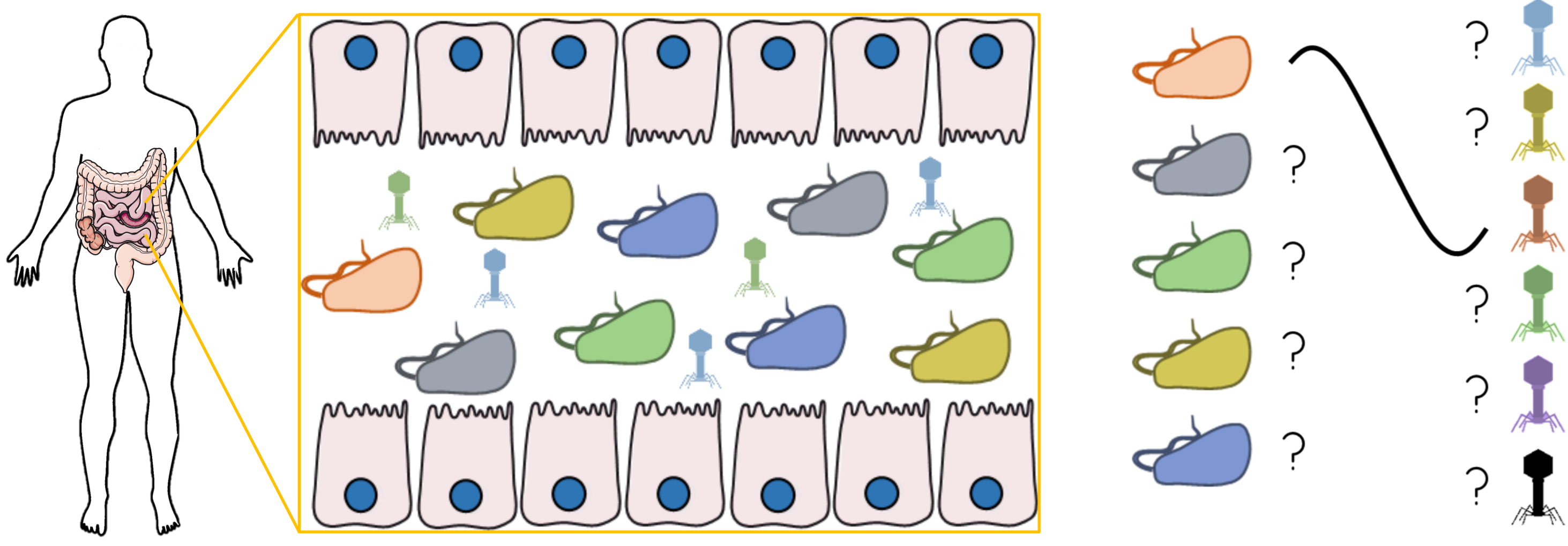




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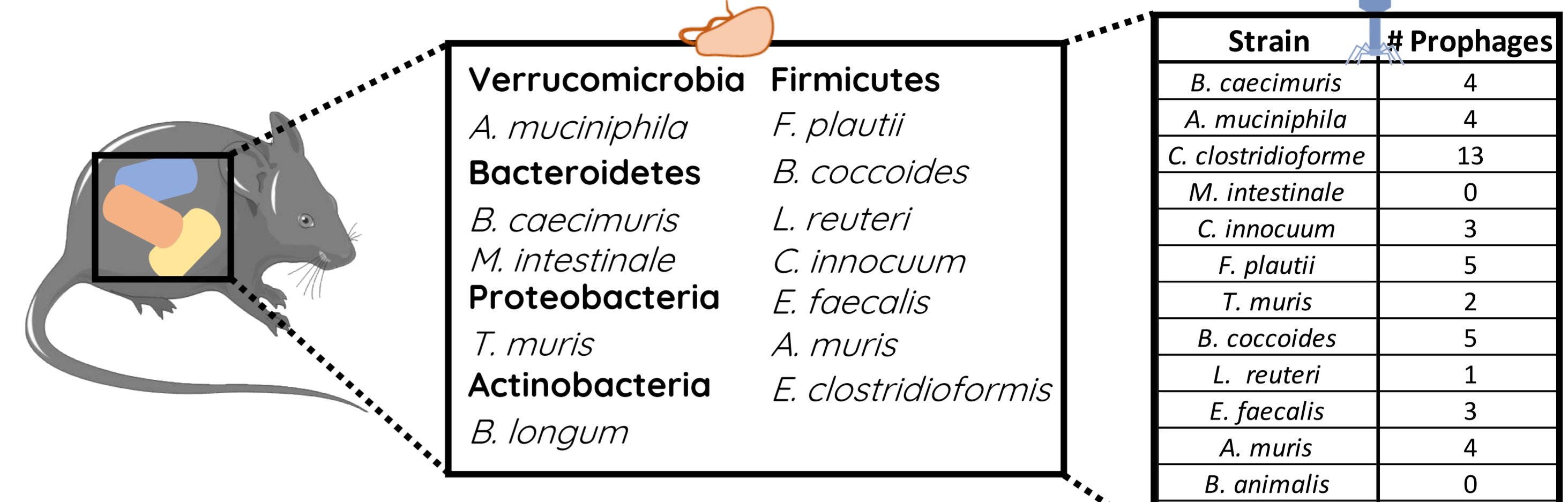
Context



