ABRINCA—
GENOMICS

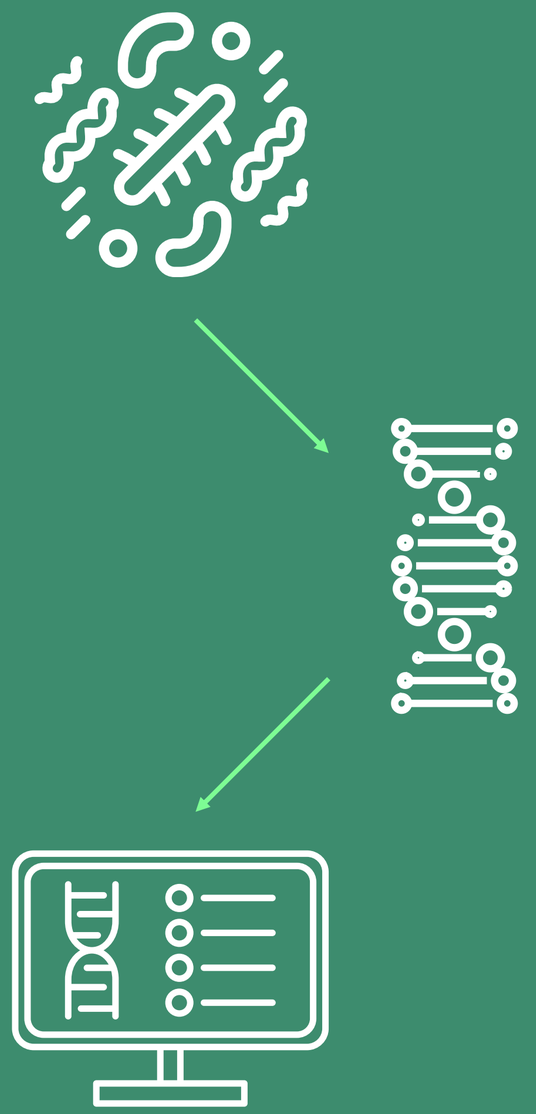
Streamlining Microbial Genomics for Food Safety

Simplifying genomics, amplifying insights.

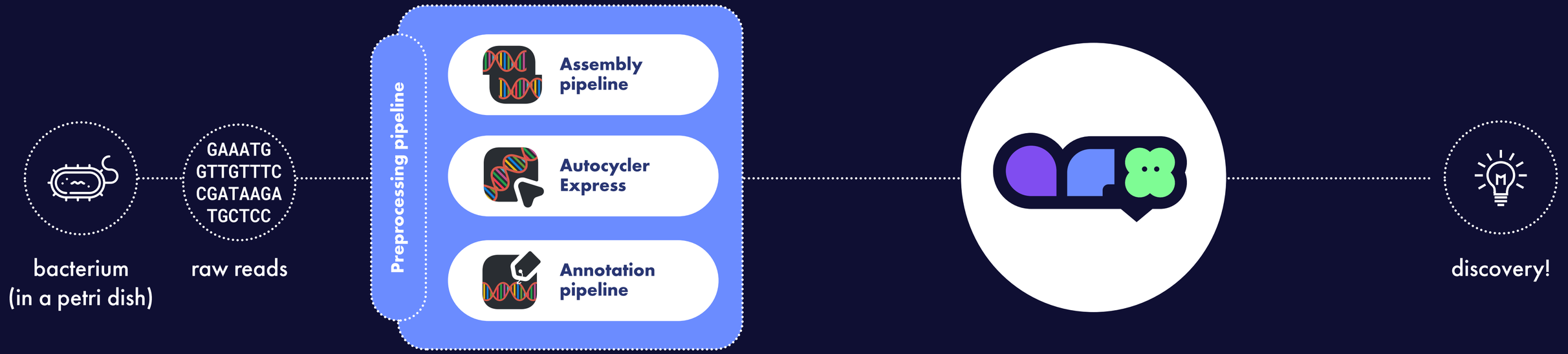
WORLD FOOD SAFETY DAY
AGROSCOPE - LIEBEFELD
8 JUNE 2026

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.

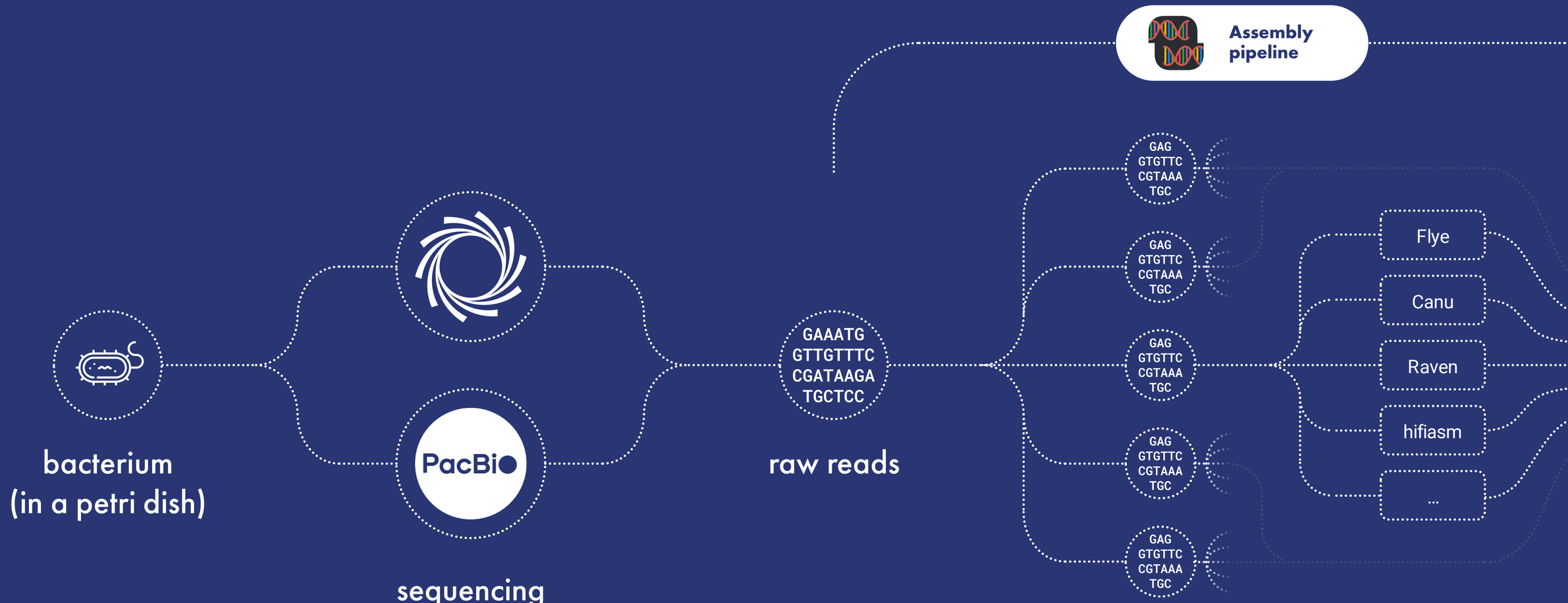
Assemblers often make errors.

