



my Baits®

Wheat Exome Kit V1

SCOPE – PERFORMANCE – OUTLOOK

25 March 2020

Jacob Enk, PhD
R&D Manager, NGS

PRESENTED BY:



arbor
biosciences

2006

Founded as
MYcroarray
Ann Arbor, MI

2017

Renamed
Arbor Bio

2019

Acquired by Chiral
Technologies

2020

- Hundreds of client publications
- Thousands of species studied

CORE TECH

Massively-
parallelized
DNA synthesis

CORE EXPERTISE

Non-model
organism
genomics



my Baits[®]

NGS target enrichment panels



my Reads[®]

Versatile NGS services



my Tags[®]

Synthetic FISH probes



Wheat Exome Kit V1

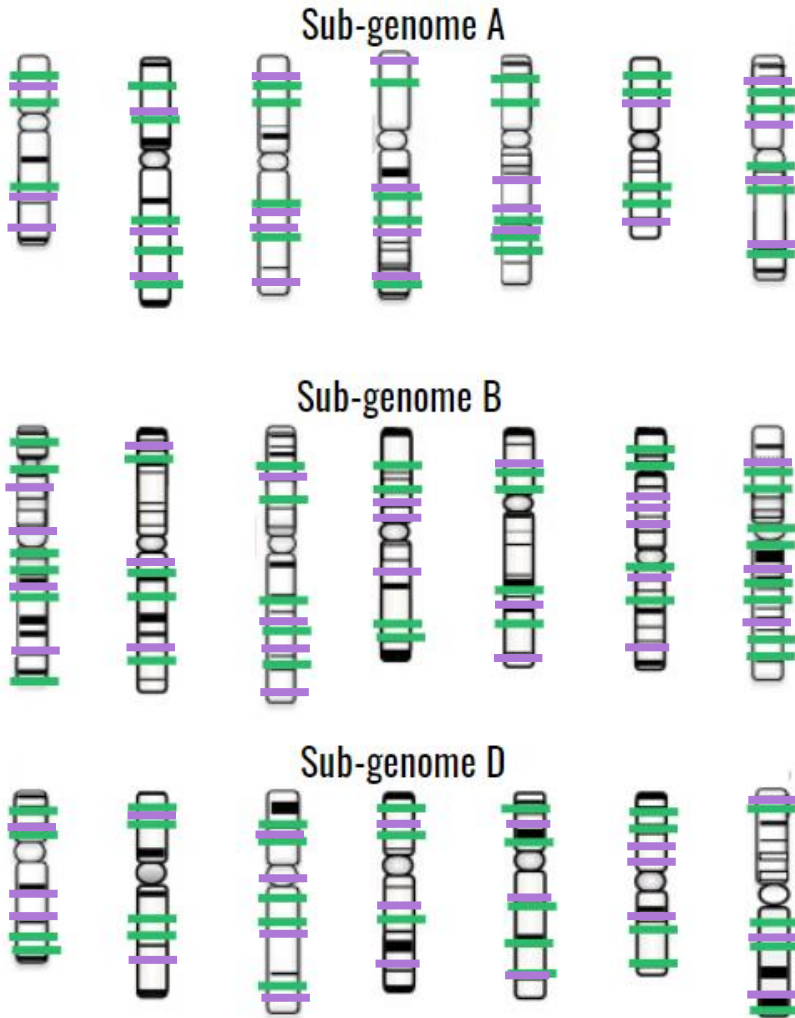
SCOPE OF DESIGN



IWGSC RefSeq 1.0

14.54 Gbp

First chromosome-scale *T. aestivum* reference assembly and annotations



High-Confidence annotations v 1.1

139,893
Gene IDs

HC exons
171 Mbp

“Promoter space” **227 Mbp**

Low-Confidence annotations v 1.1

165,016
Gene IDs

LC exons
108 Mbp

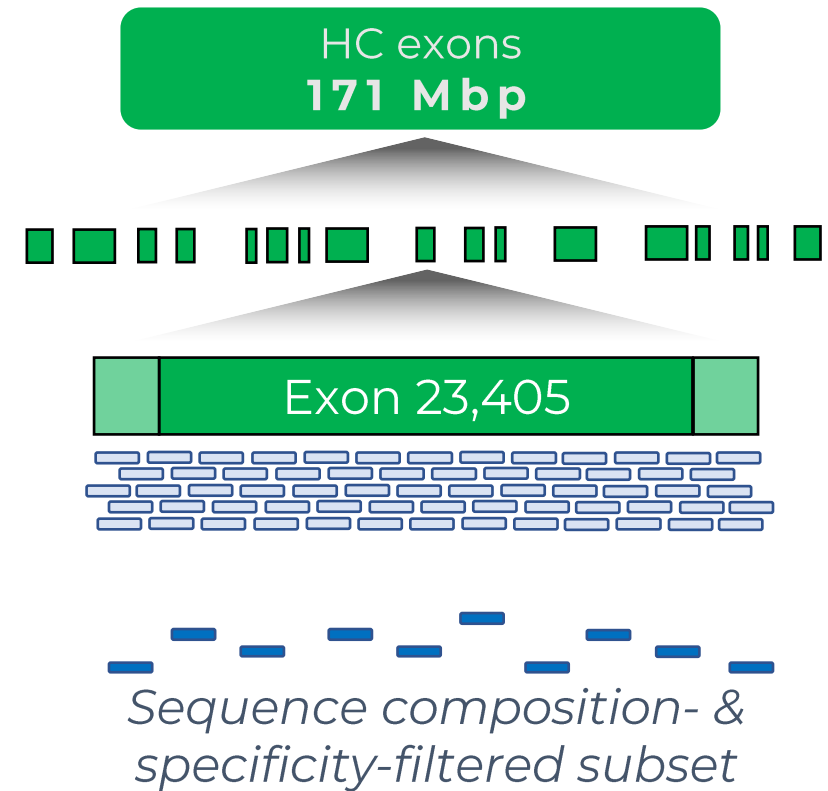
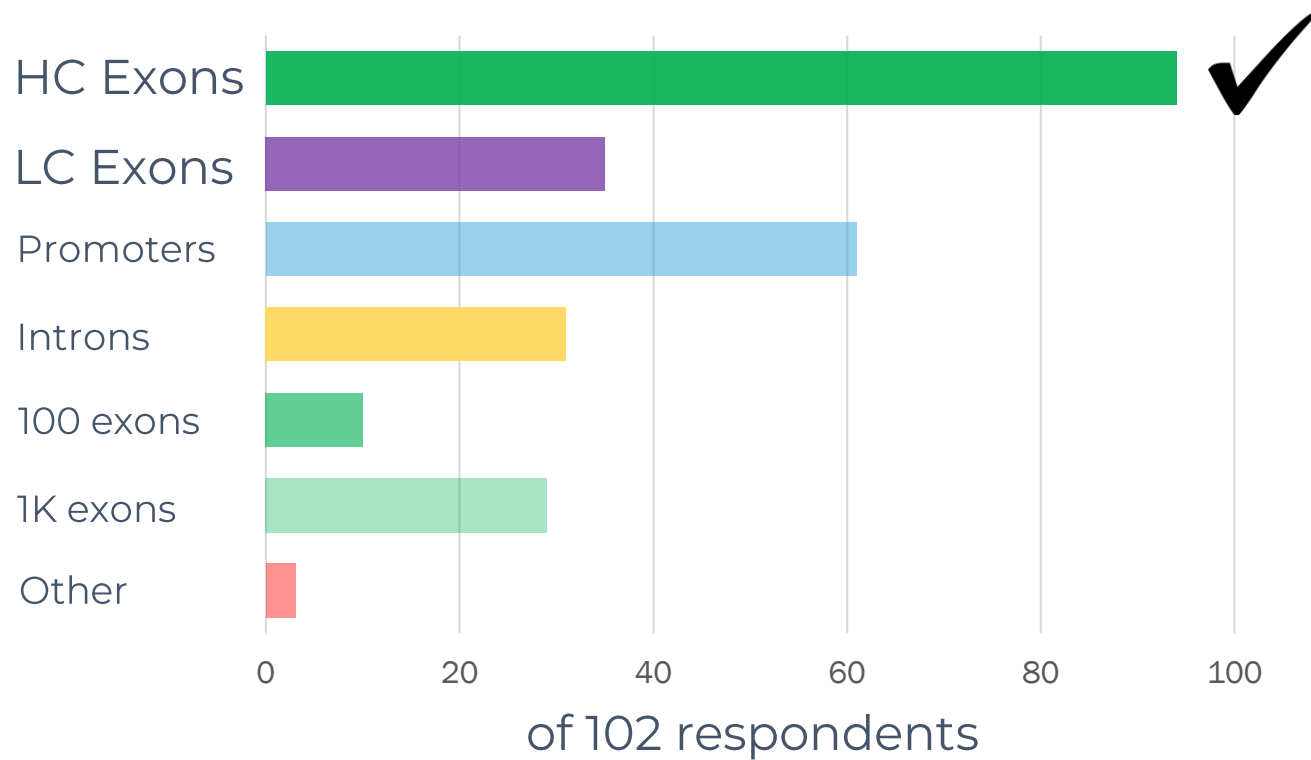
“Promoter space” **263 Mbp**

