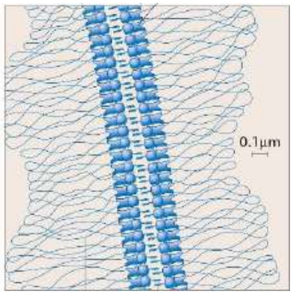
Crossover landscapes in the Arabidopsis genome



Blackwell et al 2020 *EMBO J*

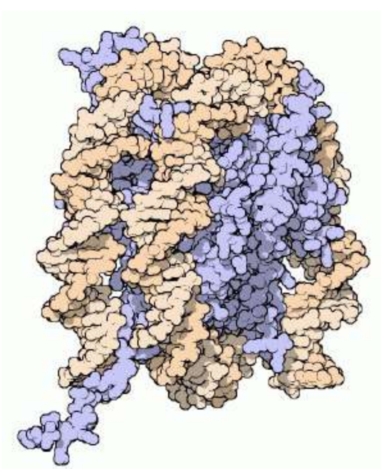
Meiotic recombination pathways

Chromatin, axis, SC



ASY1
ASY3
REC8
ZYP1a
ZYP1b

H2A.Z
H3K4^{me3}
5-mC
H3K9^{me2}



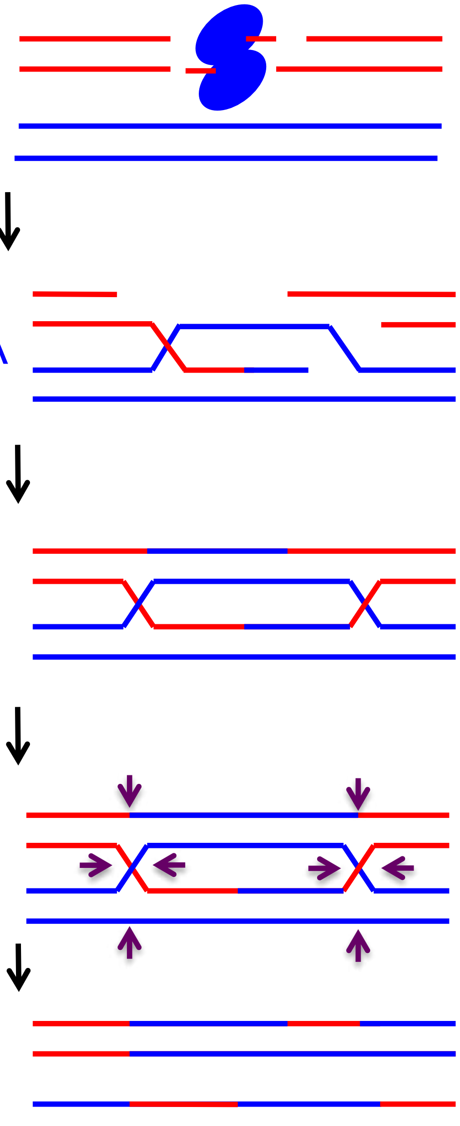
SPO11-1/SPO11-2/ MTOPVIB

DMC1, RAD51, RPA

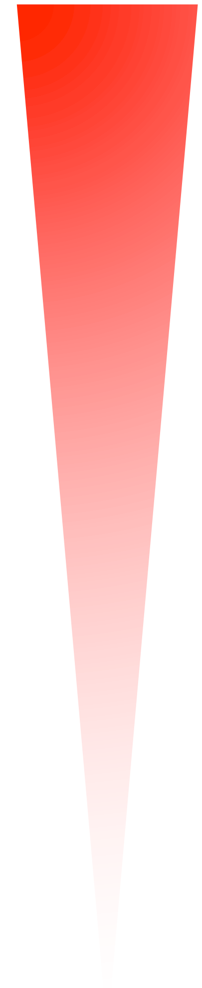
HEI10, ZIP4, MSH4, MSH5, MER3, SHOC1, PTD

MLH1, MLH3

Crossover



~200 DNA breaks

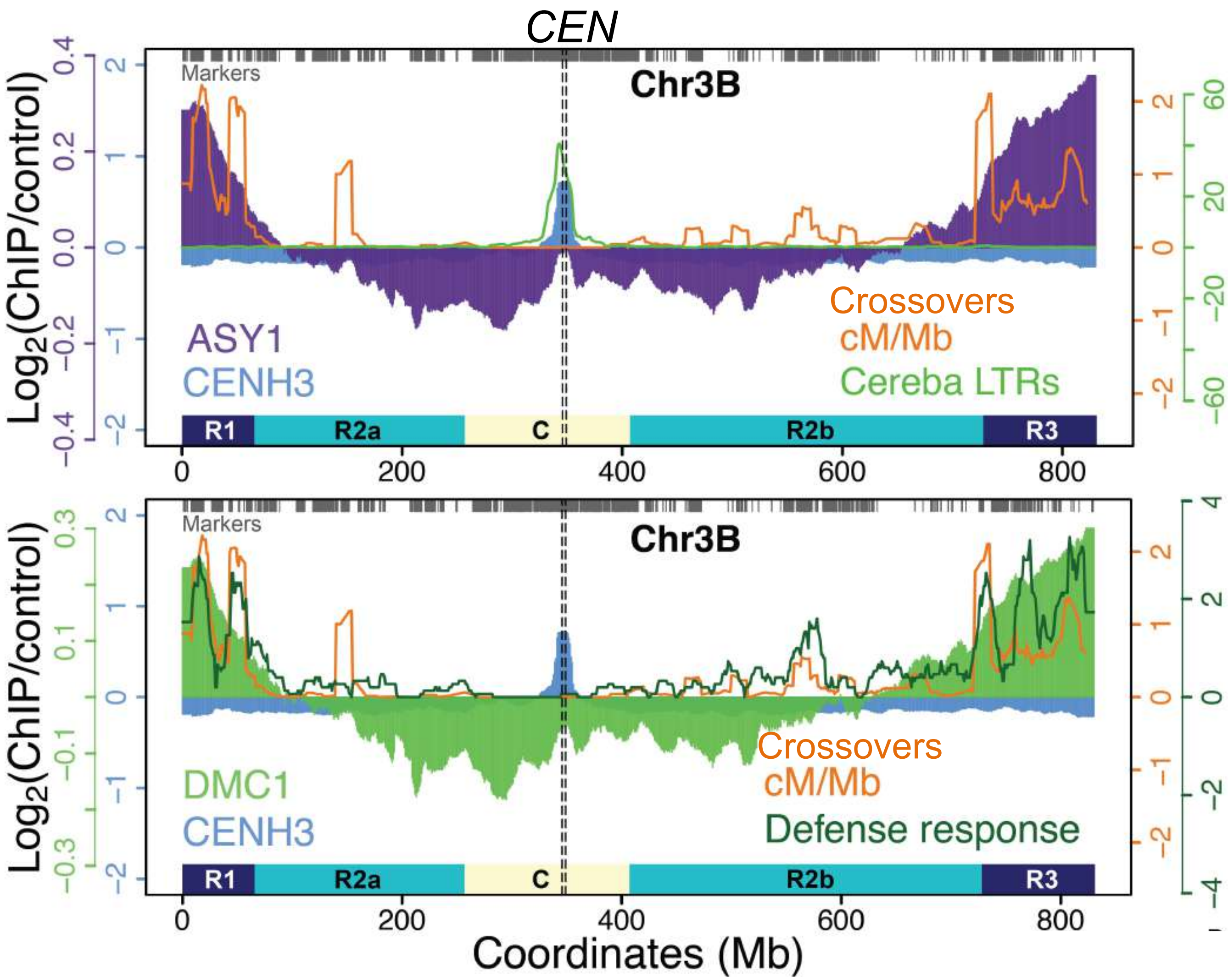


10 Crossovers

Anti-Crossover

FANCM
MHF1
MHF2
FIGL1
TOP3a
RECQ4a
RECQ4b
HCR1

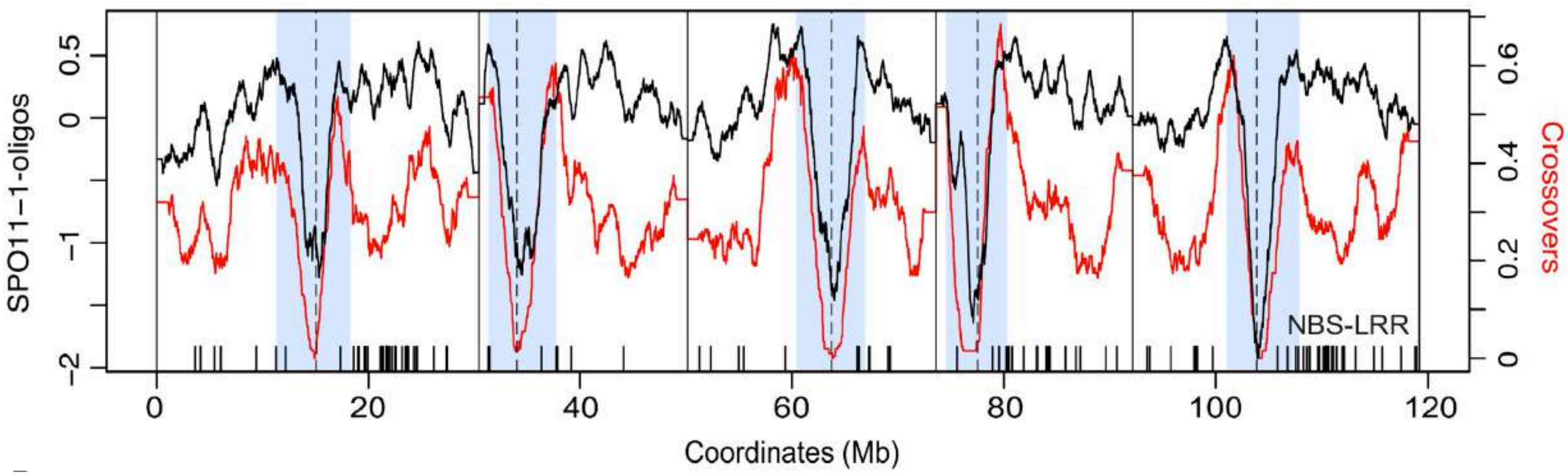
Polarized crossovers, ASY1 and DMC1 in wheat



ChIP for ASY1 and DMC1 performed against CS flowers

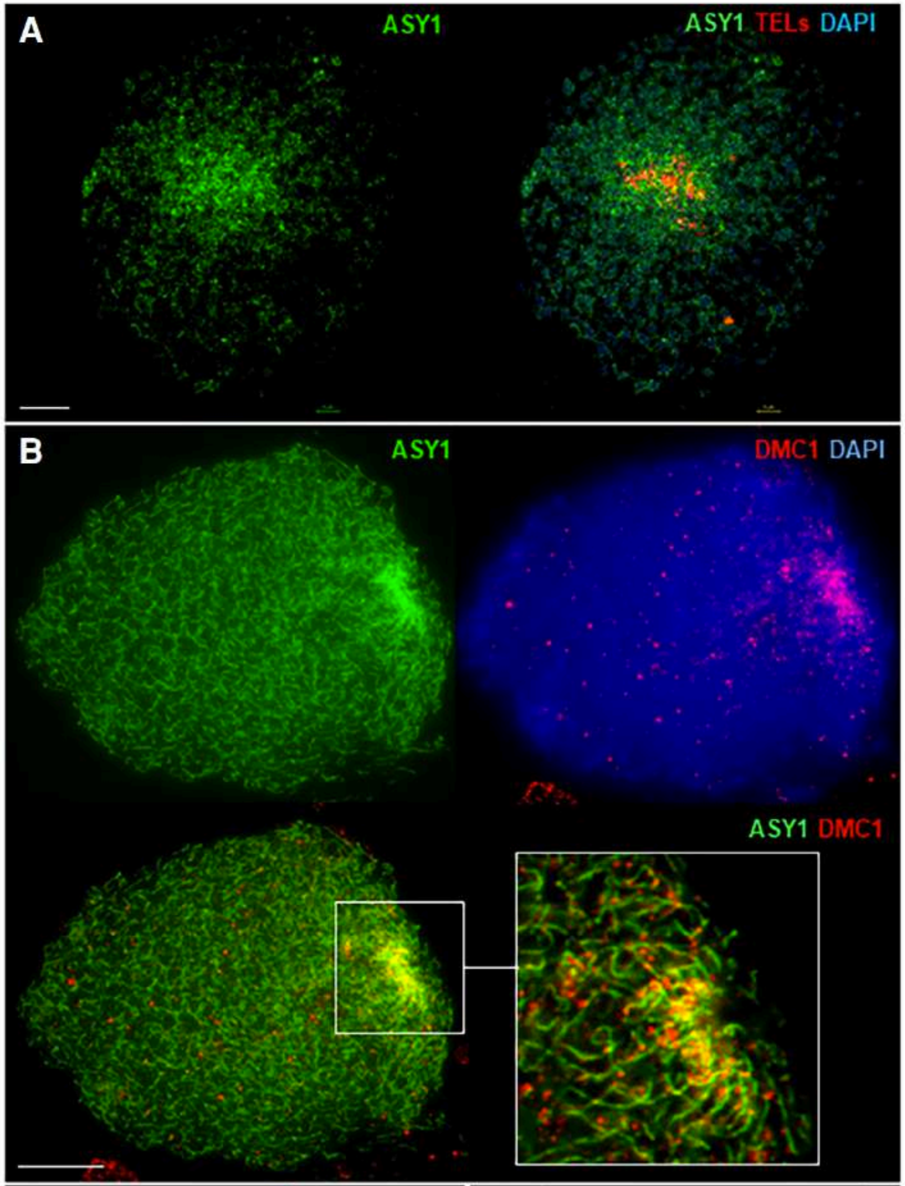
Andrew Tock & Dan Holland (2021) *Genome Res*
cM/Mb from Appels et al (2018) *Science*

