Bread wheat chromosome 7B:
genome assembly and transcript mapping

S. R. Sandve, B. Zhan, T. Belova , M.Kent , S. Lien, M. Lillemo , M. Alsheik, O.-A. Olsen

Norwegian University of Life Science & Graminor AS

H. Simkova, M. Kubalaskova, J. Dolezel. –
Lab of Molecular Cytogen. and Cytometry, Czech Republic.

F. Cattonaro , Instituto di Genomica Applicata and IGA Technology Services, Italy.

S. Kianian, A. Kumar- N. Dakota State Uni, Dept of Plant Sciences,Fargo, USA.

A. Korol, V. Frenkel University of Haifa, Israel.

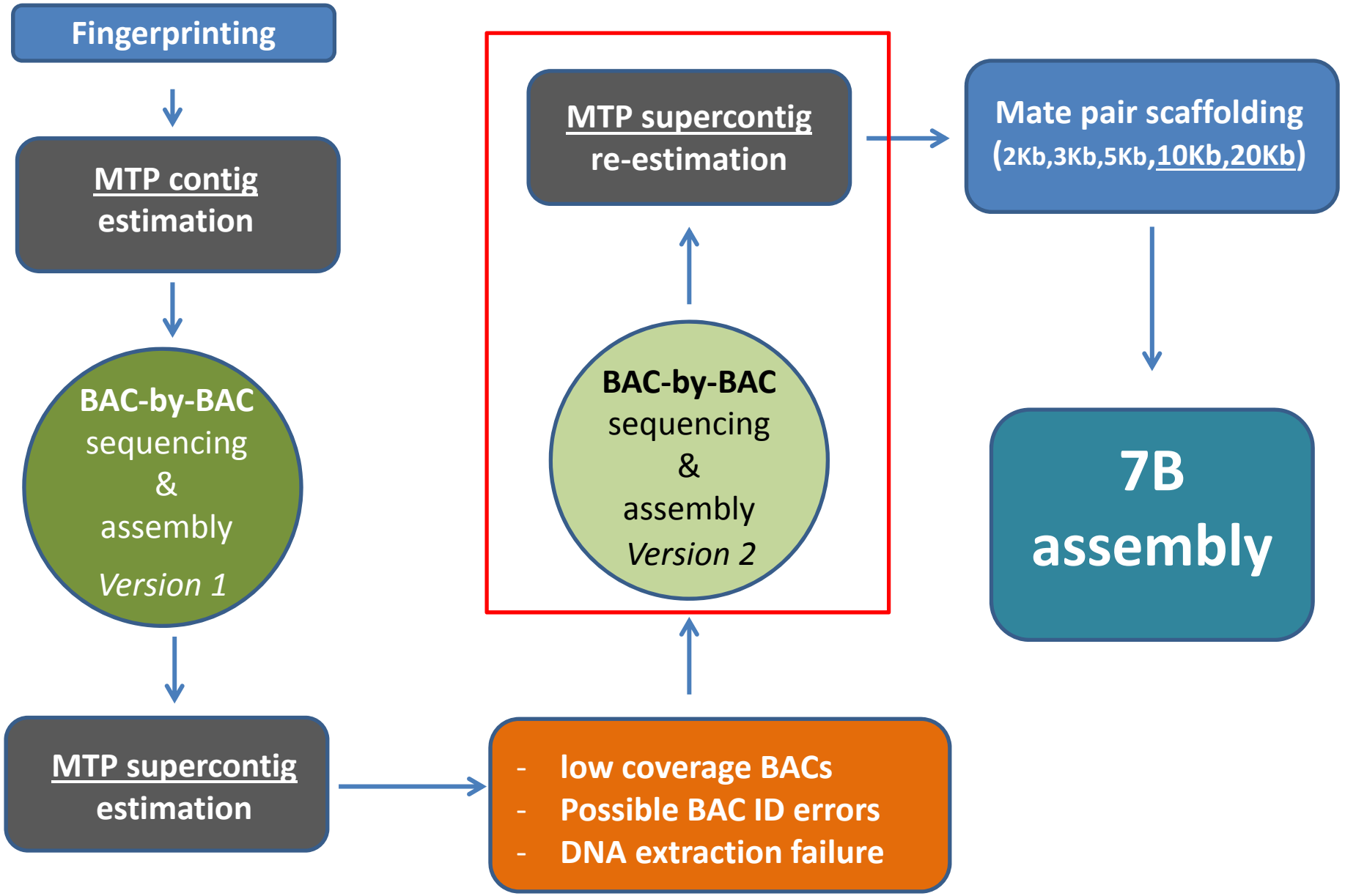
K. Mayer, M. Pfeifer, K. Kugler MIPS, Germany.

