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Joshua C Stein, Victor Llaca, Kevin Fengler, Catalina Johnson, Isabelle Caugant, Elodie Belmonte, Vincent Paillet, Hugo Zalzale, Leonardo I Pereyra-Bistrain, Clément Debiton, et al.

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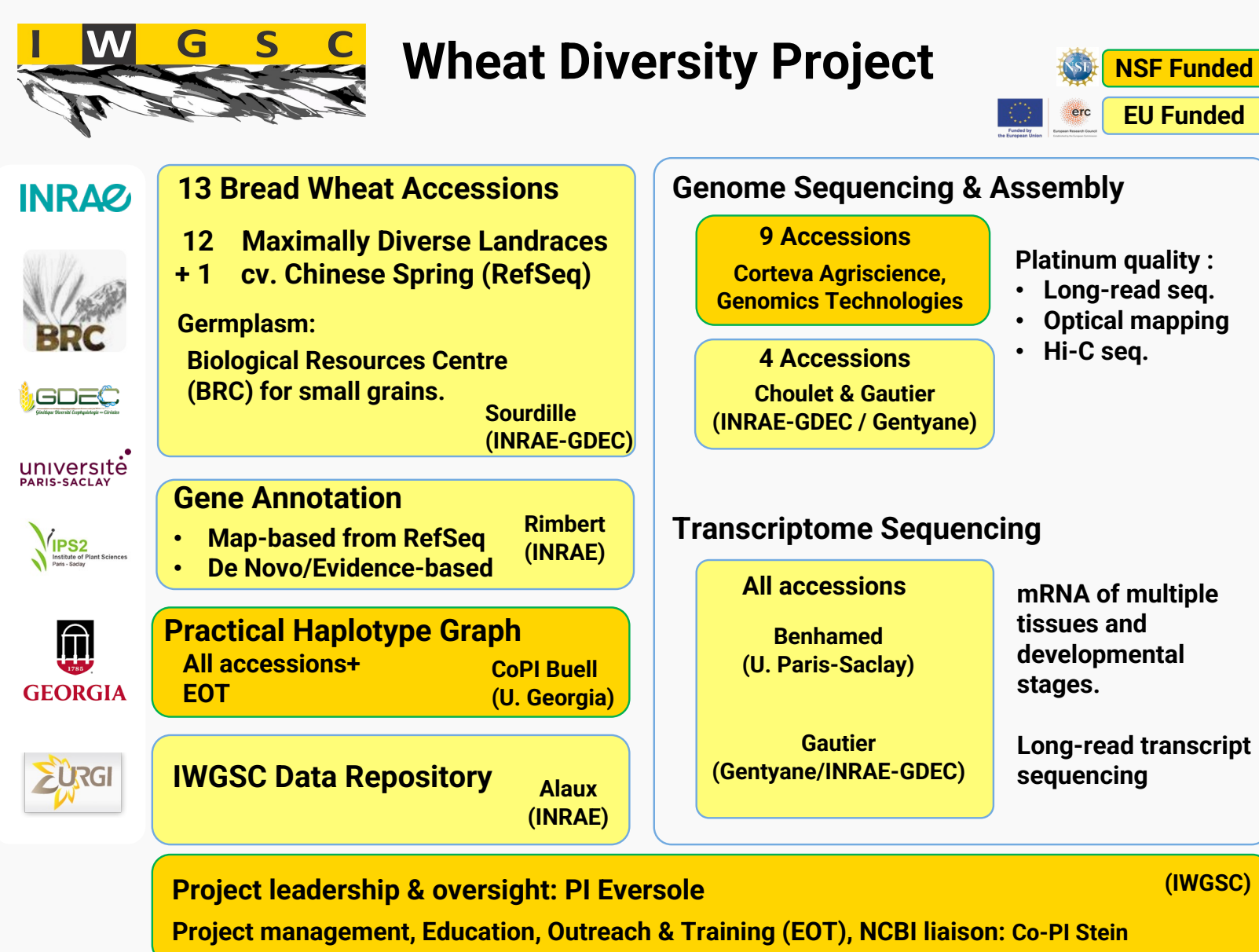
# IWGSC 2.0: Implementing the Wheat Diversity Project

