



ABRINCA—
GENOMICS

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Unlocking the Freezer: **Practical Lessons from Transforming** **Strain Collections into Dynamic R&D Assets**

Simplifying genomics, amplifying insights.

USCCN 2026 - FROM PRESERVATION TO INNOVATION
07/31/2026

Current Asset State

Vast Physical Holdings

USCCN member collections collectively preserve hundreds of thousands of characterized prokaryotic, fungal, and viral isolates across federal, academic, and specialized stock centers.

Digital Infrastructure

Many collections now have basic public portals that enable customers/ collaborators to apply simple filters like taxonomy or phenotypes.

Disconnected Sequence Data

Raw genomic data deposited in public archives is frequently detached from physical freezer vials, accession histories, and phenotypic metadata.

Current Value State

Biological Ground Truth

The authority for taxonomy, regulatory compliance, patent deposits, and reproducible global research.

Preserving Critical Biodiversity

Safeguards irreplaceable isolates from decades or even centuries of research and history.

Treasure Chest for the Future

A key reservoir for discovering novel enzymes, biosynthetic gene clusters, and functional strains for agriculture, fermented foods, health, and biomanufacturing.

Current Challenges

Data accessibility

Public portals remain static, usually lack genomic information or even simple BLAST search. This prevents potential customers from easily finding relevant strains in common scenarios.

Funding & Staffing Constraints

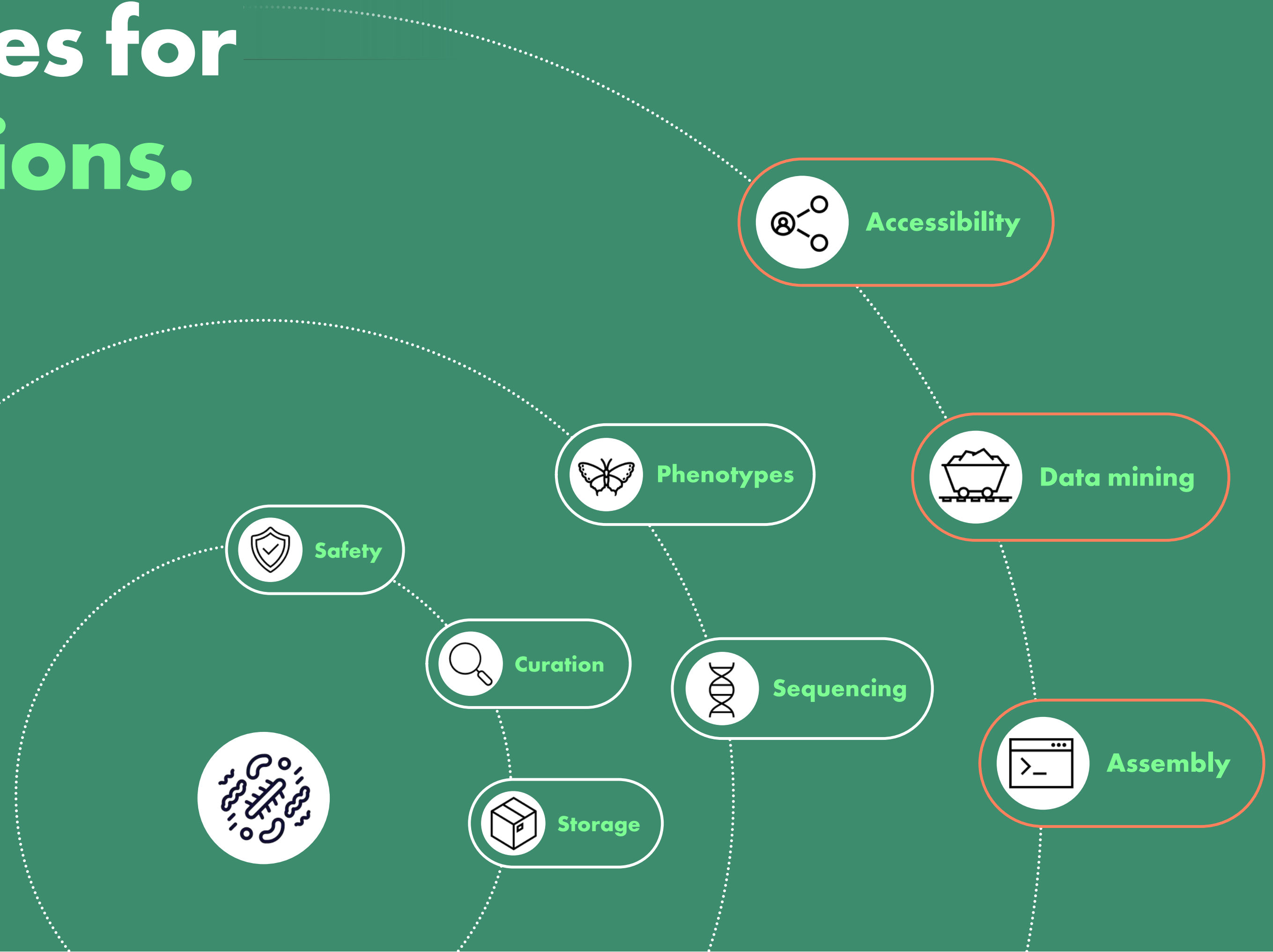
Over 70% of collections face static or declining maintenance budgets, severely limiting their ability to accession and digitize new deposits.

Bioinformatics

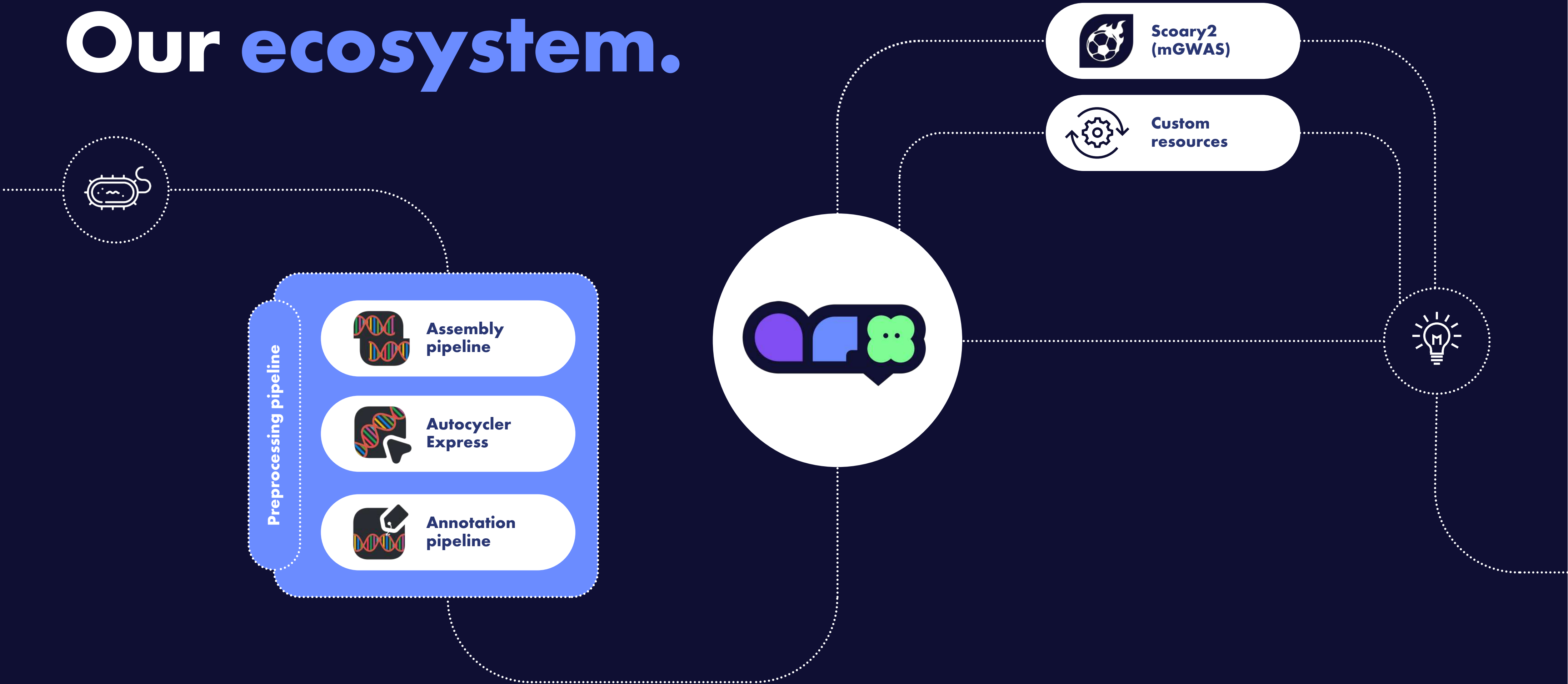
Difficulty, cost and lack of standardized protocols for sequencing and downstream processing (assembly, annotation, data management).

The challenges for strain collections.

Strain collection teams often struggle to maximize the value of their genomic data due to lack of assembly capabilities, no tools for genomic data mining, and poorly managed datasets, leaving tremendous potential and commercial value unrealized.



Our ecosystem.



Key problems for assembly

PLASMIDS AND PHAGES.



Resistance genes are often located on plasmids, phages disrupt fermentation.



Assemblers often drop plasmids / phages.

CONTAMINATION.



Sometimes, isolates are not as isolated as we hope.



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

MANUAL CURATION.

