

# Related animals with small genomes, conserved morphology, but flexible gene order: *Oikopleura dioica*

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## *Oikopleura dioica* in brief:

- Japanese name: オタマボヤ

- *Oikopleura dioica* is a globally distributed marine animal. It is evolutionarily closer to humans than model organisms such as yeast, nematodes or fruit flies. As it belongs to the chordate phylum it has features common with vertebrate embryonic development, such as a dorsal nerve cord, and the formation of a muscular tail supported by a notochord.

- **Ecological importance:** *O. dioica* is a small filter feeder that can account for up to 10 % of the total carbon mass in an area. It eats unicellular plankton and was reported to be able to ingest bacterial viruses and microplastics as well. Being an extremely efficient predator, it has an important role in the carbon chain, by producing organic matter (fecal pellets and "houses") that sediment to the sea floor.

- **Evolution:** as it belongs to the Tunicate phylum, it is among the invertebrates that are evolutionary closest to humans. Tunicates, like vertebrates, are chordates: they have a muscular tail. They also have a brain, a heart, a gut, etc.

- **Compact genome:** only 70 Mb. Nevertheless, it contains 18,020 predicted genes, which makes it an interesting model to study how to compactly encode functions homologous to some found in vertebrates.

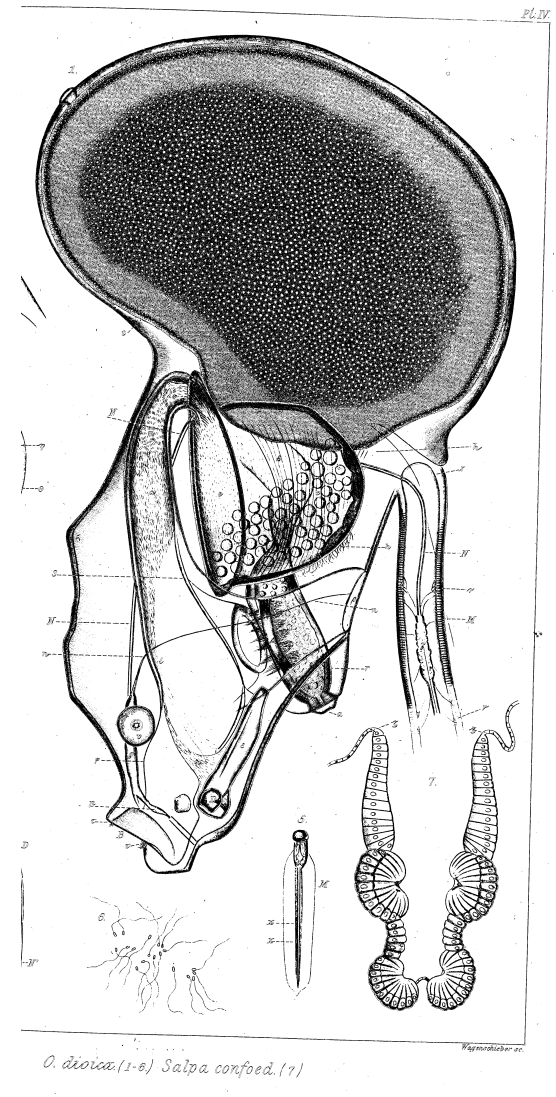
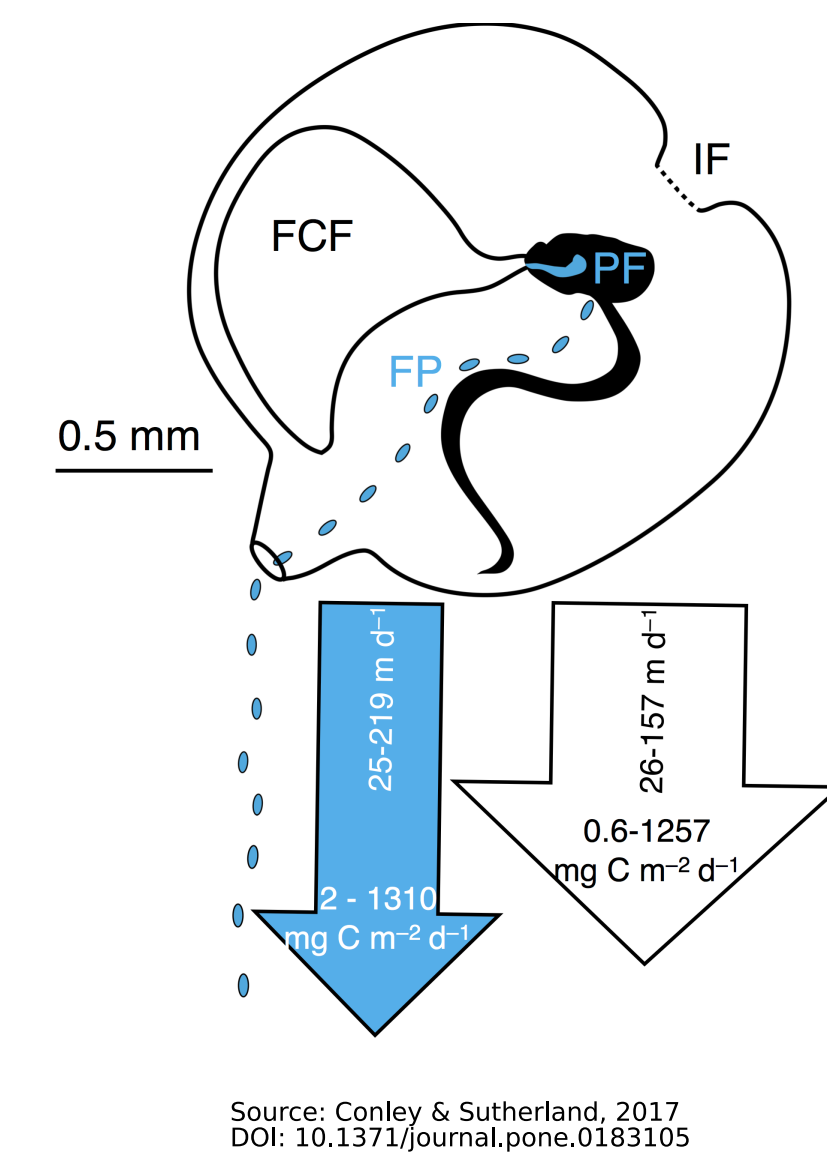
- *O. dioica* lives in a "house" made of cellulose and novel proteins. The house is a 3D microfluidic filter that enables *Oikopleura* to prey on microbes significantly smaller than itself. *Oikopleura* have even been reported to capture and ingest bacteriophage viruses. The *Oikopleura* house is synthesised from a specialised epithelium on the epidermis. The cellular arrangement in this epithelium is always the same between individuals.

