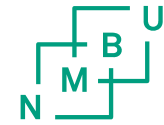


A draft sequence of bread wheat chromosome 7B based on individual MTP BAC sequencing using pair end and mate pair libraries.

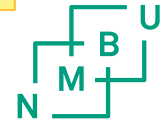
O.-A. Olsen, T. Belova , B. Zhan, S. R. Sandve, J. Hu, L. Li, J. Min, J. Chen, Y. Yang, X. Xu, M. Pfeifer, K. Kugler, A., K. Mayer, A. Korol, V. Frenkel, H. Simkova, M. Kubalaskova, J. Dolezel, F. Cattonaro, P. Sourdille, E. Paux, M. Kent, S. Lien, M. Lillemo ,M. Alsheik.



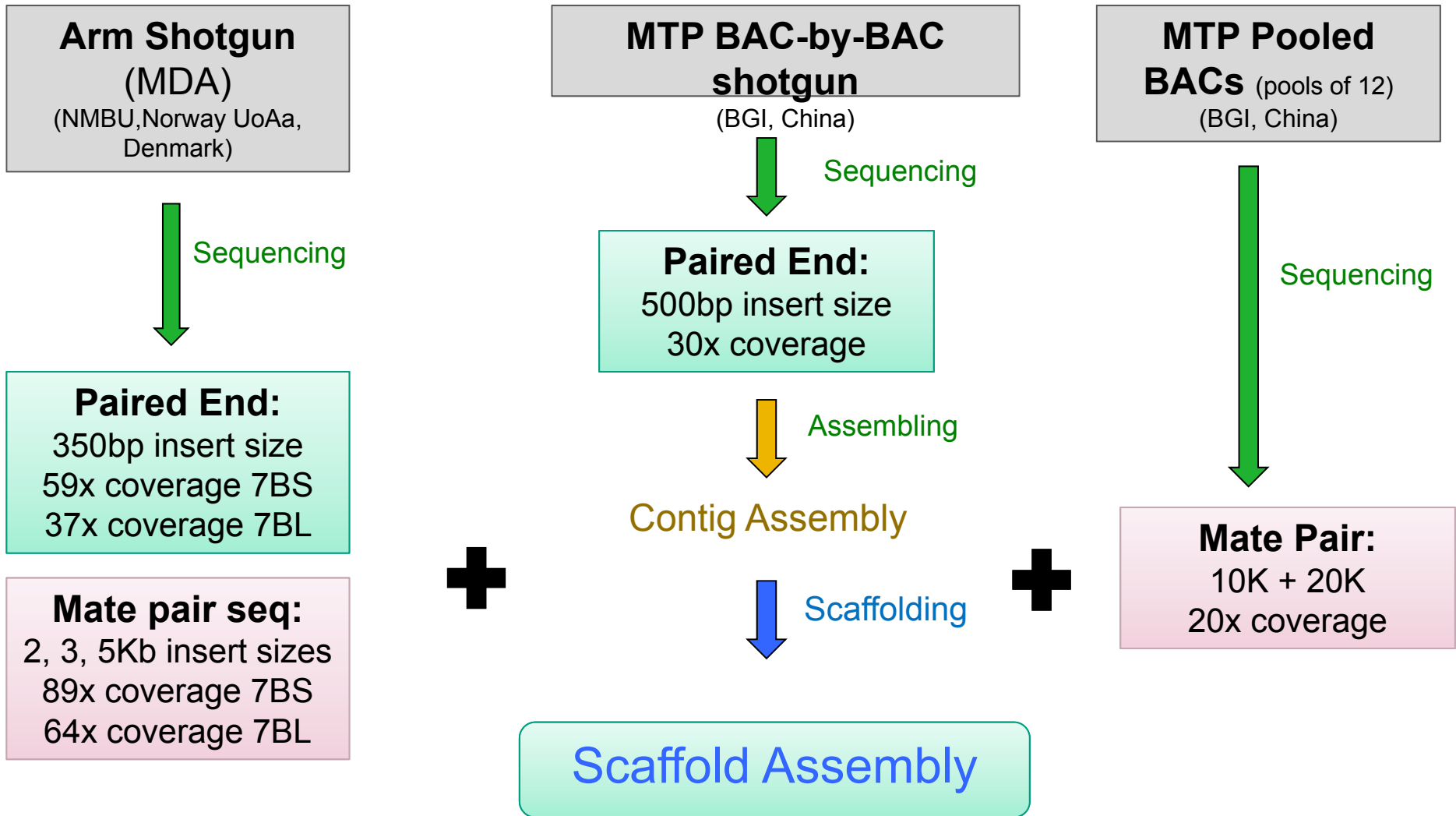
Overview

- Part I. Assembly of 7BL BACs and physical contigs
- Part II. Assembly statistics of 7B
- Part III. Mapping physical contigs on 7BL
-

