

A NGS Data Management and Analytics Platform

MOVING YOUR RESEARCH FROM ANALYSIS TO DATA INTERPRETATION



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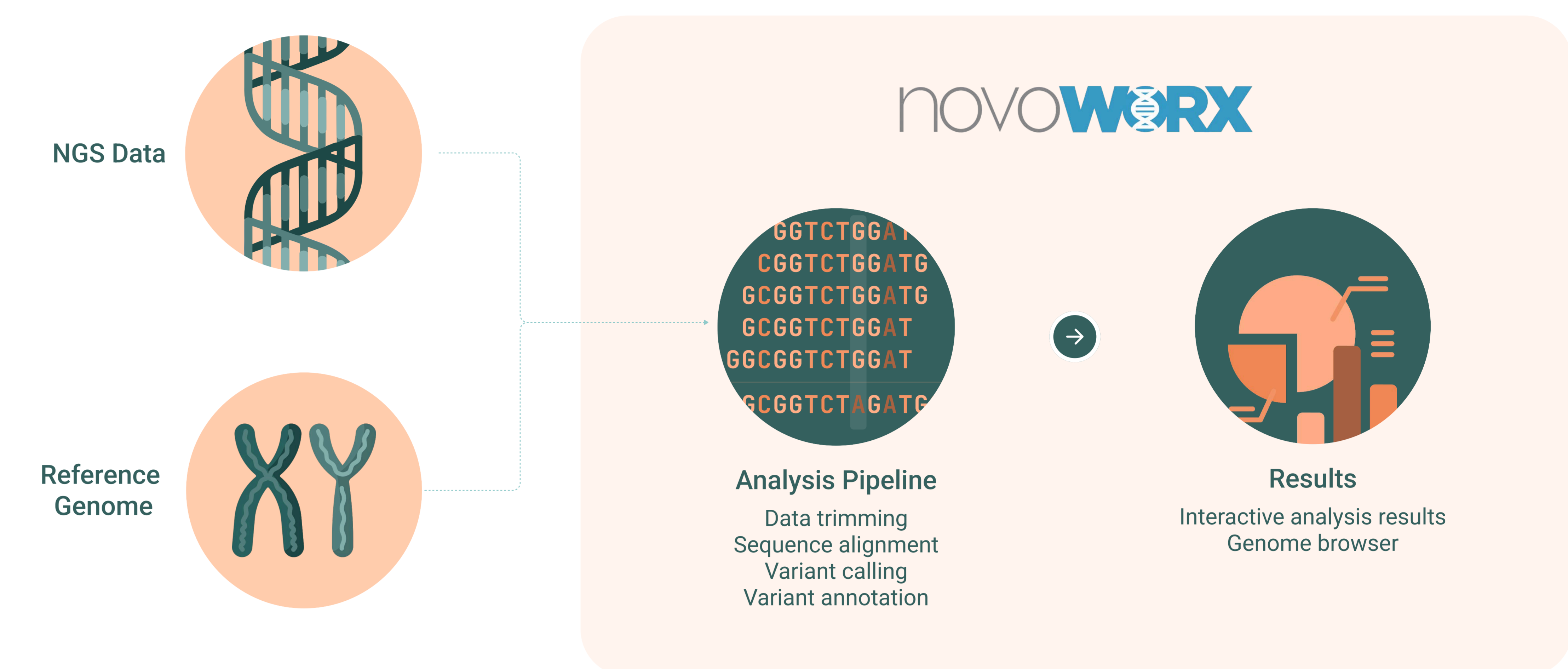
INTRODUCING NOVOWORX

From NGS Data to Discovery

As NGS continues to be one of the most popular tools in molecular biology, NGS data analysis is at the heart of making sense of your big data. Running complex bioinformatics algorithm might take away a big chunk of your time causing unnecessary delays in research progress. Here's the good news, we have a smart solution for you.

Introducing novoWorx, a Next Generation Sequencing data management and analytics platform. A comprehensive multi proprietary platform to accelerate your research by simplifying analysis using sophisticated, fully automated solutions powered by the latest technologies to handle extensive, large-scale data processing. The platform uses the best practice in running millions of reads to provide clear insights from your NGS data to drive your research further.

Why novoWorx?



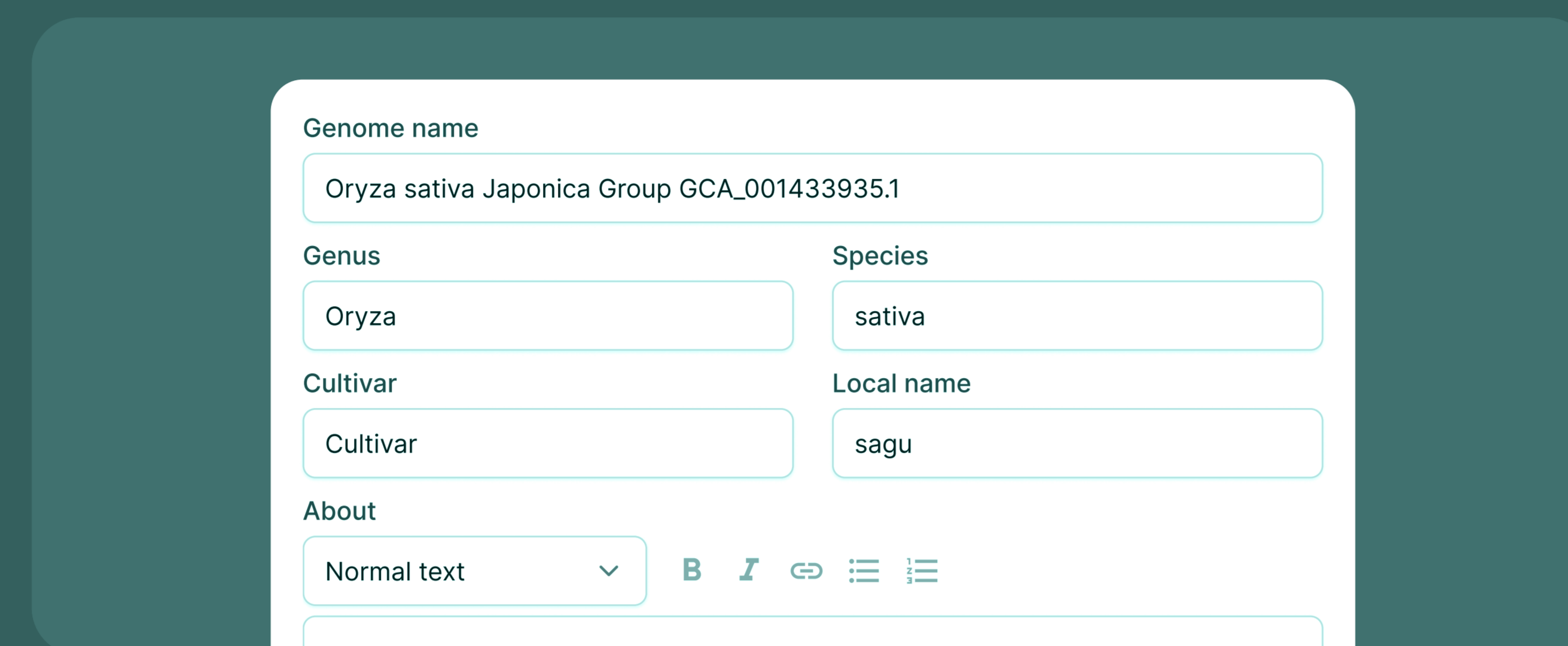
- 01 Unique Capabilities.** The only commercially available tool that offers embedded novoAlign™ and novoSort™ programs for high-throughput bioinformatics analysis.
- 02 Modular and Flexible.** Utilize ready-to-use genomics pipelines to quickly and efficiently run analyses with minimal setup.
- 03 User-Friendly Interface.** Easily process large datasets with multiple samples without any programming knowledge.
- 04 Standardized Outputs.** Generate all outputs in standard formats required for downstream and tertiary analysis by other systems.
- 05 Customizable Solutions.** Have the flexibility of integrating custom pipelines tailored to your specific research needs.
- 06 Exceptional Support.** Rely on our comprehensive after-sales support to assist with any questions or issues, to get the most out of our platform.