ASY1 and SPO11-1-oligos in Arabidopsis



Choi et al (2018) *Genome Res*

Polarized recombination in bread wheat



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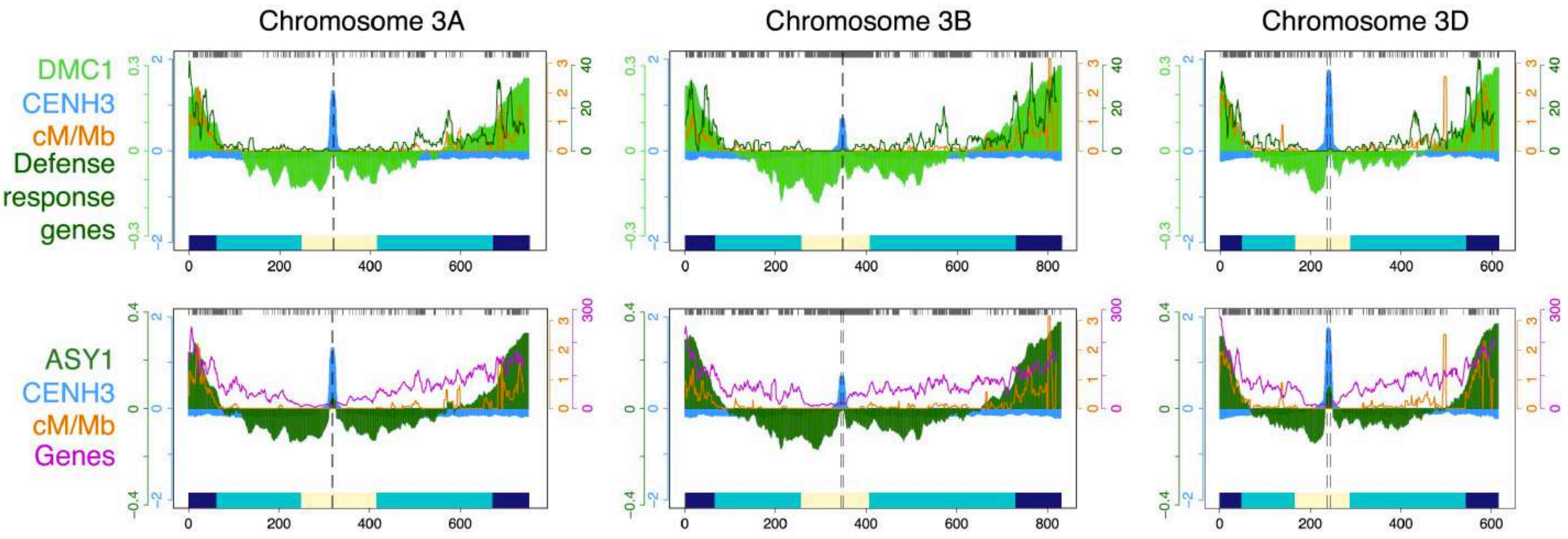
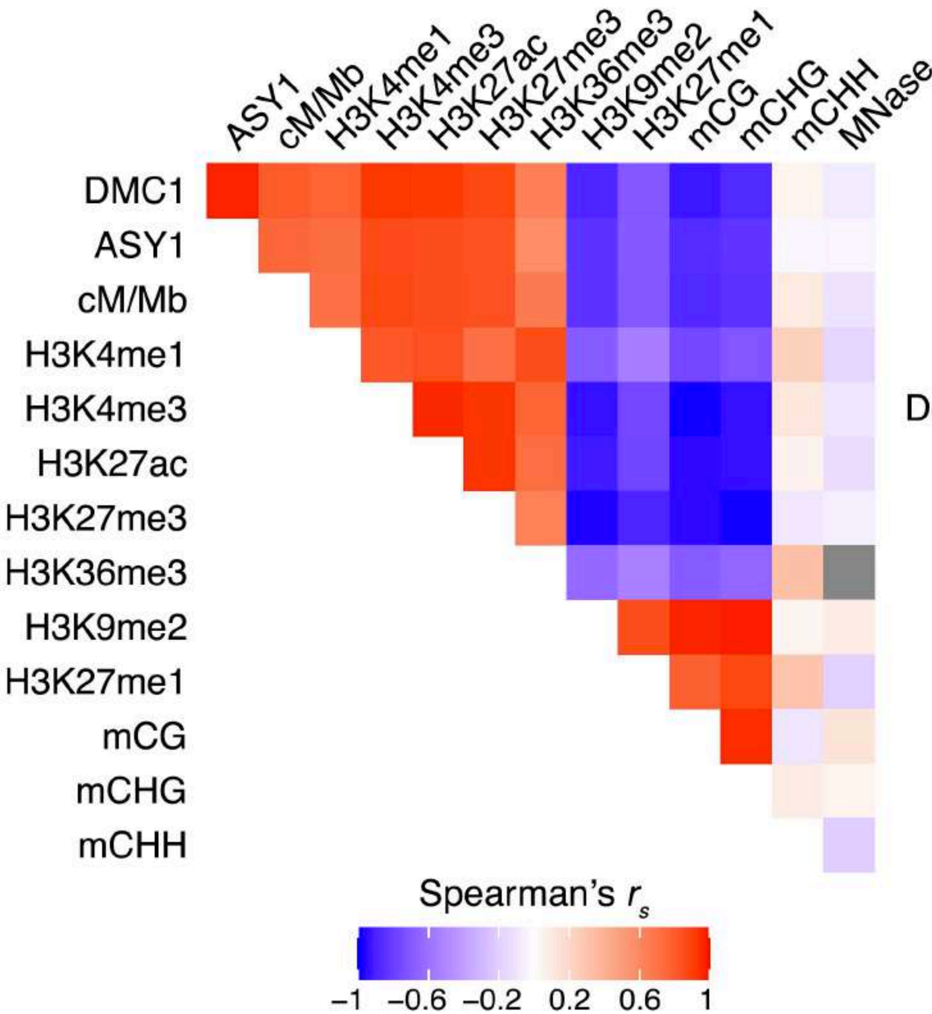
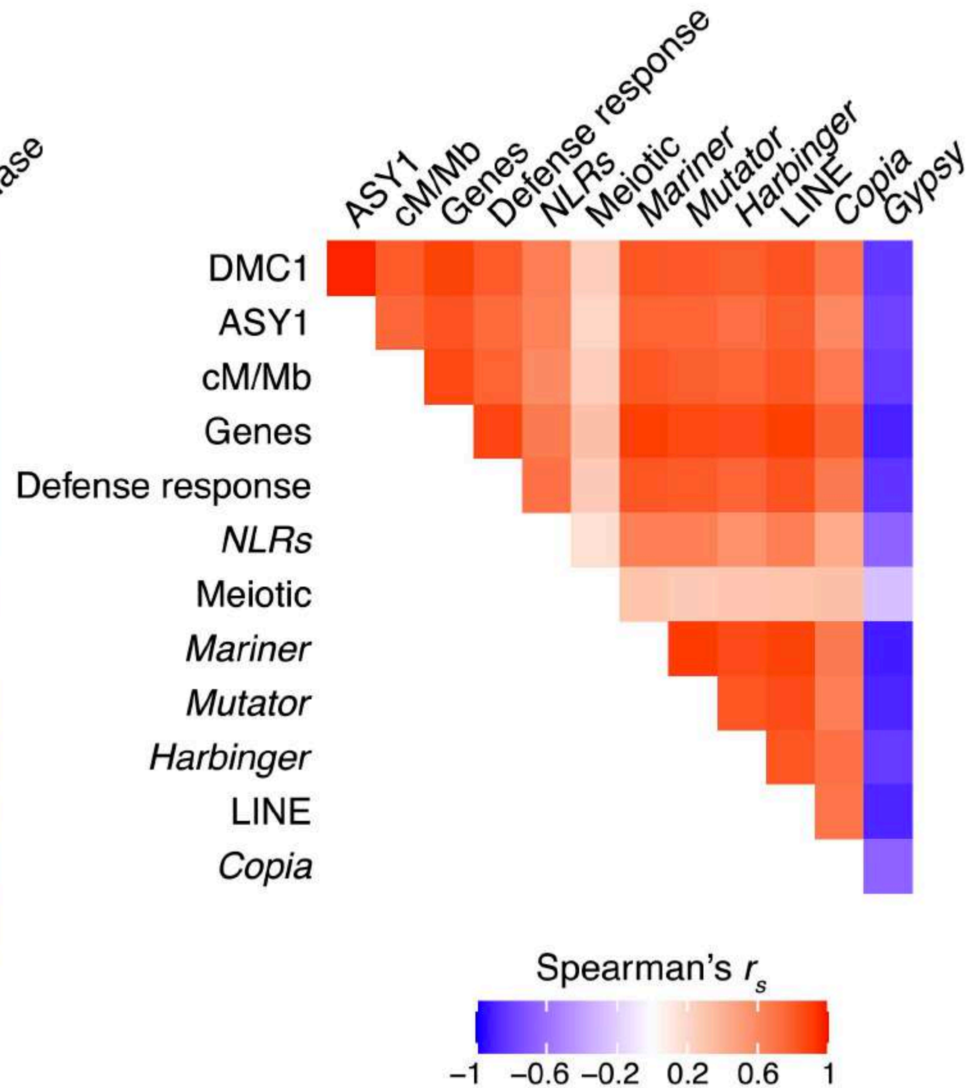
Recombination and chromatin in the wheat genome

