

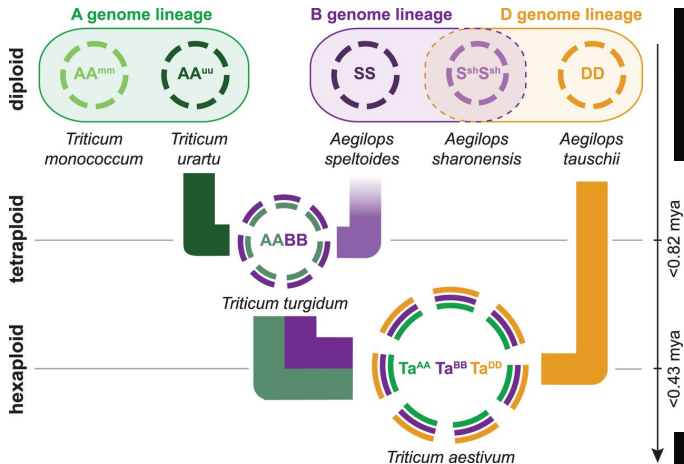
Conservation and rearrangement: gene order in peri-centromeric regions of Triticeae genomes

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IPK Gatersleben

April 13th, 2016

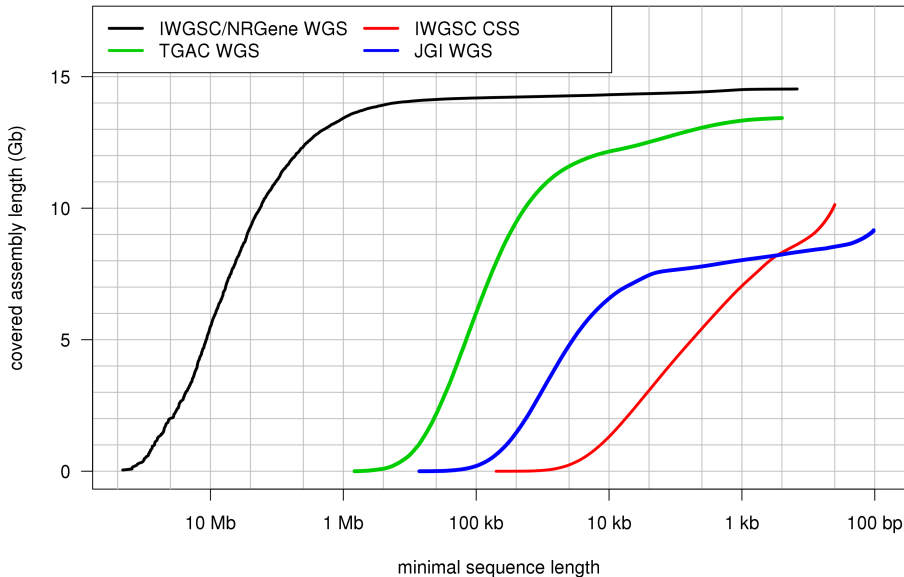
The polyploid wheat genome



IWGSC, Science, 2014

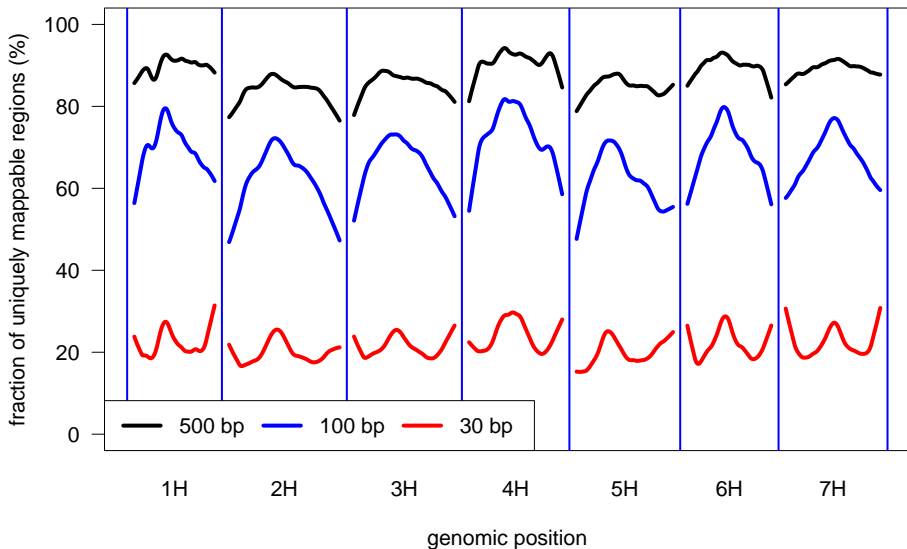
- ▶ Genome size: ~ 15 - 17 Gb, 3 × 7 pairs of chromosomes