Genome & data management



Centralised repository

Store and organise all genomic data in a single, secure location.



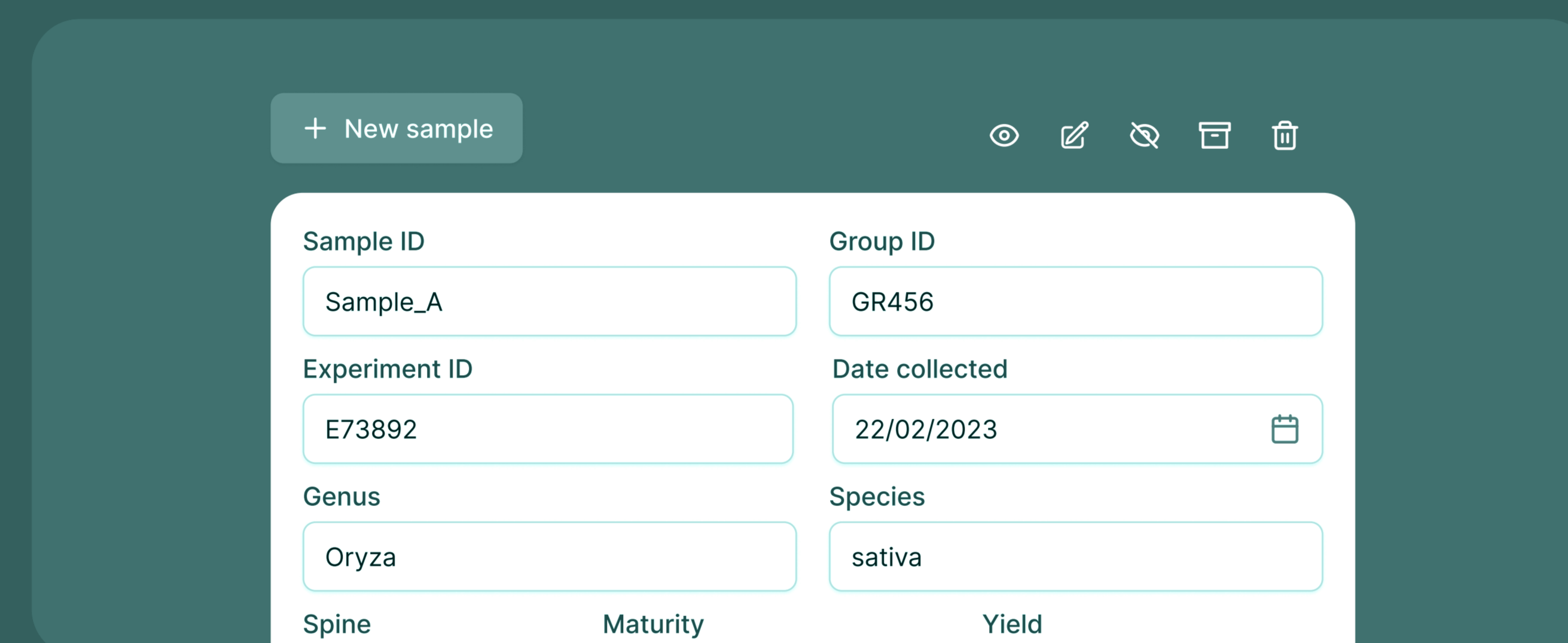
Comprehensive metadata

Attach detailed metadata to each genome, ensuring easy tracking and retrieval.