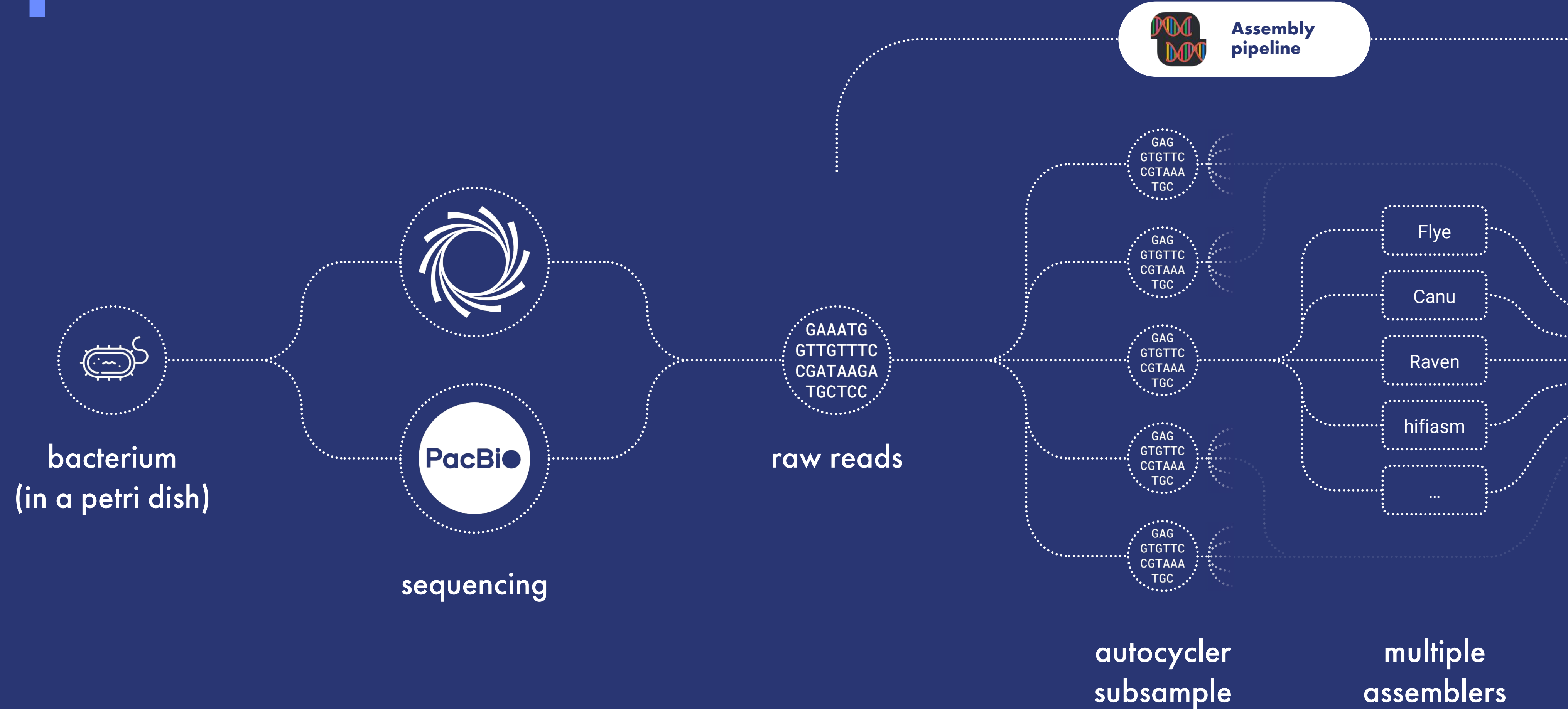


Human supervision is required for optimal results.

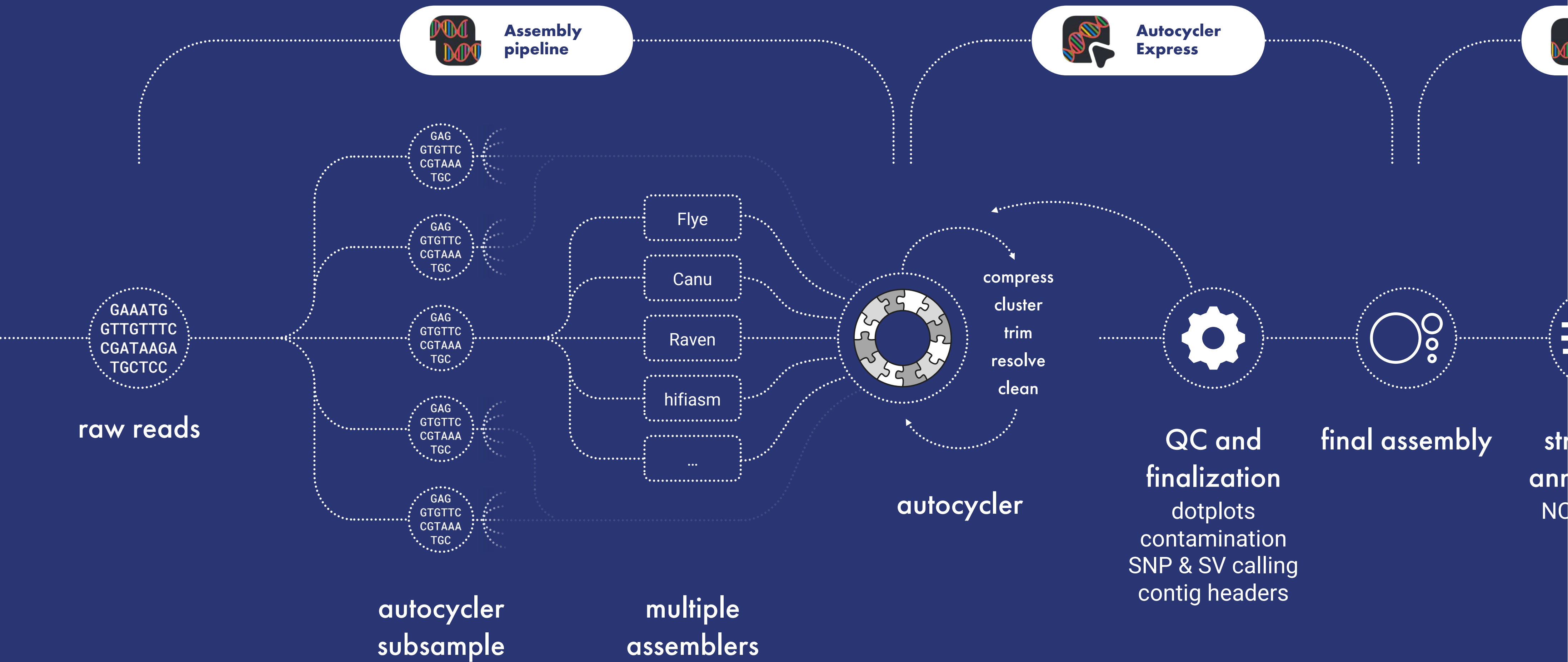


Human supervision is very slow.

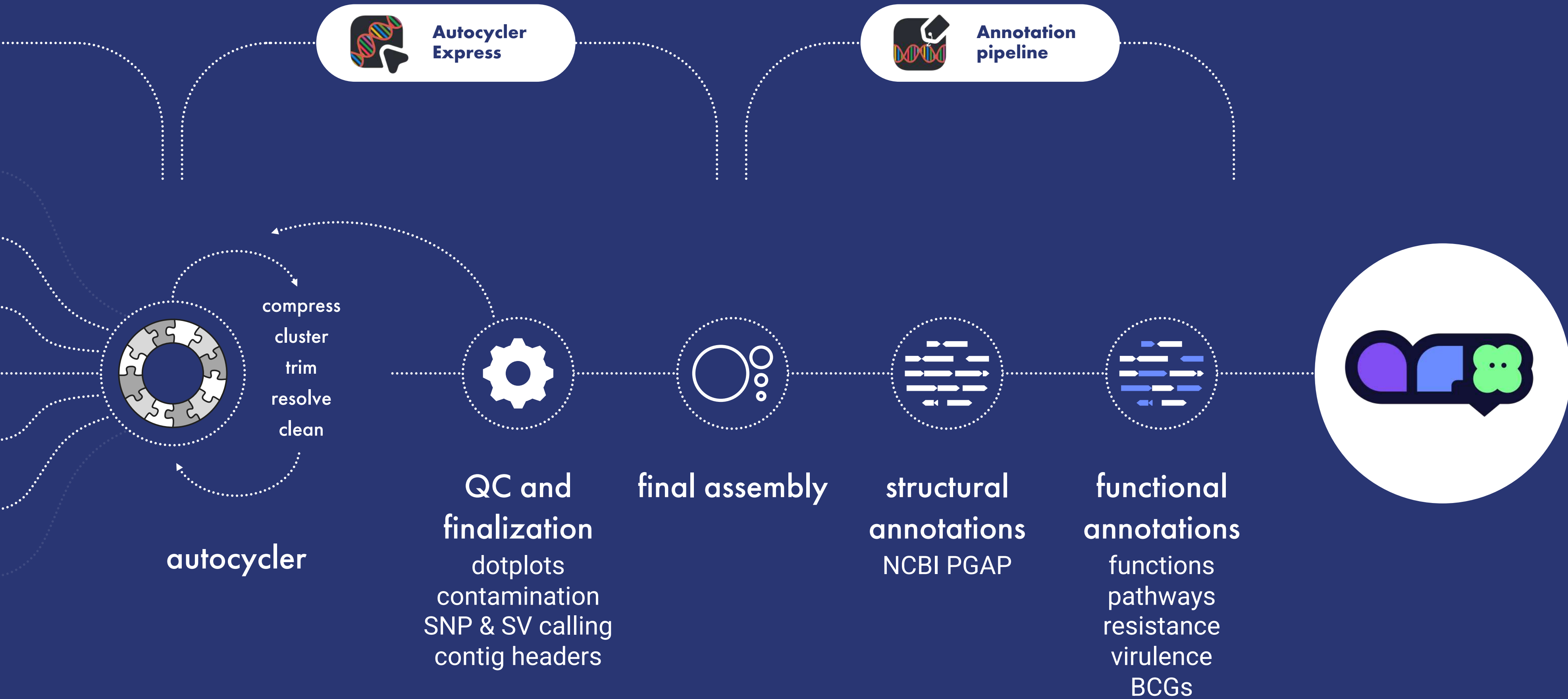
Pipeline.



Pipeline.



Pipeline.



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Autocycler Express.

**Example 1:
Contamination**

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**Example 3:
Linear Plasmid**

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**Example 2:
Missing Plasmids**

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**Example 4:
Targeted Reassembly
of Phages**

Benefit.



High throughput



Gold standard quality



Supervised curation



Connected to Arx

$10^3\times$

31%

100%

75%

Lower error rate

**More plasmids
discovered**

**Of samples
checked for
contamination
and taxonomy**

**Reduction of
processing time**

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

The Big Picture

DOWNSTREAM ANALYSES DEPEND ON THE ASSEMBLY



Flawed foundational genomes can compromise every subsequent functional prediction.