## *Oikopleura dioica*: a plankton predator that:

lives in a house made with cellulose

has a muscular tail, for flowing food to its mouth

never sleeps and closes its life cycle in only 5 days

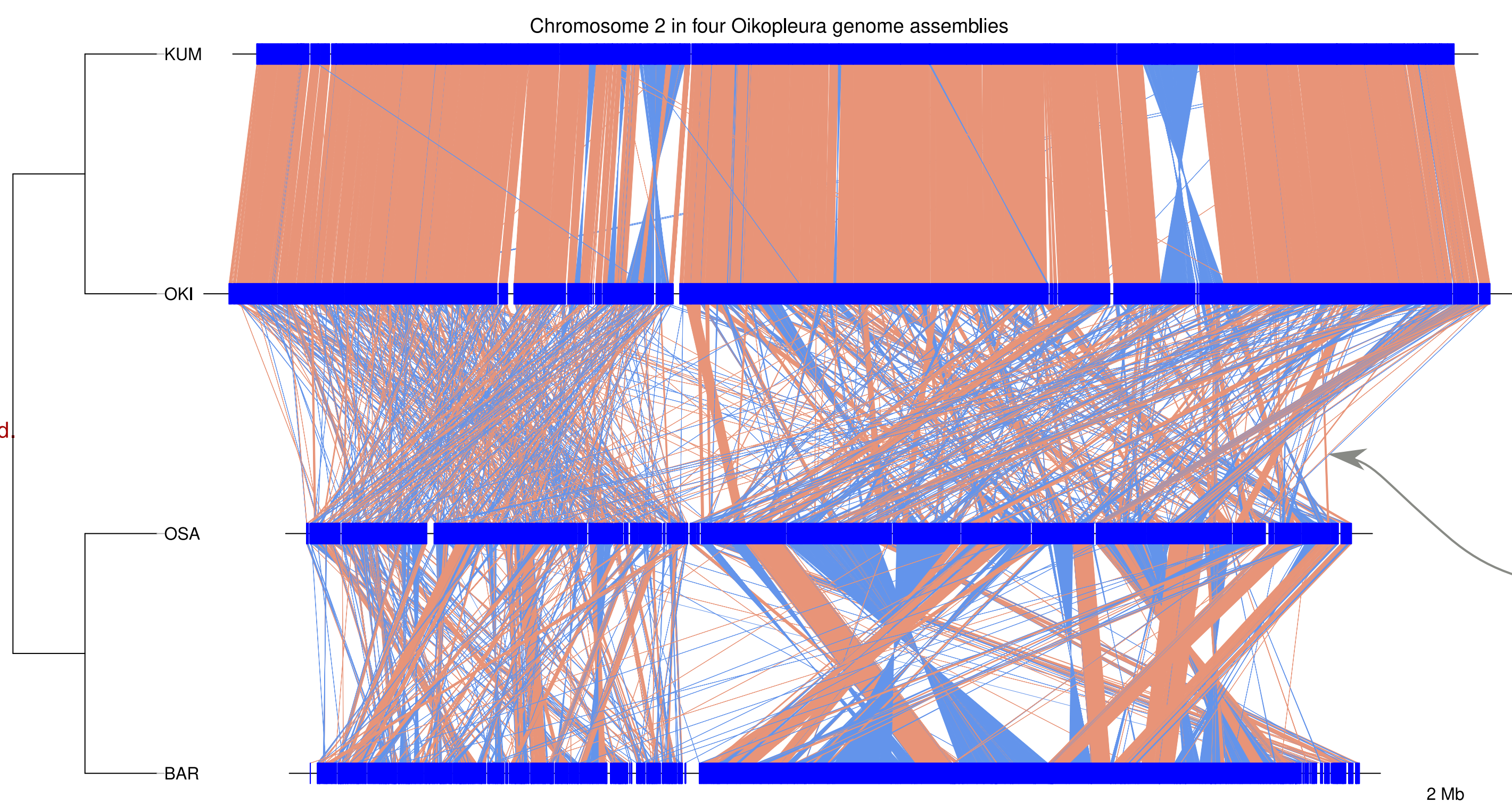
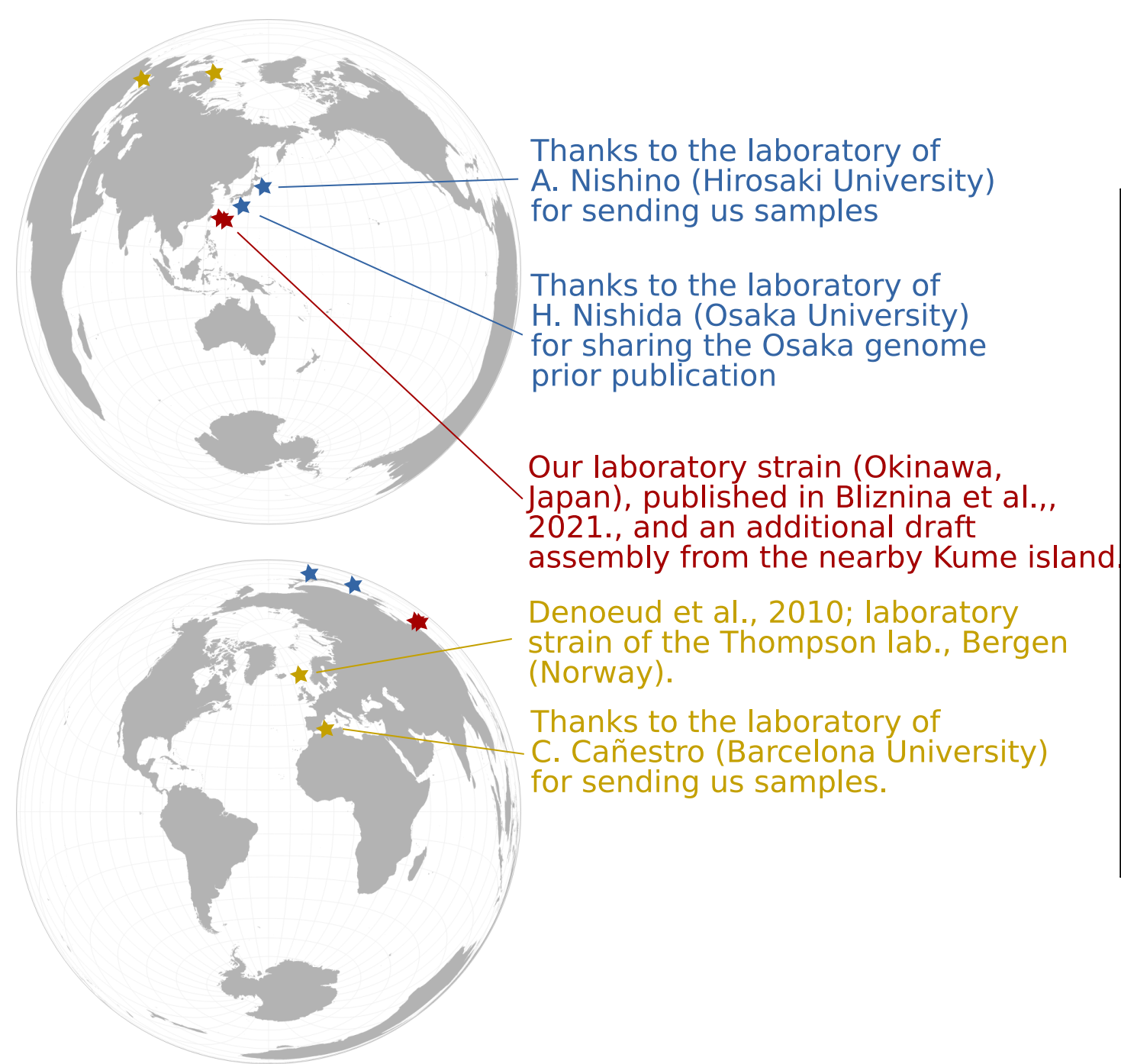