Kit composition

Guided by IWGSC community survey



Q: What would be useful to your research?

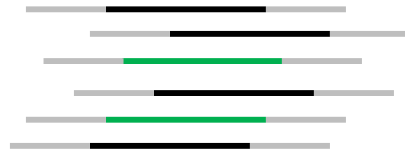


Use and development

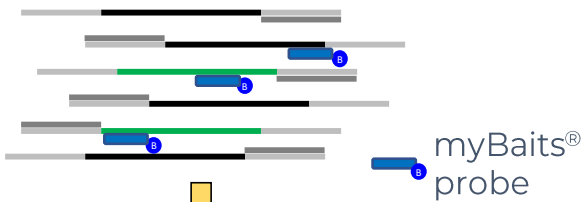
Simple myBaits[®] workflow



Amplifiable
sequencing library



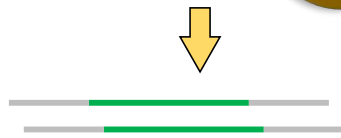
Hybridize myBaits[®]
probes



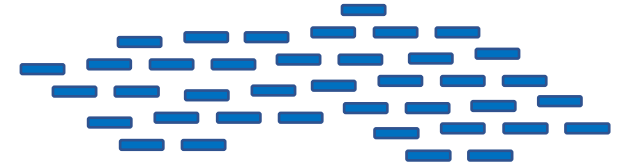
Bind hybrids to
magnetic beads



Wash, amp,
sequence

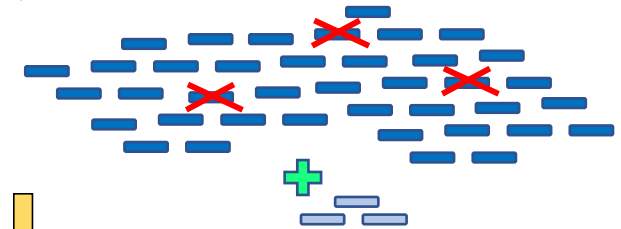


“Alpha”
probe set



Test

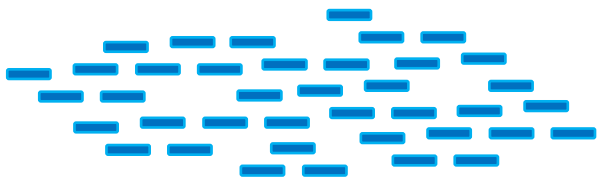
Refine to
“Beta”



