Computational Prediction and Characterization of 3D Genome Organization in *Brassica napus*

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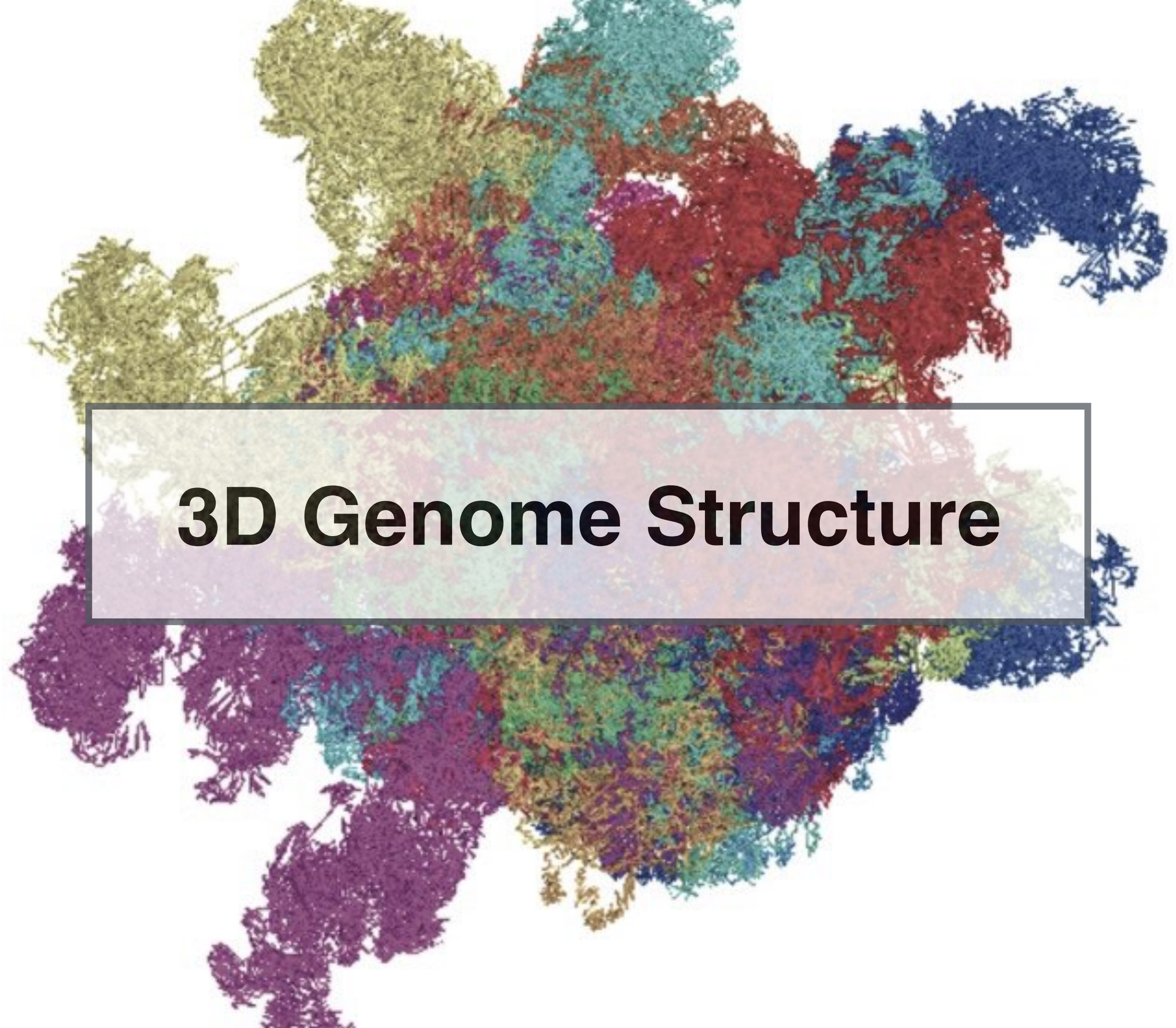
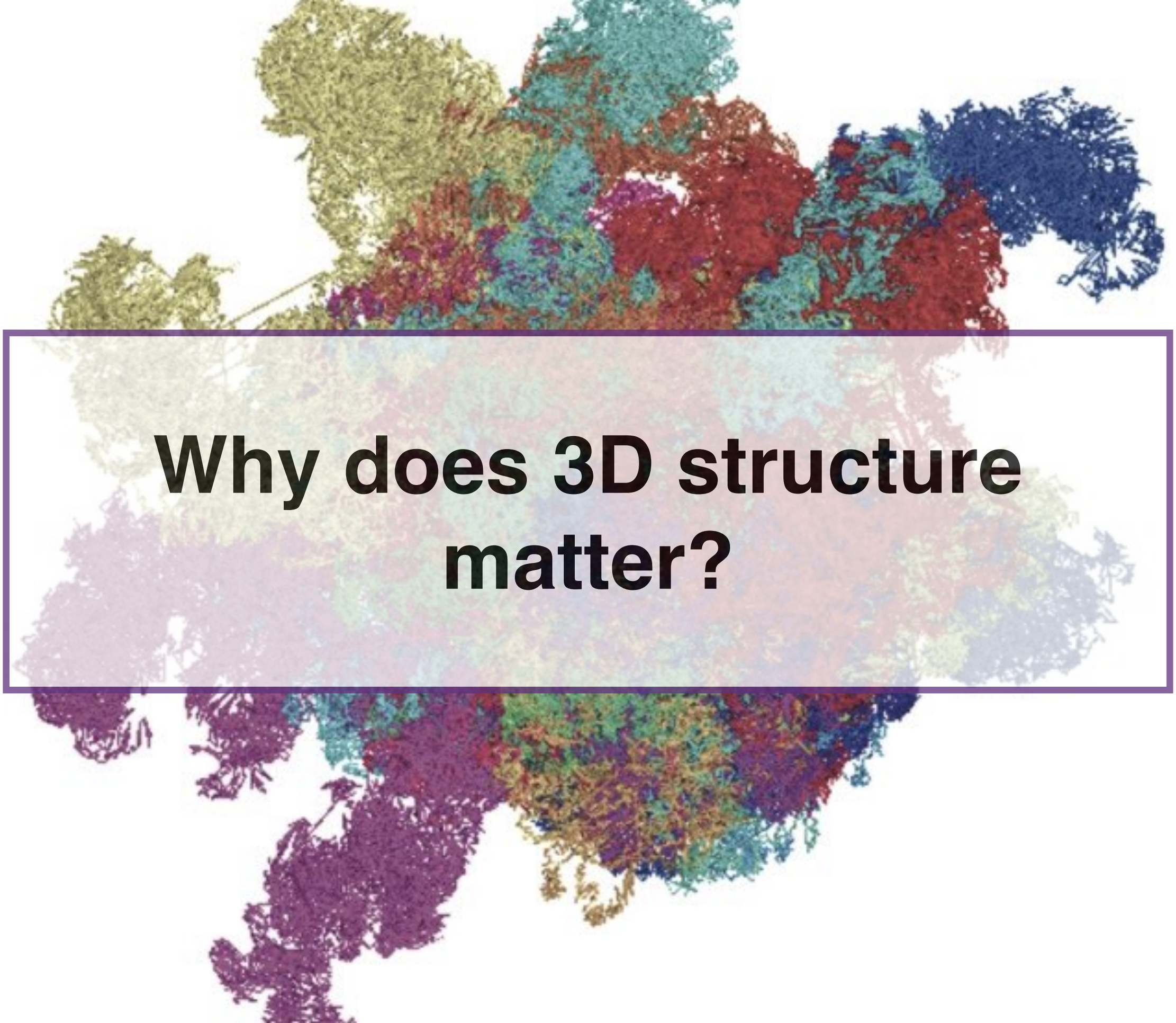
