Sequencing and analysis of chr. 1B

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Partners, funders

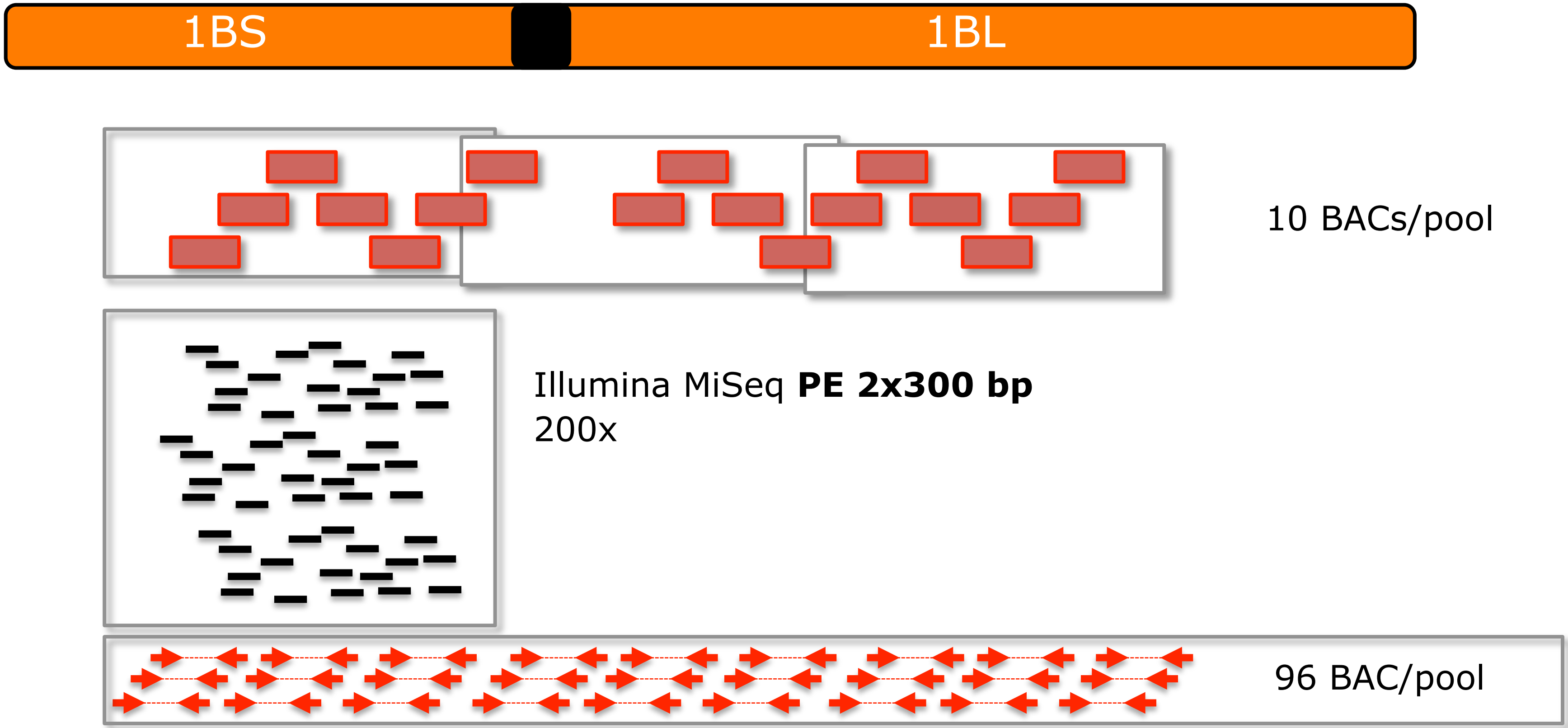
- *INRA GDEC*
- *Génoscope*
- *INRA CNRGV*
- *INRA URGI*
- *University of Haifa*

