



ABRINCA—  
GENOMICS

# Streamlining **Microbial Genomics** for Food Safety

**Simplifying genomics, amplifying insights.**

WORLD FOOD SAFETY DAY  
AGROSCOPE - LIEBEFELD  
8 JUNE 2026

# Why **microbial** **genomes** matter

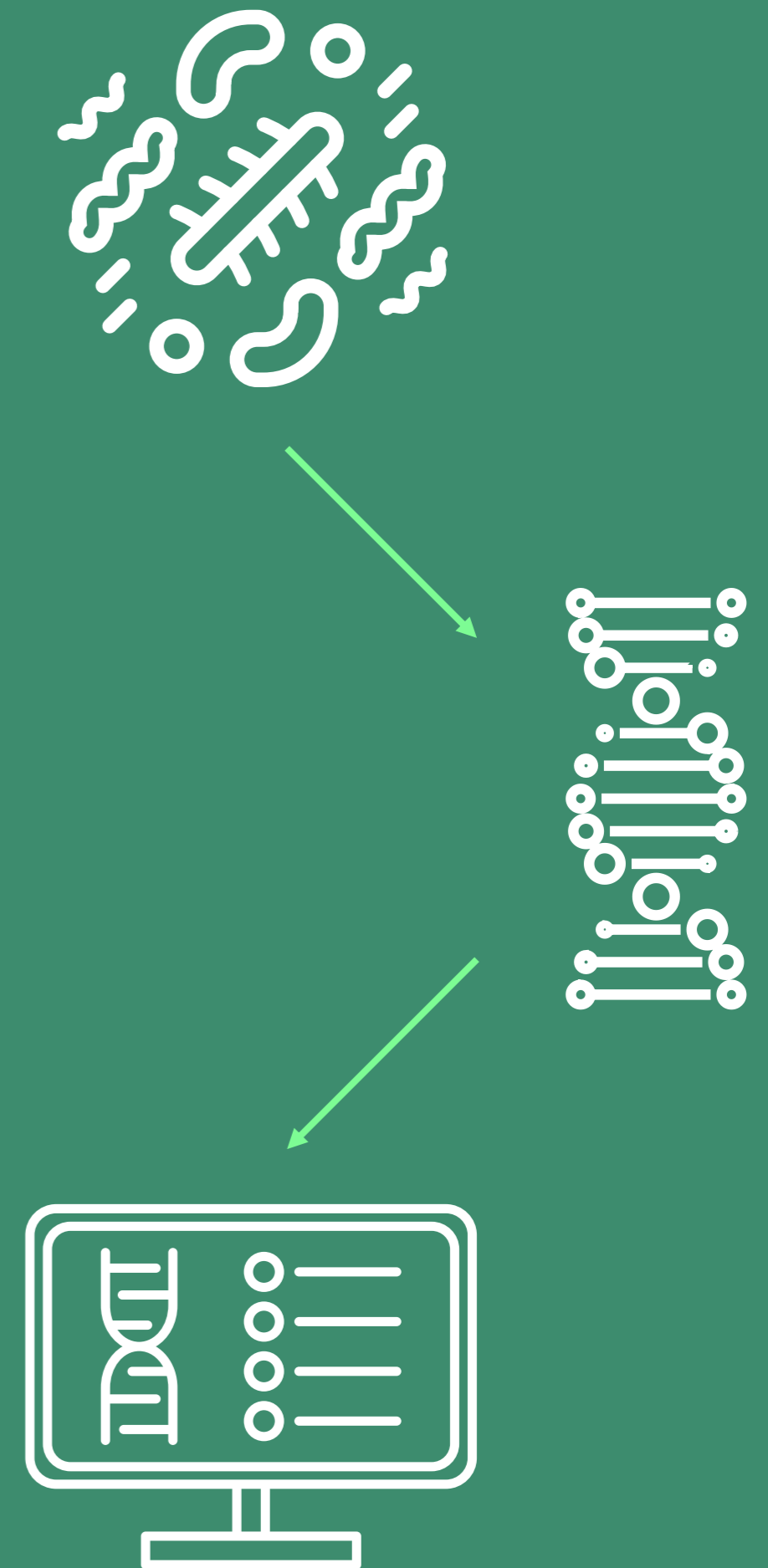
**PREDICTING RESISTANCE.**



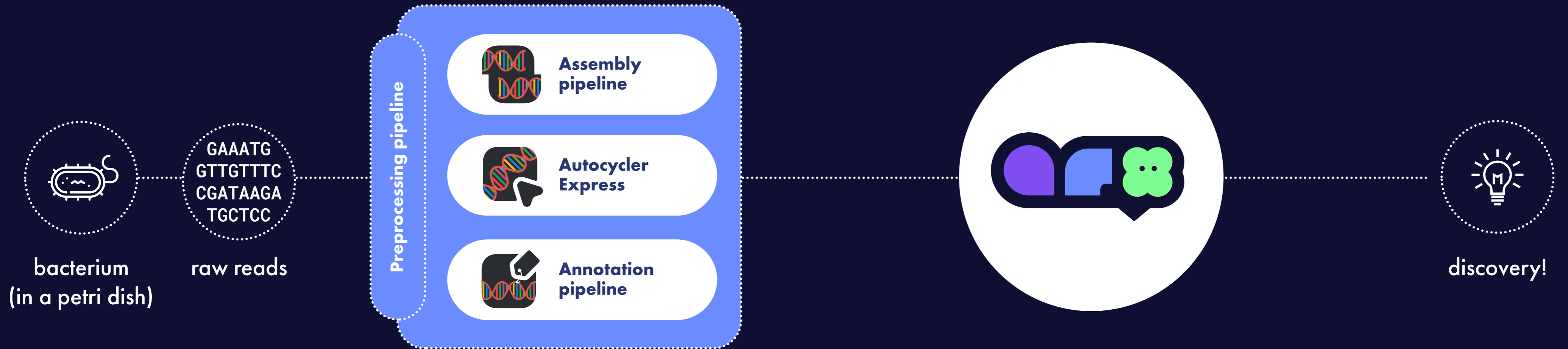
**DESIGNING BETTER CULTURES.**



**PREVENTING OUTBREAKS.**



# The Abrinca ecosystem



# Key problems for assembly

## PLASMIDS.



Resistance genes are often located on plasmids.



Assemblers often drop plasmids / phages.

## SNPs.



High base quality required for outbreak tracking.



Assemblers often make errors.