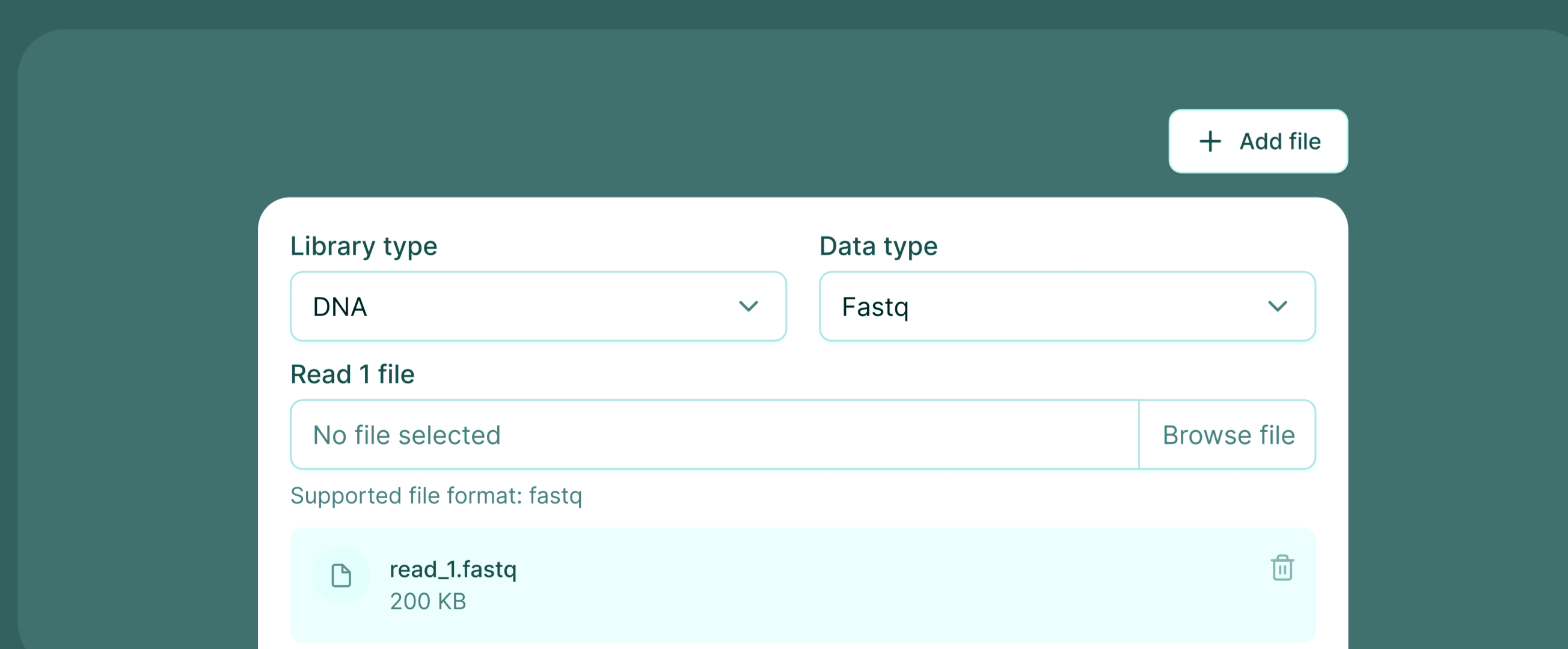
Genome version control

Maintain version histories of genomic data to track changes and updates over time.



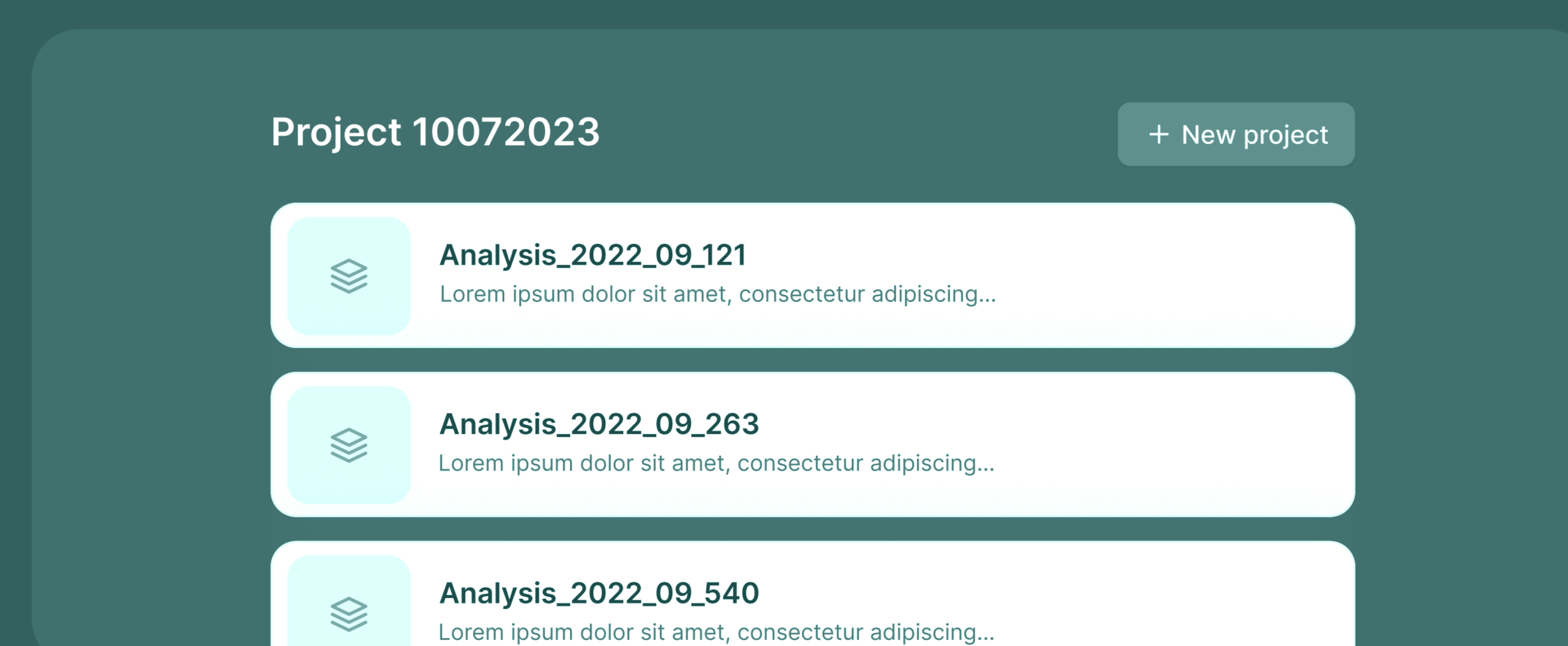
Sample management

Efficiently manage and catalog samples with detailed attributes and conditions.



Data integration

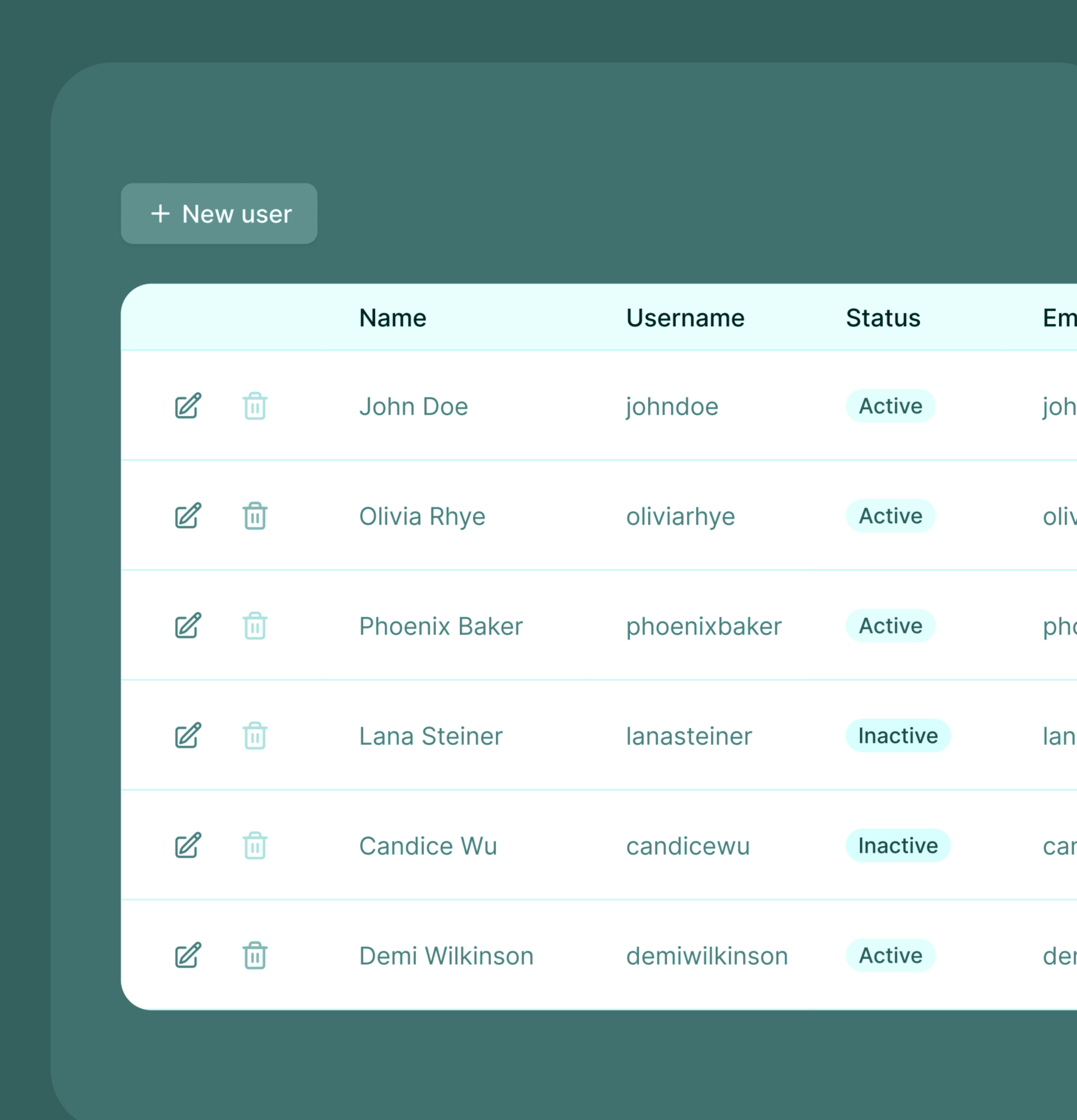
Seamlessly integrate data from multiple sources, including NGS, WGS, and WES datasets.