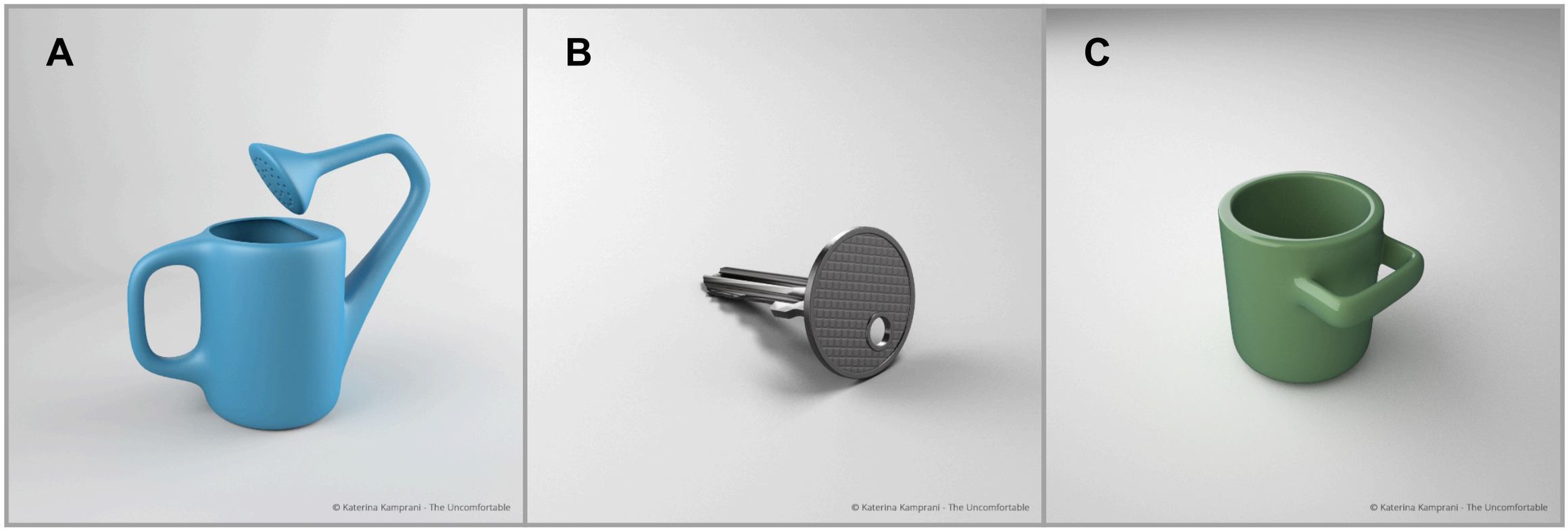
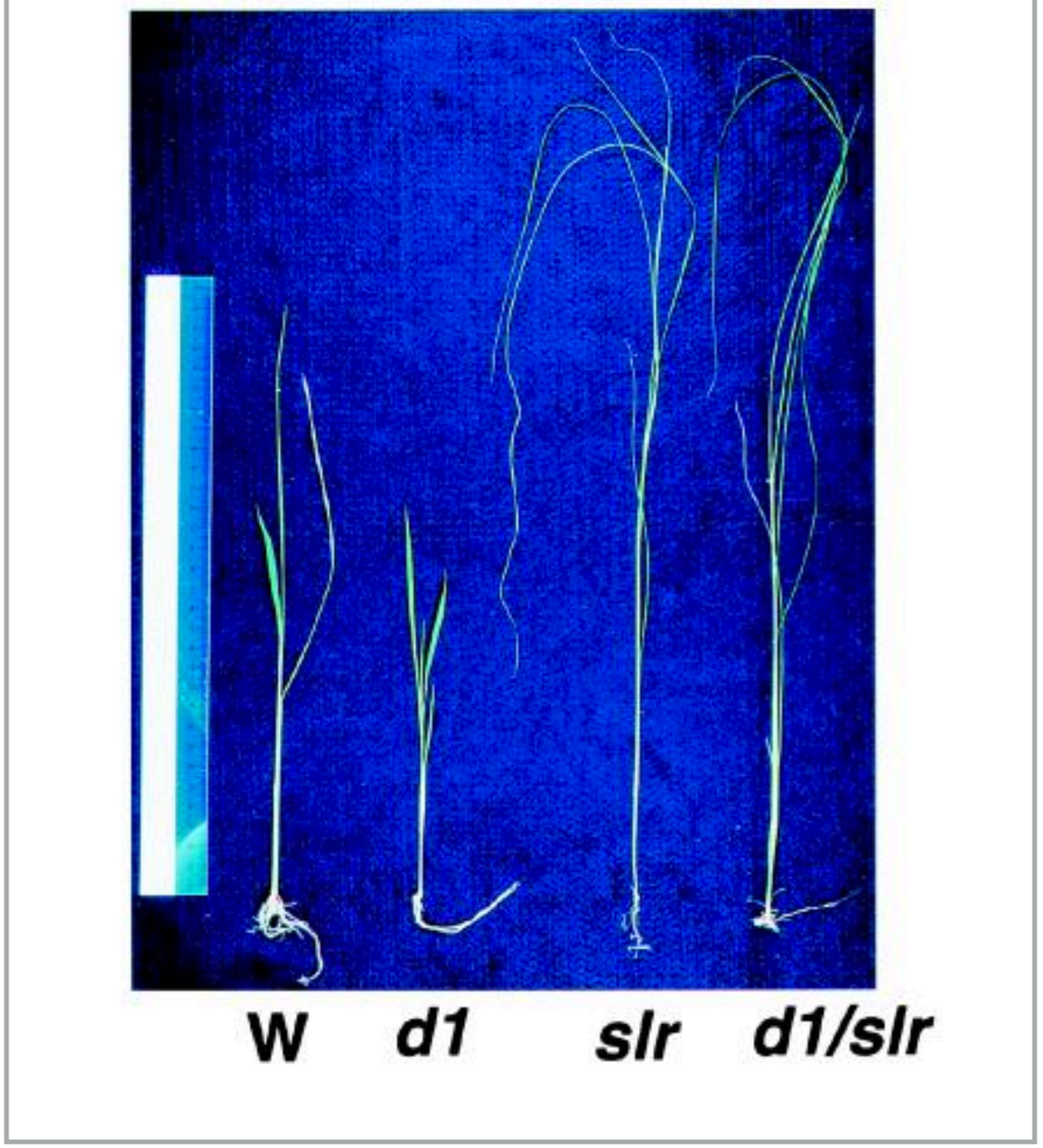


