河南農業大學
Henan Agricultural University

CASCA
2026
The First China-Australia Symposium
on Crop Stress and Climate Adaptation

# Chromosome-level genome assembly of the Durum wheat cultivar Langdon

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March 13, 2026

# Outline

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2 **Result**

3 **Summary**

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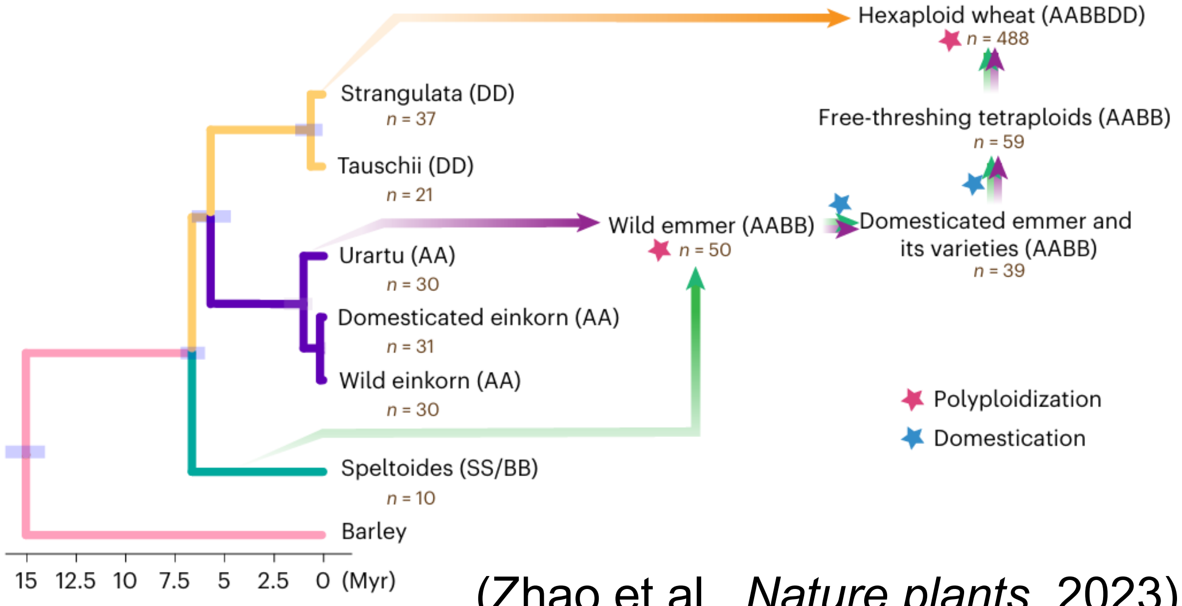
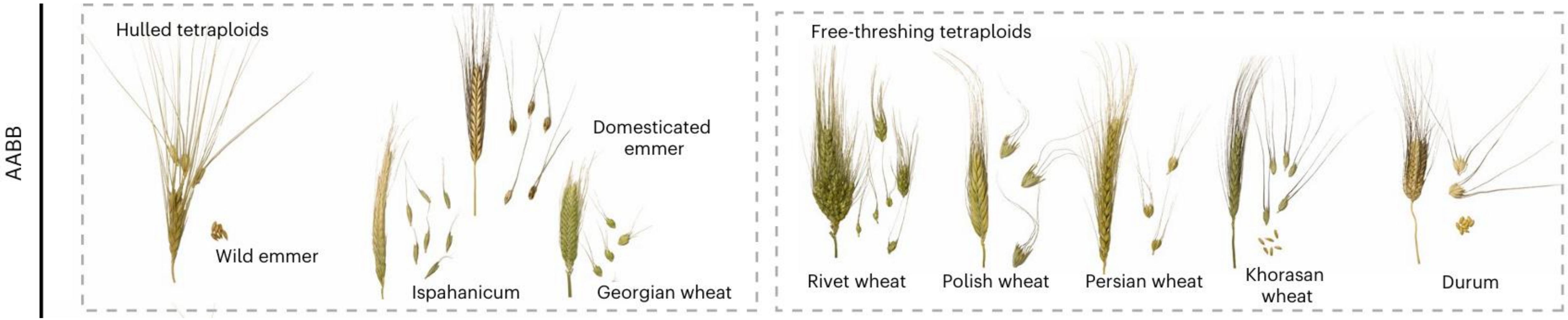
# 1. Backgroud

# 1.1 Durum wheat

- Durum wheat (*Triticum turgidum ssp. durum*, 2n = 4x = 28, BBAA) is the second most widely cultivated wheat species in the world, it plays a pivotal "bridging" role in the evolution of wheat.

