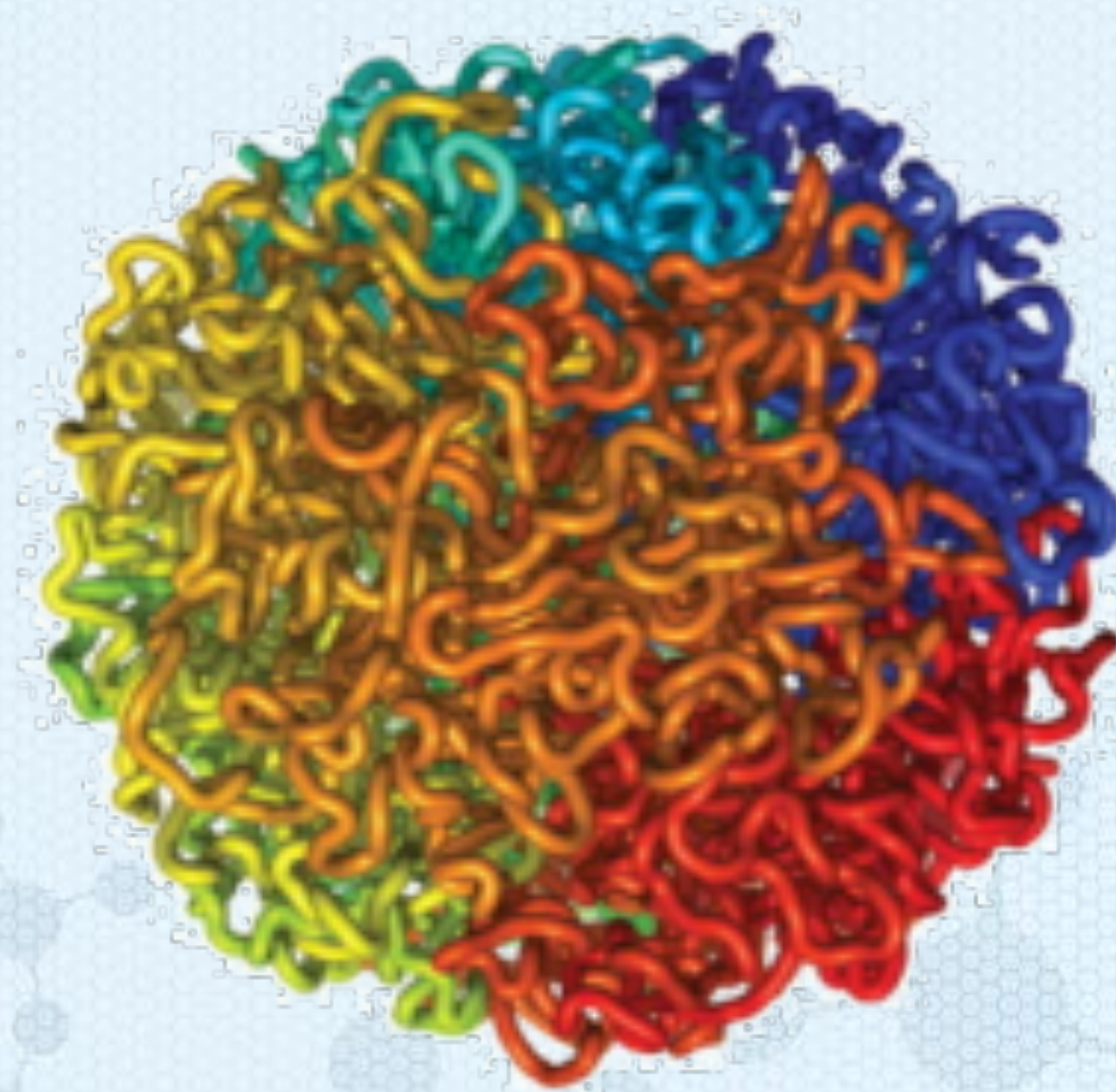# Building high quality genomes with PacBio + HiC

@PhaseGenomics
@Zevkronenberg
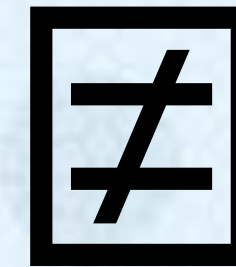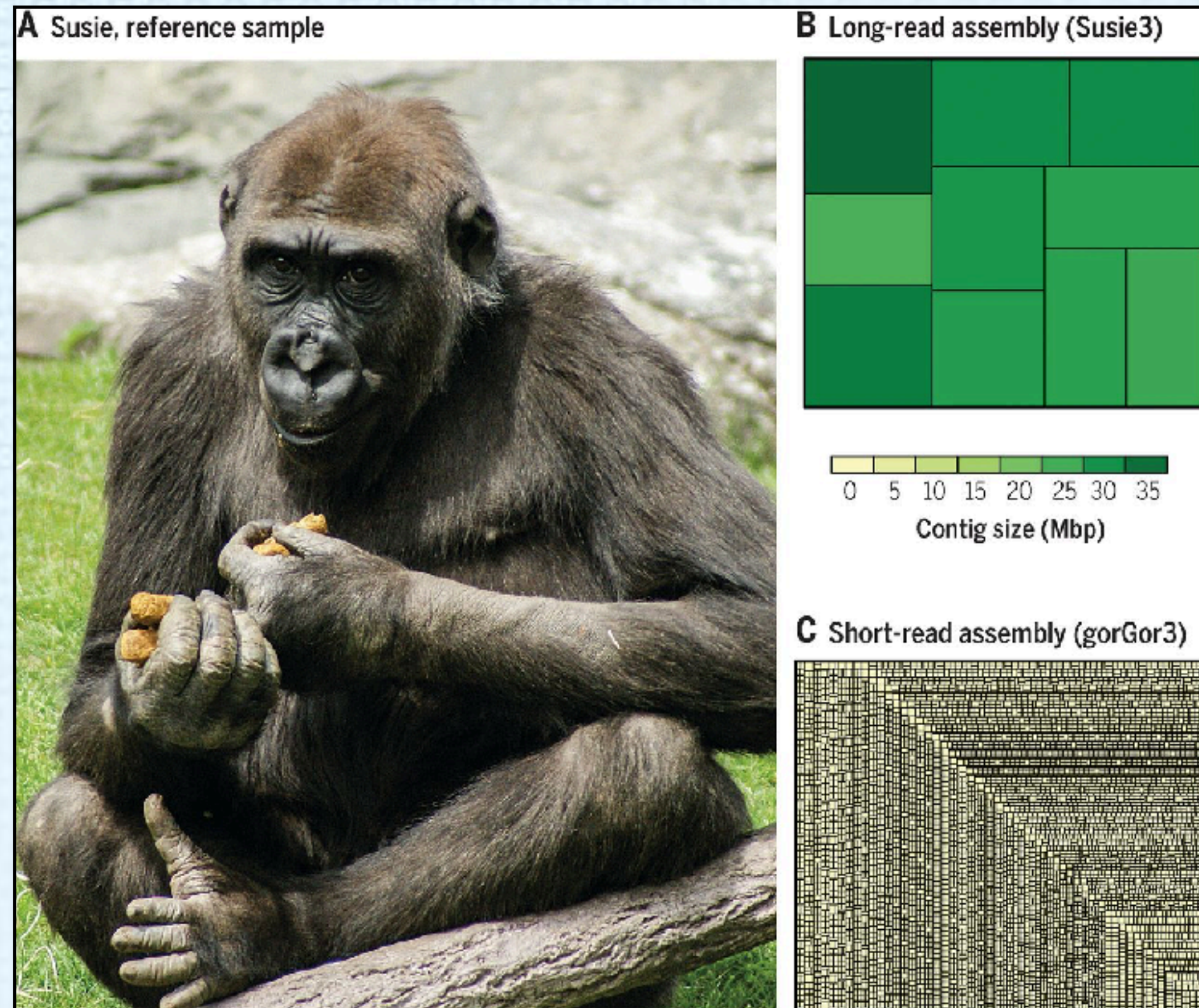info@phasegenomics.com