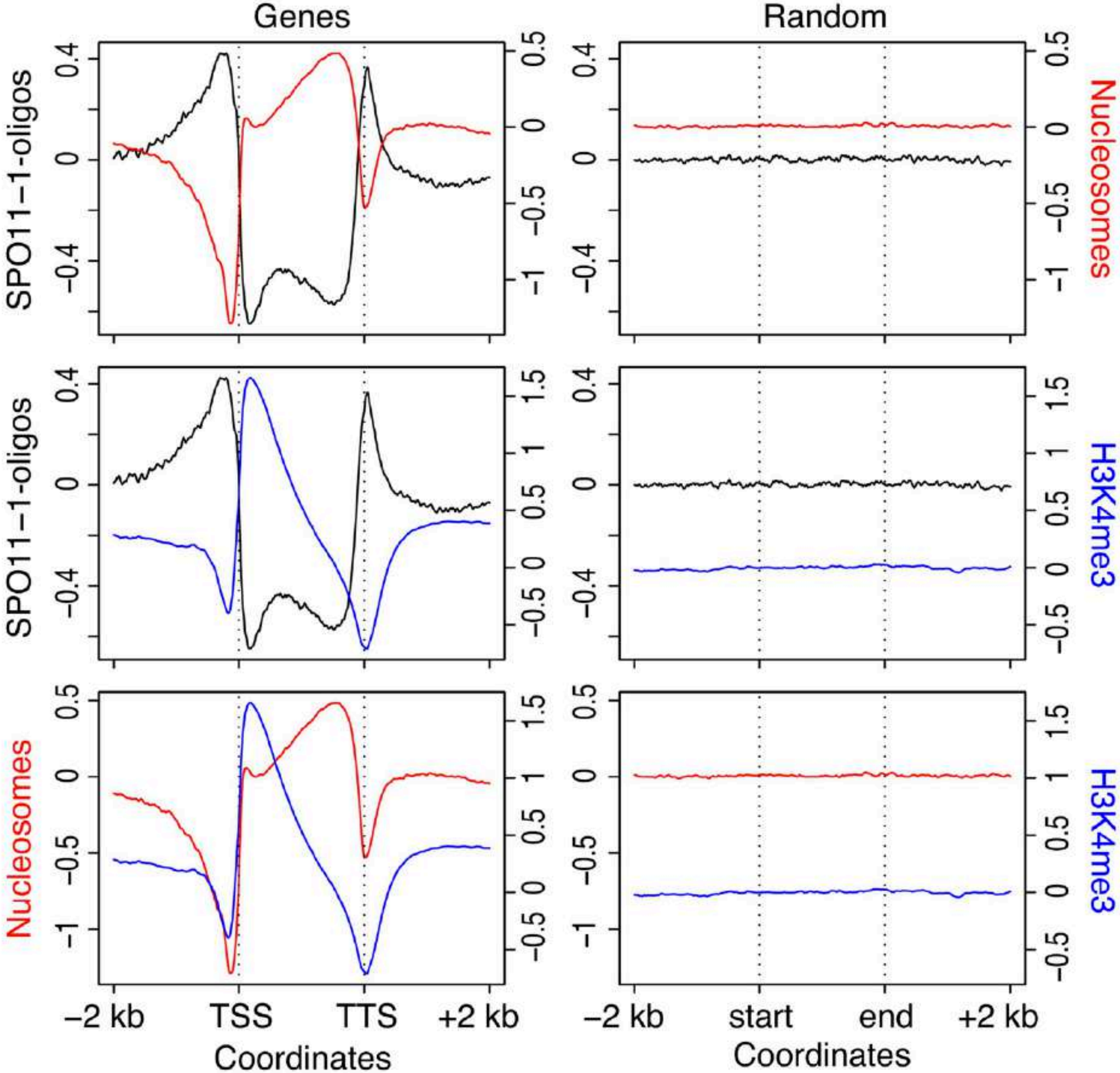


Recombination and chromatin in the wheat genome



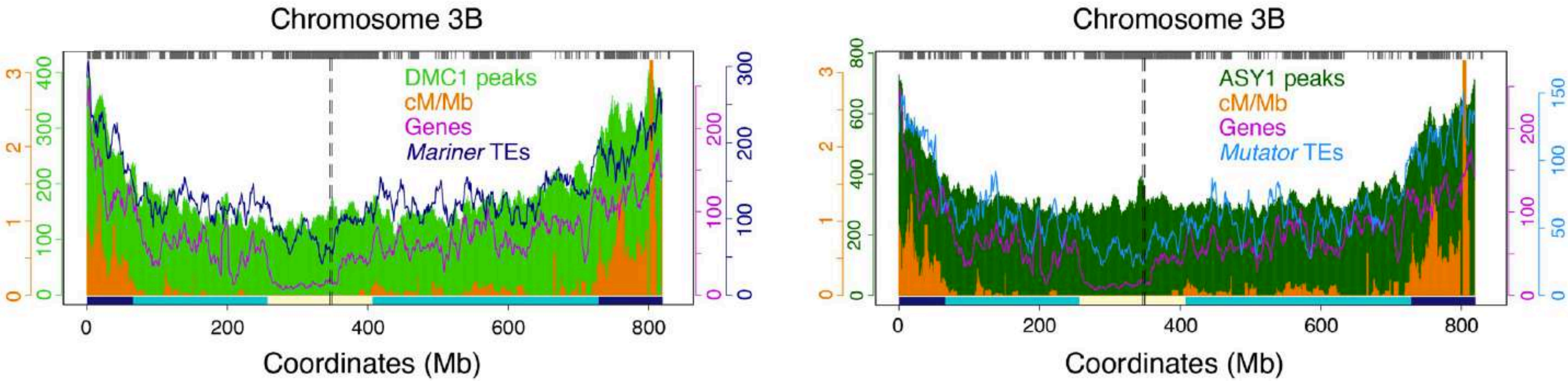


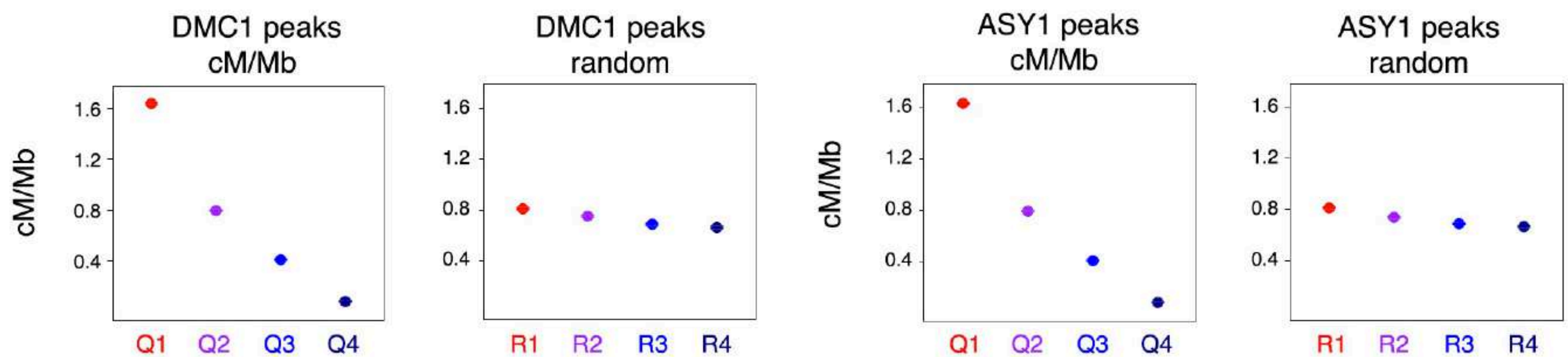
Recombination hotspots around Arabidopsis genes



Choi et al (2018) *Genome Res*

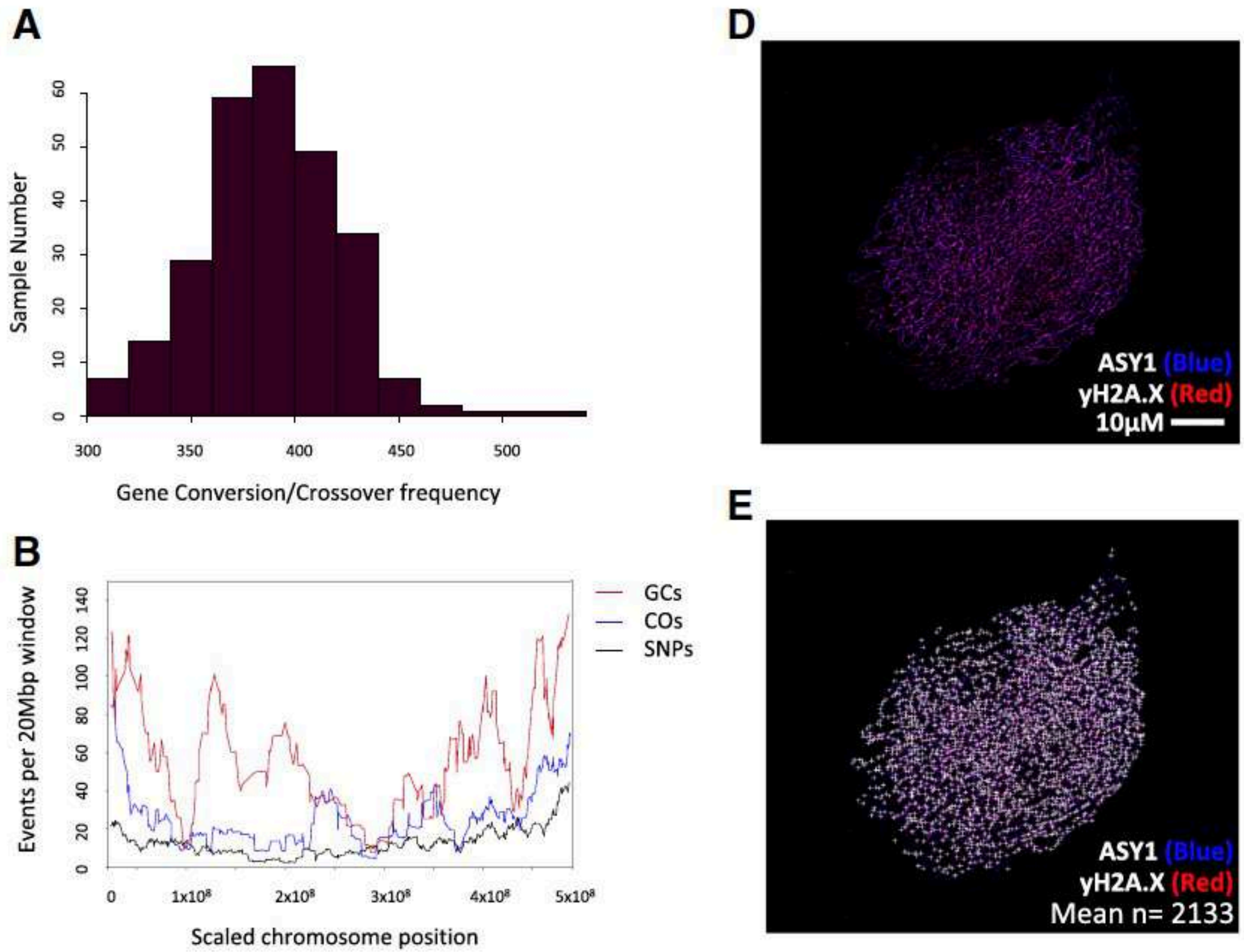
ASY1 and DMC1 hotspots in wheat





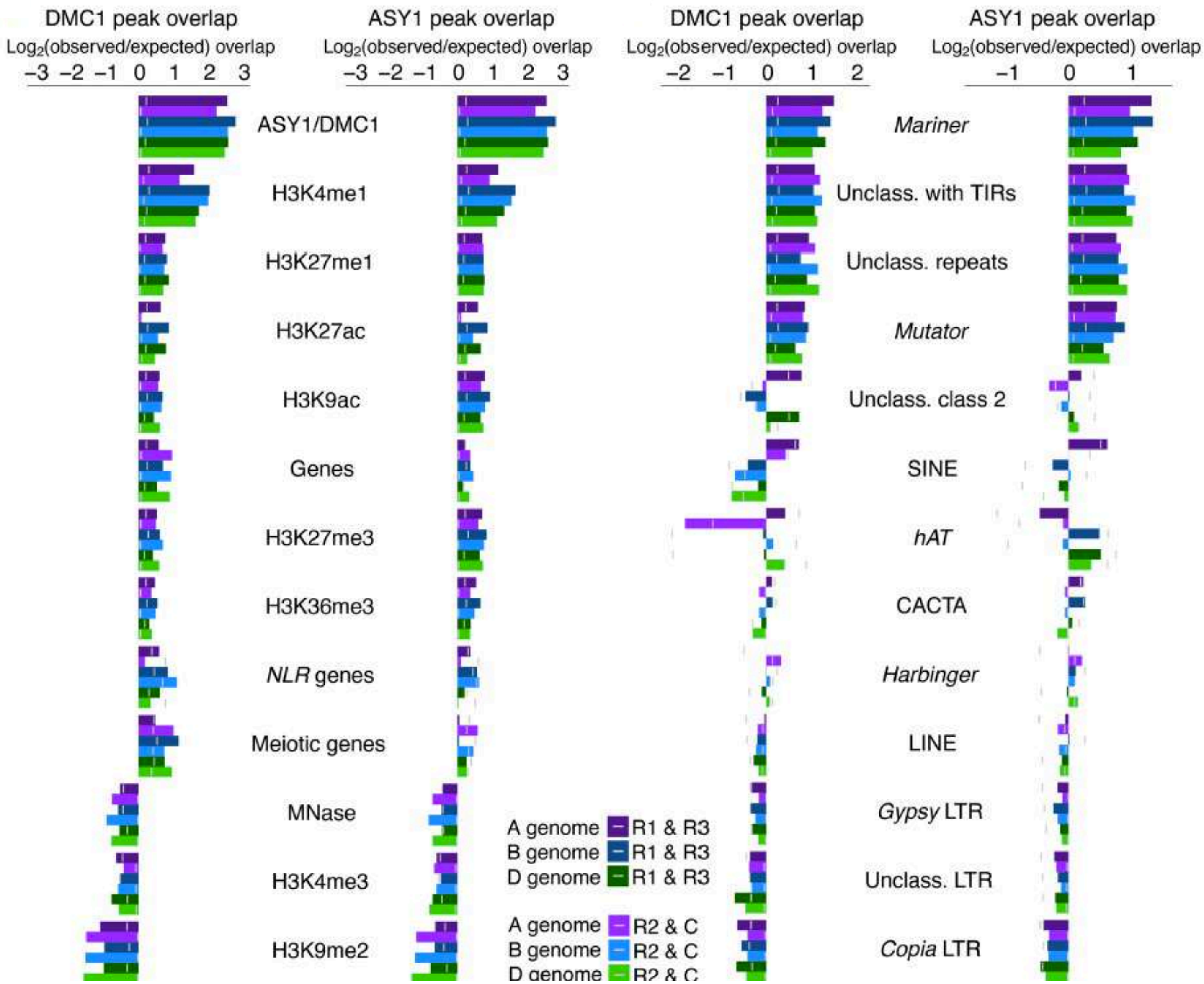
cM/Mb data from Pierre Sourdille's CS x Renan mapping experiment

