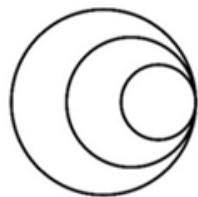# How to design and deliver pathogen genomics training for health and research professionals

Module 3B
Sample Genomic Analysis, Data
Generation, and QC

Module Overview

1. Introduction

   a. General overview of WGS methodologies (library prep and sequencing; rudimentary data analysis workflow)
   b. Summary of the workflow presented by Wilber
   c. Discussion - opportunities for error to be introduced in the earlier workflow
   d. Consideration of *Klebsiella* example; corollaries and differences compared to TB example

2. Consideration of example scenarios in small groups - interpretation and incorporation into training material
   a. Identify QC issues in
      i. the design of sample collection strategy,
      ii. DNA isolation,
      iii. sequencing, and
      iv. post-processing metrics.

3. Discussion - applicability of concepts in participants' own research and professional settings - and how these concepts would feed into training materials that they will design
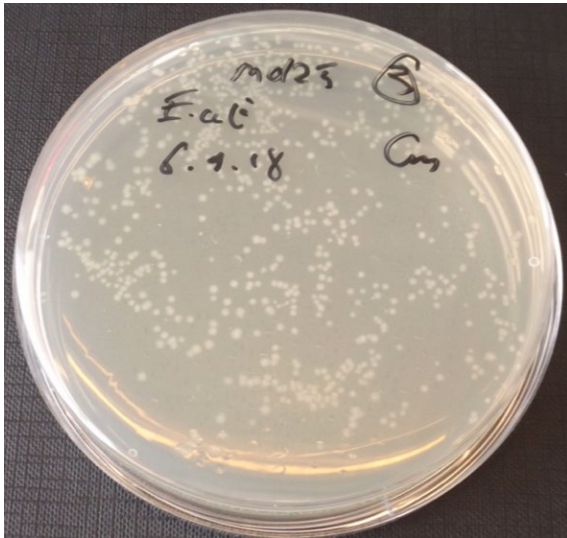
4. Questions

Whole Genome Sequencing, and why do you care for training purposes?
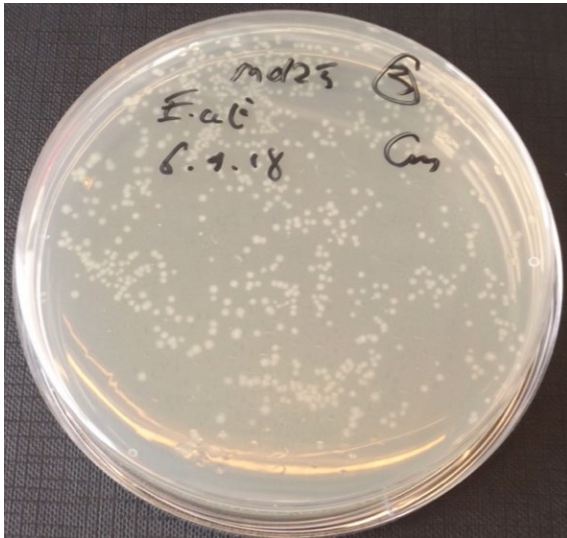
GTACCCGTAAGCAAACTTTGG

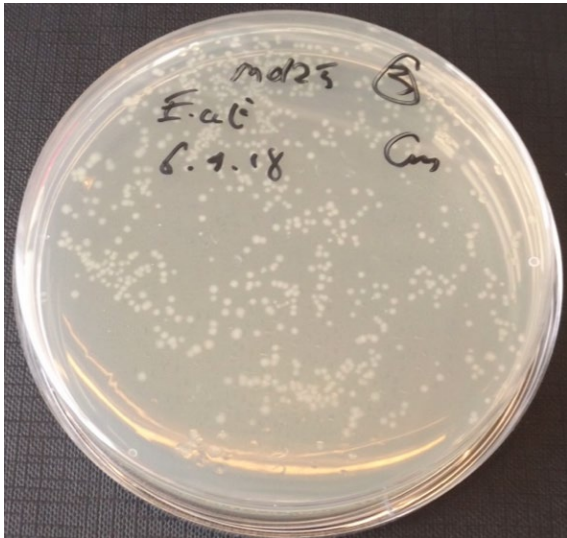# Whole Genome Sequencing, and why do you care for training purposes?