MANUAL CURATION.

Downstream analyses depend on high quality assemblies.

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

Our pipeline



bacterium
(in a petri dish)

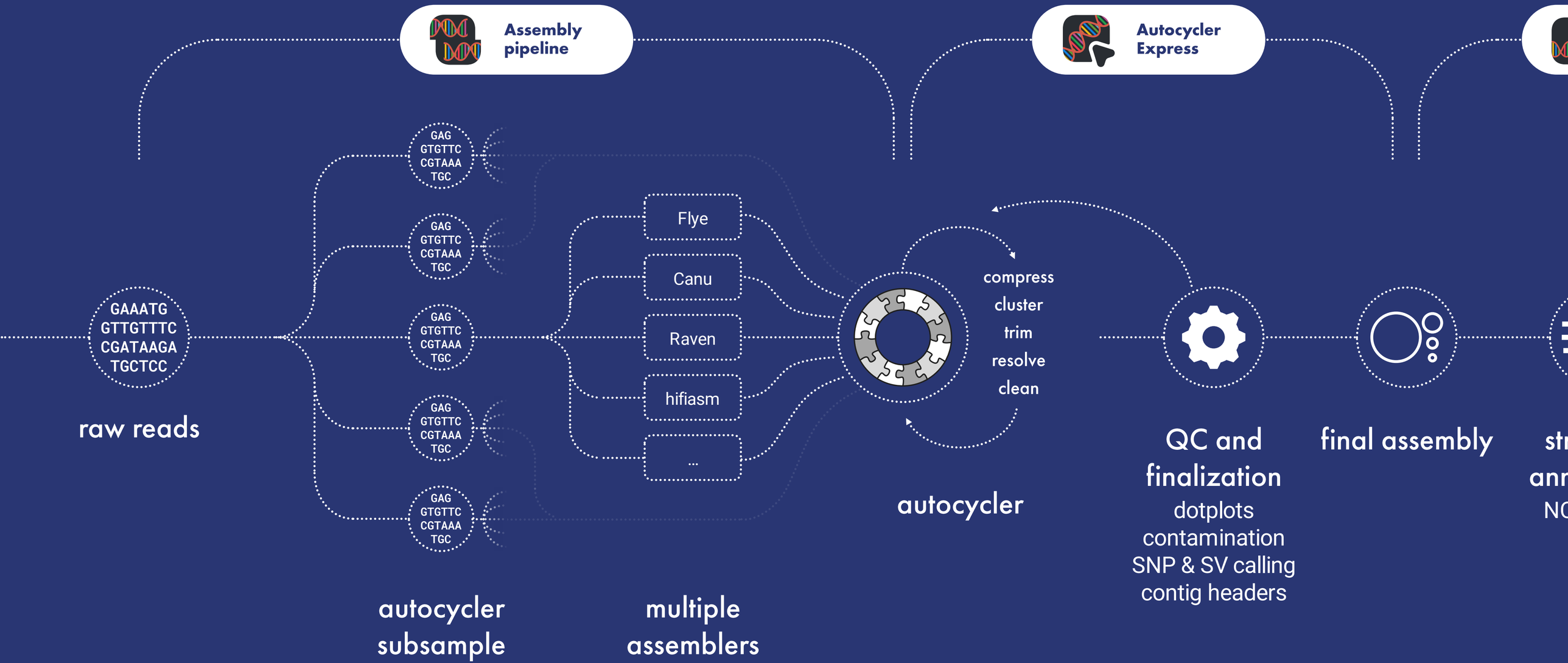
sequencing

raw reads

autocycler
subsample

multiple
assemblers

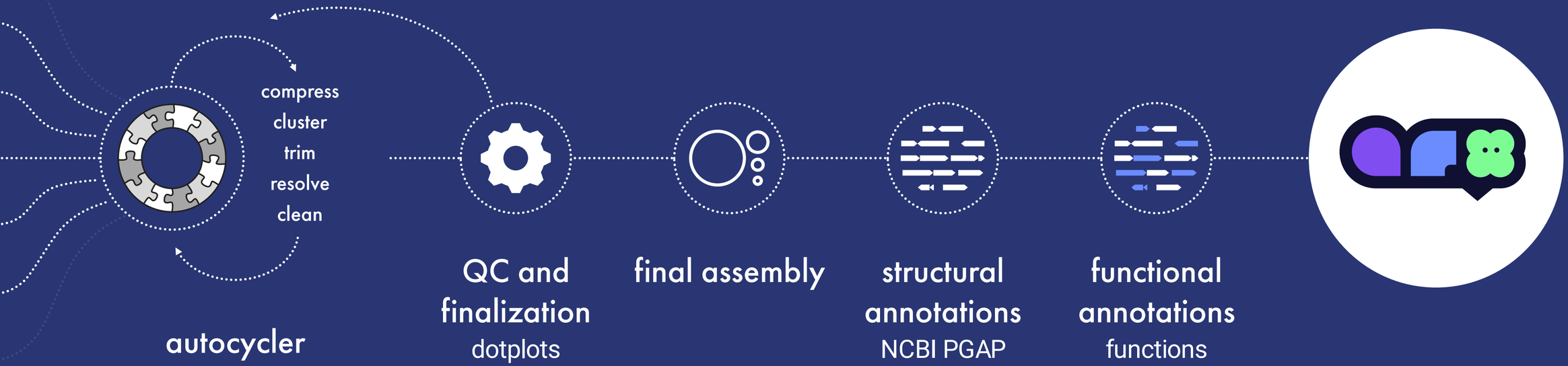
Our pipeline



Our pipeline

Autocycler Express

Annotation pipeline



autocycler

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.