Evidence for widespread DSBs in wheat

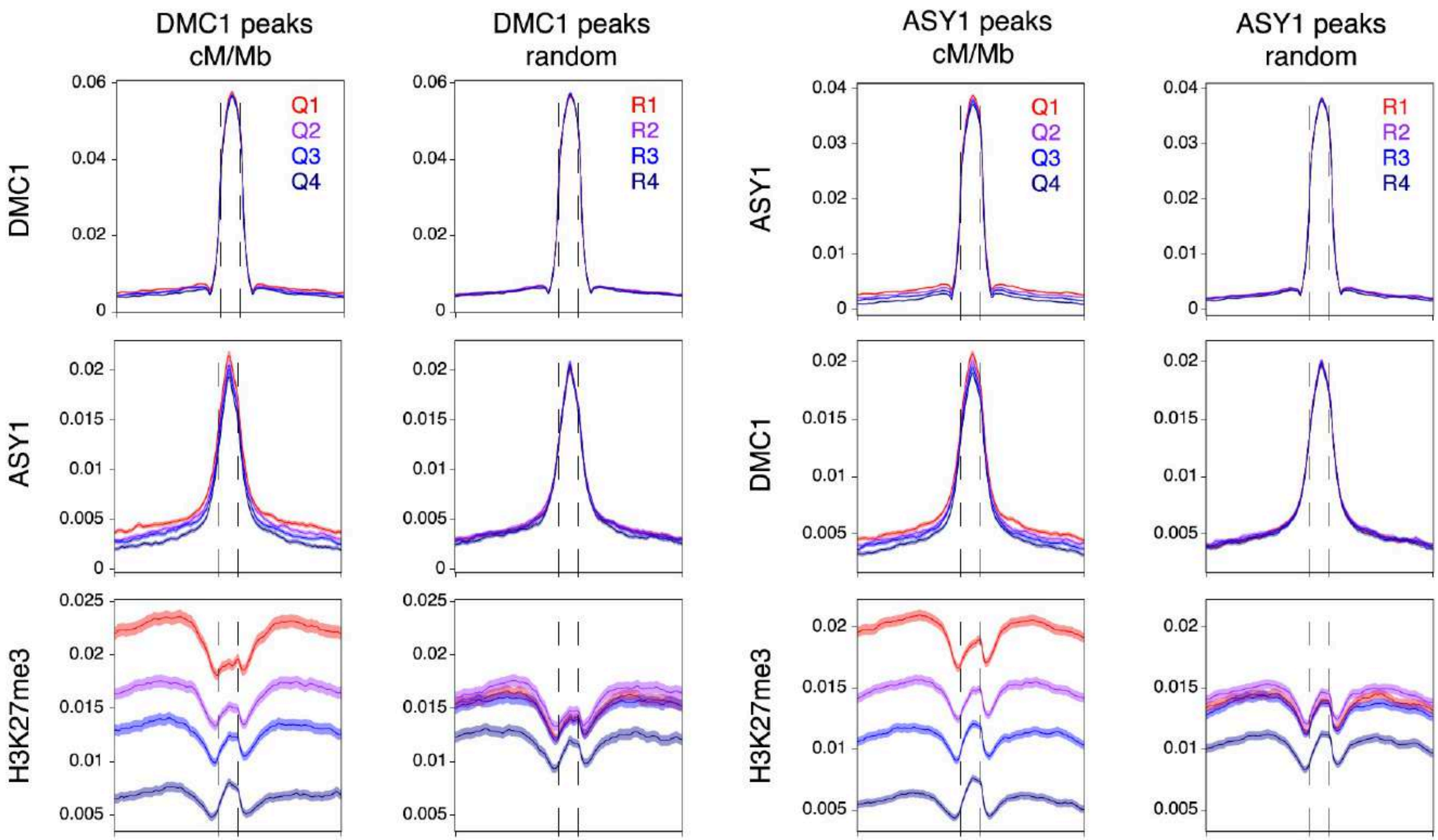


Gardiner .. Hall (2019) *Genome Biology*

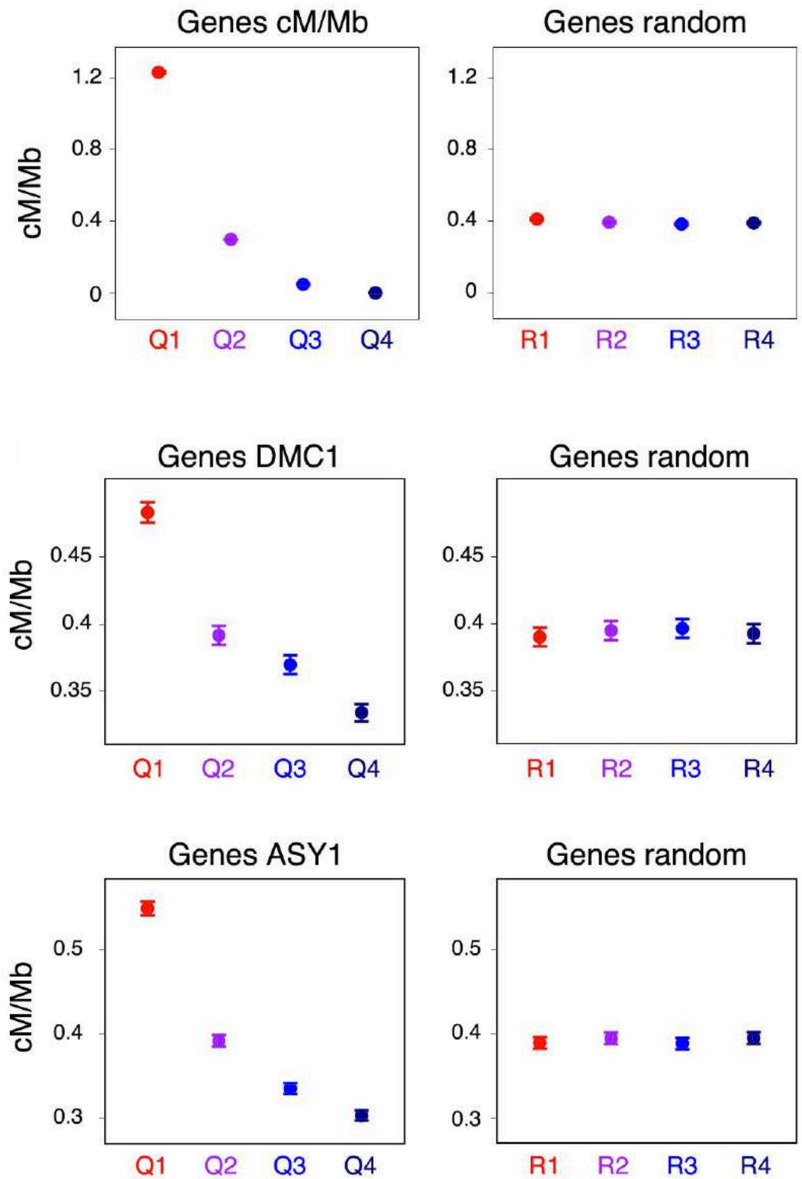
ASY1 and DMC1 hotspots in wheat



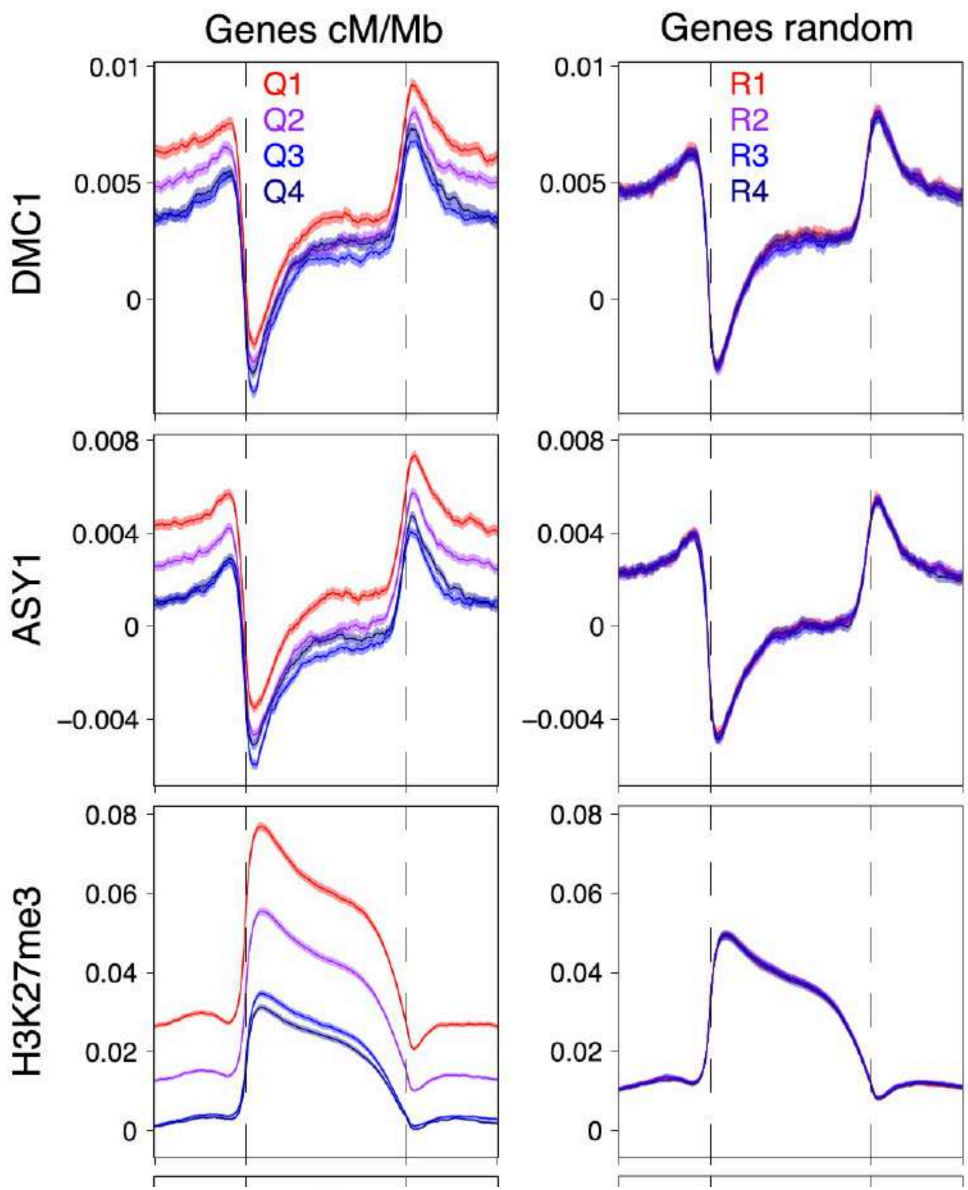
Correlation of crossovers & H3K27me3 at DMC1 and ASY1 peaks