J. Hu, L. Li, J. Min, J. Chen, Y. Yang, X. Xu, Beijing Genomics Institute, China.

Outline

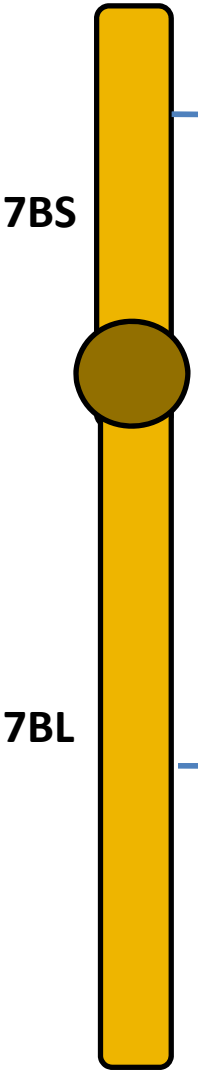
- Sequencing strategy update
- An improved Minimal Tiling Path
- 7B sequencing progress
- Progress on anchoring MTP to genetic and physical maps
- Transcriptome analyses

7B sequencing work-flow



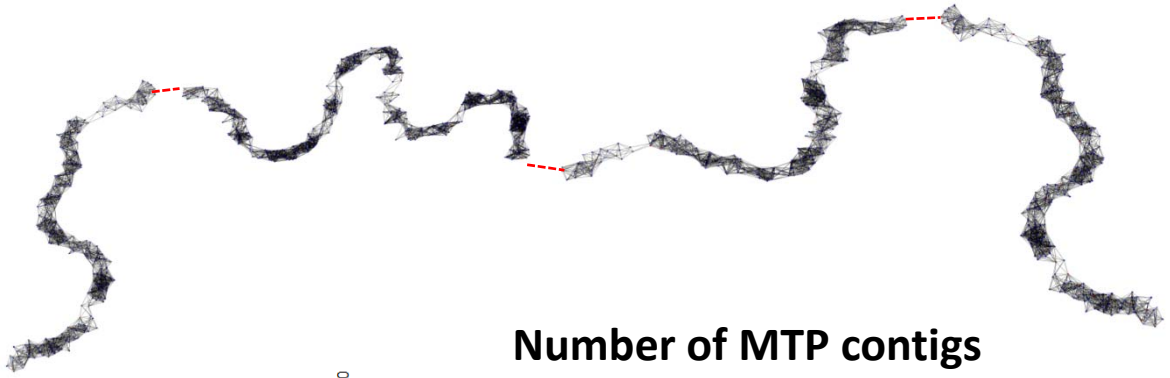
Improved 7B Minimum Tiling Path

Physical mapping

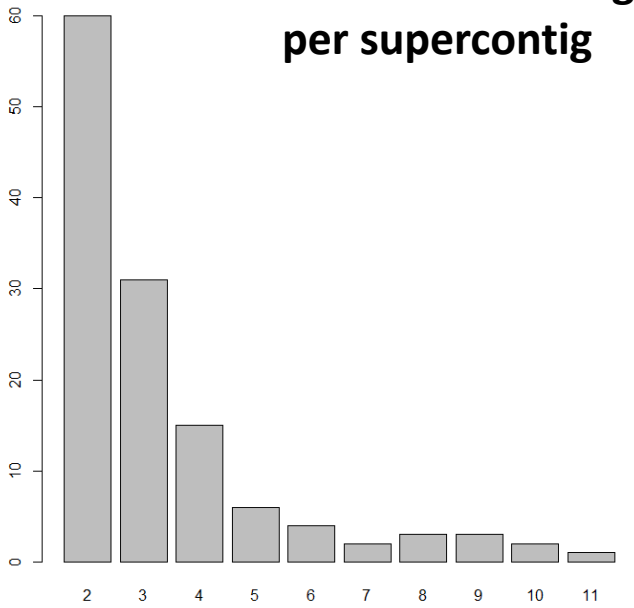


MTP BAC's: **3039**
BAC size: **185Kb**
MTP contigs: **255**
MTP supercontigs: 104

MTP BAC's: **5529**
BAC size: **150Kb**
MTP contigs: **286**
MTP supercontigs: 143