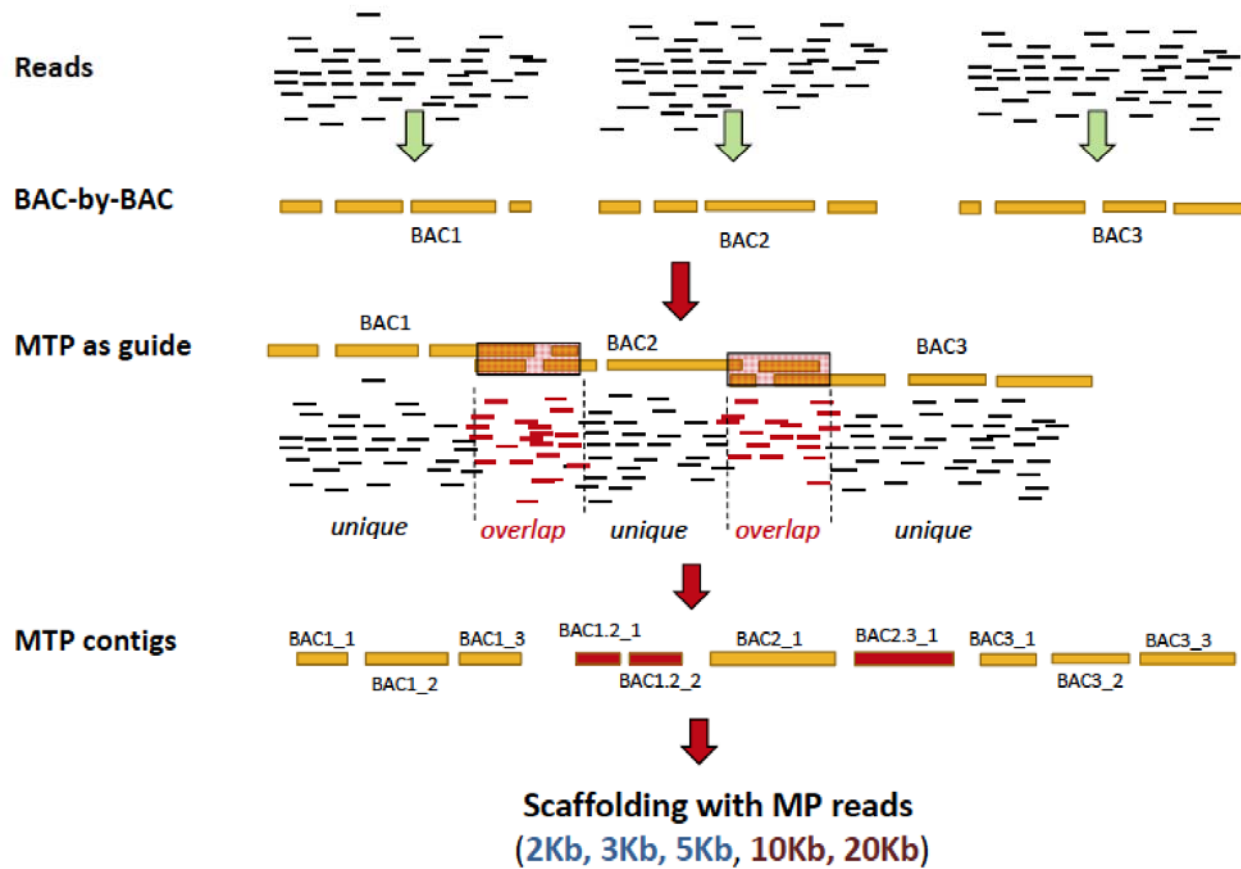
- Part I. Assembly of 7BL BACs and physical contigs