INRA

*PIA **BreedWheat** project*

*France Génomique **WheatSeq** project*

Strategy



10 BACs/pool

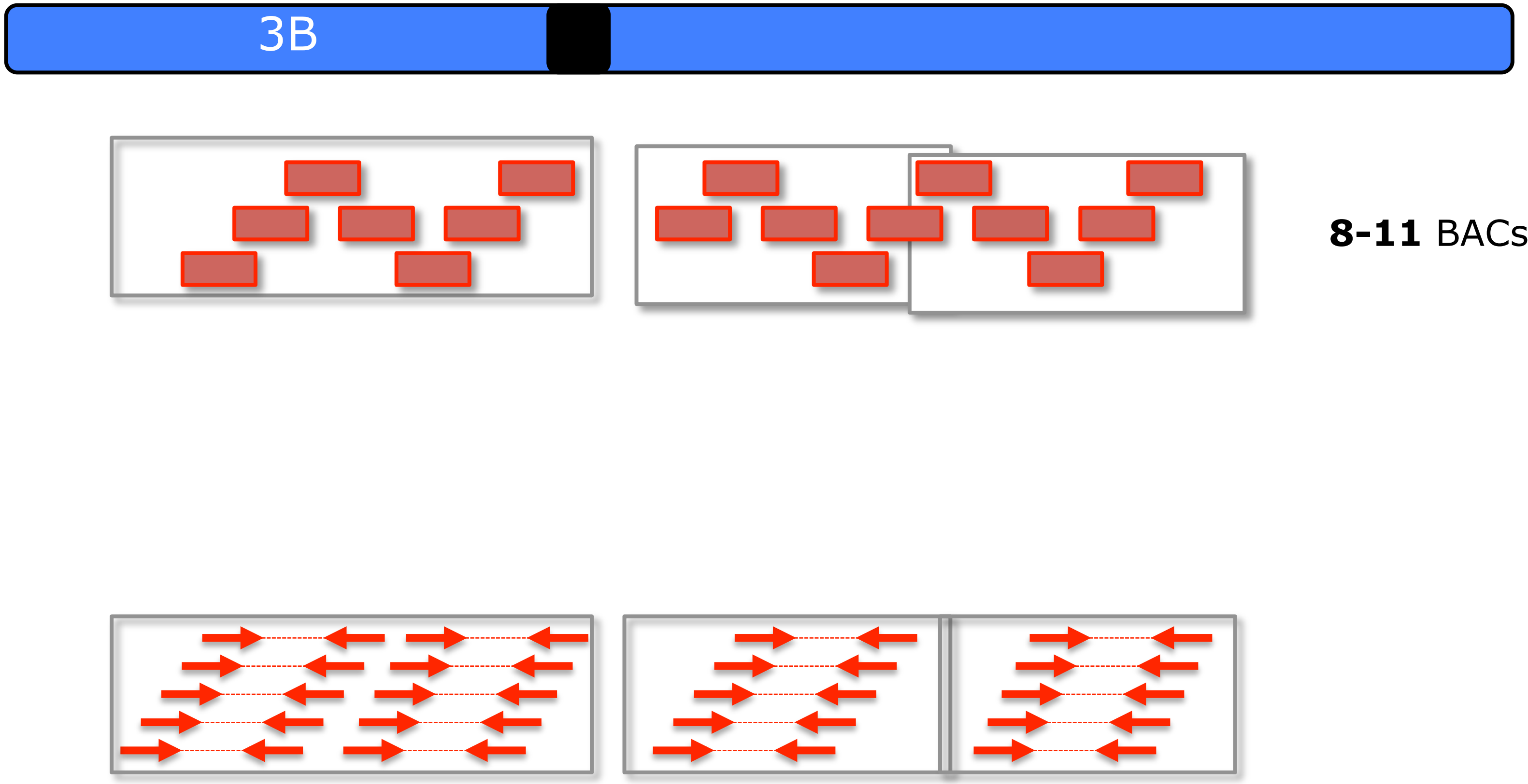
Illumina MiSeq **PE 2x300 bp**
200x

96 BAC/pool

Illumina HiSeq **5kb MP 2x150 bp**
100x

CEA-IG-Génoscope
- ○ *Valérie Barbe*
- ○ *Adriana Alberti*
- ○ *Karine Labadie*
- ○ *Sophie Mangenot*
- ○ *Arnaud Couloux*
- ○ *Jean-Marc Aury*
- ○ *Patrick Wincker*