Lieberman-Aiden, *et. al*. Science, 2009

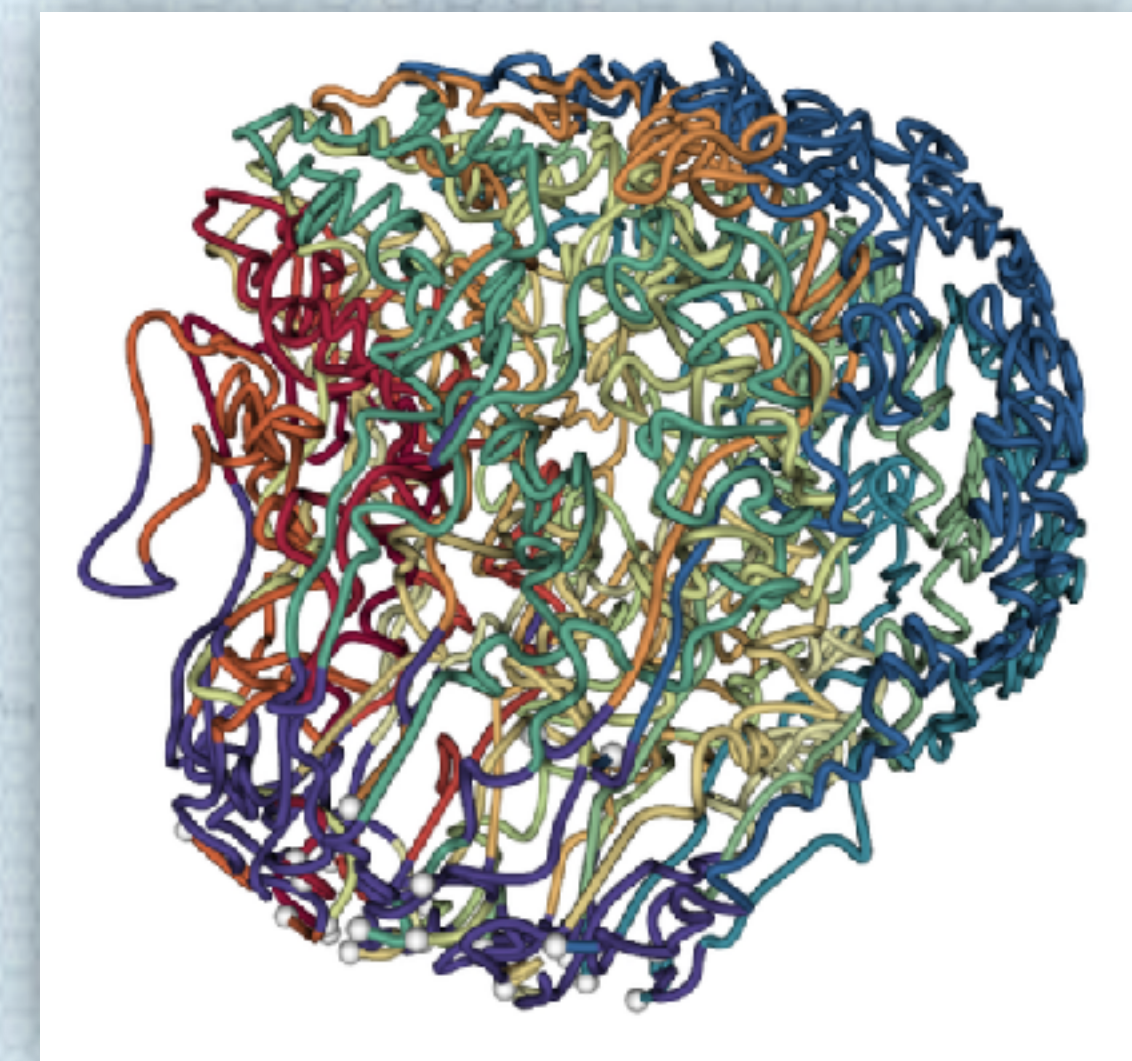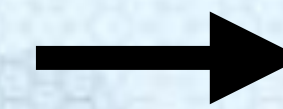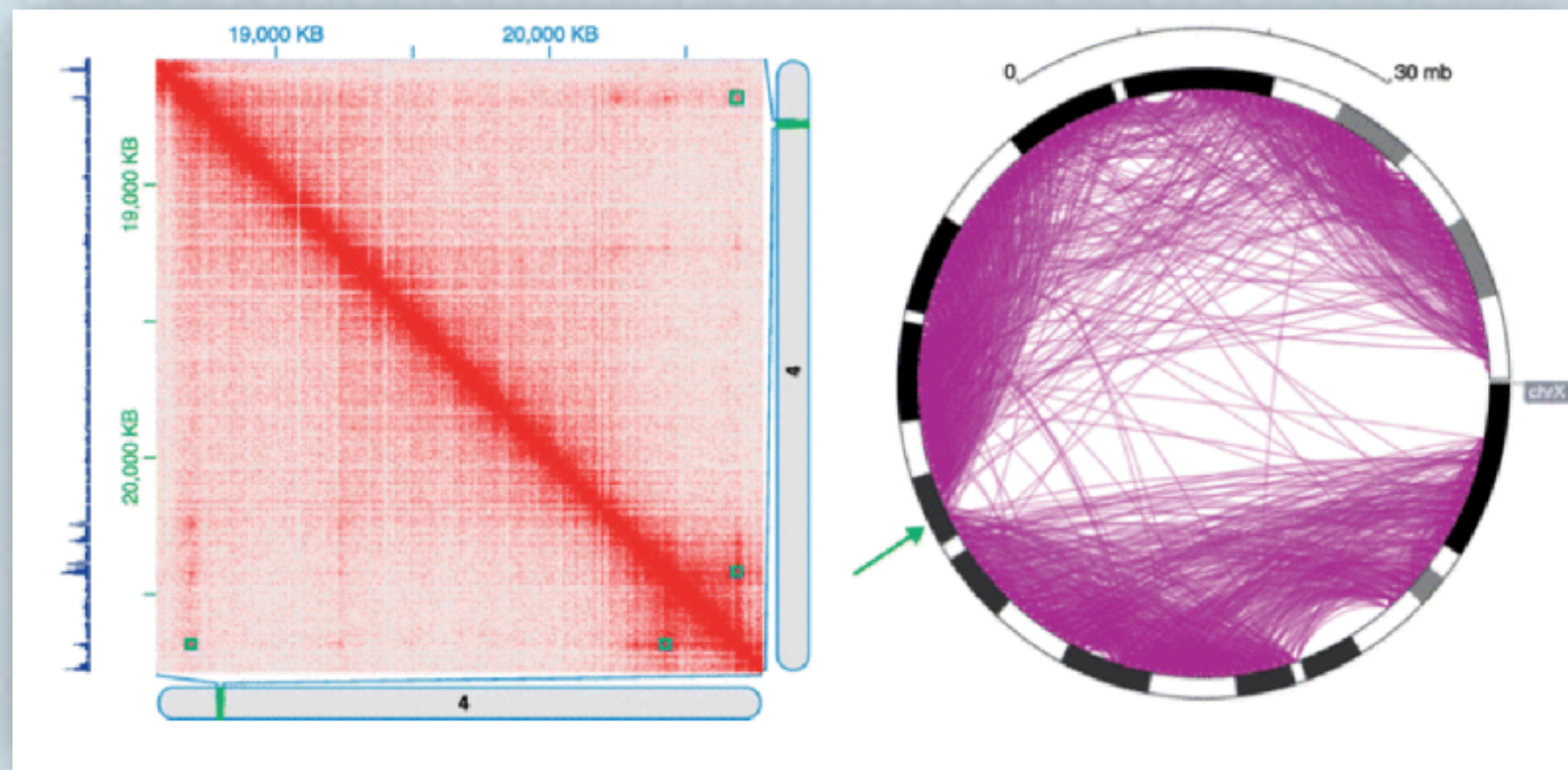