3D Genome Structure



Why does 3D structure matter?





Ueguchi-Tanaka *et al.* Rice dwarf mutant d1, which is defective in the alpha subunit of the heterotrimeric G protein, affects gibberellin signal transduction PNAS, 97(21): 11638-11643.

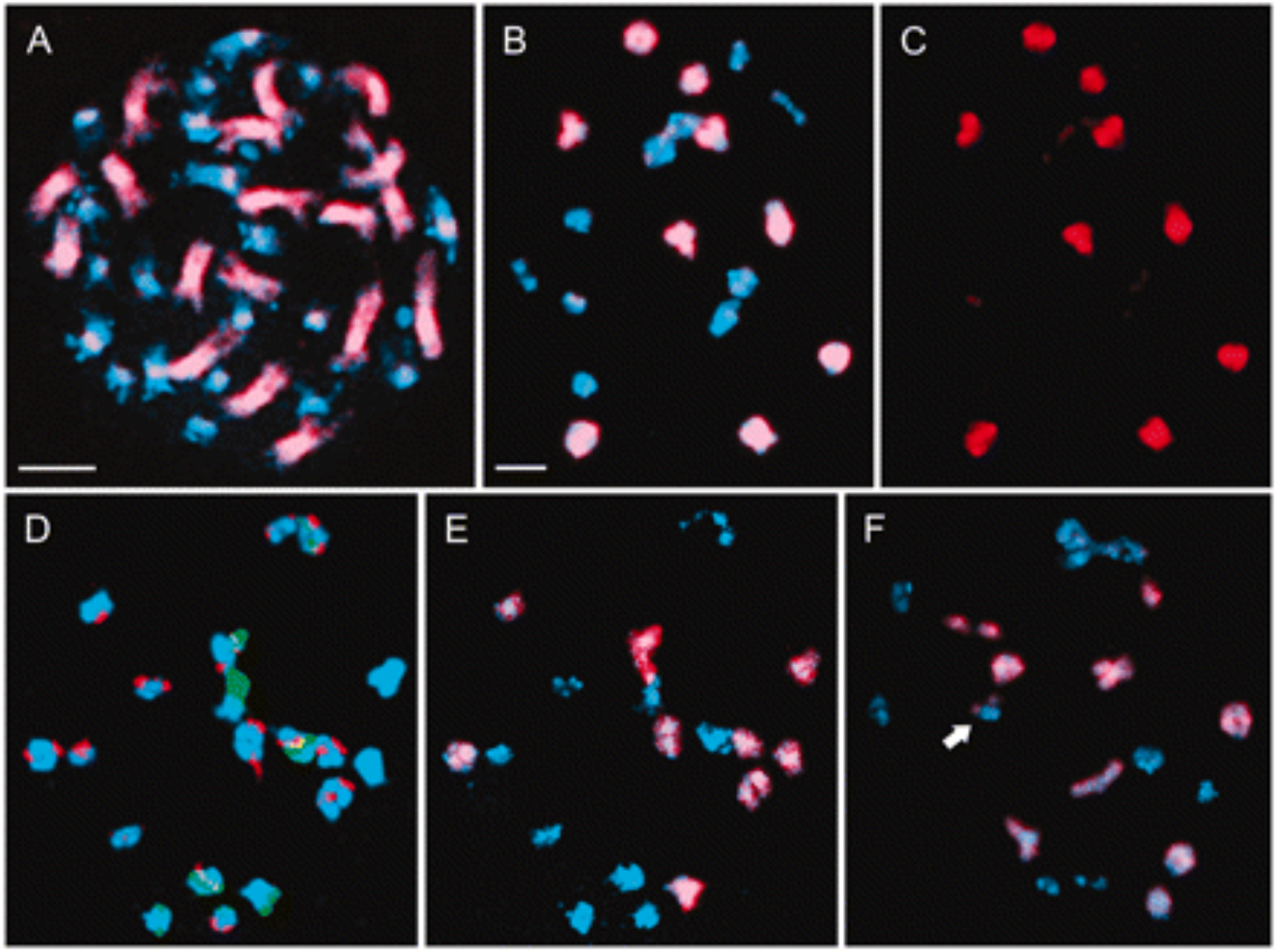
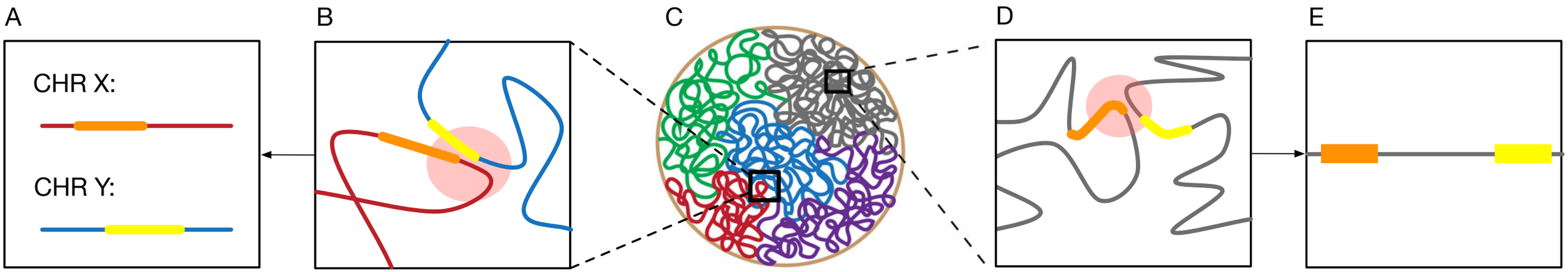