Strategy



8-11 BACs/pool

Roche454 **8kb-MP 450 bp**

40x

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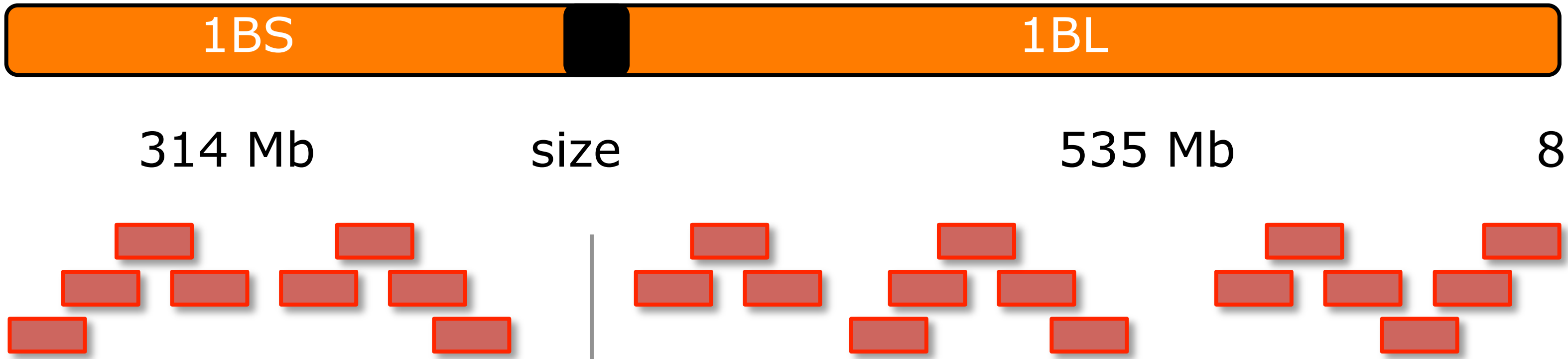
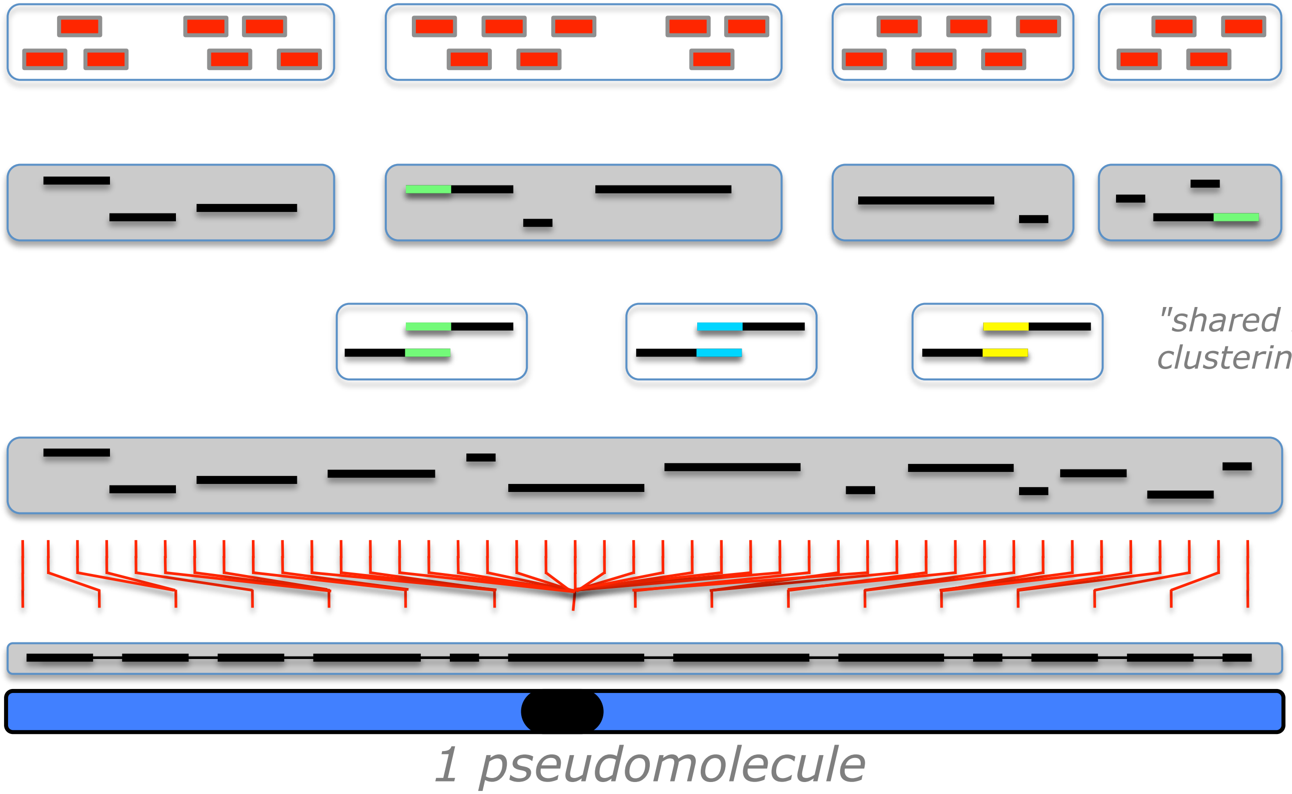
Physical maps