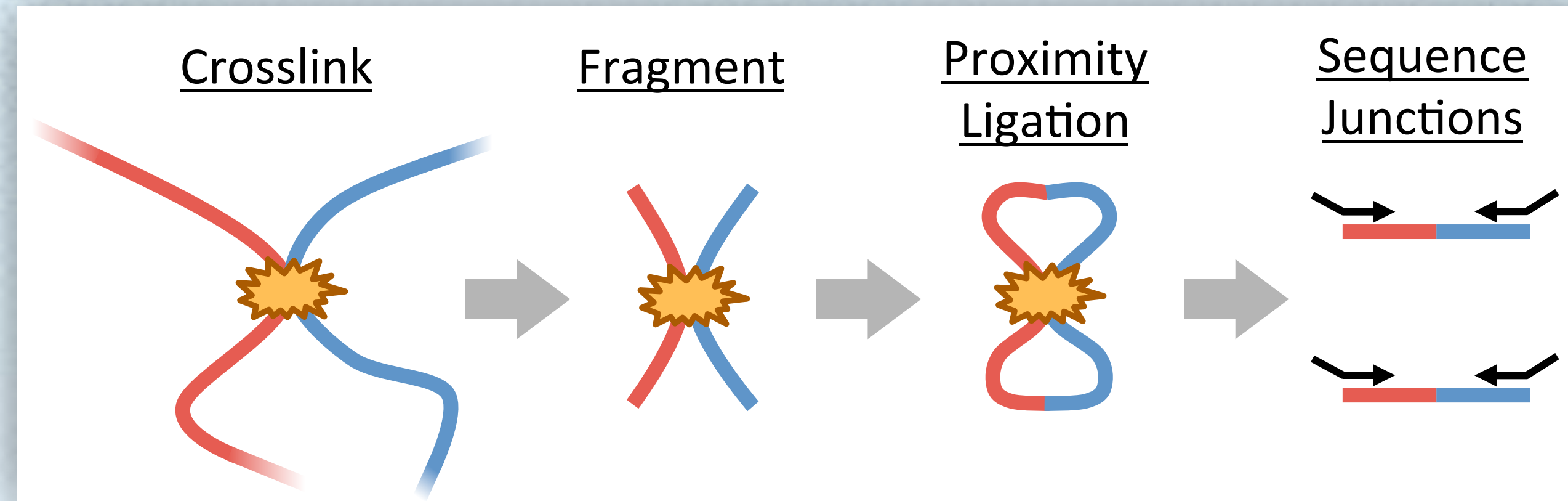# Genome assembly does not yield chromosomes

contigs

chromosomes

Gordon et al. Science 2016

How do we go from contigs from chromosomes?

