

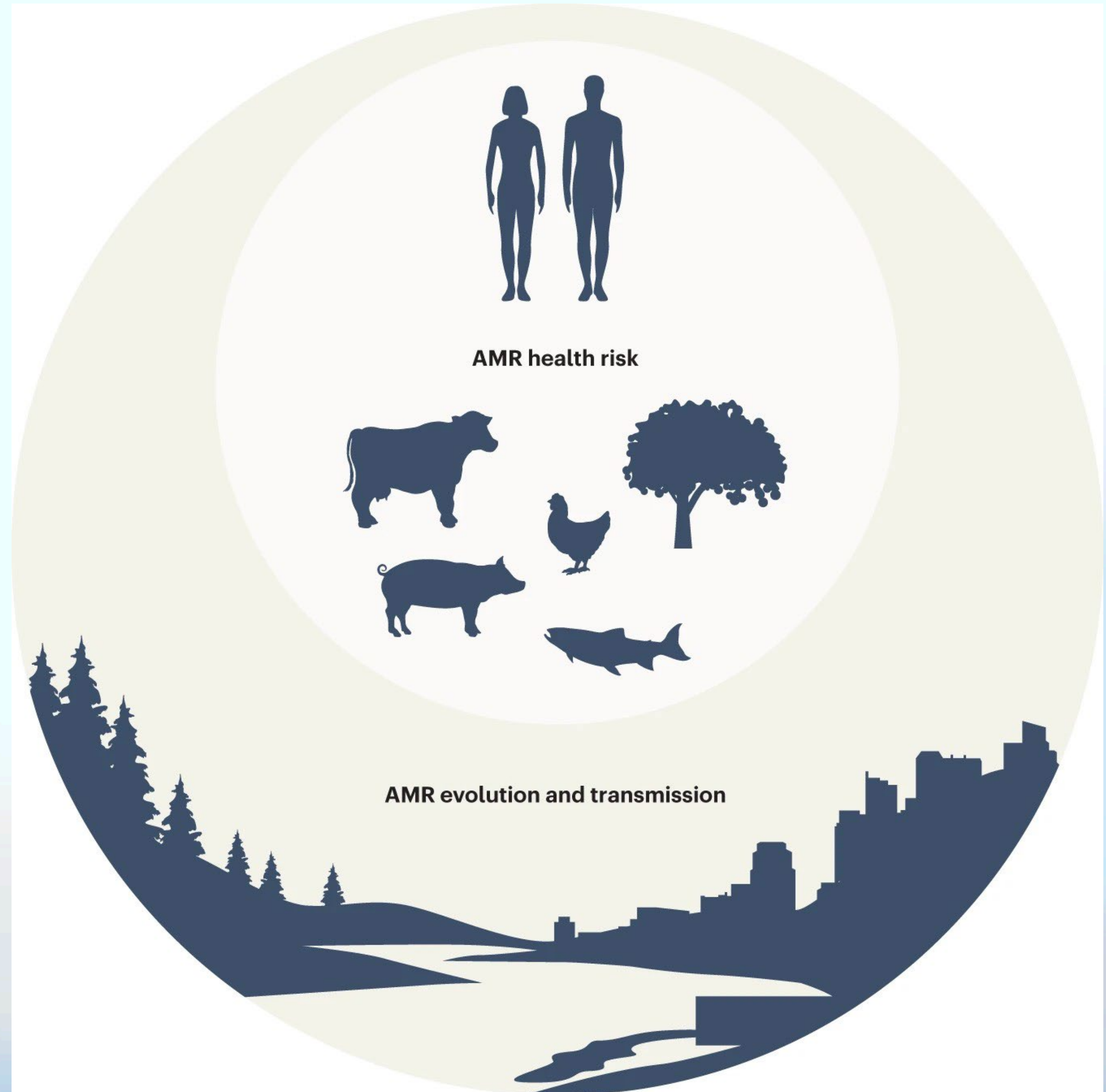
Exploring Plasmid Distribution in Bacterial Communities through Single-Cell Sequencing