314 Mb	size	535 Mb	849 Mb
4372	#MTP-BACs	6023	10395
-	#PE-pools	-	1083
-	#MP-pools	-	109

INRA CNRGV
- ○ *Arnaud Bellec*
- ○ *Hélène Bergès*

Pseudomolecule construction



BAC-pools

Assembly
Scaffolding
Gap filling

"shared ISBP"-based clustering

Merging

map

Anchoring

1 pseudomolecule

Assembly – scaffolding – merging

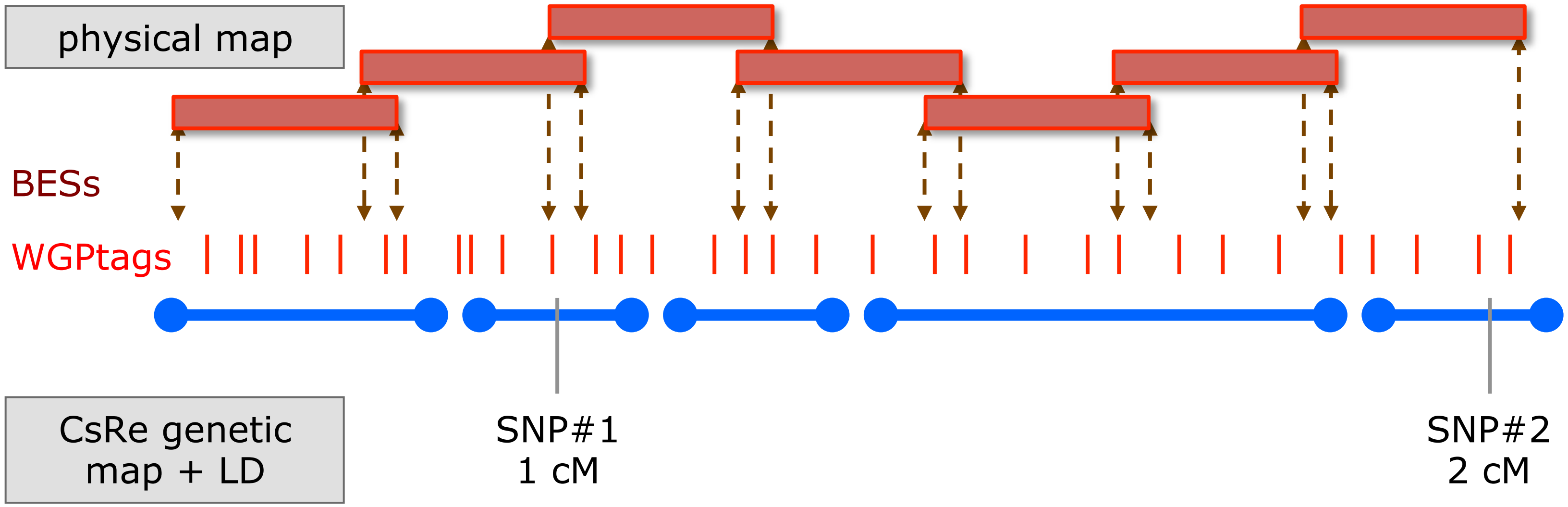
	1B	3B
expected size	849 Mb	995 Mb
pool assembly	923 Mb **13386** scaff, N50=**350 kb** **1% Ns**	1040 Mb **16136** scaff, N50=**275 kb**
Gap filling, Manual Scaffolding Improvement (BACends)	-	992 Mb **4999** scaff, N50=**463 kb** **7% Ns**
Merging	807 Mb (95%) redundancy removed=13% **10979** scaff, N50=**656 kb**	833 Mb (84%) redundancy removed=16% **2808** scaff, N50=**892 kb**
with cutoff >10kb	**2746** scaff, N50=**694 kb**	**1913** scaff, N50=**895 kb**