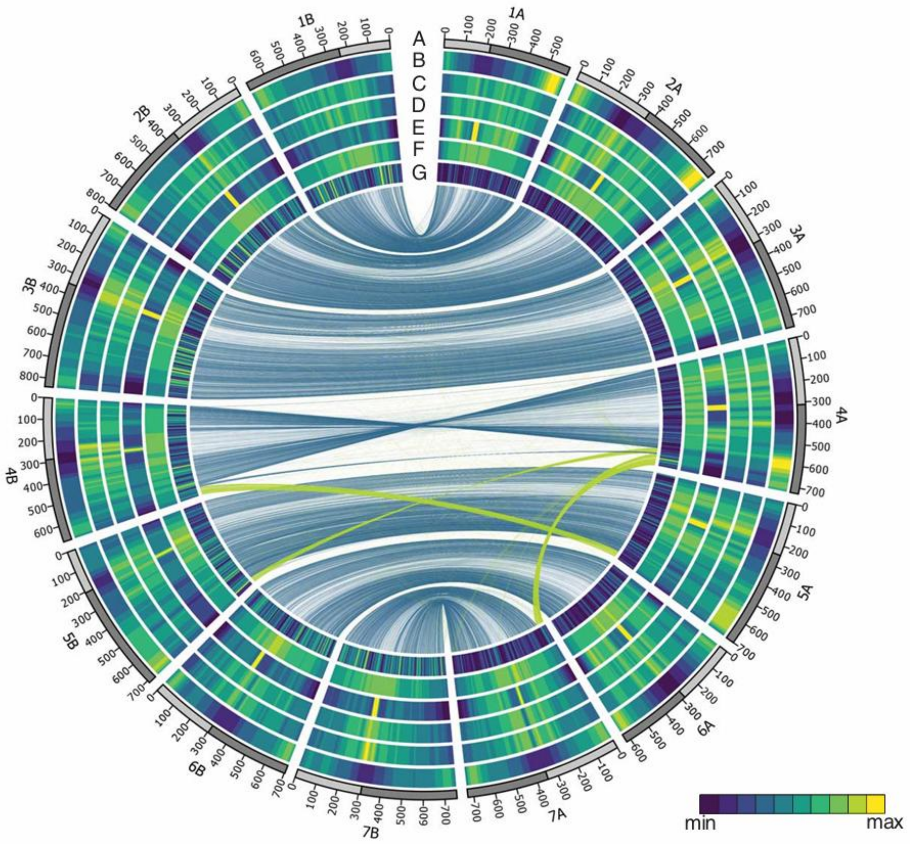


(Zhao et al., *Nature plants*, 2023)

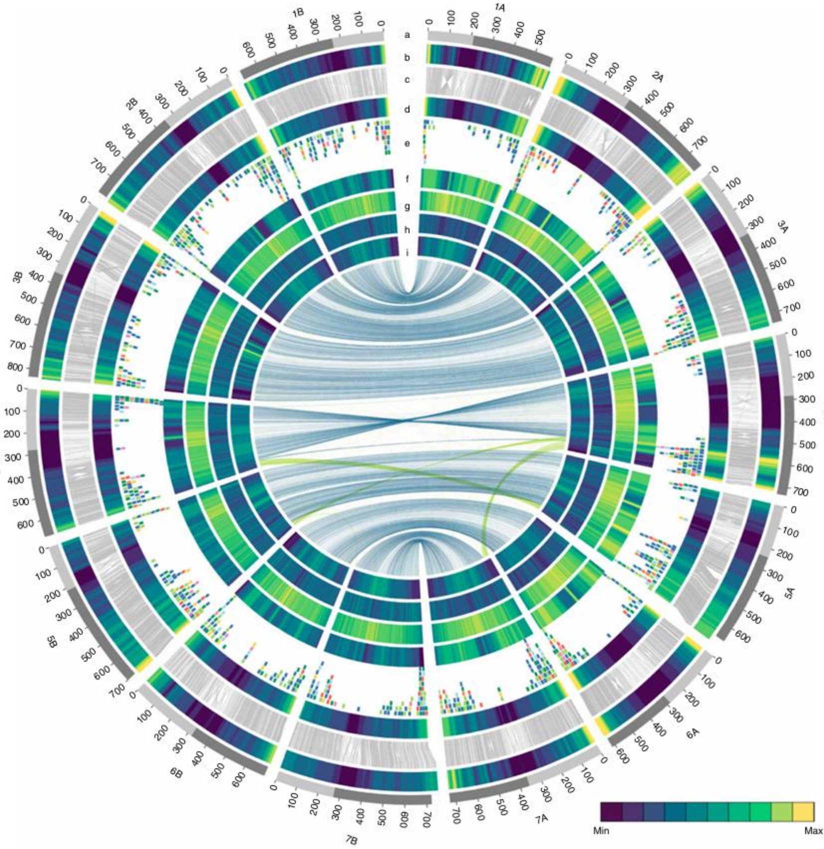


# 1.2 Previous research

- Due to the limitations of NGS technologies, the assembled genomes of Svevo and Zavitan contain numerous gaps



Wild emmer zavitan genome
(Avni et al., *Nature,* 2017)



Durum wheat svevo genome
(Maccaferri et al., *Nature Genetics*, 2019)

# 1.3 Research significance

- As the parent of synthetic wheat, durum wheat cultivar Langdon serves as a bridge to introduce elite genes from wild relatives into modern common wheat, enhance the stress resistance of wheat.

AABBCC

Langdon (AABB) **Langdon/PI551139 (AABBCC)** PI551139 (CC)

AABBMM

PI349045 (AABB) **PI349045/PI551061 (AABBMM)** PI551061 (MM)

