An aerial photograph of a university campus, showing various buildings, green spaces, and parking lots. A semi-transparent white rectangular box is overlaid on the upper portion of the image, containing the title text. The text is in a bold, black, sans-serif font, with the species name in italics.

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

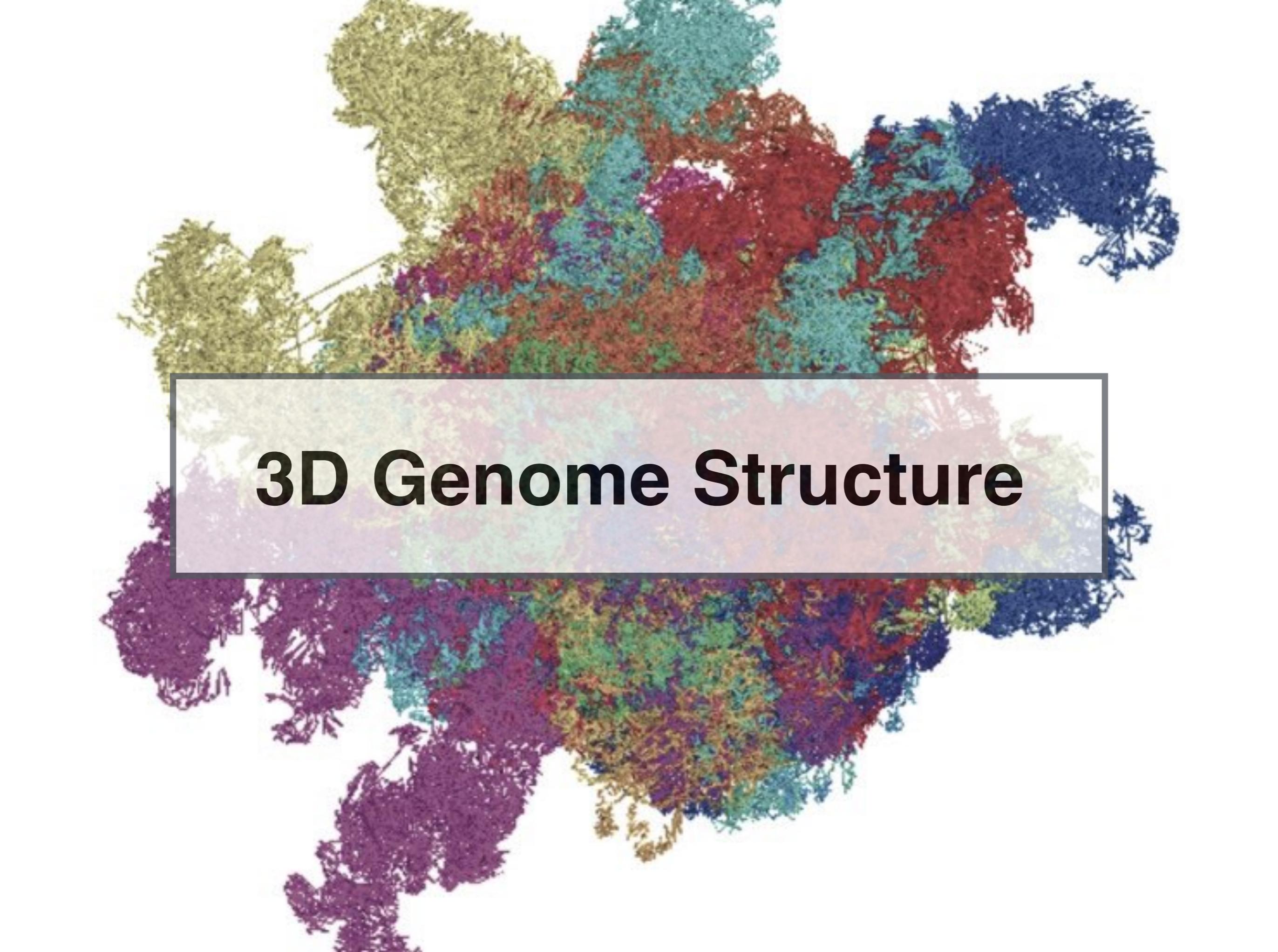
Kimberly MacKay, Tricia Bender, Isobel Parkin,
Anthony Kusalik, Stephen Robinson

An aerial photograph of a university campus, showing various buildings, green spaces, and surrounding fields. A semi-transparent white box is overlaid on the center of the image, containing contact information.