Phage-bacteria interactions in the gut environment are difficult to study

Model

OMM¹² mice 12 bacterial strains ? Phages



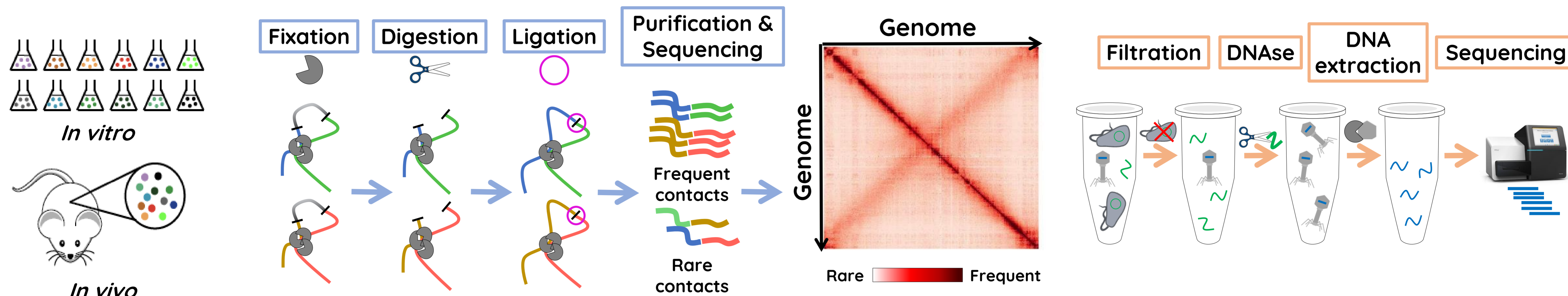
The viral community of the OMM¹² model remains unknown

Methods

Samples

3C (Chromosome Conformation Capture)