Figure 1 from Howell *et al*. 2008 (© 2008 by the Genetics Society of America, reprinted with permission)



From MacKay *et al.* 2019, unpublished

Problem

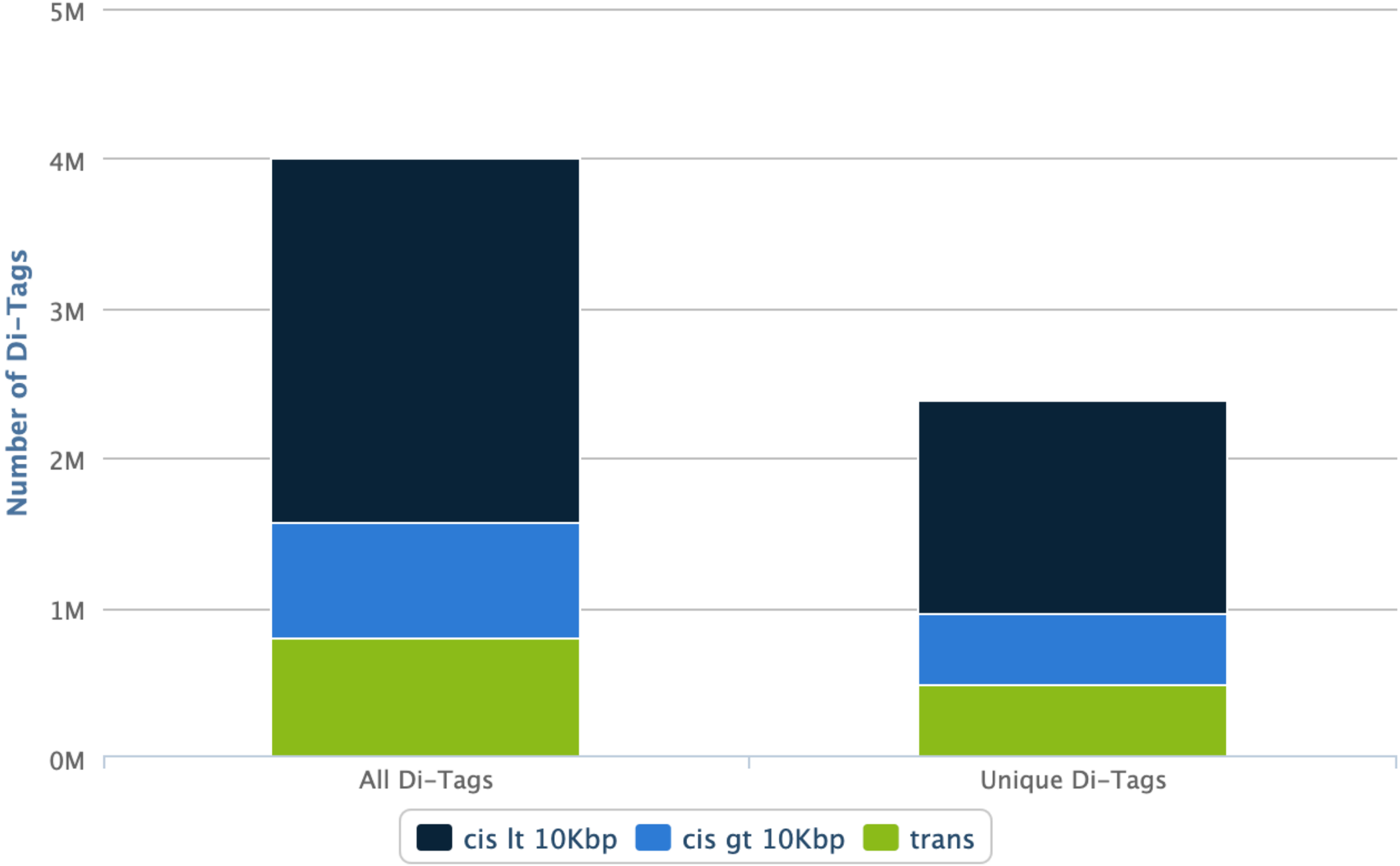
Investigations into 3D genome organization in allopolyploid organisms like *Brassica napus* are lacking. These are required to deduce links between genomic structure and phenotype.