## Massive rearrangements between *O. dioica* genomes

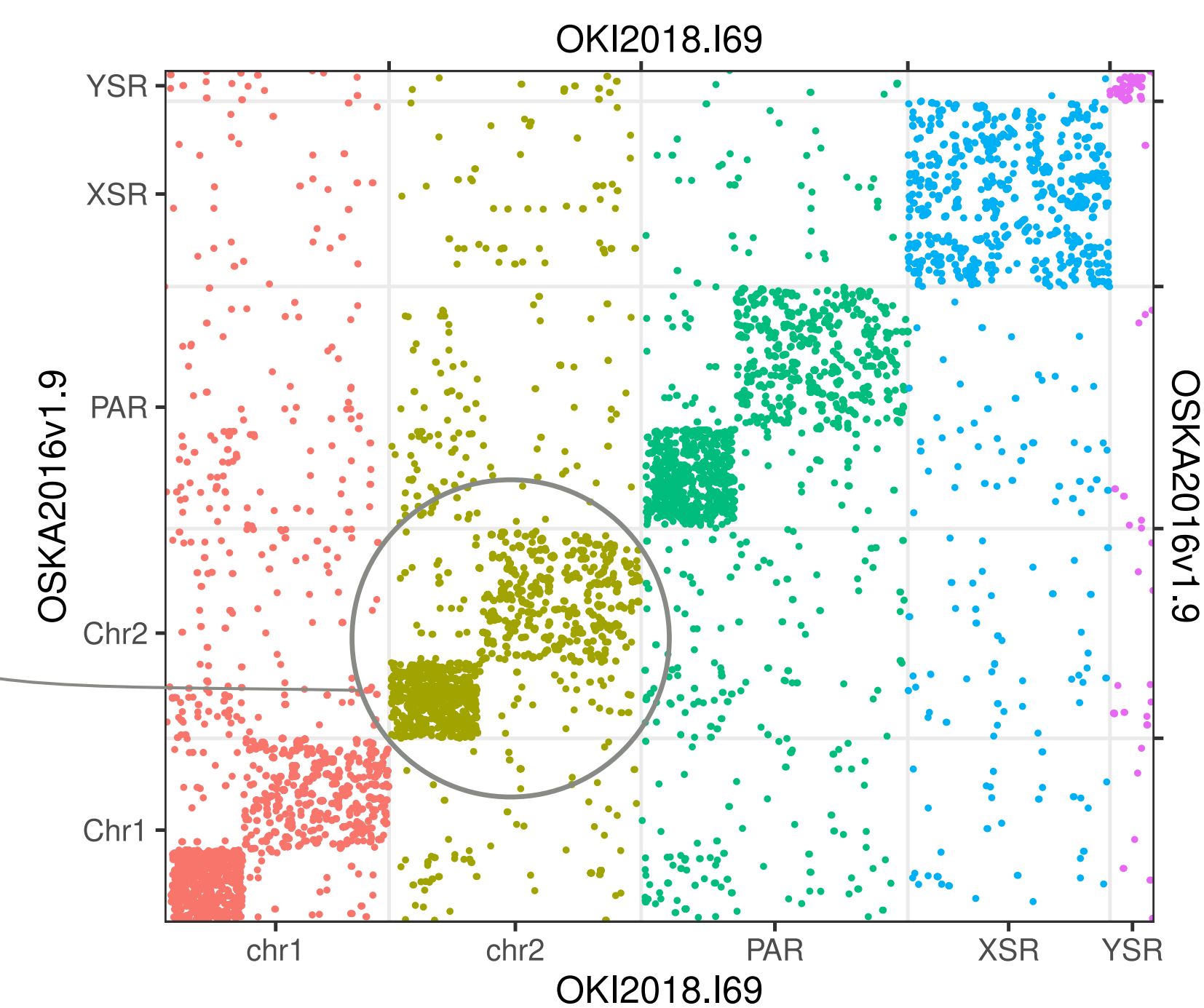
Chromosomal assemblies of different isolates revealed massive scrambling of gene order, questioning current taxonomy.