Project and analysis

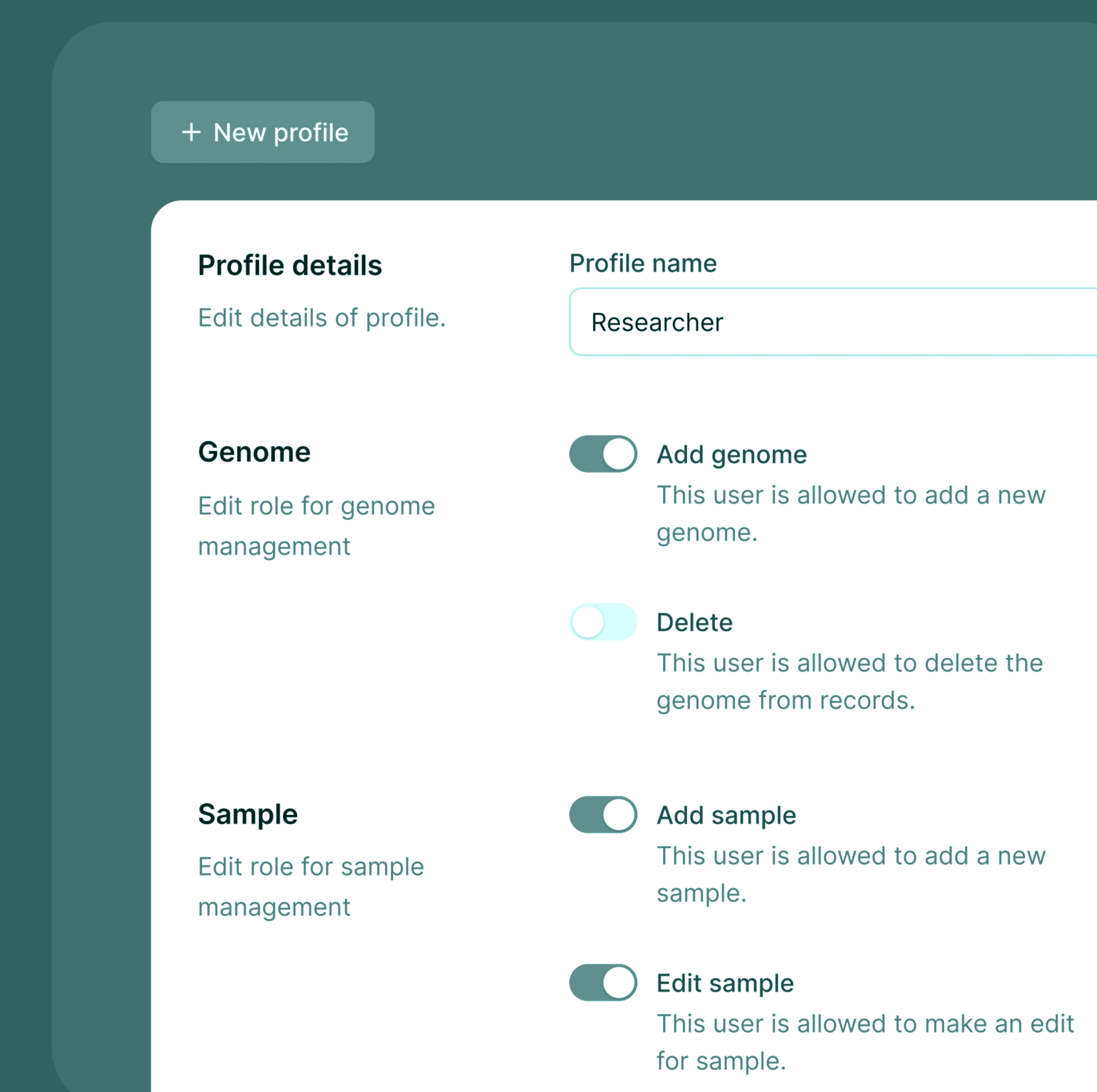
Each project includes a list of user-run analyses, with real-time job status tracking for efficient monitoring and management.

