IWGSC-WHOLE GENOME SHOTGUN ASSEMBLY OF CHINESE SPRING


Crop Development Centre Durum Wheat Breeding and Genetics Program

UNIVERSITY OF SASKATCHEWAN
Crop Development Centre
COLLEGE OF AGRICULTURE AND BIORESOURCES
AGBIO.USASK.CA

I W G S C

Dr. Curtis Pozniak

IWGSC Workshop,
PAG Jan 2016

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PotashCorp - a Founding Partner

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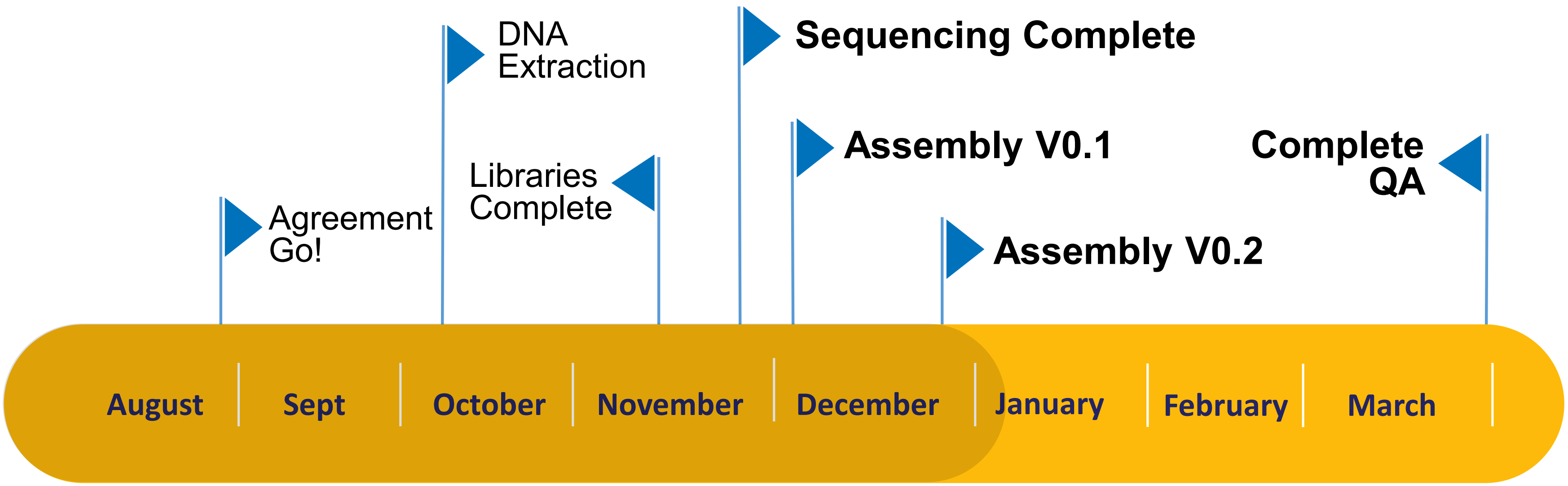
IWGSC

IWGS-Whole Genome Assembly Project

De novo assembly using **Illumnia** generated (200X) PE and MP data and **NRGene** Assembly pipline.



illumina DeNovoMAGIC™

NRGene illumina IPK GATERSLEBEN UNIVERSITY OF SASKATCHEWAN K-STATE Kansas State University TEL AVIV UNIVERSITY

IWGSC-WGA v0.2 Metrics

Total No. Scaffolds	138,484
Assembly size:	14.5 Gb
Gaps size:	262 Mb
Gaps:	1.8 %
L_{50}:	**7.1 Mb**
N_{50} (#sequences):	**566**
L_{90}:	1.26 Mb
N_{90} (#sequences):	2,363
Max size	46 Mb

