

# Vanessa genome

strikes back!



# Preliminary plan:

## 1. Basic genome statistics

- a. Summary of main characteristics
- b. Verification of existing assembly with linkage map
- c. 3D genome organization: compartmental organization, presence of TAD and loops
- d. Synteny (may have been done)

## 2. Patterns of recombination

- a. Linkage maps and recombination rate
- b. Combining patterns of recombination with gene and repeat density

## 3. Genomic regions of particular interest for migratory genomics

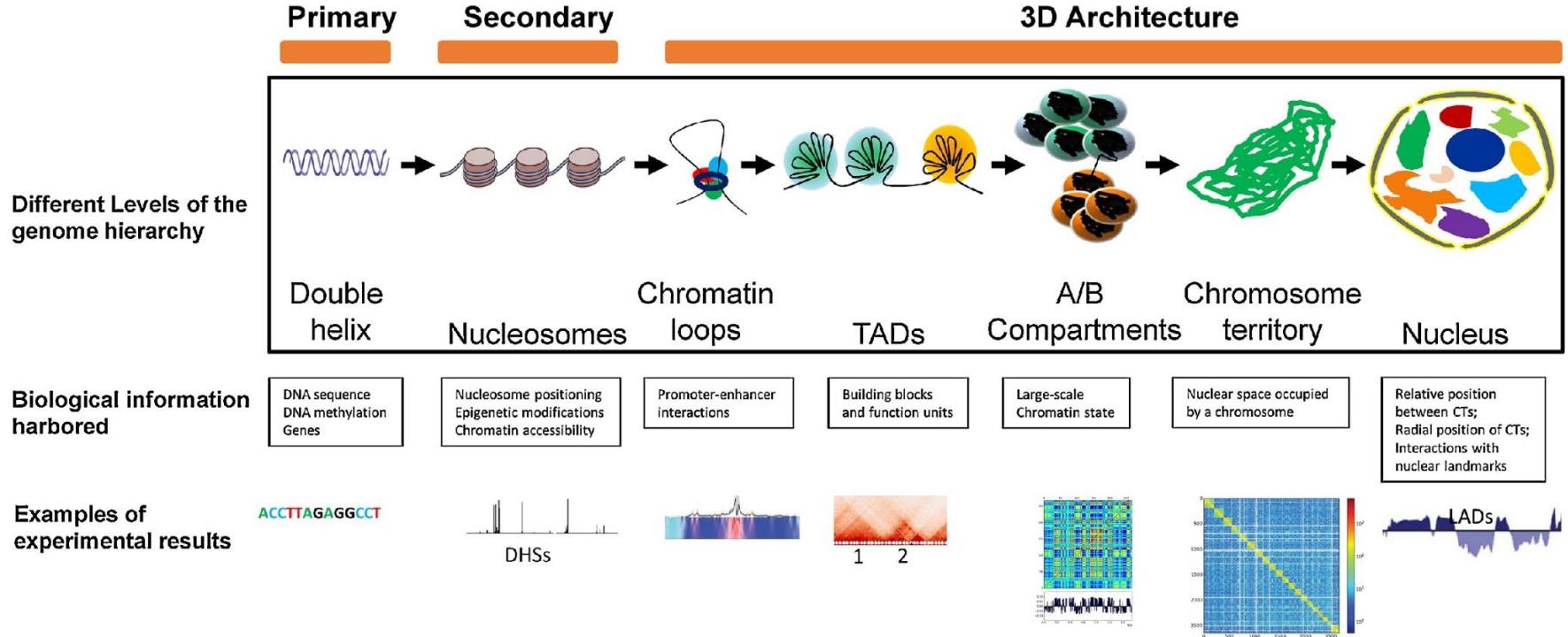
- a. Evolution of migratory phenotype: are gene family expansions and contractions related to migration?
- b. Identification of candidate genes of interest: migration locus, circadian clocks