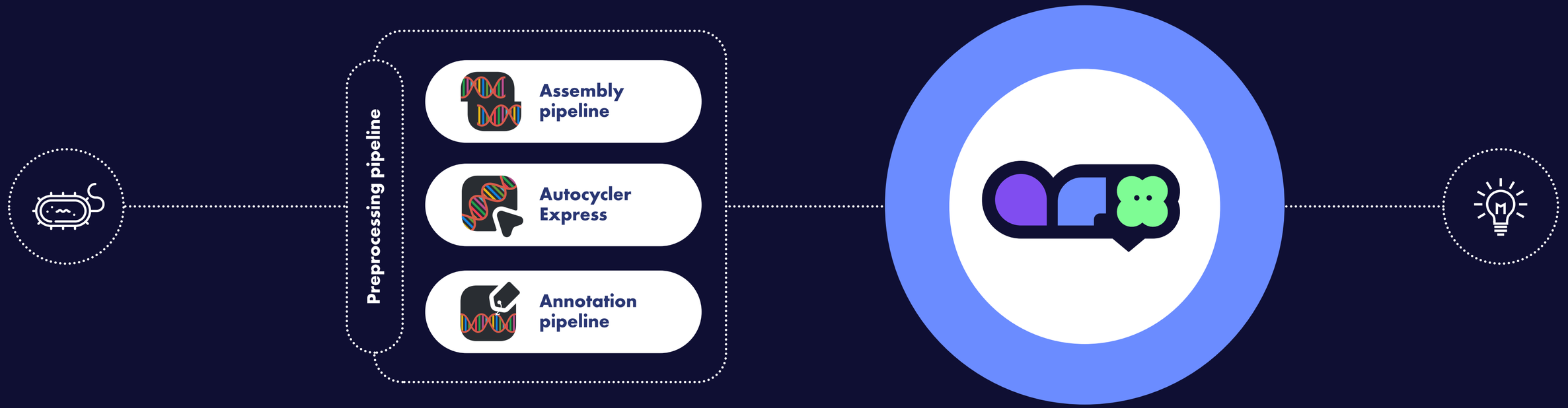
MANUAL CURATION.

Downstream analyses depend on high quality assemblies.

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

numbers are based on a comparison to conventional single-assembler-based pipelines

Our ecosystem



Data Mining Problem ☞ Solution.

Questions

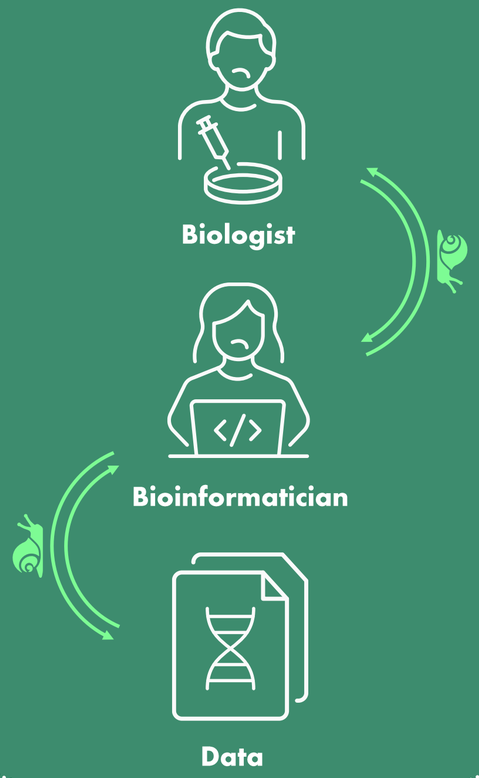
Question 1
Does this strain have resistance genes?

Question 2
Does one of our strains have this bacteriocin sequence?

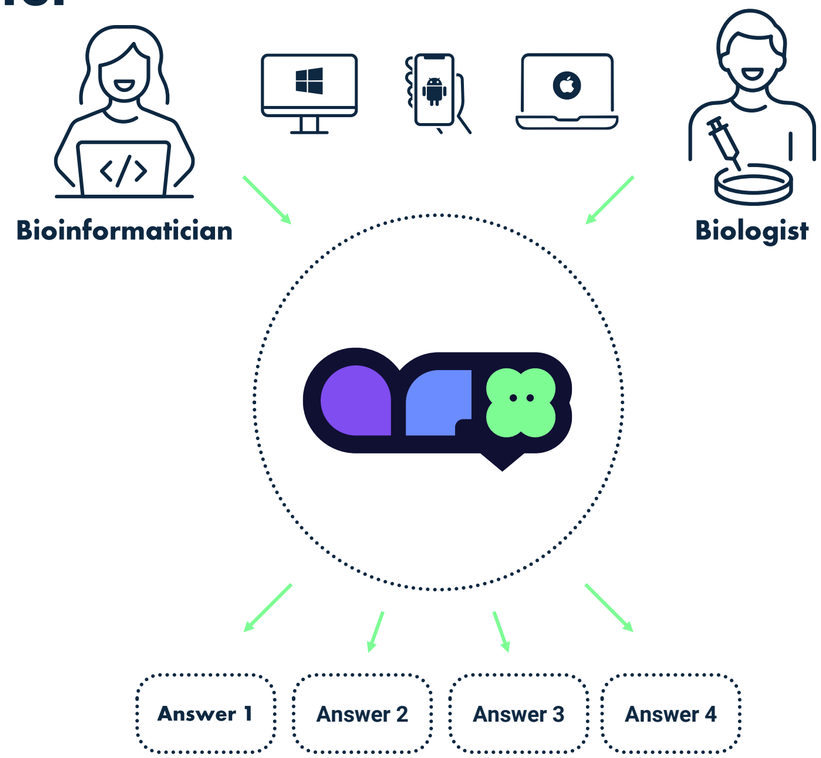
Question 3
Can this strain use lactose as a substrate?

Question 4
Which orthogene can explain this resistance pattern?