Hi-C captures the 3D structure of Chromosomes

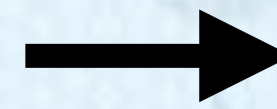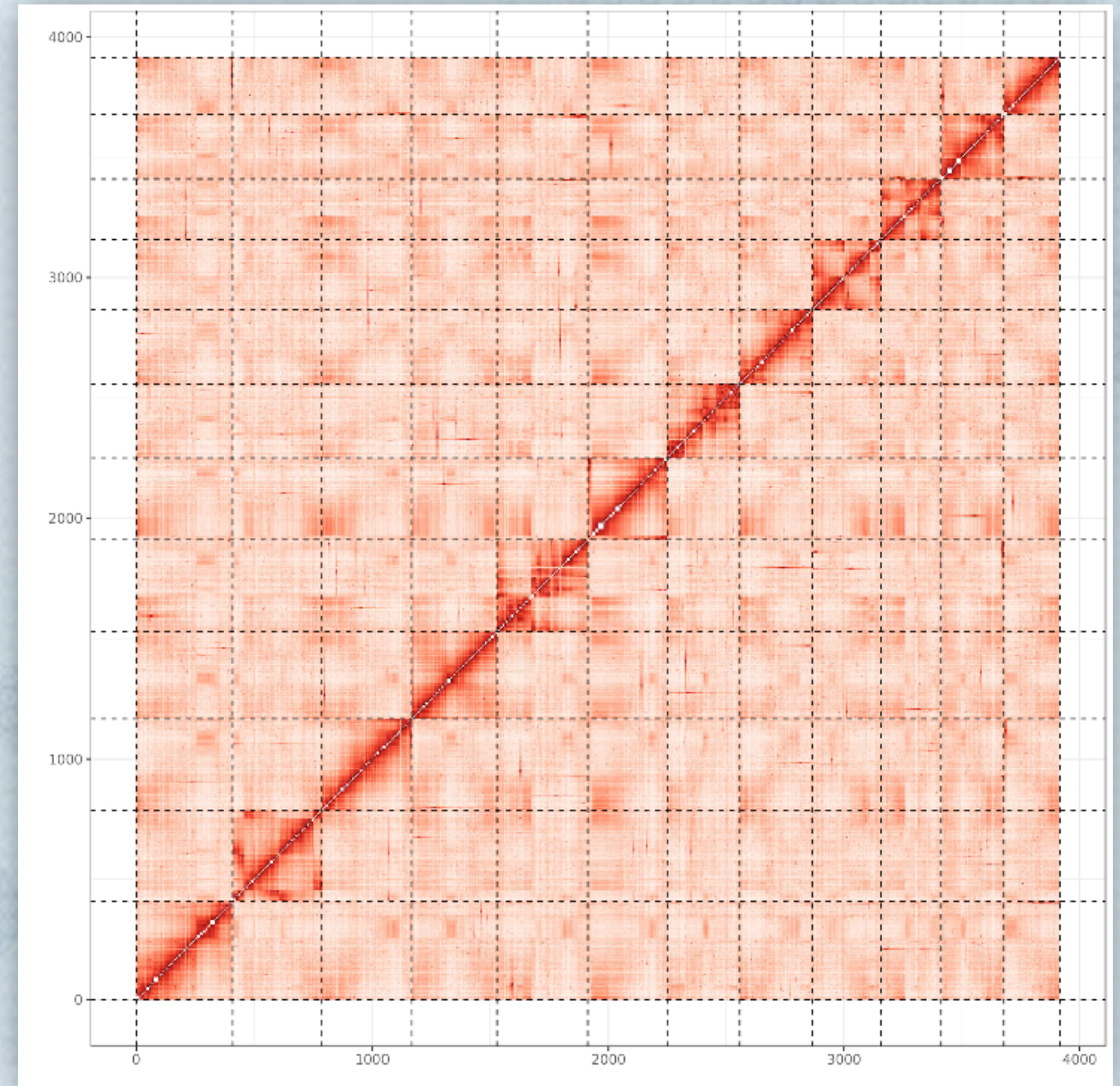# High quality scaffolding with Proximo

falcon contig to contig proximity
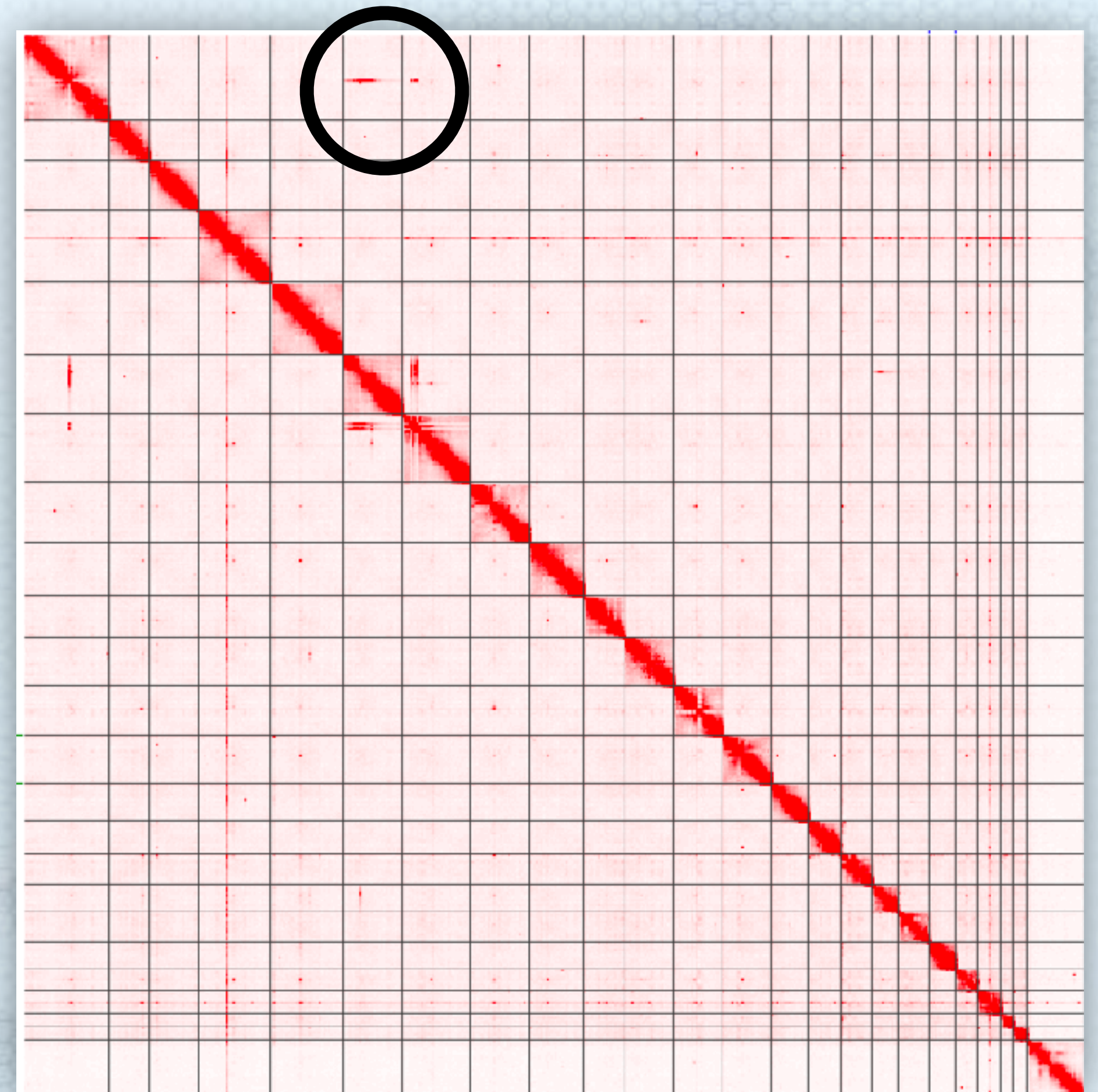
chromosome scale scaffolds