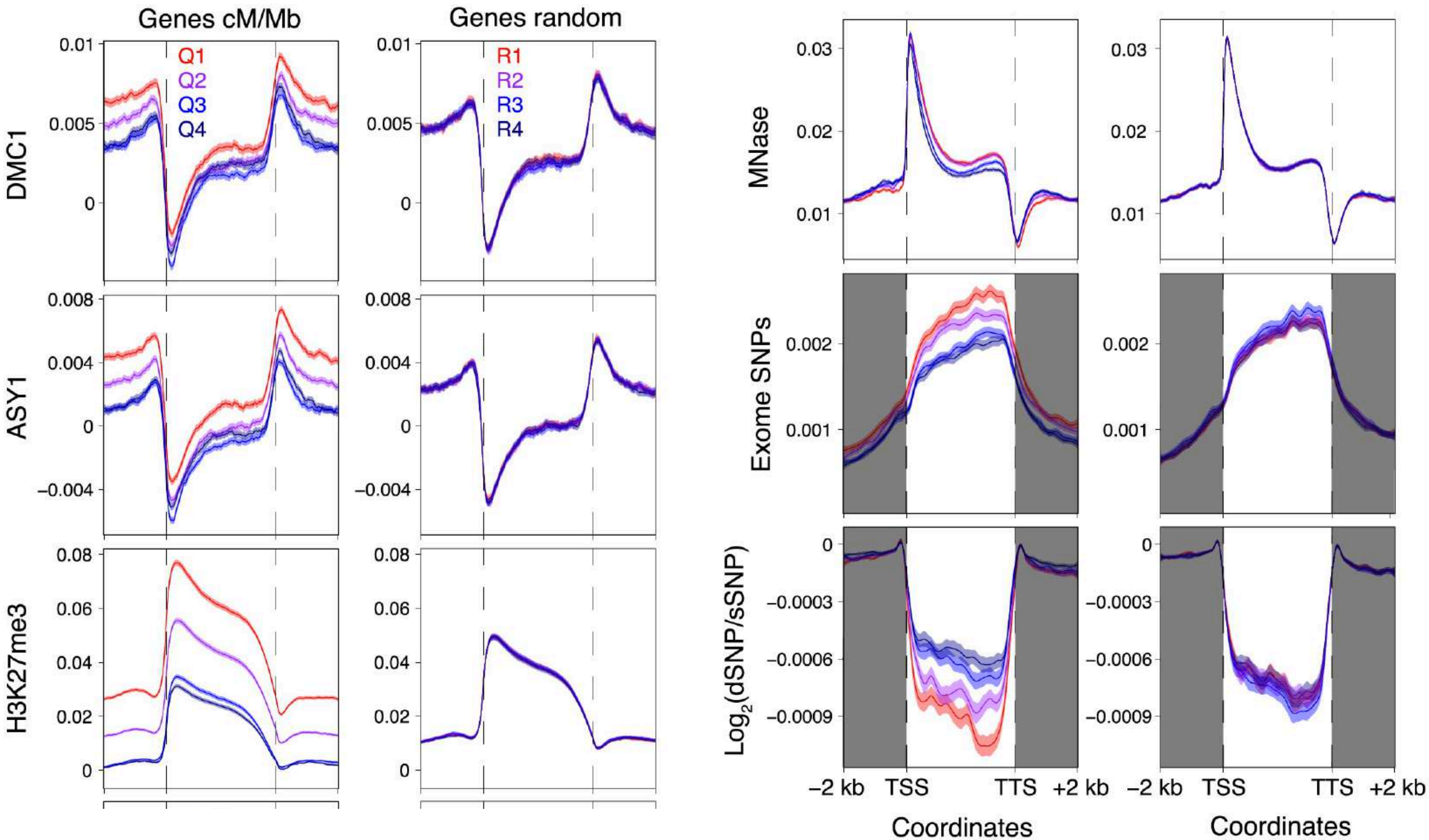
Crossovers, ASY1 and DMC1 in wheat genes



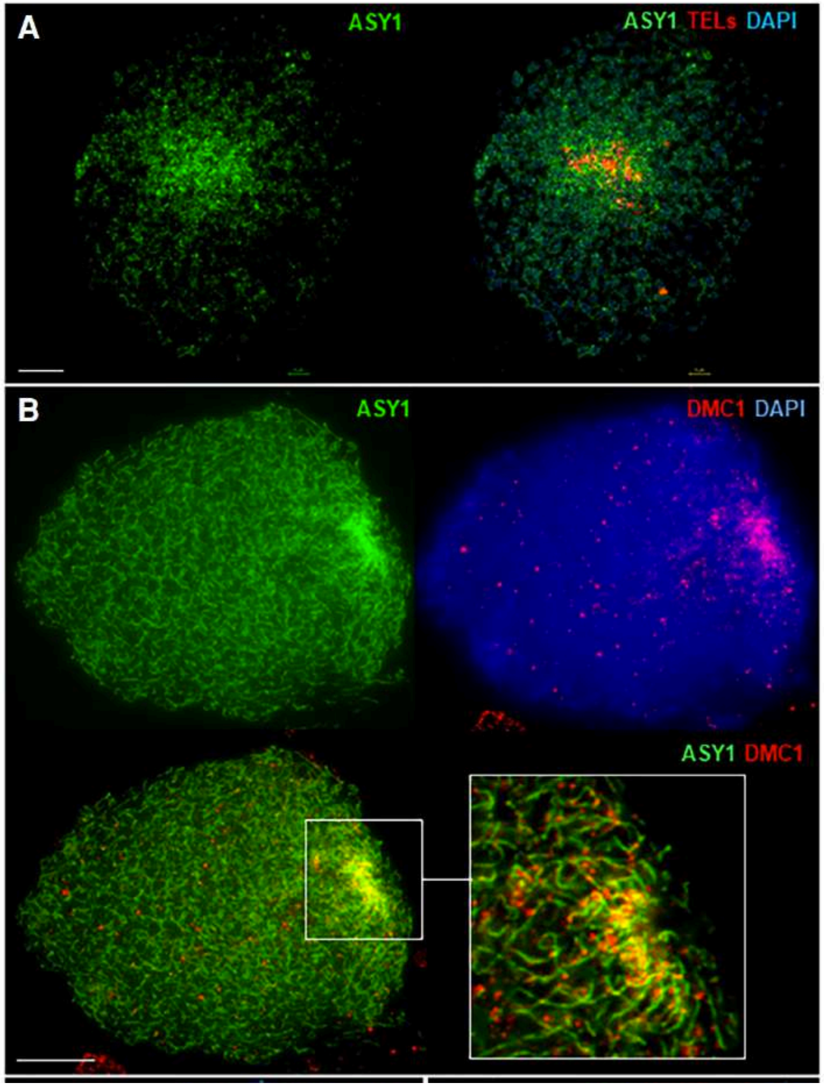
Crossovers, H3K27me3, ASY1 and DMC1 in wheat genes

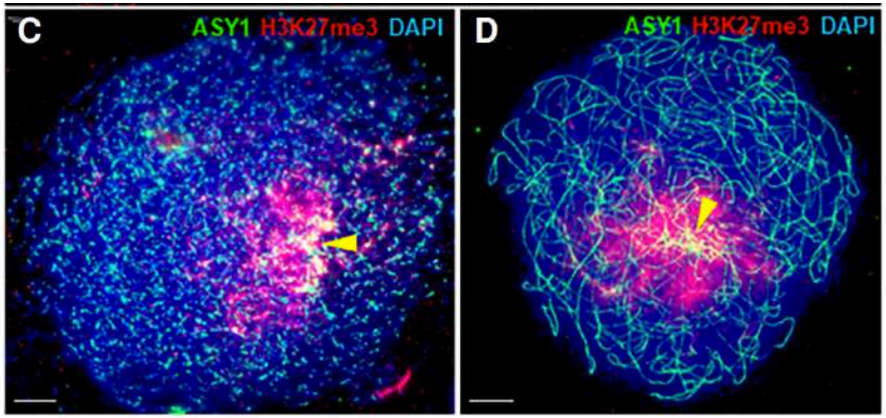


Crossovers and diversity in wheat genes



Polarized H3K27me3 and recombination in bread wheat





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What is the Polycomb mark H3K27me3?

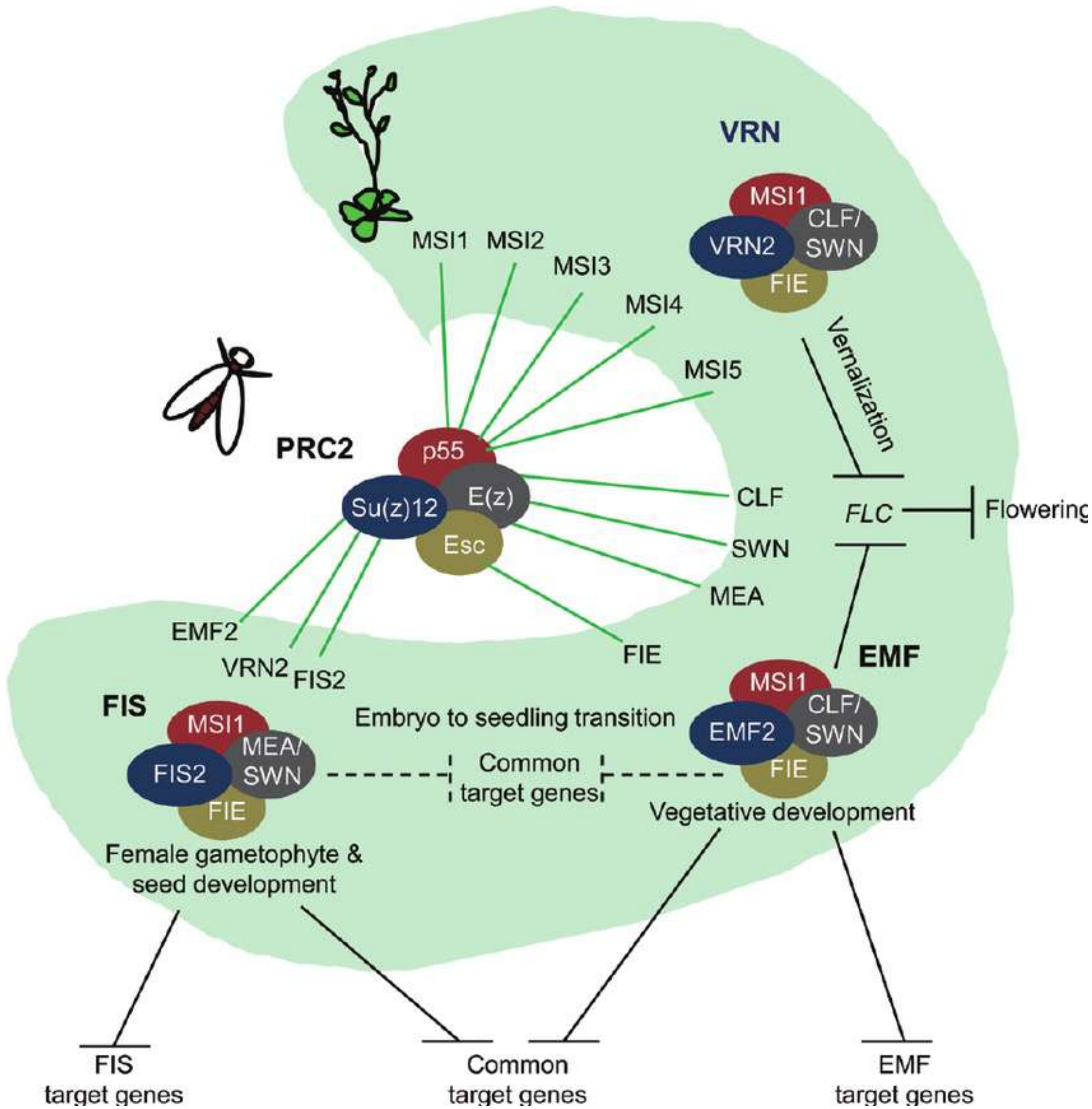
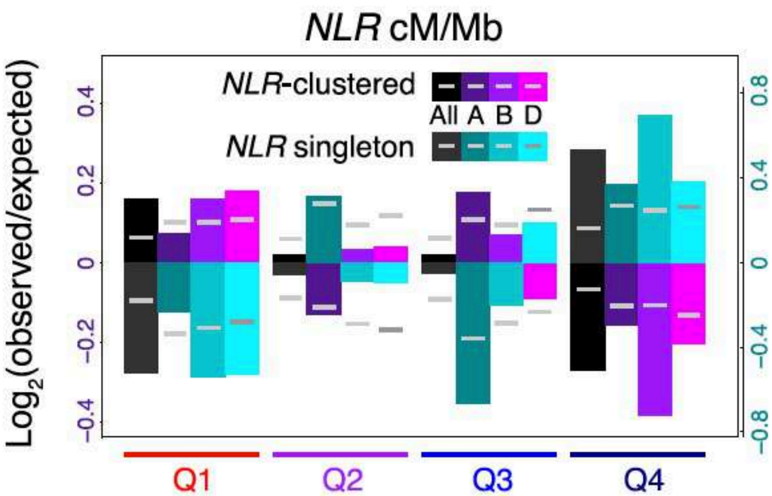
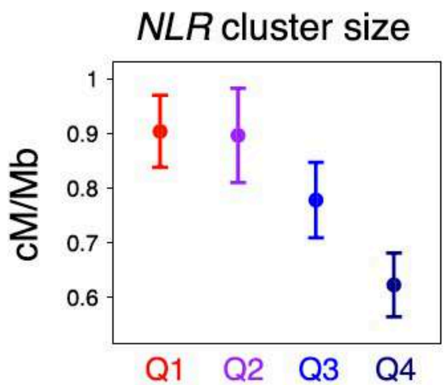