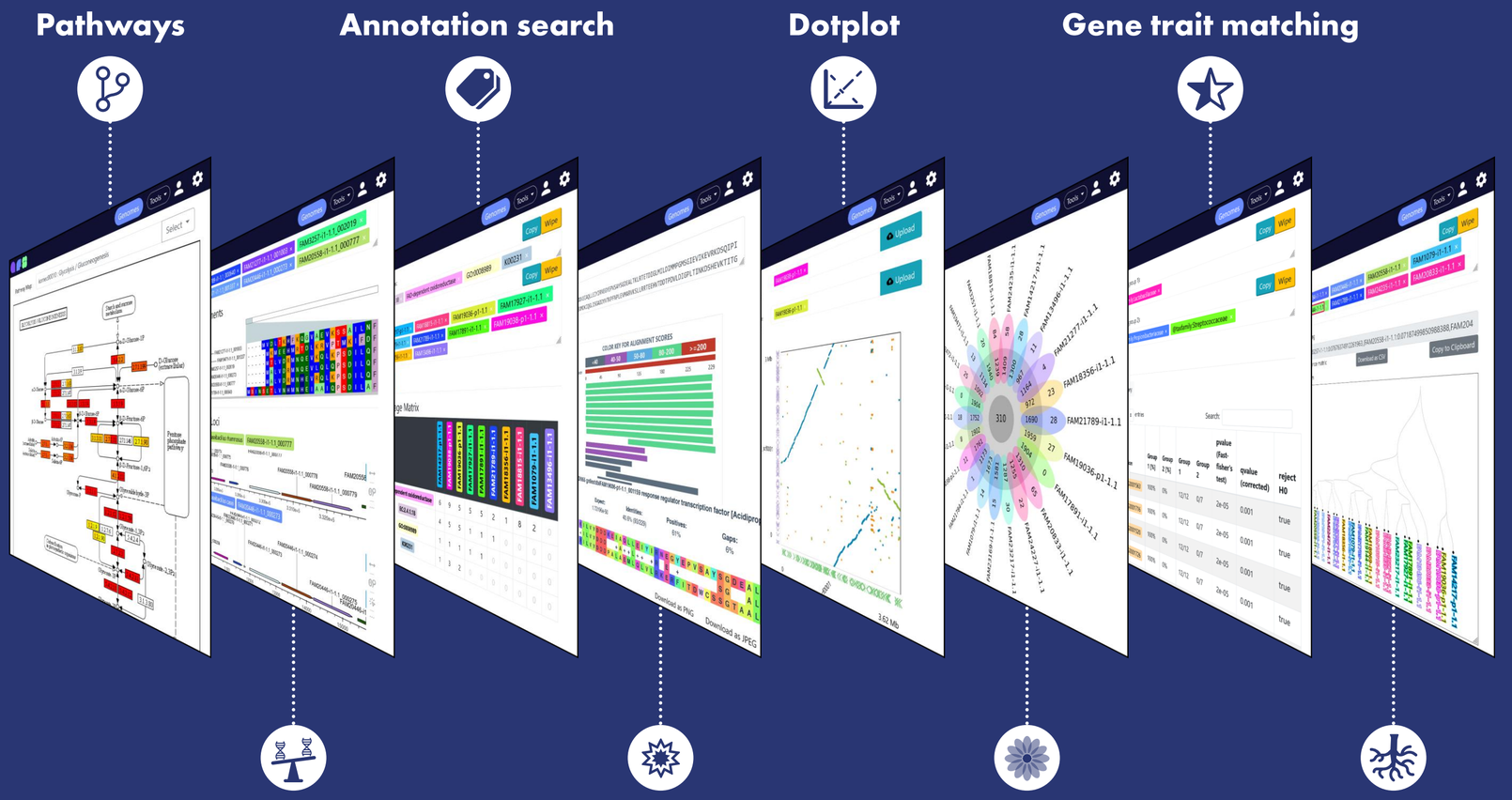
Before



After



Arx


Pathways
Annotation search
Dotplot
Gene trait matching
Gene comparison
BLAST
Flower plot
Phylogenetic trees

Resistance genes

Resistance genes

Genome overview page

Genomes Tools

/ TAXID 1282 / ORGANISM NBRC100911 / GENOME NBRC100911-p1-1.1

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

This genome is a representative of NBRC100911.