Excellent contiguity and genome representation



Longer read lengths improve assembly completeness

Uniquely mappable regions as a function of k-mer/read length

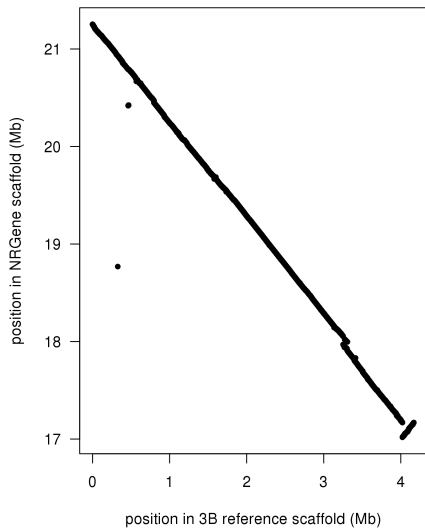


Two wheat assemblies

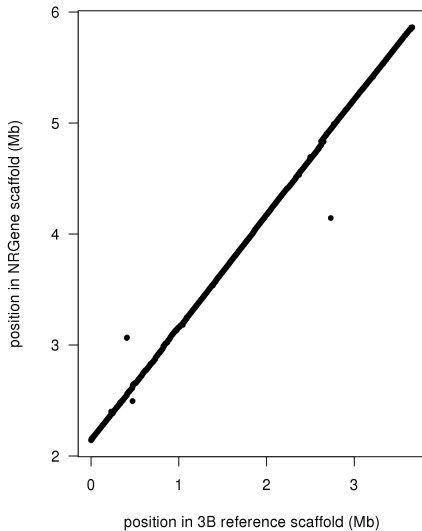
	Bread wheat	Wild emmer
ploidy	6x (AABBDD)	4x (AABB)
genome size	~ 15 – 17 Gb	~ 10 – 12 Gb
assembly size	14.5 Gb	10.5 Gb
N50	548 (7.4 Mb)	415 (7.0 Mb)
N90	2,276 (1.3 Mb)	1,828 (1.2 Mb)
genetically anchored	14.0 Gb (96.5 %)	10.1 Gb (95.6 %)

Alignment of the BAC-based reference of 3B

v443_0936 (4.2 Mb) vs. scaffold16560-2 (22.6 Mb)

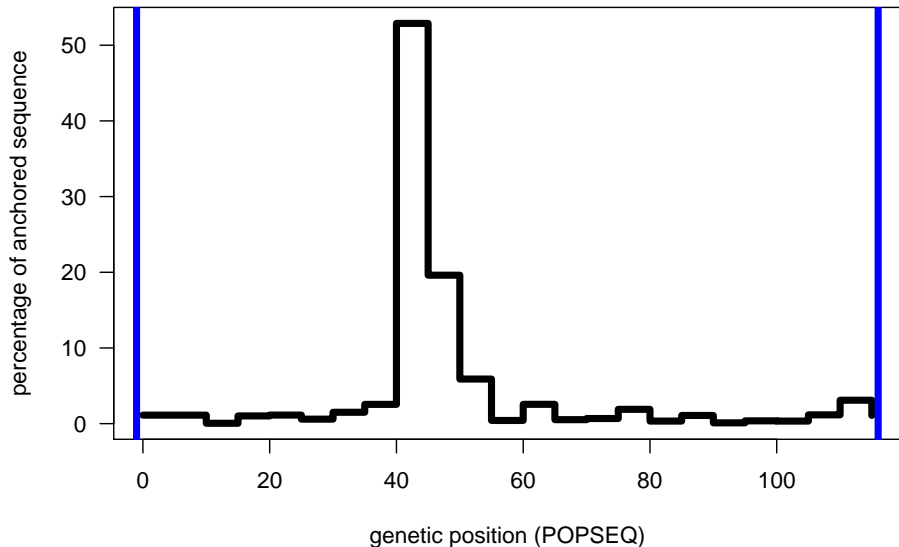


v443_0903 (3.7 Mb) vs. scaffold123840 (10.1 Mb)