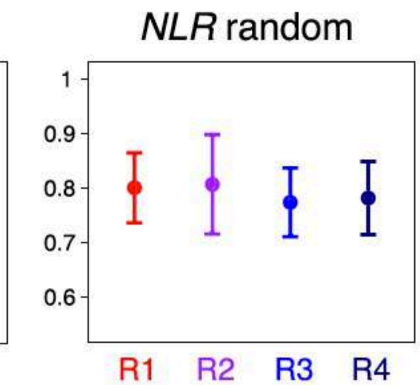
Table 4. Crossover and DNM rates. Results are presented for the sexes separately. Numbers represent the crossover rate relative to the genome average within annotated regions; values within parentheses are 95% CIs. ChromHMM categories are measured in adult ovaries. Abbreviations: Enhancers/DNase, enhancer states (EnhA1/2/AF/W1/W2/Ac) and deoxyribonuclease (DNase)–only states (DNase); Biv/Poised, bivalent and poised promoters; PRC2, polycomb-group–repressive complex 2 (ReprPC); Prom, promoter regions (PromU/D1/D2); Tx, transcribed regions (Tx5′/Tx/Tx3′/TxWk); TxEnh, enhancers within transcribed regions (TxEnh5′, TxEnh3′, TxEnhW, and TxReg); ZNF, enriched over zinc-finger genes and repeats (ZNF/Rpts); Het, heterochromatin.

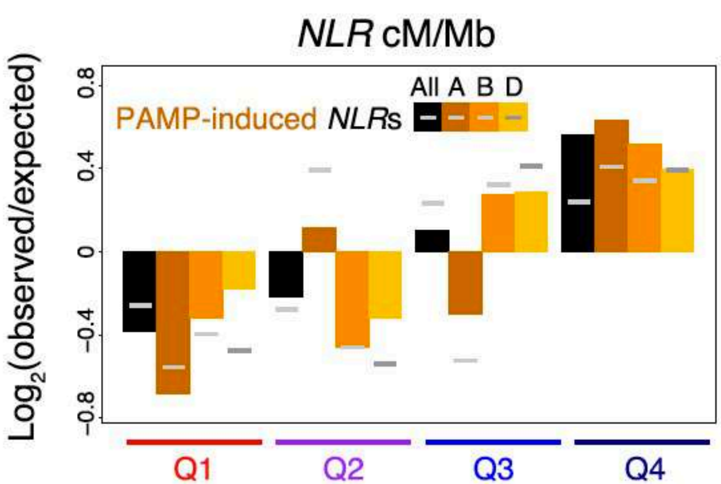
Parameter	Paternal	Maternal
Crossover recombination results		
Autosomal genetic length (cM)	2602.3 (2600.4,2604.2)	4180.4 (4177.2,4183.6)
Crossovers (cM per Mb)	0.945 (0.944, 0.946)	1.518 (1.517,1.519)
Complex crossover ratio (%)	0.53 (0.50,0.56)	1.24 (1.21,1.29)
Relative crossover rates in annotated regions		
Pratto DSB	24.90 (24.87, 24.93)	18.93 (18.91, 18.96)
Altemose PRDM9 ± 500 bp	7.28 (7.27, 7.30)	7.12 (7.11, 7.13)
Altemose H3K4me3 ± 500 bp	3.92 (3.92, 3.93)	3.99 (3.99, 4.00)
5-Hydroxymethylation	2.82 (2.80, 2.85)	2.59 (2.58, 2.60)
THE1b regions	4.32 (4.27, 4.37)	2.53 (2.50, 2.56)
ChromHMM Biv/Poised	1.56 (1.53, 1.59)	1.69 (1.67, 1.71)
ChromHMM Enhancers/DNase	1.56 (1.55, 1.57)	1.93 (1.92, 1.94)
ChromHMM Het	0.61 (0.60, 0.63)	0.32 (0.31, 0.33)
ChromHMM Prom	1.10 (1.08, 1.12)	1.32 (1.31, 1.34)
ChromHMM PRC2	2.94 (2.92, 2.97)	2.54 (2.52, 2.55)
ChromHMM TxEnh	0.71 (0.71, 0.72)	0.63 (0.62, 0.63)
ChromHMM Tx	0.56 (0.55, 0.56)	0.46 (0.46, 0.46)
ChromHMM ZNF	0.52 (0.49, 0.55)	0.18 (0.17, 0.19)
Ovary H3K27me3	2.54 (2.52, 2.56)	2.37 (2.35, 2.38)
Ovary H3K36me3	0.60 (0.59, 0.60)	0.53 (0.52, 0.53)
Ovary H3K4me3	1.19 (1.18, 1.21)	1.43 (1.42, 1.44)
Ovary H4K20me1	0.64 (0.62, 0.65)	0.55 (0.54, 0.56)
Ovary H3K27ac	1.37 (1.36, 1.38)	1.64 (1.63, 1.65)
Ovary H3K4me1	1.41 (1.40, 1.42)	1.68 (1.67, 1.69)
Sex-specific DNM rates near crossovers		
Genome-wide rate (10^{-9})	9.59 (9.48, 9.70)	2.59 (2.54, 2.64)
Enrichment within 0 to 1 kb	41.5 (33.2, 52.0)	58.4 (44.0, 77.4)
Enrichment within 1 to 3 kb	6.91 (4.76, 10.1)	11.9 (7.42, 19.2)
Enrichment within 3 to 40 kb	1.05 (0.82, 1.35)	2.21 (1.60, 3.06)
Enrichment within 3 to 40 kb (only for complex crossovers)	—	49.7 (27.5, 90.0)