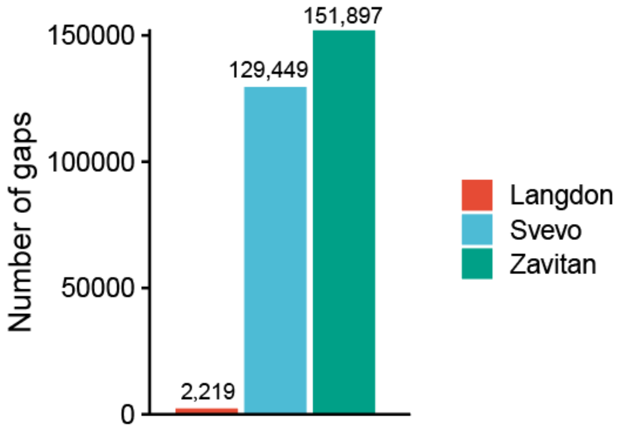
AABBUU

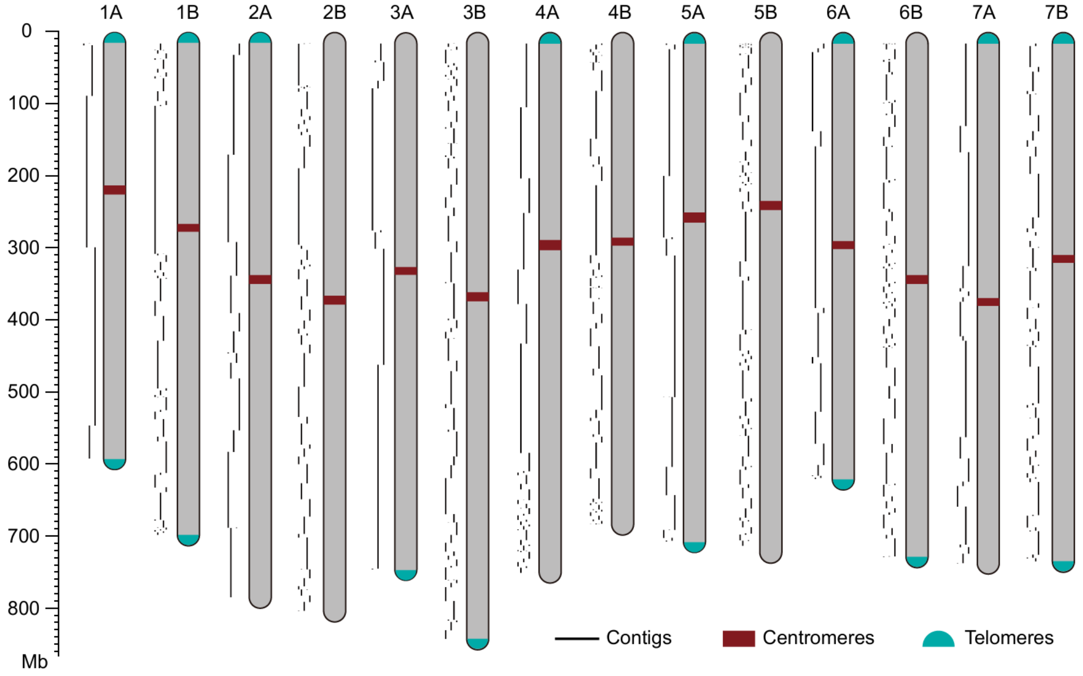
Langdon (AABB) **Langdon/PI554395 (AABBUU)** PI554395 (UU)

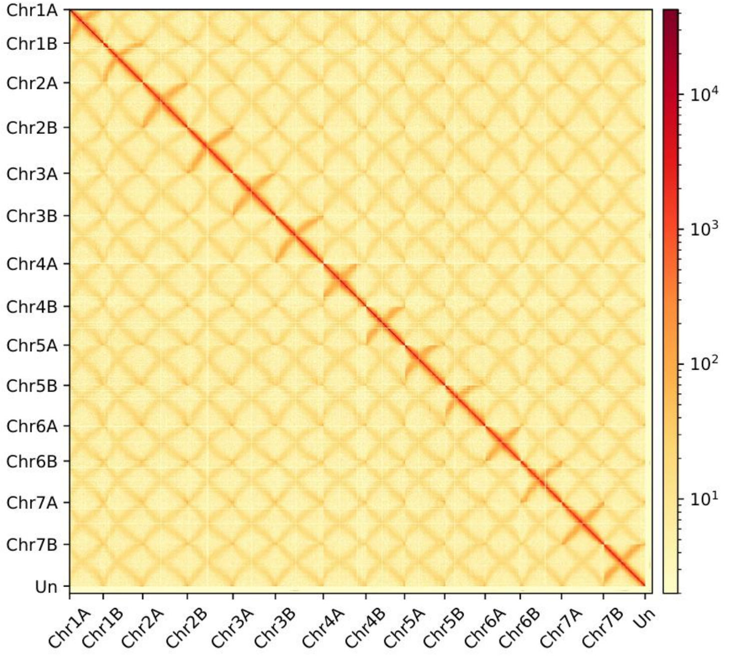
# 2. Result

# 2.1 HiFi + Hi-C assembly

- Assembled genome size : 10.47 Gbp
- Anchored onto 14 chromosomes : 10.38 Gbp (99.1%)
- Number of scaffolds : 724,   N50: 751.3 Mbp
- Number of contigs : 2,234, N50: 41.2 Mbp
- Number of gaps : 2,219