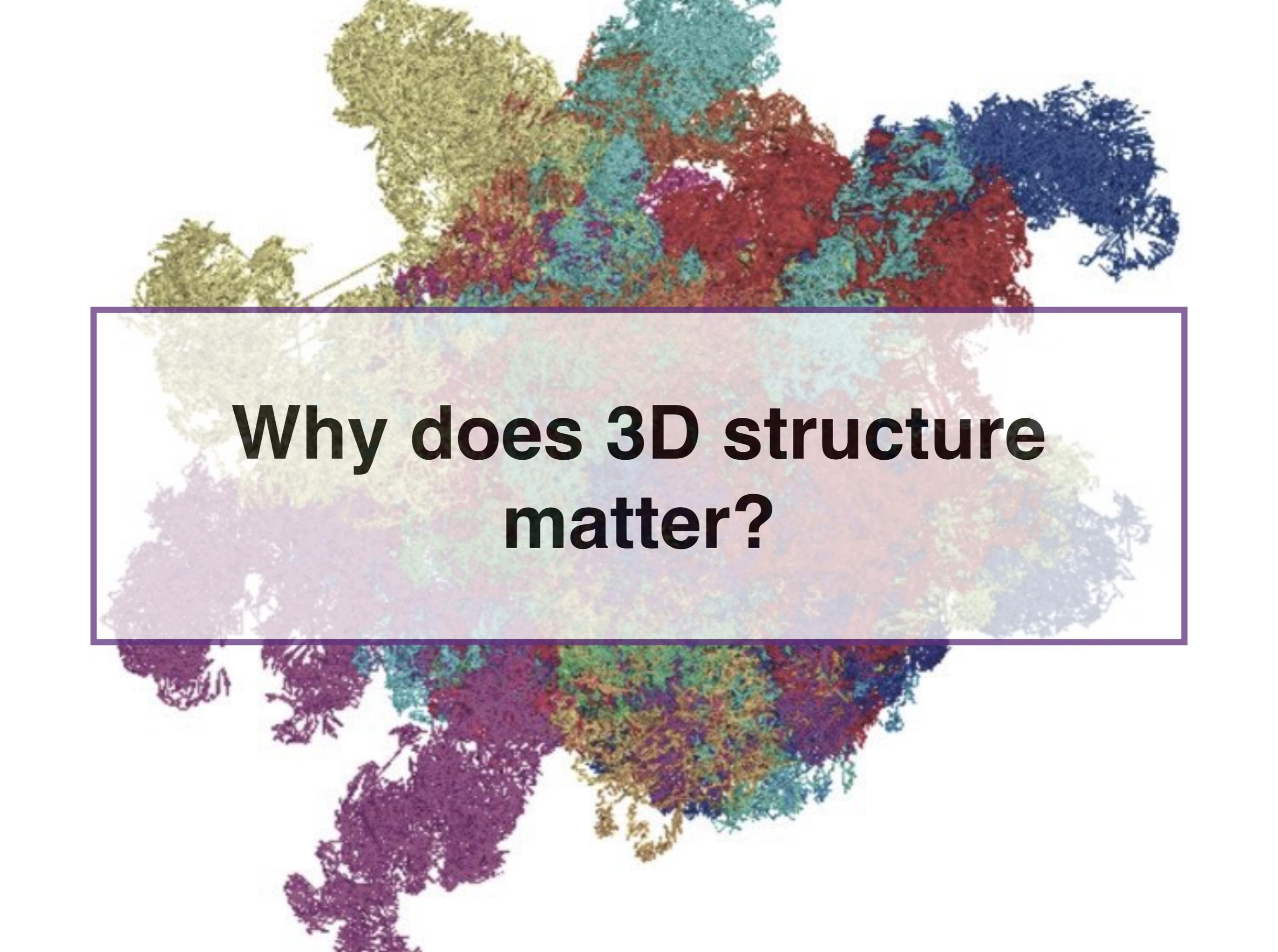
Contact Information:

e-mail: kimberly.mackay@usask.ca

twitter: [@mackayka](https://twitter.com/mackayka)



3D Genome Structure

A 3D point cloud of a tree, where different colors represent different parts of the structure. The colors include green, blue, red, purple, and yellow. The tree is shown from a top-down perspective, with a central trunk and several branches extending outwards. The point cloud is semi-transparent, allowing the text to be seen through it.

Why does 3D structure matter?