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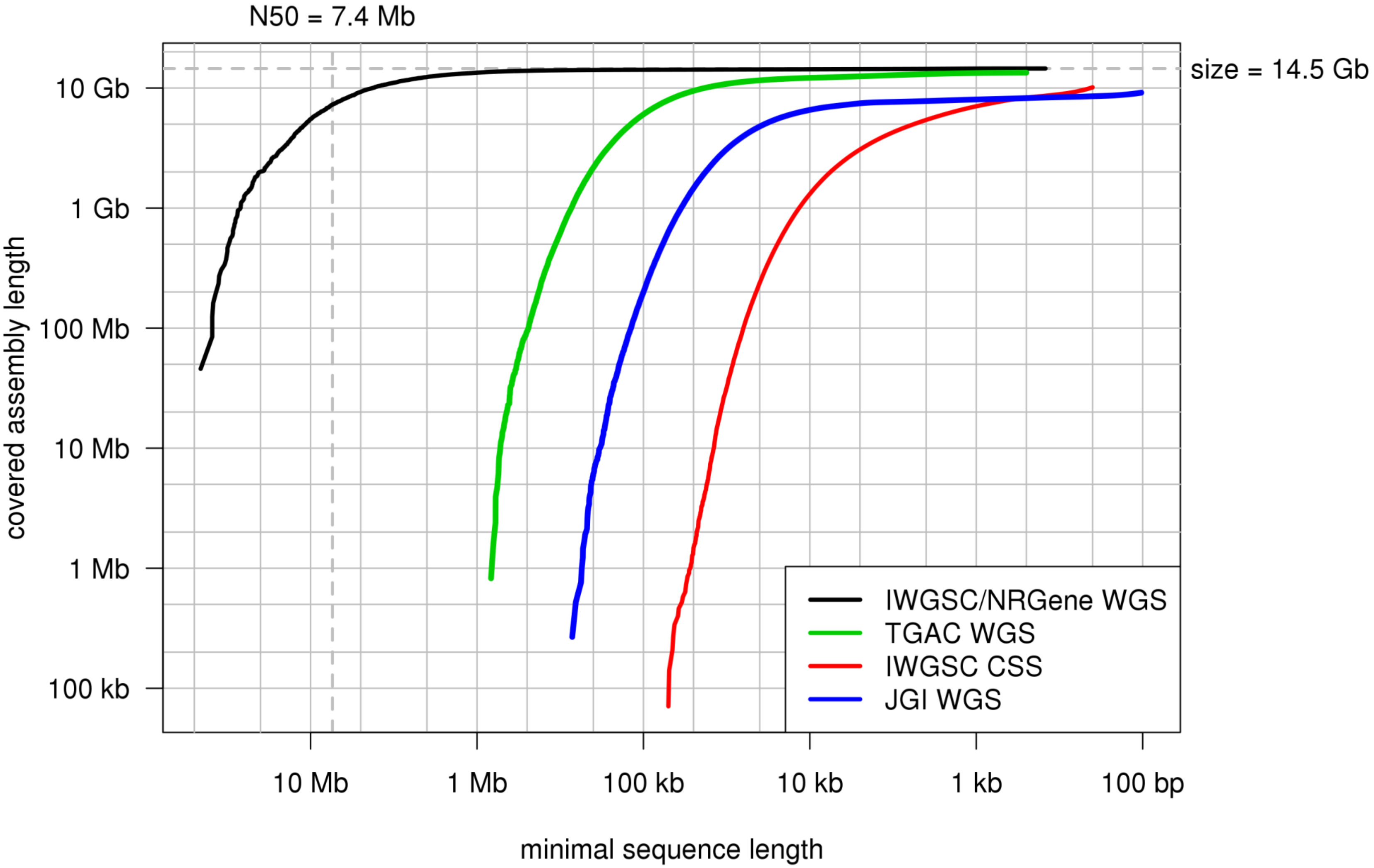
Assembly Comparisons