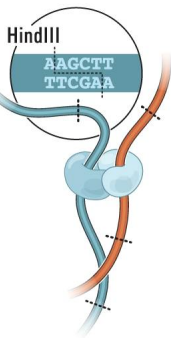
POPSEQ cannot order contigs in peri-centromeric regions

Anchored sequence along the genetic map

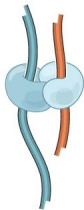


HiC: chromosome conformation capture sequencing

Crosslink DNA



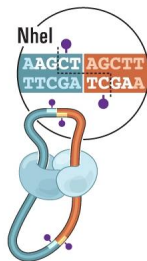
Cut with restriction enzyme



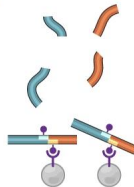
Fill ends and mark with biotin



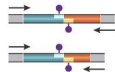
Ligate



Purify and shear DNA; pull down biotin

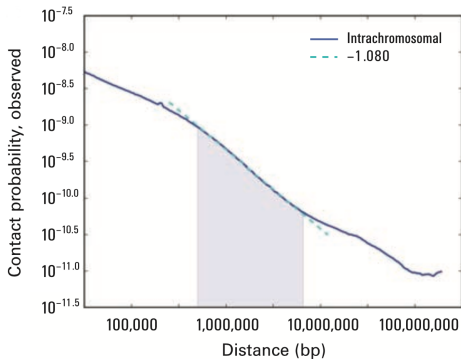


Sequence using paired-ends



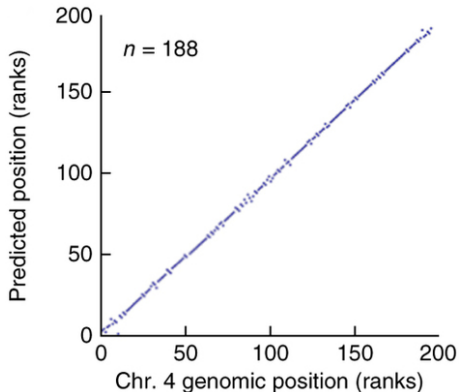
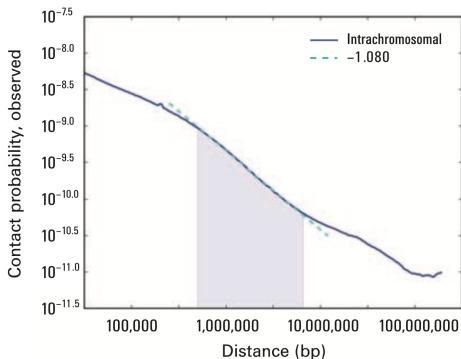
Lieberman-Aiden *et al.*, 2009