## 4. Identification of regions of interest for epigenetics using Hi-C data

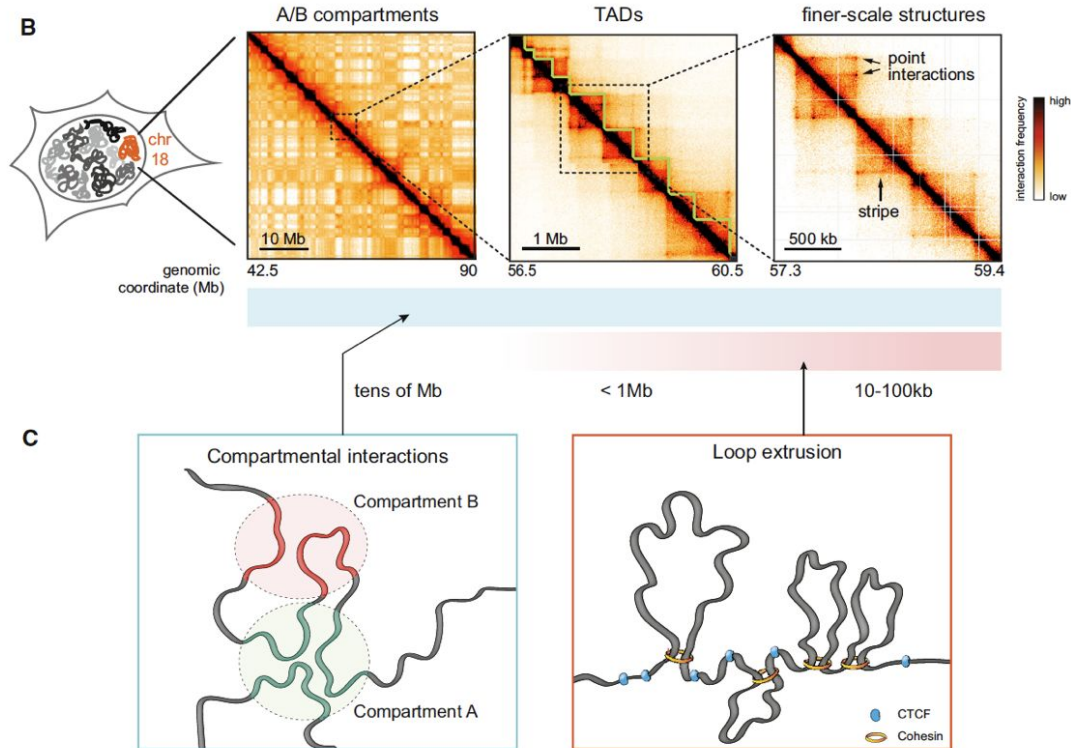
- a. Compartments, TADs, loops
- b. Combining 3D organization patterns with gene and repeat density

## 5. Comparative genomics?

# 1. Basic genome statistics: 3D organization



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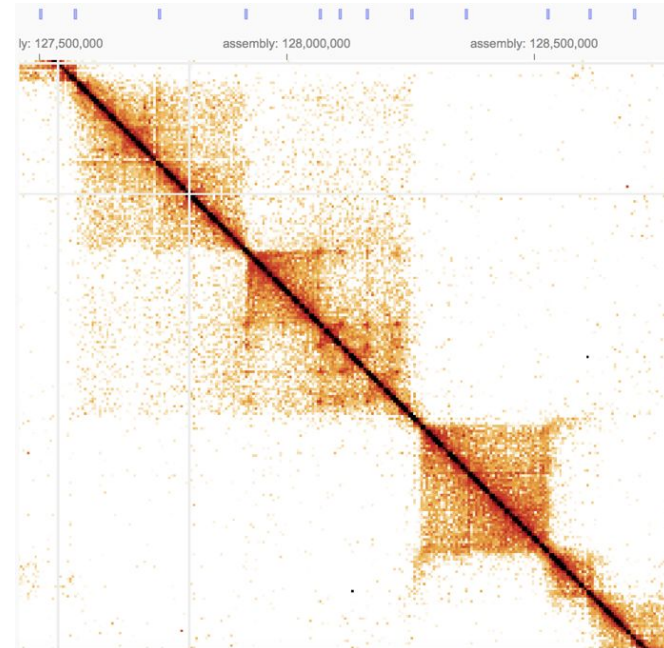
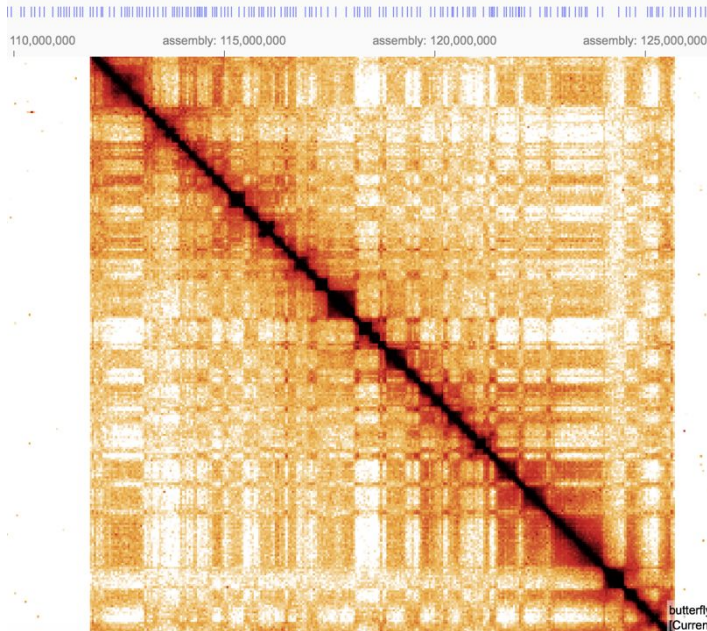