PLASMIDS AND PHAGES REALLY MATTER



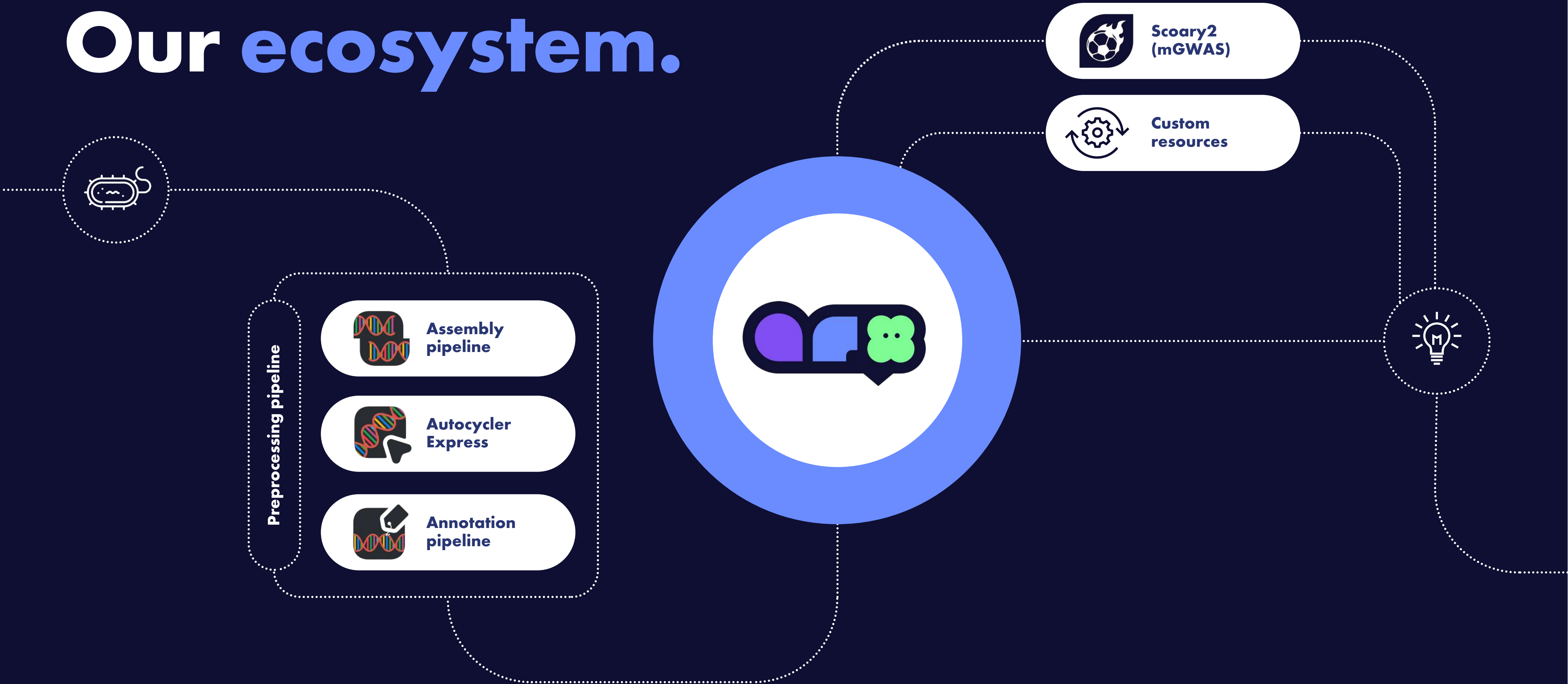
Complete data for each genome for maximum research potential.

GOLD STANDARD QUALITY AT SPEED



Autocycler Express enables curation of 100 genomes in a day and gives high confidence.

Our ecosystem.



The Solution for **data access.**

Questions

Question 1

Which strains carry the target pathway?

Question 2

Which isolate matches this reference genome?

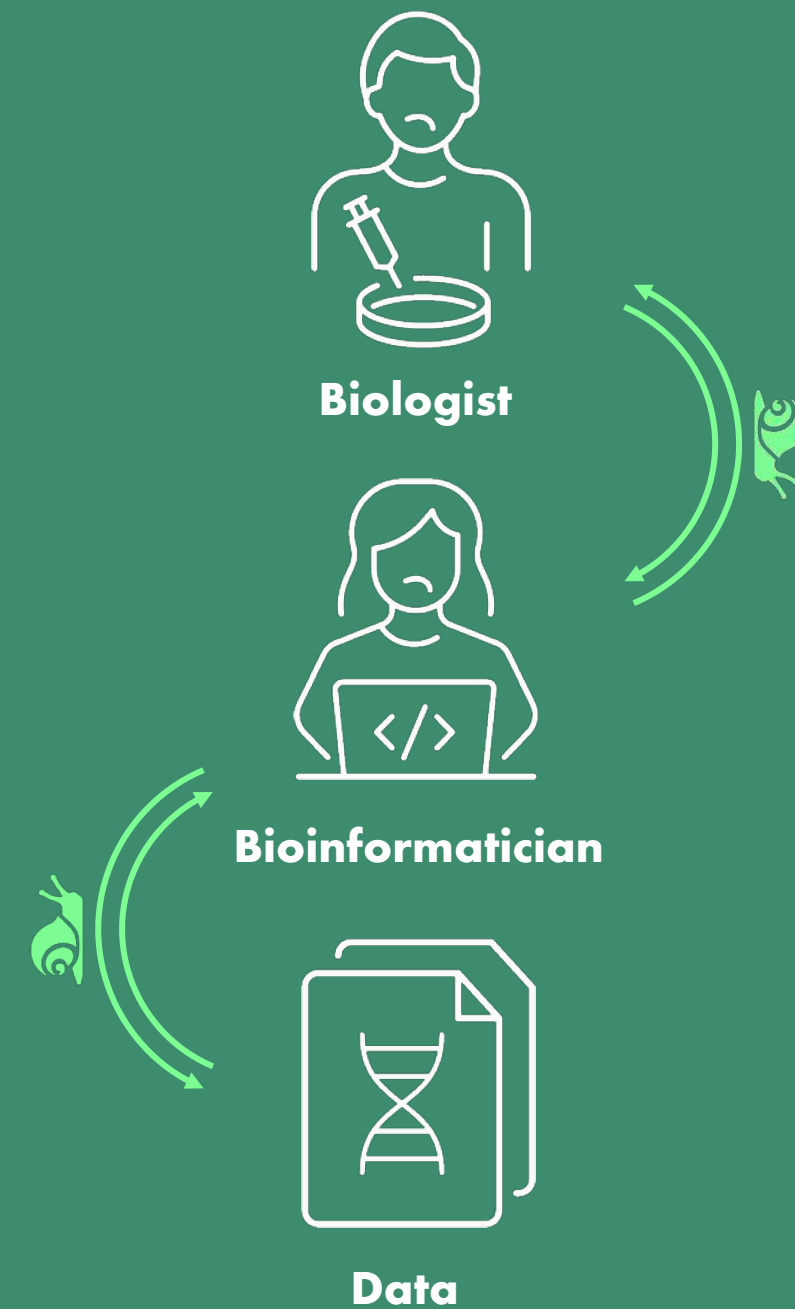
Question 3

Which genes drive this strain's phenotype?

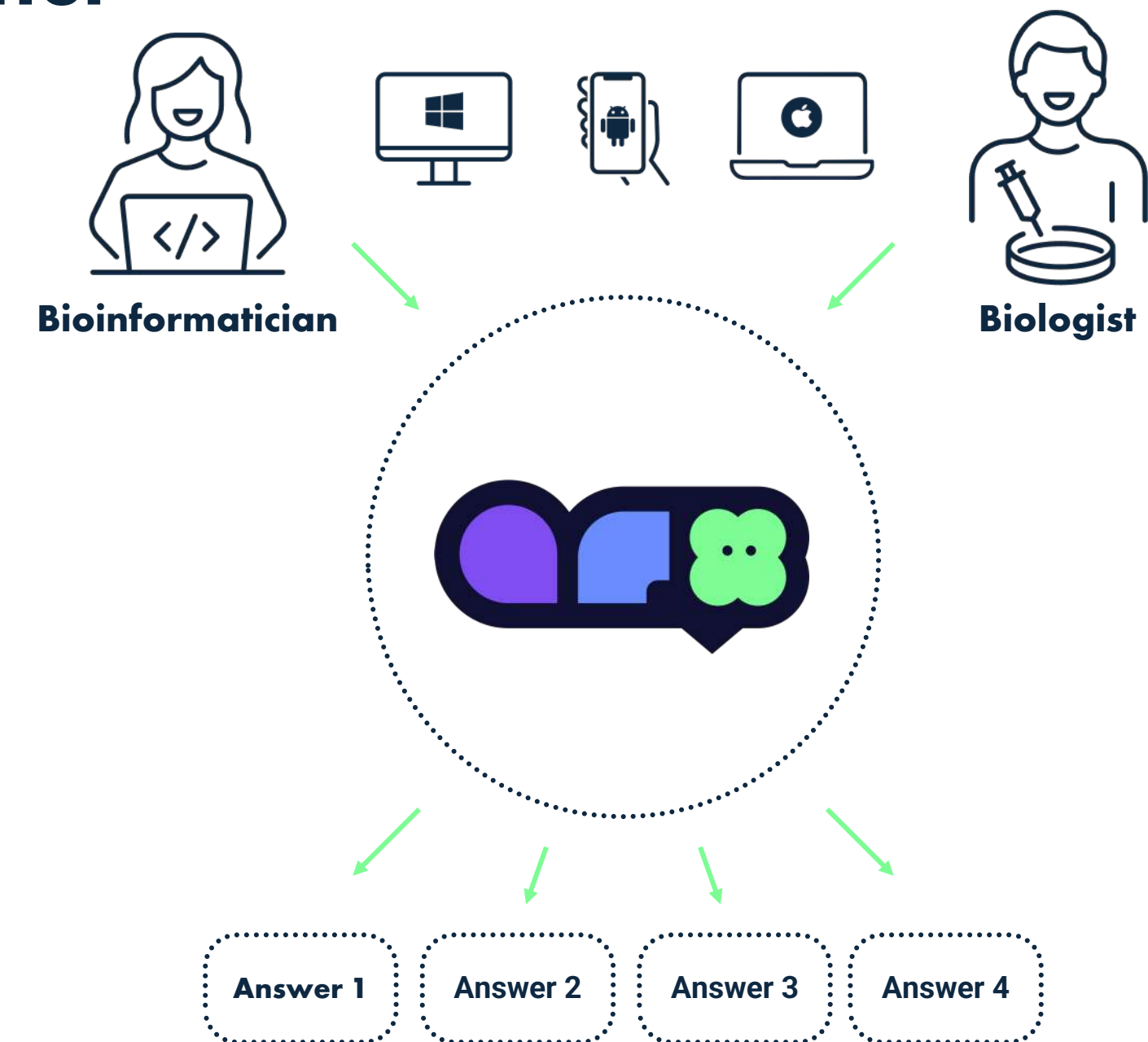
Question 4

Which accessory genes define this clade?