Solution

Characterize 3D genome organization in *Brassica napus* under “normal” conditions. Specifically, investigate the existence of previously identified 3D “hallmarks”.

(1) Results

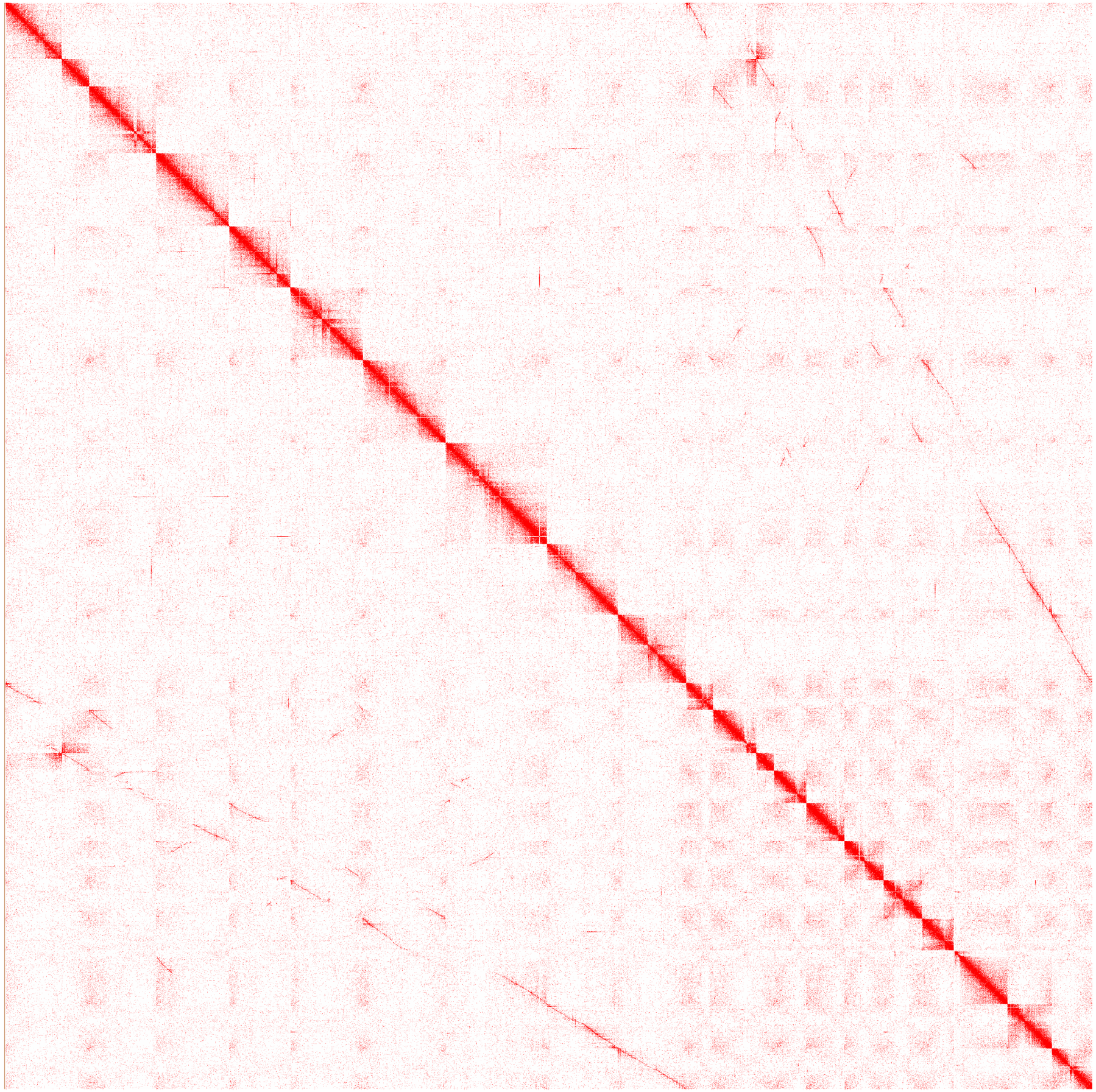
Typical Hi-C library characteristics are present