# 1. Basic genome statistics: 3D organization

Compartments

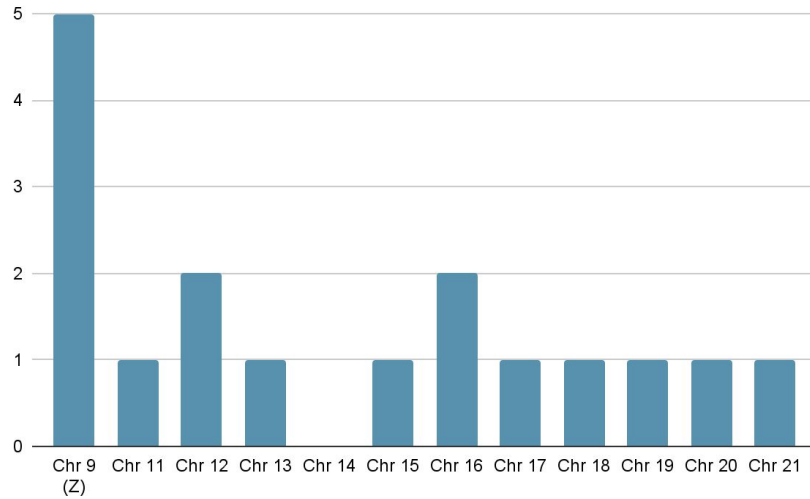
TADs (Topologically Associated Domains) - 4875

Loops

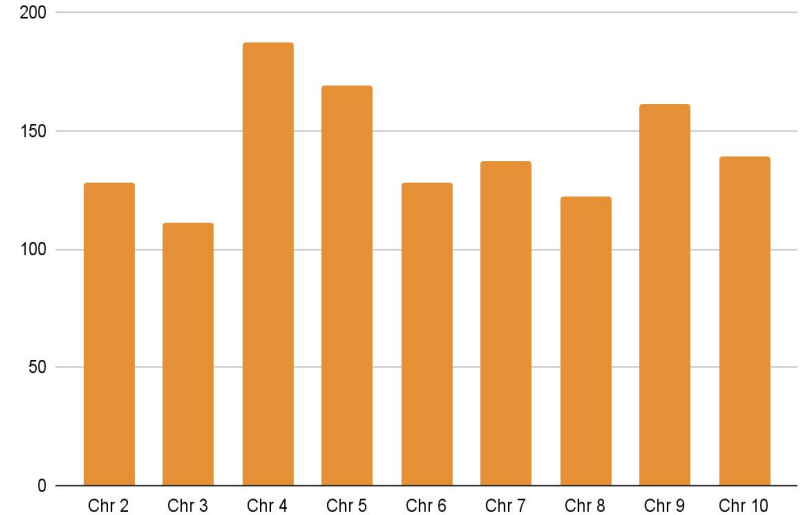


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Loops

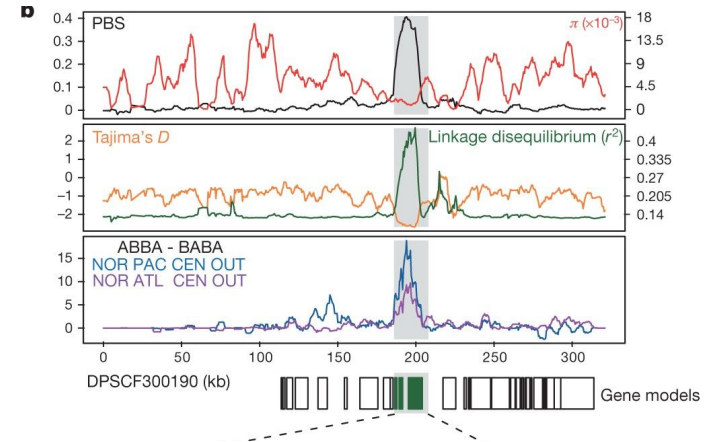


TADs (Topologically Associated Domains)