Assembly summary

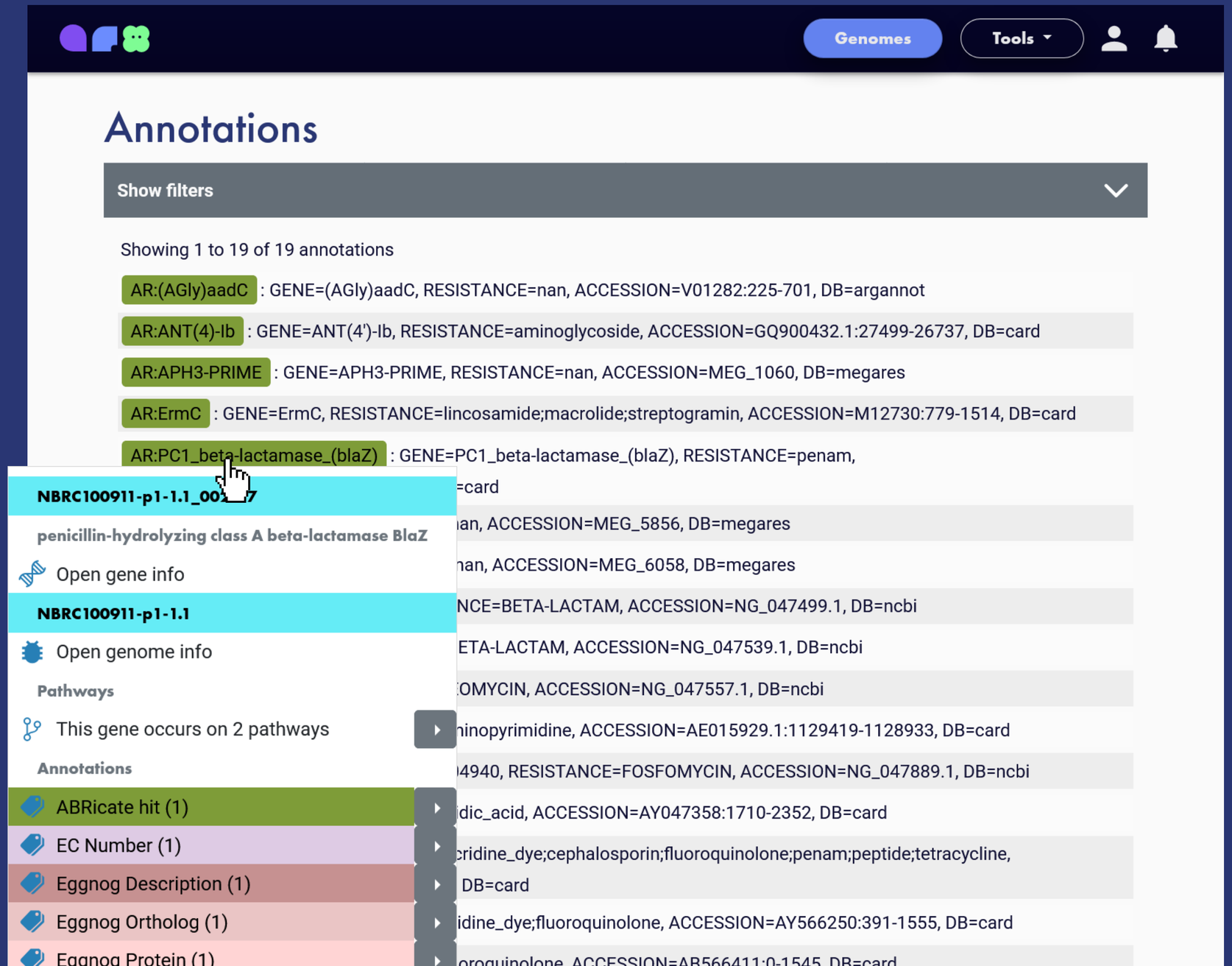
ABRicate summary

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

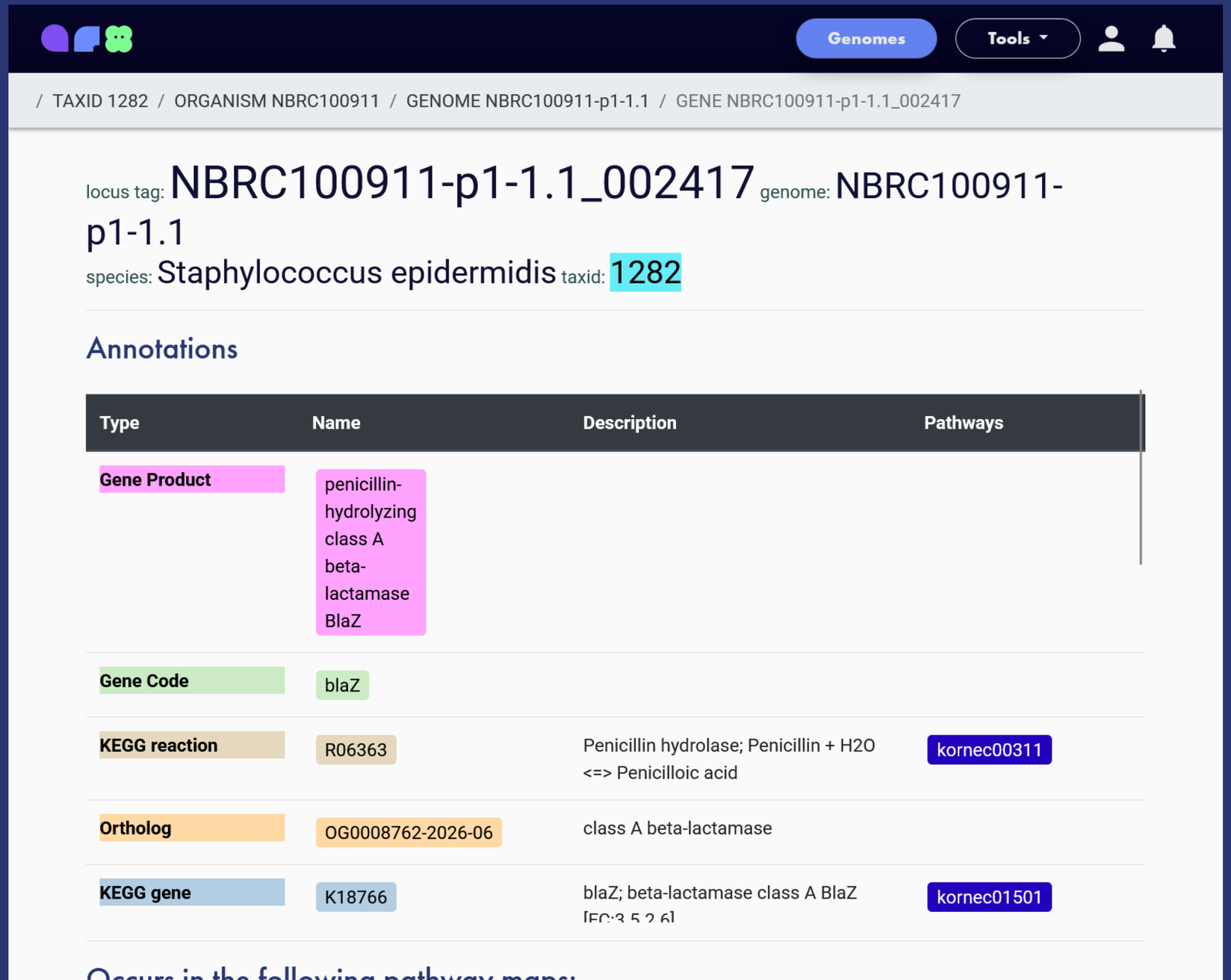
List of ABRicate annotations



Resistance genes

Gene detail view

- Annotations and pathways



ABRINCA—
GENOMICS

Resistance genes

Gene detail view

- Annotations and pathways
- Gene sequences

KEGG gene | K18766 | blaZ; beta-lactamase class A BlaZ [EC:3.5.2.6] | kornec01501

Occurs in the following pathway maps:

Pathway	Description
kornec00311	Penicillin and cephalosporin biosynthesis
kornec01501	beta-Lactam resistance

Sequences

Nucleotide sequence (GC-content: 28.0 %): Export FASTA

```
TTGAAAAAGTTAATATTTTTAATTGCAATTGCTTTAGTTTTAAGTGCATGTAATTCAAACAGTCCACATGCCAAAGAGTT
AAATGATTTAGAAAAAAAATATAATGCTCATATTGGTGTTTATGCTTTAGATACTAAAAGTGGTAAGGAAGTAAAATTTA
ATTCAGATAAGAGATTTGCCTATGCTTCGACTTCAAAAGCGATAAATAGTGCTATTTTGTTAGAACAAGTACCTTATAAT
AAGTTAAATAAAAAAATACATATTAACAAAGATGATATAGTTGCTTATTCTCCTATTTTAGAAAAATATGTAGGAAAAGA
TATCACTTTAAAAGAACTTATTGAGGCTTCAATGACATATAGTGATAATACAGCAAACAATAAAATTATAAAAGAGATCG
GTGGGATCAAAAAAGTTAAACAACGTCTAAAAGGACTAGGAGATAAAGTAACAAATCCAGTTAGATATGAGATAGAATTA
AATTATTATTCACCAAAGAGCAAAAAAGATACTTCAACACCTGCTGCTTTCGGTAAGACTTTAAATAAACTTATCGCAAA
TGGAAAATTAAGCAAAGAAAACAAAAAATTCTTACTTGATTTAATGTTAAATAATAAAAGCGGAGATACTTTAATTAAAG
ACGGTGTTTCAAAAGACTGTAAGGTTGCTGATAAAAGTGGTCAAGCAATAACATATGCTTCTAGAAATGATGTTGCTTTT
GTTTATCCTAAGGGCCAATCTGAACCTATTGTTTTAGTCATTTTTACGAATAAAGACAATAAAAGTGATAAGCCAAATGA
TAAGTTGATAAGTGAAACCGCCAAGAGTGTAATGAAGGAATTTTAA
```