Before



After



The Solution for **data management.**

Before

Data stored locally on **hard disks**.

No overview of available datasets.

Data **scattered** over different groups.

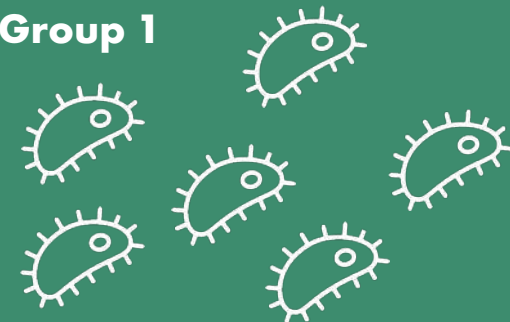
Fosters **siloeing** and protectionism.

No metadata attached to data.

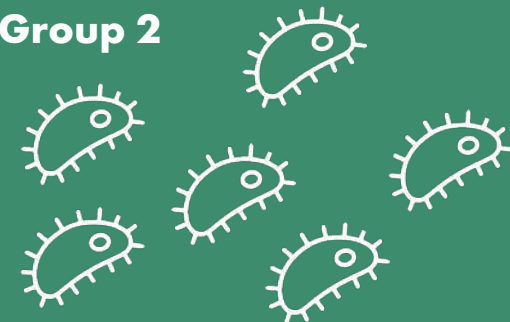
Inconsistent processing, **incompatible data**.

Automated analysis **impossible**.

Group 1



Group 2



Group 3



After

Data **centrally organized** in folder structure.

Comprehensive **overview** of the available data.

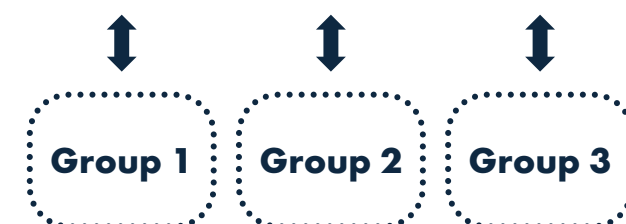
Data **available** to everyone all the time.

Enables easy **sharing** of data across groups.

Metadata **prevents costly mistakes**.

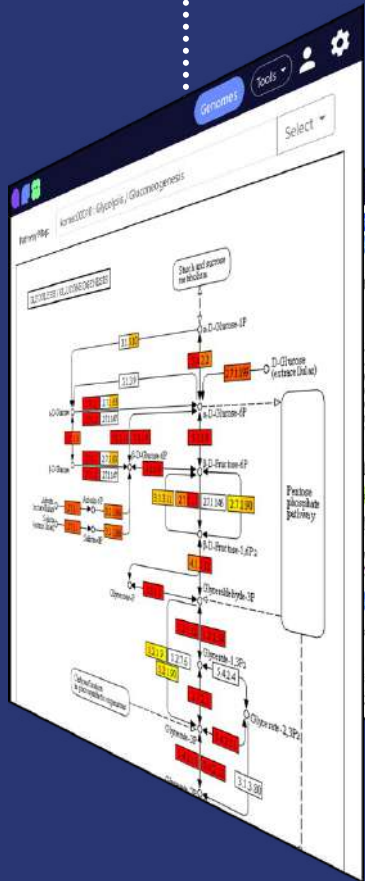
Consistent processing, **compatible data**.

Fast and simple data mining through Arx.

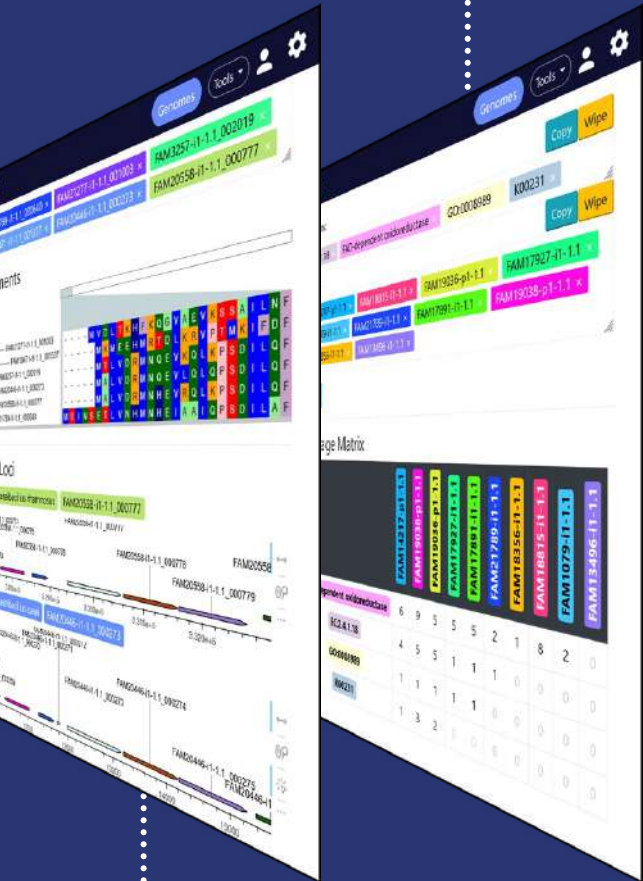


Arx software.