*Test &
Optimize*

**Final Kit and
Parameters**

- 1.7 M RNA probes
- 8-plex capture



Use and development

Enhanced wheat NGS bioinformatics



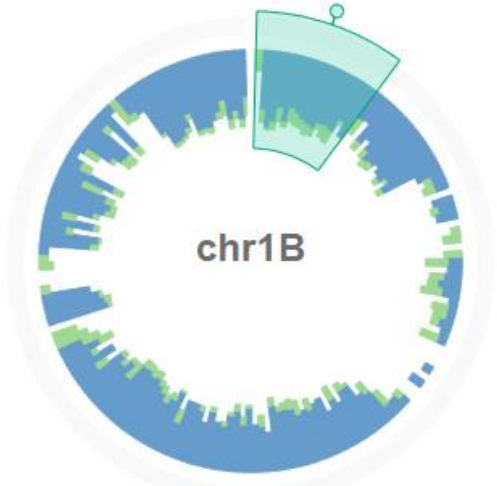
CURIO

Crop Research Solutions

curiogenomics.com

Density 86,631 variants found

Show Full Genome



Chinese Spring and Svevo fully integrated



Dynamic read alignment visualization



Rapid variant calling
Parameters tunable in real-time

Wheat Exome Kit V1

PERFORMANCE



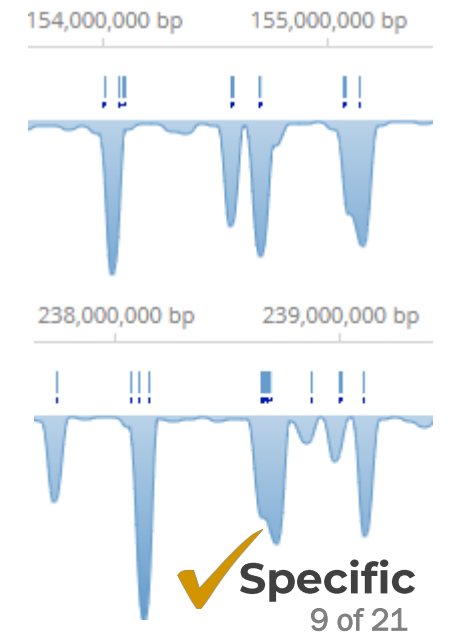
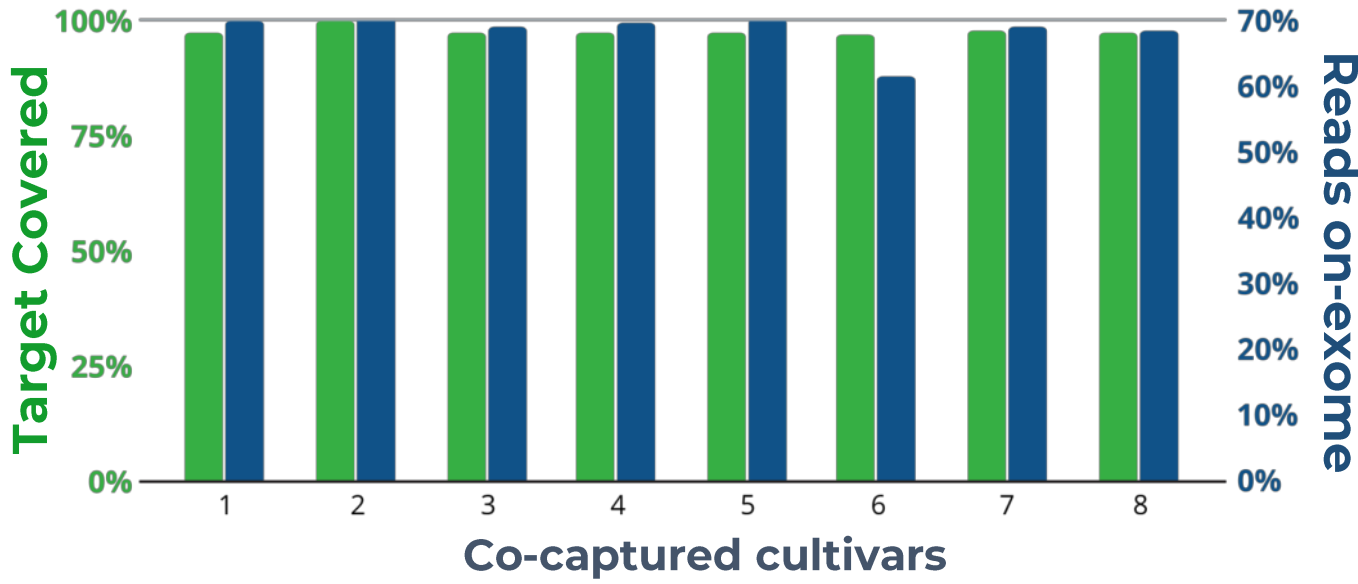
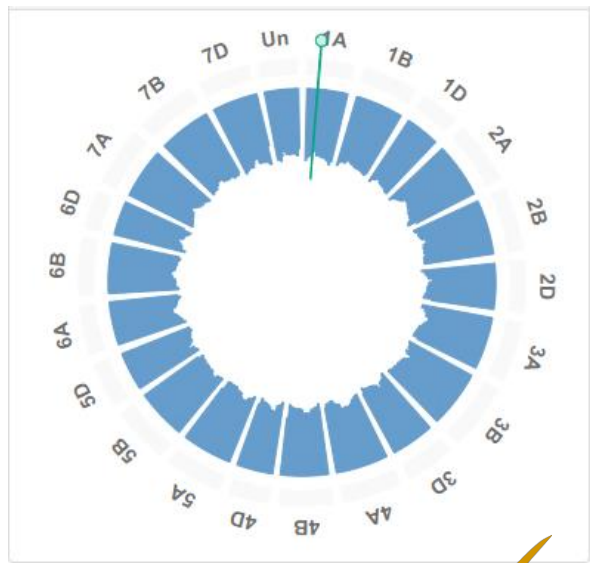
Hexaploid exome capture

Comprehensive and specific



Total Target Space	230 Mbp (158 Mbp exonic)
Recommended Sequencing	18 Gbp per sample (Illumina [®])
Target Read Depth	>32X mean unique read depth
Target Coverage	>97% high-confidence exons hit

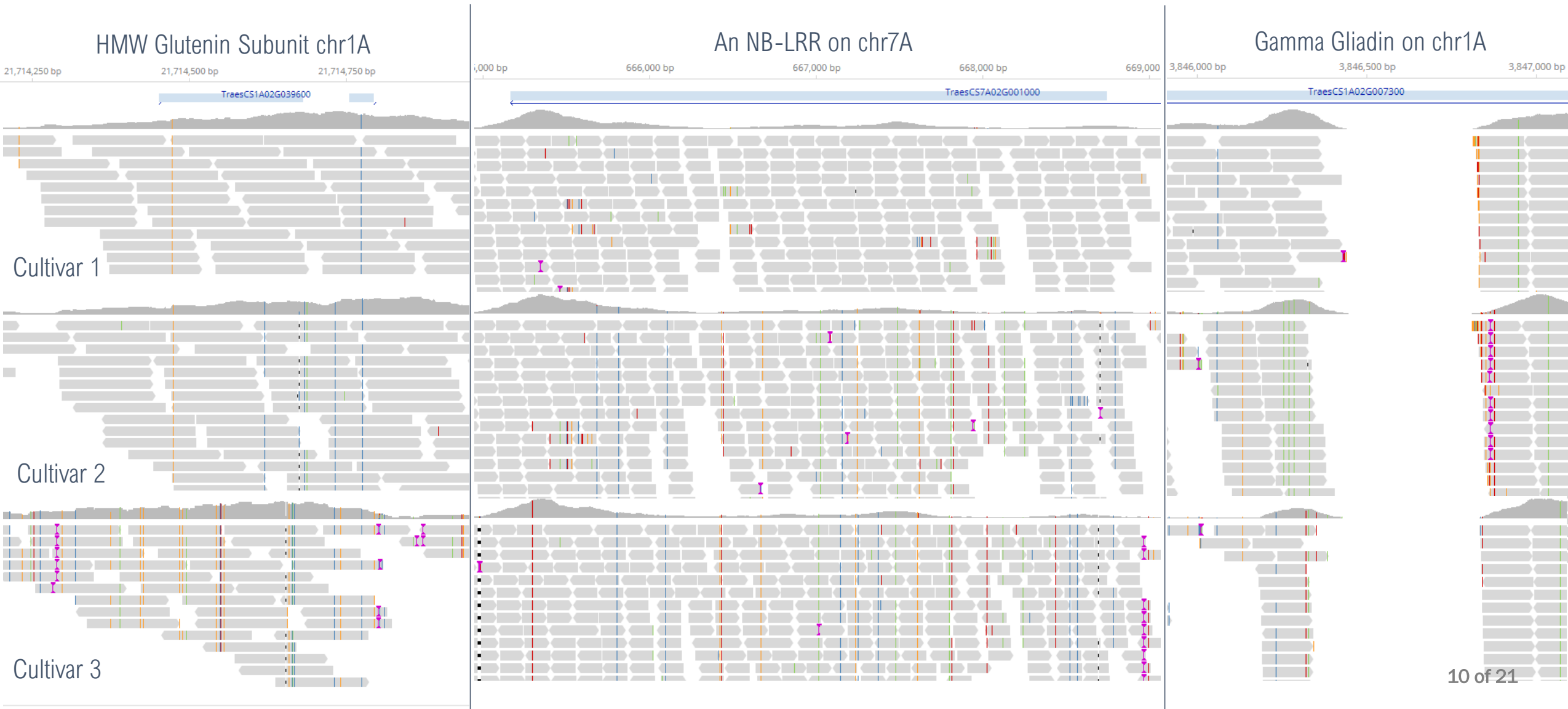
30-fold reduction in exome sequencing cost vs. WGS