Pairwise comparison of whole genomes show conservation of synteny - in the sense of "staying on the same chromosome"

*Oikopleura dioica* is known as a globally distributed species.



OKI2018.I69 vs OSKA2016v1.9 macrosynteny plot



Collaborative sampling of *Oikopleura* in major water basins of the Northern hemisphere

Pairwise alignments of homologous chromosomes (Chr 2) and species phylogenetic cladogram.

Pairwise genome alignment visualised with the dot plot method

## There are 3 genome assemblies available for *Oikopleura dioica*:

- Odb3 (Denoëud and coll., 2010), a Sanger sequencing of the laboratory strain of the Thompson laboratory in **Norway**.

- OSKA2016 (Wang and coll., 2020), a PacBio sequencing of the laboratory strain of the Nishida laboratory in **Osaka**, Japan.

- OKI2018\_I69 (Bliznina and coll., 2021), a Nanopore sequencing of a single individual of a laboratory strain of the Luscombe laboratory in **Okinawa**, Japan.

**Our OKI2018 I69 assembly has chromosome-scale resolution** thanks to Hi-C scaffolding. More details are available in our bioRxiv preprint: "Telomere-to-telomere assembly of the genome of an individual *Oikopleura dioica* from Okinawa using Nanopore-based sequencing", Bliznina and coll., 2020, <https://doi.org/10.1101/2020.09.11.292656>.