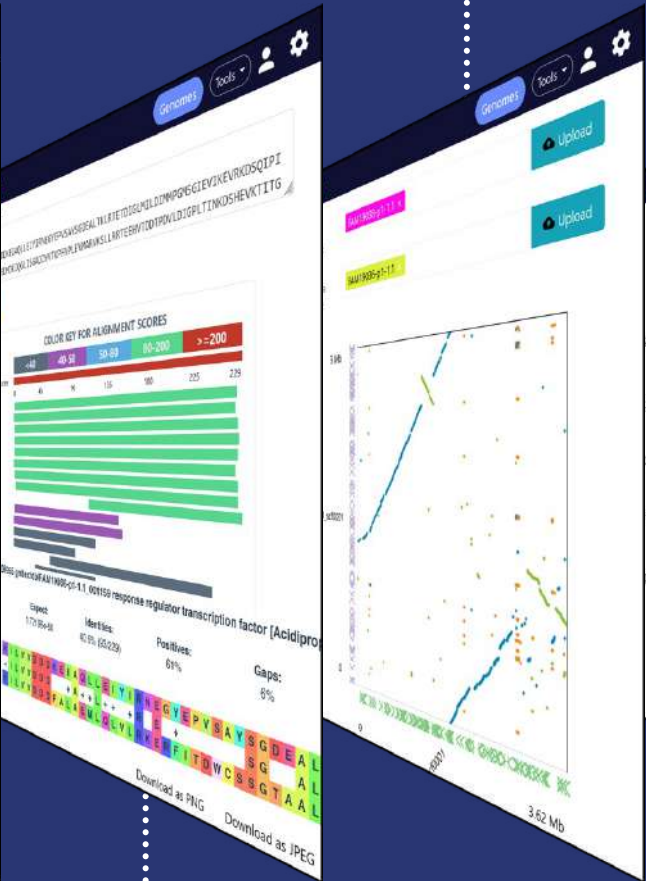
Pathways



Annotation search



Dotplot



Gene trait matching



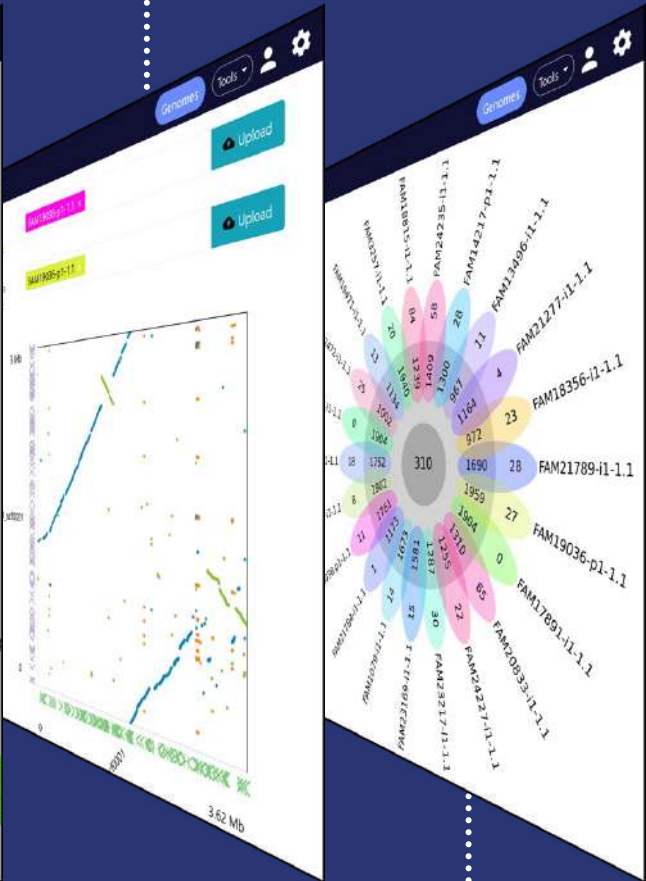
Gene comparison



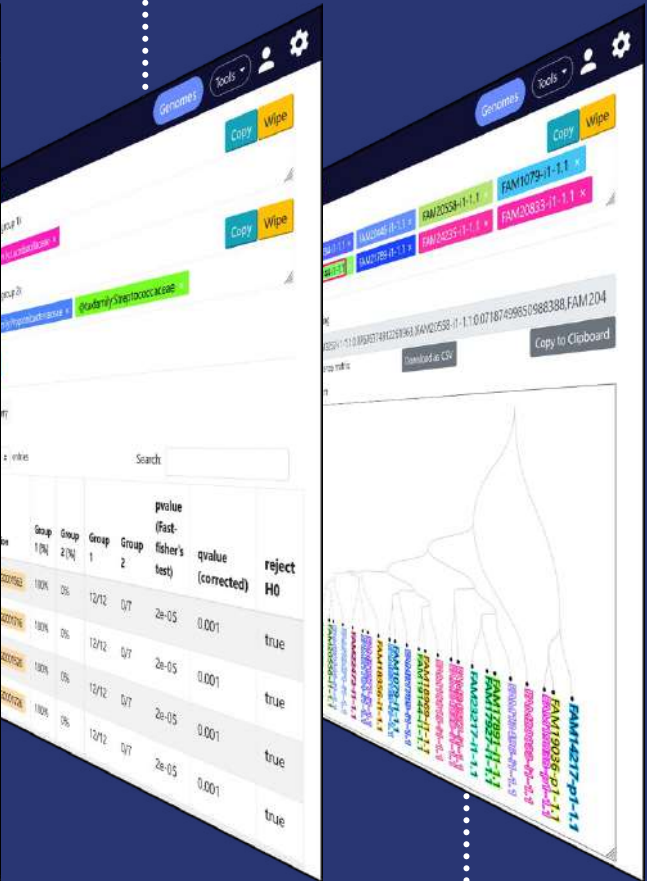
BLAST



Flower plot



Phylogenetic trees

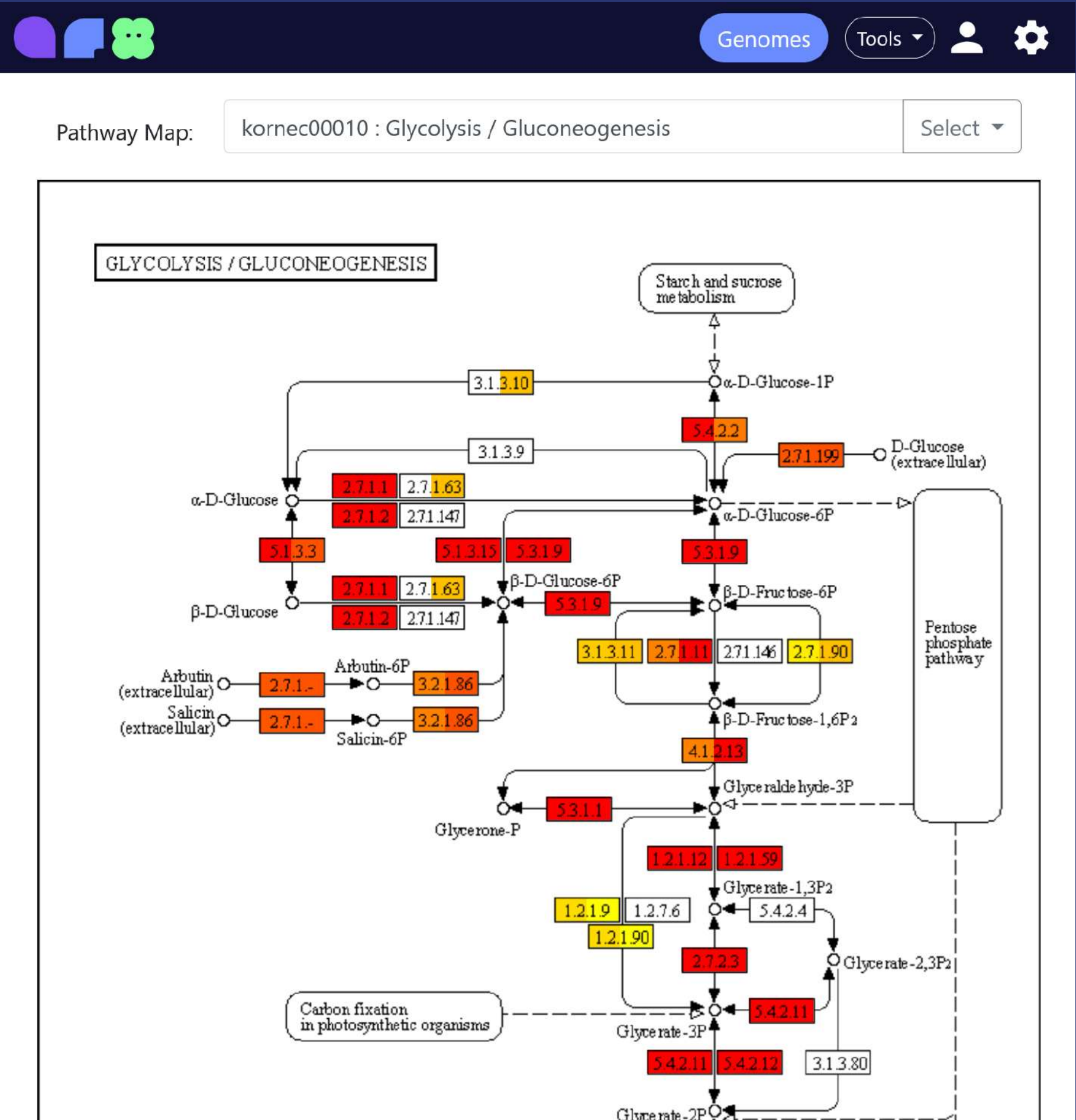


Feature: Pathways



Get instant access to the
metabolic capabilities of your
microbes.

Compare single strains or
groups of microbes concerning
metabolic pathways.