Virome Sequencing

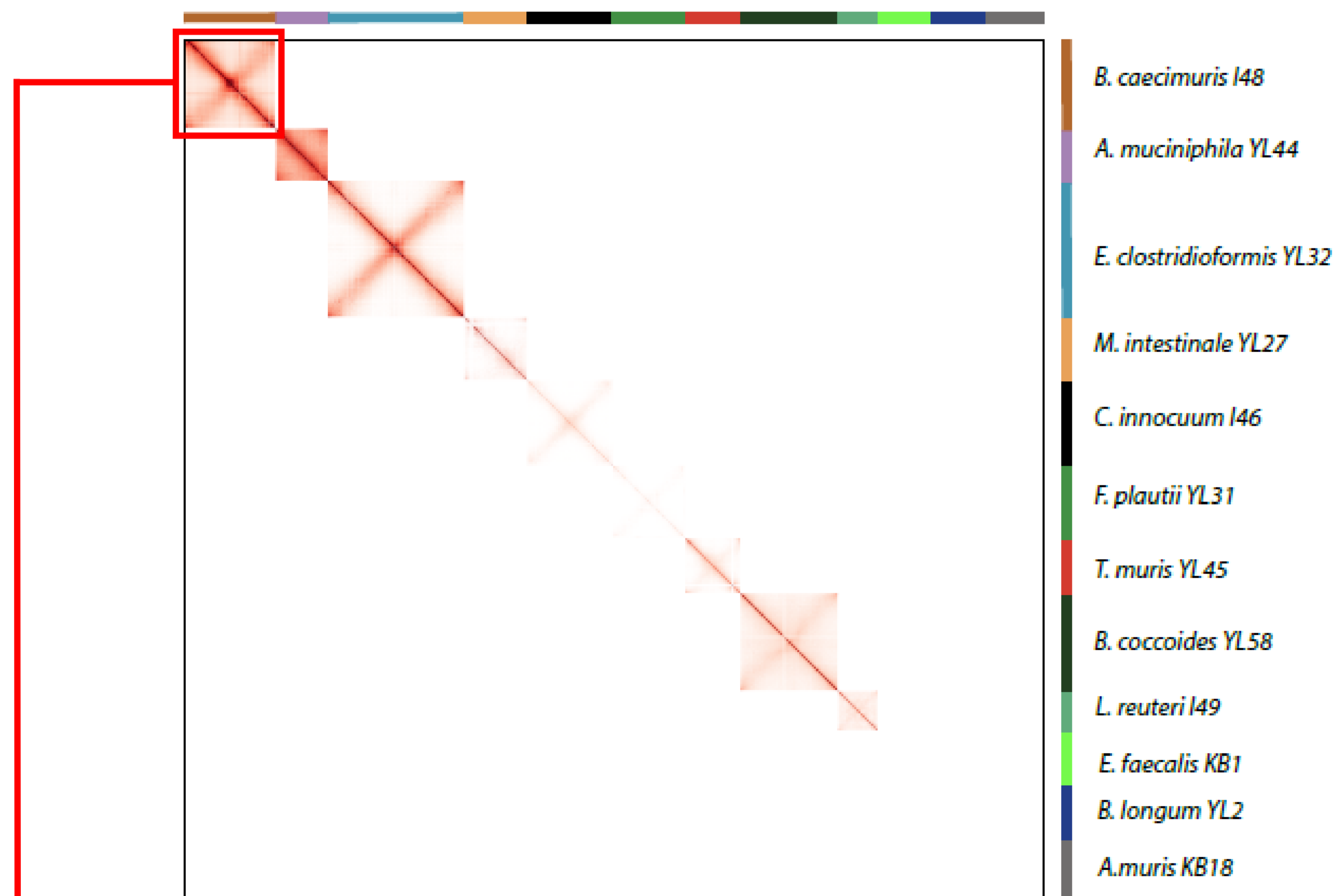


3C captures DNA contacts to reconstruct the 3D organisation of genomes

Enriching a sample in viral DNA