The International Wheat Genome Sequencing Consortium<sup>1</sup>, Joshua C. Stein<sup>1</sup>, Victor Llaca<sup>2</sup>, Kevin Fengler<sup>2</sup>, Catalina Johnson<sup>1,3</sup>, Isabelle Caugant<sup>1</sup>, Elodie Belmonte<sup>4</sup>, Vincent Pailler<sup>3</sup>, Hugo Zalzal<sup>5</sup>, Leonardo Pereyra-Bistraín<sup>5</sup>, Clément Debiton<sup>4</sup>, Pauline Lasserre-Zuber<sup>4</sup>, Sophie Bouchet<sup>4</sup>, John P. Hamilton<sup>6</sup>, Pierre Marin<sup>4</sup>, Isabelle Lhommet<sup>4</sup>, Hélène Rimbart<sup>4</sup>, Michael Alaux<sup>7</sup>, Véronique Gautier<sup>4</sup>, Pierre Sourdille<sup>4</sup>, C. Robin Buell<sup>6</sup>, Frédéric Choulet<sup>4</sup>, Moussa Benhamed<sup>5</sup>, Kellye Eversole<sup>1</sup>

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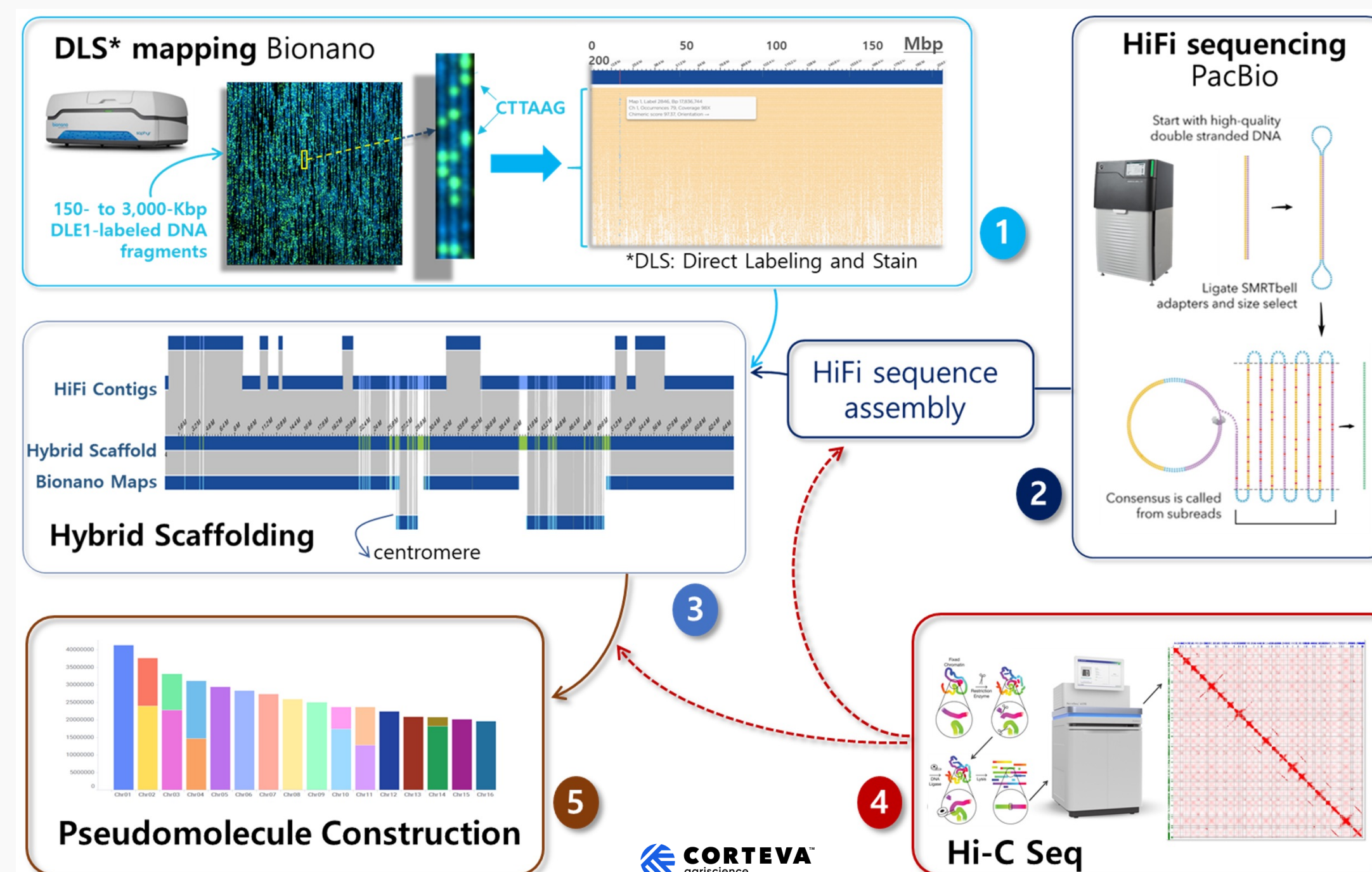
Preserve, discover, and mobilize genetic resources by sequencing landrace genomes that encompass the worldwide diversity of bread wheat.