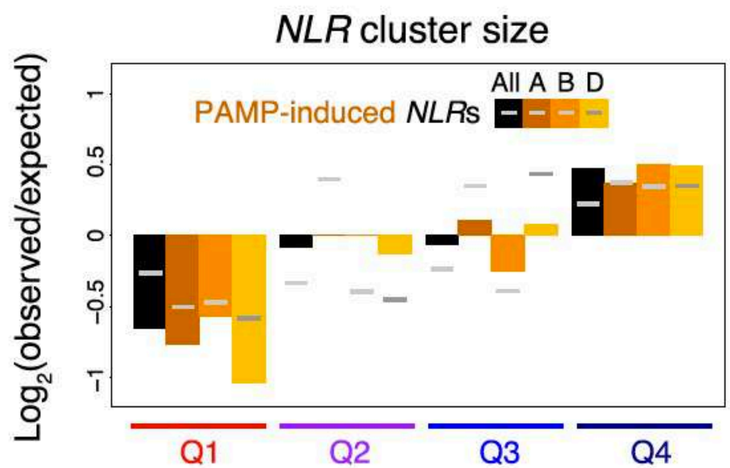
Crossovers and wheat *NLR* genes



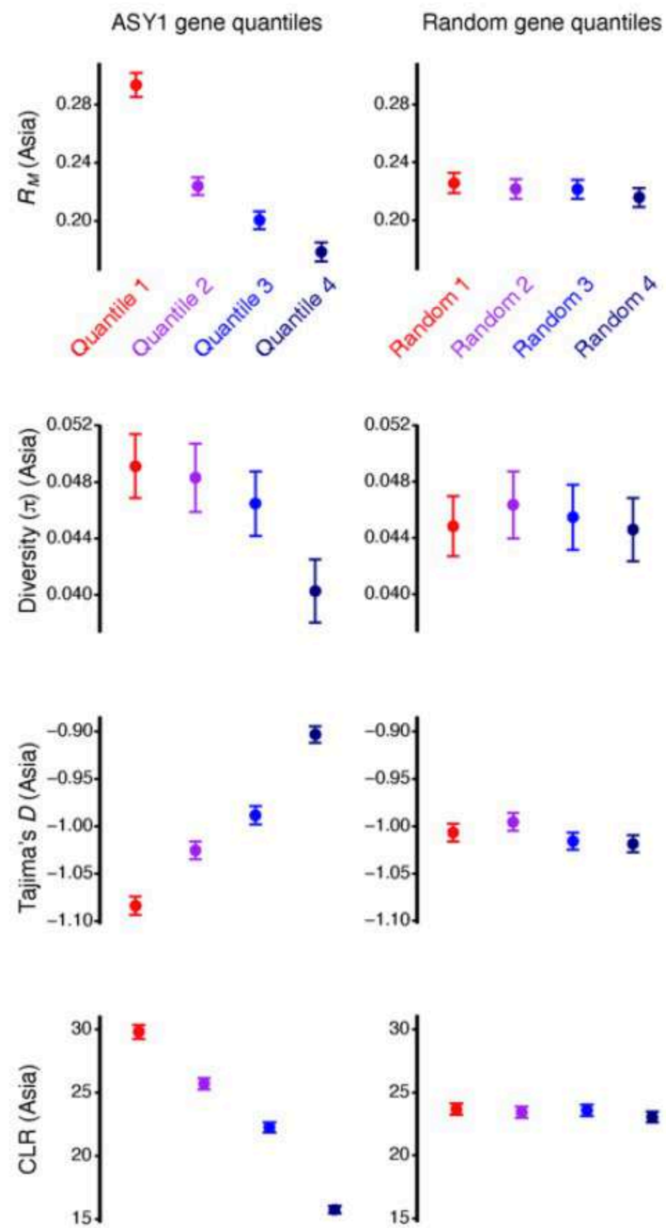




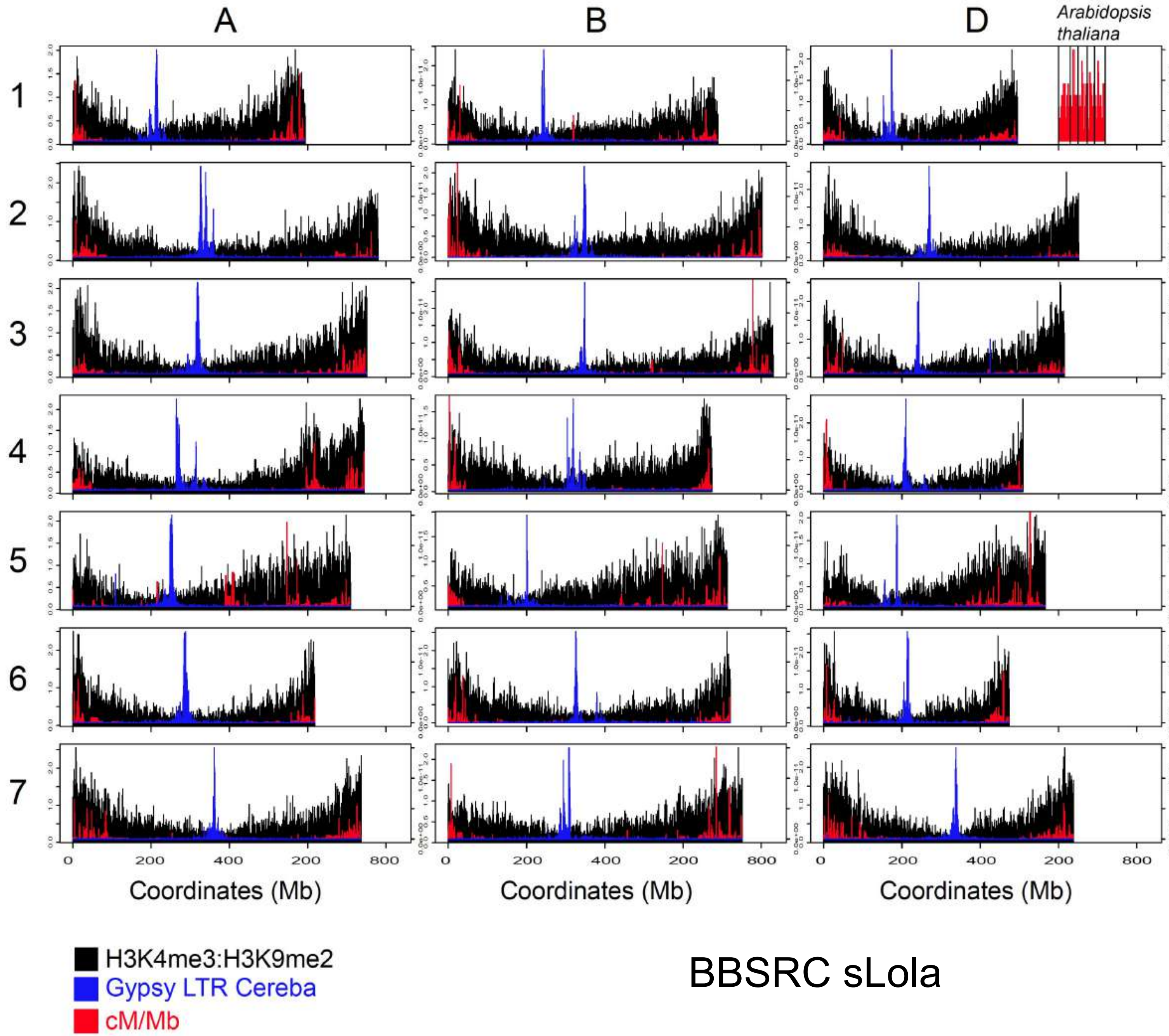




Crossovers, diversity and selection



Recombination gradients in the wheat genome



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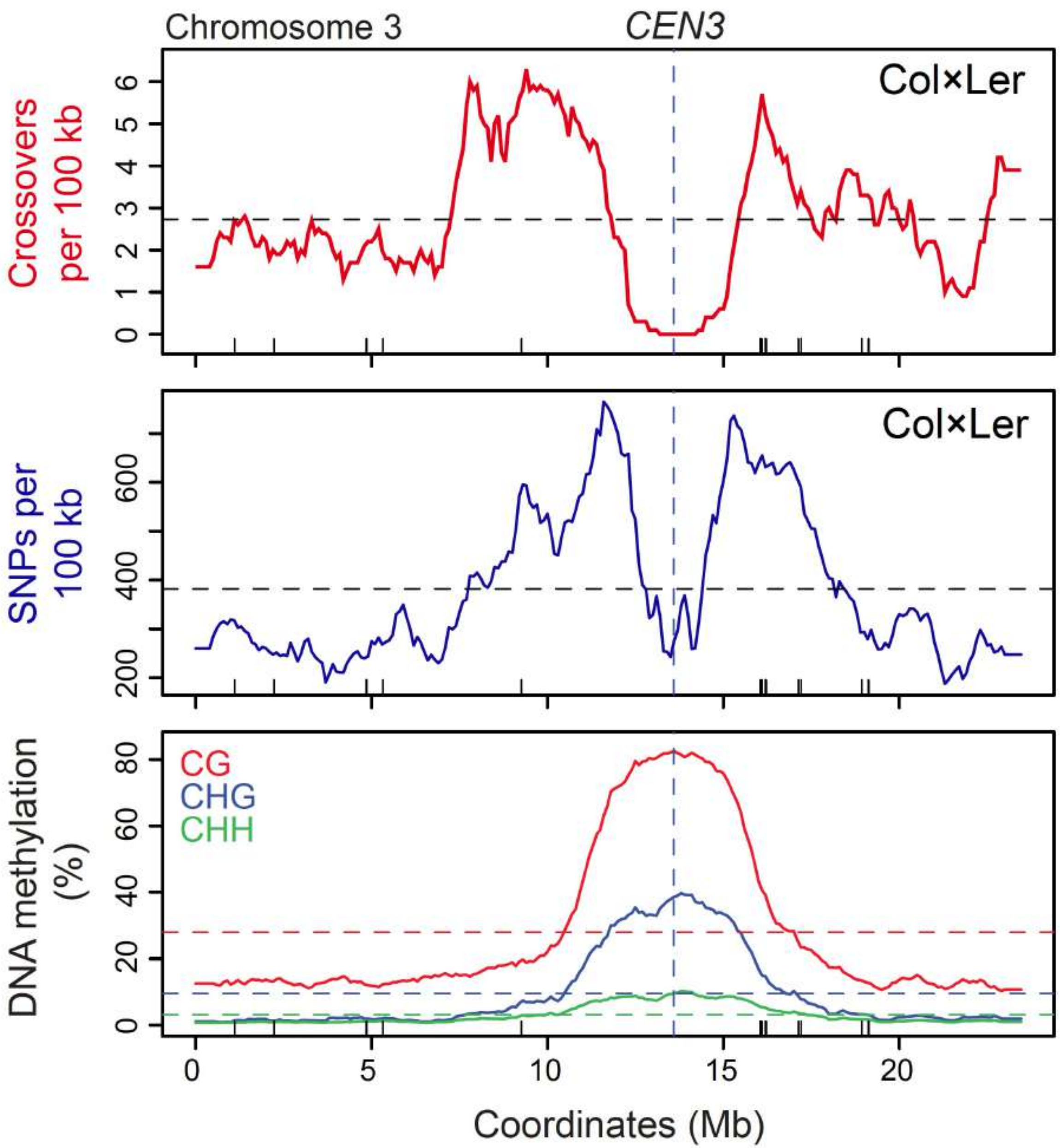
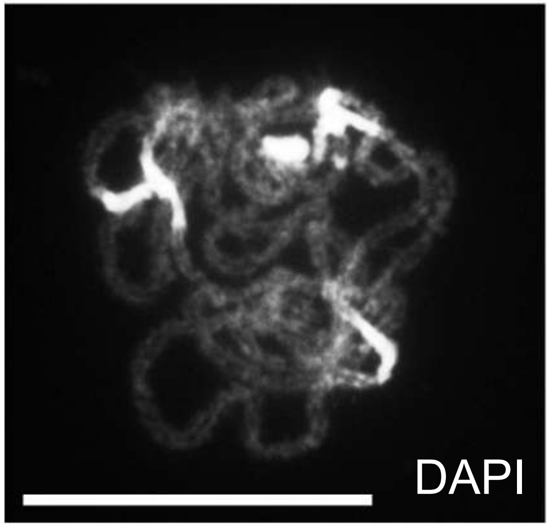
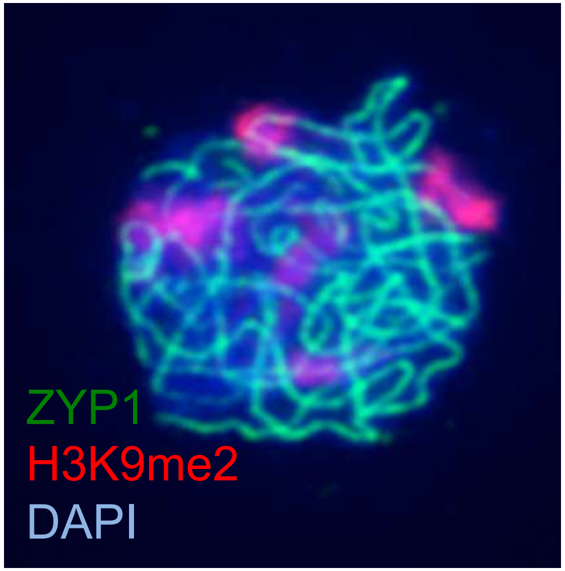
Arabidopsis crossover and polymorphism landscapes



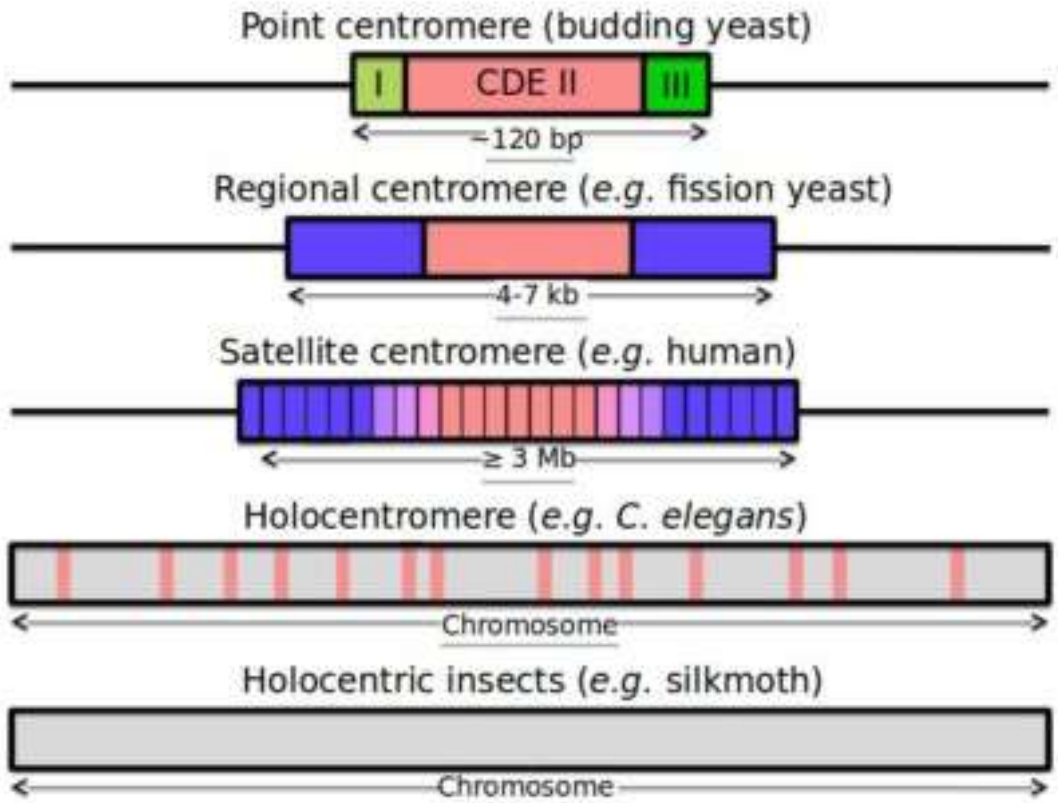




Christophe Lambing

The Centromere Paradox: Stable Inheritance with Rapidly Evolving DNA

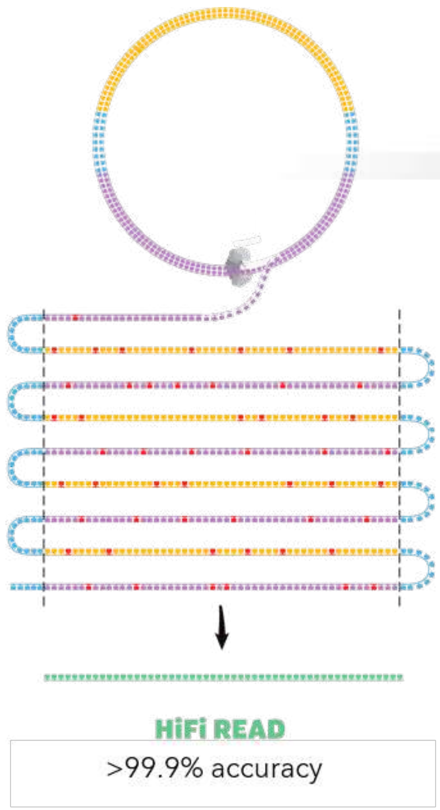
Steven Henikoff,* Kami Ahmad, Harmit S. Malik