High-Throughput Barcoding and Preliminary Data Processing

Qinqin Wang

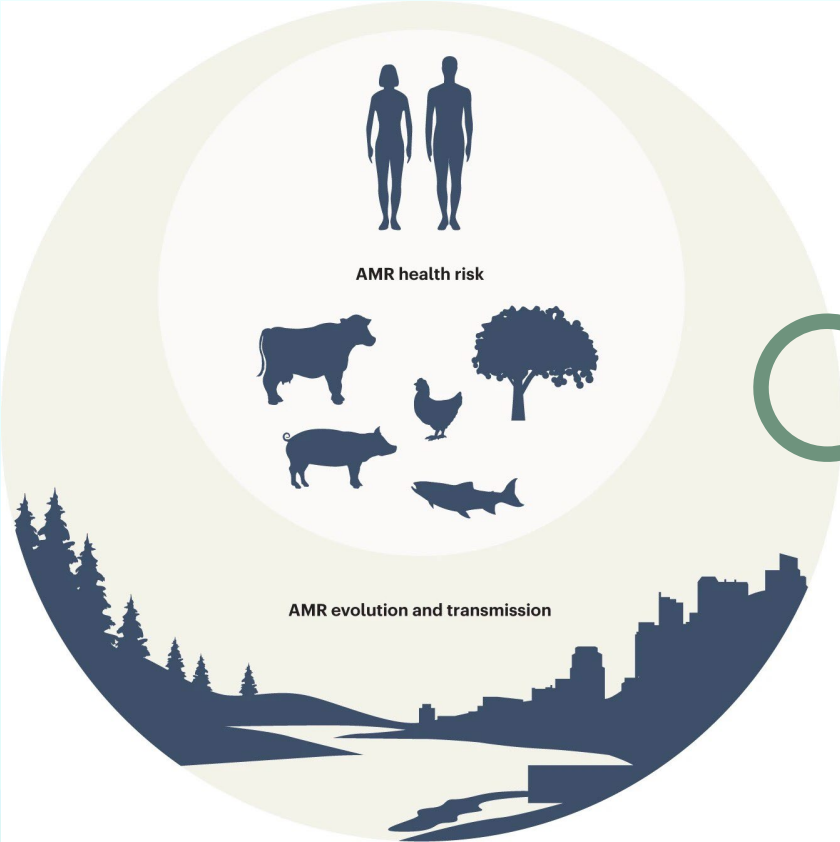
04.12.2023

AMR, One Health and the environment

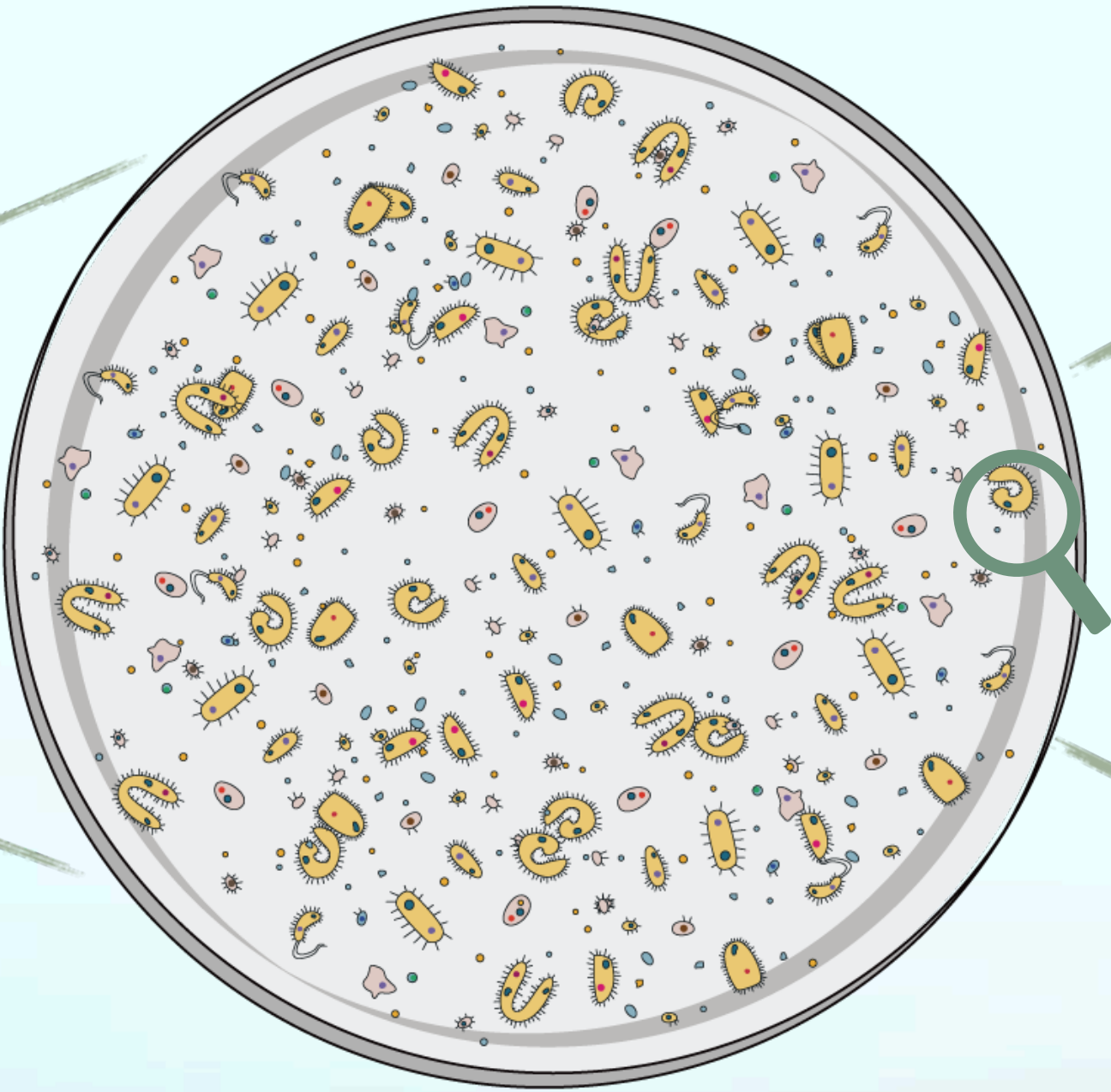


Larsson, D. G. J., et al. "AMR, One Health and the environment." *Nature Microbiology* 8.5 (2023): 754-755.

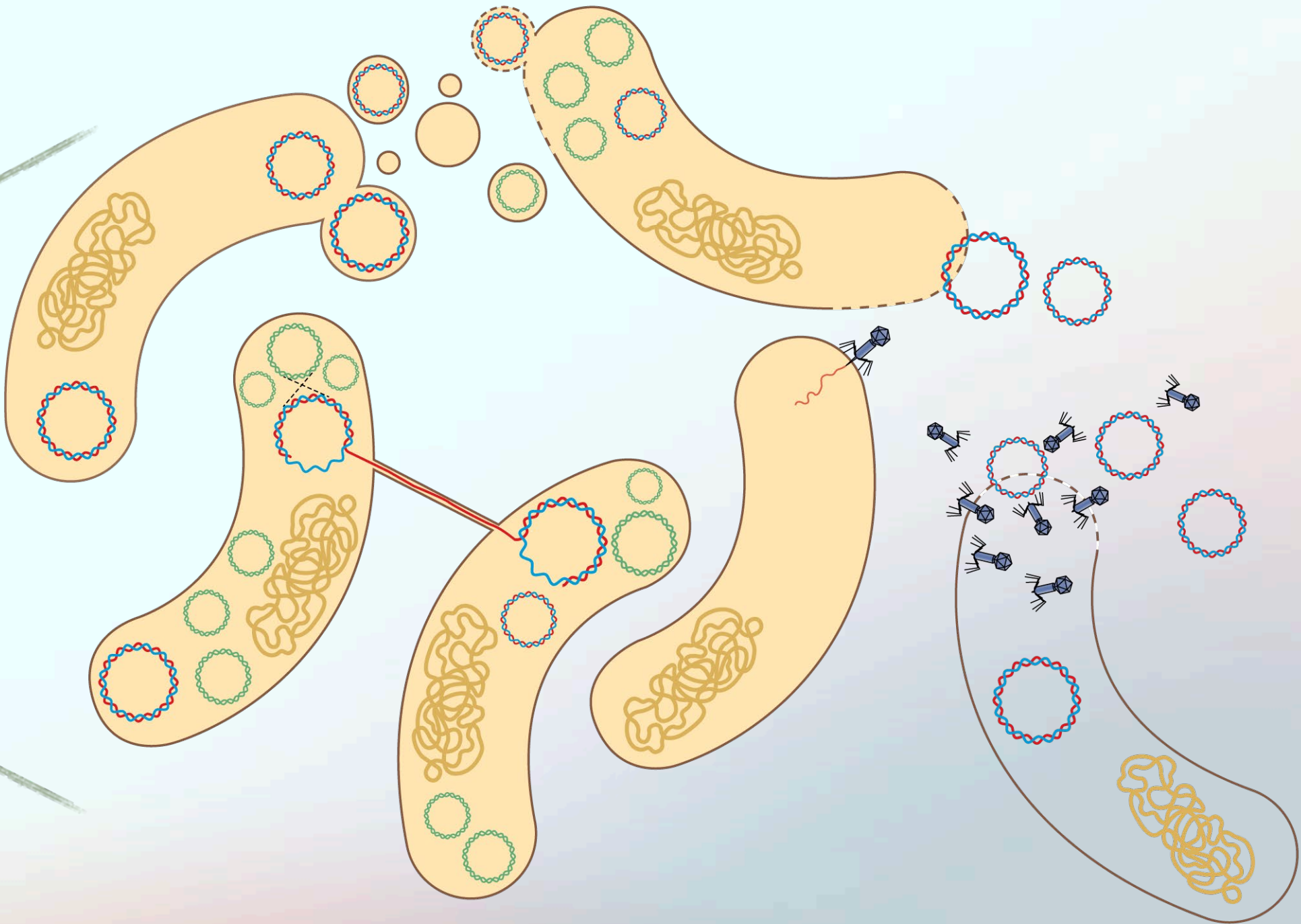
AMR spread



One health



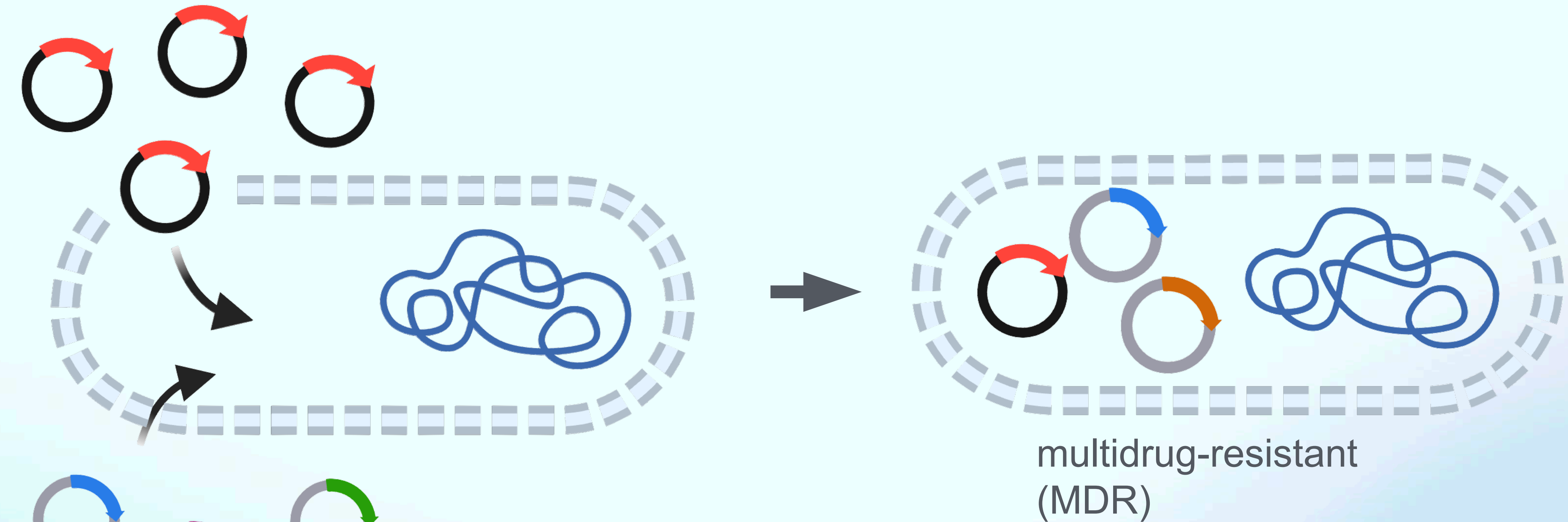
Bacterial communities



Horizontal transfer of AMR

★ Antibiotic-resistance plasmids

How plasmid help spread AMR among microorganisms?