Administration & user management



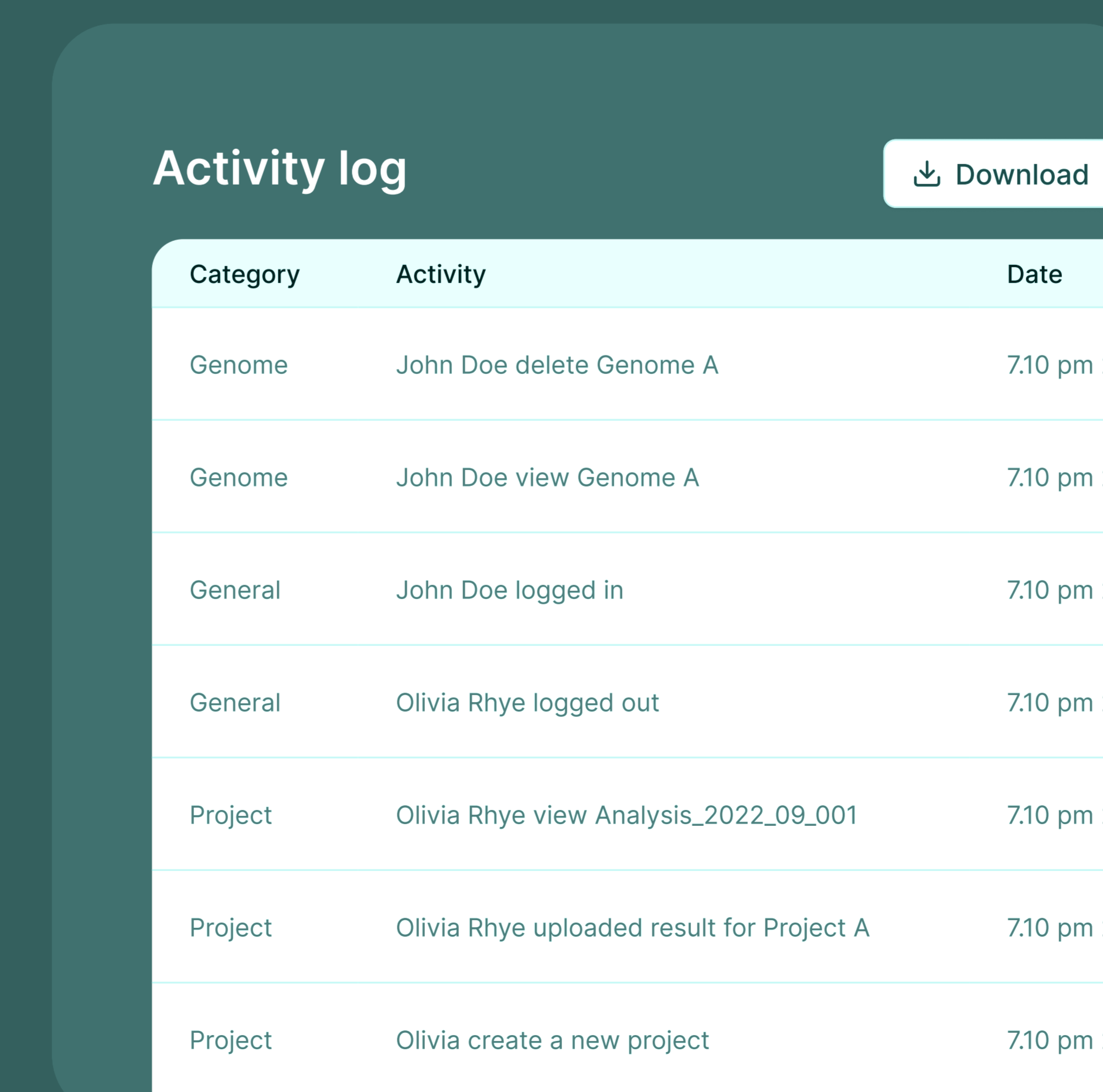
Manage users

- ▶ Easily add new users or update user details like name, email, and role.
- ▶ Remove users securely with confirmation steps to prevent accidental deletions.
- ▶ Manage user status, setting them as active or inactive based on current needs.



Profile management

- ▶ Define and manage various user profiles like Researcher, Visitor, etc.
- ▶ Manage profiles tailored to your organization's requirements.
- ▶ Assign specific roles and permissions to different profiles.



User Activity Logs

- ▶ Track all user activities within the system.
- ▶ Download the activity logs for security and auditing purposes.

Multiple pipelines in one platform

● Single Nucleotide Variants (SNVs) Analysis Pipeline

Identifies mutations or variants (including SNVs, INDELs, and SVs), in WGS, WES, and human amplicon datasets, ensuring precise variant calling for genetic analysis.

● Reference Guided Assembly Pipeline

Performs the assembly of reference-based reads.