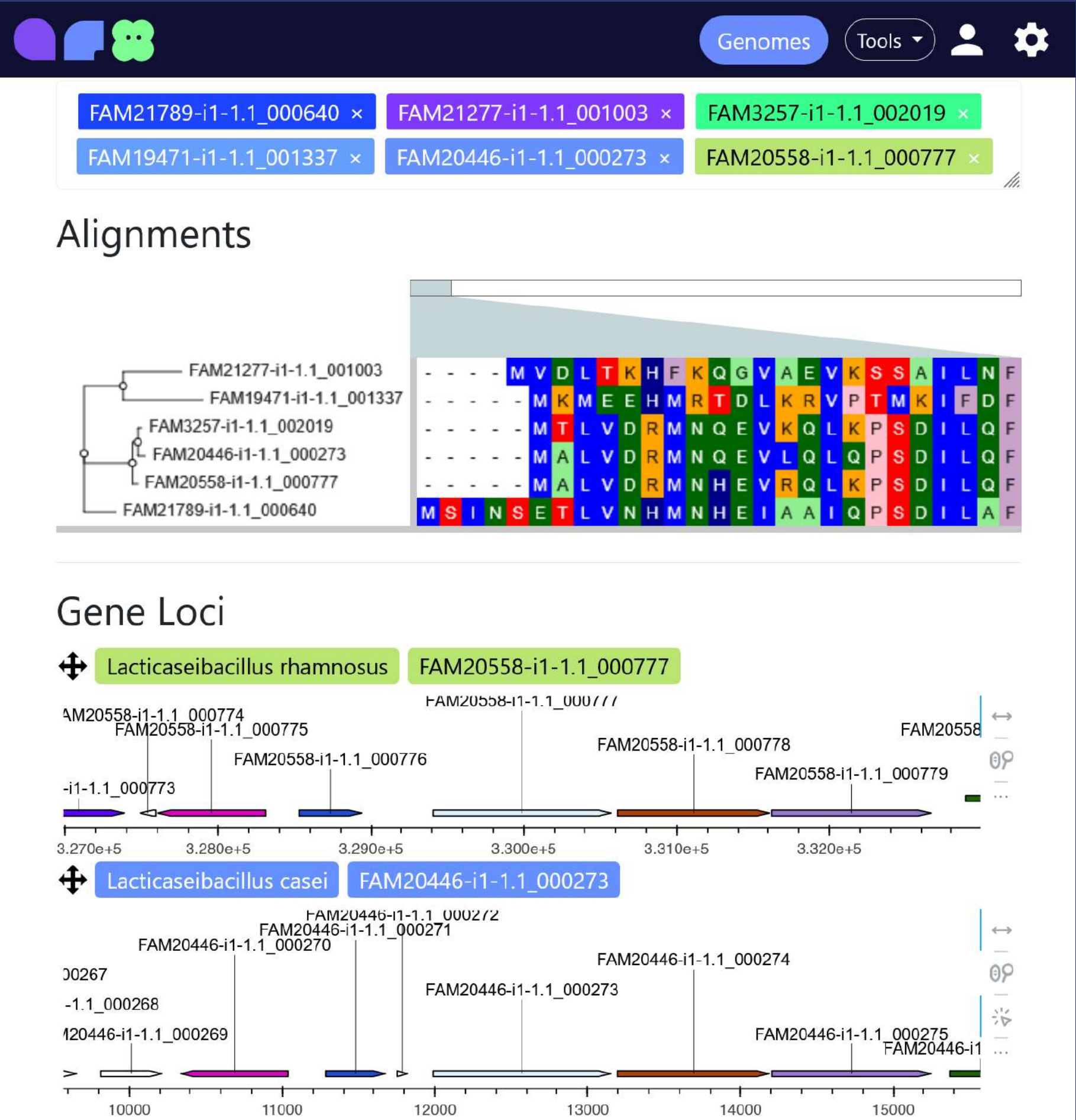


Feature: Gene comparison



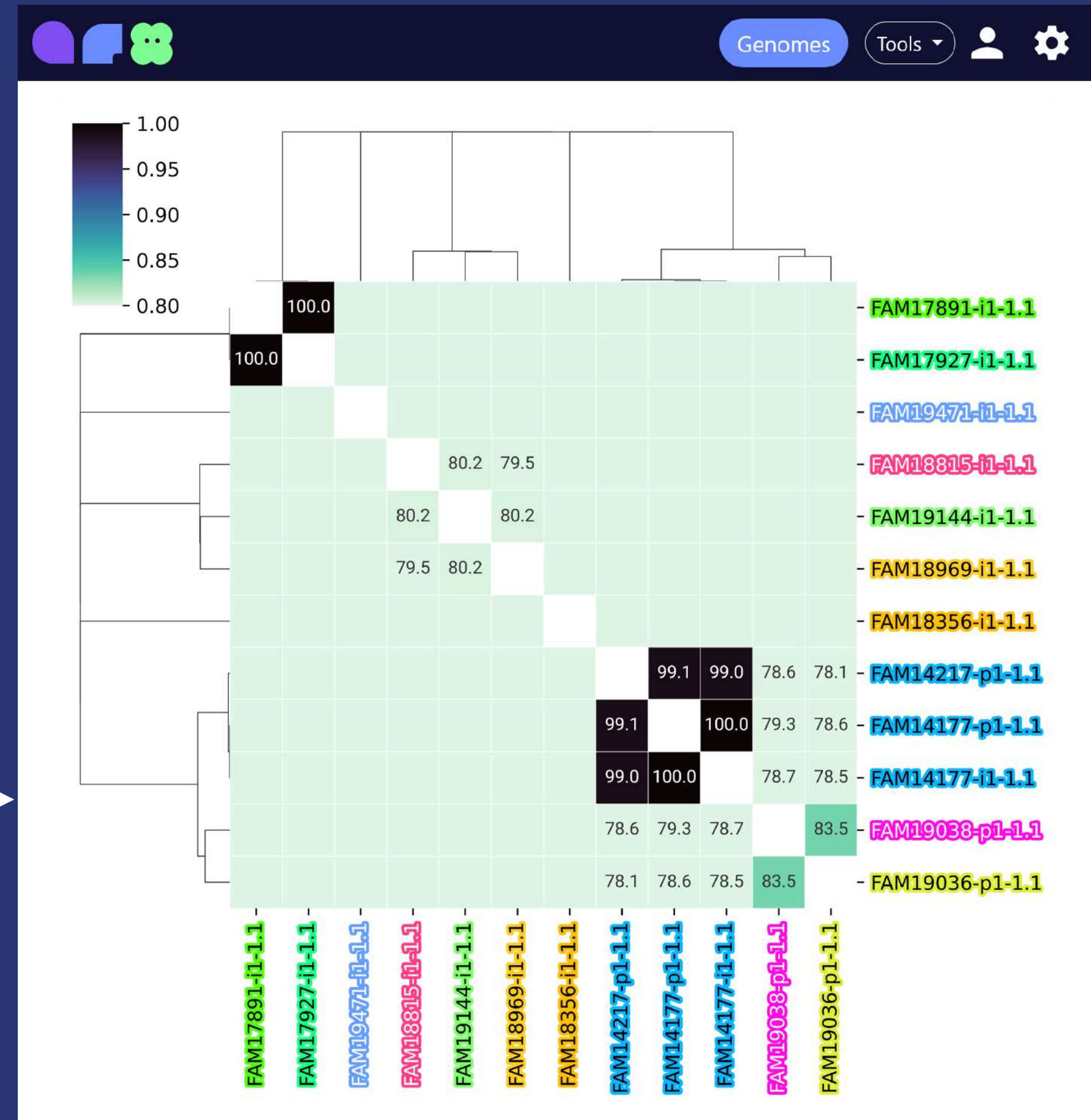
Compare the DNA and protein
sequences of genes.

Explore the genomic
neighborhood.

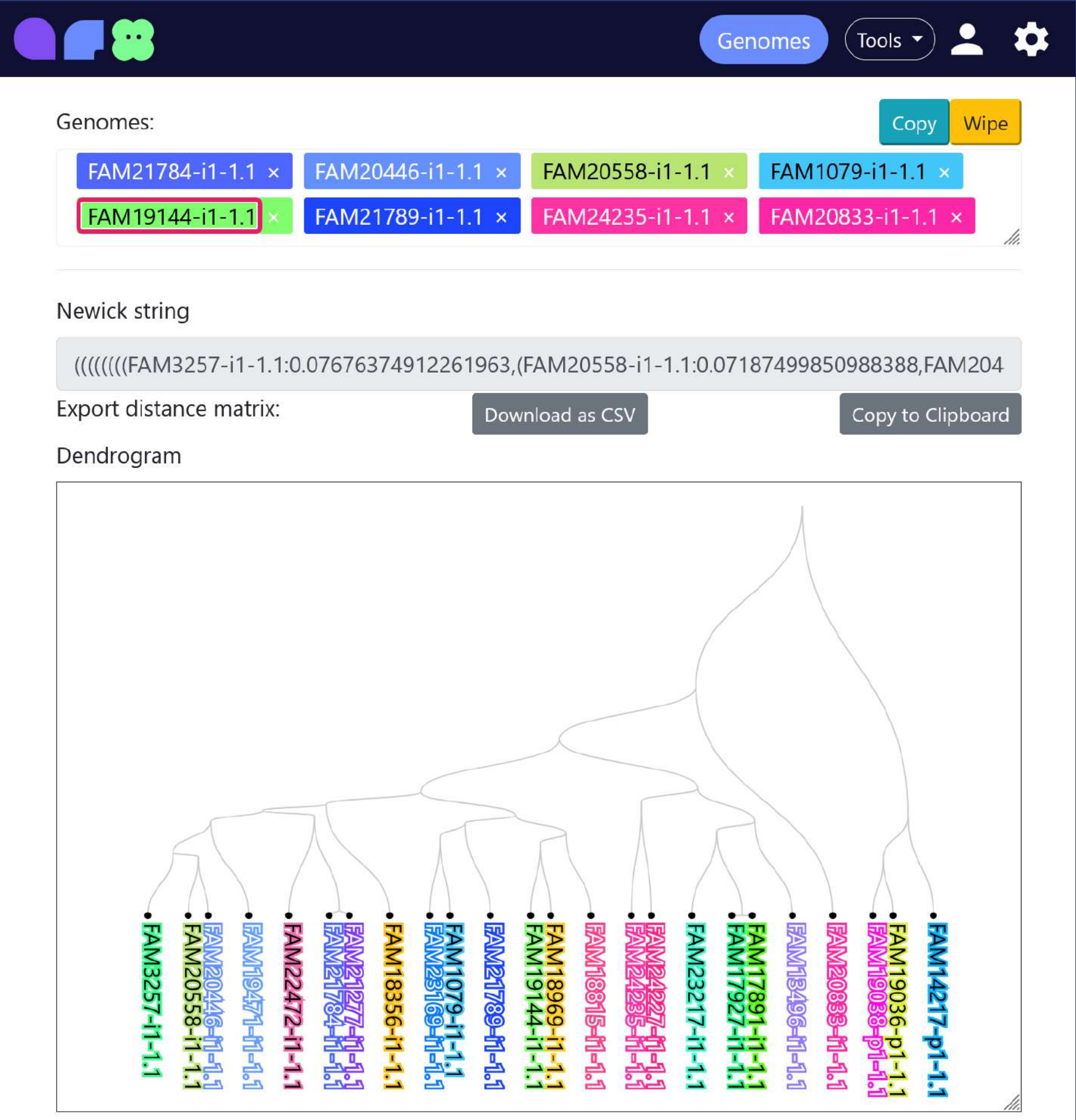
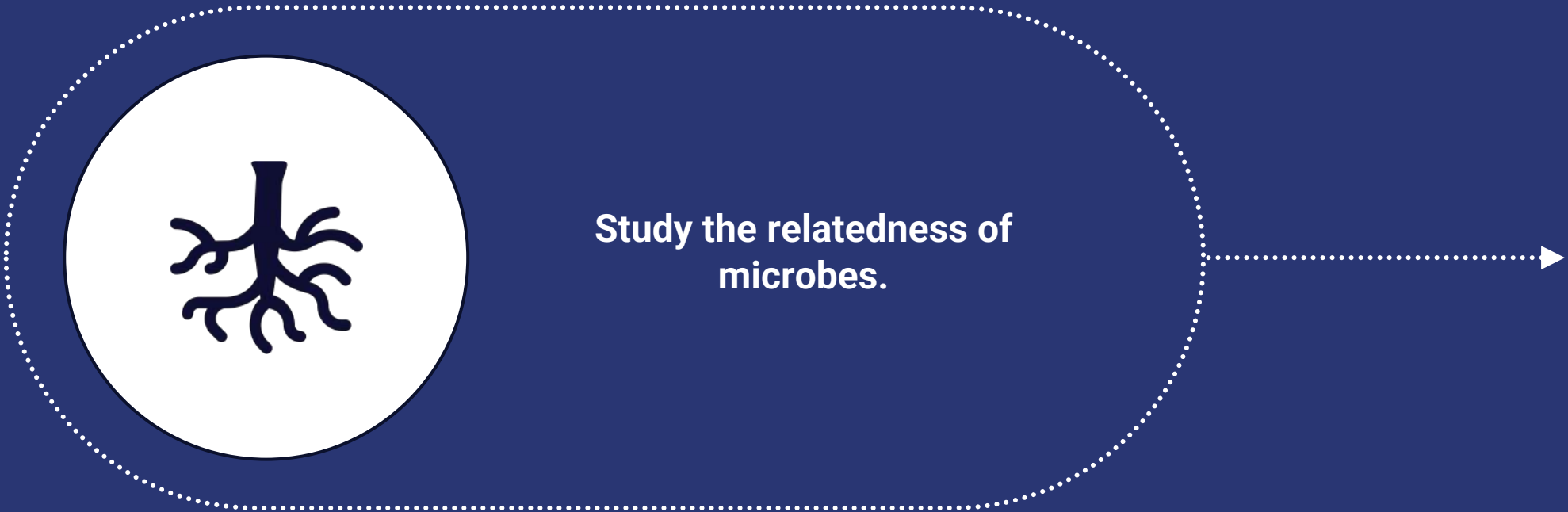


Compute Average Nucleotide Identity (ANI) using different algorithms, visualize as interactive similarity matrix.

The diagram illustrates a workflow for computing ANI. It starts with a circular icon containing a grid pattern, representing a similarity matrix. An arrow points from this icon to a rectangular box containing the text: 'Compute Average Nucleotide Identity (ANI) using different algorithms, visualize as interactive similarity matrix.' A dashed arrow points from the right side of this box to the next step in the process.