Sequencing strategy



MTP-based assembly strategy



B.Zhan

Expected overlap size in BAC-MTP sequence assembly

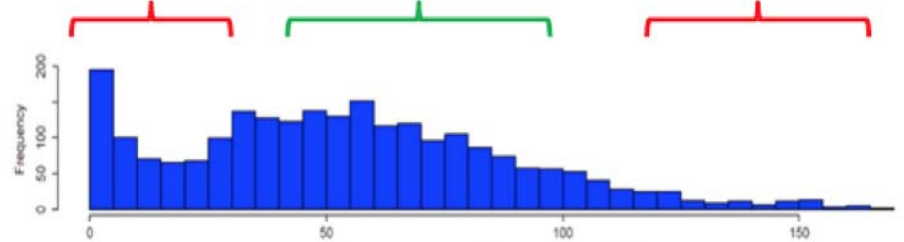


Low coverage (20%)

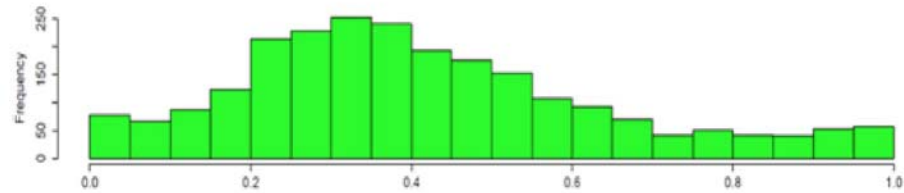
or error

Expected

Redundancy



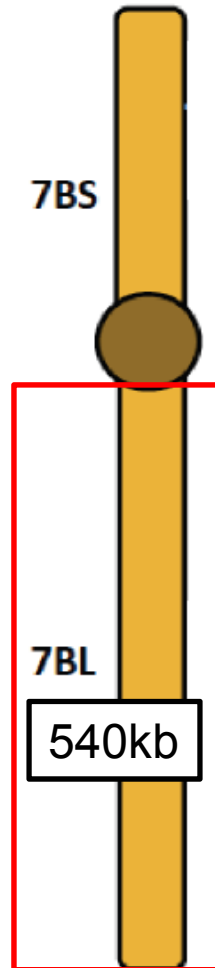
Overlap assembly size (Kb)



Proportion BAC length overlap

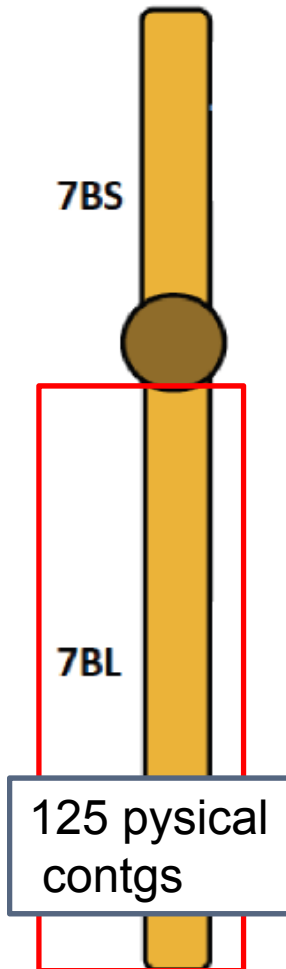
B.Zhan

BAC by BAC sequence assembly statistics for contigs and scaffolds (with MP data)



Statistics	Contigs	Scaffolds (MP 10,20Kb)	
Number of sequences	105,445	40,677	
Total size (Mbp)	538	523	
N50 (Kbp)	17,525	110,347	7X
N80	5,815	22,776	
Average (Kbp)	5,107	12,873	
No.Seq/BAC	19	7	

Summary statistics for 7BL MTP physical contig assembly assembly (LTC; manual curation) , continued

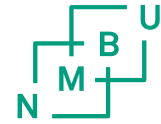


No. MTP-contig clones	5561
No. MTP physical contigs	125
Clones per MTP p. contig/min/max	44.8 / 1 / 219
Total Kbp	529407
Arm coverage*	98 %