● SARS-CoV-2 Screening and Classification Pipeline

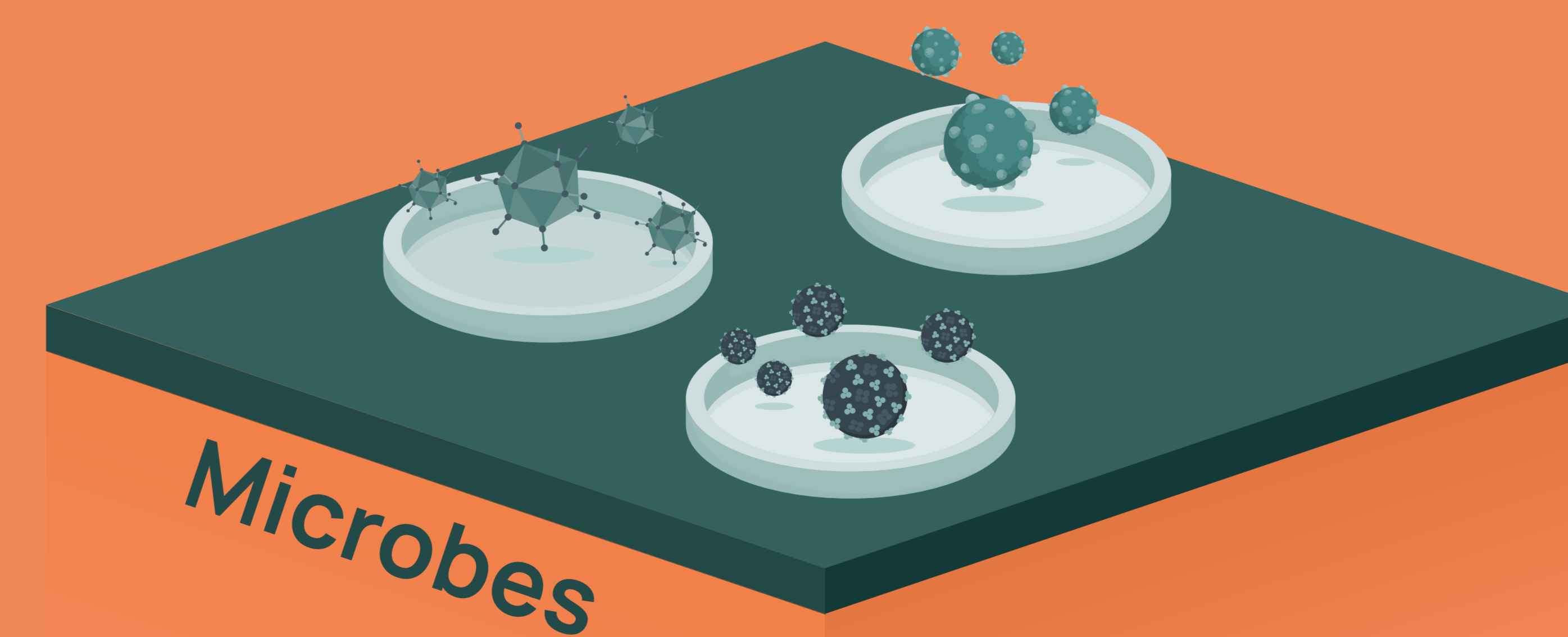
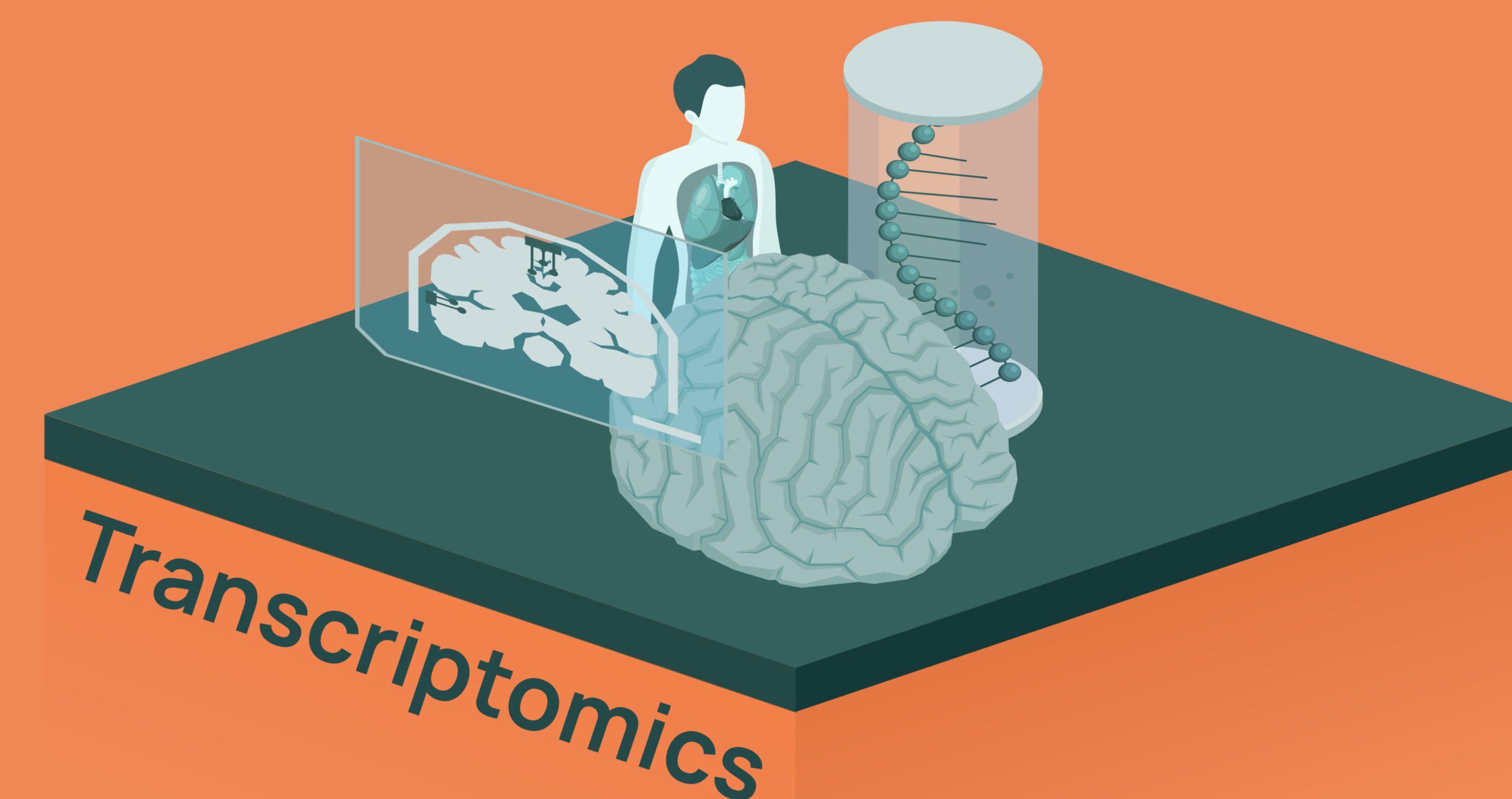
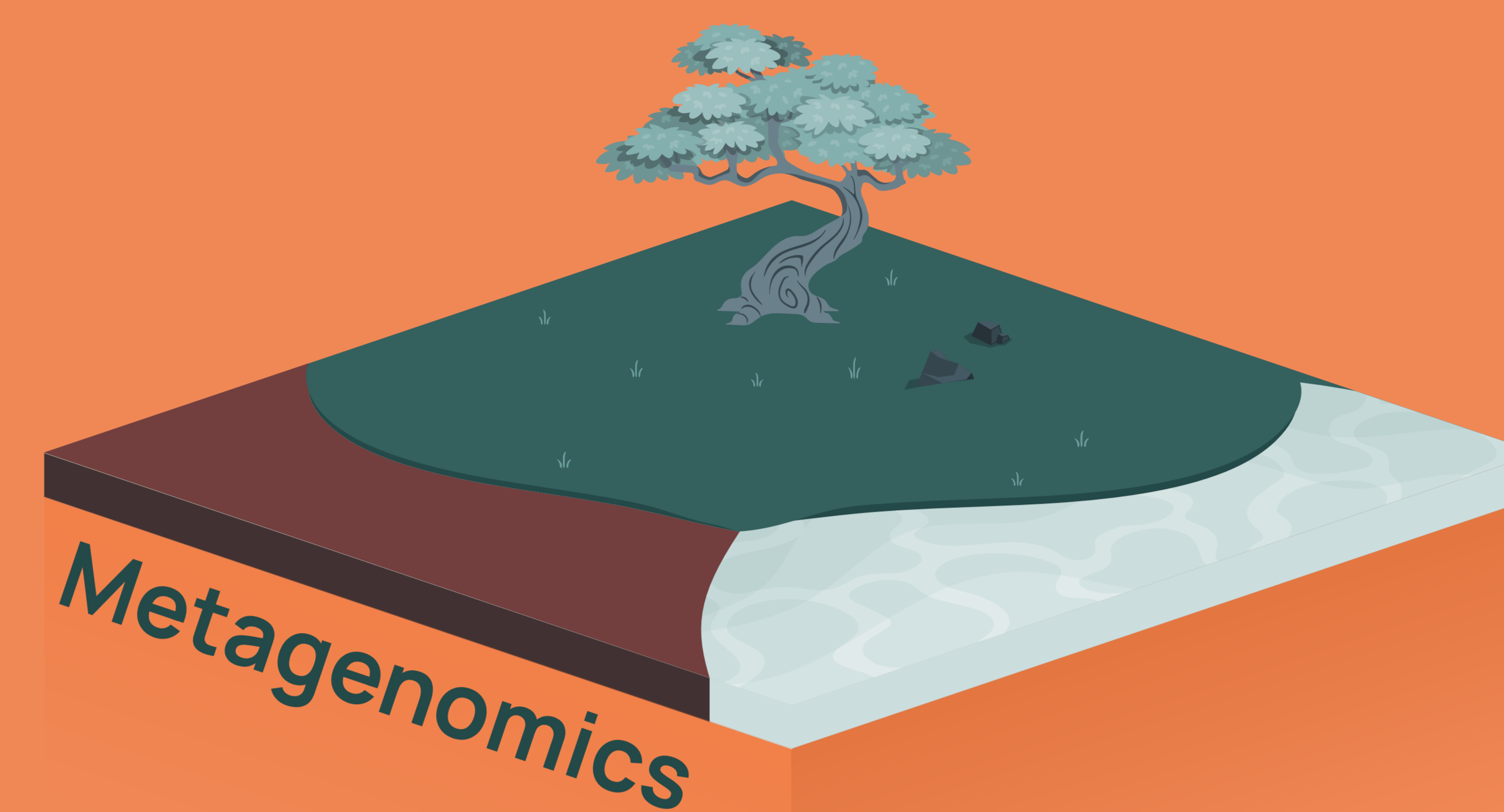