## MANUAL CURATION.

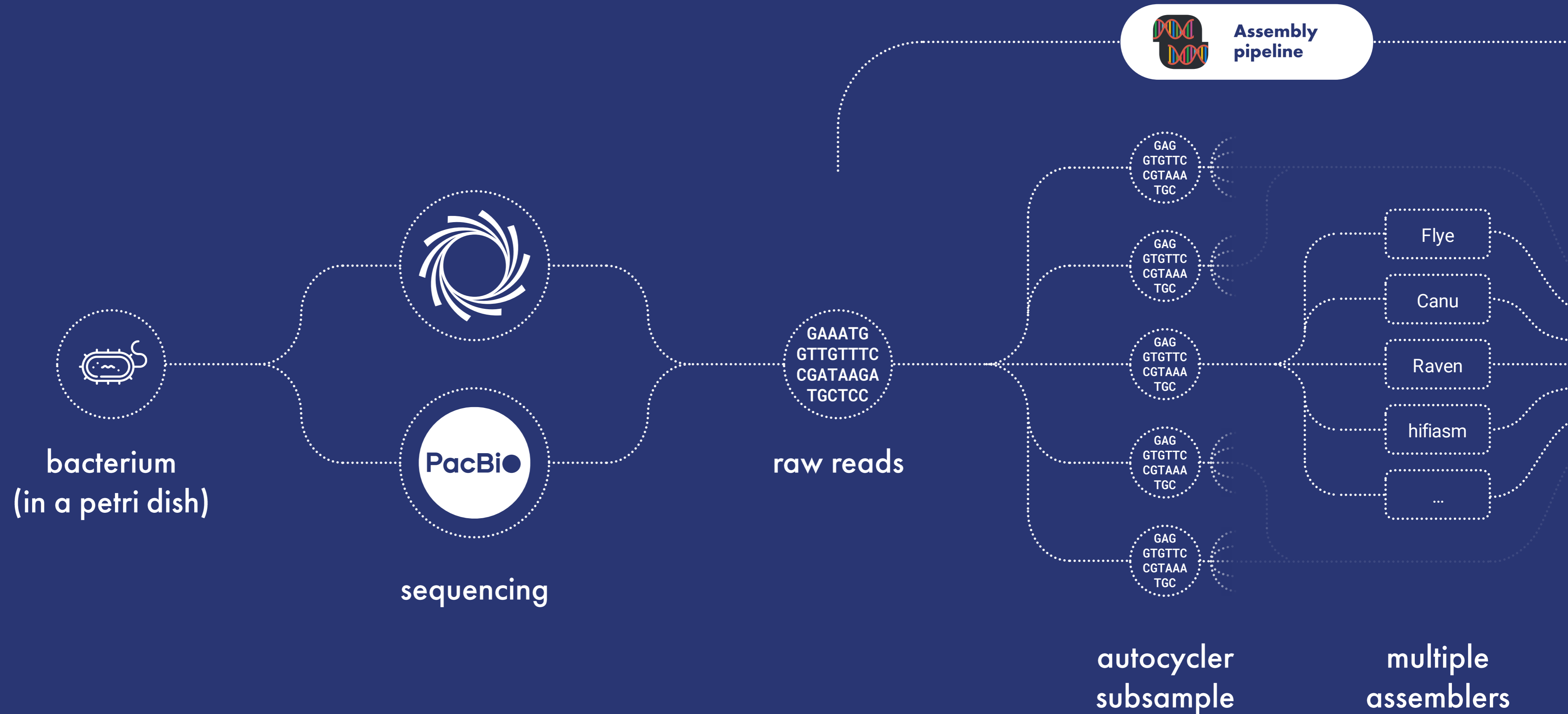


Downstream analyses depend on high quality assemblies.

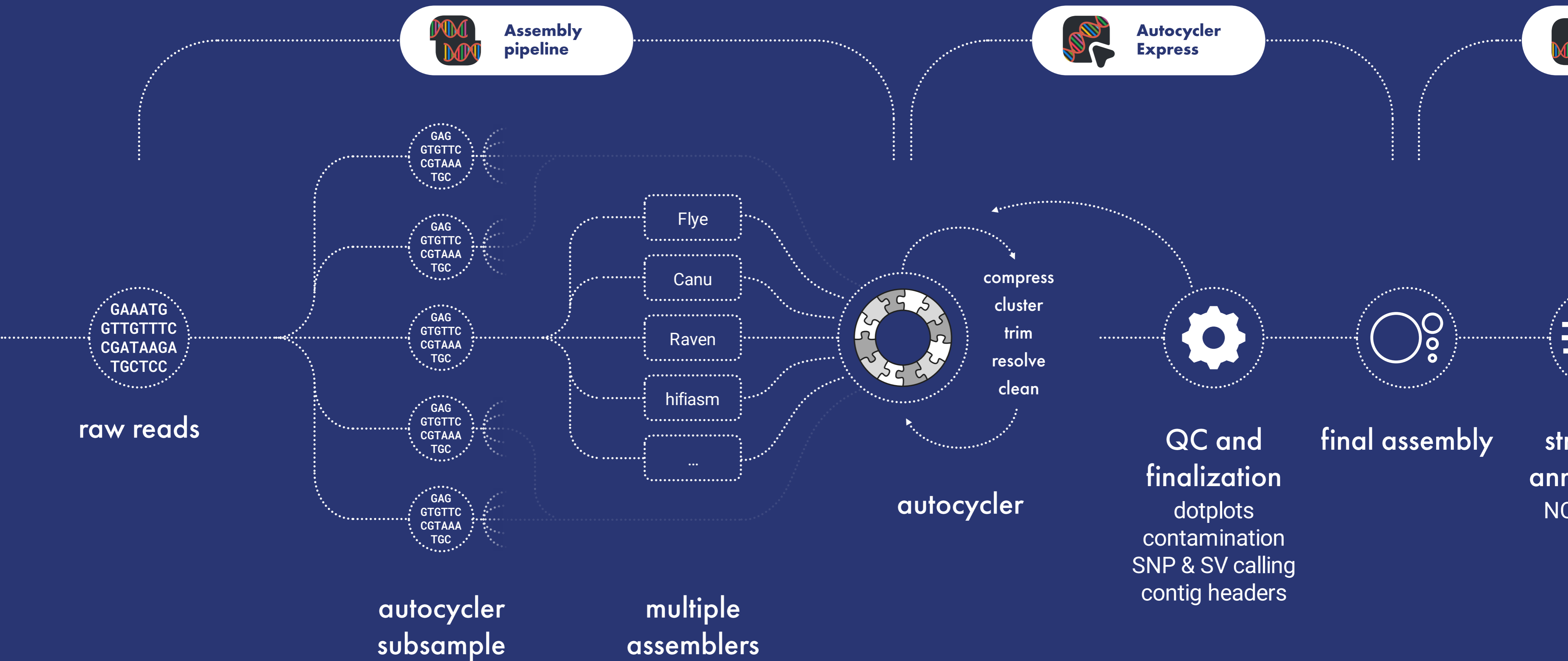


QC and taxonomy checks are cumbersome and take a lot of time.

# Our pipeline



# Our pipeline



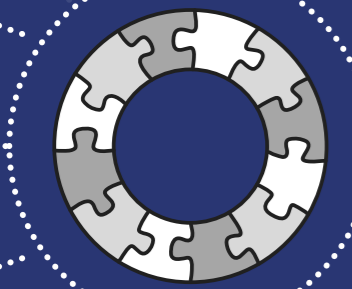
# Our pipeline



**Autocycler  
Express**



**Annotation  
pipeline**



**autocycler**

compress  
cluster  
trim  
resolve  
clean



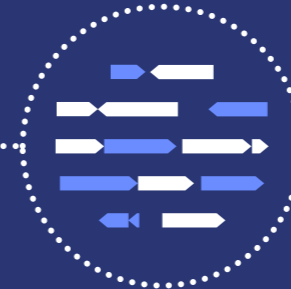
**QC and  
finalization**  
dotplots  
contamination  
SNP & SV calling  
contig headers