Feature: Trees



Feature: Annotation search



Genomes

Tools

Annotations:

EC:2.4.1.18

FAD-dependent oxidoreductase

GO:0008989

K00231

Copy

Wipe

Genomes:

FAM14217-p1-1.1

FAM18815-i1-1.1

FAM19036-p1-1.1

FAM17927-i1-1.1

FAM1079-i1-1.1

FAM21789-i1-1.1

FAM17891-i1-1.1

FAM19038-p1-1.1

FAM18356-i1-1.1

FAM13496-i1-1.1

Copy

Wipe

Submit

Coverage Matrix

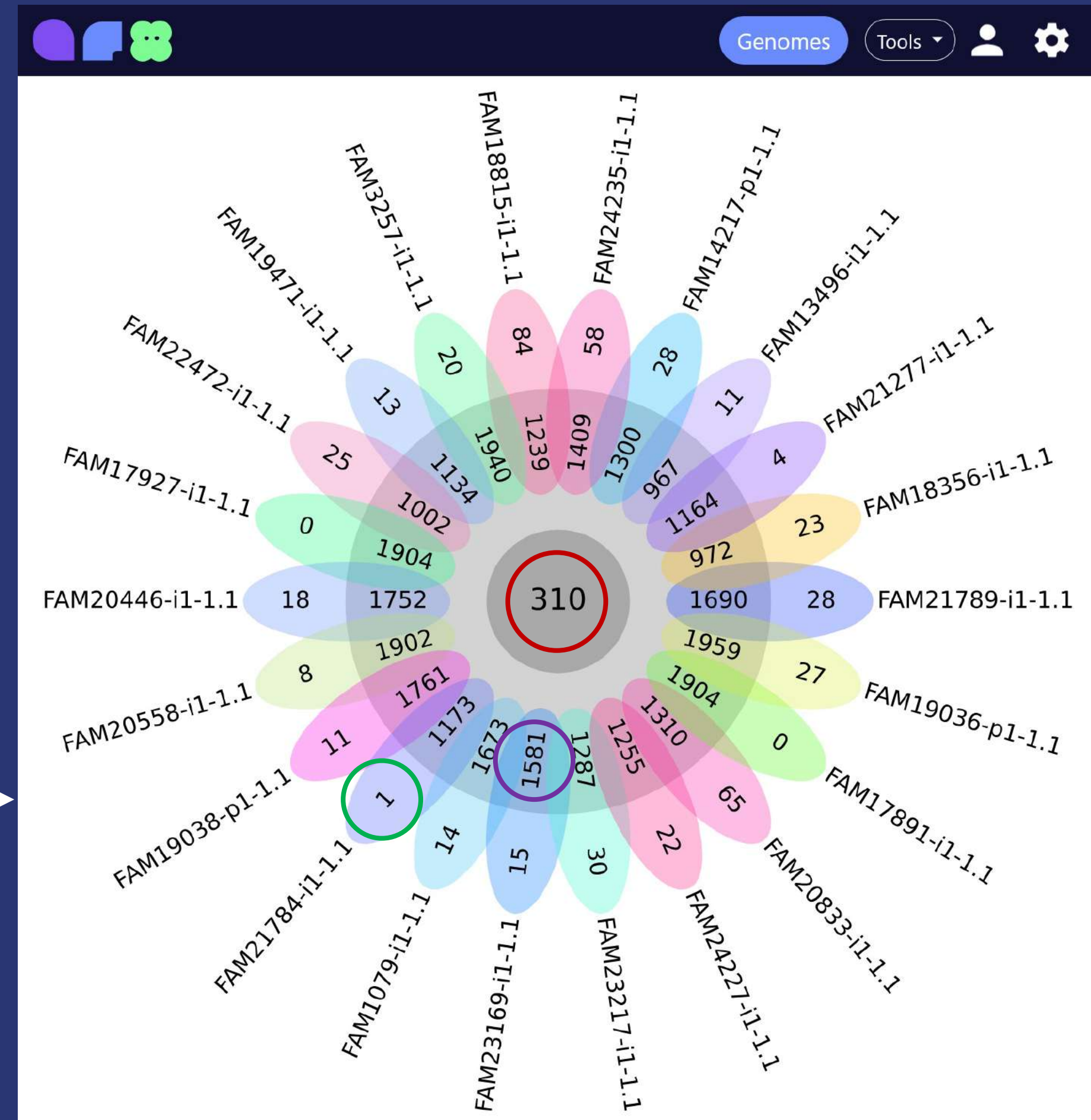
	FAM14217-p1-1.1	FAM19038-p1-1.1	FAM19036-p1-1.1	FAM17927-i1-1.1	FAM17891-i1-1.1	FAM21789-i1-1.1	FAM18356-i1-1.1	FAM18815-i1-1.1	FAM1079-i1-1.1	FAM13496-i1-1.1
FAD-dependent oxidoreductase	6	9	5	5	5	2	1	8	2	0
EC:2.4.1.18	4	5	5	1	1	1	0	0	0	0
GO:0008989	1	1	1	1	1	0	0	0	0	0
K00231	1	3	2	0	0	0	0	0	0	0

Feature: Dotplot



Compare the structure of
genomes.
Discover repetitive regions and
structural variation.





Feature: Gene trait matching



Find candidate genes that may explain certain traits.

Genomes (group 1):

@taxfamily:Lactobacillaceae x

CopyWipe

Genomes (group 2):

@taxfamily:Propionibacteriaceae x @taxfamily:Streptococcaceae x

CopyWipe

Submit

Show query

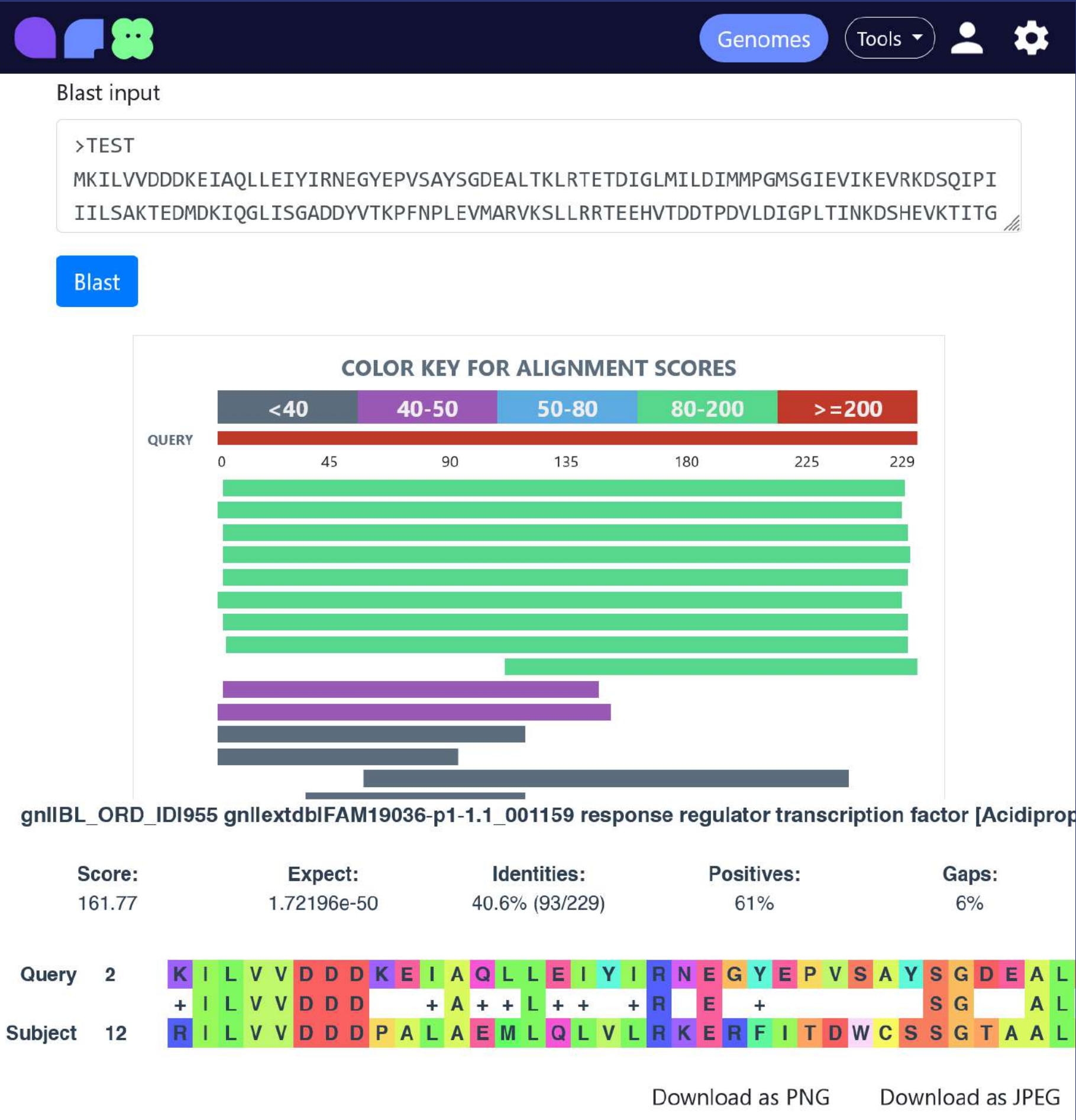
Show 25 entries Search:

Annotation	Group 1 [%]	Group 2 [%]	Group 1	Group 2	pvalue (Fast-fisher's test)	qvalue (corrected)	reject H0
N0.HOG0001563	100%	0%	12/12	0/7	2e-05	0.001	true
N0.HOG0001716	100%	0%	12/12	0/7	2e-05	0.001	true
N0.HOG0001520	100%	0%	12/12	0/7	2e-05	0.001	true
N0.HOG0001726	100%	0%	12/12	0/7	2e-05	0.001	true

Feature: BLAST



Search for genes based on a
nucleotide/protein sequence
using the NCBI BLAST
algorithm.



The Big Picture

DATA MANAGEMENT FOR THE LONG TERM



Arx manages user permissions and stores the genomic data in a simple and transparent folder structure.

ENABLES DIRECT ACCESS TO GENOMIC DATA



Enables people to quickly and autonomously answer many questions.

MAXIMIZE THE VALUE OF THE DIGITAL ASSETS



Arx leads to a qualitative shift in how people interact with the strain collection.