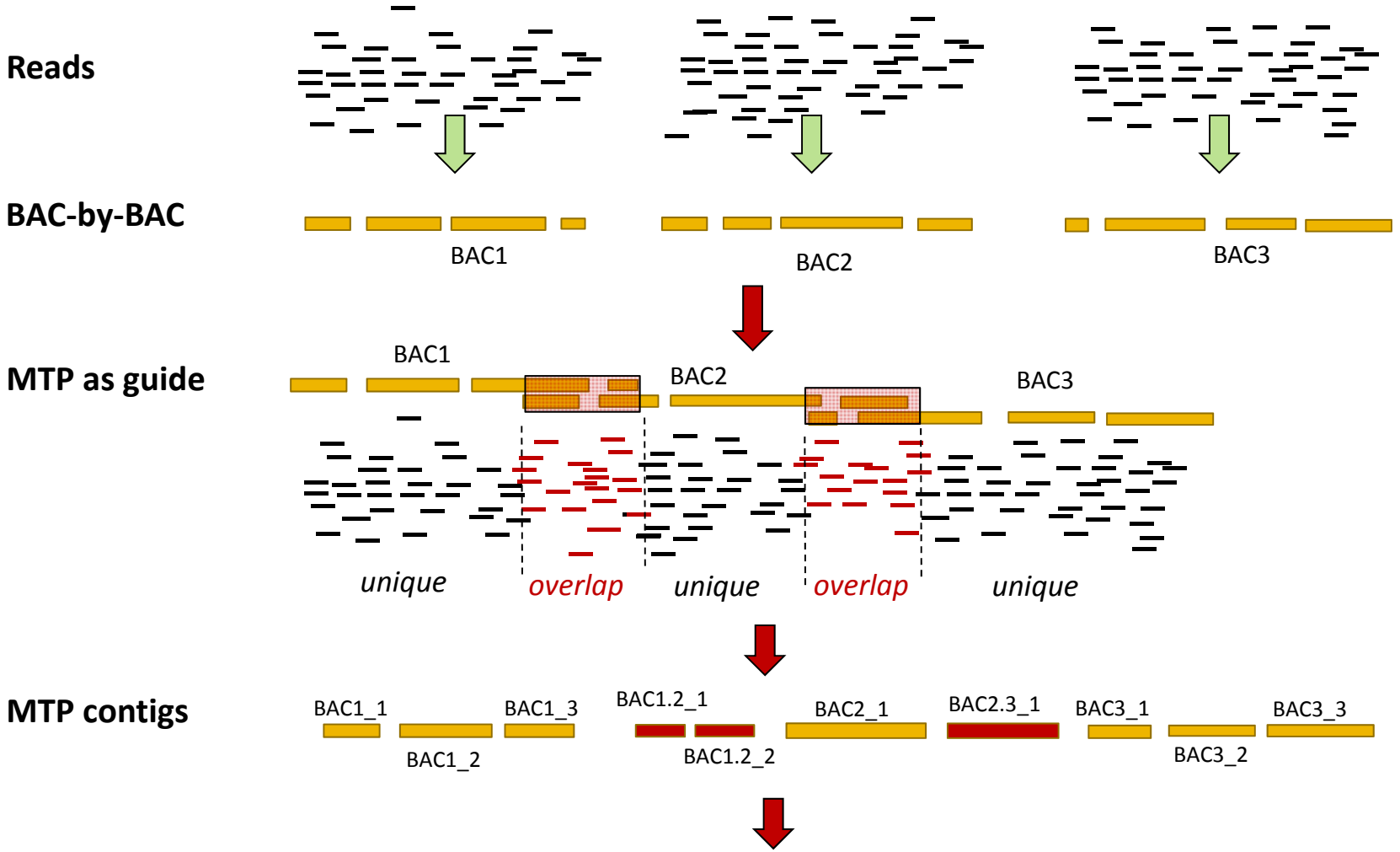
Number of MTP contigs per supercontig



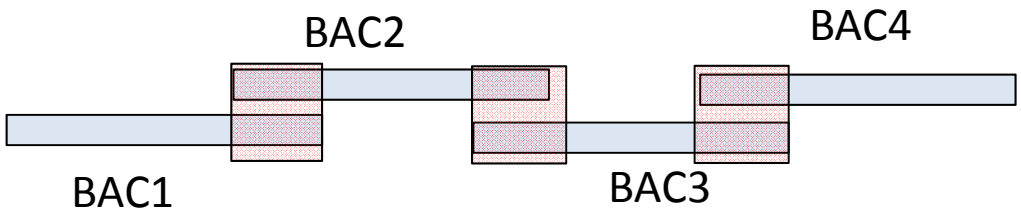
- 127 supercontigs > 1 MTP contig

Korol, Frenkel, Uni. Haifa

MTP-based assembly strategy



Expected overlap size in BAC-MTP sequence assembly

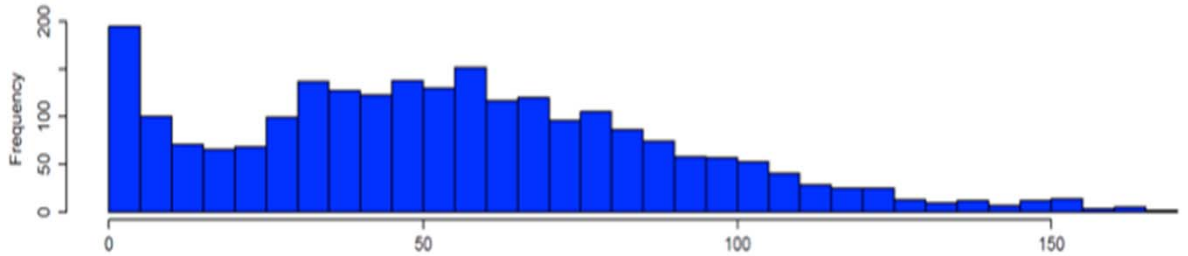


~30% overlap

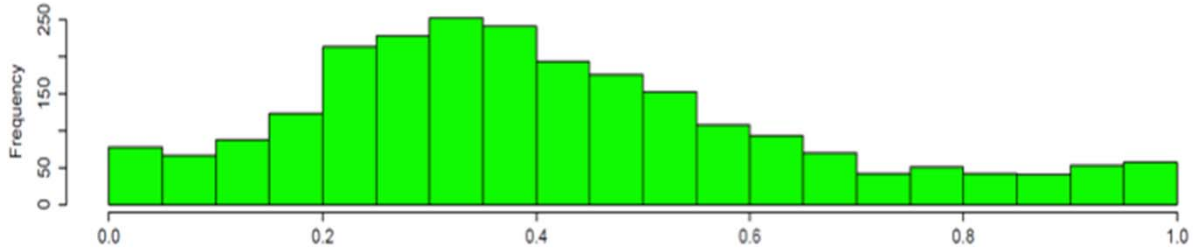