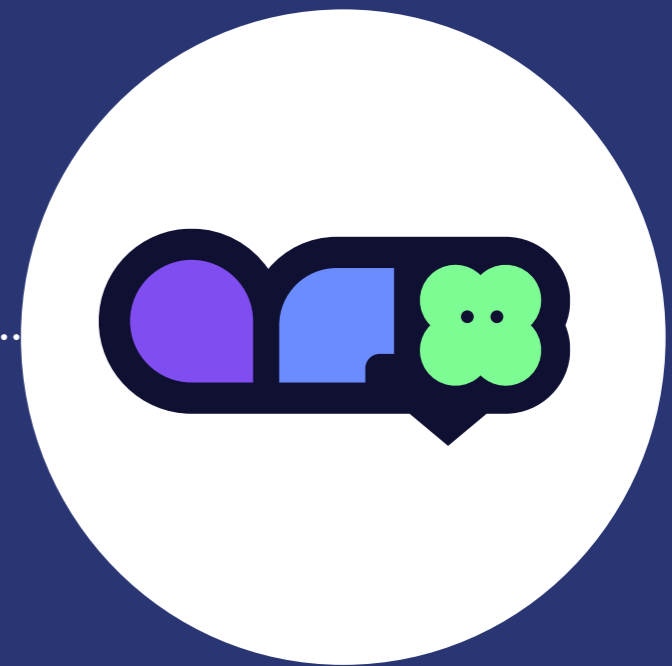
**final assembly**



**structural  
annotations**  
NCBI PGAP



**functional  
annotations**  
functions  
pathways  
resistance  
virulence  
BCGs



# Key solutions for assembly

## PLASMIDS.



Resistance genes are often located on plasmids.



~31% **more plasmids**  
even better **phage** detection

## SNPs.



High base quality required for outbreak tracking.



Reach the limit of what is possible with your data – **virtually base-perfect** sequences. This is critical for outbreak tracking, for example.

## MANUAL CURATION.

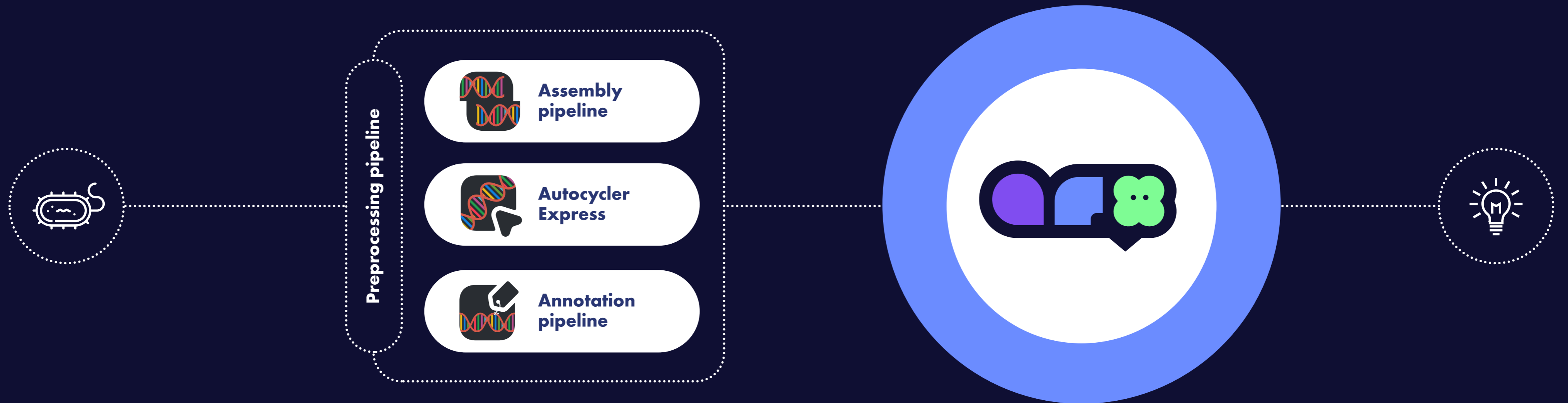


Downstream analyses depend on high quality assemblies.



Autocycler Express dramatically increases your **confidence** in the assemblies and therefore your downstream data analysis

# Our ecosystem



# Data Mining Problem Solution.

## Questions

### Question 1

Does this strain have resistance genes?

### Question 2

Does one of our strains have this bacteriocin sequence?

### Question 3

Can this strain use lactose as a substrate?

### Question 4

Which orthogene can explain this resistance pattern?