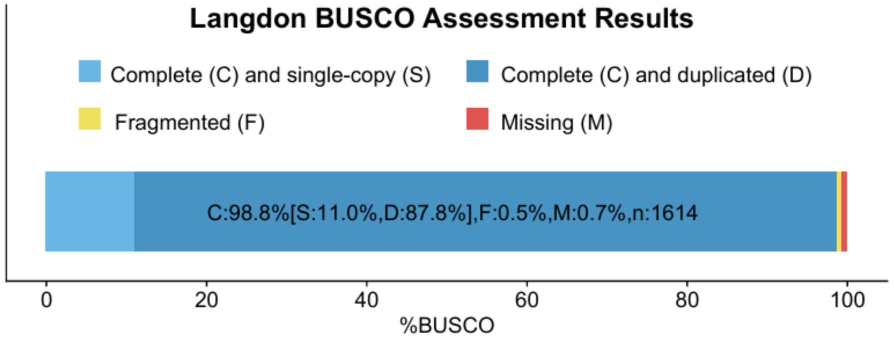


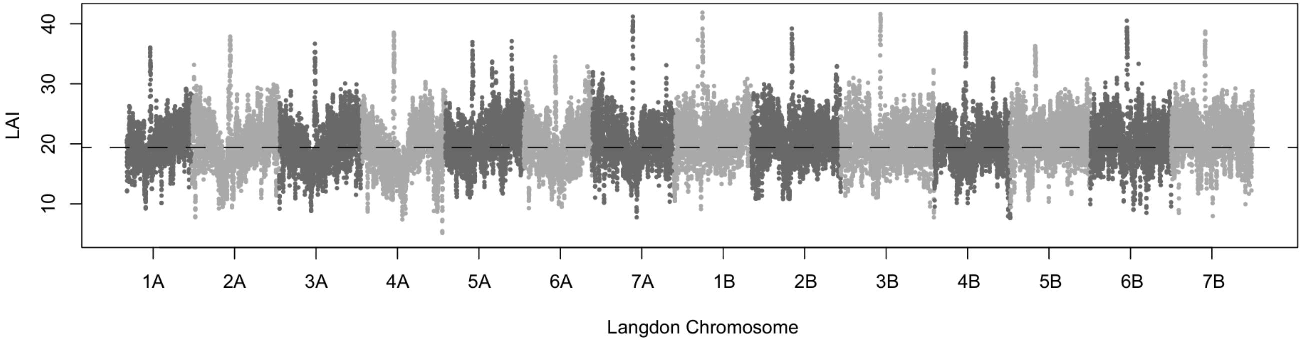


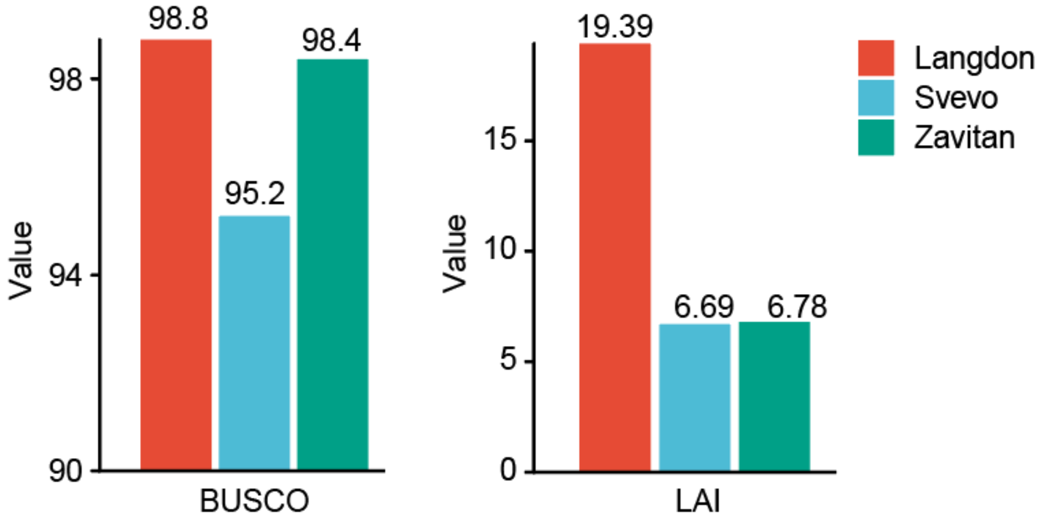


# 2.2 Quality assessment

- BUSCO score : 98.80%
- Consensus nucleotide quality value (QV) score : 50.31
- Whole genome long terminal repeat assembly index (LAI) : 19.39