Proximo

In collaboration with Kelly Vining

Flagging scaffolding issues with Hi-C

Clint the chimpanzee

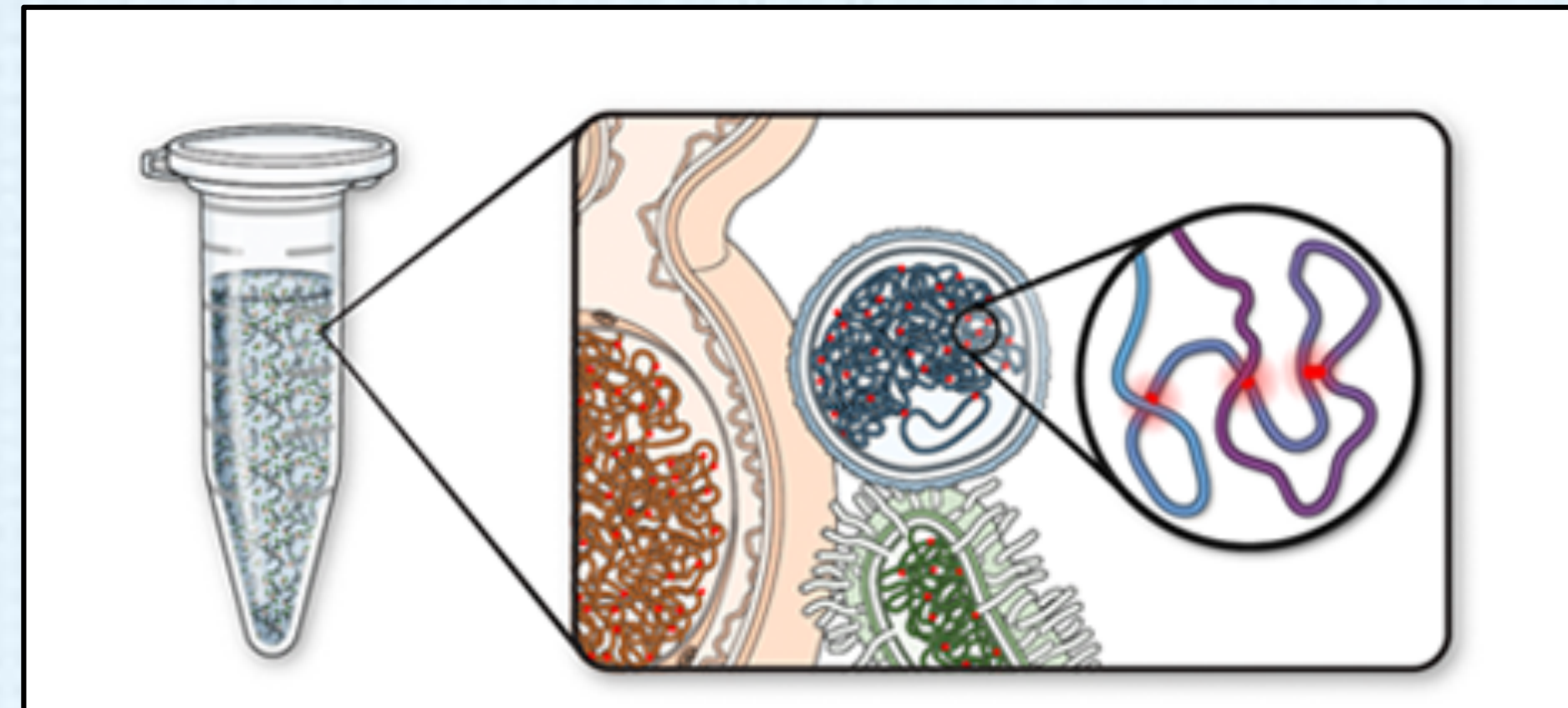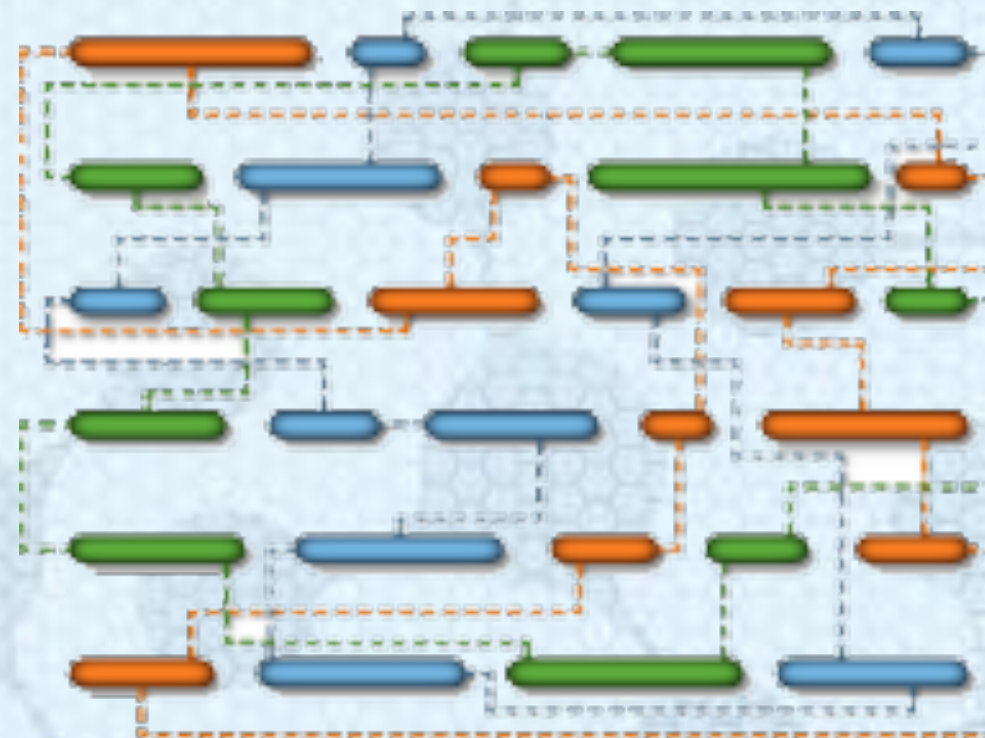**Clint scaffolds**