Protein sequence: Export FASTA

```
MKKLIFLIAIALVLSACNSNSPHAKELNDLEKKYNAHIGVYALDTKSGKEVKFNSDKRFAYASTSKAINSAILLEQVPYN
KLNKKIHINKDDIVAYSPILEKYVGKDITLKELIEASMTYSDNTANNKIIKEIGGIKKVKQRLKGLGDKVTNPVRYEIEL
NYYSPKSKKDTSTPAAFGKTLNKLIANGKLSKENKKFLLDLMLNNKSGDTLIKDGVSKDCKVADKSGQAITYASRNDVAF
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

ABRINCA—
GENOMICS

Resistance genes

Gene detail view

- Annotations and pathways
- Gene sequences
- Neighboring genes

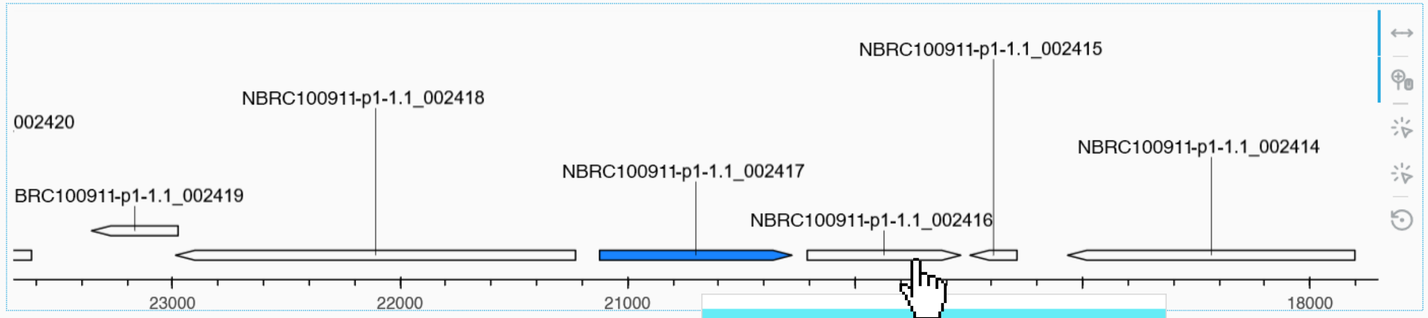
MKKLIFLIAIALVLSACNSNSPHAKELNDLEKKYNAHIGVYALDTKSGKEVKFNSDKRFAYASTSKAINSAILLEQVPYN
KLNKKIHINKDDIVAYSPILEKYVGKDITLKELIEASMTYSDNTANNKIIKEIGGIKKVKQRLKGLGDKVTNPVRYEIEL