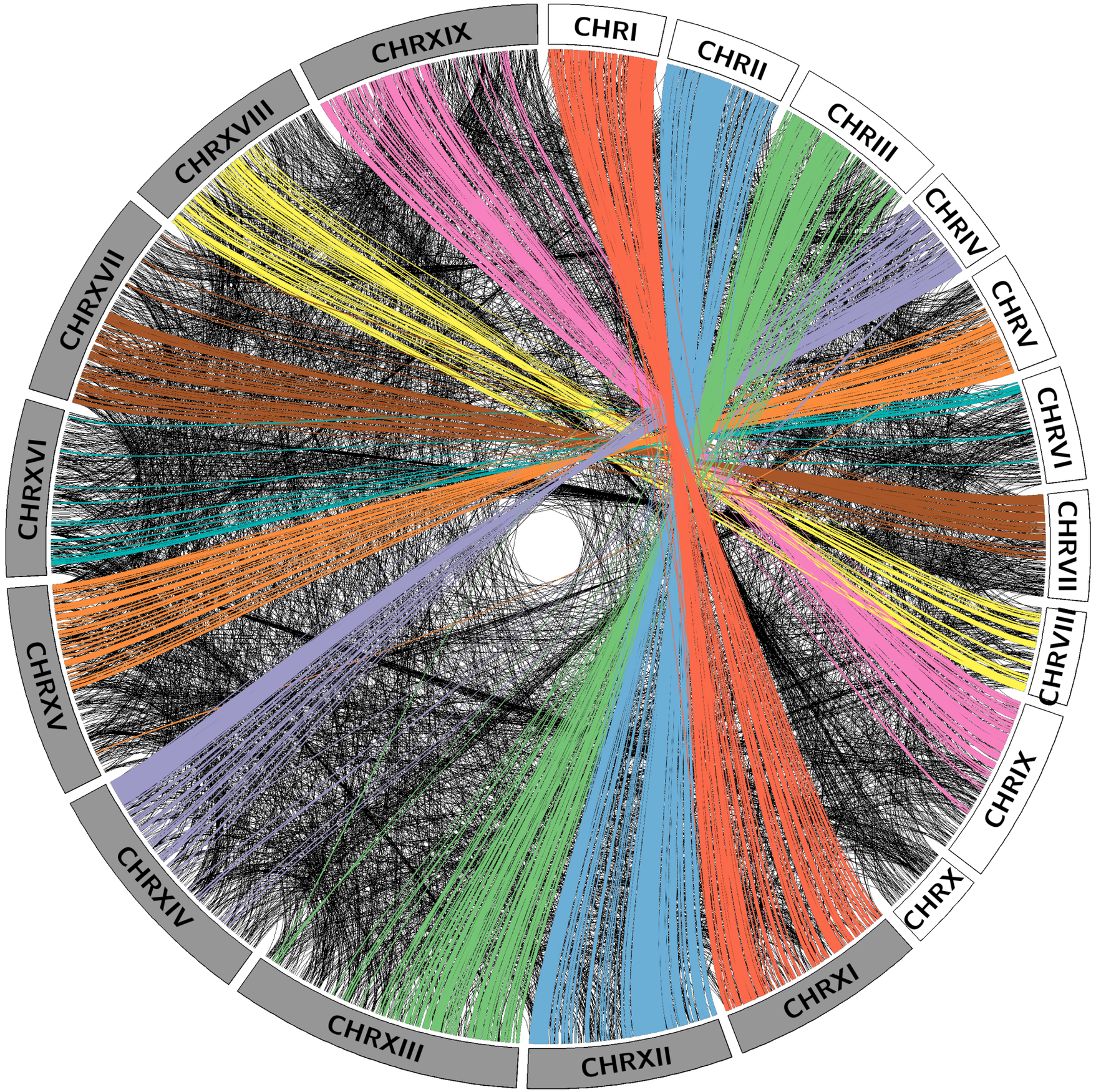


60 % *cis*-interactions vs.
40% *trans*-interactions

(2) Results

Novel interaction pattern detected in *trans*-chromsomal interactions between homoeologous chromosomes