Preliminary QC of IWGS-WGA

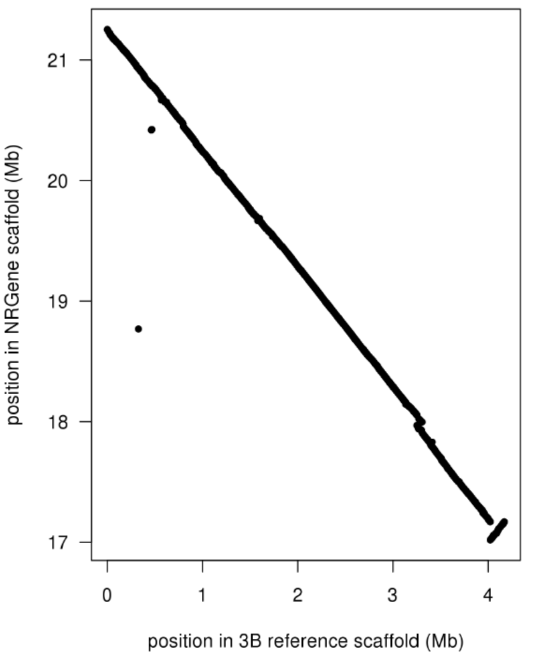
Martin Mascher,
IPK Gatersleben

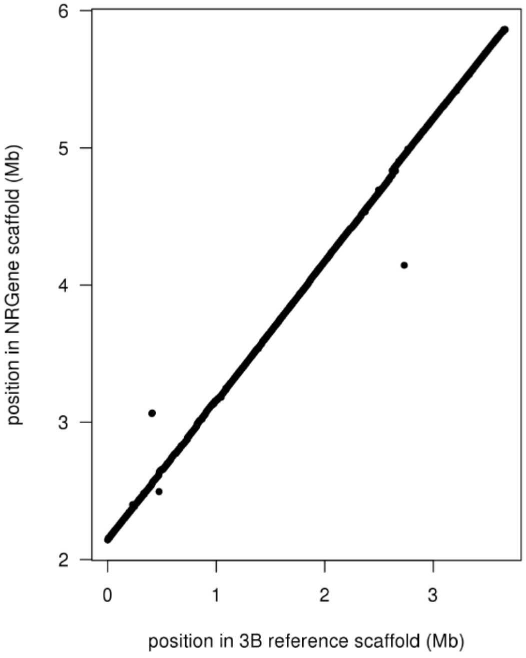
- Alignment to MTP-based assemblies
- Alignment to physical maps
- Genic/Intergenic space
- Anchoring of assembly

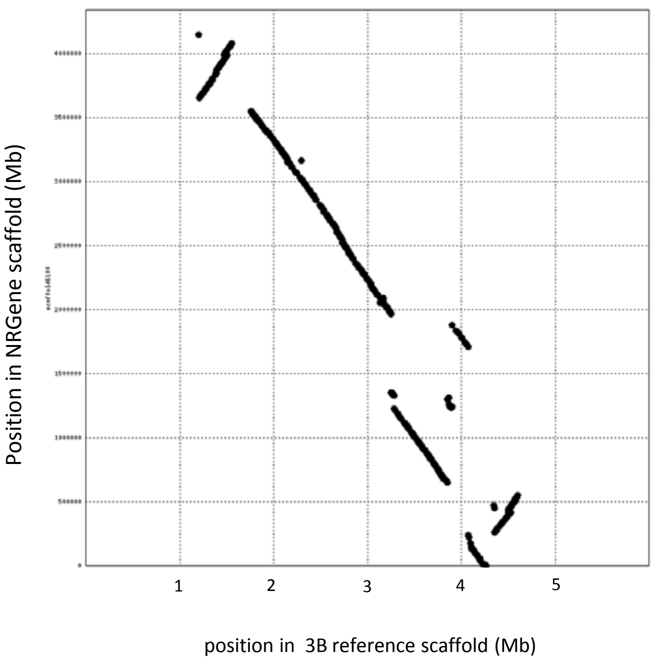
Fred Choulet
INRA Clermont

Alignment to MTP-based Assemblies

>95% of the 3B Pseudomolecule is present in the IWGSC-WGA


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

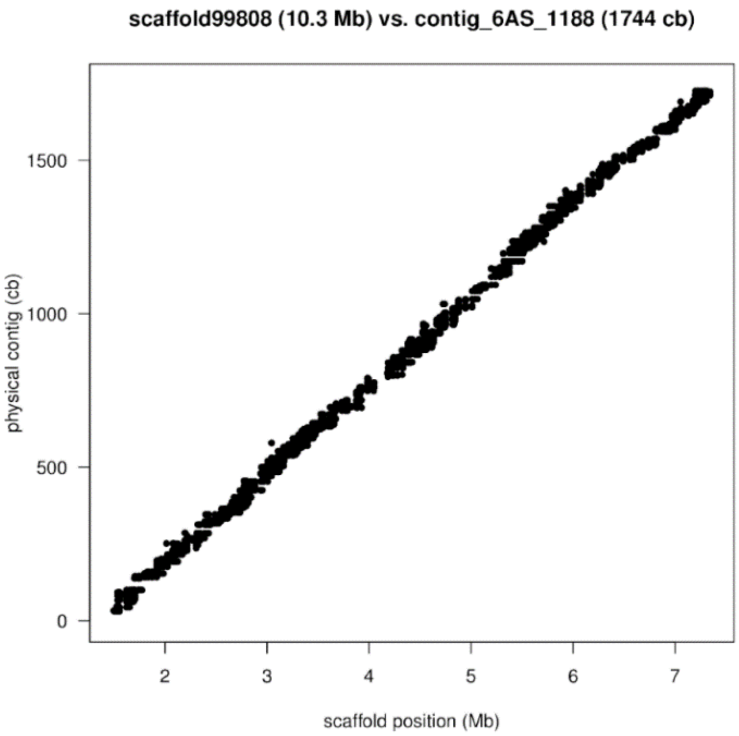

v443_0903 (3.7 Mb) vs. scaffold123840 (10.1 Mb)