A



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B



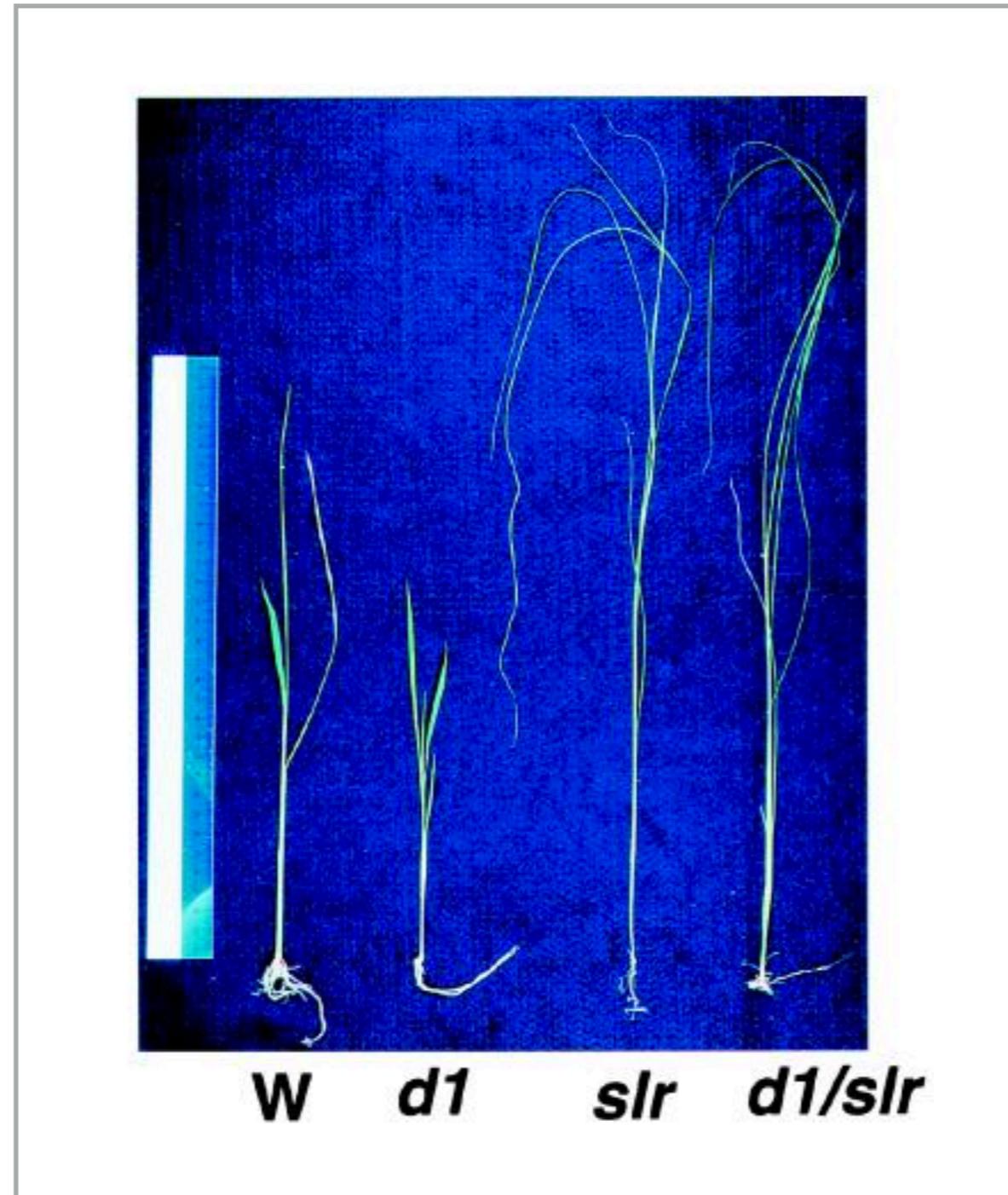
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C