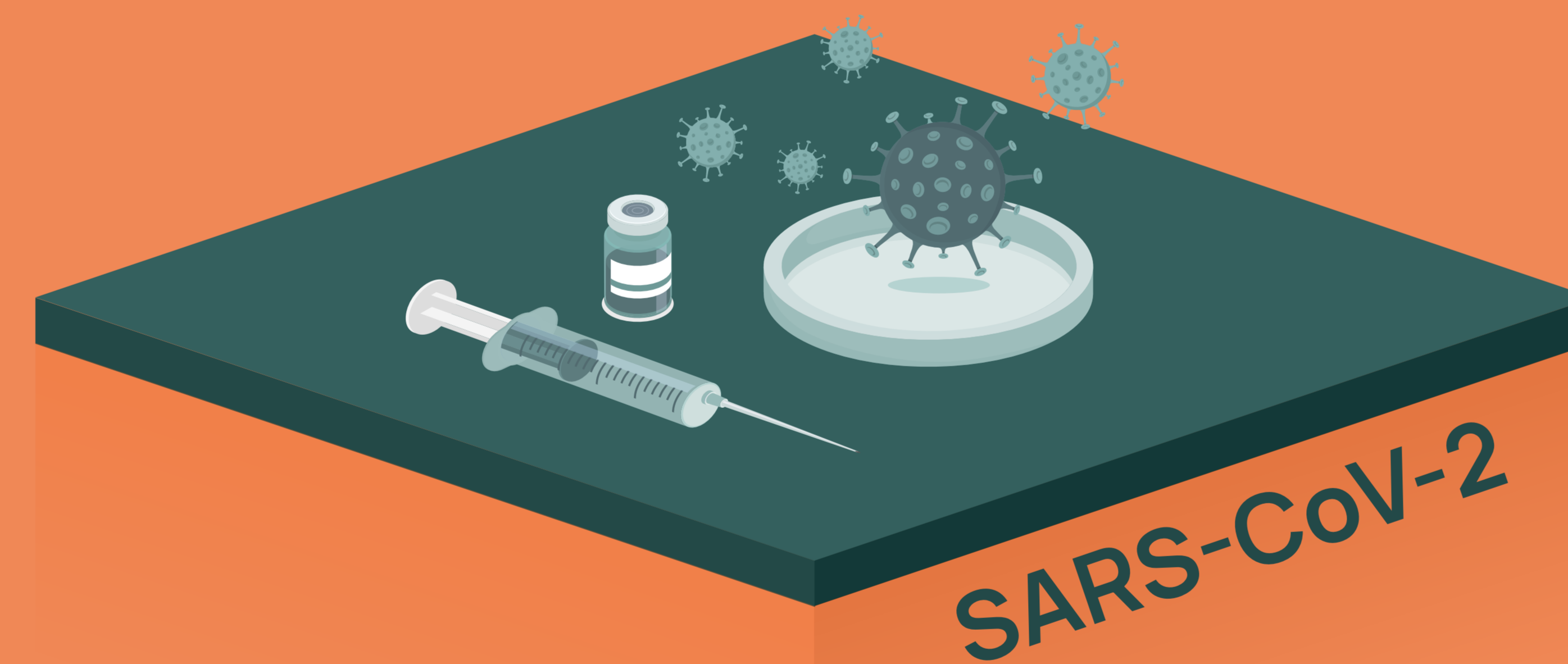
Classifies the proportion of microbes, archaea, and viruses in samples, performs robust comparative analysis, and removes contamination for metagenomics.