Low coverage (20%) or error

Expected

Redundancy



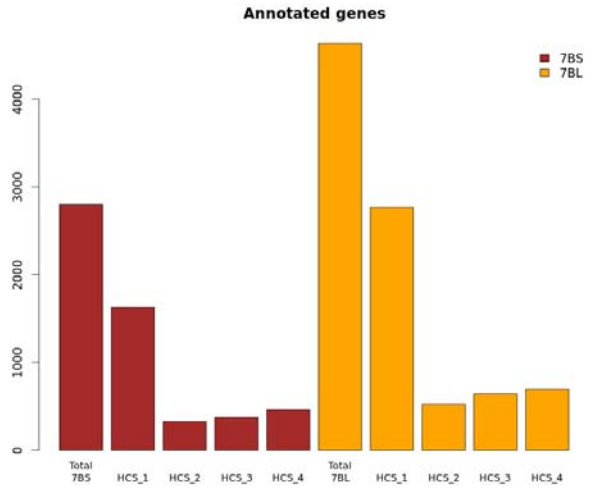
Overlap assembly size (Kb)



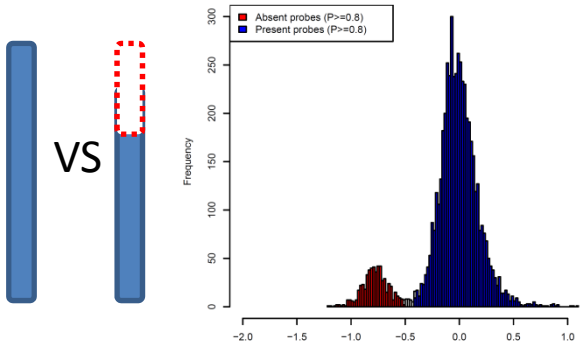
Proportion BAC length overlap

Improved MTP BAC-by-BAC assembly

Statistics	Assembly v1 OLC *(20% low coverage)*		Assembly v2 OLC *(1-5% low coverage)*	
	7BS	**7BL**	**7BS**	**7BL**
Total size	337 Mbp	550 Mbp	-	580 Mbp
Scaffold #	55,109	72,020	-	71,000
Max scaffold size	274 Kb	597 Kb	-	600 Kb
N50 scaffold size	23 Kb	36 Kb	-	46 Kb
Mean scaffold size	6.1 Kb	7.6 Kb	-	7.2 Kb
Scaffolds per BAC	15	13	-	13



Anchoring of MTP to genetic and physical maps



Recombination/LD maps

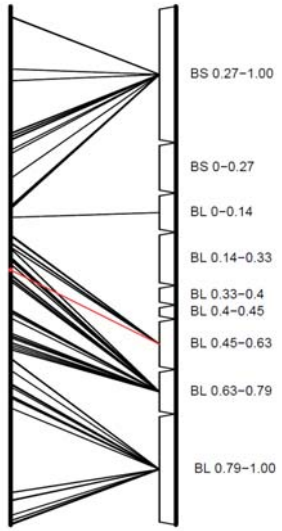
- Naxos*Synthetic (629 markers)
- Collaboration INRA (autumn 13)