## Before



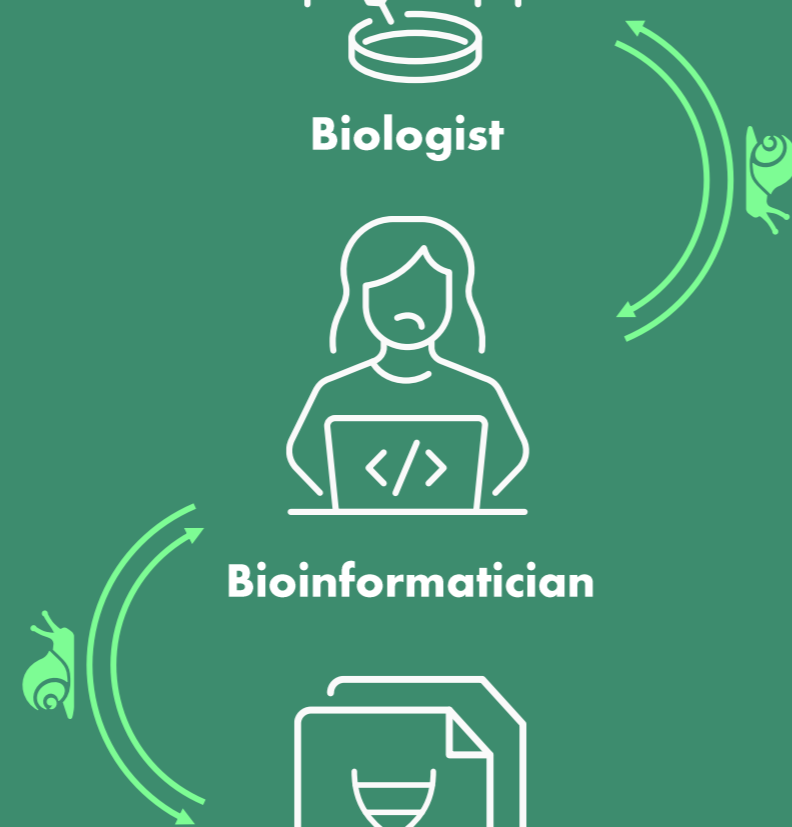
Biologist



Bioinformatician



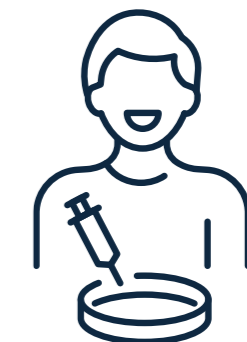
Data



## After



Bioinformatician



Biologist

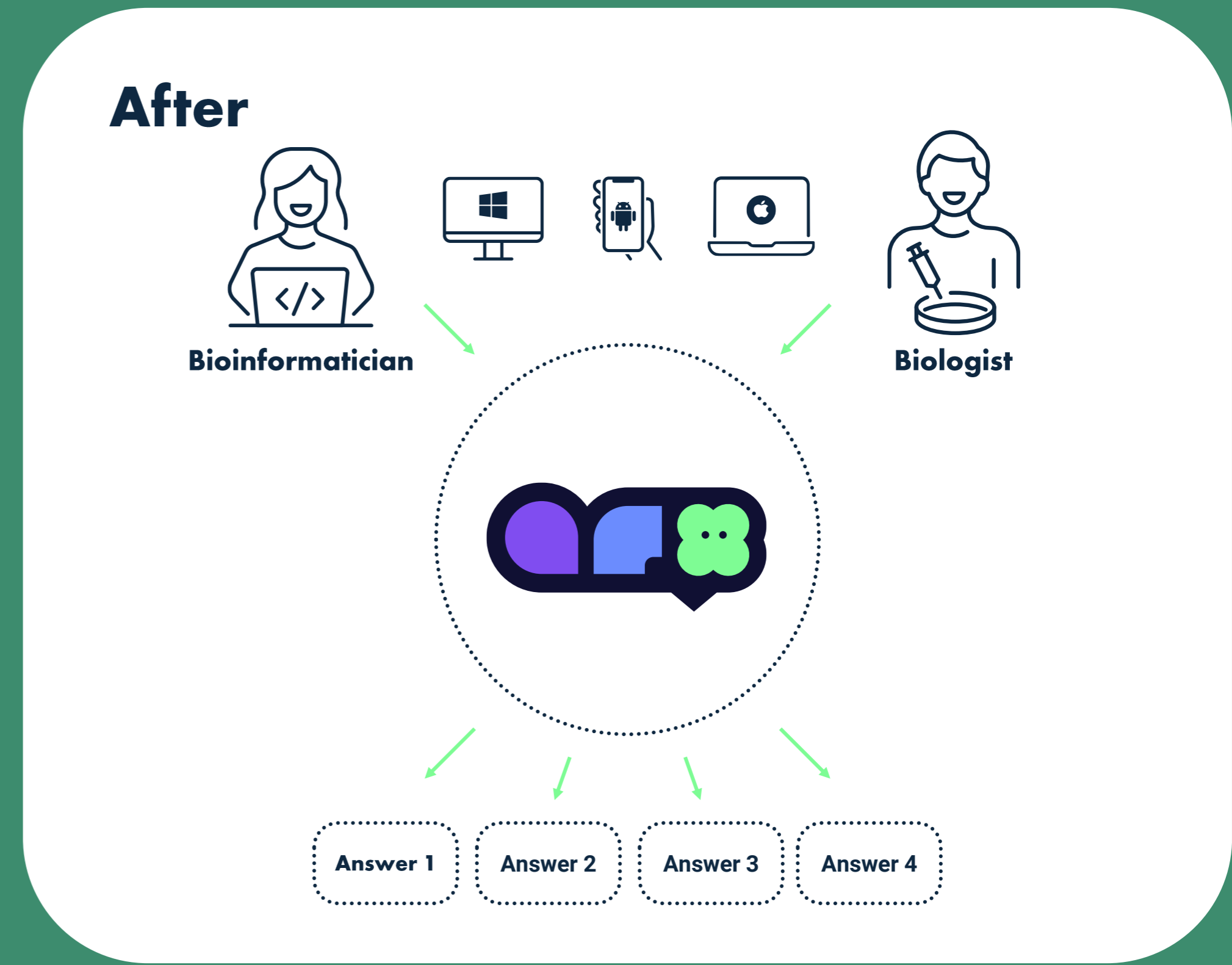


Answer 1

Answer 2

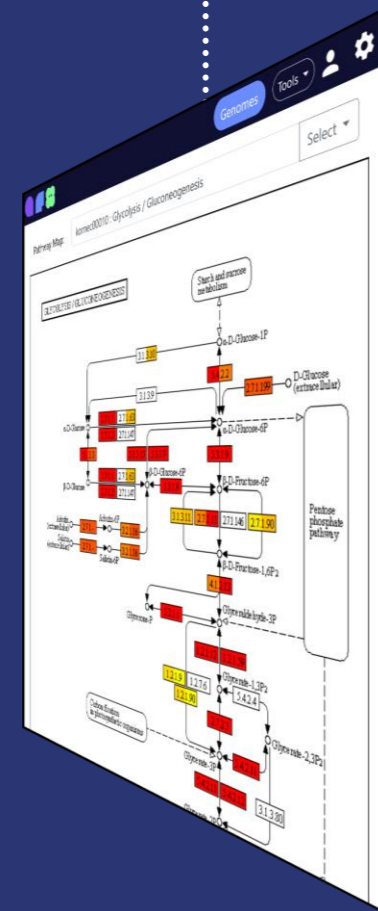
Answer 3

Answer 4

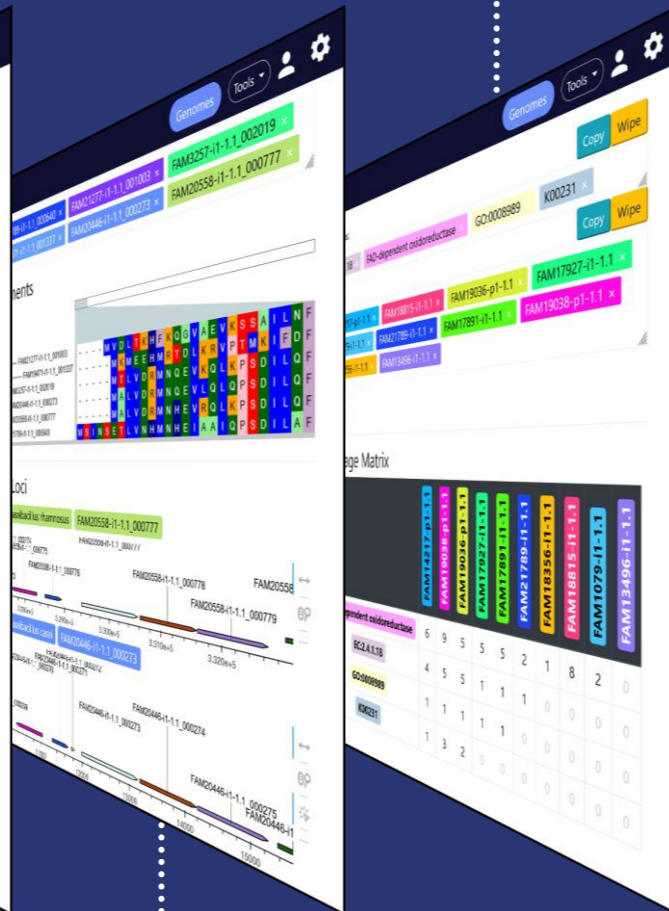


# Arx

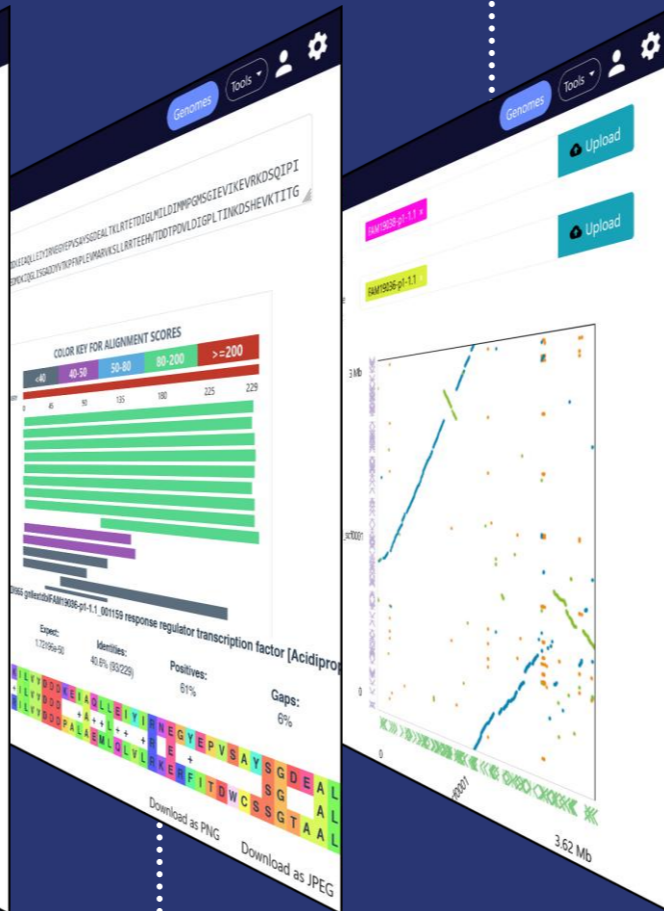
Pathways



Annotation search



Dotplot



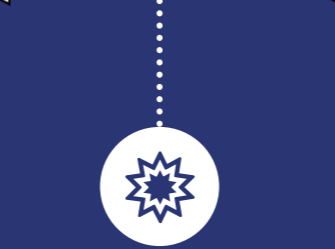
Gene trait matching



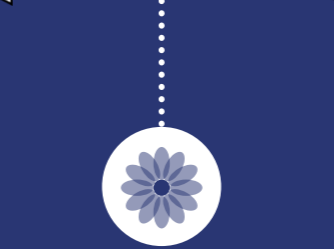
Gene comparison



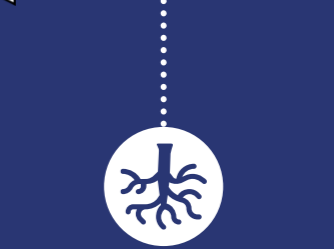
BLAST



Flower plot



Phylogenetic trees



# Resistance genes



# Resistance genes

Genome overview page

The screenshot shows a web interface for a genome browser. At the top, there are navigation buttons for 'Genomes' and 'Tools', along with user and notification icons. The breadcrumb path is '/ TAXID 1282 / ORGANISM NBRC100911 / GENOME NBRC100911-p1-1.1'. The main content area displays the genome name 'NBRC100911-p1-1.1' and the organism 'Staphylococcus epidermidis' with taxid '1282'. A green box states 'This genome is a representative of NBRC100911.' Below this is the 'Assembly summary' section, which contains two circular diagrams representing the genome components. The larger circle represents the chromosome with the following metadata: length=2.5mbp, coverage=266x, location=chromosome, GC-content=32.2%, and dnaapler=reoriented:dnaA. The smaller circle represents a plasmid with the following metadata: length=30.1kbp, coverage=579x, location=plasmid, GC-content=30.4%, and dnaapler=reoriented:repA. The 'ABRicate summary' section indicates that the genome was analyzed with abricate 1.0.1 using various databases and that 19 genes with putative antibiotic resistance markers were identified. The 'VIBRANT summary' section is partially visible at the bottom.

genome: **NBRC100911-p1-1.1** organism: NBRC100911  
species: **Staphylococcus epidermidis** taxid: **1282**

This genome is a representative of NBRC100911.

### Assembly summary

length=2.5mbp  
coverage=266x  
location=chromosome  
GC-content=32.2%  
dnaapler=reoriented:dnaA

length=30.1kbp  
coverage=579x  
location=plasmid  
GC-content=30.4%  
dnaapler=reoriented:repA