International initiative to unlock bread wheat diversity by sequencing 12 maximally diverse landrace genomes & update RefSeq Chinese Spring

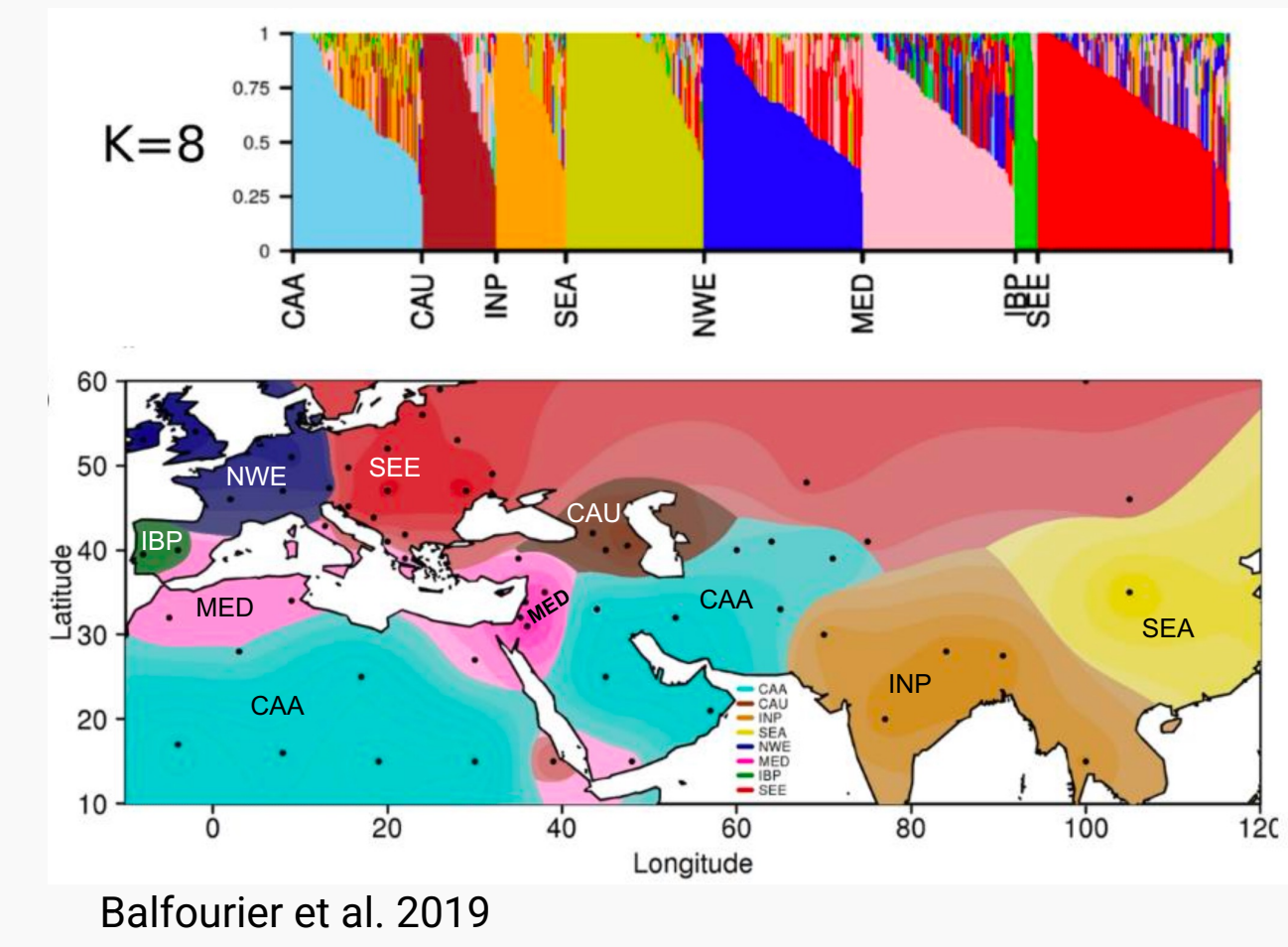


**Aim 1) Platinum genome assemblies for 12 maximally diverse landraces and Chinese Spring (CS)**  
**Aim 2) Transcriptome long-reads and gene annotation for 12 landraces while sustaining IWGSC CS RefSeq as a community-curated resource**  
**Aim 3) Practical Haplotype Graph (PHG) to catalog all genetic diversity in bread wheat and enable community-driven discoveries across the species;**  
**Aim 4) Increase STEM diversified workforce through education outreach, and training.**