* Assuming estimated size 7BL of 540Mb

V.Frenkel, T.Belova

- Part II. Assembly statistics of 7B

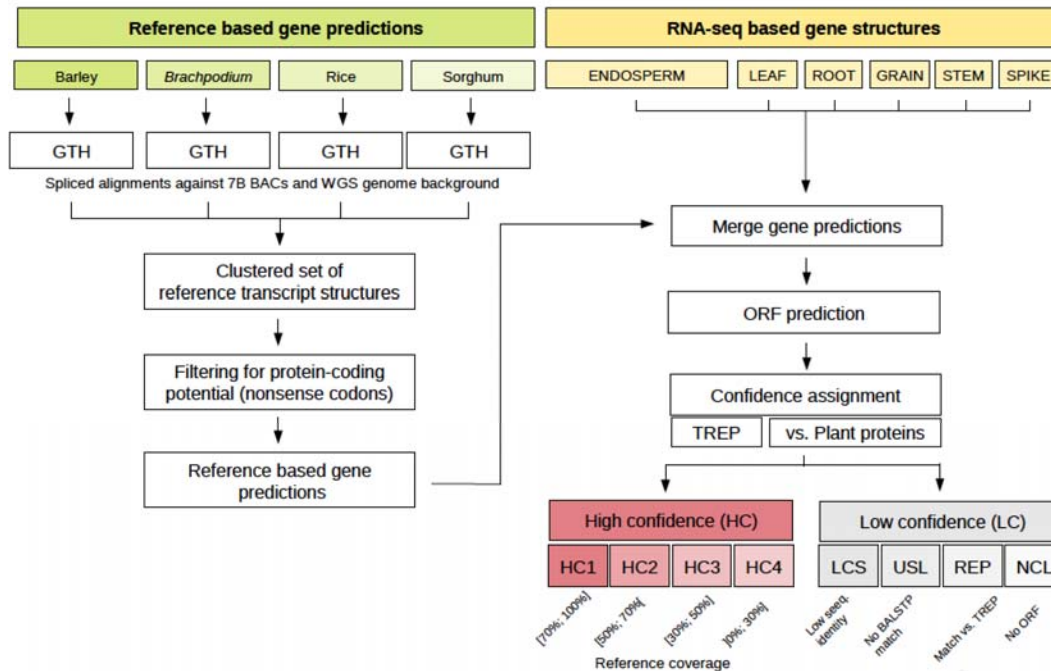


Annotation of 7B BAC gene assembly (1st version)

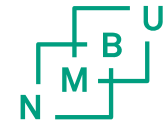
7B gene calls:

- Gene/transcript structures found via spliced-alignments of reference proteins (barley, brachy, rice and sorghum)
- Wheat fl-cDNAs
- RNAseq of endosperm, leaf, root, grain, spike and stem.

Gene prediction pipeline



M.Pfeifer, K.Kugler, K.Mayer, unpublished



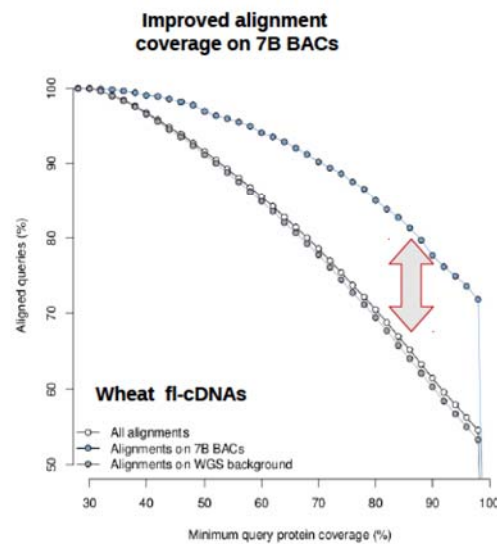
Key results

- High sequence (>95%) overlap between IWGSC 7B CSS and the 7B BACs:
 - 95 % of the CSS bp are contained in the 7b BAC assemblies (>= 100 bp perfect hit)
 - 97 % of the 7B BACs are already present in the IWGSC contigs, only in shorter stretches
 - 7B BACs contain more repeated sequences, but no substantial amount of new unique sequences (only ~3%)
 - On average 10x increase of sequence length in the BAC assemblies