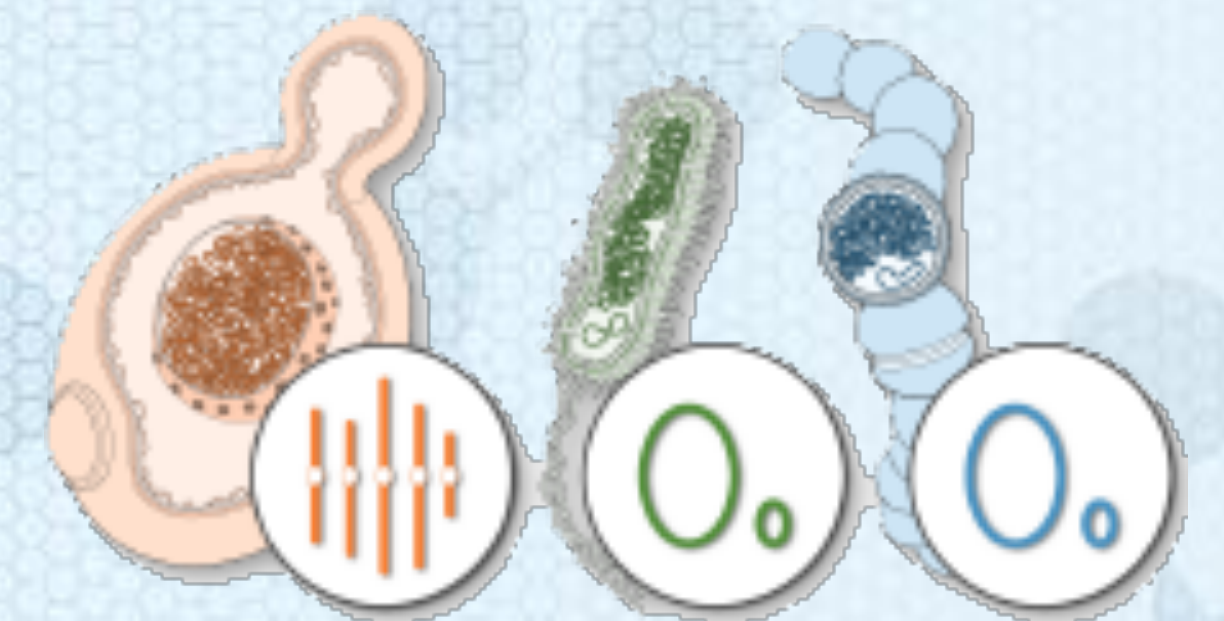ProxiMeta leverages Hi-C information to deconvolve metagenomic samples
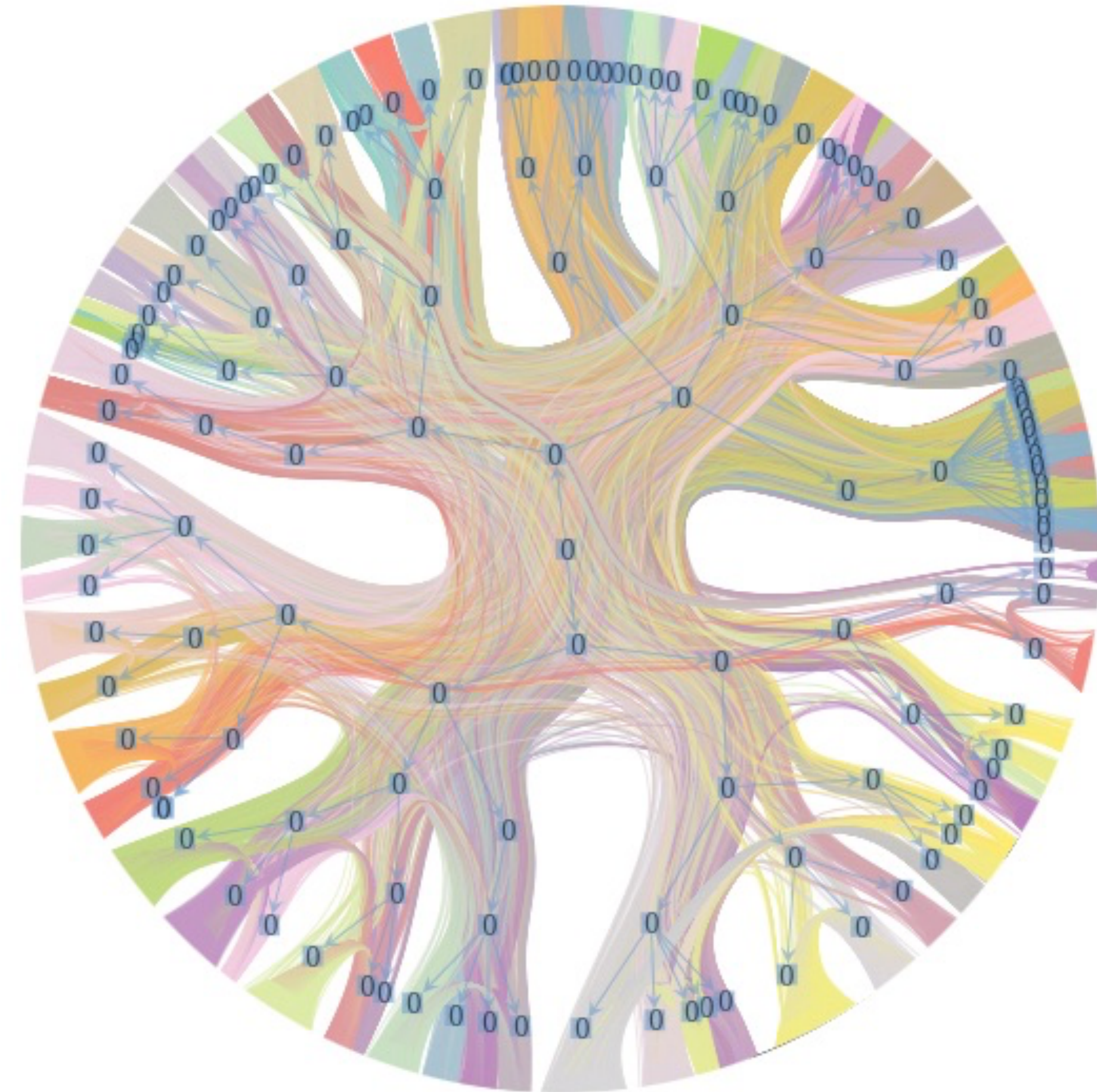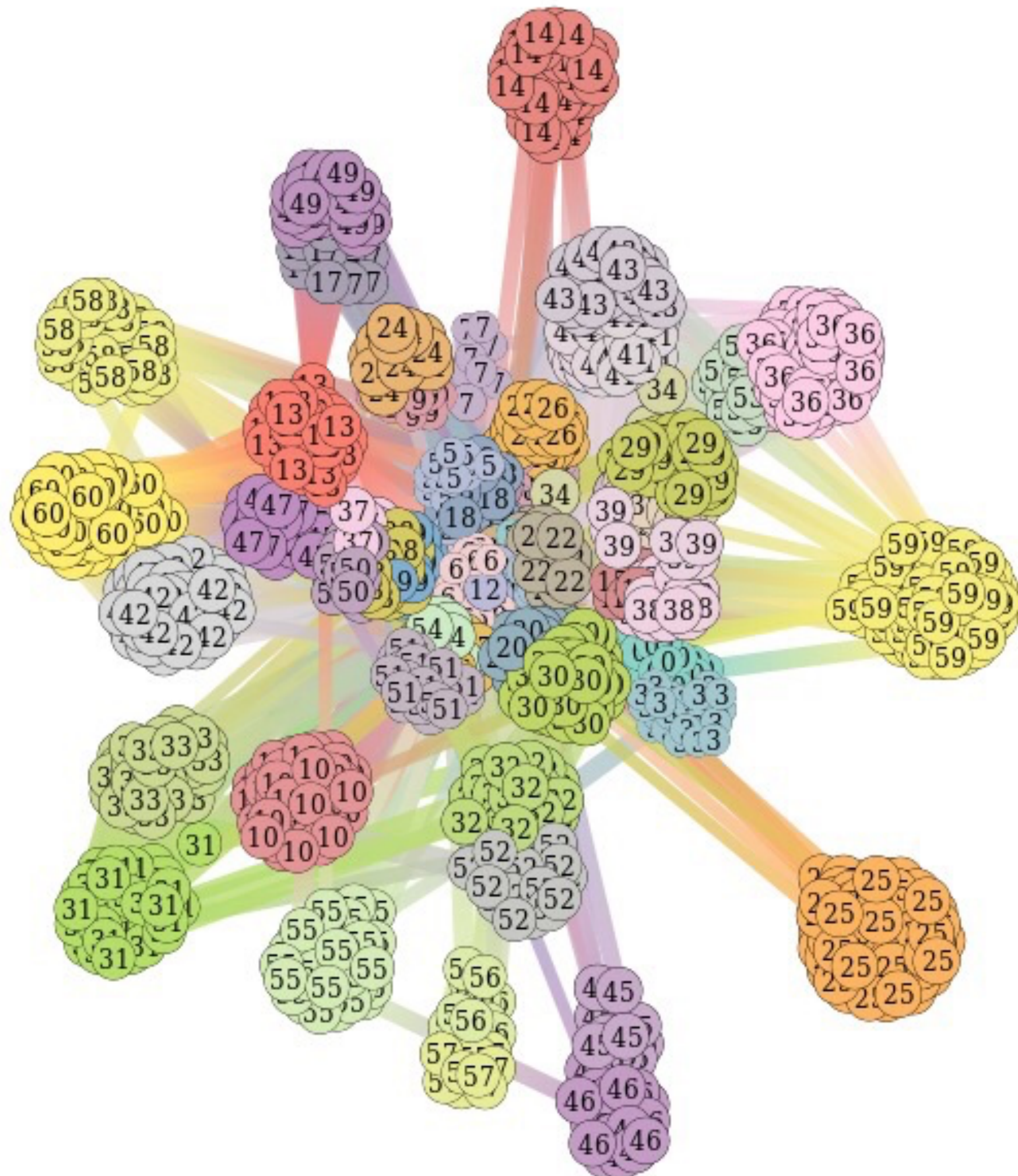
Assembly → Assembly + Hi-C → Genome clusters