- Plasmid mobility

- Plasmid compatibility

- Plasmid function

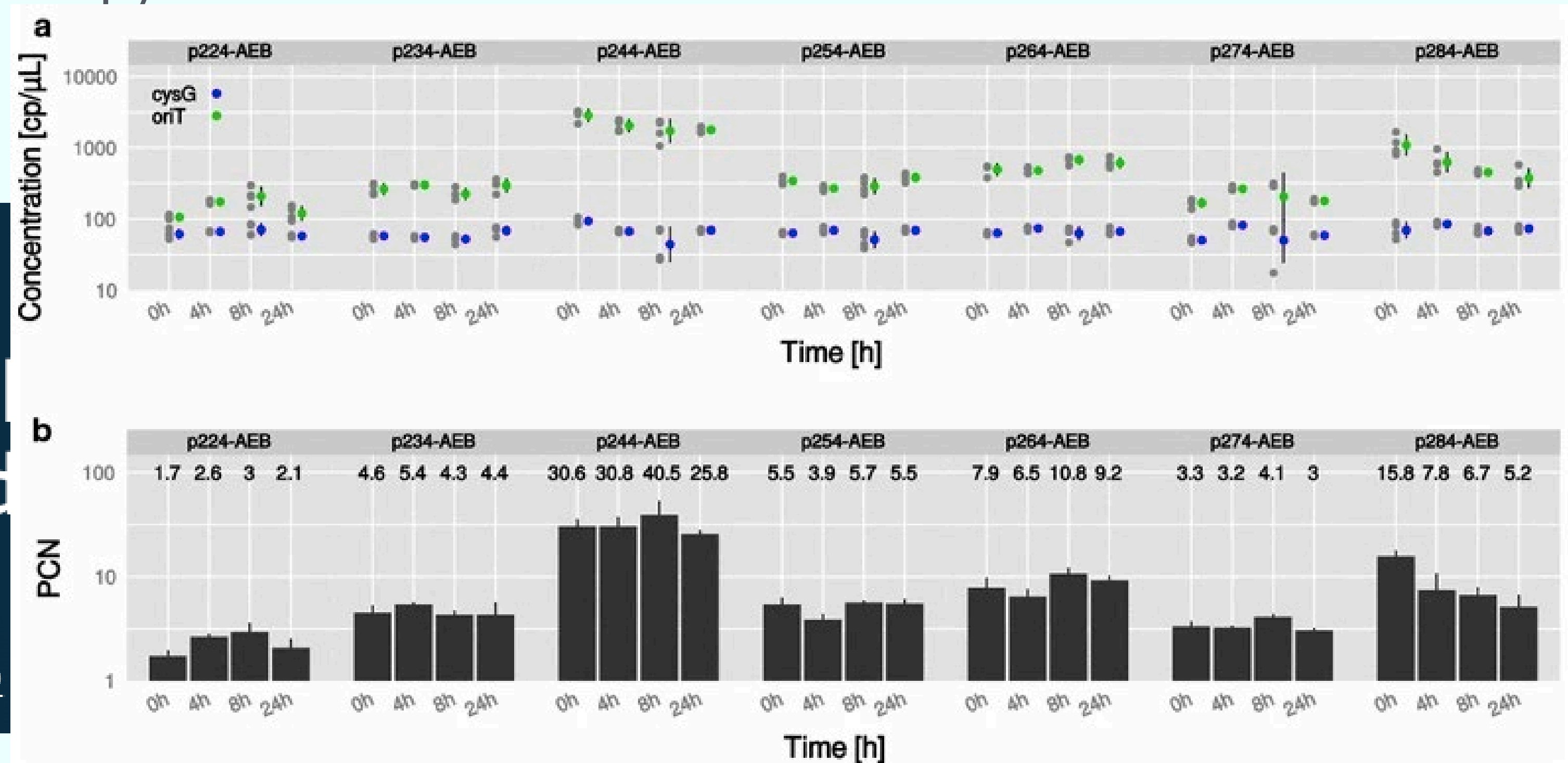
- Fitness cost

- Use qPCR to get the average plasmid copy number
- Use droplet digital PCR (ddPCR)

Home > Microbial Cell Factories > Article

Copy number variability of plasmids determined by Droplet Digital PCR

Research | Open access | Published: 19 December 2016



- Use fluorescent reporters

nature communications

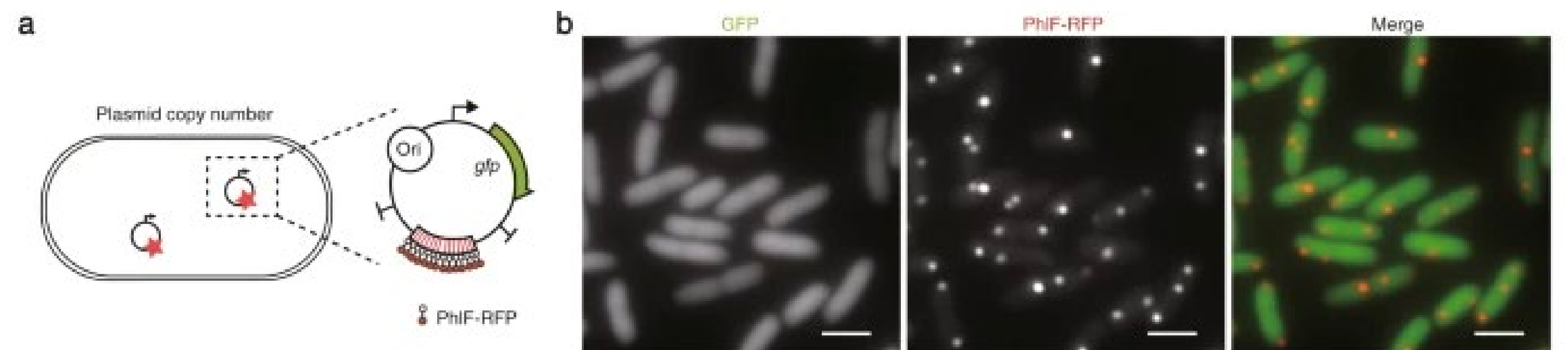
Explore content ▾ About the journal ▾ Publish with us

[nature](#) > [nature communications](#) > [articles](#) > article

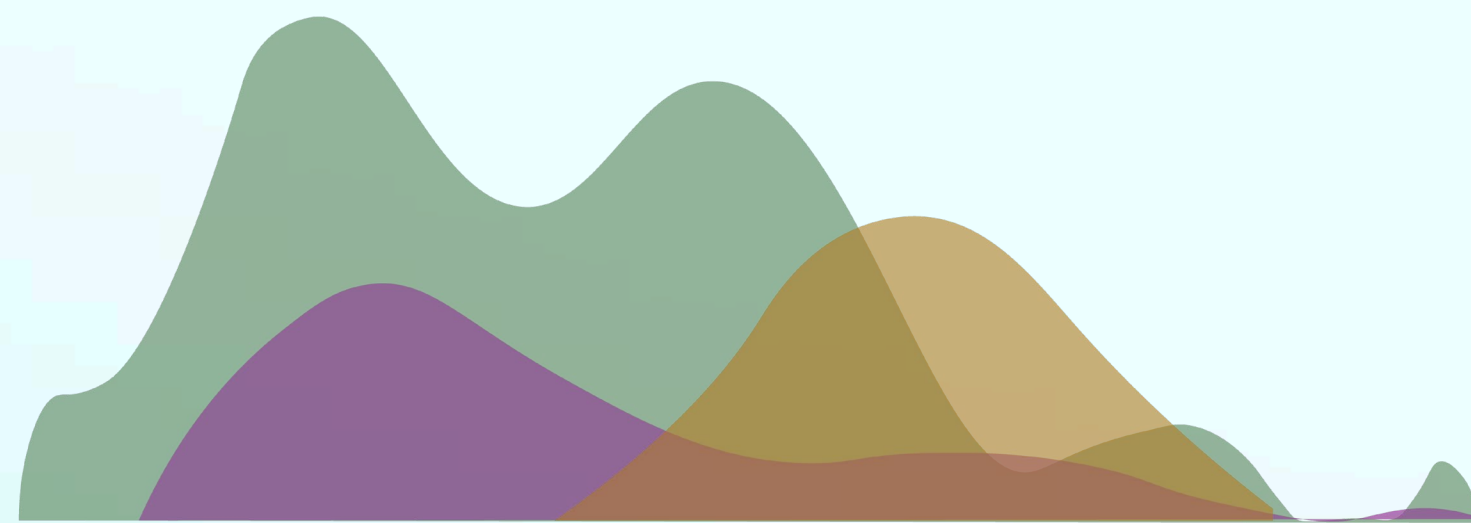
Article | [Open access](#) | Published: 05 March 2021

Single-cell measurement of plasmid promoter activity

Fig. 1: Measurement of plasmid copy number and transcript number.