GTACCCGTAAGCAAACTTTGG → **Useful Information**

Whole Genome Sequencing, and why do you care for training purposes?

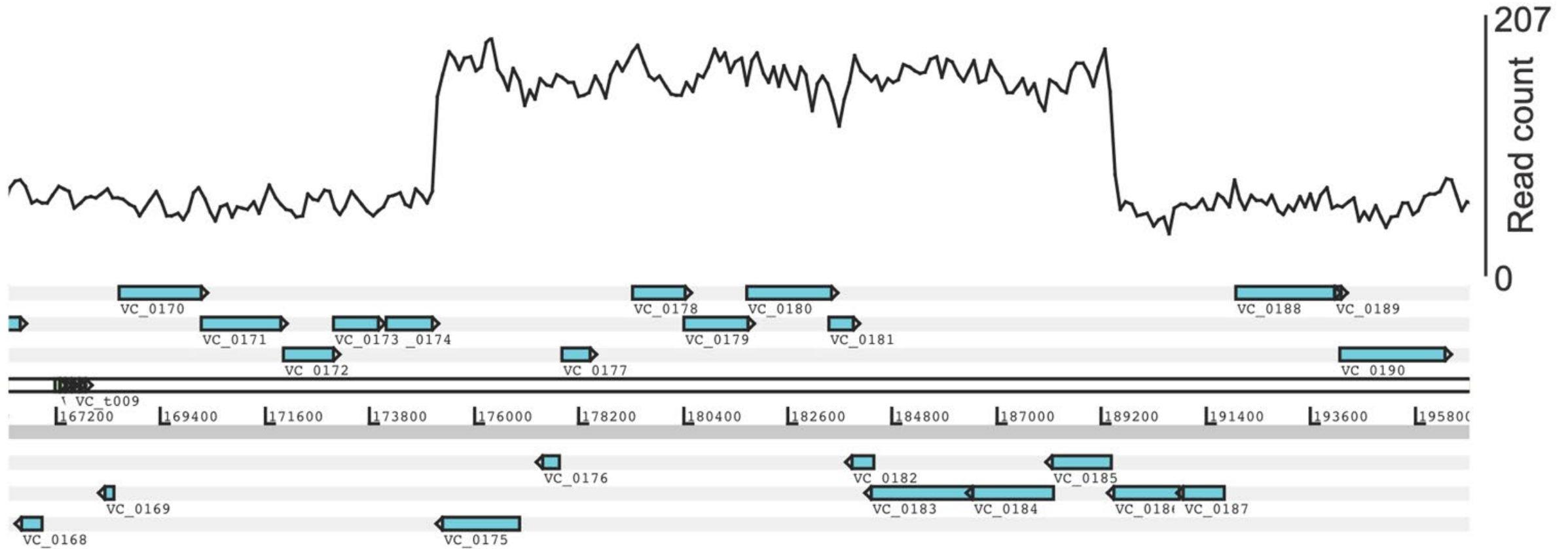

GTACCCGTAAGCAAACTTTGG → **Useful Information**

Whole Genome Sequencing, and why do you care for training purposes?
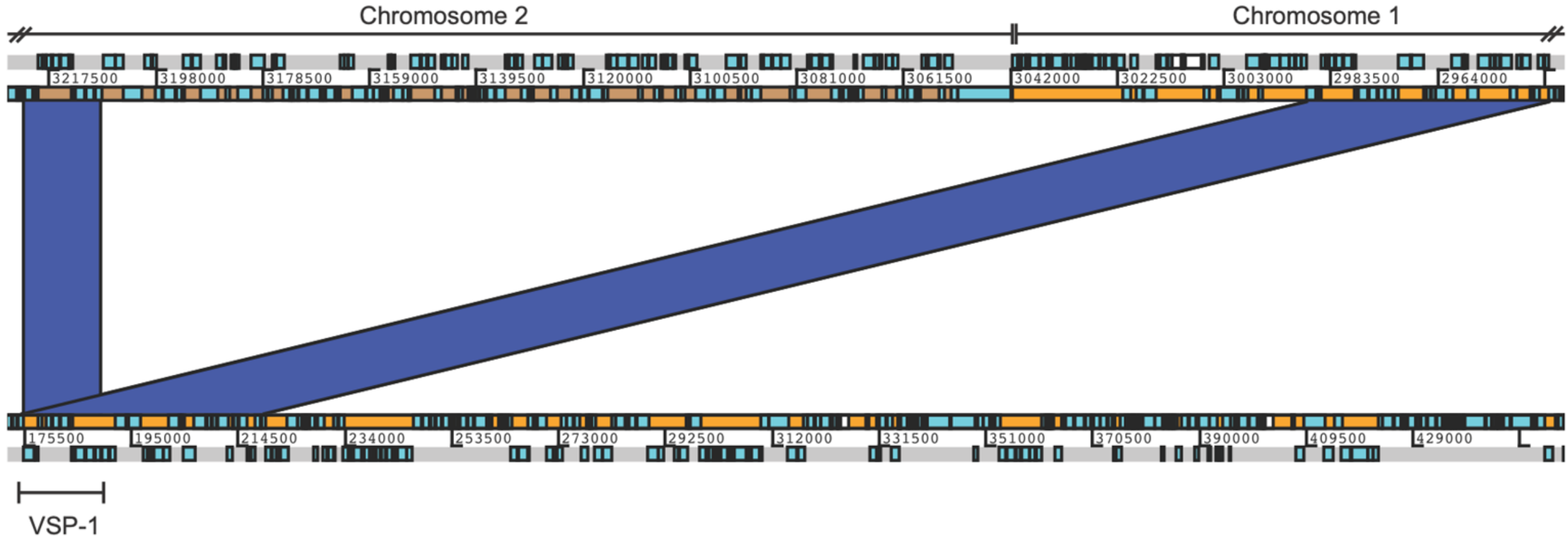
Short-read vs long-read