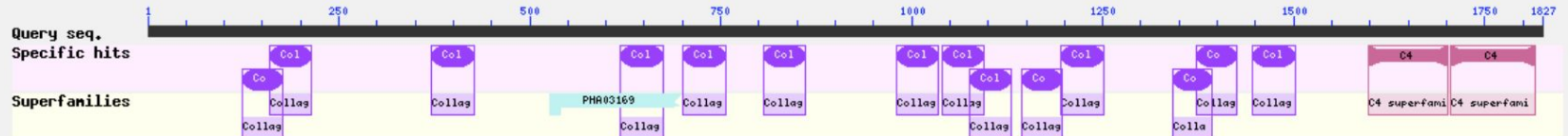


## 3b. Migratory genes presence/absence

Candidate genes: does monarch “migratory locus” present in Vanessa?



**?** Putative conserved domains have been detected, click on the image below for detailed results.



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## **3. Genomic regions of particular interest for migratory genomics**

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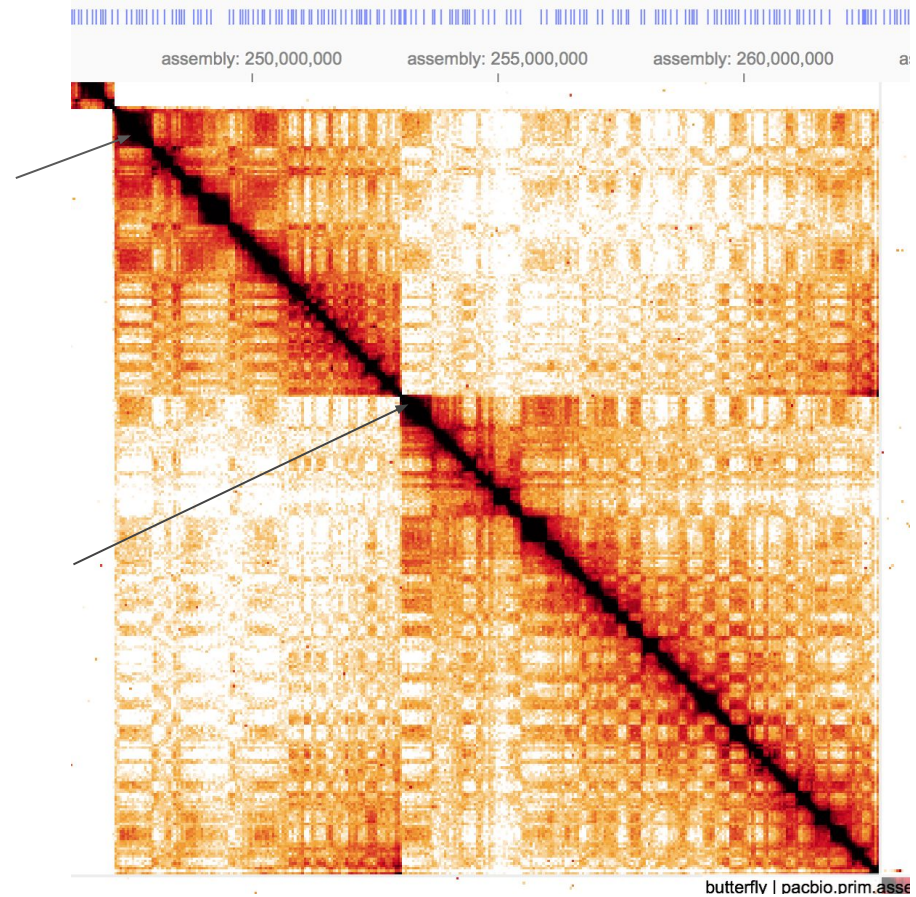
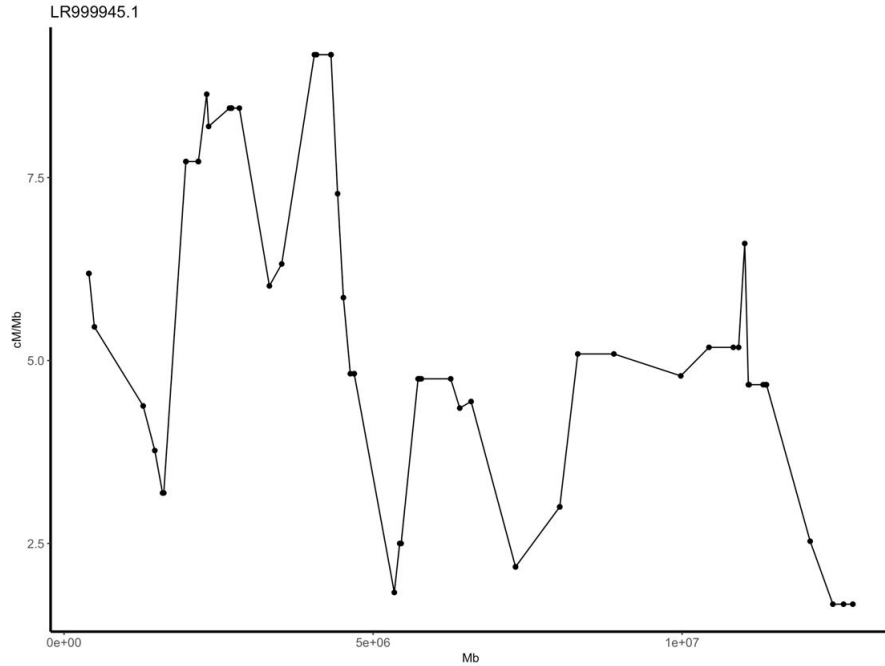
## **4. Identification of regions of interest for epigenetics using Hi-C data**