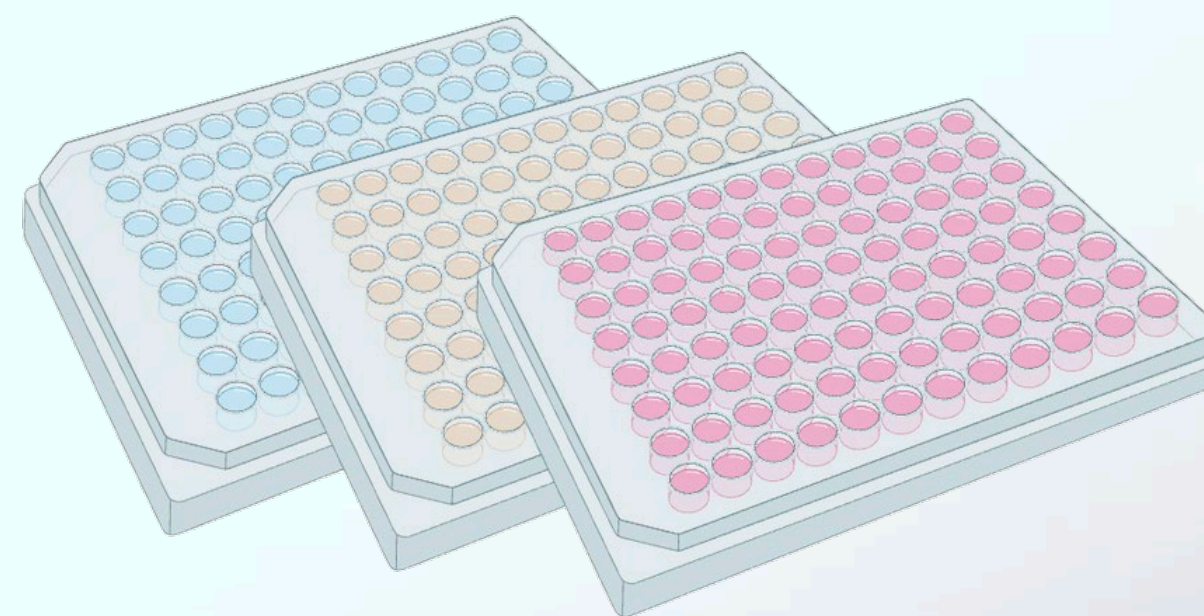
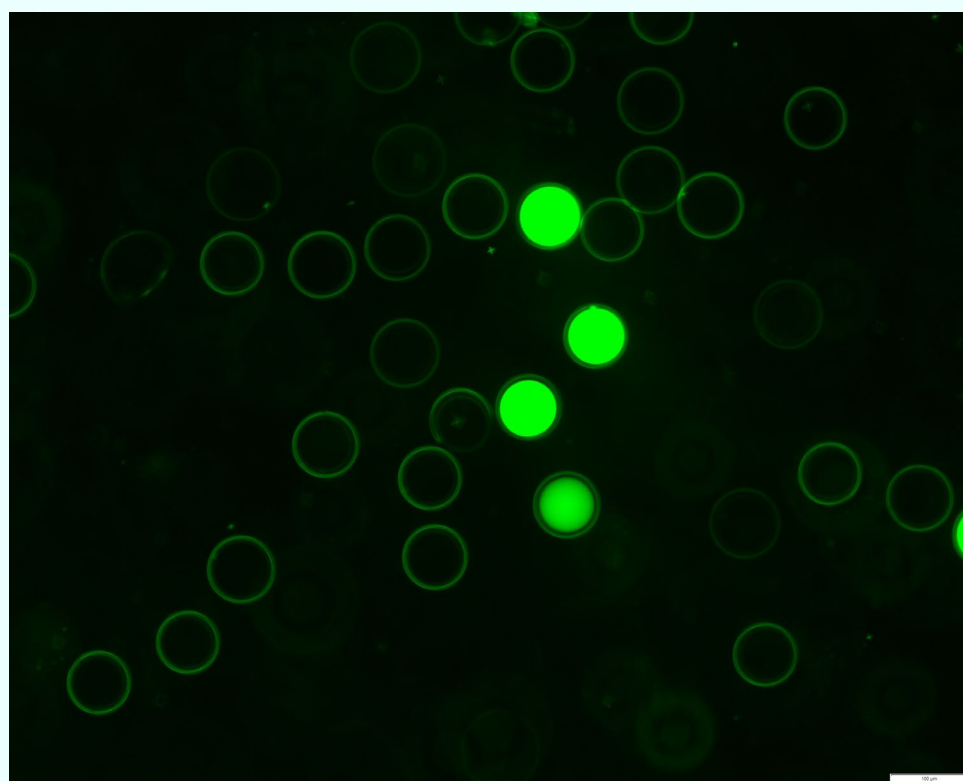
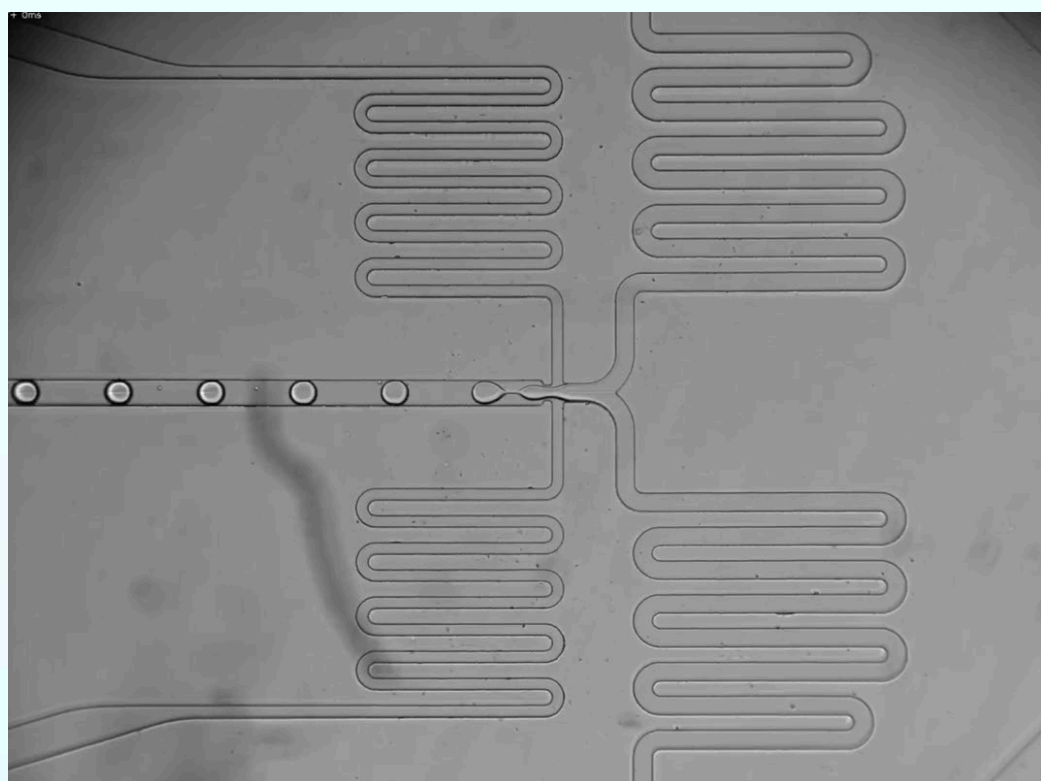
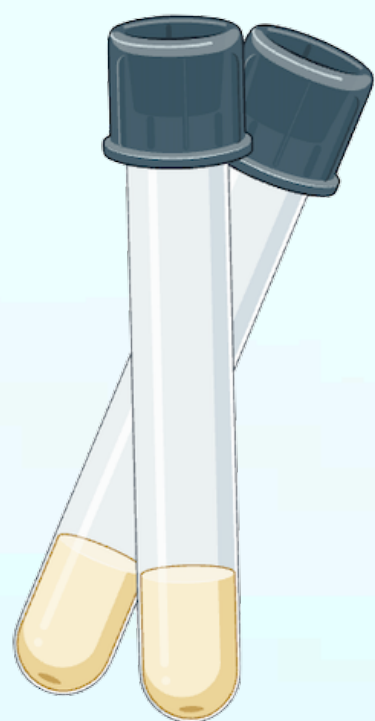
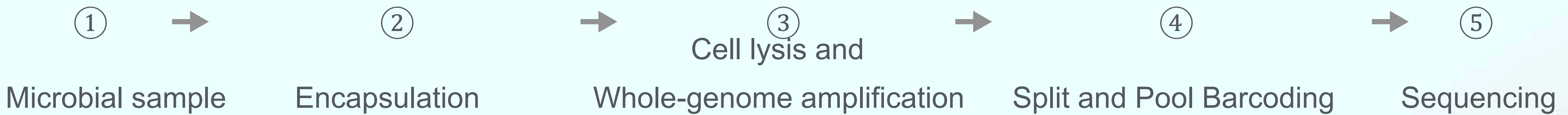