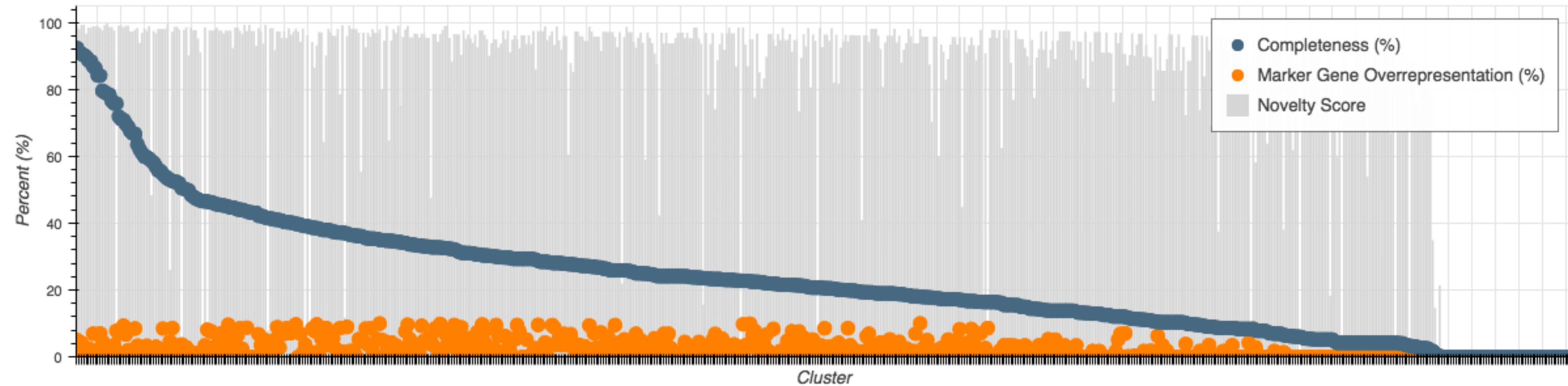# ProxiMeta is a MCMC clustering algorithm to deconvolve metagenomic assemblies