M.Pfeifer, K.Kugler, K.Mayer, unpublished

20% improved coverage of wheat fl-cDNAs in 7B BAC assembly compared to the shotgun assembly

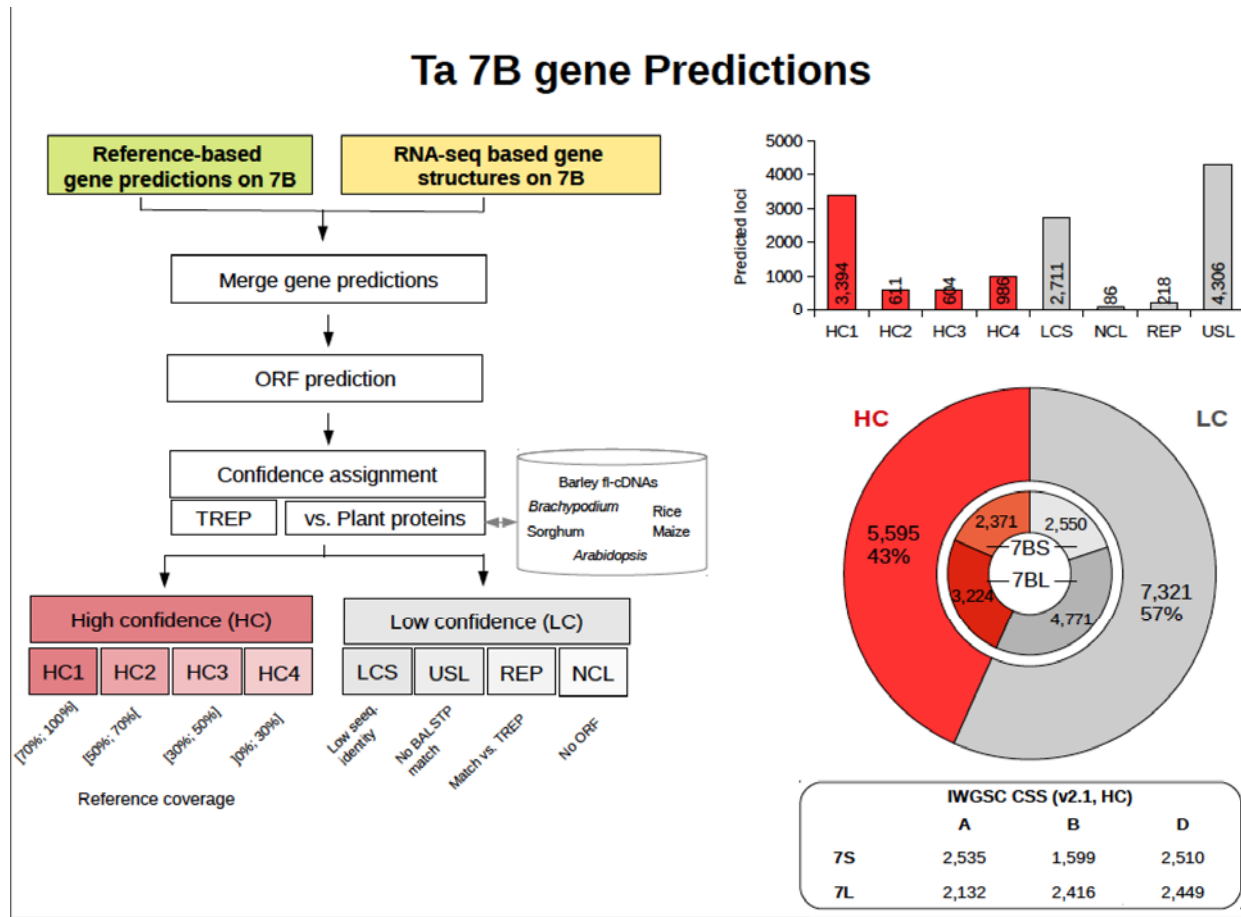
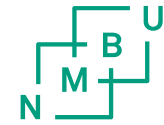
Protein coverage of aligned reference proteins



	7BS	7BL	7B
Loci	2,663	3,511	6,174
Transcripts	3,724	4,677	8,401
Avg. transcript length (bp)	983	925	951
Avg. exon length (bp)	268	280	274

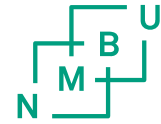
M.Pfeifer, K.Kugler, K.Mayer, unpublished

5,595 high confidence (HC) genes predicted in the BAC assembly; around 1,500 more compared to the shotgun assemblies.