Heterogeneity



Single-Cell Sequencing

Workflow

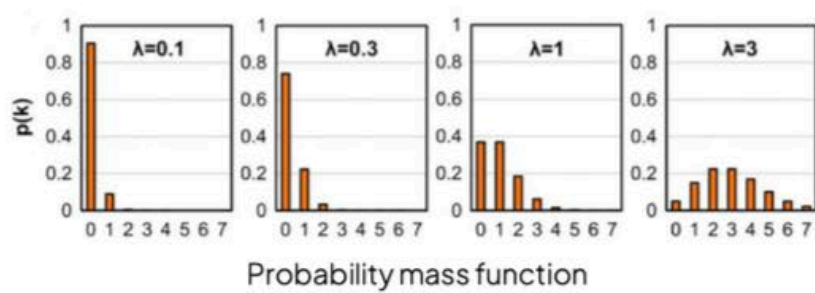
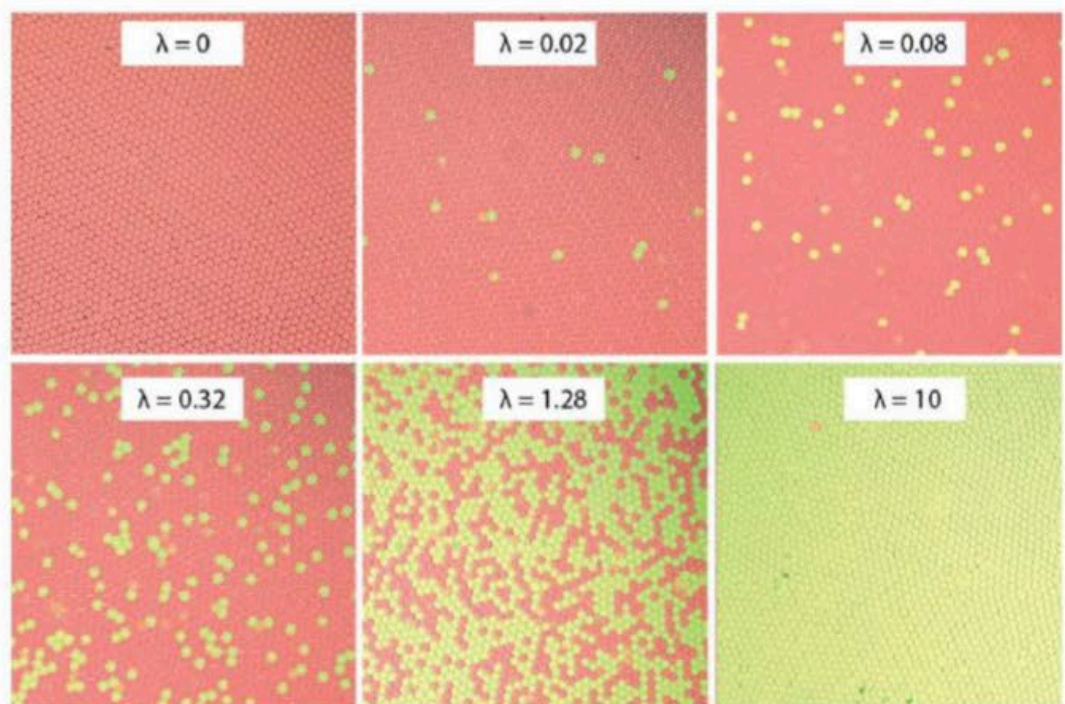


Get single cell in a droplet –Poisson distribution

$$\lambda = \frac{\text{number of cells}}{\text{number of droplets}}$$

$$P(k) = \frac{e^{-\lambda} \cdot \lambda^k}{k!}$$

λ – mean number of events in interval
 k – events
 $P(k)$ – probability of events in interval
 e – Euler's constant (~ 2.72)



Lambda value = 0.05-0.1

To get less contamination or doublets

$$10 \times 10 \times 10 = 1,000$$

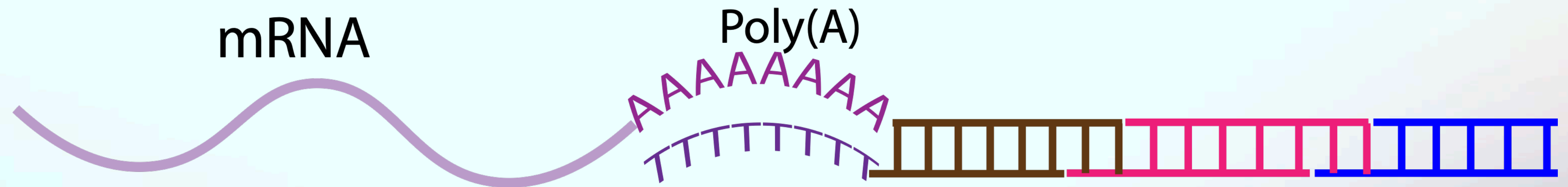
$$48 \times 48 \times 48 = 110,592$$

$$96 \times 96 \times 96 = 884,736$$

...