Differences due to:

- Physical map 1B > 3B
- Sequencing tech 1B > 3B
- BAC pooling 3B > 1B
- Manual finishing 3B >> 1B

	1B	3B
expected size	849 Mb	995 Mb
all scaffolds	807 Mb (95%)	833 Mb (83%)
completeness	96%	94%

Anchoring



	1B	3B
expected size	849 Mb	995 Mb
all scaffolds	807 Mb (95%)	833 Mb (83%)
completeness	96%	94%

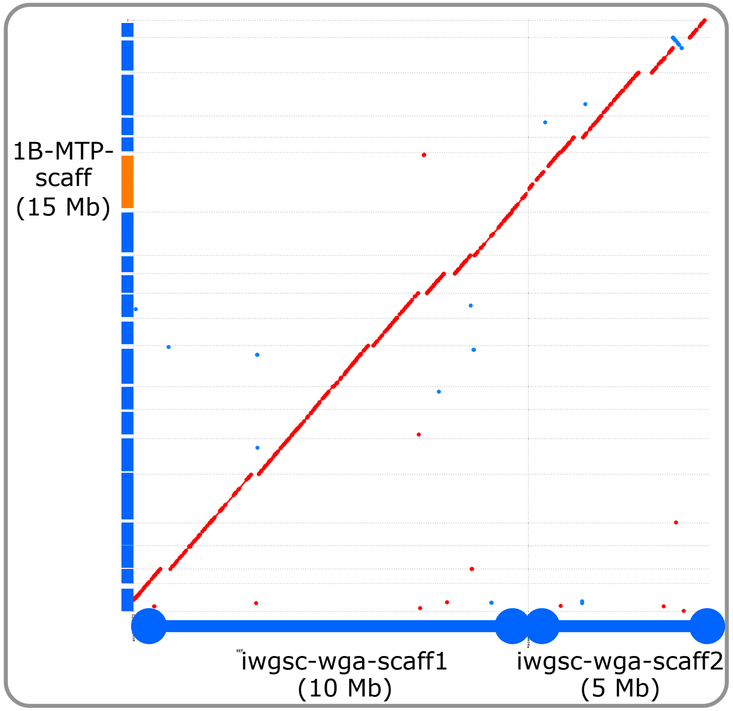
Anchoring

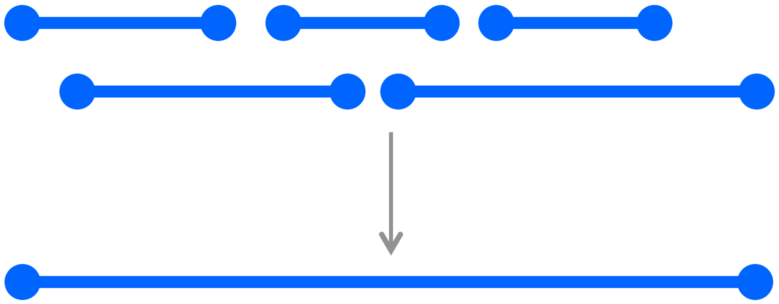
physical map		
BESs	**9706** BACs with BESs	**20953** BACs with BESs
WGPtags	WGPtags to come !!!! ☺	**14199** BACs with WGPtags
CsRe genetic map + LD	**5636** SNPs	~**2000** SNPs
Pseudomolecule	`v0.2.0` **1356 scaff / 552 Mb / 71%**	*Choulet et al. 2014* 1358 scaff / 774 Mb / **93%**