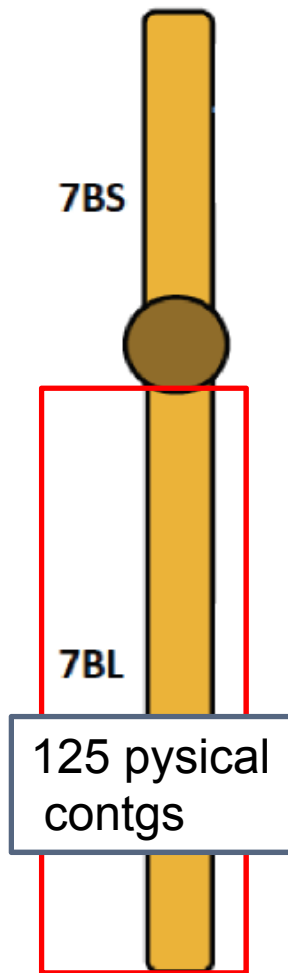


M.Pfeifer, K.Kugler, K.Mayer, unpublished

- Part III. Mapping physical contigs on 7BL



Strategy for anchoring the 125 physical contigs of 7BL:



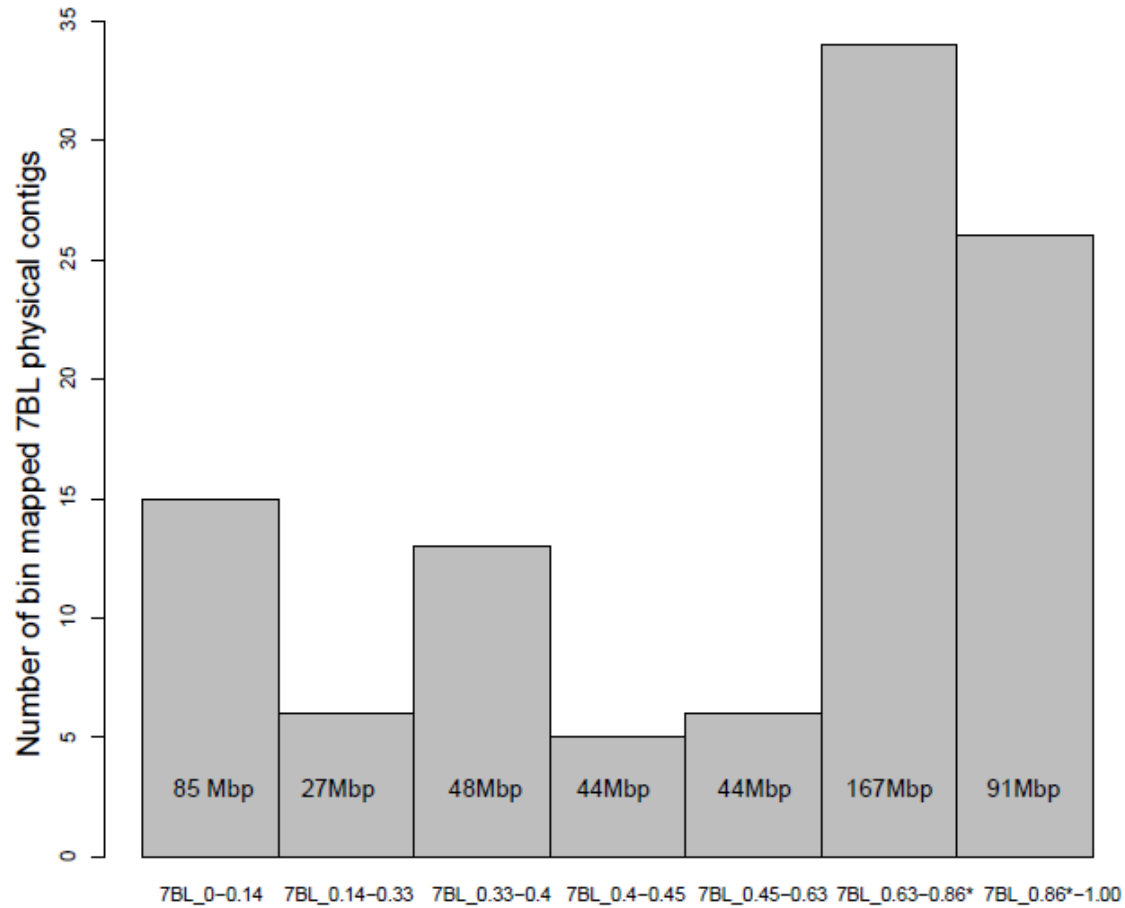
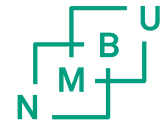
7B Deletion bin mapping