Comprehensive ✓

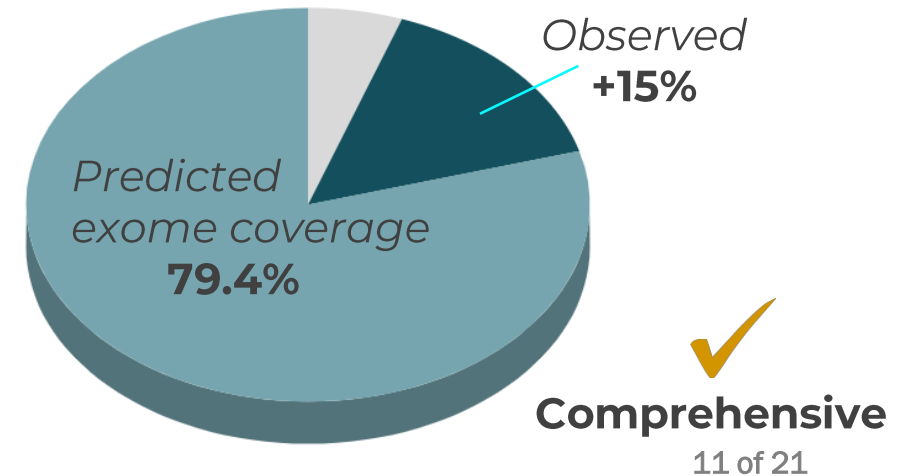
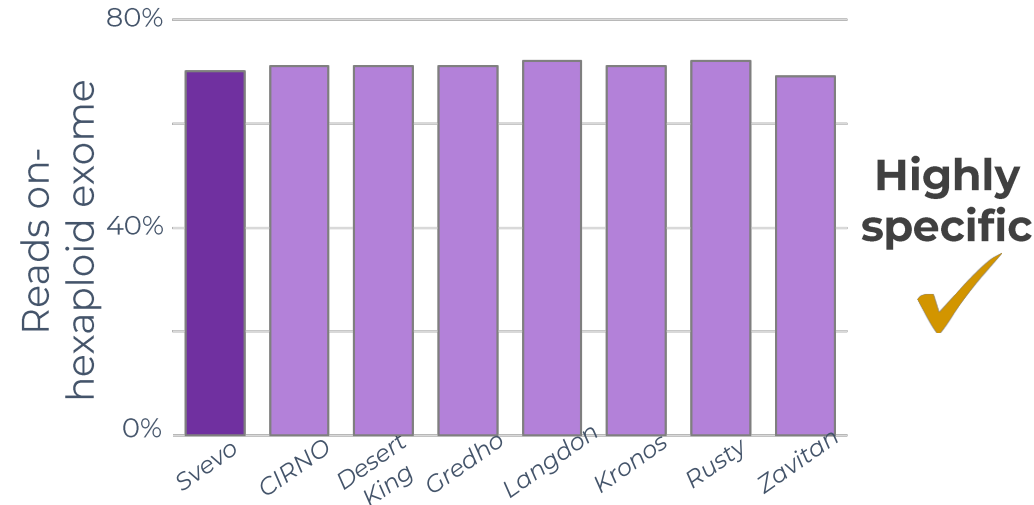
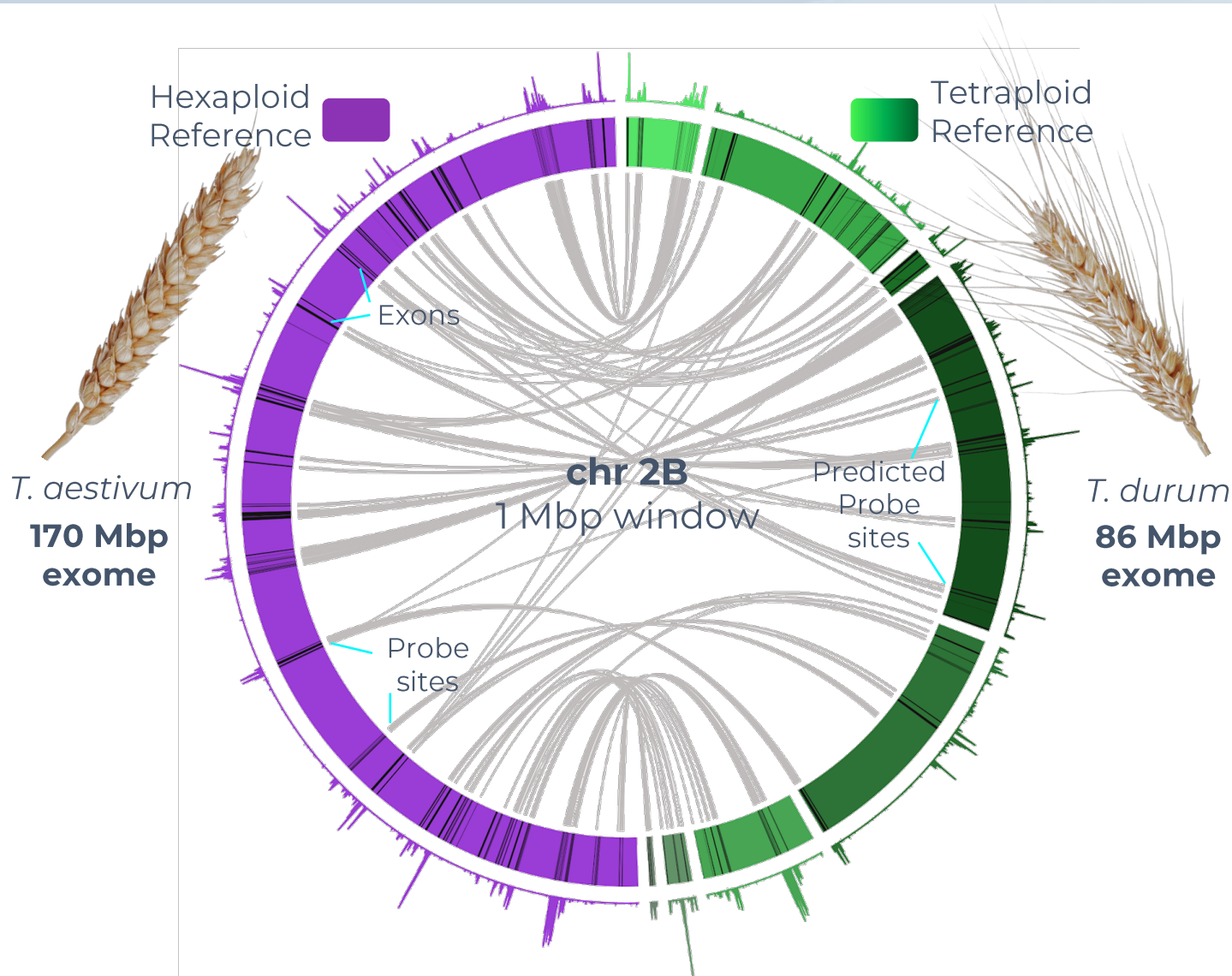
Hexaploid wheat exome capture