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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.

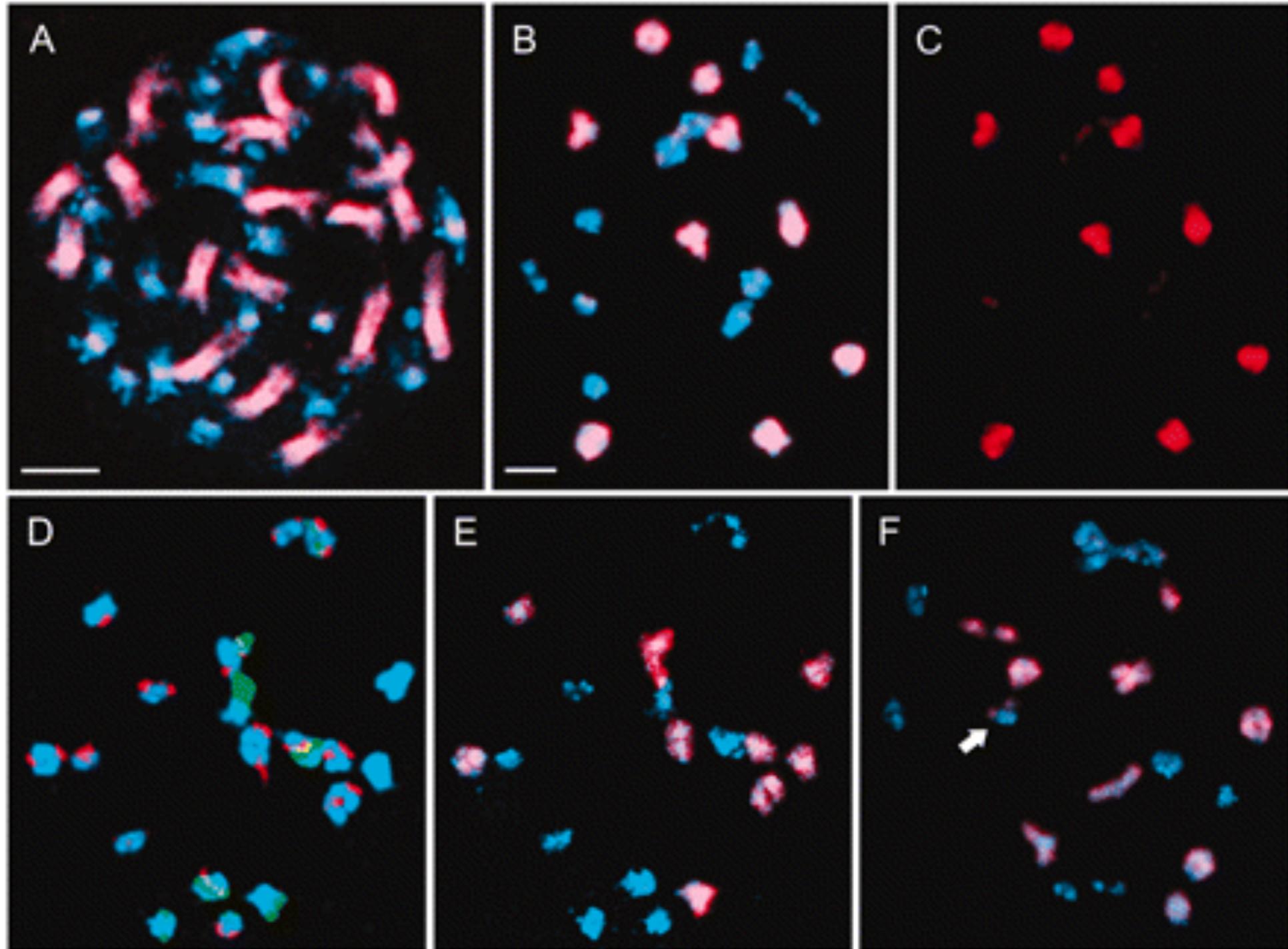
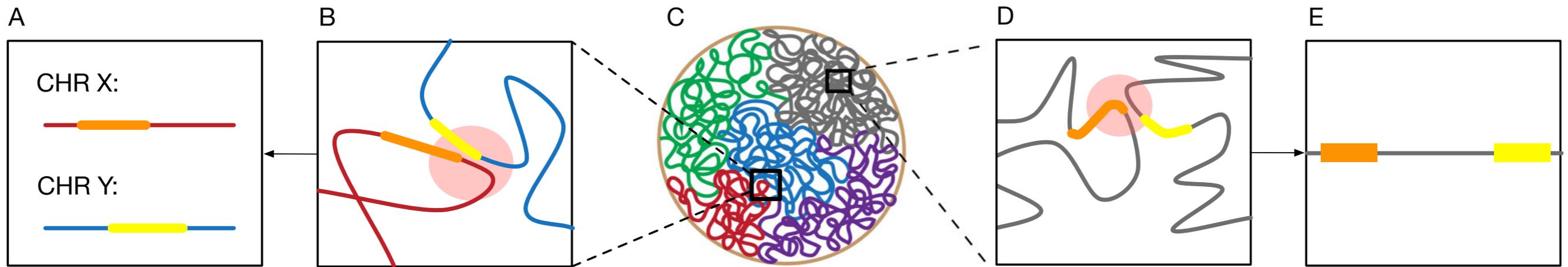