Barcoding for RNA

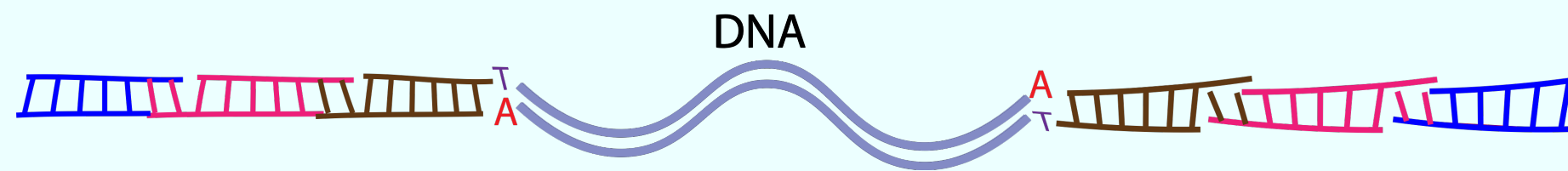
Single-stranded



Barcoding for Genome

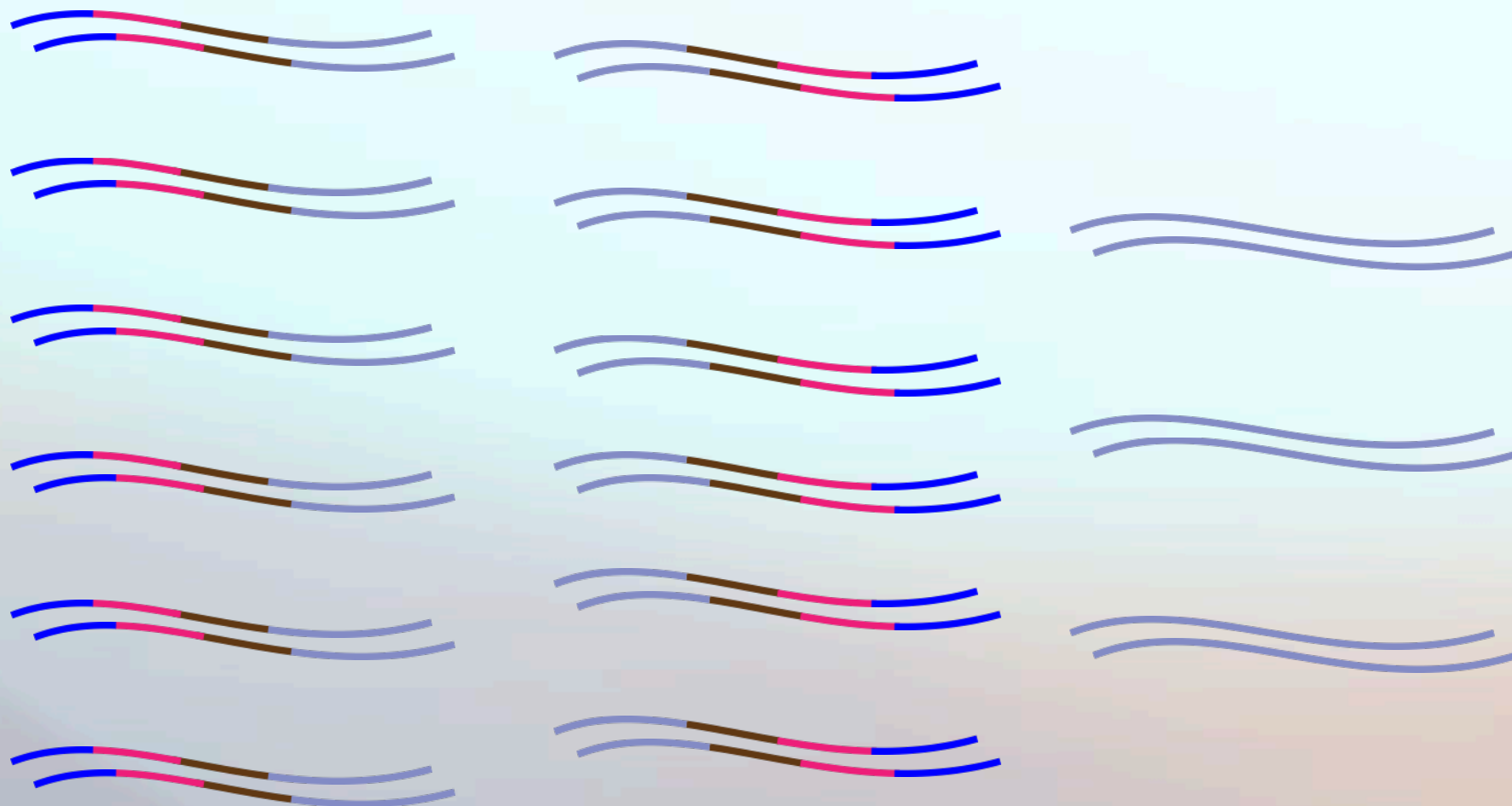
1. T4 ligation

① Barcoding via 3x ligation



② Fragmentation

③ Sequencing Library



Advantage: Reduce bias caused by PCR

Shortcoming: Higher cost, cumbersome process, the ligation efficiency is not high