← Arabidopsis

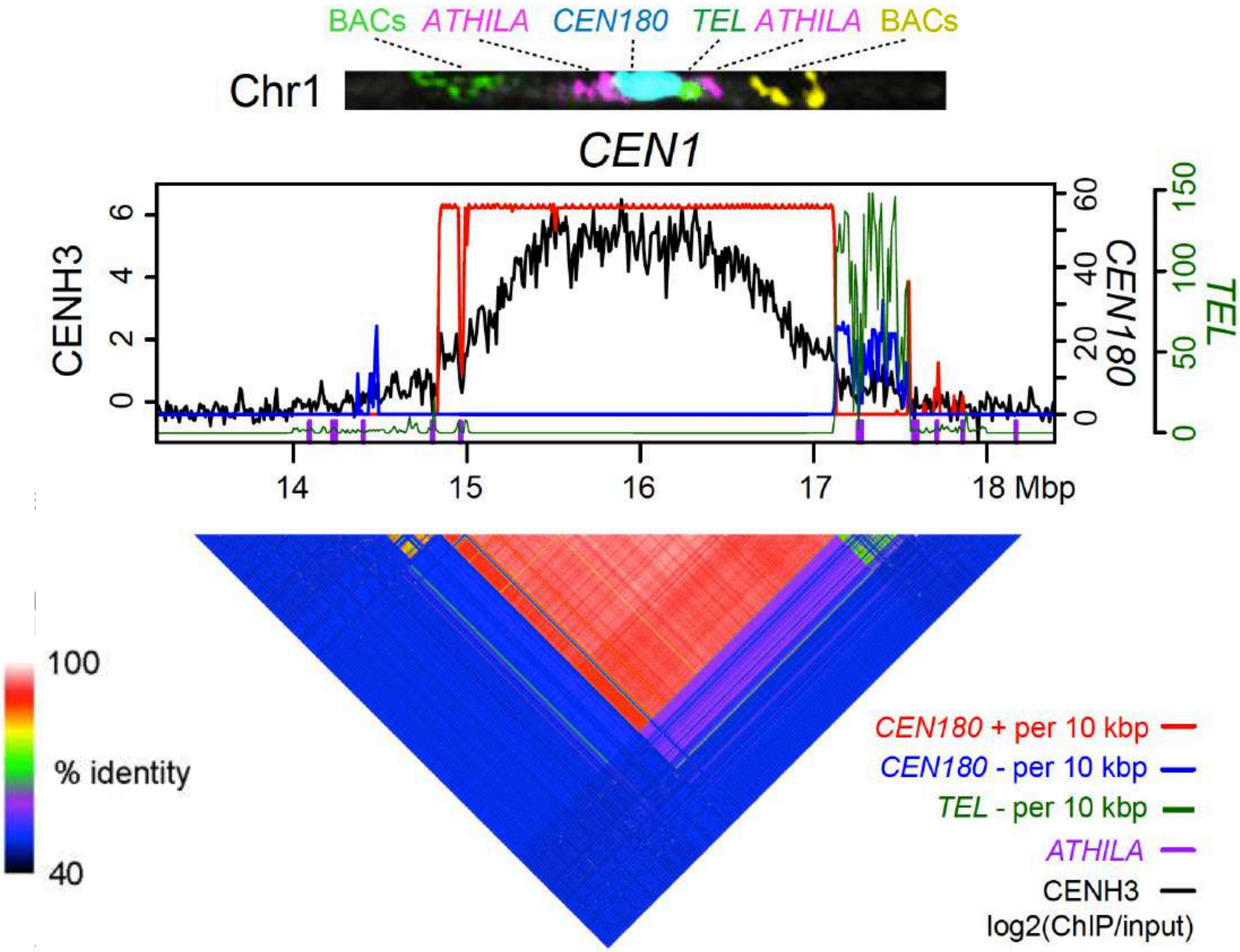
Long read DNA sequencing

Oxford Nanopore Technologies
>100 kb
95-99% accuracy
Methyl-detection



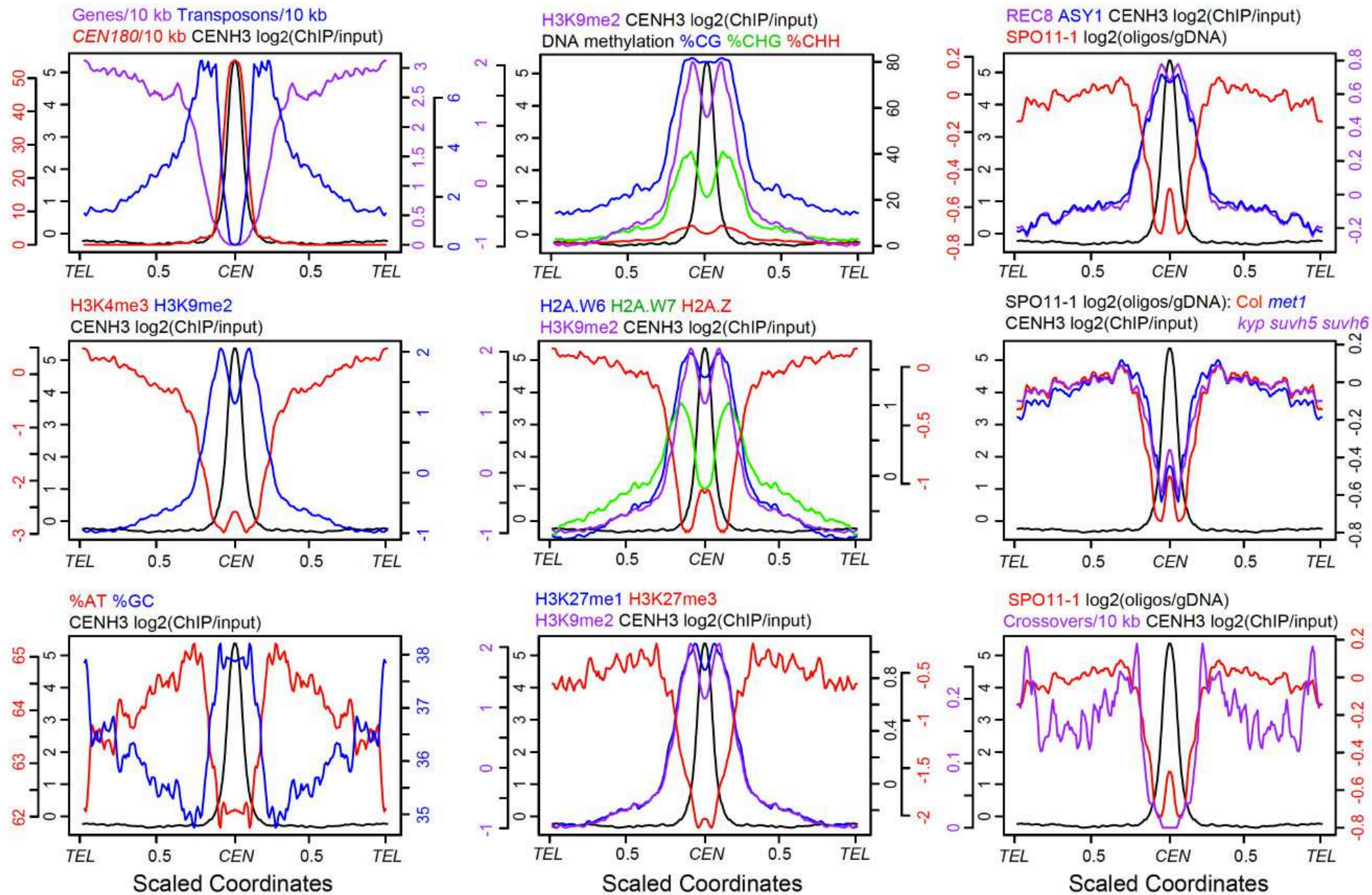
Pacific Biosystems
HiFi CCS
~15 kbp
>99% accuracy

Centromeres are massive tandem arrays of *CEN180* repeats that support CENH3



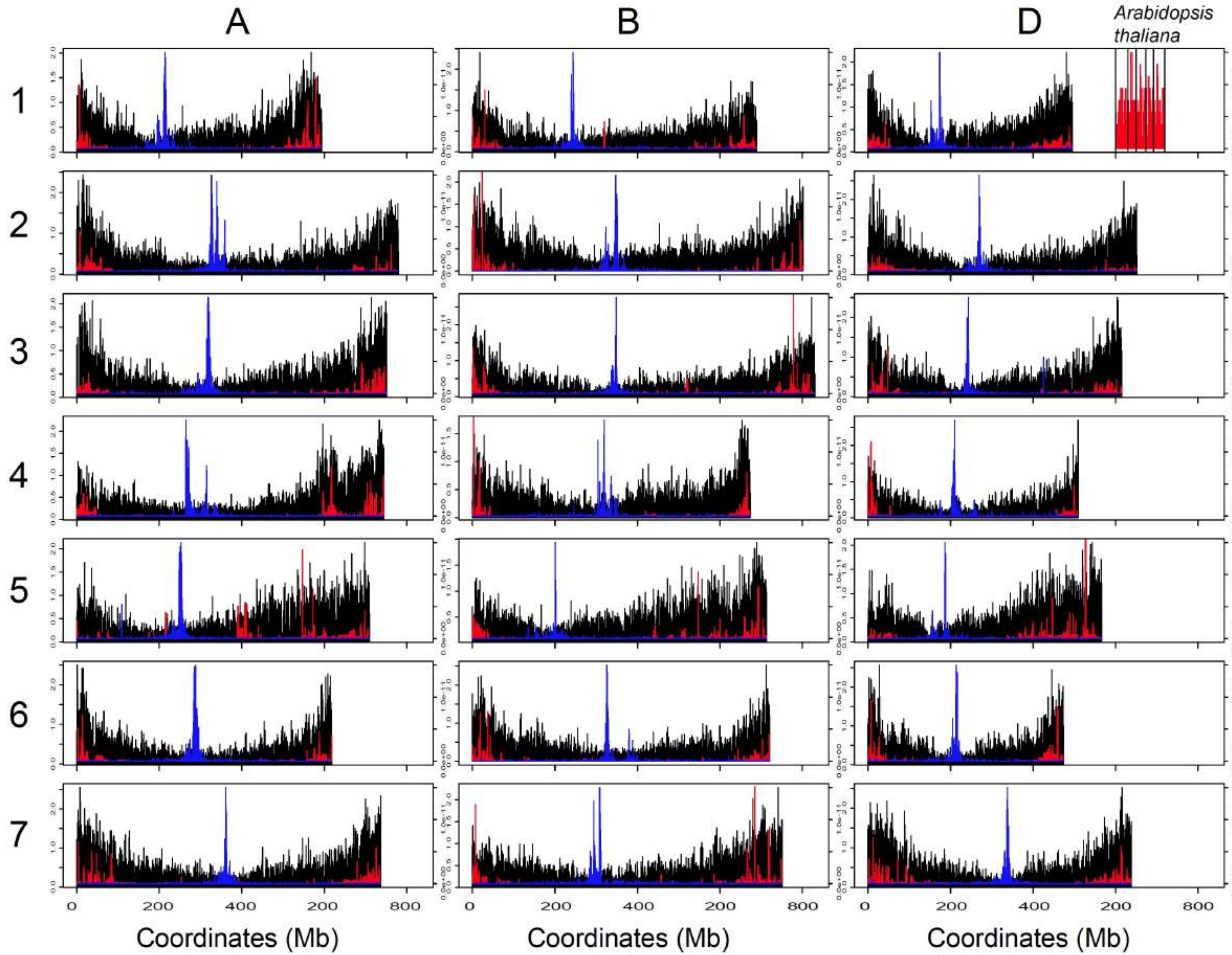
CENH3 ChIP-seq data - Maheshwari et al *Genome Res*

Genetic and epigenetic landscape of the centromeres



Centromeric chromatin is distinguished from pericentromeric heterochromatin

Recombination gradients in the wheat genome



H3K4me3:H3K9me2
Gypsy LTR Cereba
cM/Mb

BBSRC sLola

Questions:

1. The wheat genome is highly polarized in terms of recombination (crossover), DMC1 and ASY1

2. DMC1 and ASY1 hotspots are widespread

3. The polycomb mark H3K27me3 distinguishes regions of high crossover activity

4. Recombination correlates with gene diversity, signatures of selection and annotation

5. Arabidopsis may not be an adequate model for the wheat genome!

Acknowledgements

Lab members
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