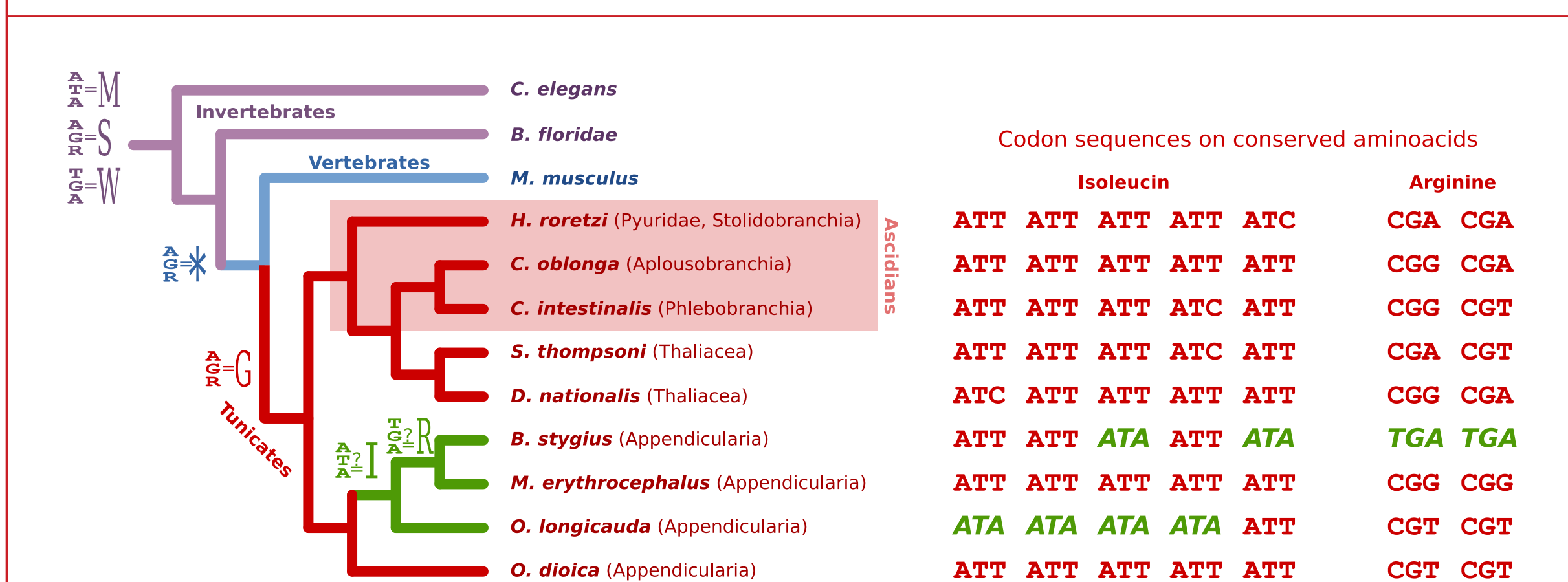
**In simple terms: our study shows that the genes move a lot, but within their chromosome arm.**

These large-scale rearrangements are likely to cause reproductive isolation and question the assumption that *Oikopleura dioica* is a single species.

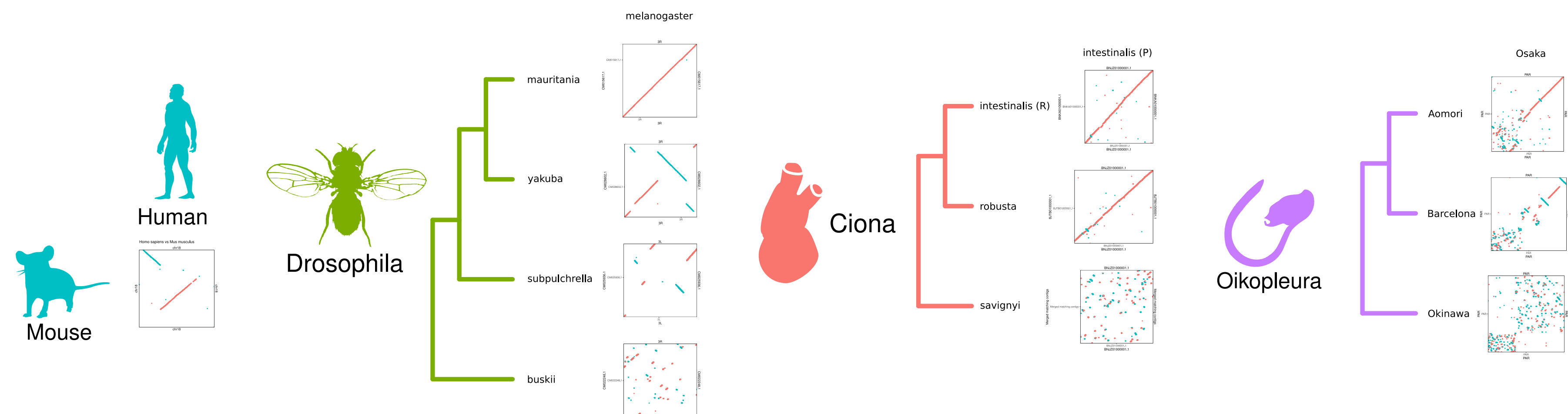
## Conclusions and perspectives:

Each change of chromosomal location of a DNA sequence from one genome to the other is related to a break of the DNA molecule. We are now studying the sequence context of these breaks to understand what makes the *Oikopleura* genome so "fluid" and how we can utilise this to simplify the design of artificial genomes.