Figure 1 from Howell *et al.* 2008 (© 2008 by the Genetics Society of America, reprinted with permission)



From MacKay *et al.* 2019, unpublished

Problem

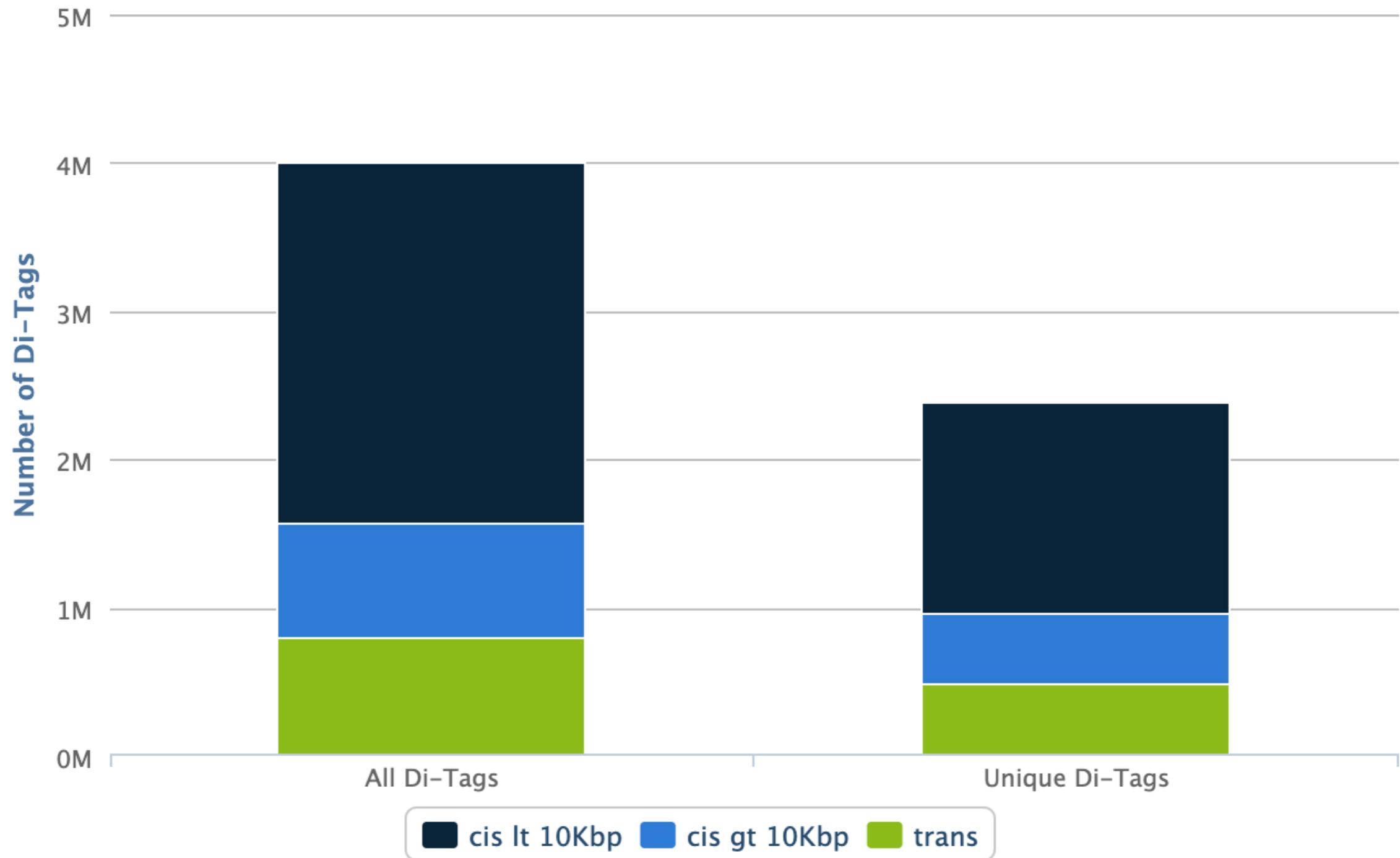
Investigations into 3D genome organization in allopolyploid organisms like *Brassica napus* are lacking. These are required to deduce links between genomic structure and phenotype.