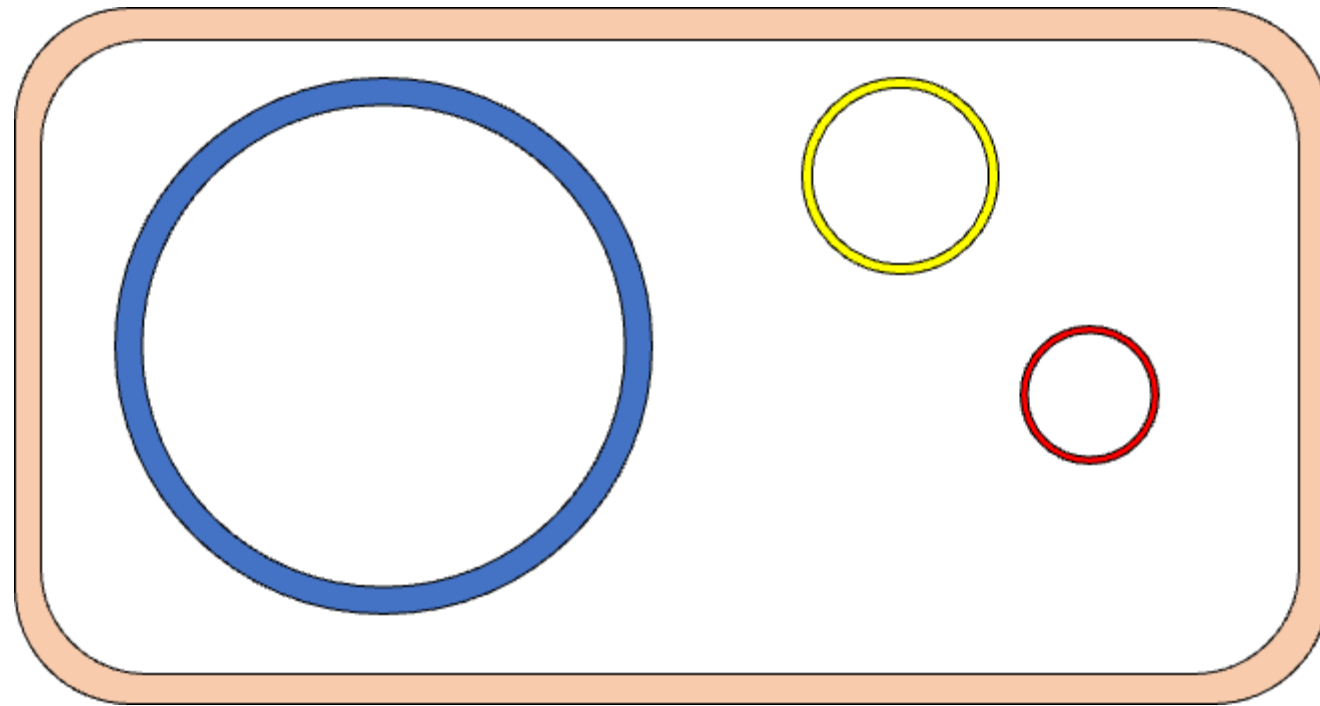**Local settings**

Best practice

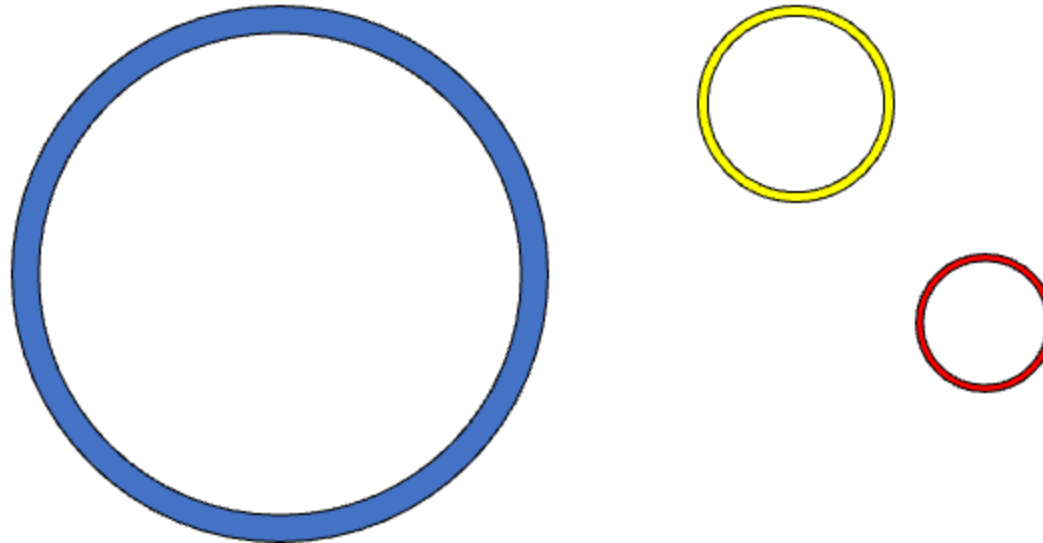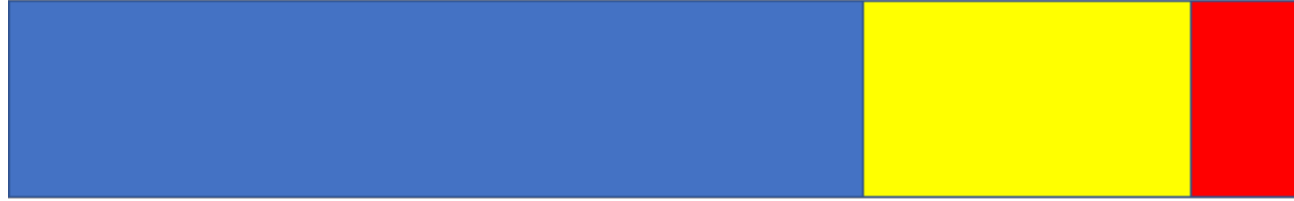# What's wrong with this picture?

What's wrong with this picture?