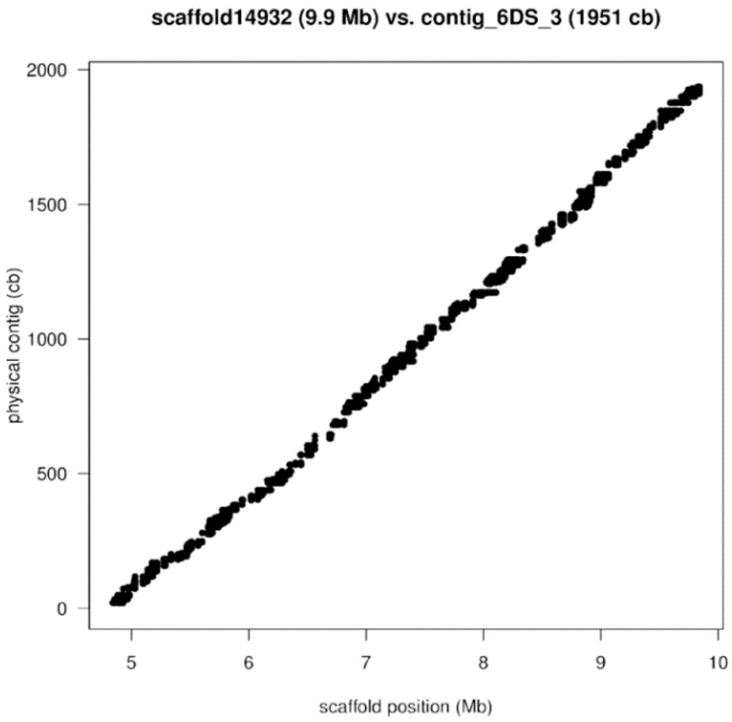

SSt1 ta3B Interval (4 Mb)

IWGSC

Comparison of Physical Maps to CS-WGS Assembly

Mapping of whole genome profiling tags of LTC-derived physical maps to IWGSC-WGA reveals near perfect colinearity


scaffold99808 (10.3 Mb) vs. contig_6AS_1188 (1744 cb)


scaffold14932 (9.9 Mb) vs. contig_6DS_3 (1951 cb)

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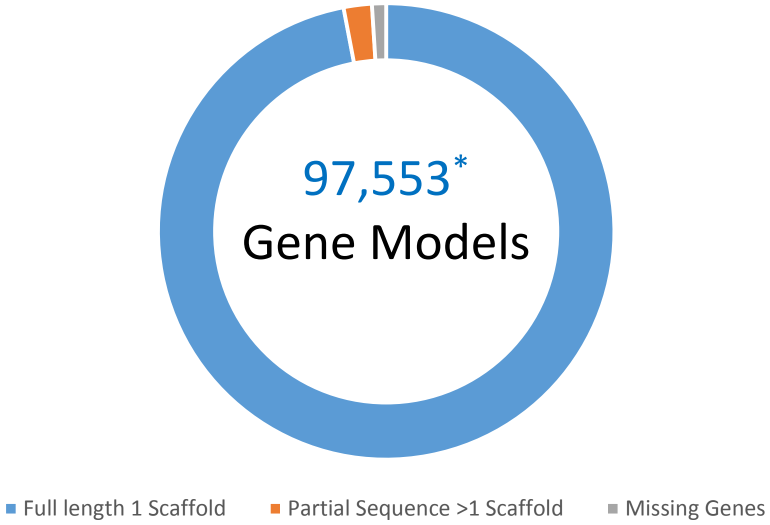
Analysis of Genic / Intergenic Space

>97% of the CSS coding exons are present on a single scaffold

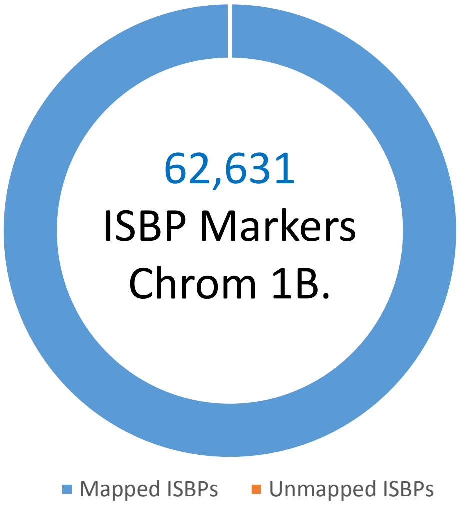
>98% of ISBP markers map to the IWGSC-WGA