Mapping the linear genome with 3D contact matrices



Lieberman-Aiden *et al.*, 2009; Kaplan and Dekker, 2013

Mapping the linear genome with 3D contact matrices

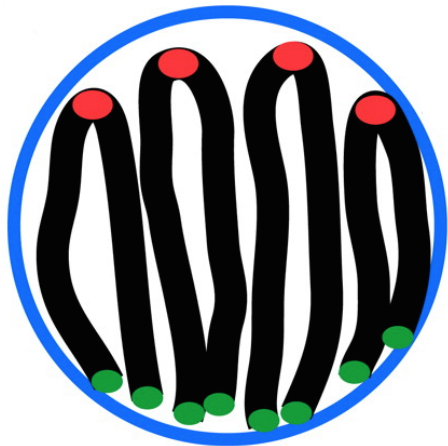


Lieberman-Aiden *et al.*, 2009; Kaplan and Dekker, 2013

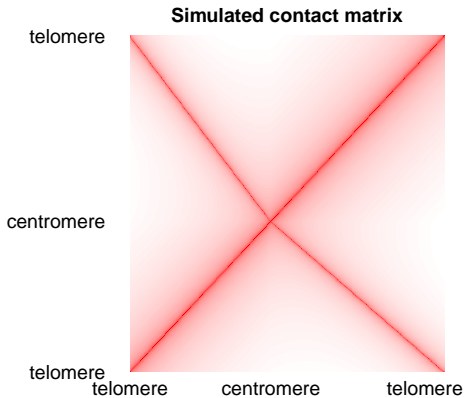
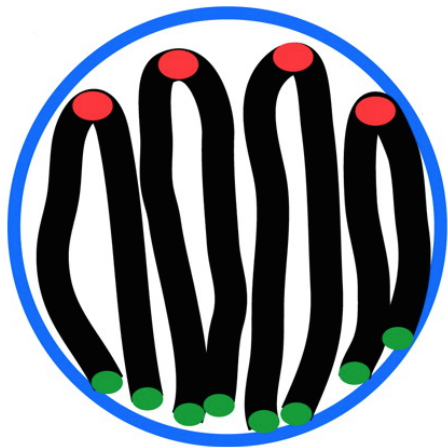
HiC maps of bread wheat and emmer

	Bread wheat	Wild emmer
assembly size	14.5 Gb	10.5 Gb
# HiC links	3.7 M	6.5 M
ordered by HiC	14.0 Gb (96.3 %)	10.1 Gb (96.0 %)
oriented by HiC	–	9.7 Gb (92.5 %)
# scaffolds per chr.	177	199