**Aim 1: Platinum genomes of 12 maximally diverse landraces and cv. Chinese Spring**



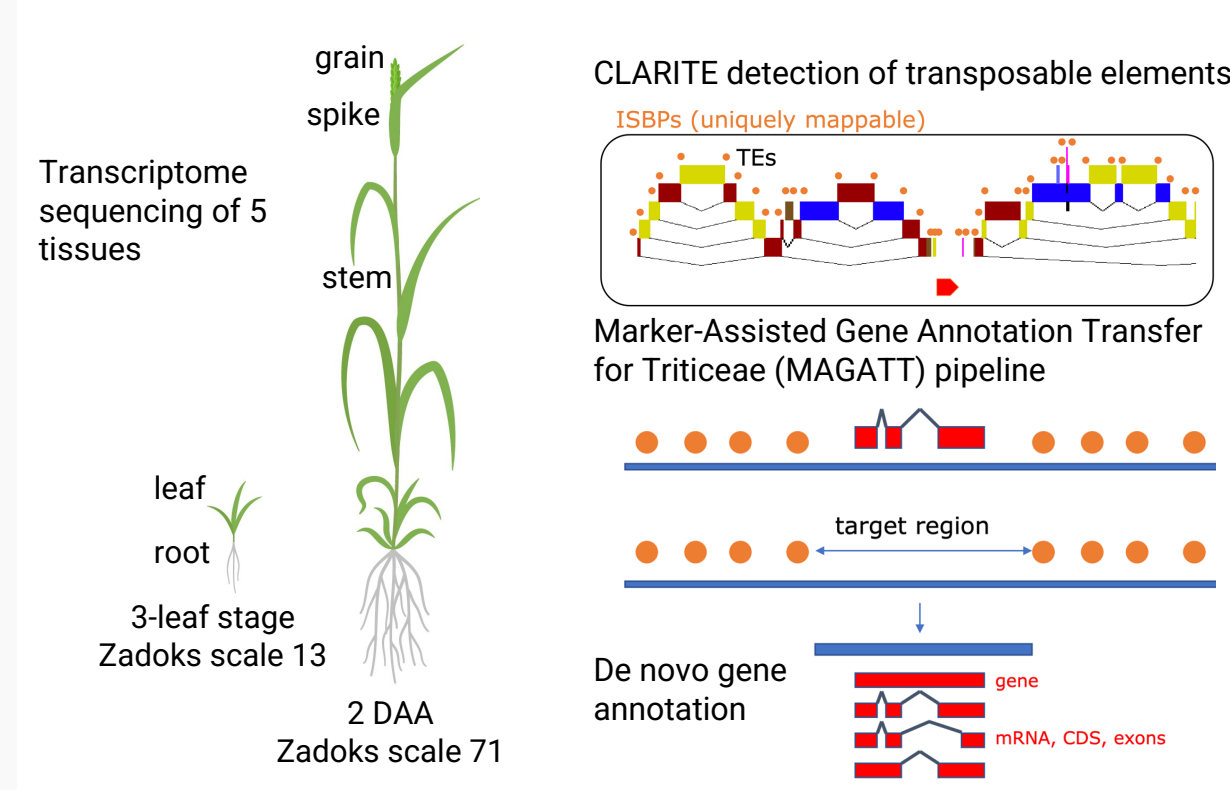
- 8 phylogeographic haplogroups among 632 genotyped landraces = subpopulations corresponding to early regional growing centers.
- Genome sequence & assembly using long-reads, optical mapping, and conformational capture sequence.



**Aim 2: Transcriptome long-reads and gene annotation for 12 landraces and sustain IWGSC CS RefSeq as a community-curated resource**