Genetic mapping

Synteny-based mapping

T.Belova

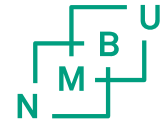
7B Deletion bin mapping



105 7BL physical contigs mapped to 7 7BL deletion bins

T.Belova,

Genetic mapping



Summary on genetic mapping using 3 populations:

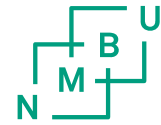
- 282 F8 Renan*CS (INRA) ————— 420K Axiom SNP chip
- 131 F6 lines SY1 x Naxos ————— 90K Illumina SNP chip
- 181 F6 lines Sh3CBRD x Naxos ————— 90K Illumina SNP chip

Statistics	Re*CS	SY*Nax	SHA3/CBRD*Nax
Number unique loci on chromosome 7 group	308	71	38
Genetic length cM	127.3	220.2	100.67
Number of markers mapped to 7BL BACs	1259	289	247
7BL physical contig markers	79	52	46

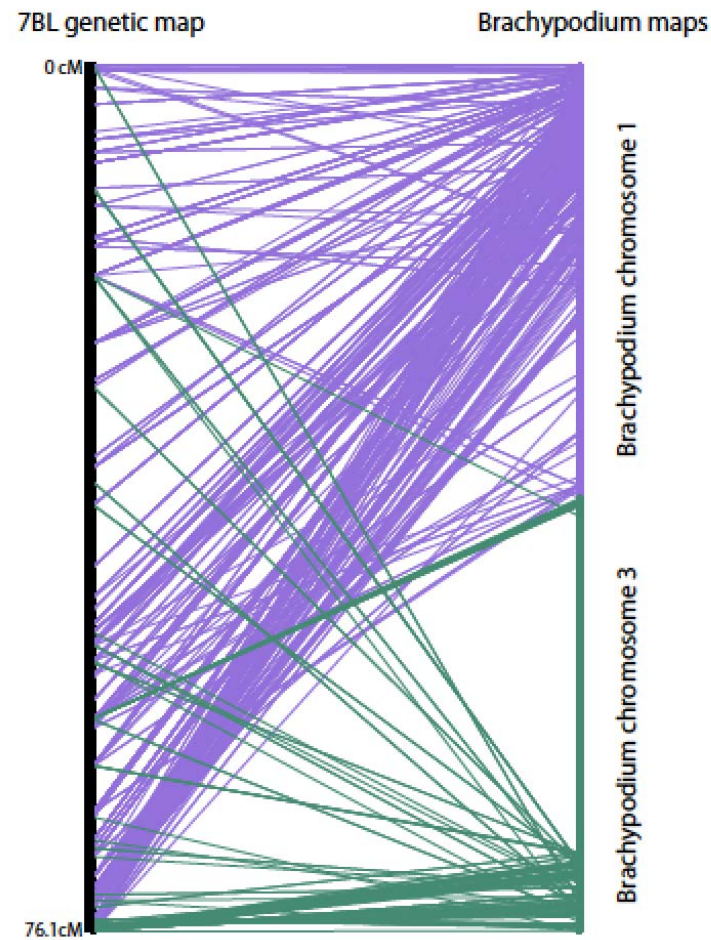
Combining 3 maps, 83 7BL physical contigs were genetically mapped