Solution

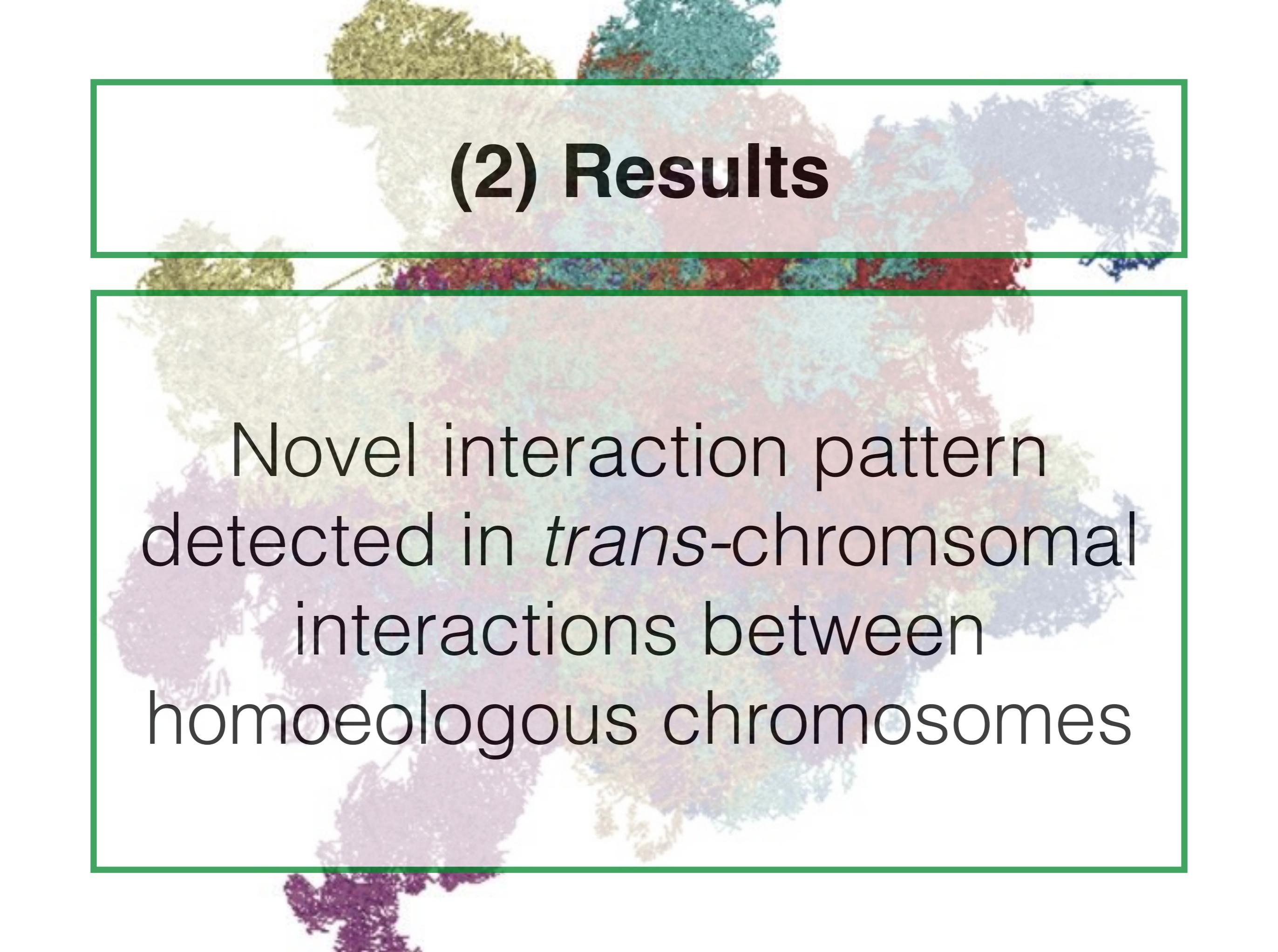
Characterize 3D genome organization in *Brassica napus* under “normal” conditions. Specifically, investigate the existence of previously identified 3D “hallmarks”.