IWGSC-CSS Gene Models



**99% identity, 90% coverage*

TE junction-based markers



4315 scaffolds (14.0 Gb) with 1 + CSS genes

3197 scaffolds (13.6 Gb) with 3 + CSS genes

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Anchoring of IWGSC-WGA

High density marker data allows anchoring of 14.0 Gb to genetic maps

Source	No. markers	% Mapped
CSS Survey Sequence	(337,000 contigs)	99.3%
Cs x Re	272,218	92.1%
Syn x Opata	(437,973 contigs*)	98.3%
90K iSelect	81,987	97.6%
U of Bristol Axiom**	819,572	98.1%

>14.1 Gb (**96.5 %**) assigned to chromosome arms

>431,617 anchored scaffolds map to Syn x Opata

*Number of JGI Contigs anchored to Syn x Opata genetic map
** U of Bristol WISP Project (www.cerealsdb.uk.net)

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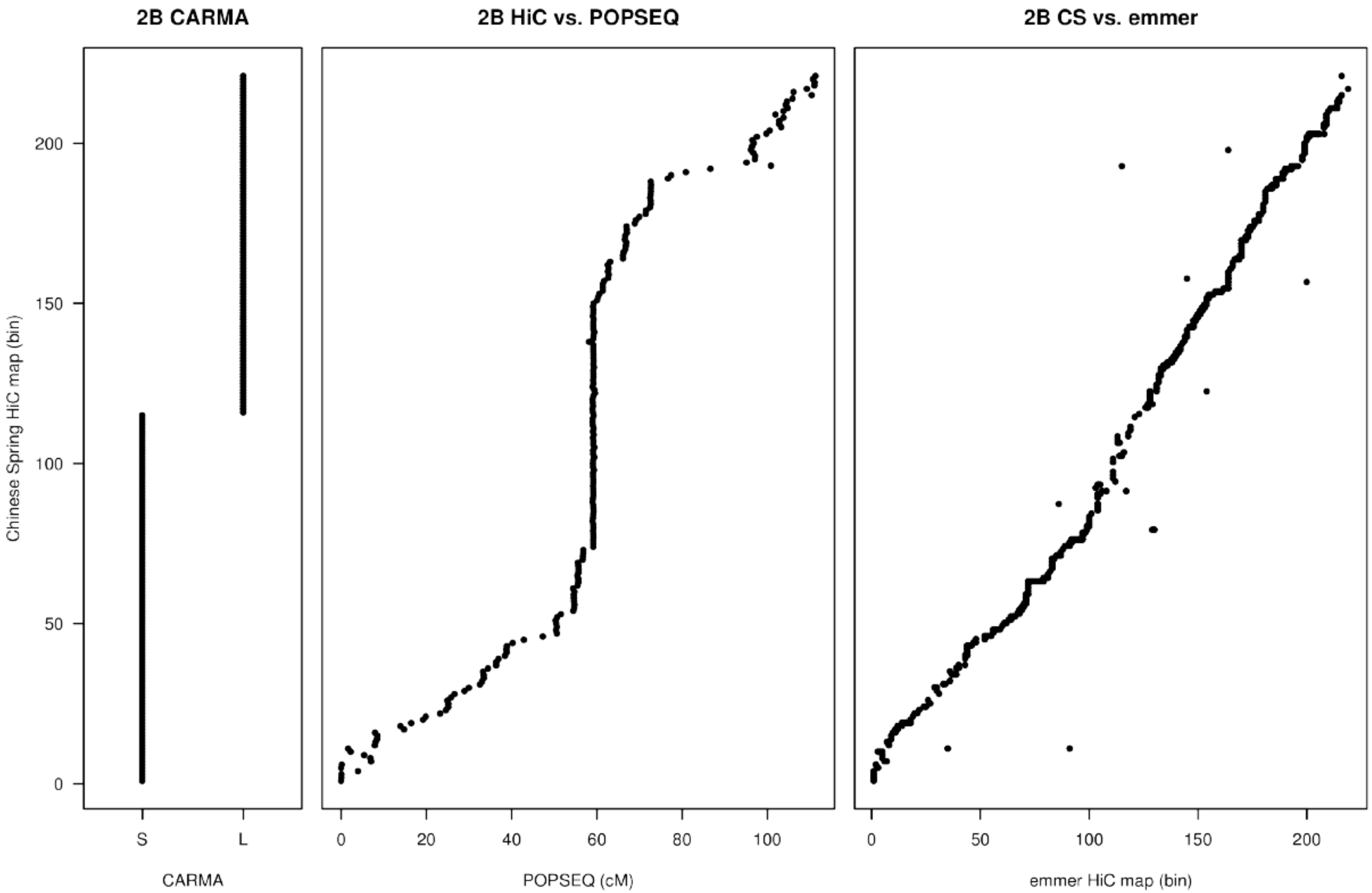
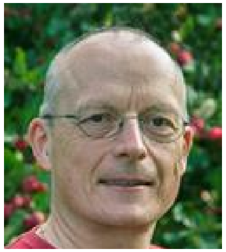
Chromosome arm assignment and Hi-C