T.Belova, P. Sourdille, E. Paux

Syntenly-based mapping

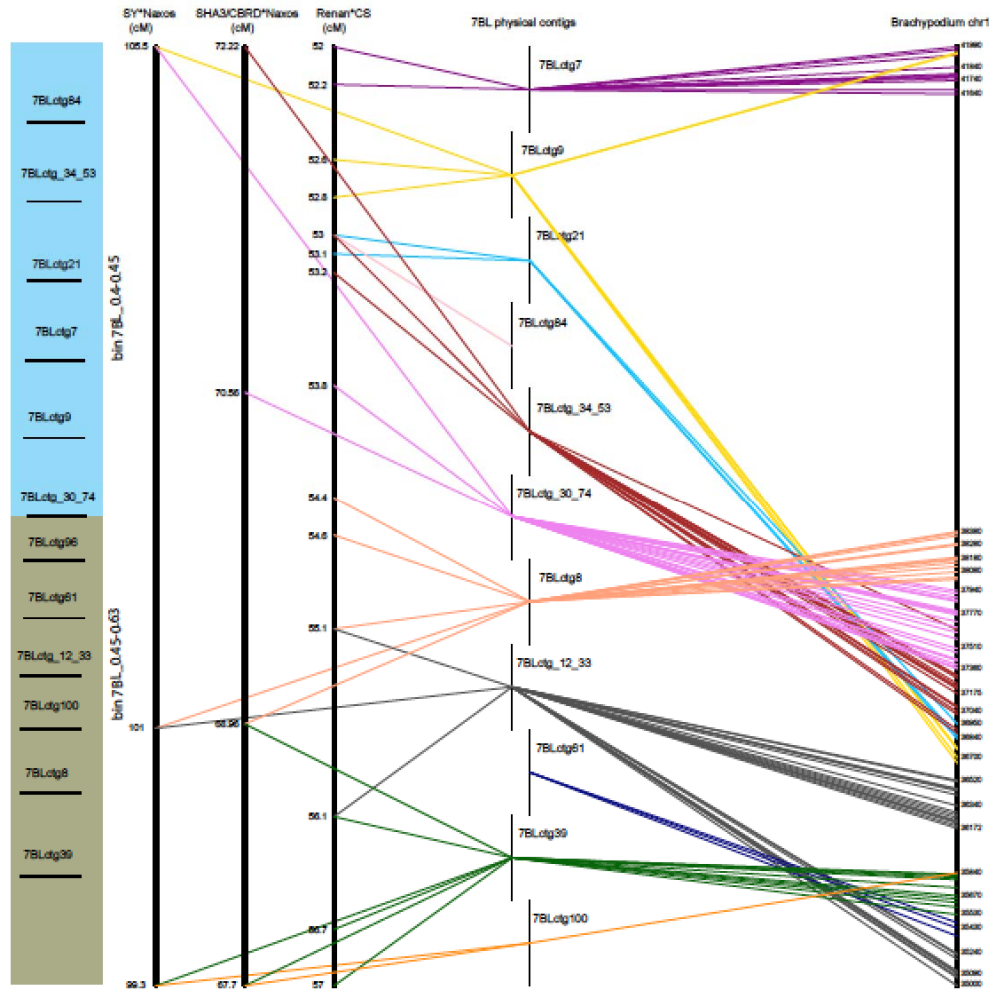
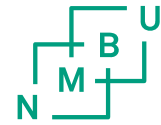


Syntenly blocks between bread wheat 7BL and Brachypodium

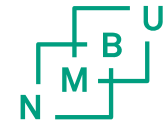


T.Belova, PhD dissertation, 2014

An integrated map for 2 deletion bins of chromosome 7BL



T.Belova

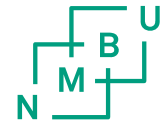


Summary of 7BL anchoring

- 109 (~514Mbp) out of the 125 7BL physical contigs assigned positional information.
- 96 physical contigs (96% of sequence scaffold length) arranged in linear order with unique positions based on genetic and synteny data
- 16 7BL physical contigs remained unanchored, representing only 1.7% of the 7B sequence scaffolds.
- Most of unanchored contigs contained a small number of BACs.

T.Belova, PhD dissertation, 2014

Acknowledgements



- T. Belova, B. Zhan S. R. Sandve,, M.Kent , S. Lien, M. Lillemo, O.-A. Olsen, *Norwegian University of Life Science*
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- P. Sourdille, E. Paux, *INRA*

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