(1) Results

Typical Hi-C library characteristics are present

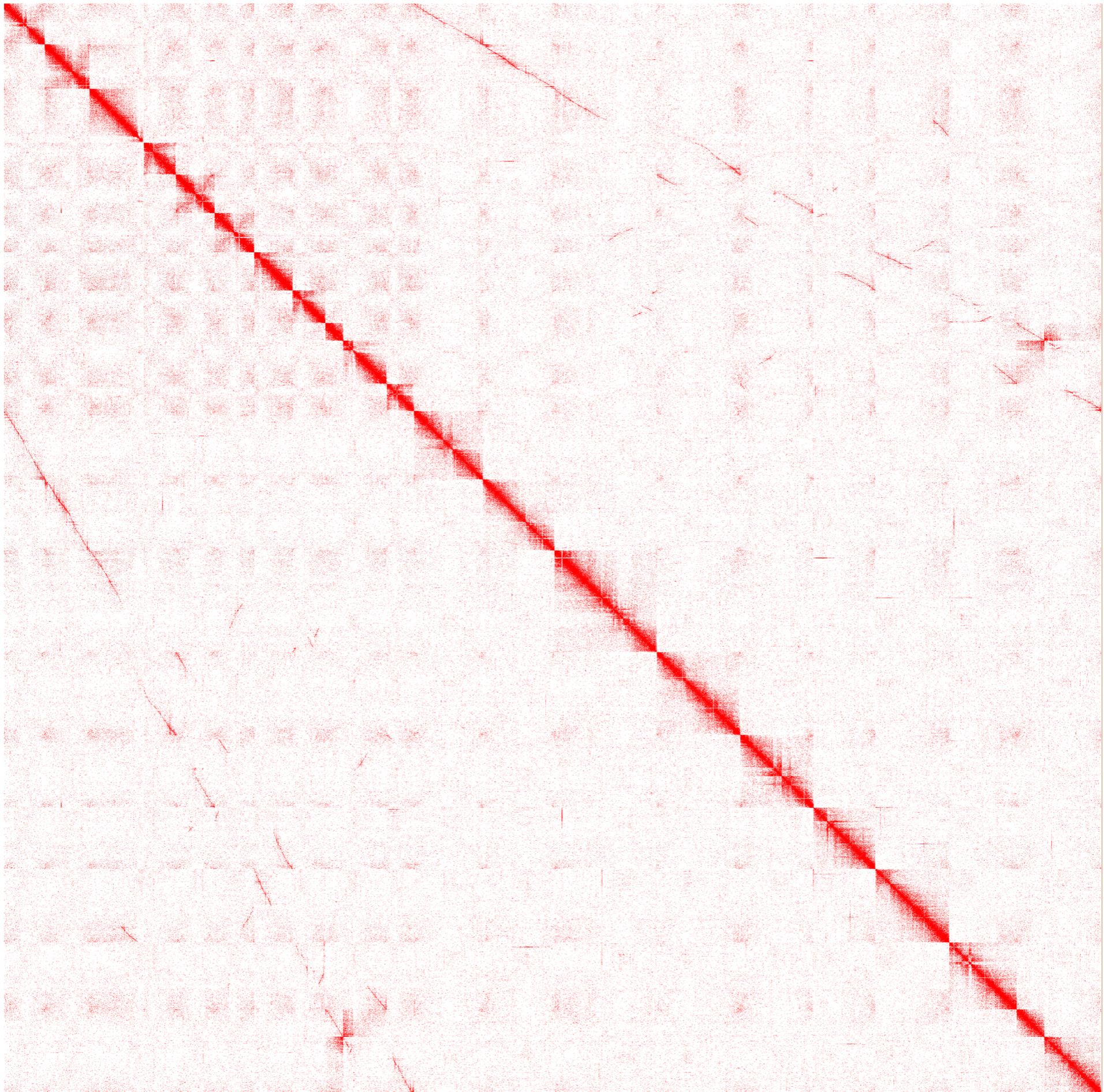


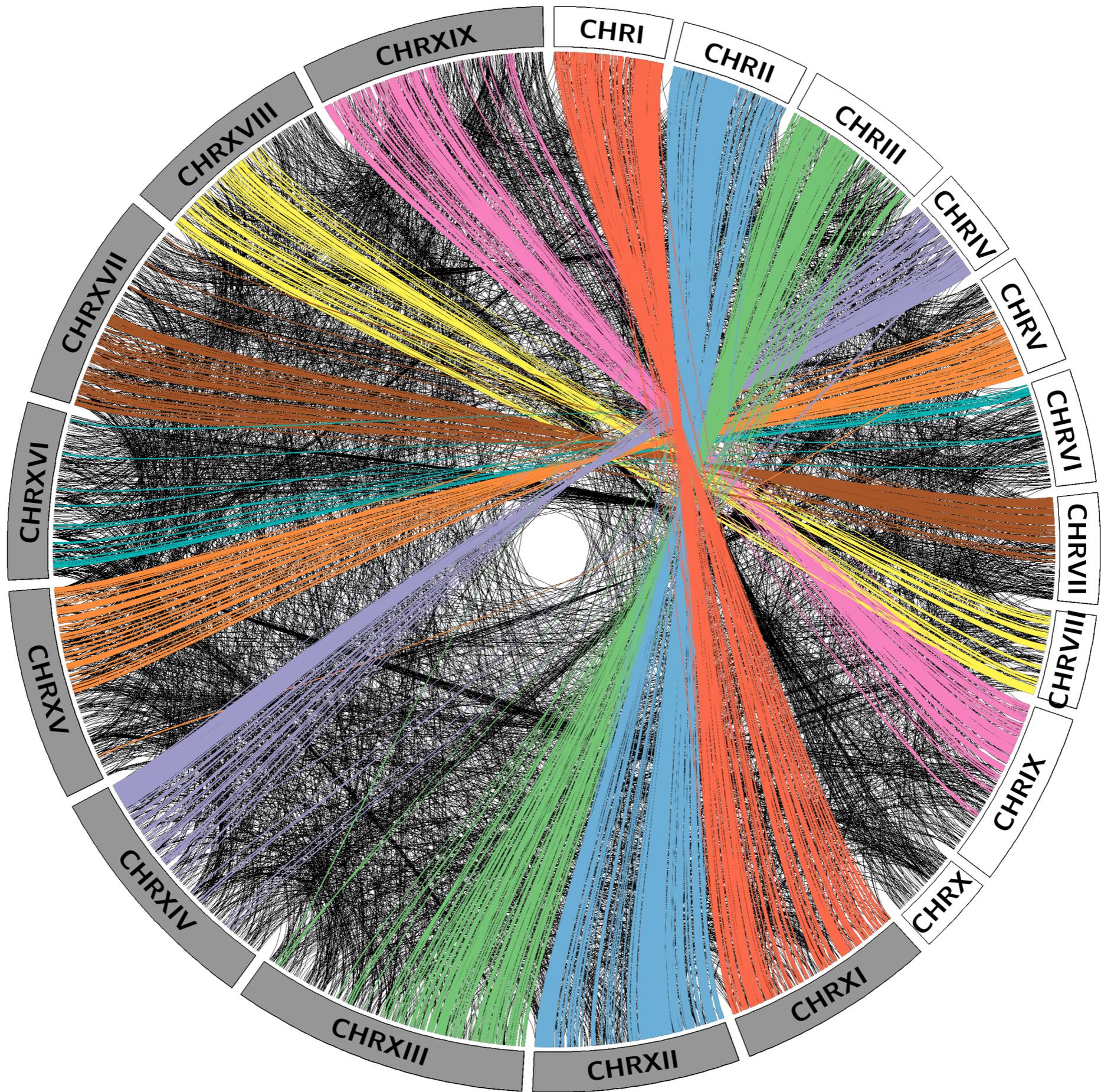
60 % *cis*-interactions vs.
40% *trans*-interactions