PMID 30971707

Choice of methods

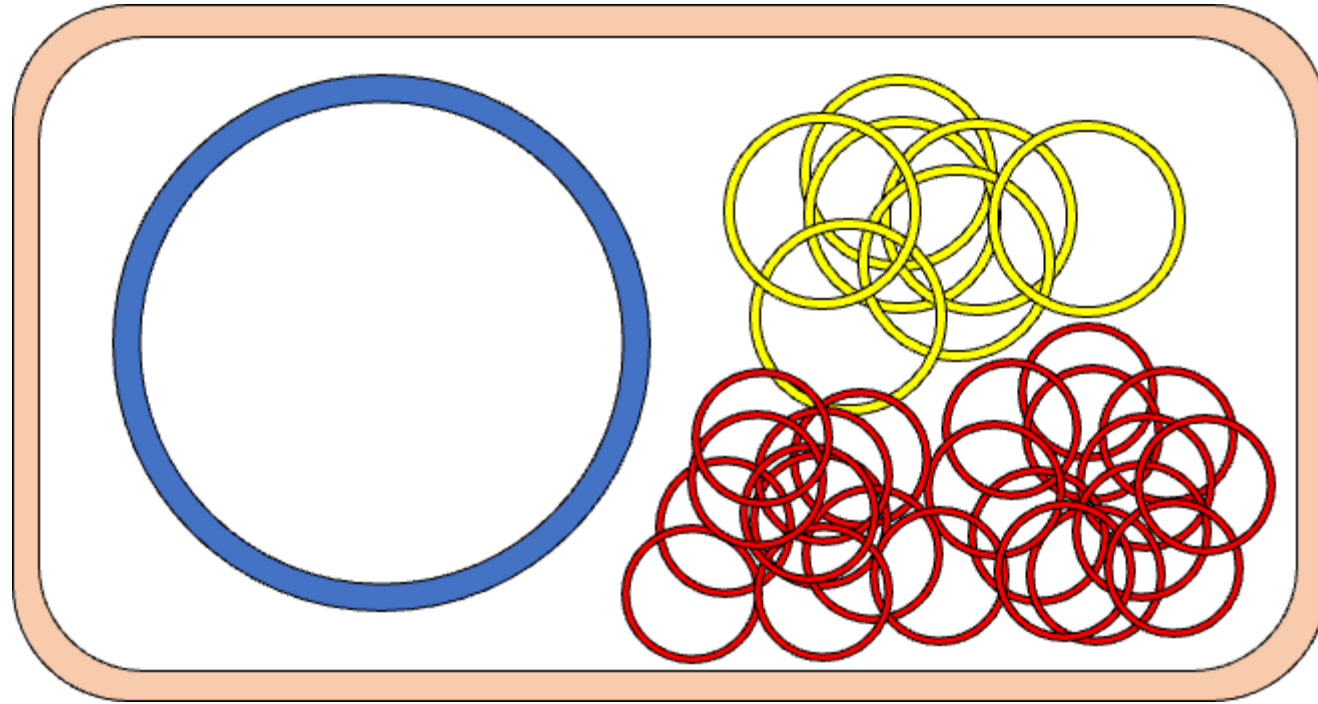