Zhu et al. 2021  
 Leroy et al. 2012  
 Daron et al. 2014



**Aim 1 Progress: primary data production and preliminary assemblies**

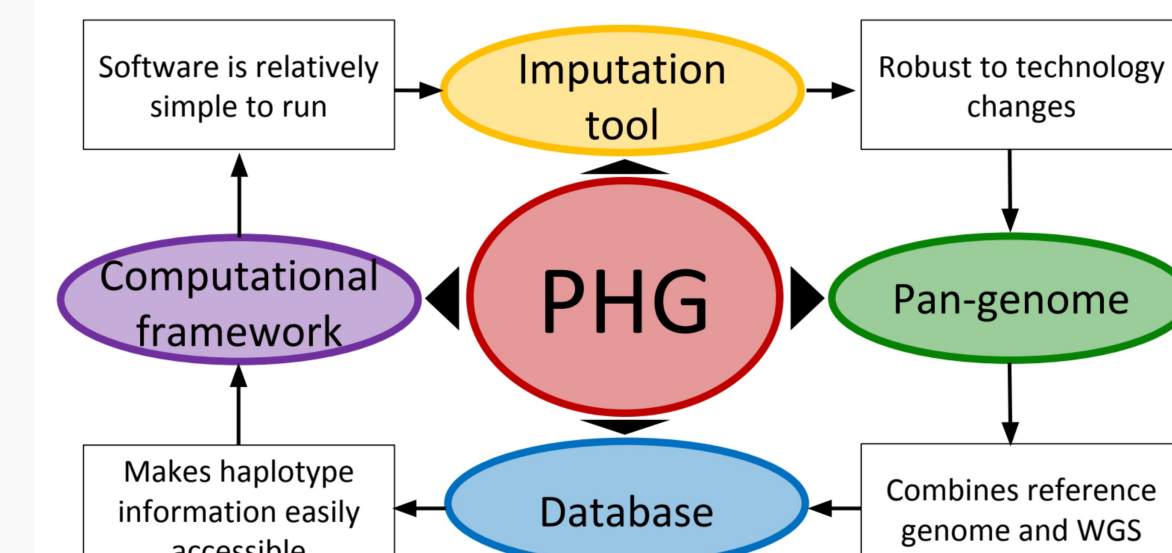
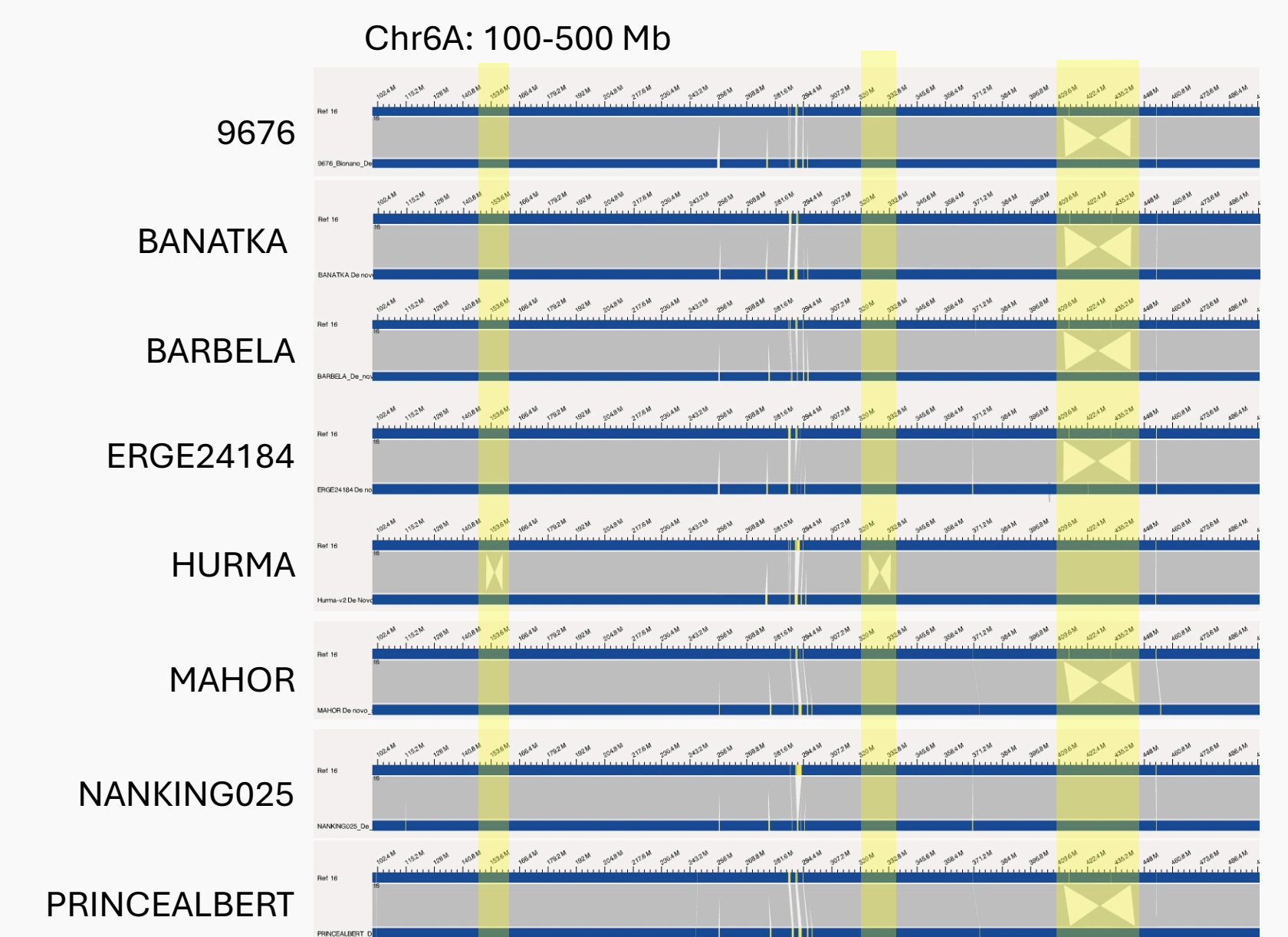
Accession	1 Bionano DLS	2 PacBio HiFi	3 Hybrid Scaffold	4 Illumina Hi-C	5 Pseudo molecule
CHINESE SPRING					
HURMA					
ERG324184					
9676					
NANKING-NO-25					
PRINCE-ALBERT					
MAHOR					
BARBELA					
BANATKA					
BLANC DE HAUTE SAONE					
POCHO					
BINTANE					
SBEI					