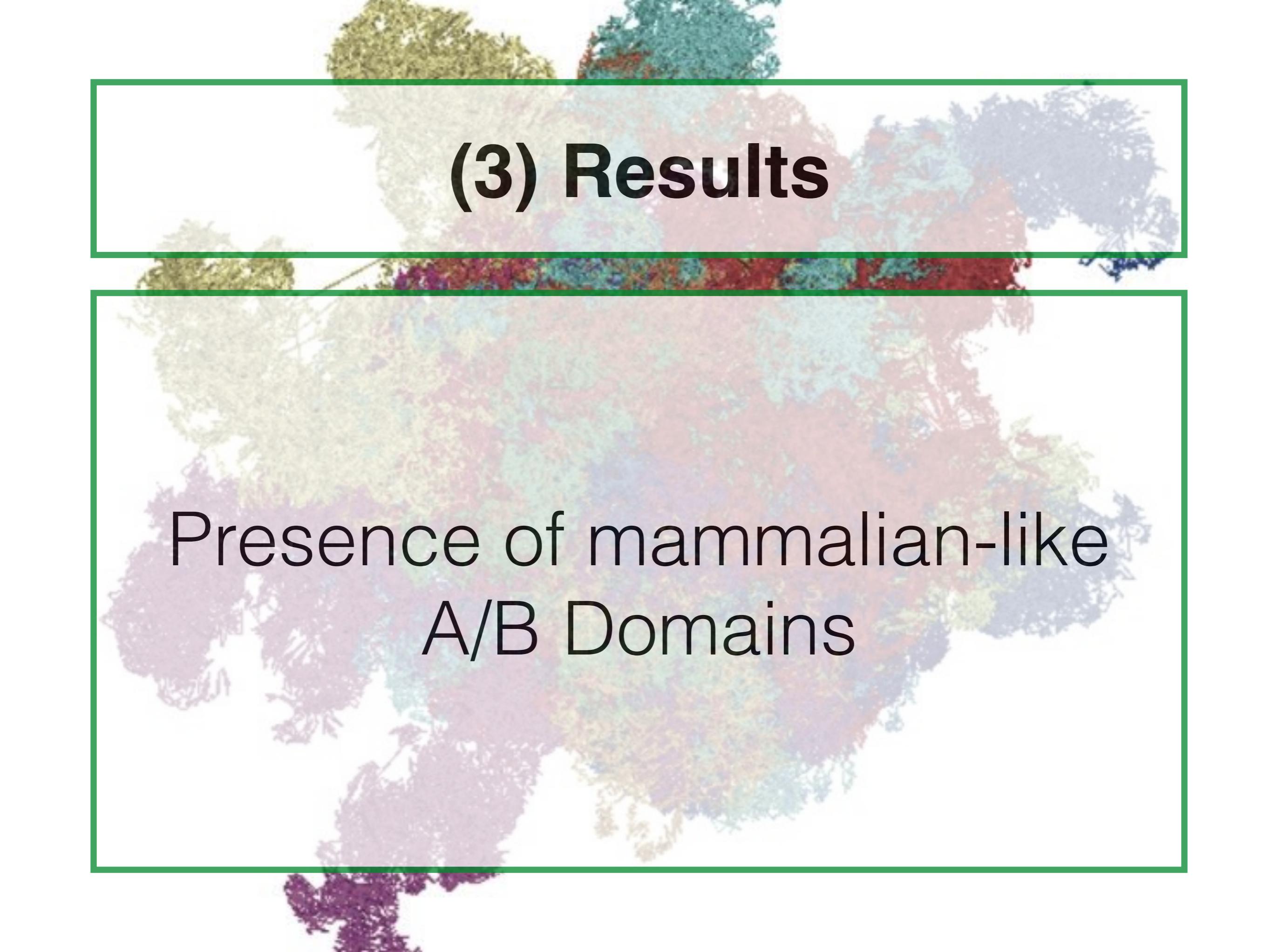


(2) Results

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

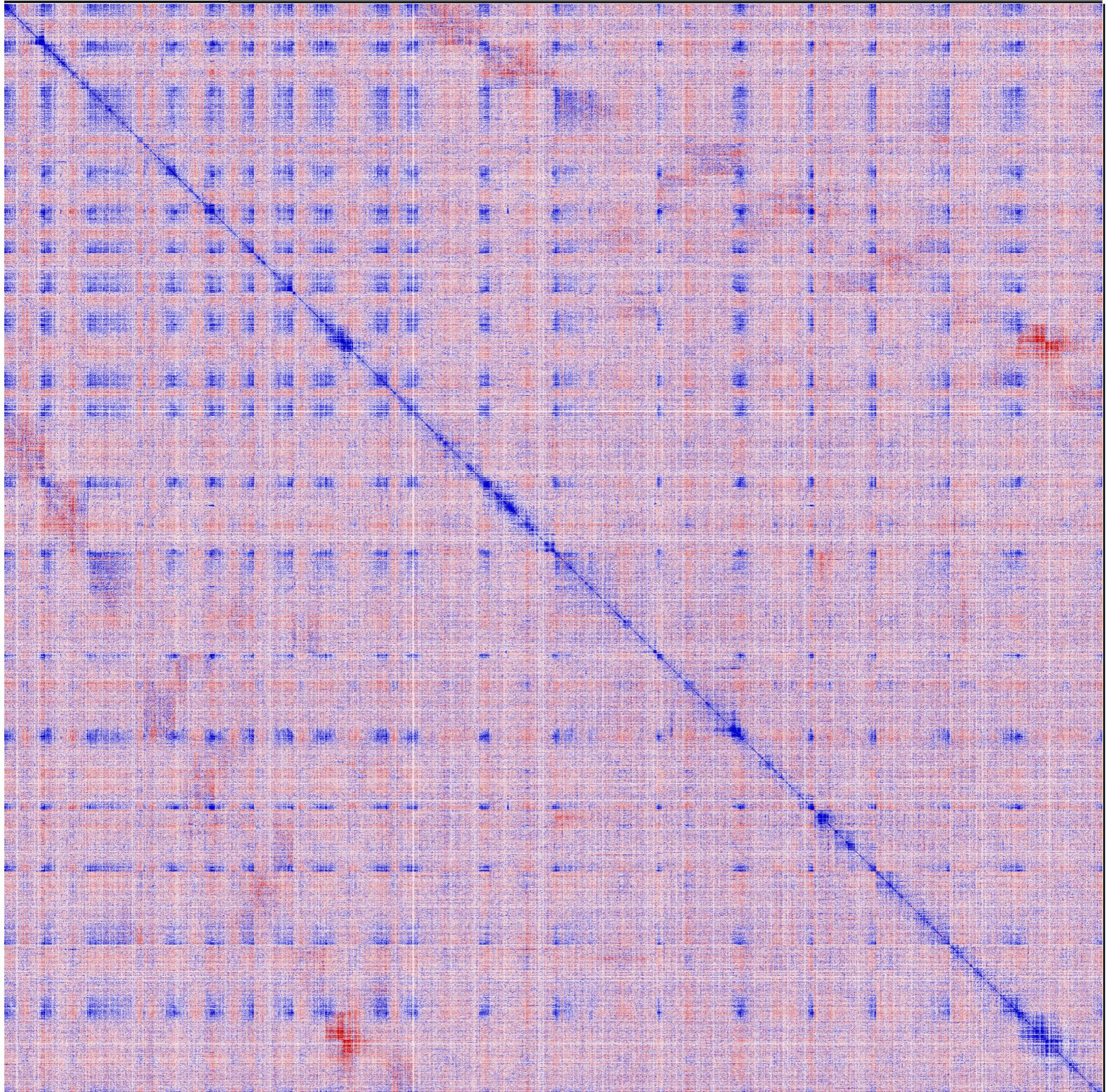






(3) Results

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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Github: <https://github.com/kimmackay/>



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