CGH based bin-mapping

- 8% 7B bin mapped
- 9 bins
- 72% MTP contigs anchored

RH maps

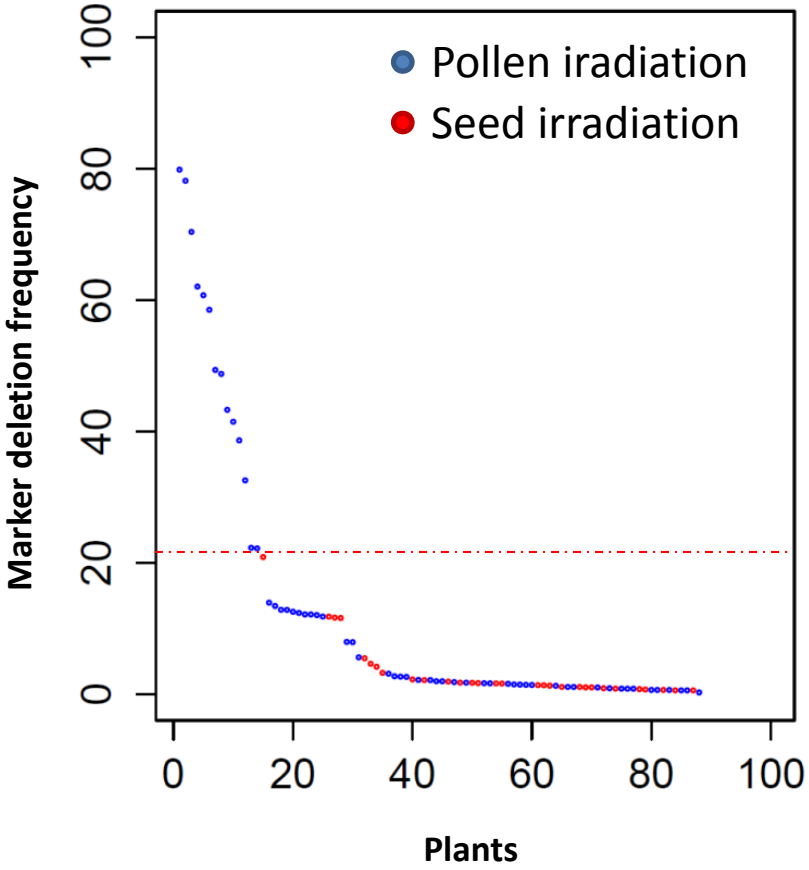
- 700 DARTseq markers
- 85 RH lines

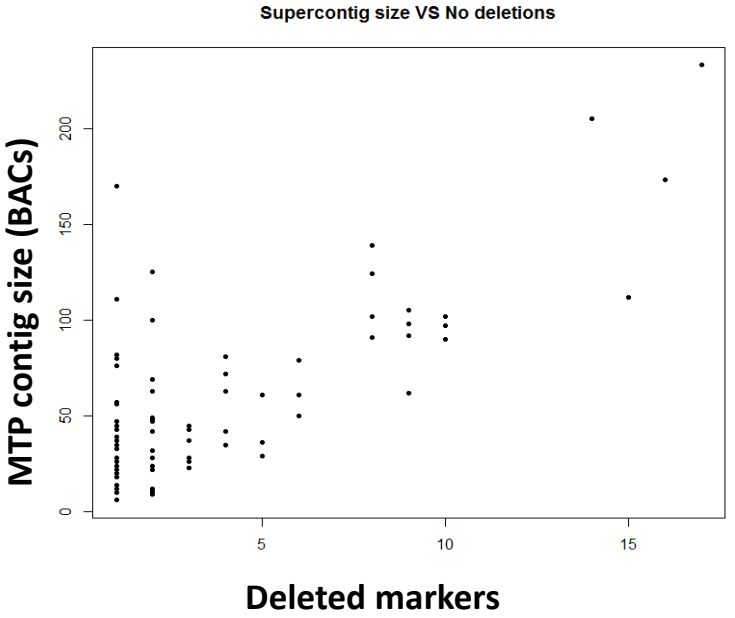


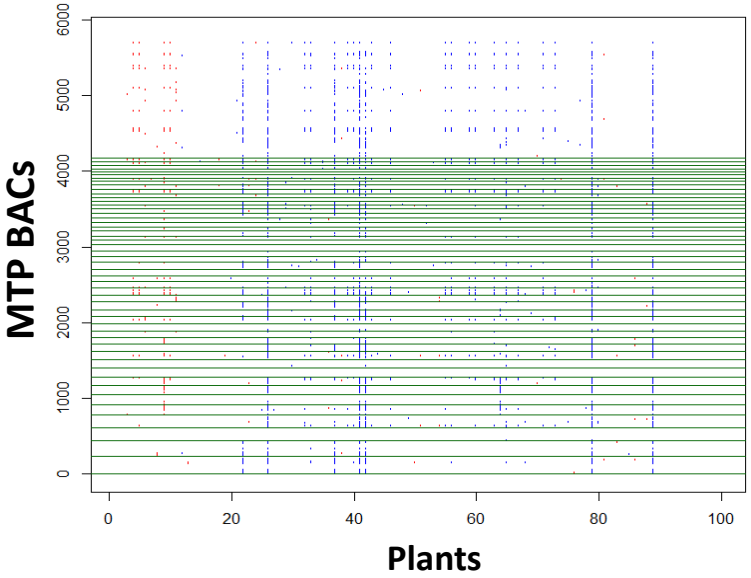
DARTseq genotyping of RH-lines

- total ~40,000 DARTseq markers

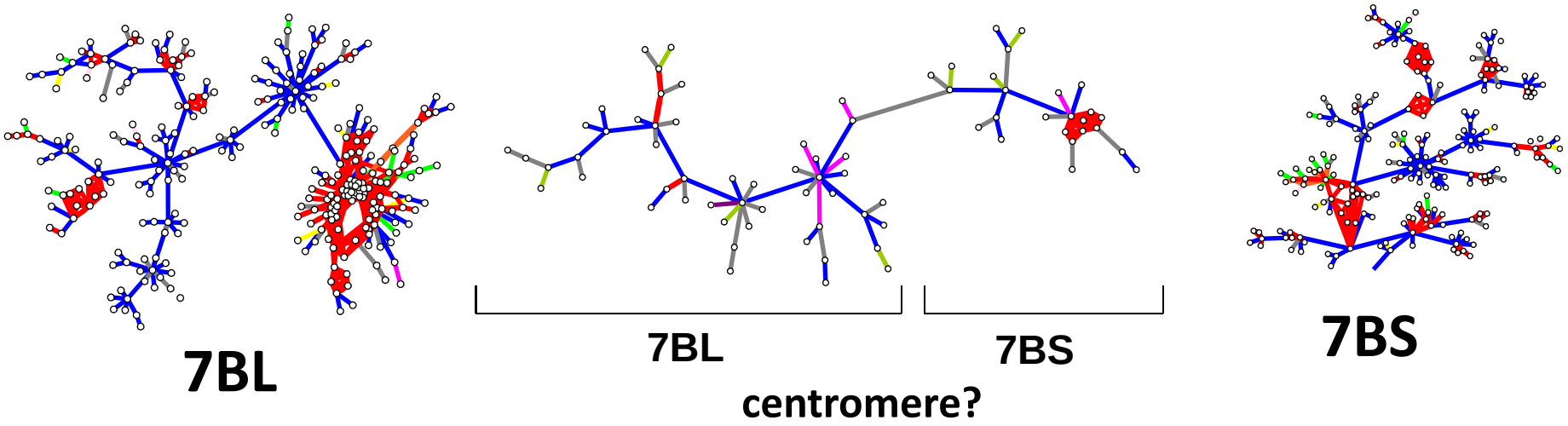
- 692 unique polymorphic 7B markers







Preliminary results: RH-mapping



- Three linkage groups
- Markers from same physical scaffolds are close in RH map
- Low resolution
- Non-stable maps (non linear topology)

Korol, Frenkel, Uni. Haifa

7B Collaborators:

H. Simkova, M. Kubalaskova, J. Dolezel.
Lab of Molecular Cytogen. and Cytometry, Czech Republic.

F. Cattonaro
Instituto di Genomica Applicata and IGA Technology Services, Italy.

S. Kianian, A. Kumar
N. Dakota State Uni, Dept of Plant Sciences,Fargo, USA/USDA Minnesota

A. Korol, V. Frenkel
B. University of Haifa, Israel.

K. Mayer, M. Pfeifer, K. Kugler
MIPS, Germany.

J. Hu, L. Li, J. Min, J. Chen, Y. Yang, X. Xu
Beijing Genomics Institute, China.

Pierre Sourdille, Etienne Paux
INRA, France.