Comprehensive and specific across cultivars



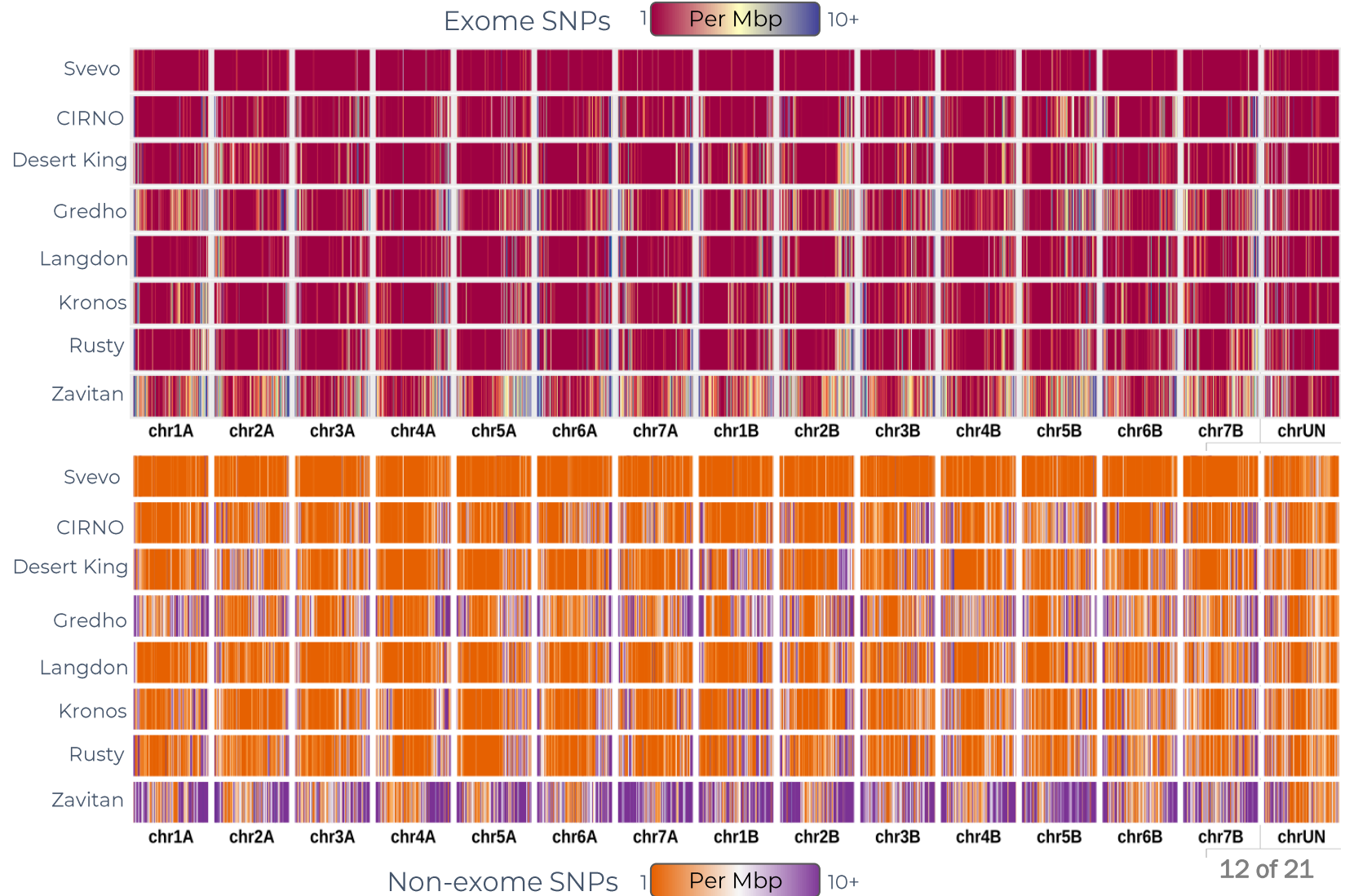
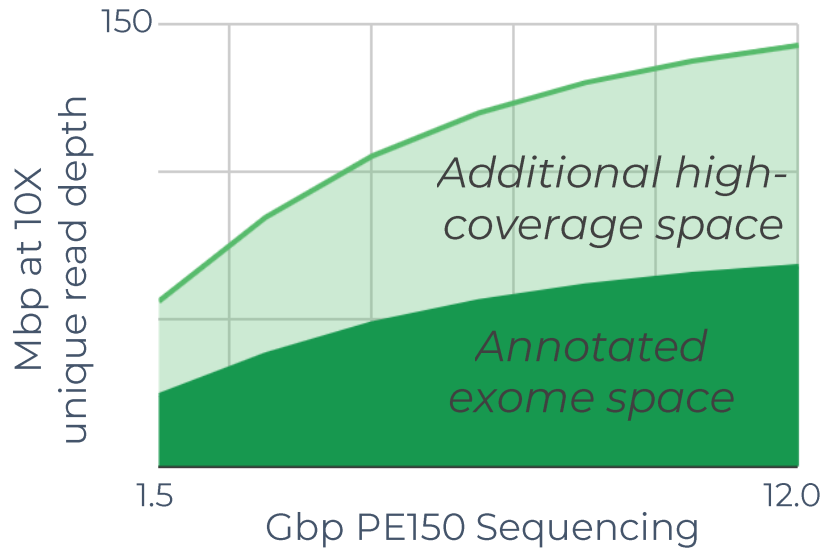
Tetraploid exome capture

Comparably high-performing



Tetraploid exome capture

Excellent genome-wide mutation discovery potential

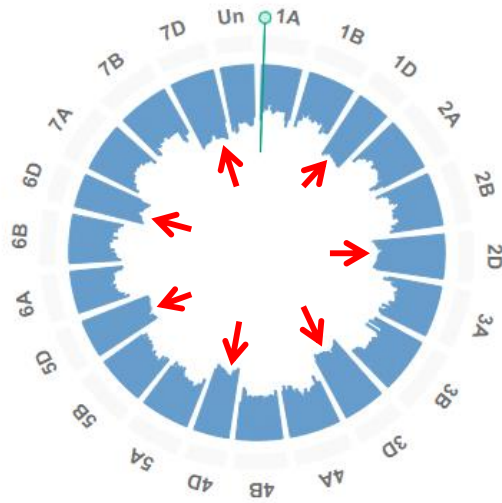


Diploid exome capture

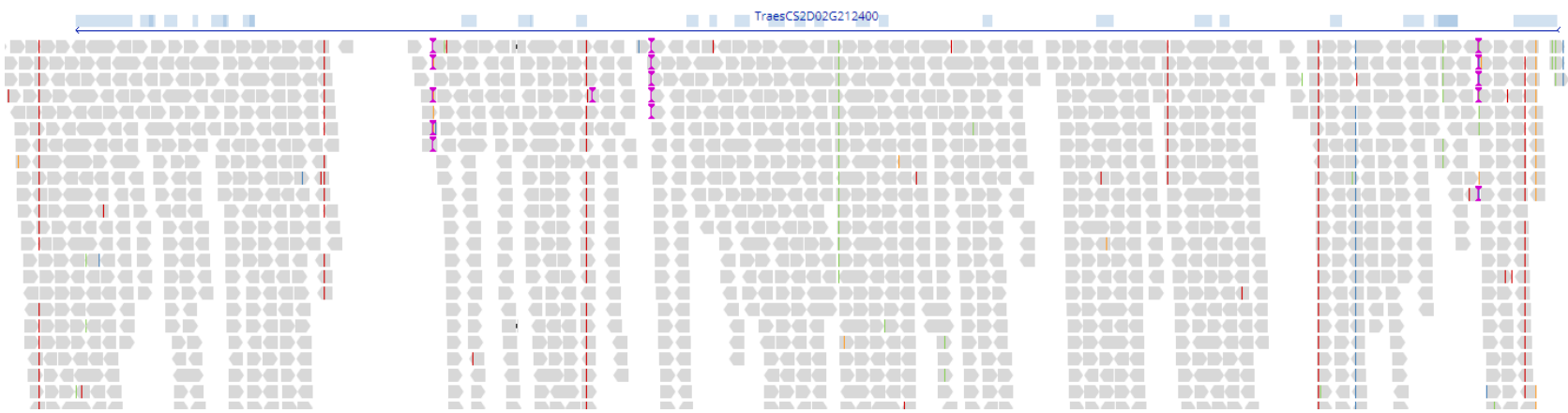
Good coverage even at highly divergent loci