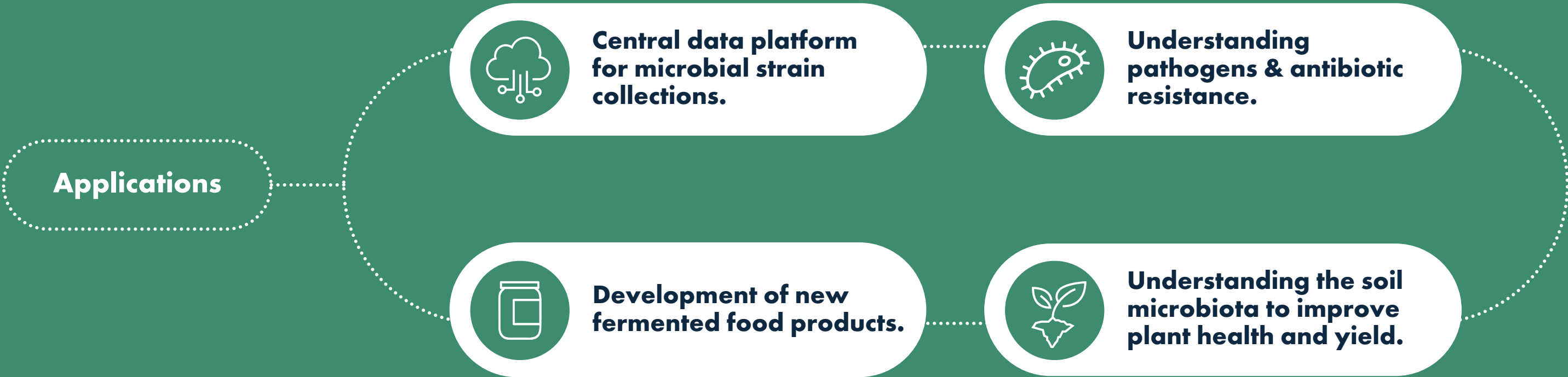
Try out our demo server.



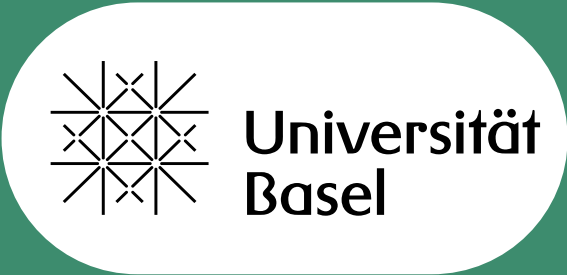
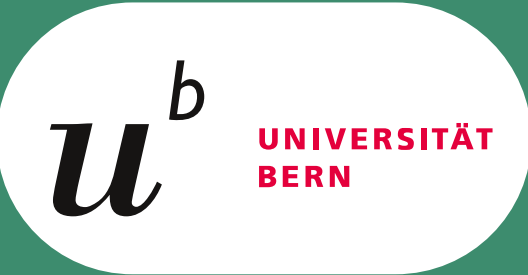
Open **demo.abrinca.com**
to experience Arx, your
microbial genome center.



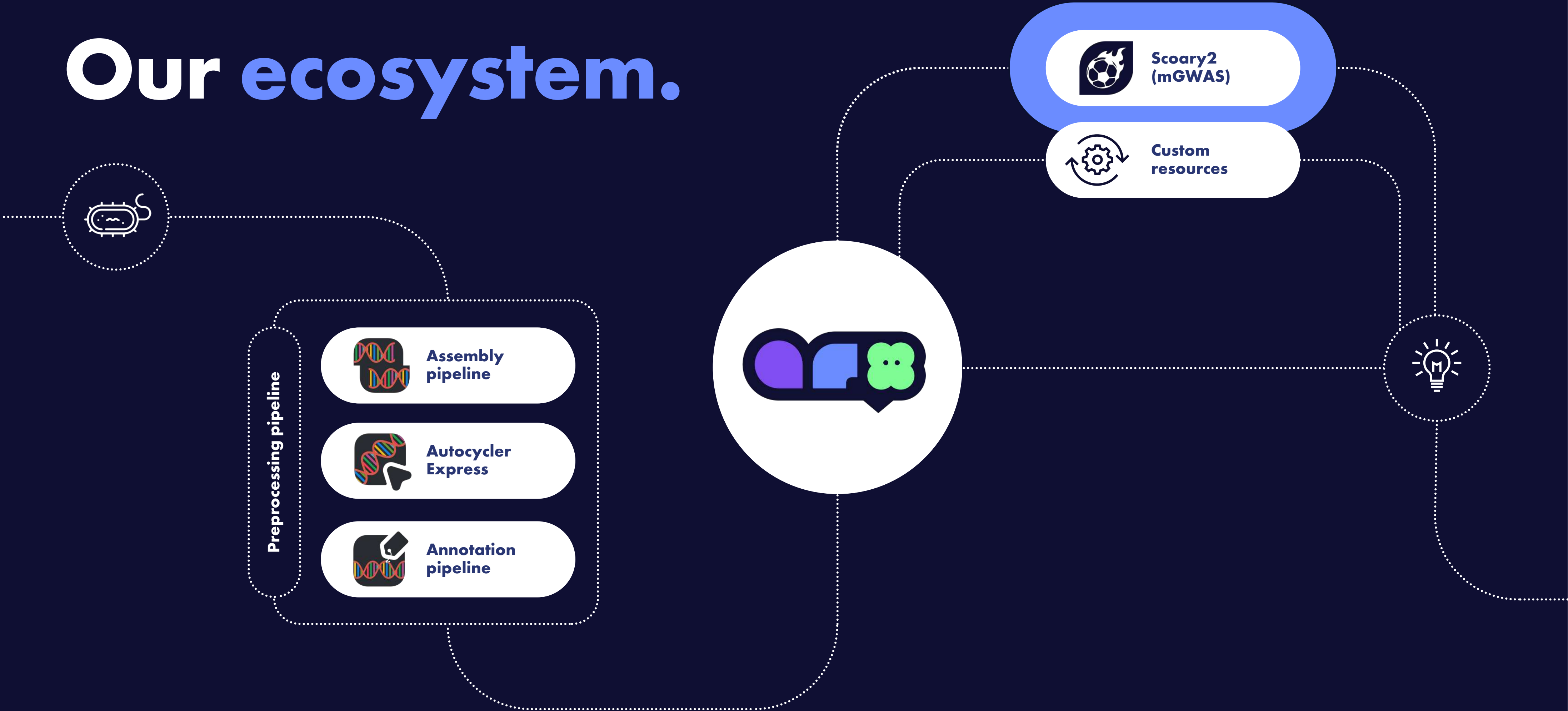
Users.



Current Users



Our ecosystem.



Scoary2.

Only ~60 metabolites identified!
~4,000 metabolites

40-60% of genes unknown
~10,358 genes

182 yogurts
made with different bacteria

	Cpd 1	Cpd 2	Cpd 3	Cpd 4
	6.0	0.2	3.1	8.0
	2.8	1.8	3.2	1.4
	6.9	2.0	9.0	1.1
	1.4	2.2	6.7	7.8
	6.1	4.8	7.4	8.8
	6.0	0.2	3.1	8.0

Gene 1	Gene 2	Gene 3	Gene 4
1	0	0	1
0	0	1	1
1	0	0	1
1	1	1	1
1	0	1	0
0	0	0	0



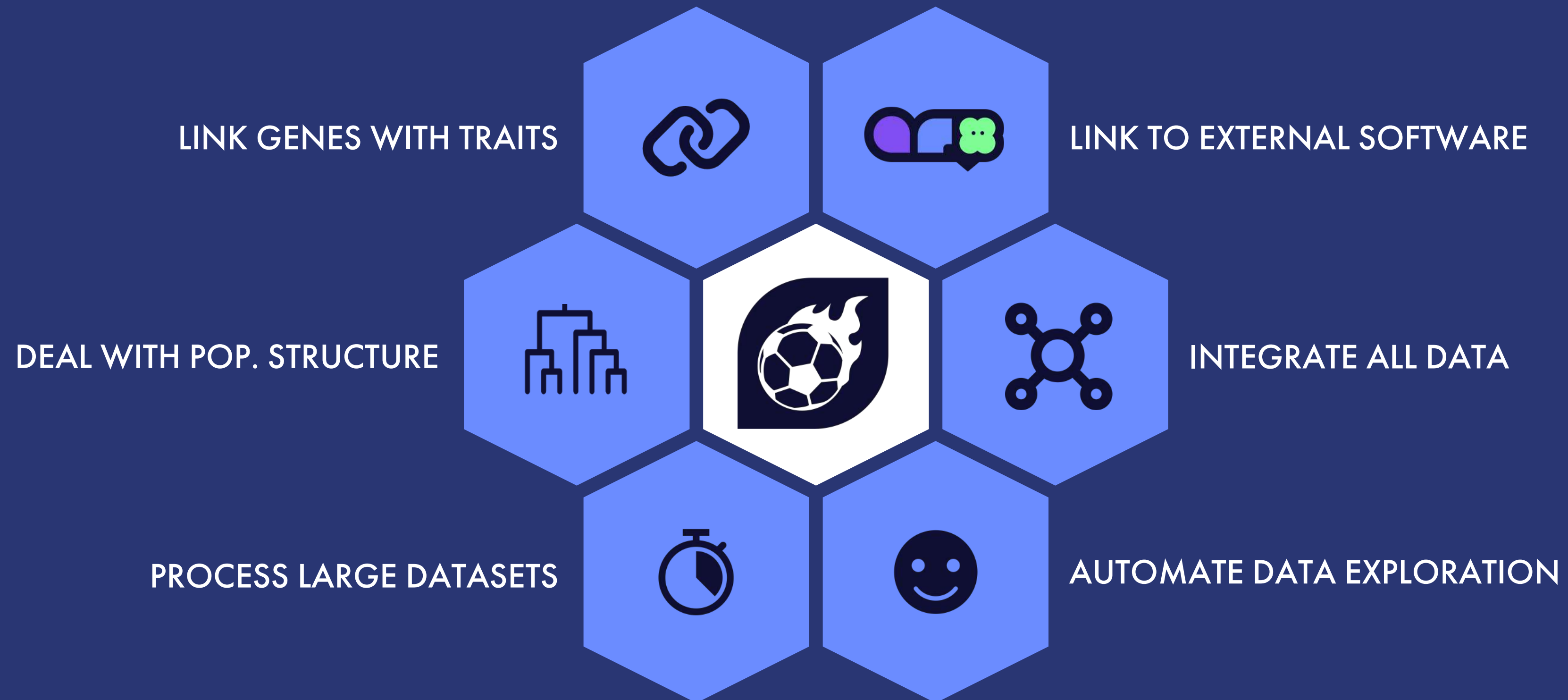
Strong confounder!

Goal: “Link the genes with the metabolites!”

Original Scoary.



New Scoary2.



**Scoary2 is the first software that makes
the study of large phenotypic datasets using mGWAS feasible.**

The Big Picture

**Helps strain collections discover new links
between phenotypes and genes.**



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Questions & **answers.**



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TOM HOWZE

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