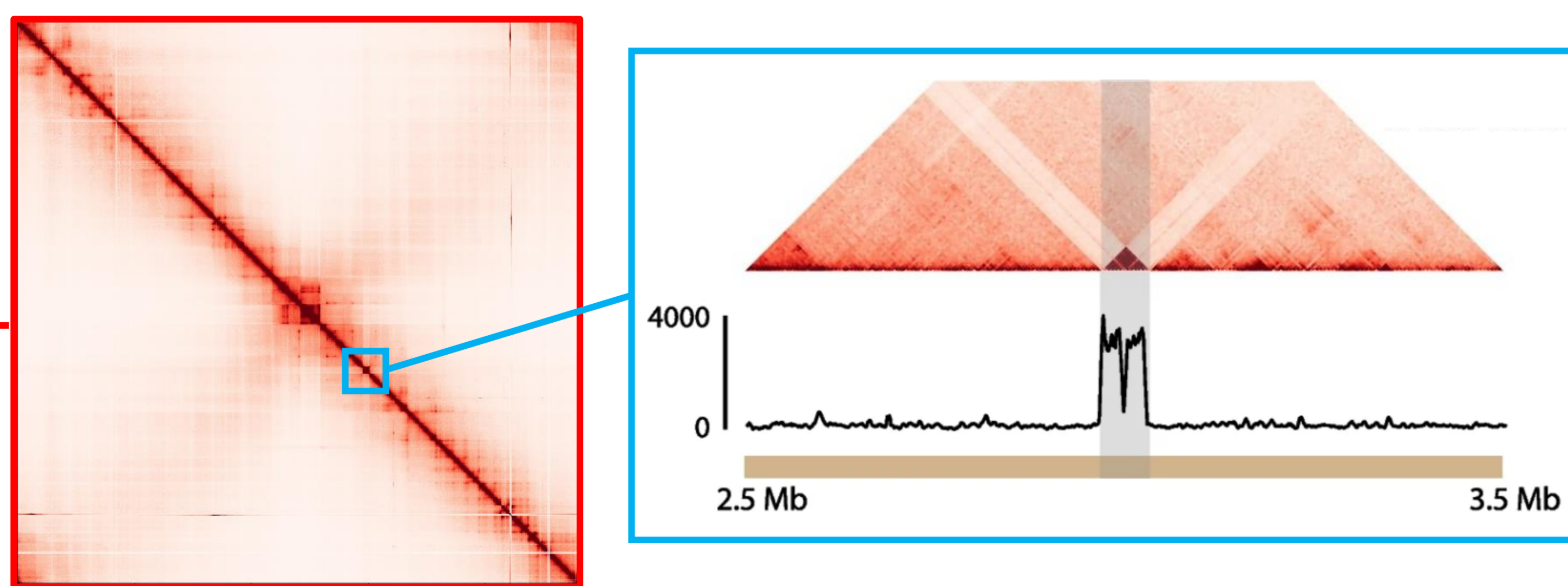
Results

Genome architecture of OMM¹² bacteria



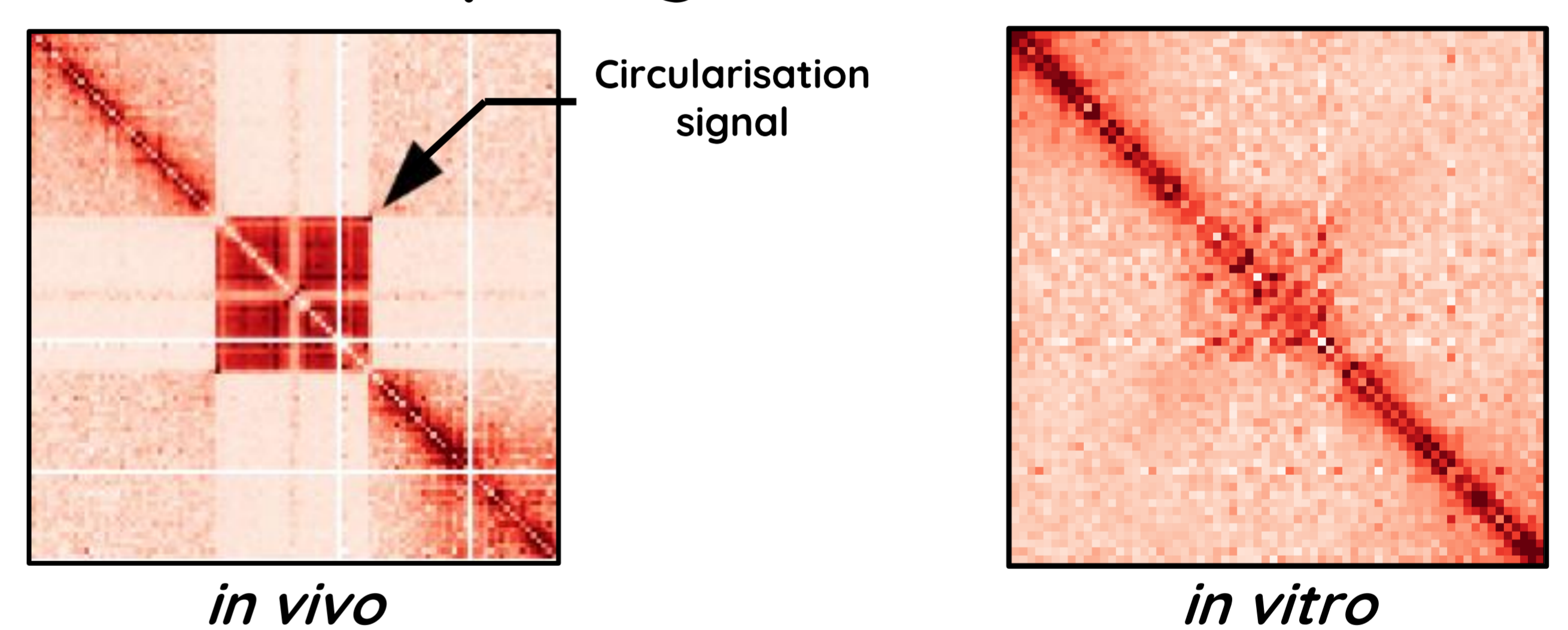
Uncovering the diversity of bacterial genome architectures