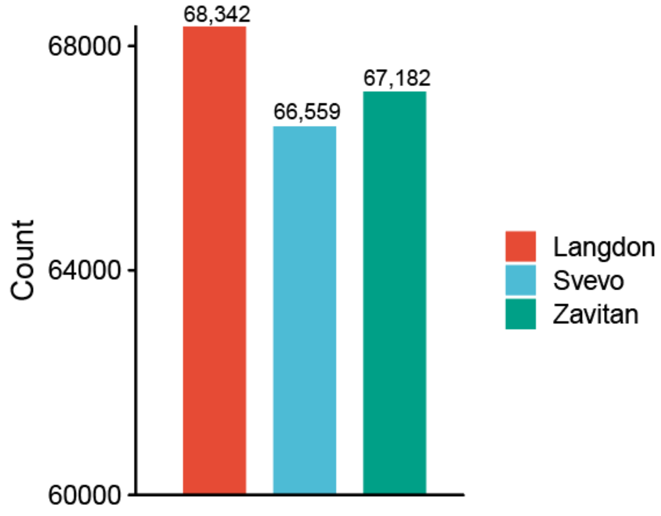


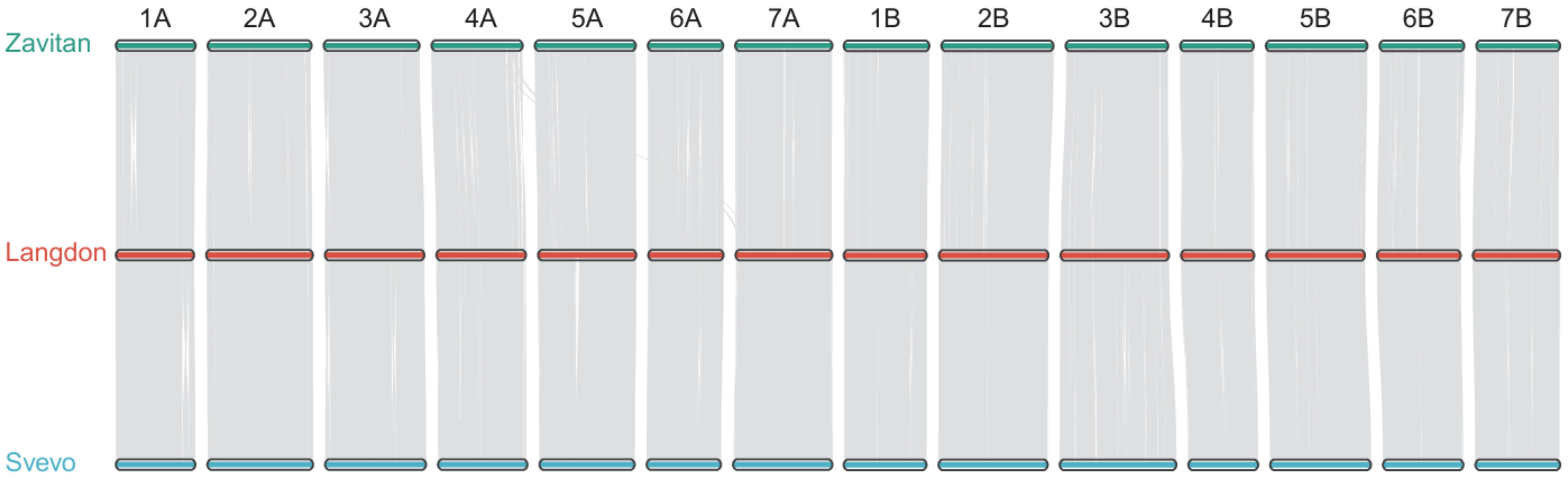




# 2.3 Gene annotation

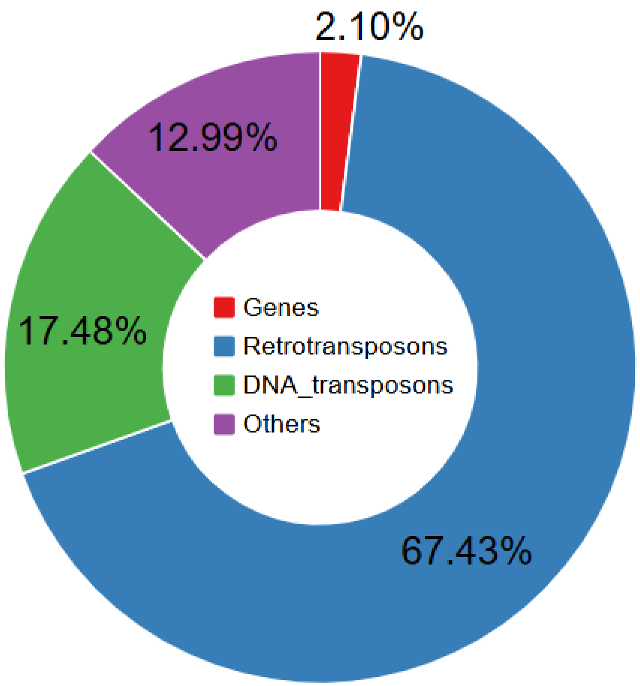
- Number of high confidence genes : 68,342
- Number of transcripts : 73,942
- Genes of Langdon, Svevo, and Zavitan show good collinearity





# 2.4 TE annotation

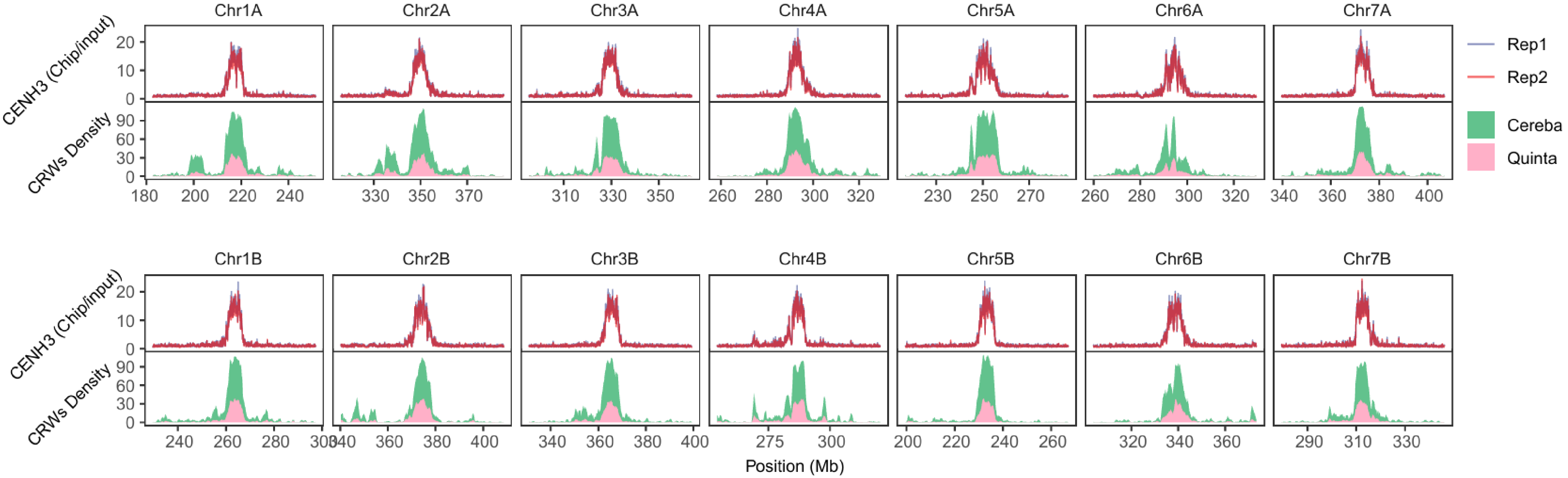
- Total TE
  9.24 Gpb (88.22%)