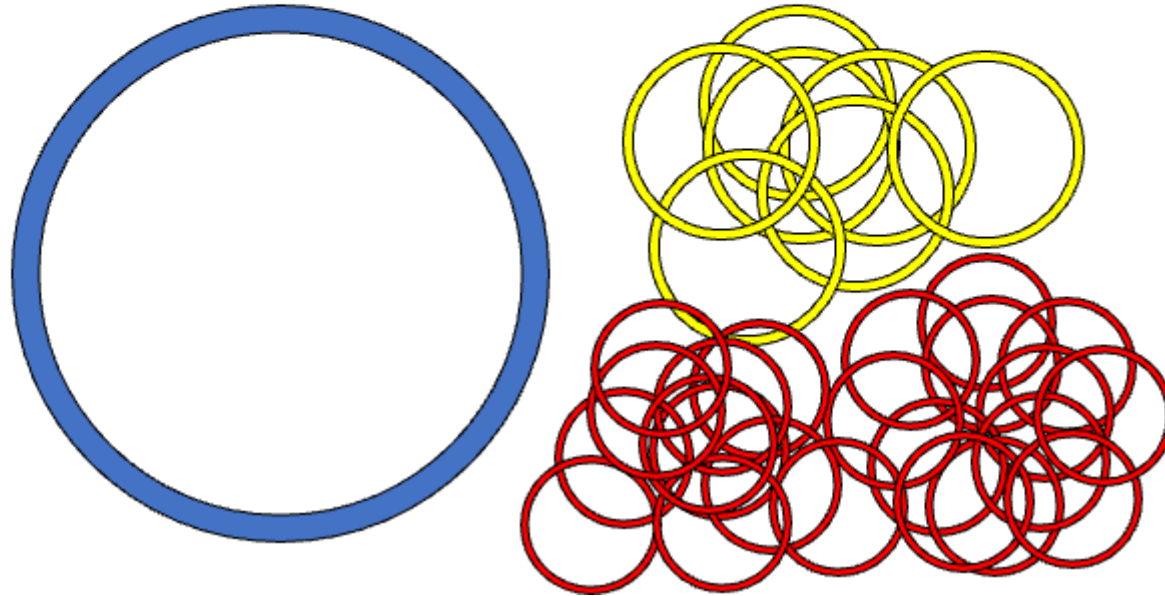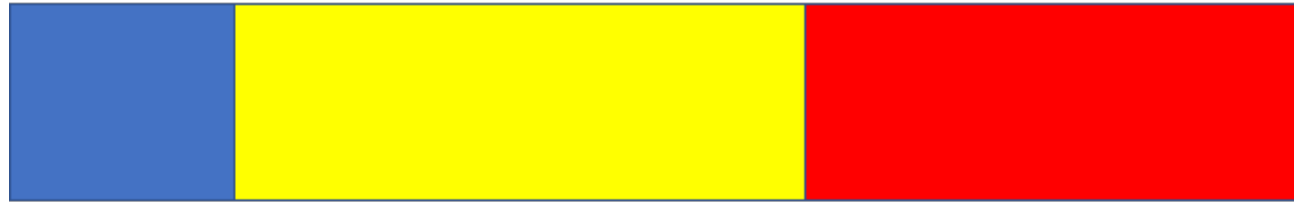# Choice of methods