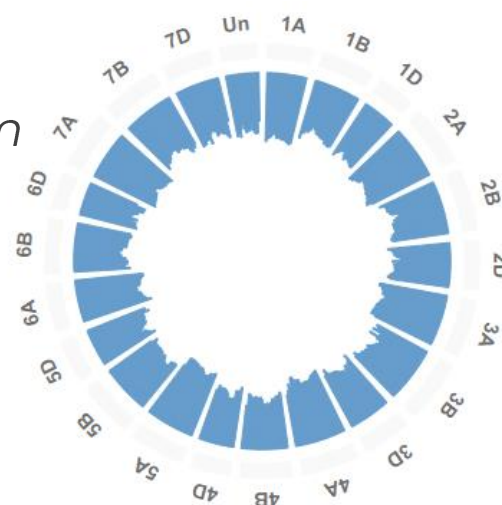
Aegilops tauschii
48%
on-target



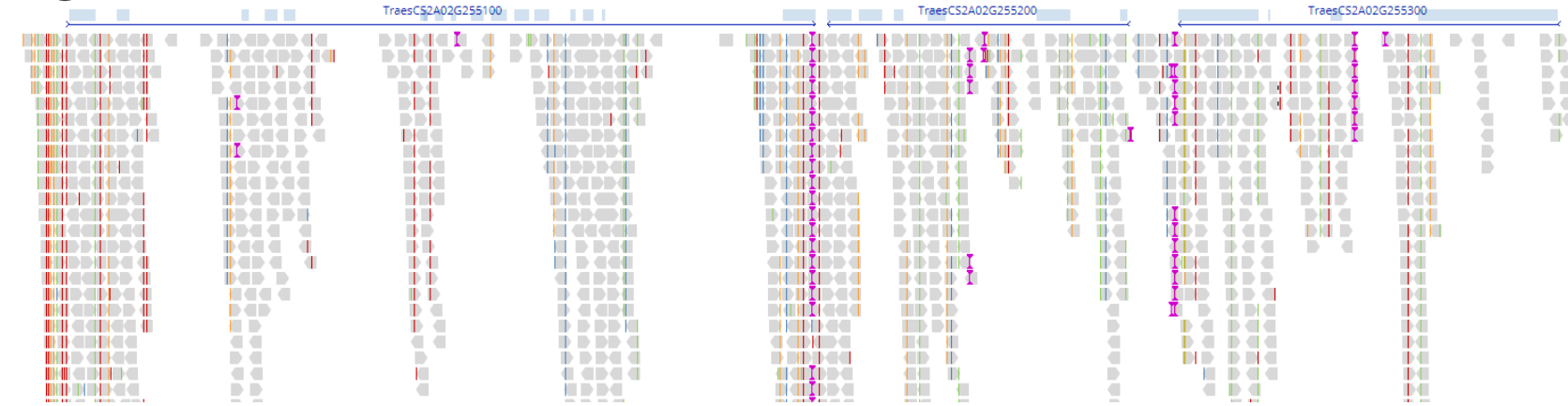
Locus on chr 2D



Triticum monococcum
45%
on-target



3 genes on chr 2A

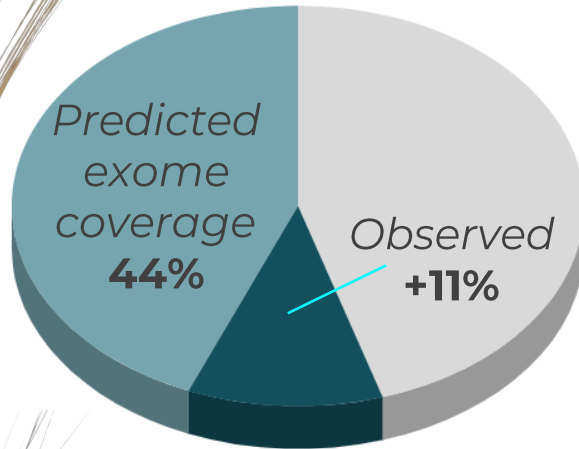


Non-wheat exome capture

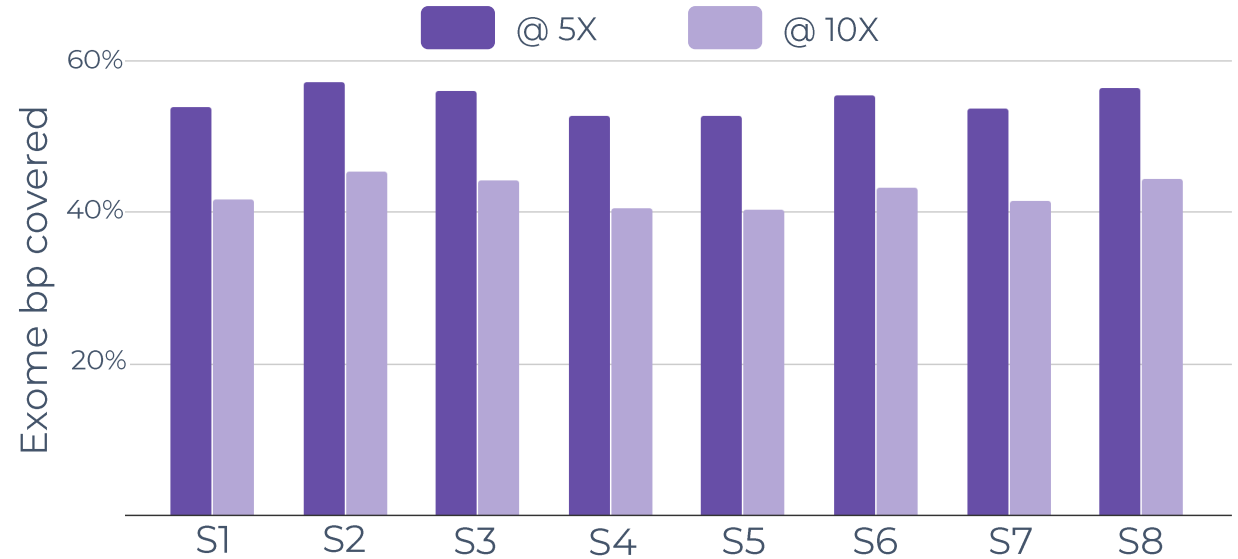
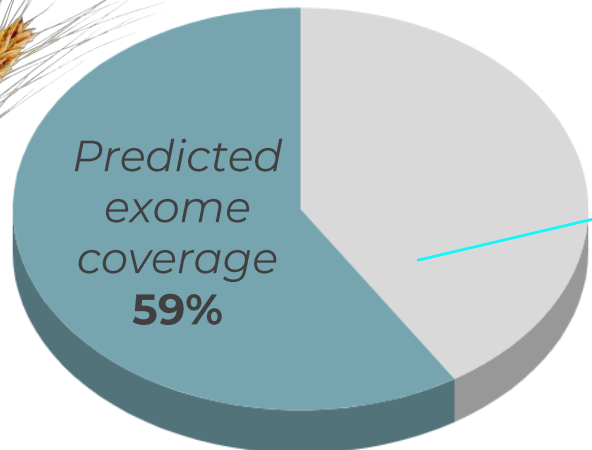
Potential for multi-taxon use