### ABRicate summary

This genome was analyzed with [abricate 1.0.1](#) using the following databases: card, ncbi, megares, argannot, vfdb, resfinder, ecoli\_vf, ecoh, plasmidfinder, insaflu. ABRicate found **19 genes** with putative antibiotic resistance markers.

### VIBRANT summary

# Resistance genes

List of ABRicate annotations

**Annotations**

Show filters

Showing 1 to 19 of 19 annotations

- AR:(AGly)aadC : GENE=(AGly)aadC, RESISTANCE=nan, ACCESSION=V01282:225-701, DB=argannot
- AR:ANT(4)-Ib : GENE=ANT(4)-Ib, RESISTANCE=aminoglycoside, ACCESSION=GQ900432.1:27499-26737, DB=card
- AR:APH3-PRIME : GENE=APH3-PRIME, RESISTANCE=nan, ACCESSION=MEG\_1060, DB=megares
- AR:ErmC : GENE=ErmC, RESISTANCE=lincosamide;macrolide;streptogramin, ACCESSION=M12730:779-1514, DB=card
- AR:PC1\_beta-lactamase\_(blaZ) : GENE=PC1\_beta-lactamase\_(blaZ), RESISTANCE=penam,

**NBRC100911-p1-1.1\_001**

penicillin-hydrolyzing class A beta-lactamase BlaZ

Open gene info

**NBRC100911-p1-1.1**

Open genome info

**Pathways**

This gene occurs on 2 pathways

**Annotations**

- ABRicate hit (1)
- EC Number (1)
- Egnog Description (1)
- Egnog Ortholog (1)
- Egnog Protein (1)

# Resistance genes

## Gene detail view

- Annotations and pathways

The screenshot shows a web interface for a genomic database. At the top, there are navigation buttons for 'Genomes' and 'Tools', along with user and notification icons. The breadcrumb path is: / TAXID 1282 / ORGANISM NBRC100911 / GENOME NBRC100911-p1-1.1 / GENE NBRC100911-p1-1.1\_002417. The main content area displays the locus tag 'NBRC100911-p1-1.1\_002417' and genome 'NBRC100911-p1-1.1'. The species is identified as 'Staphylococcus epidermidis' with taxid '1282'. Below this is an 'Annotations' section containing a table with columns for Type, Name, Description, and Pathways.

Type	Name	Description	Pathways
Gene Product	penicillin-hydrolyzing class A beta-lactamase BlaZ		
Gene Code	blaZ		
KEGG reaction	R06363	Penicillin hydrolase; Penicillin + H2O <=> Penicilloic acid	kornec00311
Ortholog	OG0008762-2026-06	class A beta-lactamase	
KEGG gene	K18766	blaZ; beta-lactamase class A BlaZ [EC:3.5.2.6]	kornec01501

Occurs in the following pathway maps:

# Resistance genes

## Gene detail view

- Annotations and pathways
- Gene sequences

Occurs in the following pathway maps:

Pathway	Description
<a href="#">kornec00311</a>	Penicillin and cephalosporin biosynthesis
<a href="#">kornec01501</a>	beta-Lactam resistance

## Sequences

Nucleotide sequence (GC-content: 28.0 %):