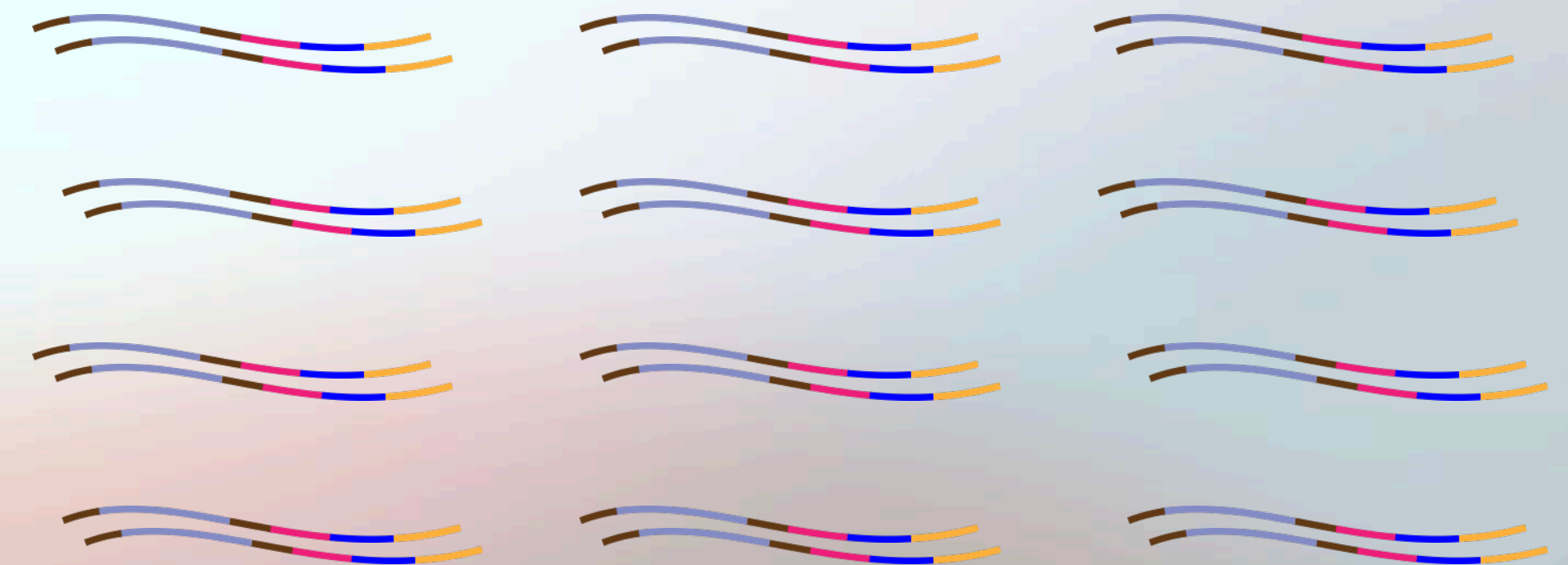
2. PCR

① Fragmentation

② Barcoding via 3x PCR



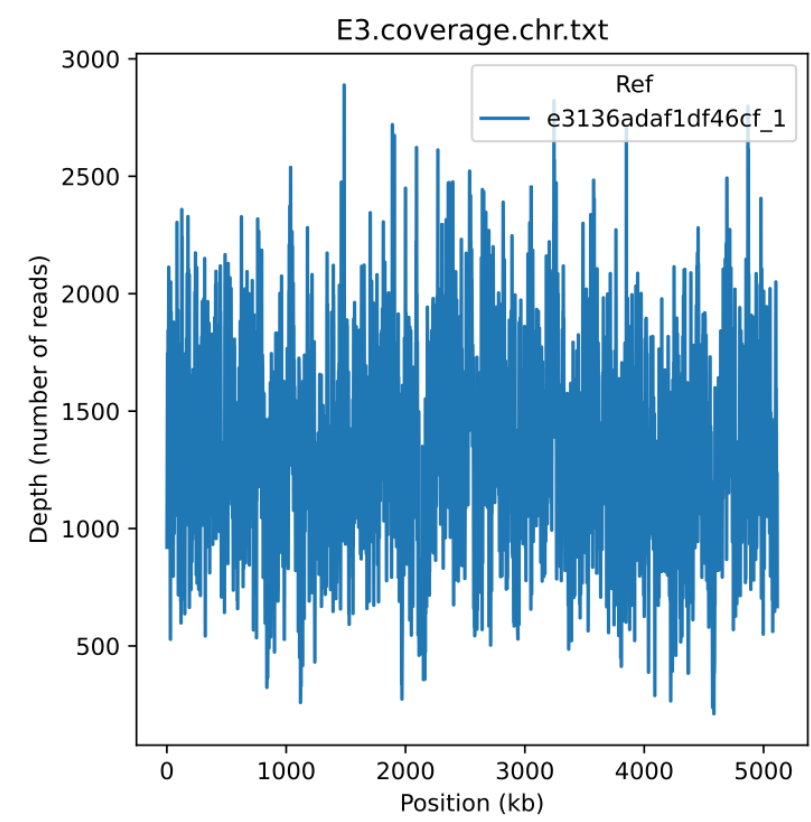
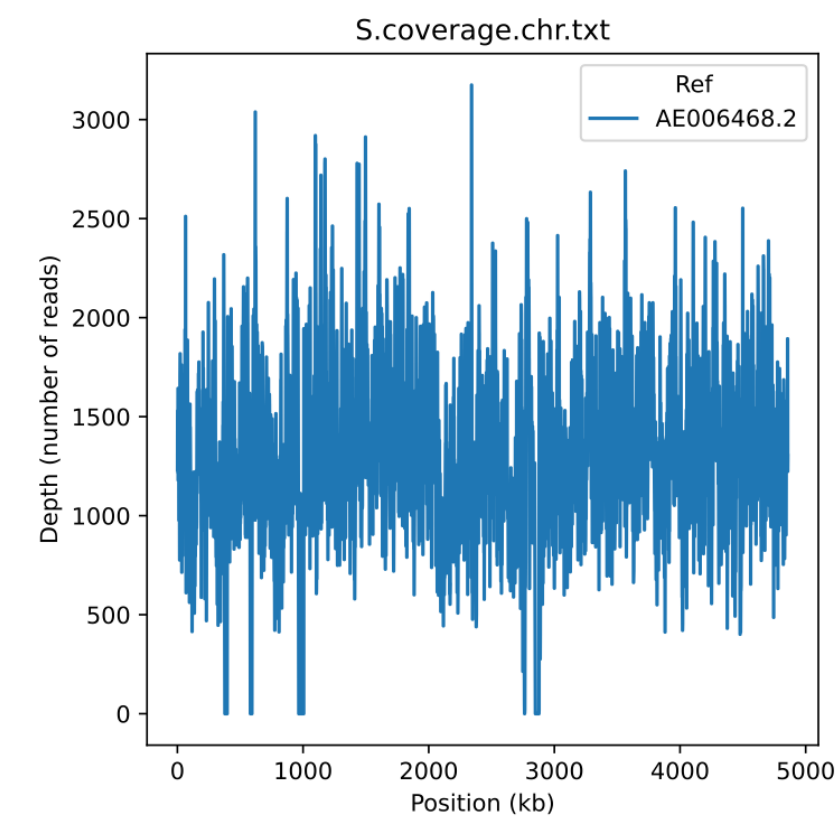
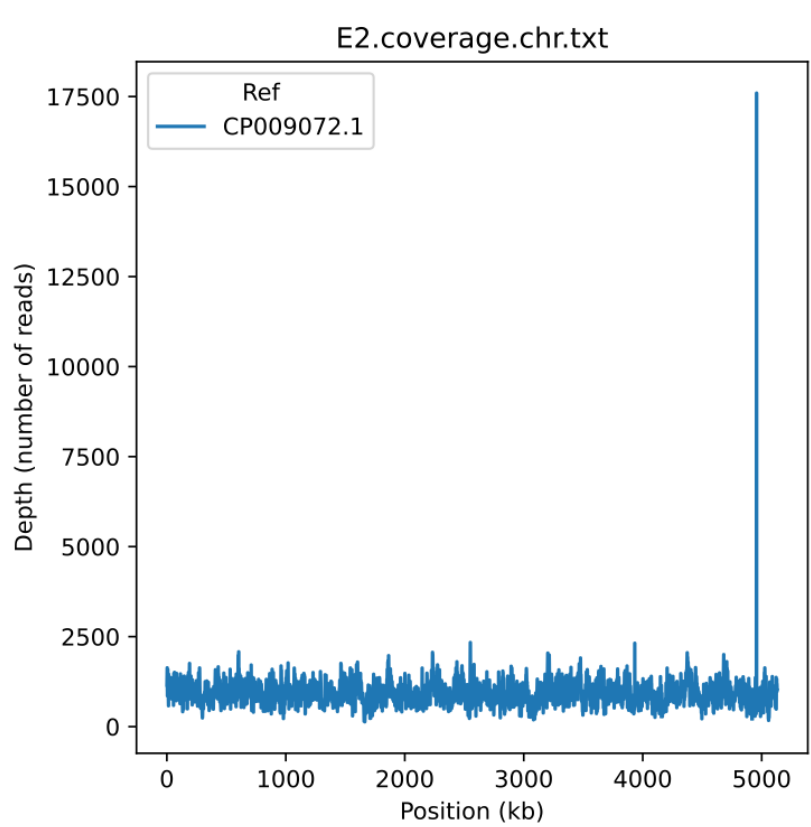
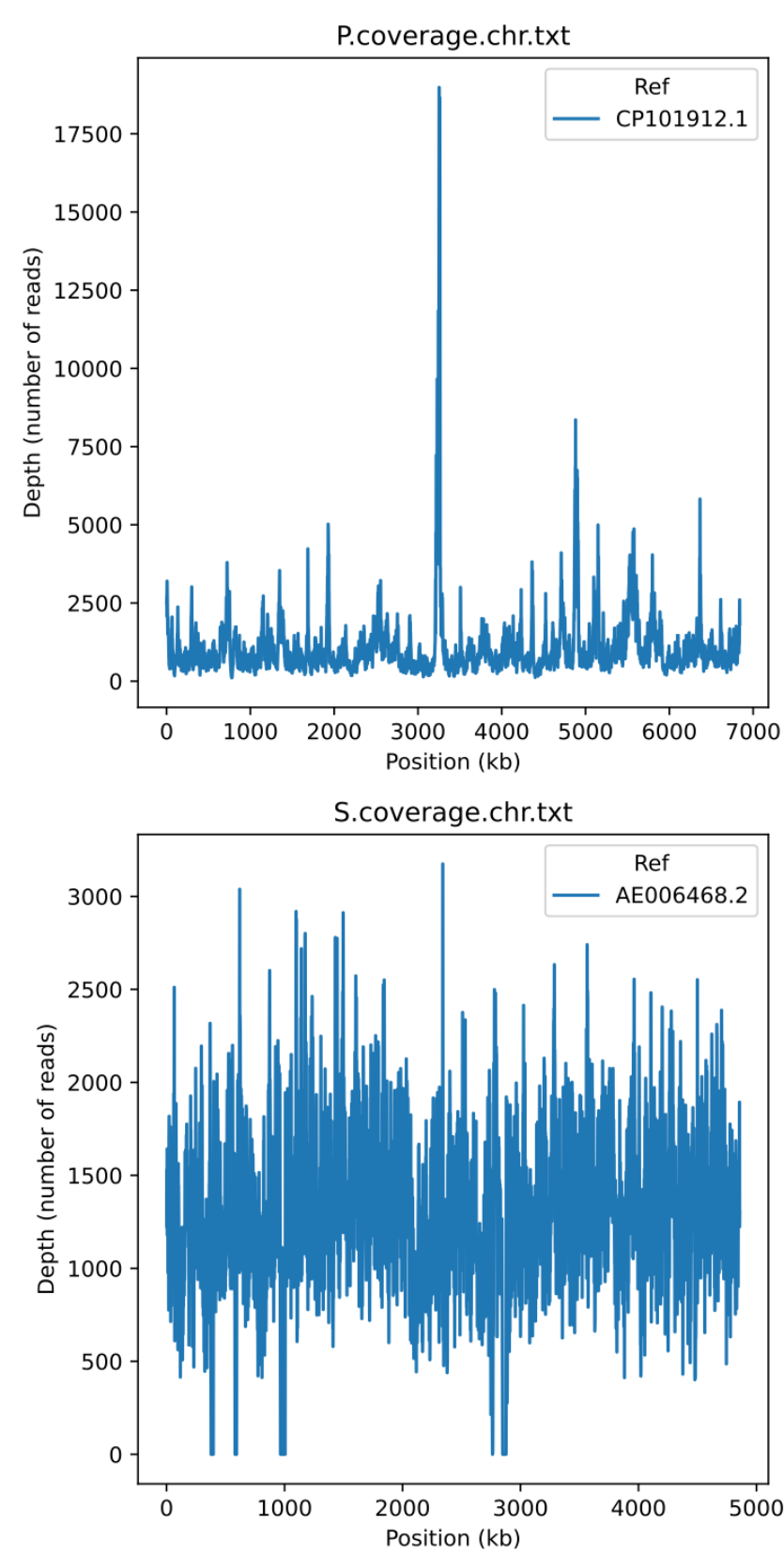
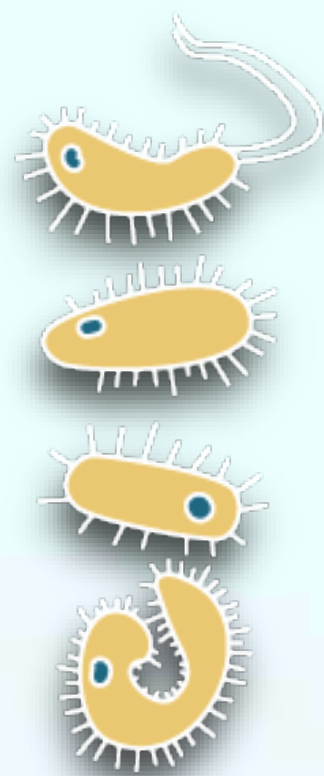
③ Sequencing Library