**GENTYANE (France)** (In Progress)

Legend: In Progress (light purple), Completed (dark purple)

Summary for 9 genomes:	Average Fold Coverage (X)	Average Assembly N50 (Mb)	Average Total Length (Mb)
Bionano DLS	94 ± 8	78.9 ± 9.5	14,683 ± 81
PacBio HiFi	35 ± 2	51.3 ± 8.5	14,485 ± 22
DLS/HiFi Hybrid Scaffold	NA	226.7 ± 28.8	14,478 ± 28
Illumina Hi-C	38 ± 7	NA	NA

**Initial comparative genomic views (Bionano maps) show value in revealing conserved and novel structural variation**



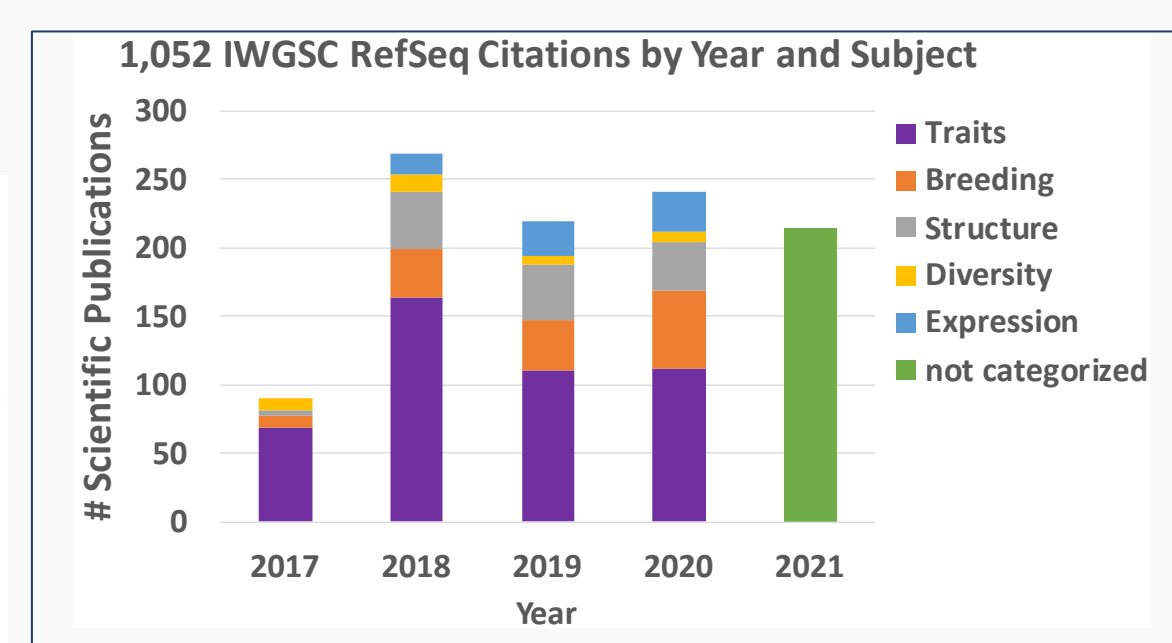
**Aim 3: Construct a Practical Haplotype Graph (PHGv2) to catalog all genetic diversity within bread wheat and enable community-driven discoveries across the species**