[Export FASTA](#) ▼

```
TTGAAAAAGTTAATATTTTTAATTGCAATTGCTTTAGTTTTAAGTGCATGTAATTCAAAACAGTCCACATGCCAAAAGAGTT
AAATGATTTAGAAAAAATAATAATGCTCATATTGGTGTATTATGCTTTAGATACTAAAAGTGGTAAGGAAGTAAAATTTA
ATTCAGATAAGAGATTTGCTTATGCTTCGACTTCAAAGCGATAAATAGTGCTATTTTGTTAGAACAAGTACCTTATAAT
AAGTTAAATAAAAAAATACATATTAACAAGATGATATAGTTGCTTATTCTCCTATTTTAGAAAAATATGTAGGAAAAAGA
TATCACTTTAAAAGAACTTATTGAGGCTTCAATGACATATAGTGATAATACAGCAAACAATAAAAATTATAAAAAGAGATCG
GTGGGATCAAAAAAGTTAAACAACGTCTAAAAGGACTAGGAGATAAAGTAACAATCCAGTTAGATATGAGATAGAATTA
AATTATTATTCACCAAAGAGCAAAAAAGATACTTCAACACCTGCTGCTTTTCGGTAAGACTTTAAATAAACTTATCGCAA
TGGAAAAATTAAGCAAAGAAAAAATAAAATTTCTTACTTGATTTAATGTTAAATAATAAAAGCGGAGATACTTTAATTAAAG
ACGGTGTTTCAAAGACTGTAAGGTTGCTGATAAAAGTGGTCAAGCAATAACATATGCTTCTAGAAATGATGTTGCTTTT
GTTTATCCTAAGGGCCAATCTGAACCTATTGTTTTAGTCATTTTTACGAATAAAGACAATAAAAGTGATAAGCCAAATGA
TAAGTTGATAAGTGAAACCGCCAAGAGTGTAATGAAGGAATTTTAA
```

Protein sequence:

[Export FASTA](#) ▼

```
MKKLIFLIAIALVLSACNSNSPHAKELNDLEKKYNAHIGVYALDTKSGKEVKFNSDKRFAYASTSKAINSAILLEQVPYN
KLNKKIHINKDDIVAYSPILEKYVGKDI TLKELIEASMTYS DNTANNKIIKEIGGIKKVKQRLKGLGDKVTNPVRYEIEL
NYYS PKSKKDTSTPAAF GKTLNKL IANGKLSKENKKFLLDLMLN NKS GDTL IKDGVSKDCKVADKSGQAITYASRNDVAF
VYPKGQSEPIVLVIF TNKDNKSDKPN DKLISETAKSVMKEF
```

## GenBank Info

gene - blaZ

locus\_tag - NBRC100911-p1-1.1\_002417

Located on: NBRC100911-p1-1.1\_scf2 (plasmid)

inference - COORDINATES: similar to AA sequence:RefSeq:WP\_000733274.1

note - Derived by automated computational analysis using gene prediction method: Protein Homology; GO function: GO:0008999

# Resistance genes

## Gene detail view

- Annotations and pathways
- Gene sequences
- Neighboring genes

MKKLIFLIAIALVLSACNSNSPHAKELNDLEKKYNAHIGVYALDTKSGKEVKFNSDKRFAYASTSKAINSAILLEQVPYN  
KLNKKIHINKDDIVAYSPILEKYVVGKDITLKELEASMTYSDNTANNKIIKEIGGIKKVKQRLKGLGDKVTNPVRYEIEL  
NYYSPKSKKDTSTPAAFGLTLNKLIANGKLSKENKKFLLDLMLNKNKSGDTLIKDGVSKDCKVADKSGQAITYASRNDVAF  
VYPKGQSEPIVLVIFTNKDNKSDKPNDKLISETAKSVMKEF

## GenBank Info

gene - blaZ

locus\_tag - NBRC100911-p1-1.1\_002417

Located on: NBRC100911-p1-1.1\_scf2 (plasmid)

inference - COORDINATES: similar to AA sequence:RefSeq:WP\_000733274.1

note - Derived by automated computational analysis using gene prediction method: Protein Homology. GO\_function: GO:0008800 - beta-lactamase activity [Evidence IEA]