| Class | Super family | Family name | Count | Length (bp) | Percentage (%) |
|---|---|---|---|---|---|
| ClassI (Retrotransposon) | LTR | | | | |
| | | Gypsy | 1,456,157 | 4,857,389,235 | 46.27 |
| | | Copia | 561,792 | 1,718,008,862 | 16.37 |
| | | Unclassified | 249,883 | 431,855,766 | 4.11 |
| | Non-LTR | | | | |
| | | LINE | 69,387 | 55,485,854 | 0.53 |
| | | SINE | 4,361 | 839,911 | 0.01 |
| ClassII (DNA transposon) | DNA TE | | | | |
| | | CACTA | 1,159,570 | 1,448,008,558 | 13.79 |
| | | Mutator | 203,107 | 87,640,115 | 0.83 |
| | | Unclassified TIRs | 68,174 | 18,523,194 | 0.18 |
| | | PIF/Harbinger | 123,310 | 54,623,978 | 0.52 |
| | | Tcl/Mariner | 334,781 | 110,043,307 | 1.05 |
| | | Unclassified | 9,619 | 6,986,316 | 0.07 |
| | | hAT | 70,825 | 29,448,846 | 0.28 |
| | Helitron | | 171,582 | 76,154,228 | 0.73 |
| Others | | | 634,070 | 344,199,261 | 3.28 |
| Total | | | 5,116,618 | 9,239,207,431 | 88.22 |

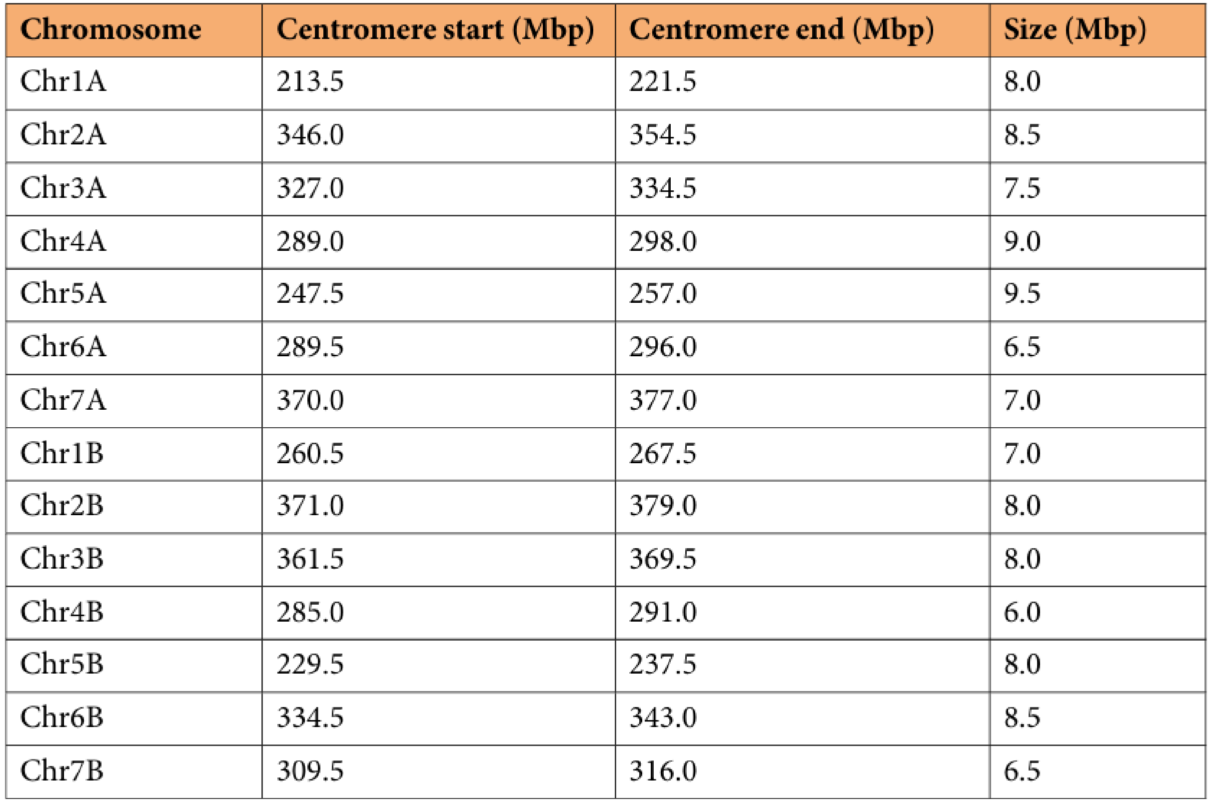
# 2.5 Centromere identification

- CENH3 Chip-seq maps centromere locations
- *Cereba* and *Quinta* LTRs are enriched in the centromeric region