1B will reach a gold standard…

- ○ Completeness +++
- ○ Contiguity ++
- ○ %Anchored + (->to be increased)
  - WGP-tags
  - TGAC WGS assembly
  - IWGSC WGA *(Illumina+NRGene)*

Combine all available resources ***-> 1B gold standard pseudomol***

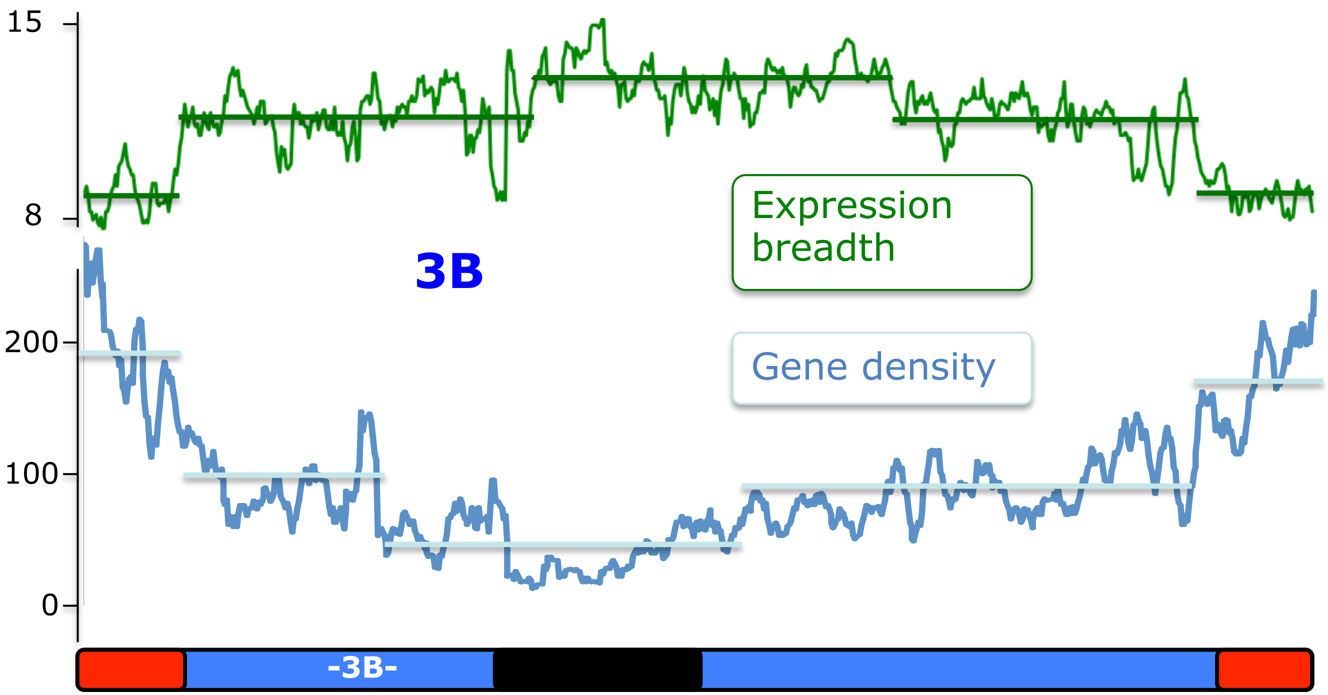




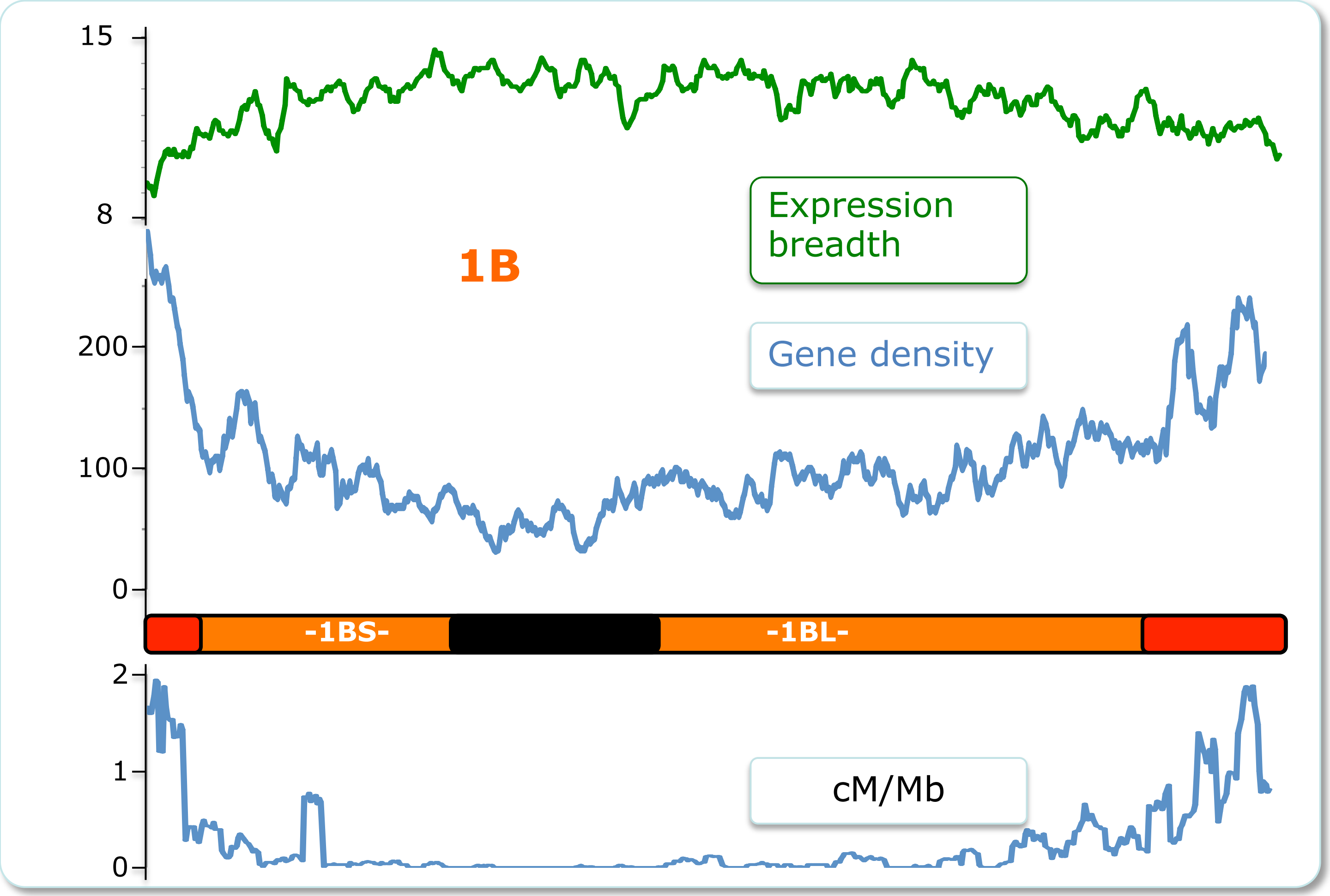
Sequence content

- Gene and TE annotation (TriAnnot):
  - **6369** gene models
  - **70%** expressed (RNASeq 15 samples *Pingault et al. 2015*)
  - **88%** TEs

Chromosome organization



Chromosome organization



❑ Acknowlegments

GDEC

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Gene name nomenclature

TRAES1BS**000000**CFD	*gene*
TRAES1BS**000000**CFD_t1	*transcript*
TRAES1BS**000000**CFD_c1	*CDS*
TRAES1BS**000000**CFD_p1	*protein*

6 digits

#scaff #gene

TRAES3BF**000100010**CFD