codon\_start - 1

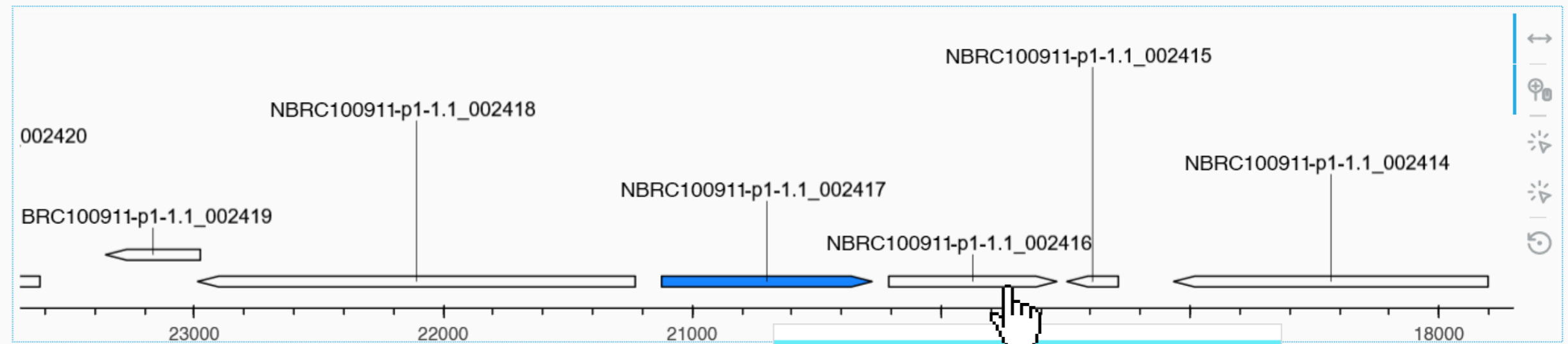
transl\_table - 11

product - penicillin-hydrolyzing class A beta-lactamase BlaZ

protein\_id - extdb:NBRC100911-p1-1.1\_002417

## Gene locus (click to toggle display options)

Located on scaffold **NBRC100911-p1-1.1\_scf2**



## Cellular location

**NBRC100911-p1-1.1\_002416**

IS6 family transposase

Open gene info

**NBRC100911-p1-1.1**

Open genome info

Annotations

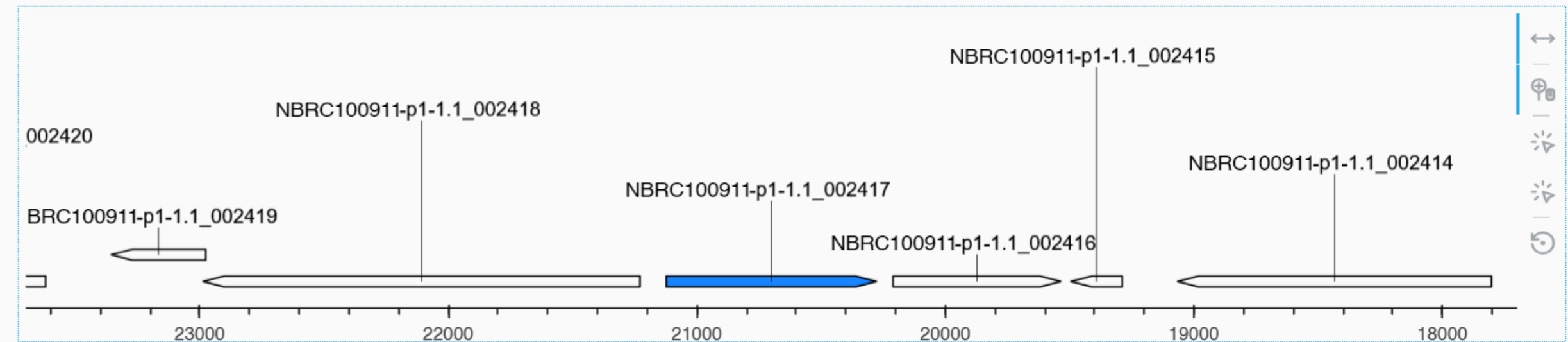
# Resistance genes

## Gene detail view

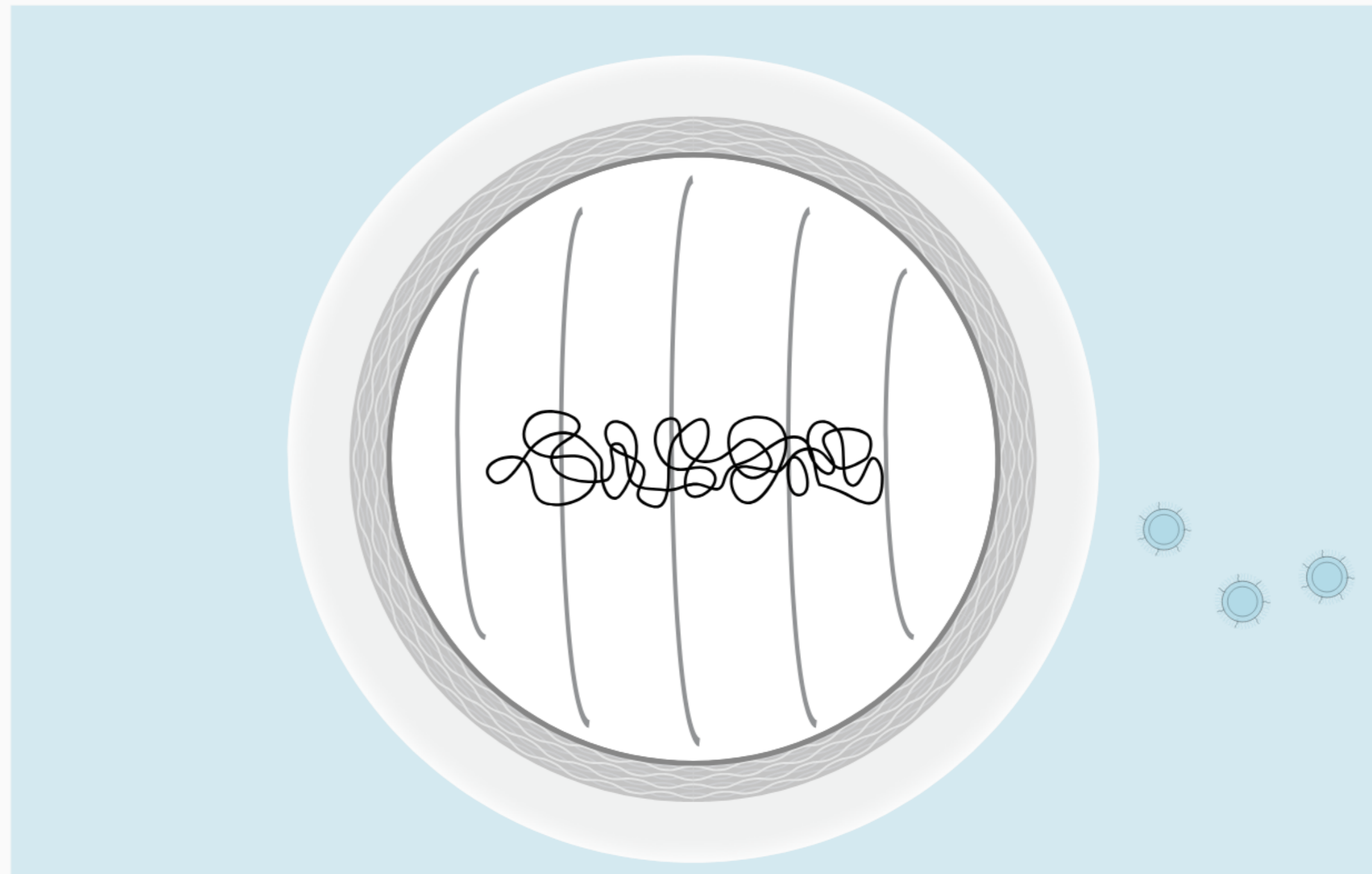
- Annotations and pathways
- Gene sequences
- Neighboring genes
- Subcellular location (secreted)

## Gene locus (click to toggle display options)

Located on scaffold NBRC100911-p1-1.1\_scf2



## Cellular location






# Pathways



# Pathways

Select two taxonomic groups for comparison


[Genomes](#)
[Tools ▾](#)



## Pathway analysis

Identify functional differences by projecting annotations onto biochemical pathway maps. Compare single genomes or groups, and click on shapes to find the underlying annotations and genes.

**To start:** search for a **pathway map** (e.g., “citrate cycle”), pick it, then select **one or more genomes** (or groups) and click **Submit**.  
(Tip: use [magic strings](#) to select genomes.) [Guide](#) →