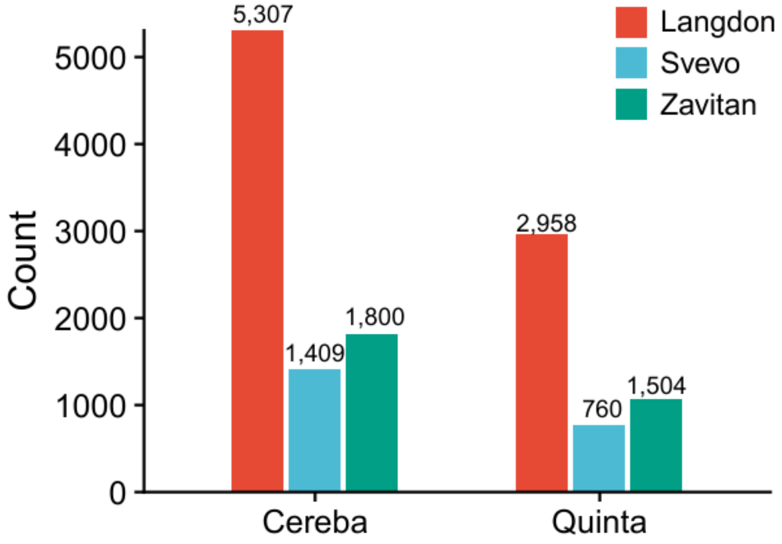


# 2.6 Near-complete centromere assembly

- Average centromere size : subA: 8 Mbp, subB: 7.4 Mbp
- Number of intact *Cereba* and *Quinta* : subA: 4,417, subB: 3,848
- Centromeres assembly in Langdon is far more complete than Svevo and Zavitan



| Chromosome | Centromere start (Mbp) | Centromere end (Mbp) | Size (Mbp) |
|---|---|---|---|
| Chr1A | 213.5 | 221.5 | 8.0 |
| Chr2A | 346.0 | 354.5 | 8.5 |
| Chr3A | 327.0 | 334.5 | 7.5 |
| Chr4A | 289.0 | 298.0 | 9.0 |
| Chr5A | 247.5 | 257.0 | 9.5 |
| Chr6A | 289.5 | 296.0 | 6.5 |
| Chr7A | 370.0 | 377.0 | 7.0 |
| Chr1B | 260.5 | 267.5 | 7.0 |
| Chr2B | 371.0 | 379.0 | 8.0 |
| Chr3B | 361.5 | 369.5 | 8.0 |
| Chr4B | 285.0 | 291.0 | 6.0 |
| Chr5B | 229.5 | 237.5 | 8.0 |
| Chr6B | 334.5 | 343.0 | 8.5 |
| Chr7B | 309.5 | 316.0 | 6.5 |



# 3. Summary

- Overall, the higher-quality assembly of Langdon serves as a valuable reference genome for advancing gene and centromere research in durum wheat