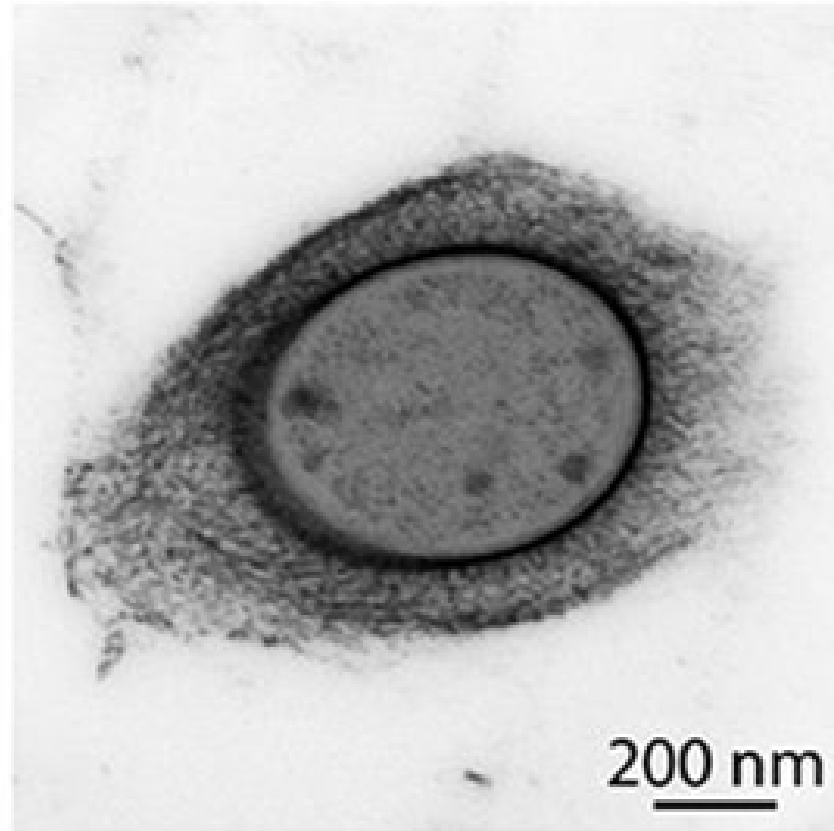**Total reads**

Choice of methods

Choice of methods

Workflow, opportunities for issues

Klebsiella pneumoniae

Klebsiella pneumoniae

200 nm

Klebsiella pneumoniae vs. Mycobacterium tuberculosis

Workflow, opportunities for issues

Thank you

T3connect