Barley
H. vulgare
121 Mbp exome*
(Morex V1)



Rye
S. cereale
28 Mbp exome





Exome Kit V1 target

vs. other wheat capture probe designs



Genome Biology

A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes

Katherine W Jordan^{1†}, Shichen Wang^{1†}, Yanni Lun^{1,2}, Laura-Jayne Gardiner³, Ron MacLachlan⁴, Pierre Huel⁴, Krysta Wiebe⁴, Debbie Wong⁵, Kerrie L Forrest⁵, IWGS Consortium, Andrew G Sharpe⁶, Christine HD Sidebottom⁶, Neil Hall⁷, Christopher Toomajian¹, Timothy Close⁷, Jorge Dubcovsky^{8,9}, Alina Akhunova^{1,2}, Luther Talbert¹⁰, Urmil K Bansal¹¹, Harbans S Bariana¹¹, Matthew J Hayden⁵, Curtis Pozniak⁴, Jeffrey A Jeddelloh¹², Anthony Hall³ and Eduard Akhunov^{1*}



Uncovering hidden variation in polyploid wheat

Ksenia V. Krasileva^{a,b,c}, Hans A. Vasquez-Gross^a, Tyson Howell^a, Paul Bailey^c, Francine Paraiso^a, Leah Clissold^c, James Simmonds^d, Ricardo H. Ramirez-Gonzalez^{c,d}, Xiaodong Wang^a, Philippa Borrill^d, Christine Fosker^c, Sarah Ayling^c, Andrew L. Phillips^e, Cristobal Uauy^{a,1,2}, and Jorge Dubcovsky^{a,1,2}

^aDepartment of Plant Sciences, University of California, Davis, CA 95616; ^bThe Sainsbury Laboratory, Norwich NR4 7UH, United Kingdom; ^cThe Earlham Institute, Norwich NR4 7UG, United Kingdom; ^dJohn Innes Centre, Norwich NR4 7UH, United Kingdom; ^eRothamsted Research, Harpenden AL5 2JQ, United Kingdom; and ¹Howard Hughes Medical Institute, Chevy Chase, MD 20815

Contributed by Jorge Dubcovsky, December 20, 2016 (sent for review November 22, 2016; reviewed by Beat Keller and Joachim Messing)

PNAS

Integrating genomic resources to present full gene and putative promoter capture probe sets for bread wheat

Laura-Jayne Gardiner^{1,2}, Thomas Brabbs¹, Alina Akhunov^{1,3}, Katherine Jordan^{1,3}, Hikmet Budak^{1,4}, Todd Richmond^{1,5}, Sukhwinder Singh⁶, Leah Catchpole¹, Eduard Akhunov^{1,3} and Anthony Hall^{1,7,*}

OXFORD GIGA SCIENCE

230 Mbp

107

Total target sequence in design

104

Target sequence mappable to RefSeq

61 Mbp

Portion @ 5X w/Arbor kit
(Hexaploid, ~18 Gbp sequencing)

59%

84

65

57 Mbp

88%

518

450

238 Mbp

53%

Wheat Exome Kit

WHAT'S NEXT

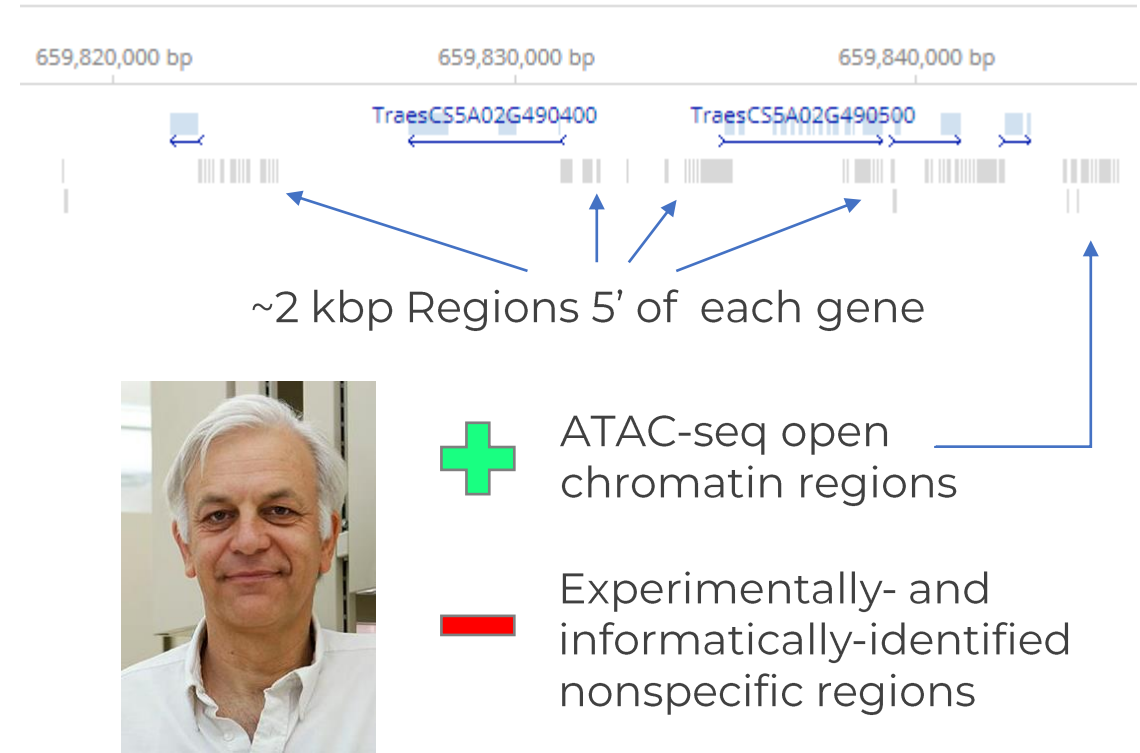
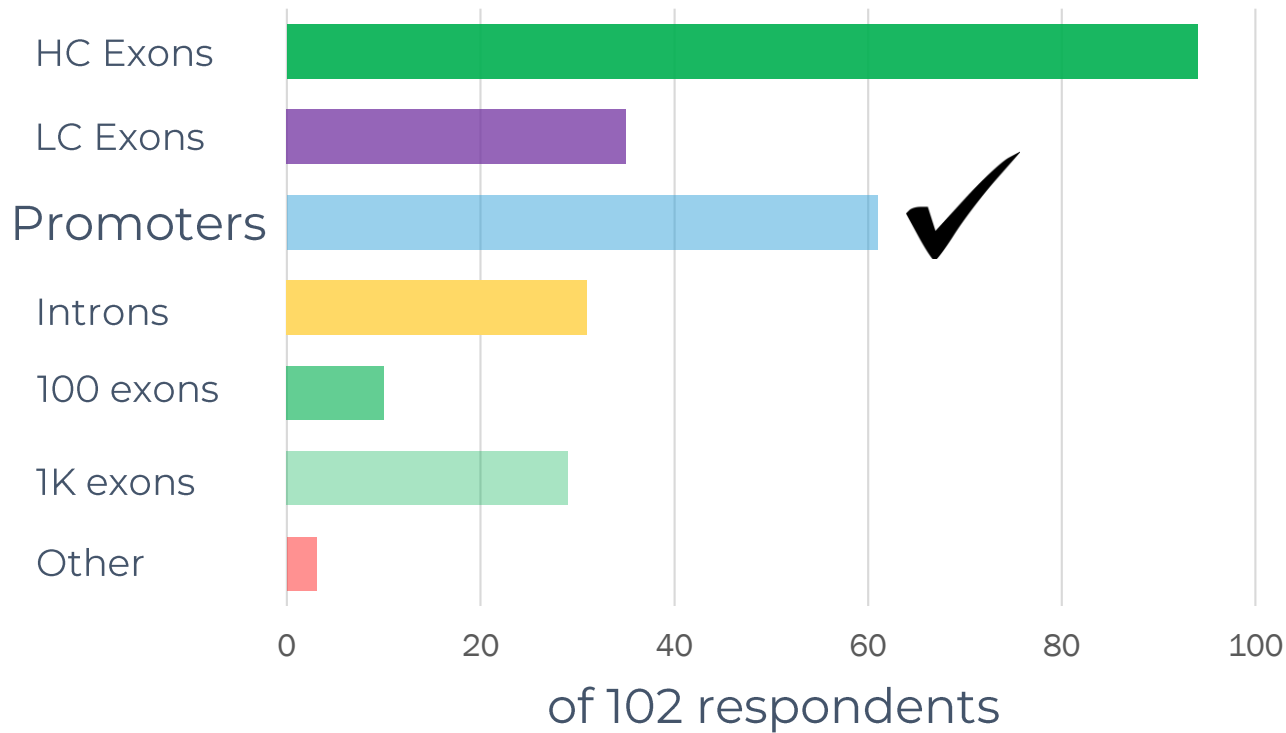