Many genome clusters from complex communities

Collaboration with USDA, NHGRI, Roslin Inst.

Collaboration with AnimalBiome

Many genome clusters from complex communities
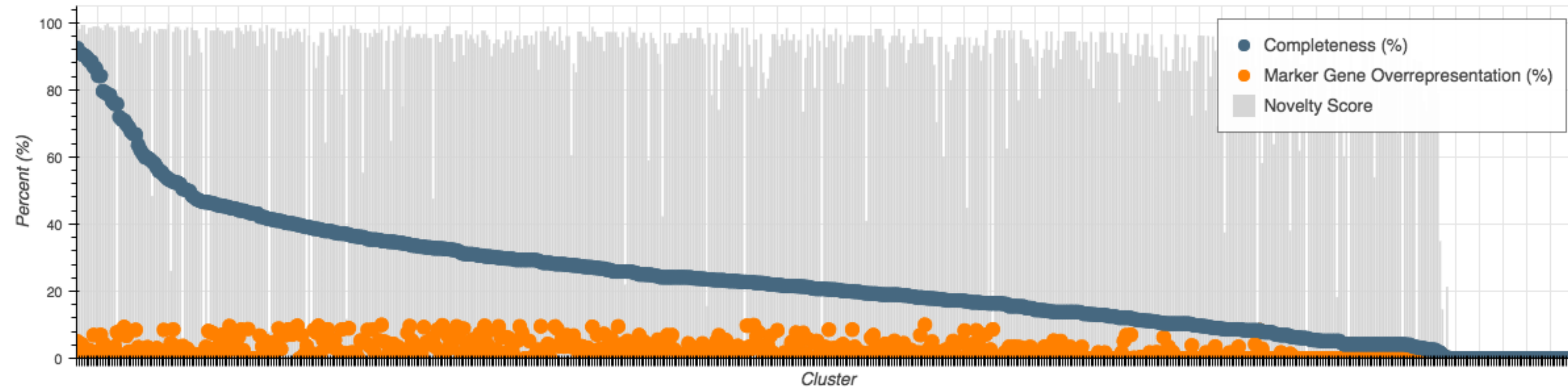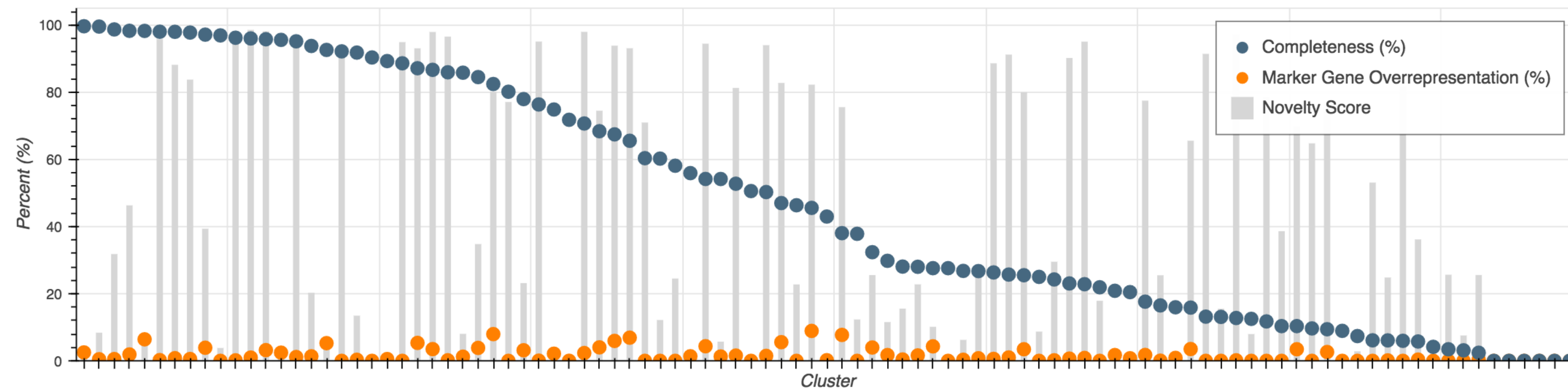
Hi-C low stress

- **Fast (1 day)**
- **Easy to use**
- **Affordable**
- **Simple sample requirements**
- **No HMW DNA**

Metagenomics　　**Animals**　　**Plants**