- a. Compartments, TADs, loops
- b. Combining 3D organization patterns with gene and repeat density
- c. 3D organization of genes of interest

## **5. Comparative genomics**



# And then we got wild...

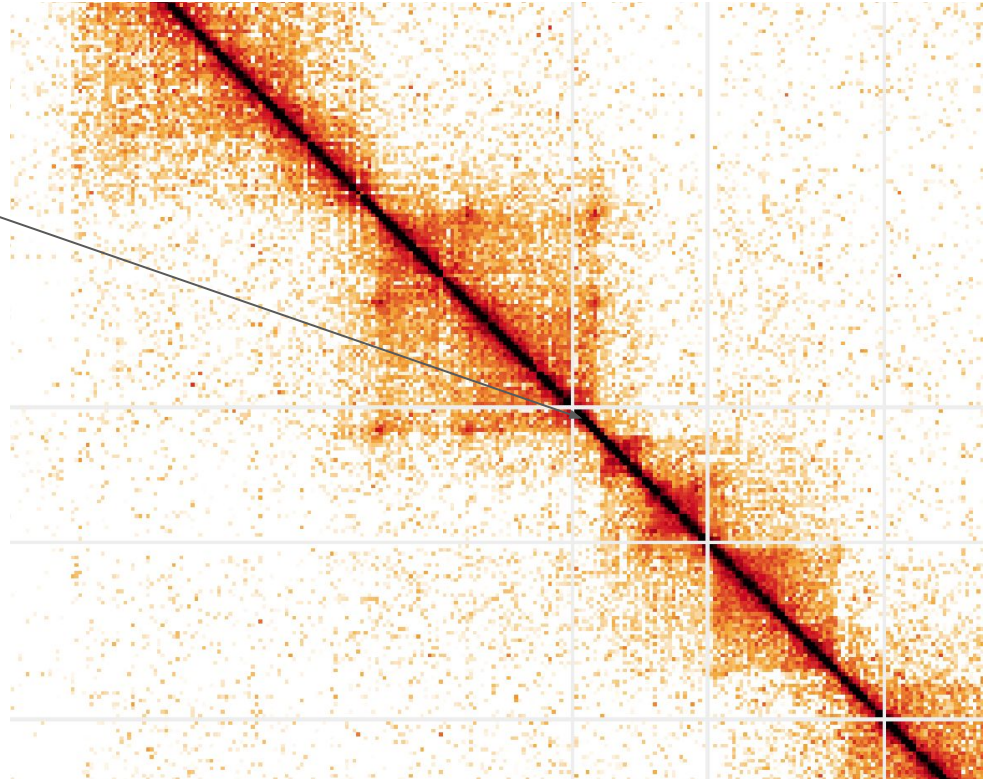


# And then we got wild...

## BAZ1A

BAZ1A along with [SMARCA5](#), [POLE3](#), and [CHRAC1](#) comprise the WCRF/CHRAC ATP-dependent [chromatin-remodeling complex](#).<sup>[3][4]</sup>

The purified CHRAC complex can mobilize [nucleosomes](#) into a regularly spaced nucleosomal array, and the spacing activity is ATP-dependent.<sup>[4]</sup> Furthermore, the BAZ1A-SMARCA5 complex enables [DNA replication](#) through highly condensed regions of [chromatin](#).<sup>[5]</sup>



# And then we got wild...

## Collagen type IV