Advantage: Cost saving and high efficiency

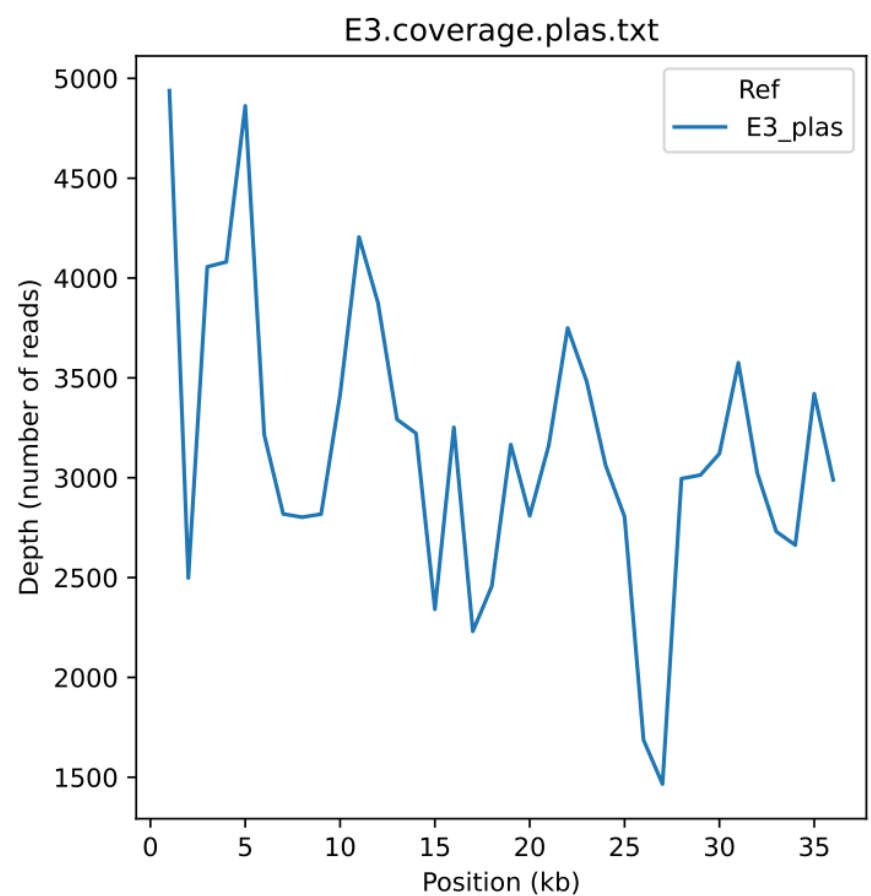
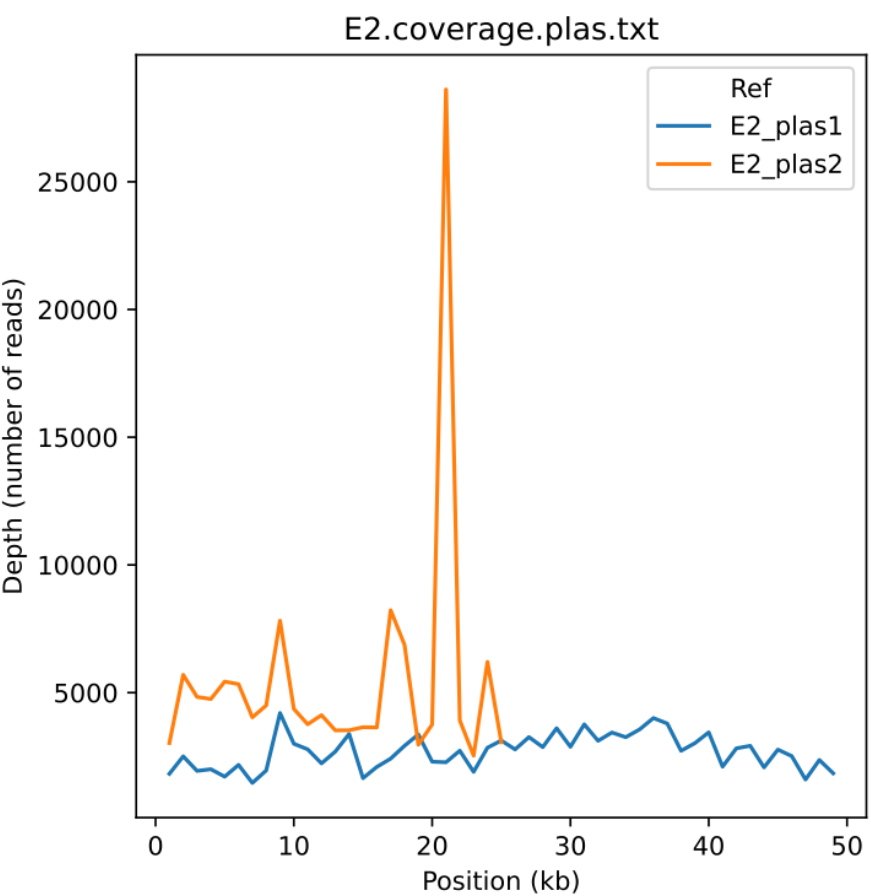
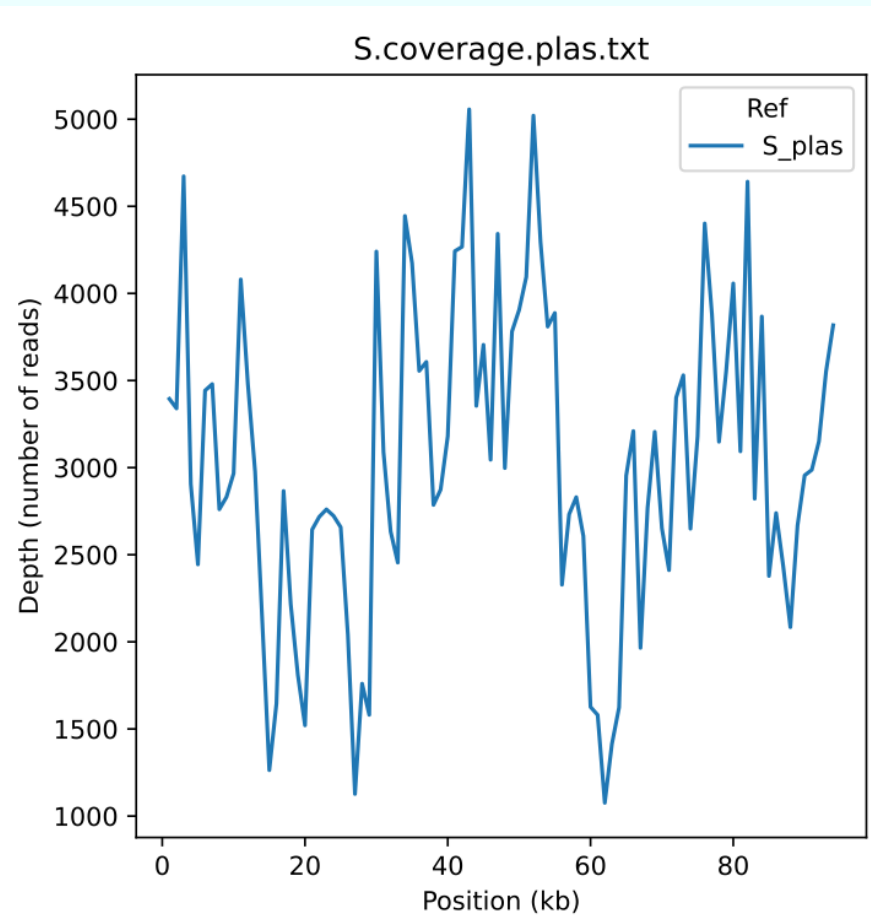
Shortcoming: biased

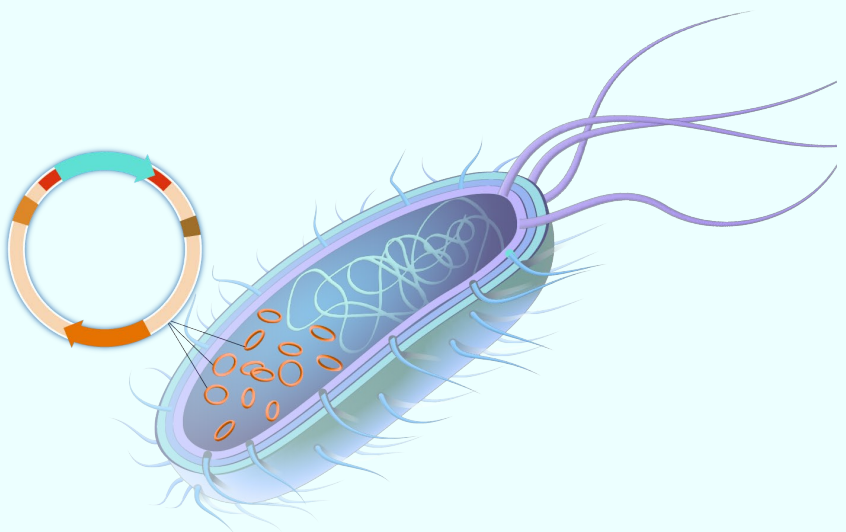
Small trial



👉Chromosome

Plasmid👉





Challenge:

- Obtain more and higher quality sequencing reads
- Analysis of downstream research



Thank you for your attention