CHRI
CHRII
CHRIII
CHRIV
CHRV
CHRVI
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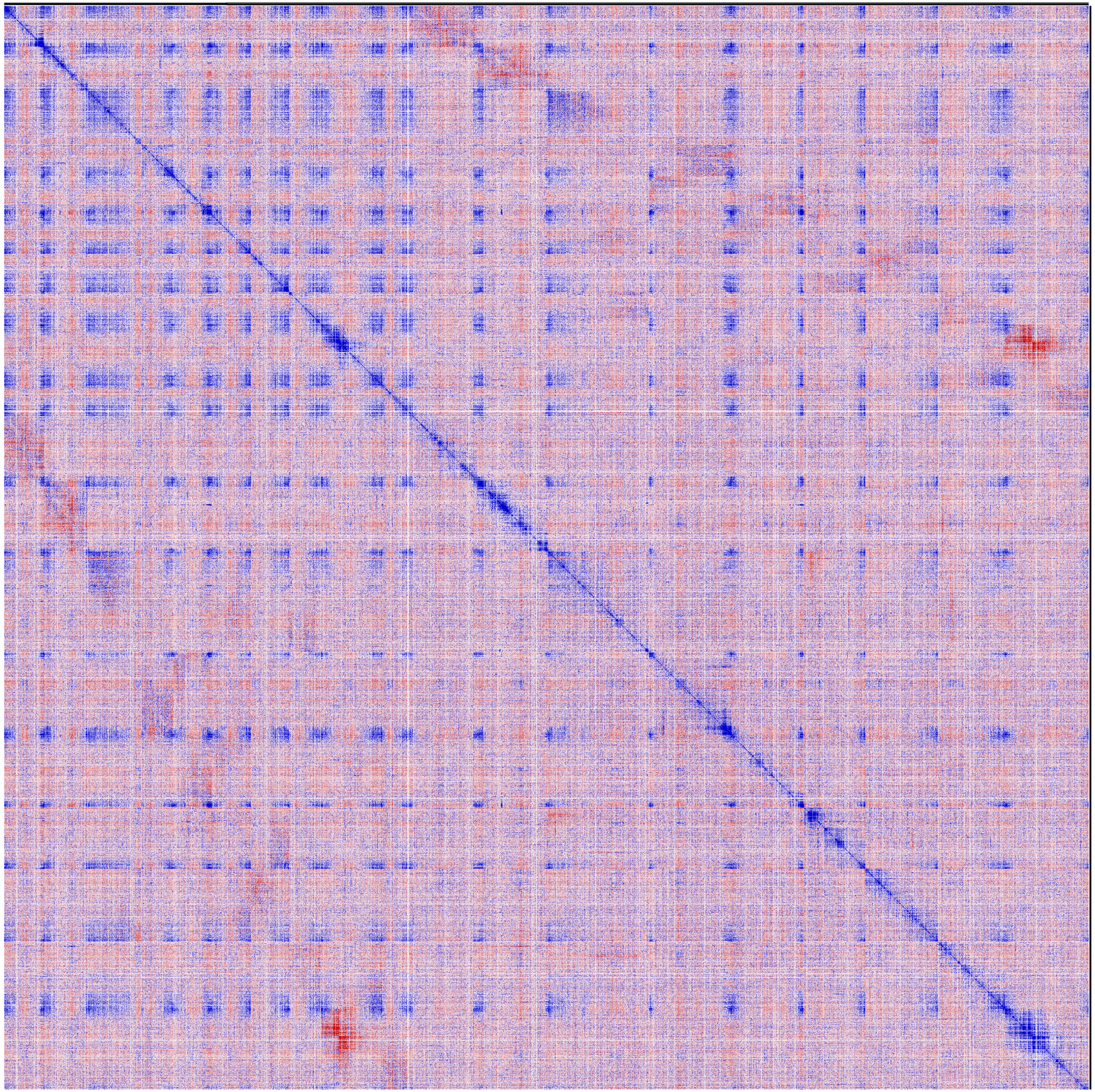
CHRVIII
CHRIX
CHRX
CHRXI
CHRXII
CHRXIII
CHRXIV
CHRXV
CHRXVI
CHRXVII
CHRXVIII
CHRXIX

(3) Results

Presence of mammalian-like A/B Domains



(4) Results

Greater proportion of statistically significant interactions involve *trans*-interactions (76%) opposed to *cis*-interactions (24%)

(4) Results

These *trans*-interactions are predominantly between corresponding regions in the A and C genomes

(5) Results

Mammalian-like TADs do not appear exist in *Brassica napus*, more similar to what was found in *Arabidopsis thaliana*

(6) Results

Chromosome Territories??

- Not likely, extensive intermingling between homeologous chromosomes
- Needs biological validation with imaging studies

Remaining Problem

	Read 1	Read 2
Unique Alignments	38,618,949	38,558,902
Multiple Alignments	134,048,570	132,370,646

- **Solution:** Multi-Mapping

Future Research Directions

- Generate higher-resolution contact maps
  - Extraction of single-gene regulatory interaction networks
  - Investigation of transcription factories
  - Integration with epigenetic data

Future Research Directions

- Solving the 3D-Genome reconstruction problem in *Brassica napus*
- Investigation of links between 3D genome structures and phenotypes

Questions?

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