NYYSPKSKKDTSTPAAFGKTLNKLIANGKLSKENKKFLLDLMLNNKSGDTLIKDGVSKDCKVADKSGQAITYASRNDVAF
VYPKGQSEPIVLVIFTNKDNKSDKPNDKLISETAKSVMKEF

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

ABRINCA—
GENOMICS

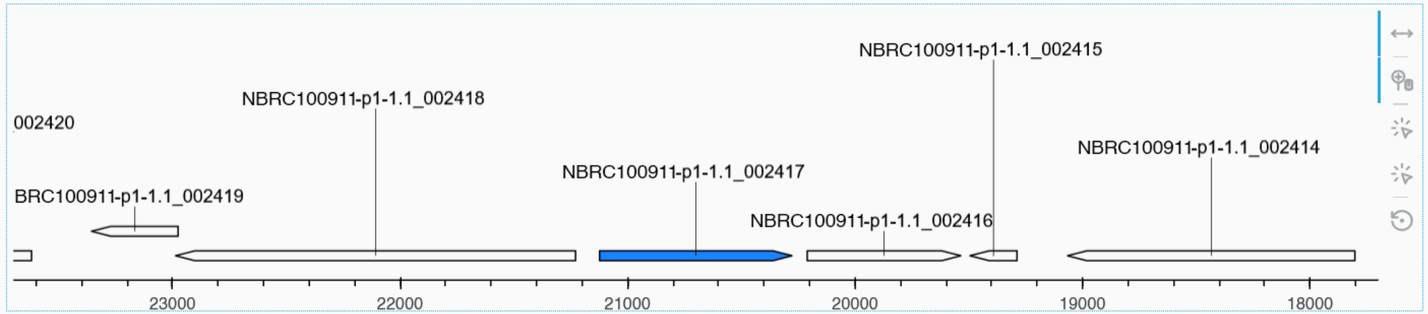
Resistance genes

Gene detail view

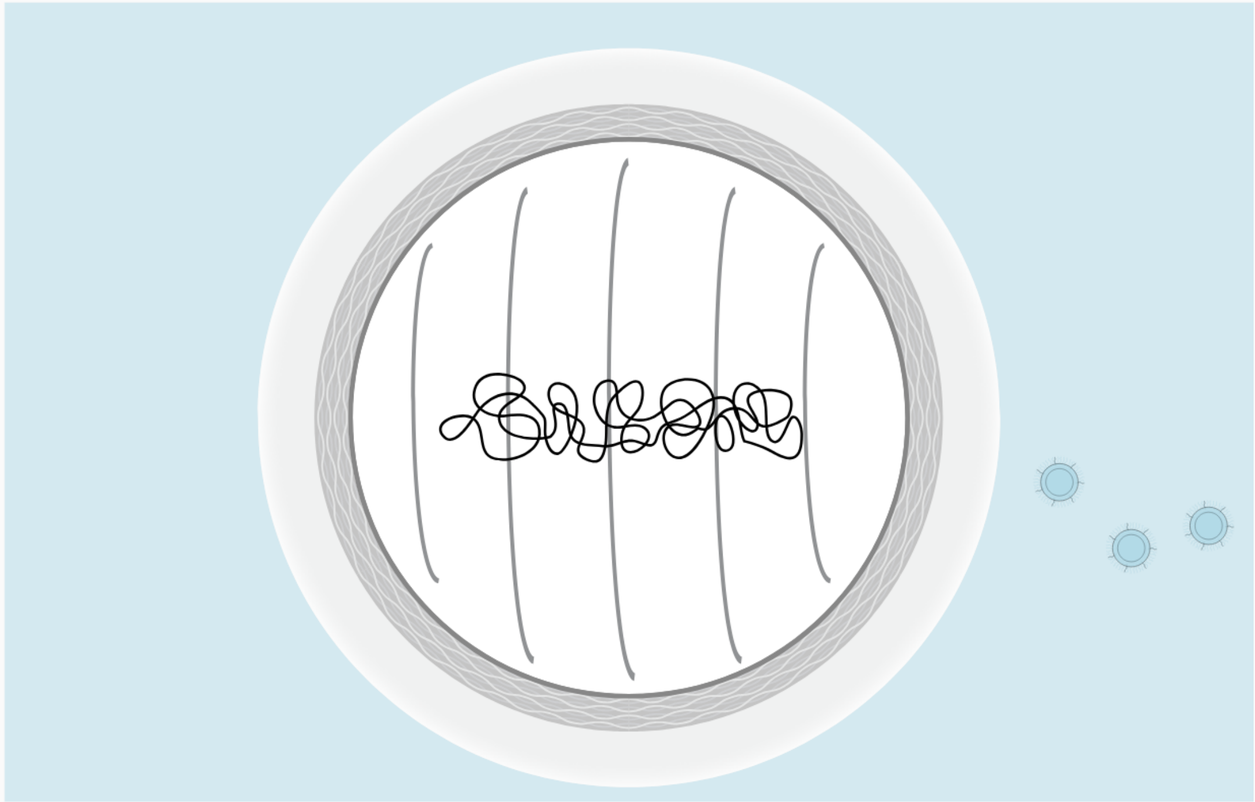
- Annotations and pathways
- Gene sequences
- Neighboring genes
- Subcellular location (secreted)

Gene locus (click to toggle display options)

Located on scaffold NBRC100911-p1-1.1_scf2



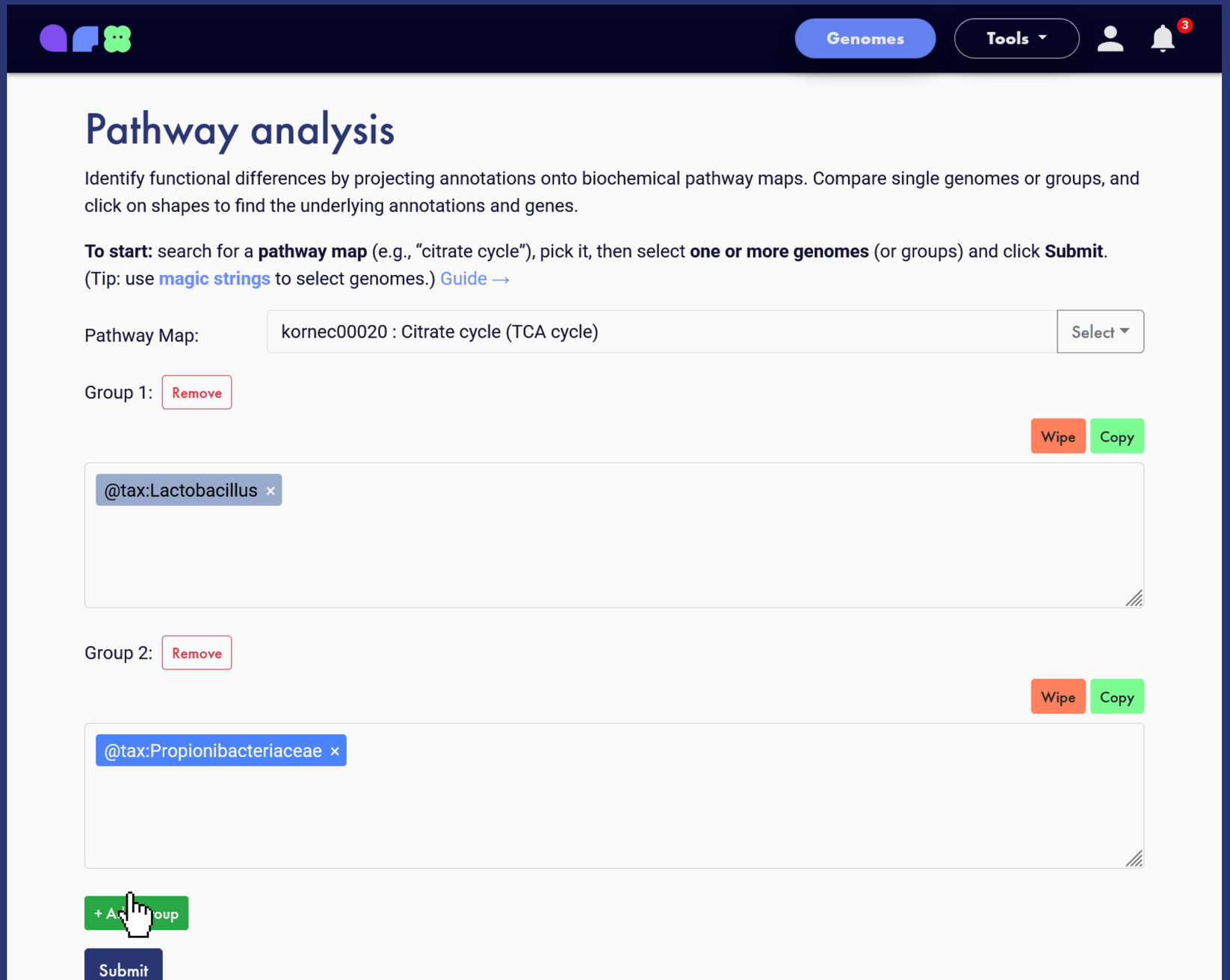
Cellular location



Pathways

Pathways

Select two taxonomic groups for comparison