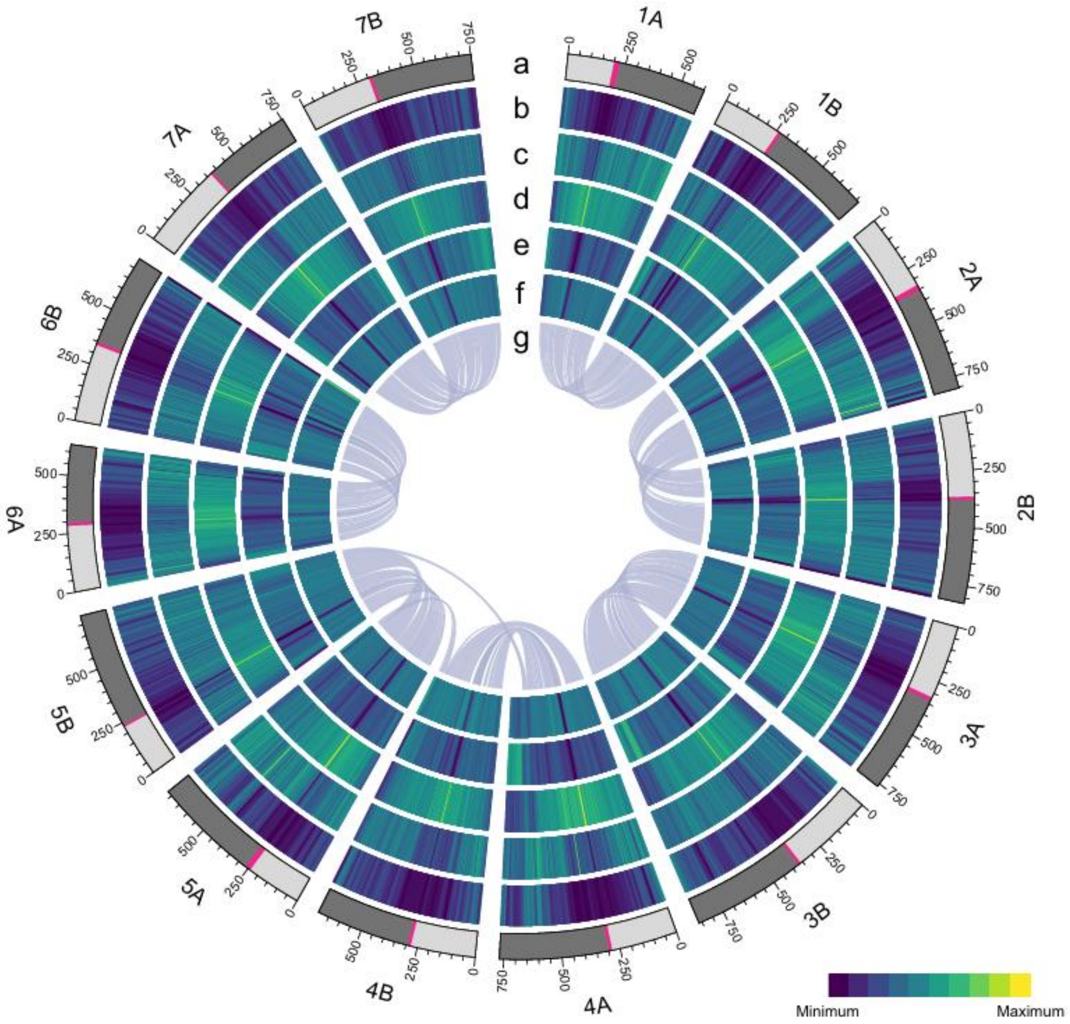
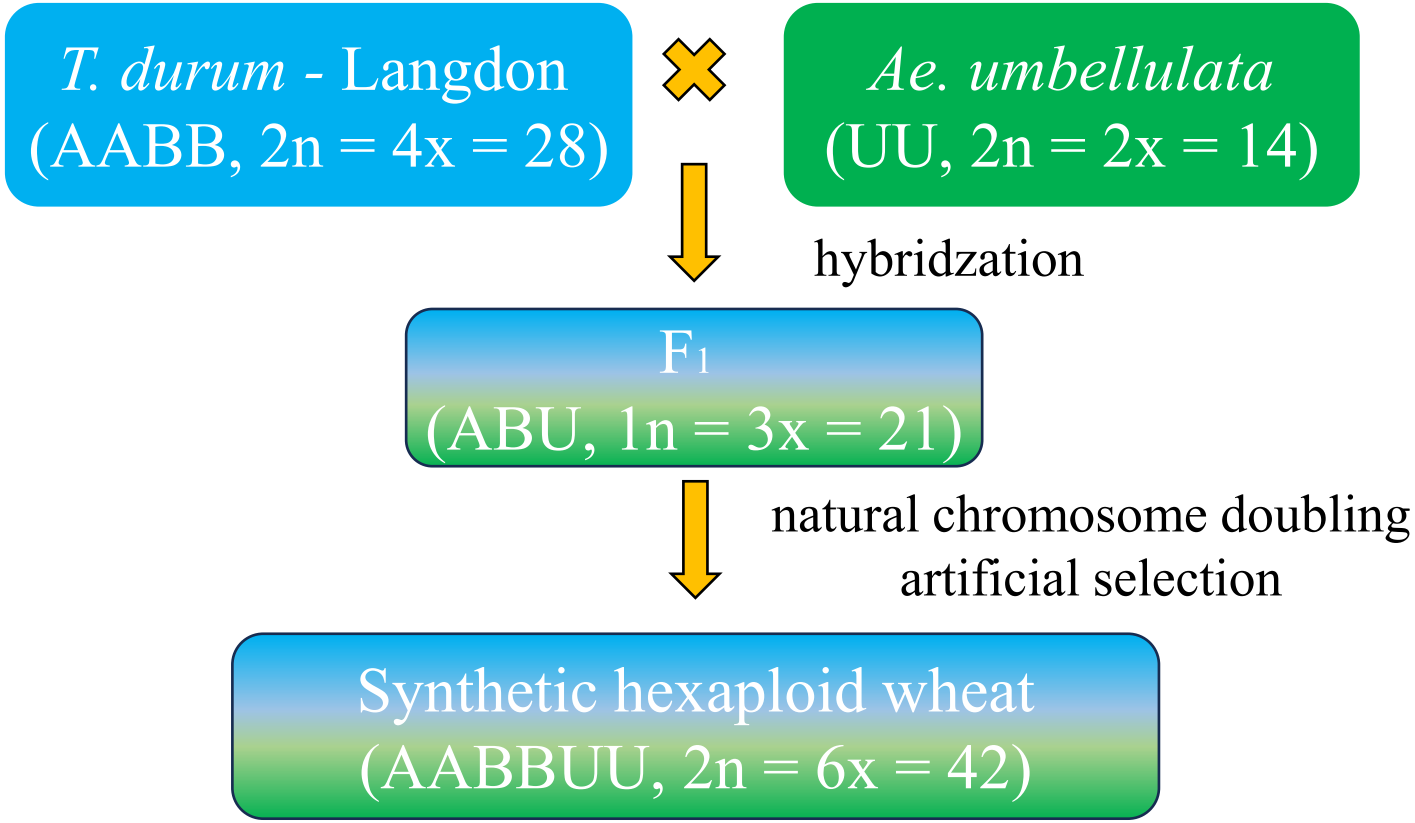


**Fig. 1** Circos display of important features of the assembled Langdon genome. The seven layers depict chromosome names and sizes, with centromere positions marked in red (**a**), density of HC genes (**b**), density of Copia retrotransposons (**c**), density of Gypsy retrotransposons (**d**), density of DNA TEs (**e**), distribution of GC content in each chromosome (**f**) and links between the syntenic chromosomes of two subgenomes (**g**). The gene and TE densities shown in circos were obtained by scanning the chromosome sequence in 3 Mbp windows.

# 4. Prospect

- Utilizing Langdon to develop synthetic hexaploid wheat, which serves as a bridge, enables the creation of translocation lines harboring elite chromosomal segments from wild relatives, thereby facilitating wheat improvement.



*T. durum* - Langdon (AABB, 2n = 4x = 28)

×

*Ae. umbellulata* (UU, 2n = 2x = 14)

hybridzation

$F_1$ (ABU, 1n = 3x = 21)

natural chromosome doubling
artificial selection

Synthetic hexaploid wheat (AABBUU, 2n = 6x = 42)

| | | |
|---|---|---|
| *Aegilops umbellulate* (UU) | Langdon (AABB) | SHW (AABBUU) |

# Acknowledgement

河南農業大學
Henan Agricultural University

Prof. Daowen Wang

Prof. Guangwei Li

四川農業大学
SICHUAN AGRICULTURAL UNIVERSITY

Prof. Zehong Yan

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