Bradbury et al. 2022

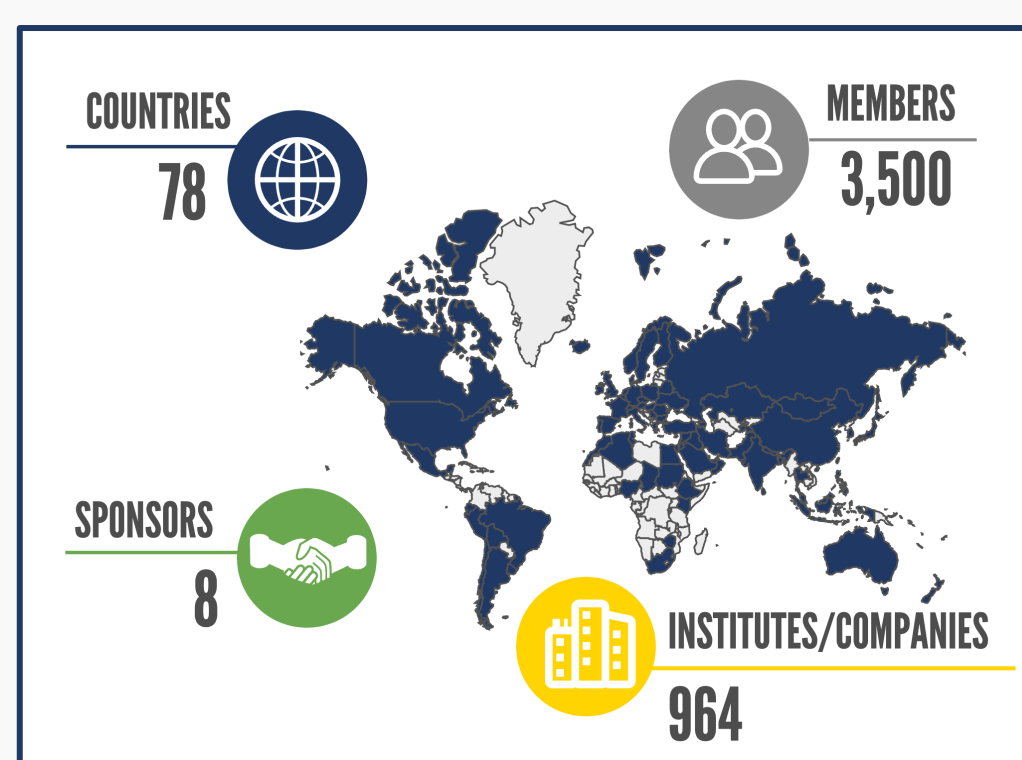
**IWGSC: 19 years delivering essential genomic tools by and for the wheat community**

**Scientific impact of Chinese Spring RefSeq & annotation**

- 2021: Version 2.1 Chinese Spring RefSeq and annotation
- 2018: Publication and analysis of IWGSC RefSeq v1.0
- 2016: Shotgun assembly (IWGSC WGA v0.4)
- 2015: Physical maps for all chromosomes
- 2014: First chromosome-based draft
- 2005: IWGSC formed



**Education, outreach, and training**



- Annual IWGSC workshops at PAG since 2007
- IWGSC and Catherine Feuillet Early Career Award
- IWGSC Webinar Series since 2020
- IWGSC Newsletter
- IWGSC General Membership
- IWGSC 2024 Undergraduate Summer Intern

**Sponsors**



**References**

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