ABRINCA—
GENOMICS

Pathways

No Lactobacillus has this gene

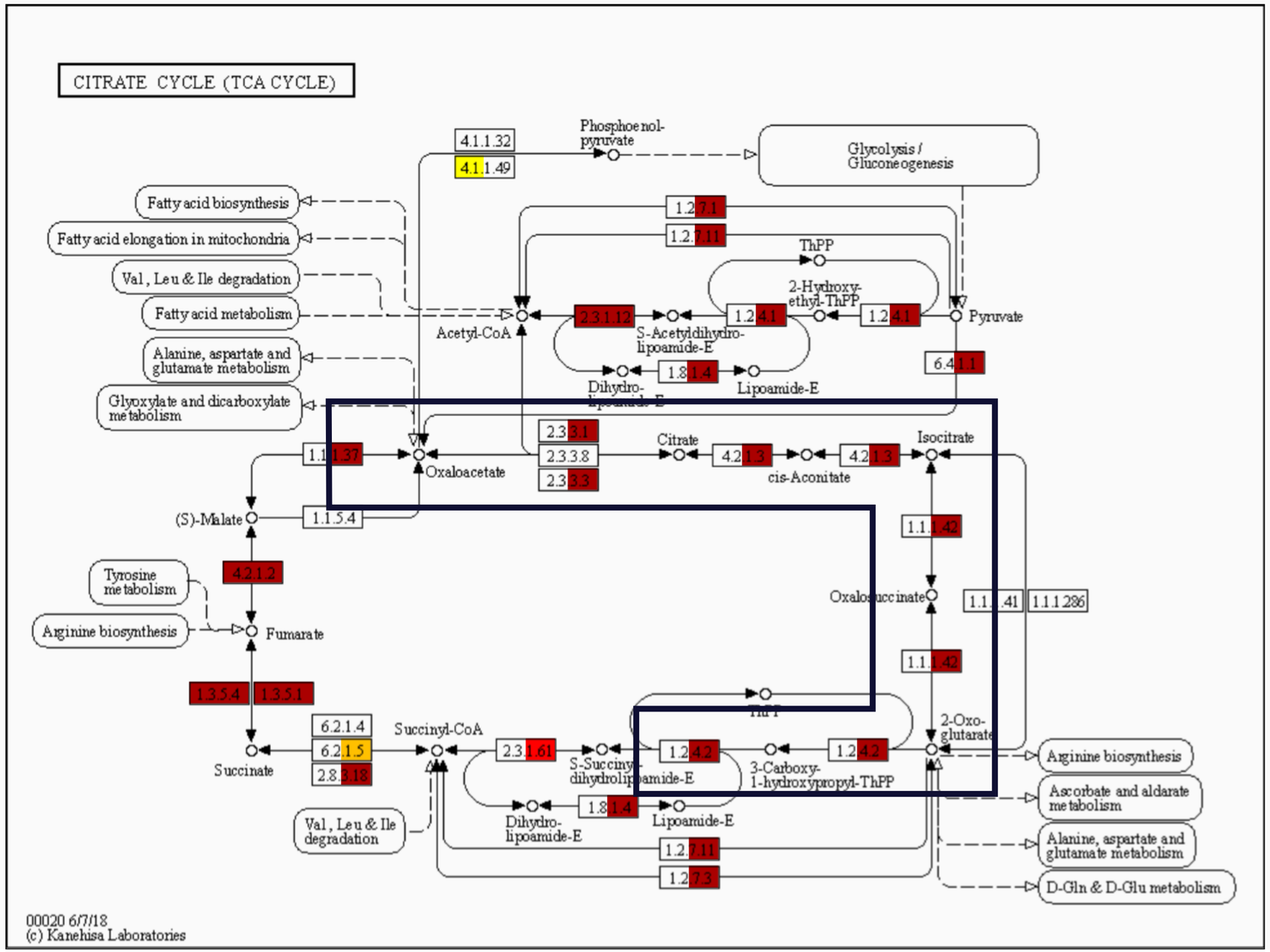
All Propionibacteria have this gene

→ Choose a Propionibacterium, they can!

Submit

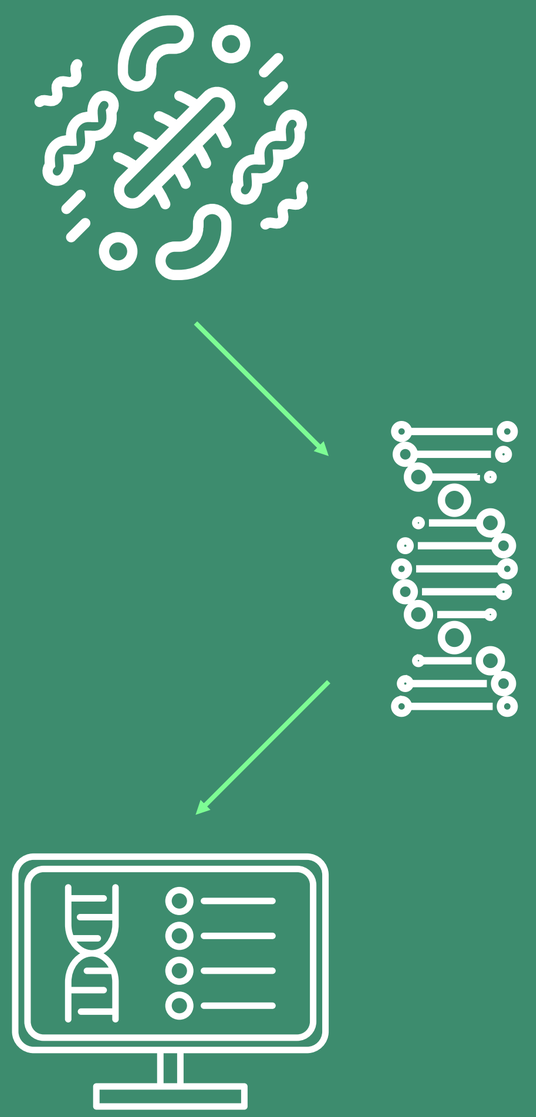
Show query Download

Change pathway colors (click to toggle)

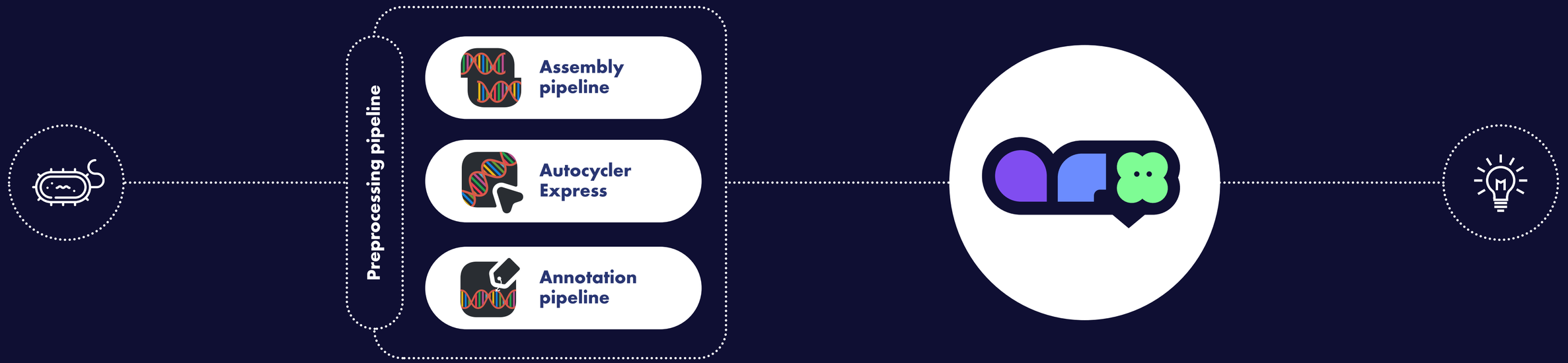


Why microbial genomes matter.

- PREDICTING RESISTANCE.
- DESIGNING BETTER CULTURES.
- PREVENTING OUTBREAKS.



Our ecosystem.



ABRINCA—
GENOMICS

Questions & answers.

TOM HOWZE
COFOUNDER, CHIEF COMMERCIAL OFFICER
TOM@ABRINCA.COM
WWW.ABRINCA.COM

CATALYSE/AGROSCOPE WORLD FOOD SAFETY DAY
8 June 2026