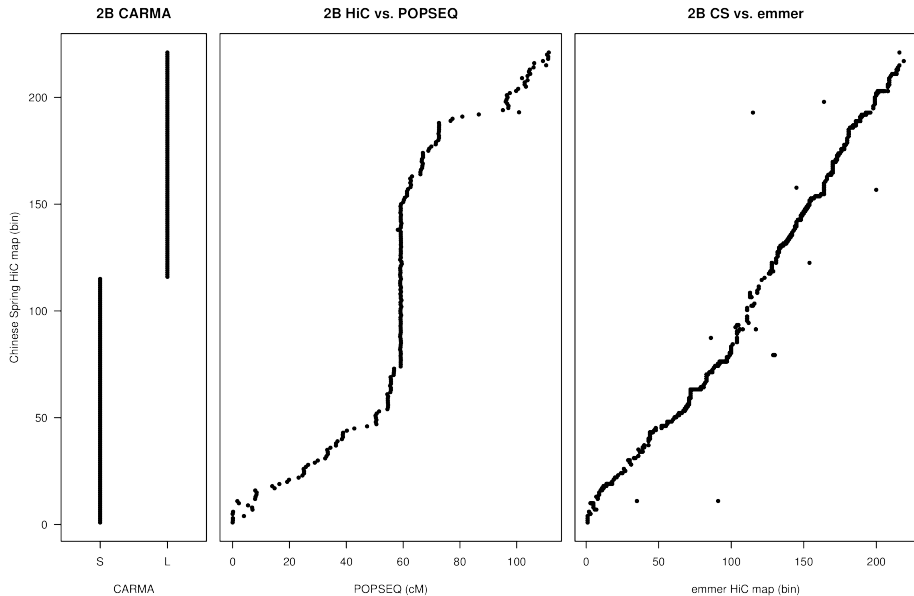
Rabl configuration of interphase nuclei



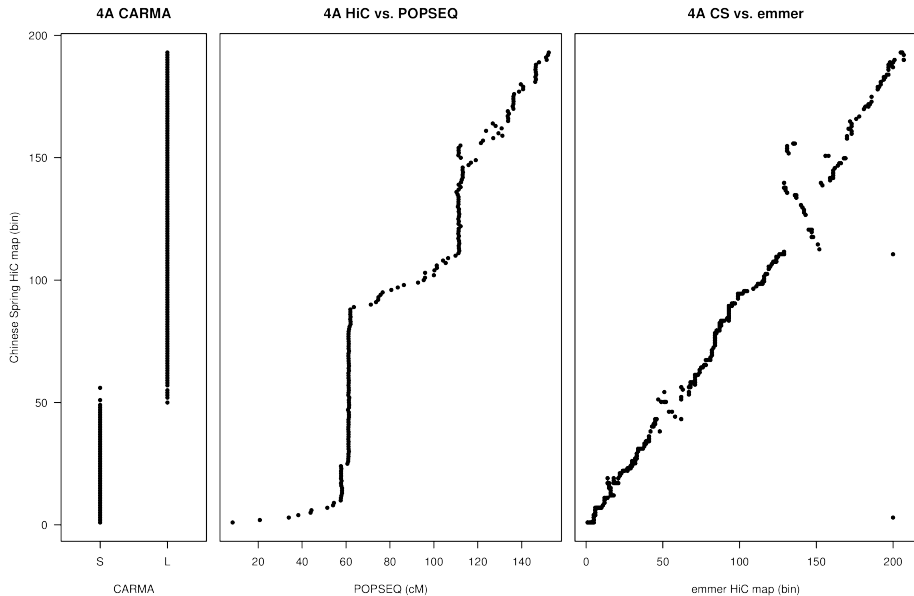
Rabl configuration of interphase nuclei



Colinearity of the HiC maps of bread wheat and emmer

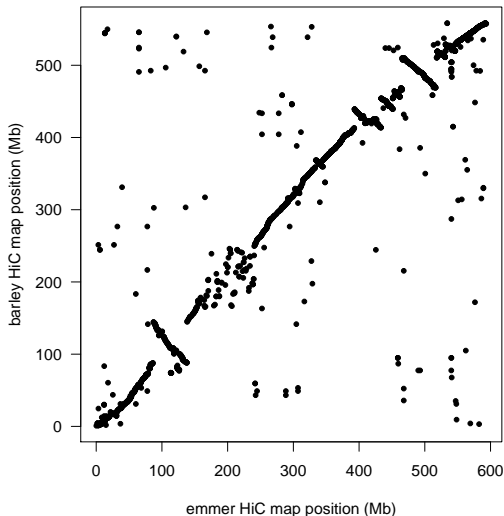


Large inversions and reduced recombination

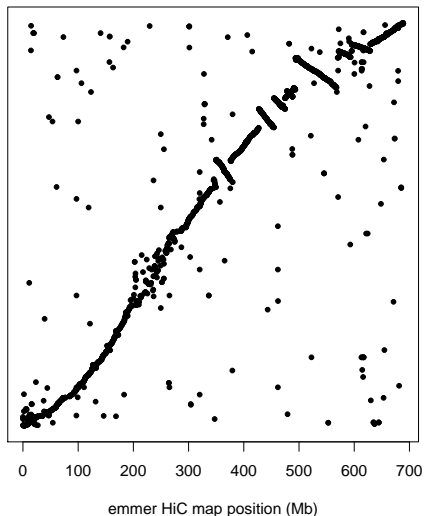


Centromeric rearrangements between wheat and barley

emmer 1A vs. barley 1H



emmer 1B vs. barley 1H



- ▶ Improved HiC map of bread wheat and construction of pseudomolecules
- ▶ NRGene assembly and HiC map of durum wheat
- ▶ HiC maps for other wheat varieties to find large structural variants (inversions, deletions, insertions)

Bread wheat assembly team

- ▶ Curtis Pozniak, Andy Sharpe, University of Saskatoon
- ▶ Jesse Poland, Kansas State University
- ▶ Assaf Distelfeld, Tel Aviv University
- ▶ Gil Ronen, Omer Barad, Kobi Baruch, NRGene
- ▶ Mike Thompson, Illumina
- ▶ Fred Choulet, INRA
- ▶ Jane Rogers, Kellye Eversole, IWGSC
- ▶ Nils Stein, Axel Himmelbach, Ines Walde, IPK Gatersleben

Wild Emmer Wheat Sequencing consortium (WEWseq)

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Tzion Fahima
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Abraham Korol

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Klaus Mayer
Mark Mikel

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Zvi Peleg
Curtis Pozniak
Silvio Savi
Ines Walde



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Roberto Tuberosa
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Daniel Chamovitz



IDT