IPK GATERSLEBEN


Nils Stein


Axl Himmelbach


Ines Walde


Martin Mascher

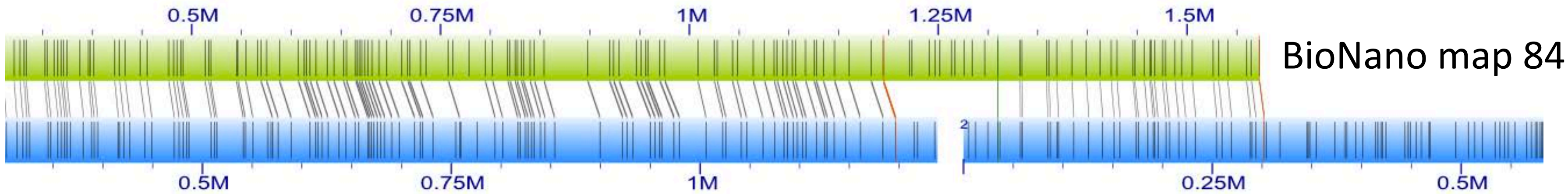
With support from

Federal Ministry
of Food
and Agriculture

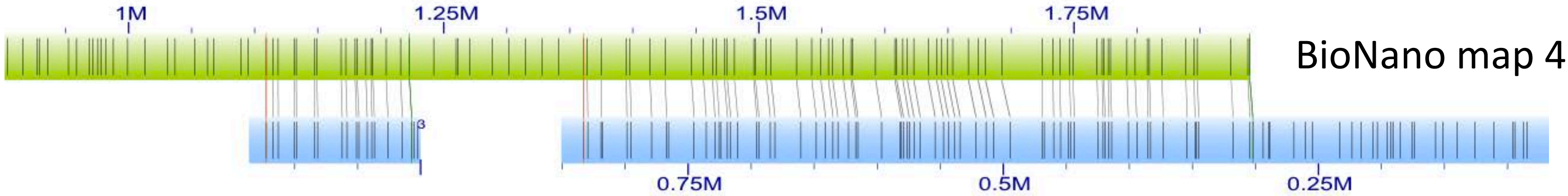
by decision of the
German Bundestag

Optical Mapping

Bionano single molecule maps of chrom. 7A confirm assembly order and allow super-scaffolding of IWGSC-WGA



