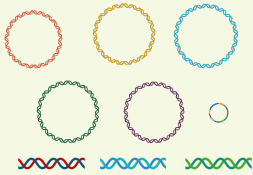


## Genome

### Assembly circled genome

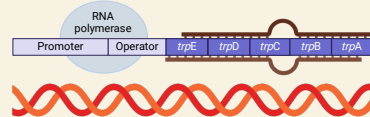
- Assembly complete genome
- Establish microbiome reference catalogue
- Investigate phylogenomics



## Gene

### Predict gene and elements

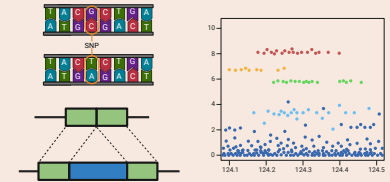
- Recovering full-length biosynthetic gene clusters
- Discovery mobile genetic element



## Population

### Microbial variation and population heredity

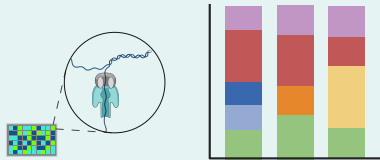
- Characterize Structural variation
- Quantify Population heterogeneity



## Tanxonomy

### Rapid identification of community composition

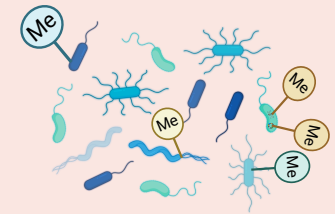
- Identification of pathogen types
- Monitoring of the environmental community



## Epigenetic

### Epigenetic and association

- Methylation profile
- Mobile elements-host association
- Assist Binning



### Long read Metagenome Application