Additional modules

Promoters from RefSeq and others



Q: What would be useful to your research?



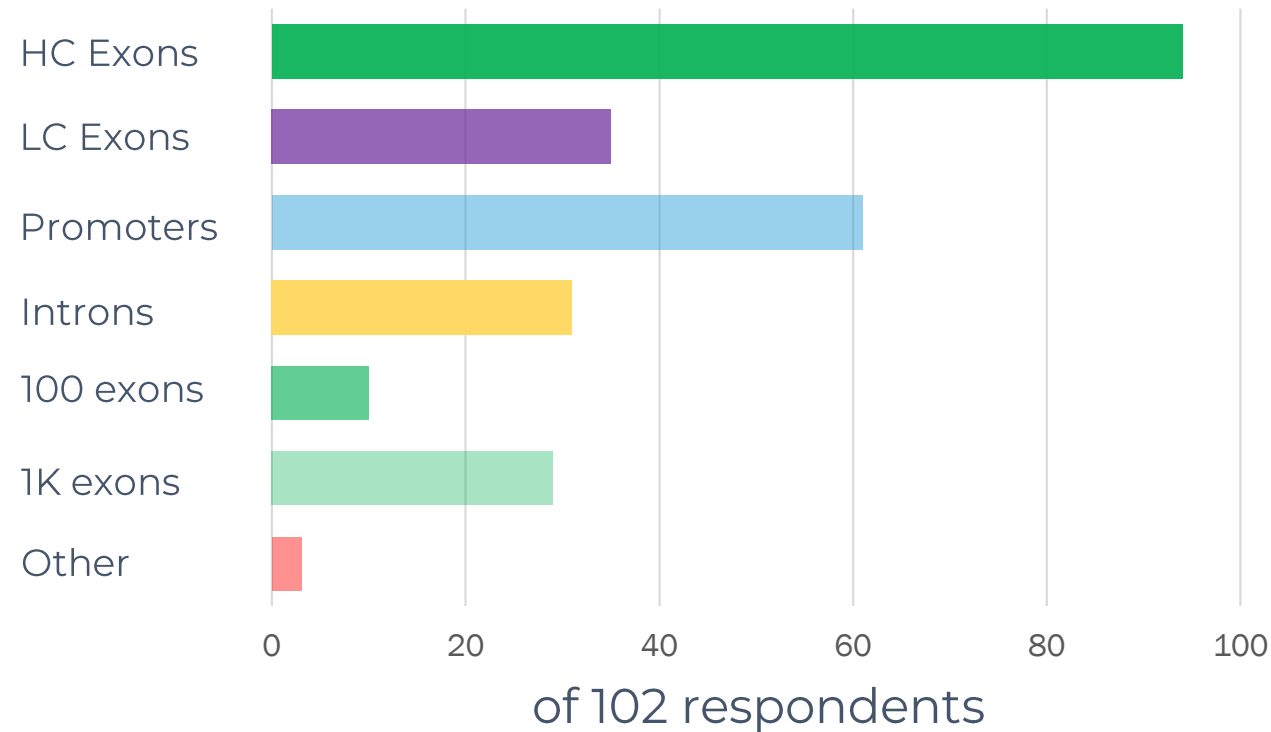
Final: 191 Mbp optional add-on

Additional modules

Reference sequence and annotation updates



Q: What would be useful to your research?



+ New RefSeq 1.0 annotations

+ RefSeq 2.0 sequence updates

+ Genome-wide SNPs

Offerings in perspective

Cost-effective exome capture and custom options



Your Lab

+ USD \$37/sample

Your gDNA

Your Library Prep

my Baits[®]

Your Sequencing

my Reads[®]

USD \$539/sample (hexaploid)

Your gDNA

Arbor Library Prep

my Baits[®]

Arbor Sequencing

 **CURIO**

CUSTOM ADD-ONS

- Introns
- New exons
- NB-LRR candidates

25%

discount

For the rest of 2020 with purchase
of Wheat Exome Core Kit

Special Thanks



Advisors and Beta Testers

Burkhard Steuernagel



Sreya Ghosh



Ute Baumann



Etienne Paux



Sébastien Praud



Expansion Leaders

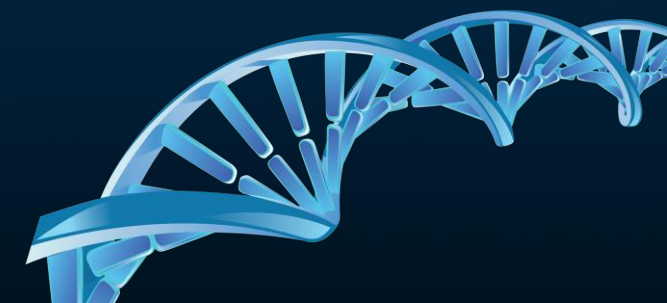
Jorge Dubcovsky



Jan Gielen



Vijay Tiwari





myBaits Expert — Predesigned Panels

myBaits Expert Wheat Exome



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Thanks!