BioNano map 84



BioNano map 49

Analysis courtesy of Rudi Appels and Gabriel Keeble

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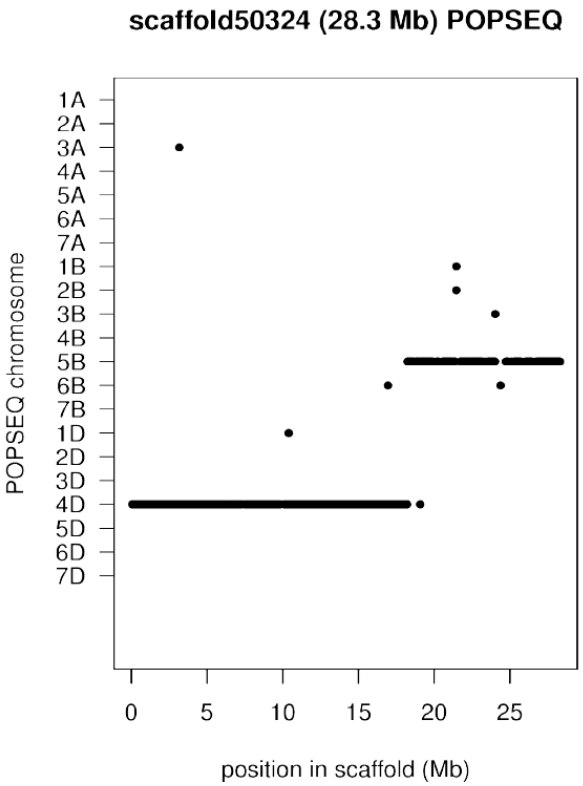
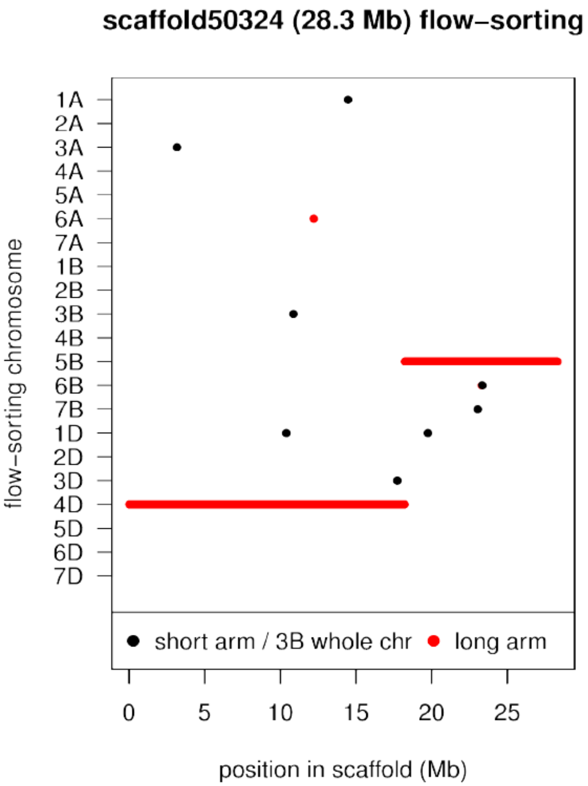
Evidence for Chimeric Assemblies

Approx. 5 % scaffolds >1 Mb are putative chimeras



scaffold50324 (28.3 Mb) POPSEQ

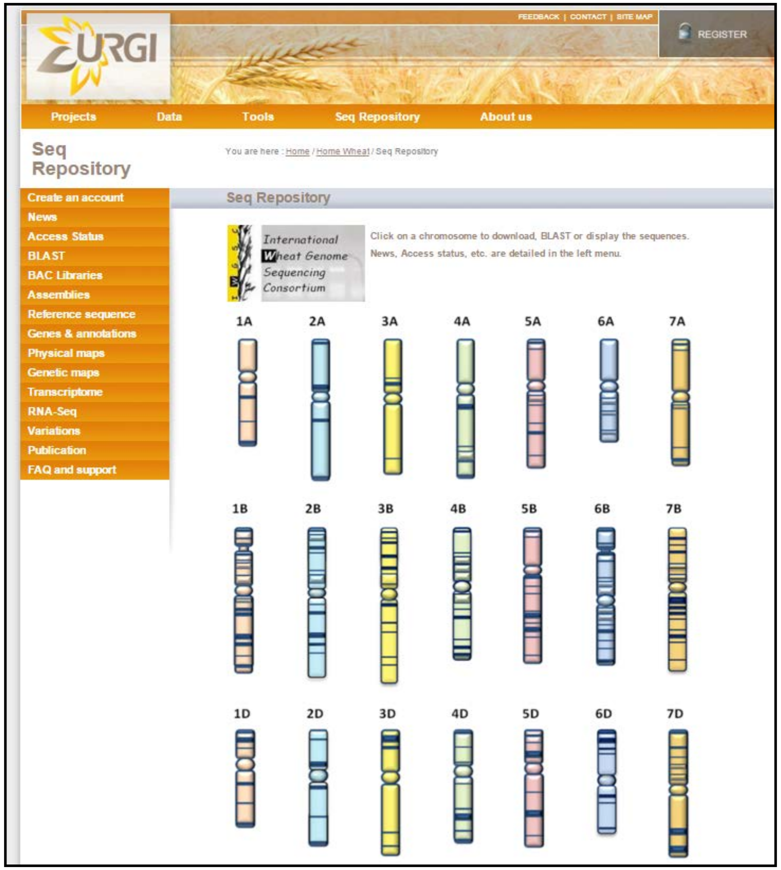


scaffold50324 (28.3 Mb) flow–sorting

IWGSC Whole Genome Assembly Data Release

Initial QA suggests that the IWGSC-WGA is impressively complete

IWGSC Data Repository hosted by INRA-URGI
http://wheat-urgi.versailles.inra.fr/Seq-Repository



Seq Repository

You are here : Home / Home Wheat / Seq Repository

Seq Repository

Click on a chromosome to download, BLAST or display the sequences.
News, Access status, etc. are detailed in the left menu.