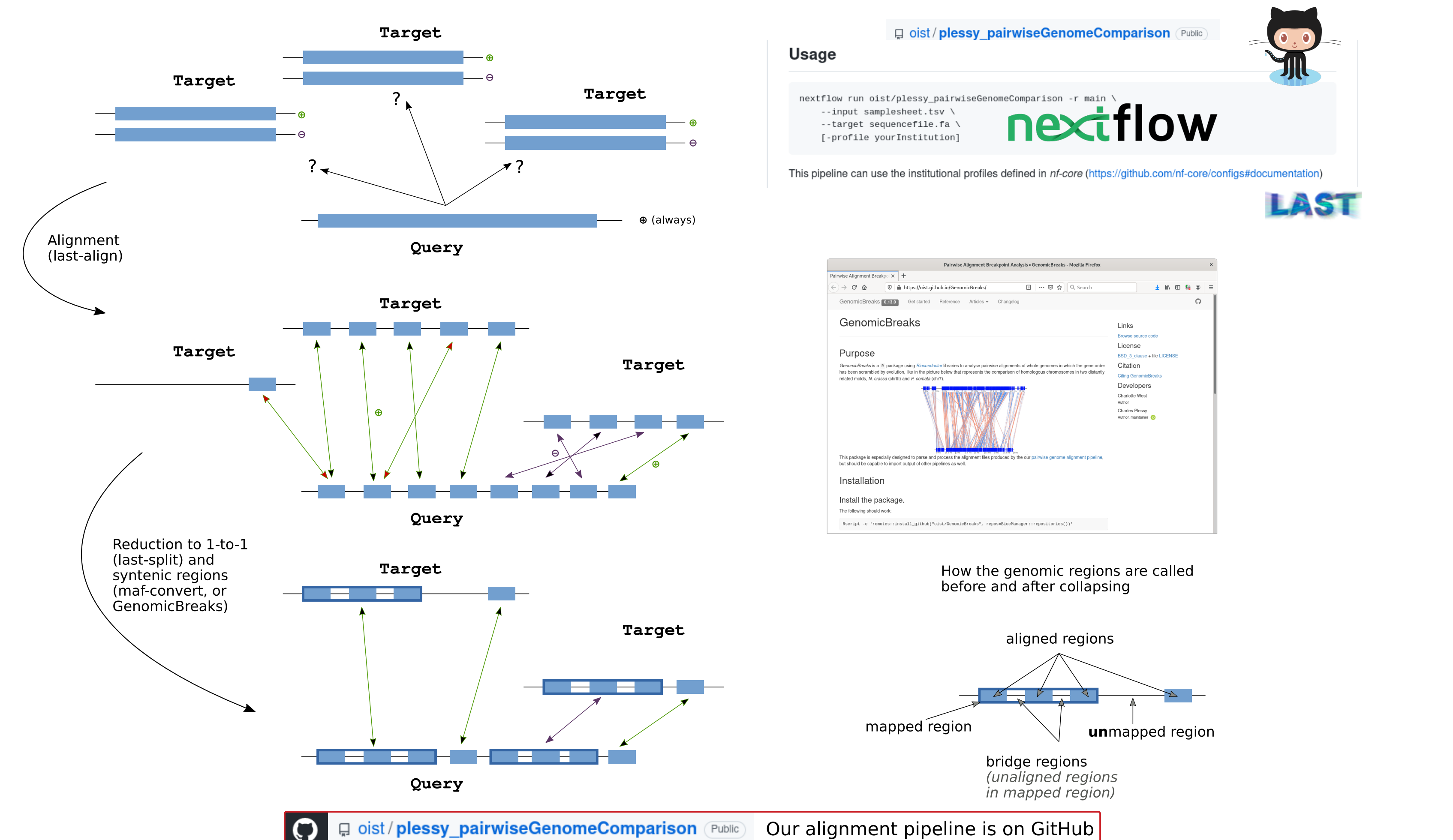
By the way... *O. dioica* uses the "ascidian" mitochondrial genetic code but some other larvaceans use a different code that was not described before.



## Alignment of 10-Mbp windows in pairs of increasingly distant species.



At a similar alignment distance, pairs of *Oikopleura* genomes (in purple) show much stronger changes of gene order than pairs of ascidian genomes (*Ciona*, in red). Both *Oikopleura* and ascidians belong to the Tunicate group of marine organisms. In comparison with pairs of *Drosophila* species (in green), *Oikopleura* distinguishes itself by a differential speed of evolution on its chromosome arms.



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