3D signature of induced prophages



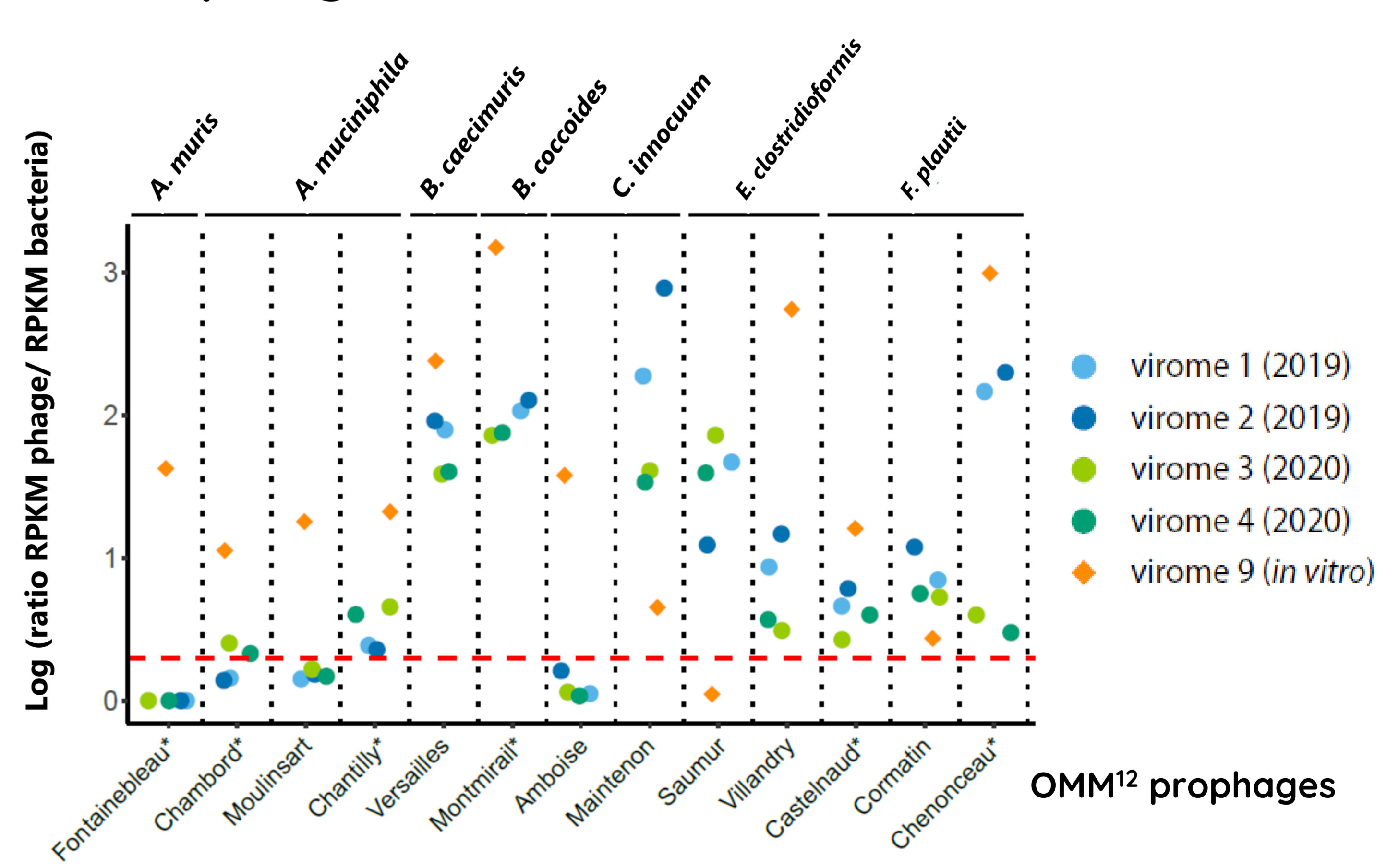
Prophage regions have specific 3D signatures

Comparing *in vitro* vs *in vivo*



Differences in the 3D signatures *in vivo/in vitro*

Prophage induction *in vitro* and *in vivo*



The OMM¹² virome is stable and composed of 10 induced prophages

Take home messages

- ✓ 3C is a promising approach to study phage-bacteria interactions, including prophage induction
- ✓ First in-depth characterisation of the OMM¹² viral community
- ✓ The OMM¹² model possesses no eukaryotic viruses or virulent phages, which makes it an ideal tool to study the role of these elements or of prophage induction on the gut microbiota