After QC, IWGSC-WGA will be released under **Toronto agreement** through the IWGSC sequence repository

April 2016

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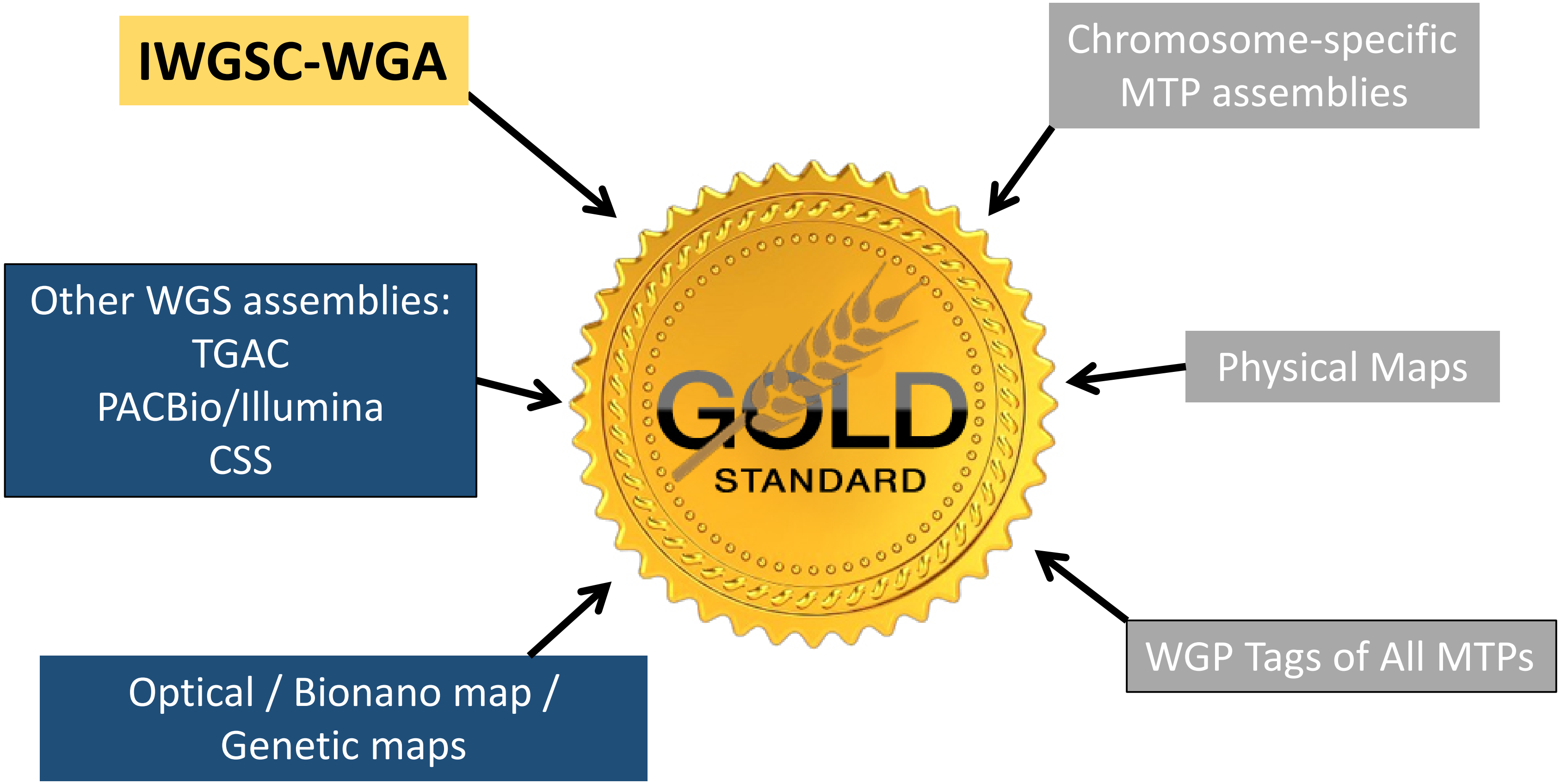
A Path Forward: Integration of all Resources

A Complete Wheat Genome Sequence by 2017



IWGSC-WGA

Chromosome-specific
MTP assemblies

Other WGS assemblies:
TGAC
PACBio/Illumina
CSS

Physical Maps

WGP Tags of All MTPs

Optical / Bionano map /
Genetic maps

Discussion initiated and ongoing!

Thanks to Our Funders!

CTAG²
Canadian Triticum Applied Genomics

NSF

USDA

GenomeCanada

GenomePrairie

Federal Office for
Agriculture and Food

SaskWheat
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