Pathway Map:  Select ▾

Group 1: Remove

Wipe Copy

@tax:Lactobacillus ×

Group 2: Remove

Wipe Copy

@tax:Propionibacteriaceae ×

+ Add Group

Submit

# Pathways



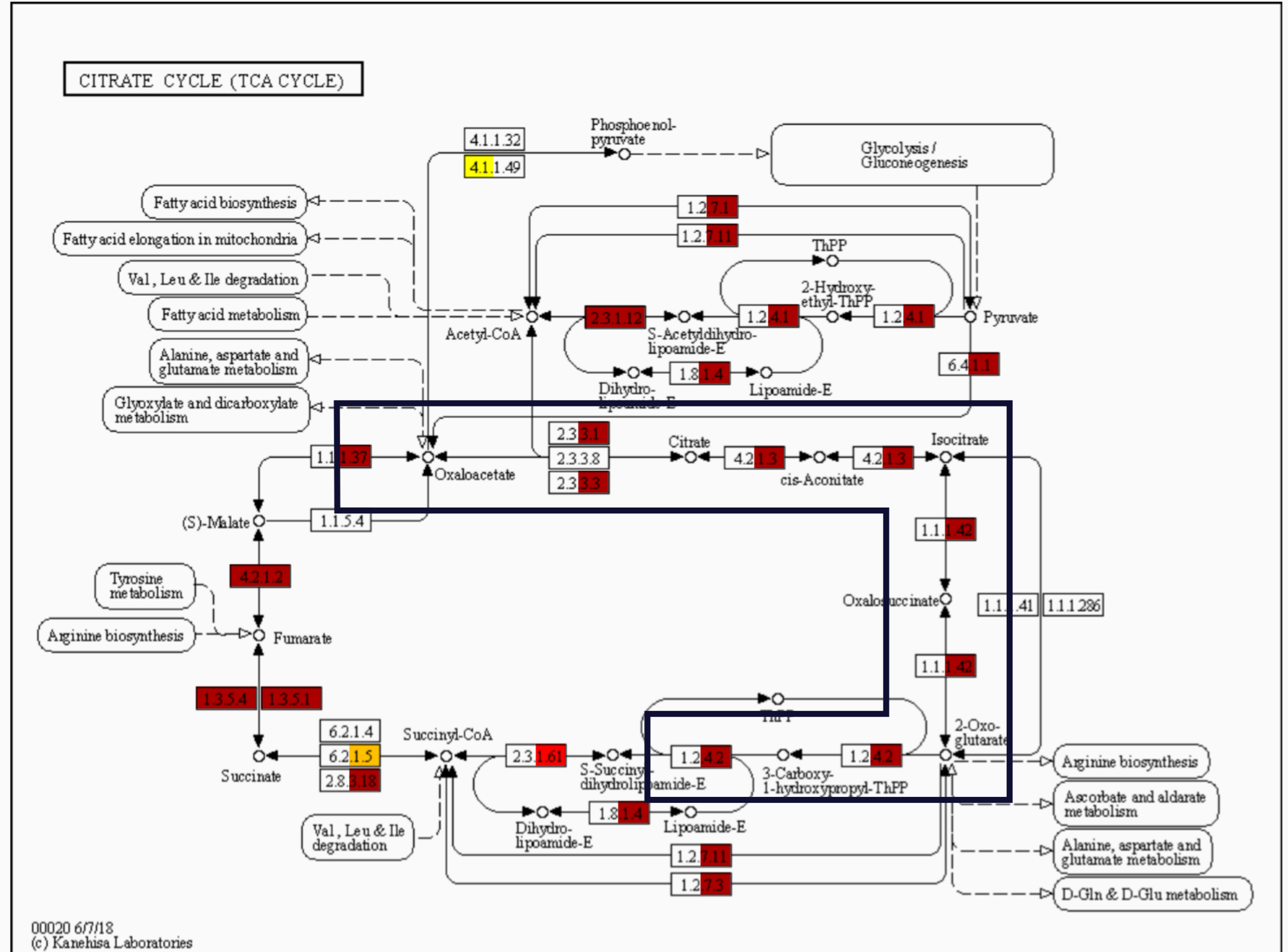
No Lactobacillus  
has this gene

All Propionibacteria  
have this gene

→ Choose a Propionibacterium,  
they can!

Show query Download ▾

Change pathway colors (click to toggle)



# Why **microbial genomes** matter.

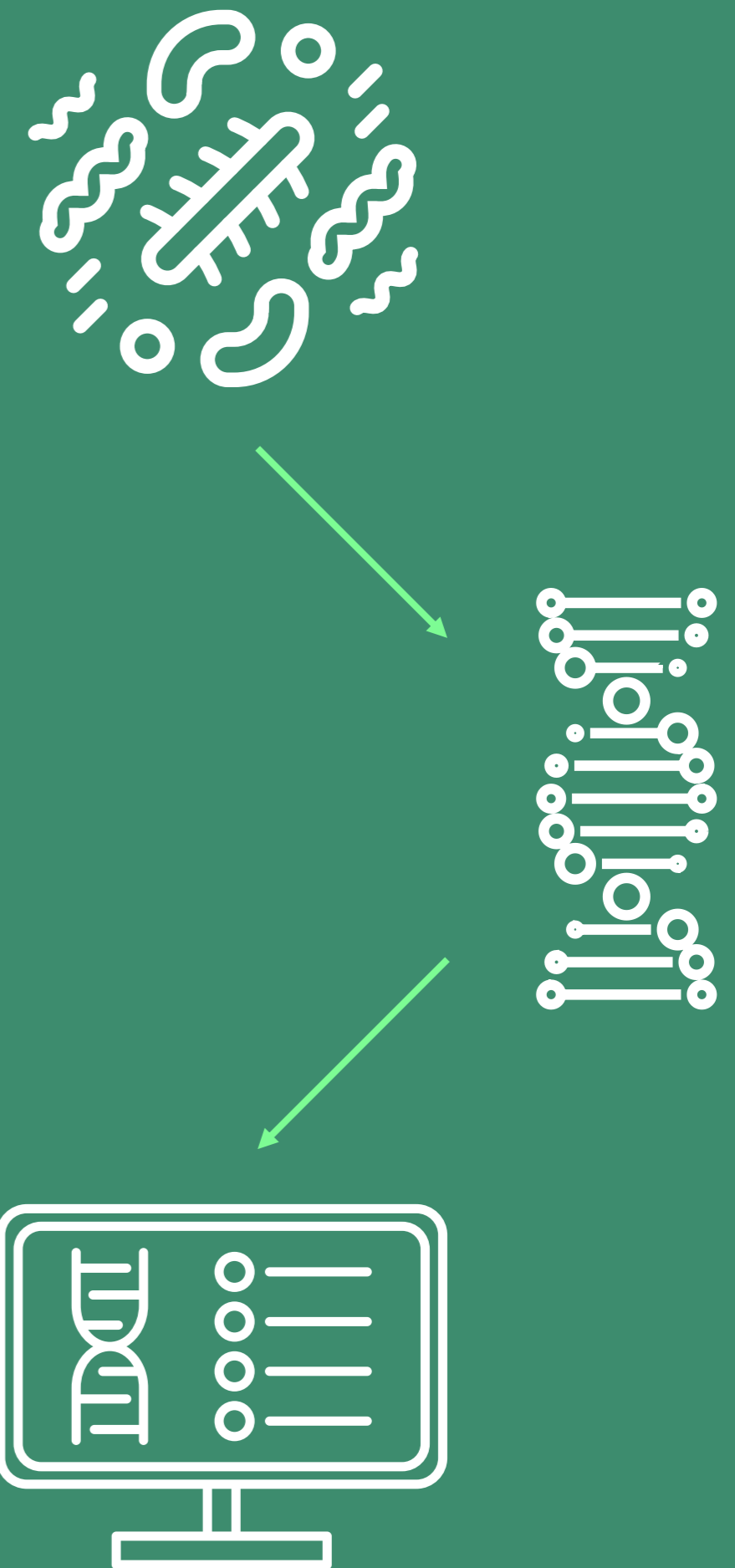
**PREDICTING RESISTANCE.**



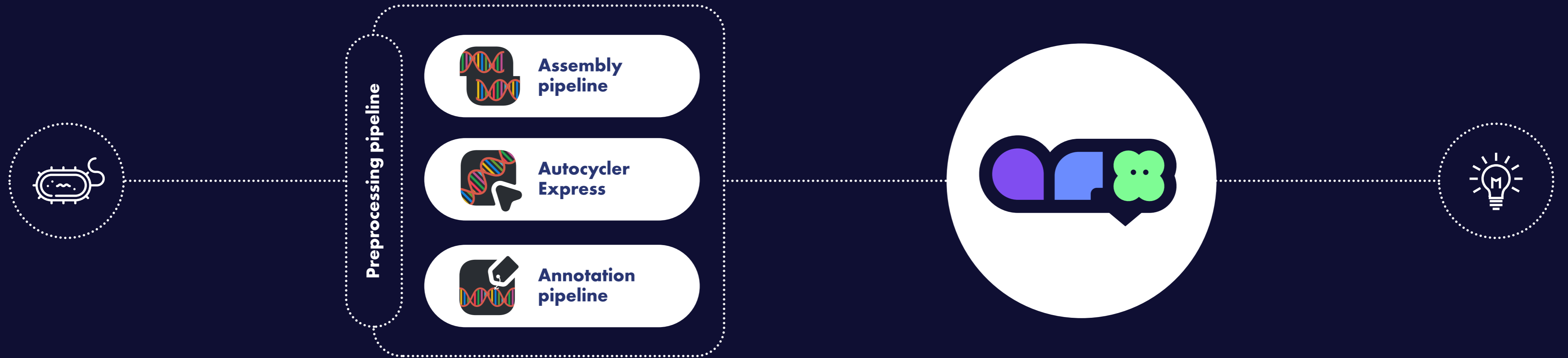
**DESIGNING BETTER CULTURES.**



**PREVENTING OUTBREAKS.**



# Our ecosystem.





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GENOMICS

# Questions & **answers.**

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WWW.ABRINCA.COM

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8 June 2026