● Reference Guided Assembly Pipeline (SARS-CoV-2 as reference)

Performs the assembly of reference-based reads where SARS-CoV-2 will be a reference.

● Reference Guided Assembly Pipeline (SARS-CoV-2 and GRCh38 as reference)

Performs the assembly of reference-based reads where SARS-CoV-2 and GRCh38 genomes will be the references.



● Metagenomics Screening & Classification Pipeline

Performs profiling analysis of bacteria, virus and protozoa in gut/environment samples.

● Metagenomics Differential Abundance Pipeline

Performs differential abundance analysis of bacteria, virus and protozoa in gut or environment samples.

● Shotgun Metagenomics Pipeline

An automated pipeline for taxonomic and functional analysis, identifying organisms and metabolic processes in a community.

● RNA Analysis Pipeline

Performs known differential gene expression analysis on RNA samples.

● miRNA Analysis Pipeline

Performs novel and known differential gene expression analysis on micro-RNA samples.

● PacBio IsoSeq Analysis Pipeline

Performs the isoform abundance analysis, structural and quality annotation of isoforms of PacBio Long Reads sequencing.

● Reference Guided Assembly Pipeline

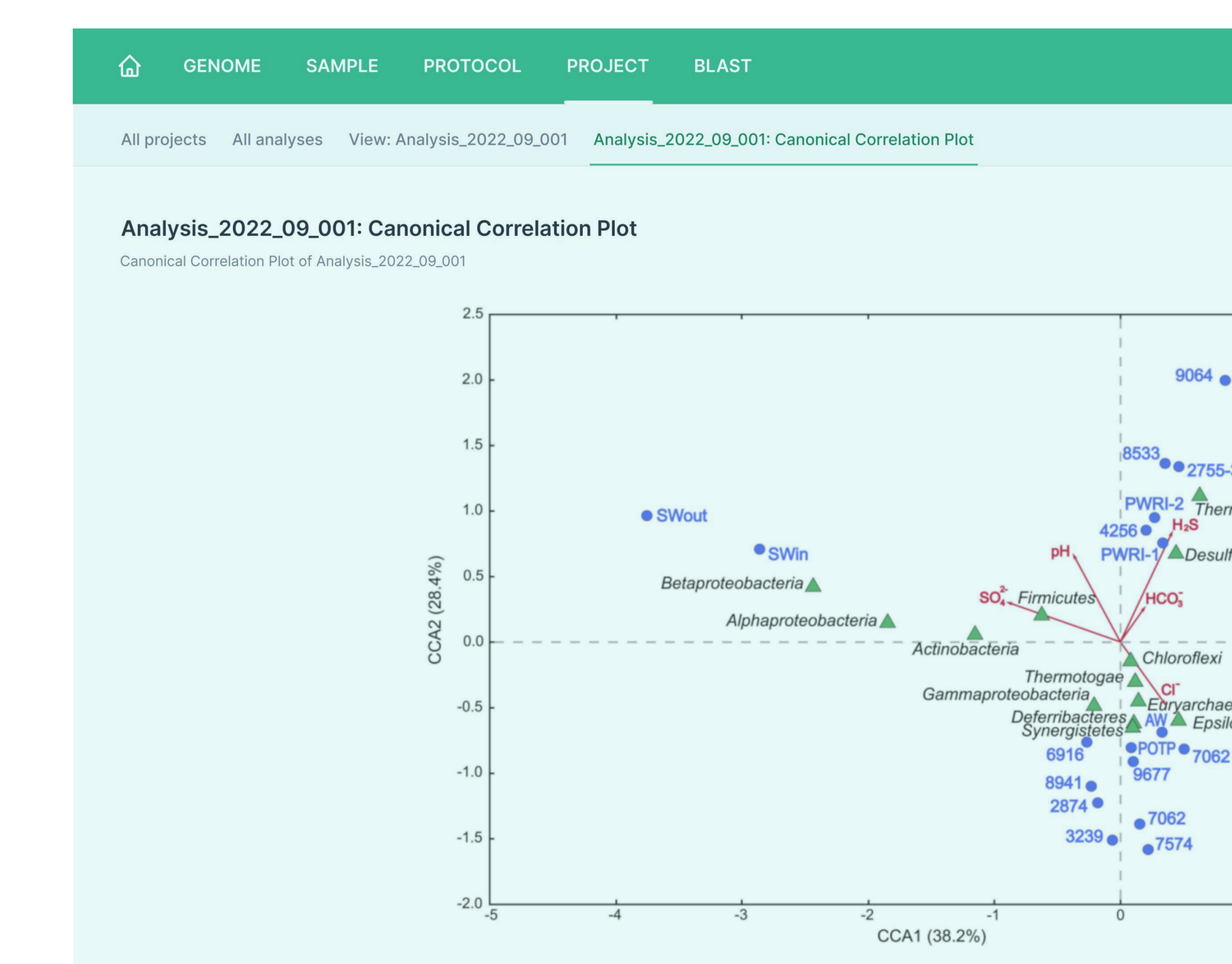
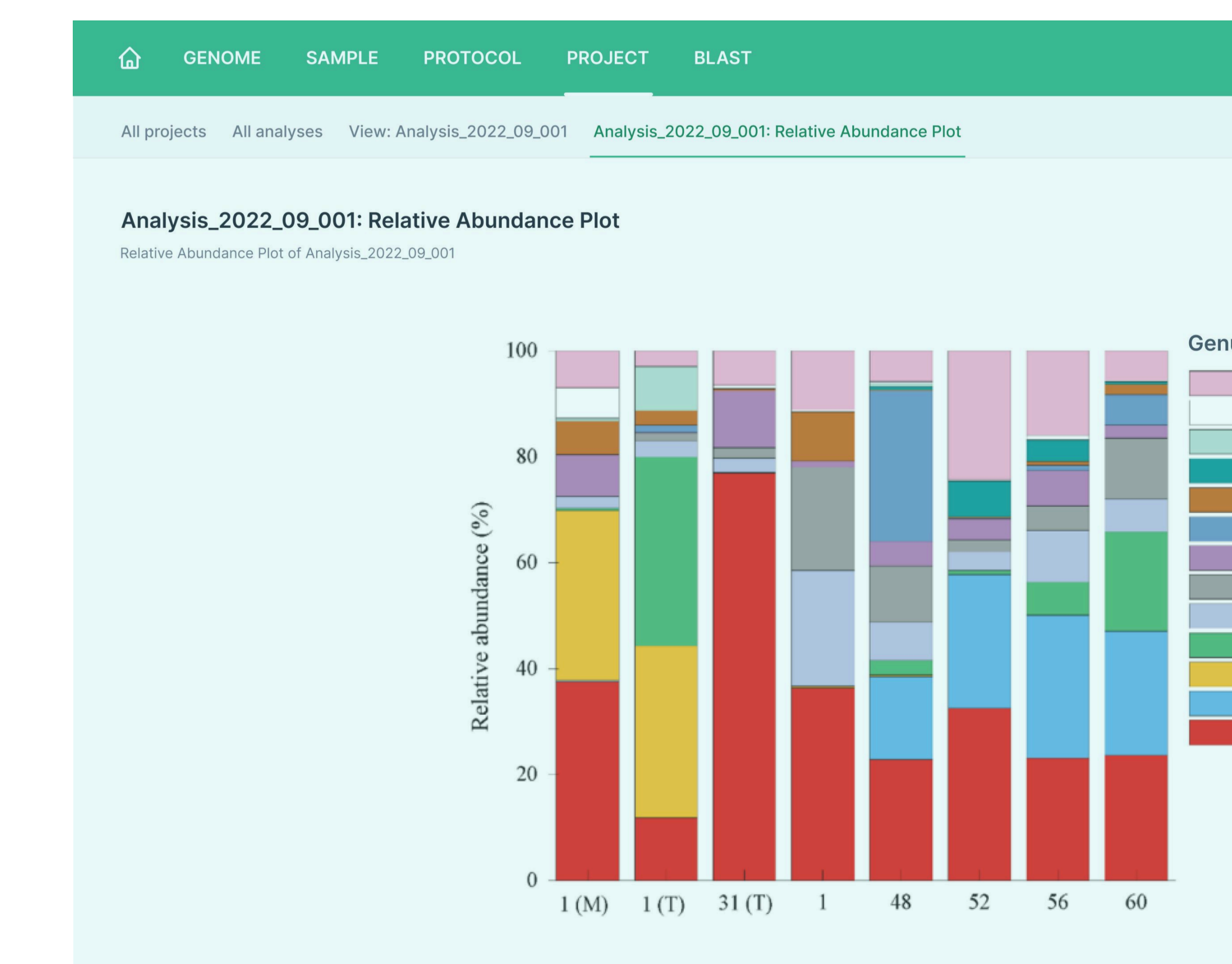
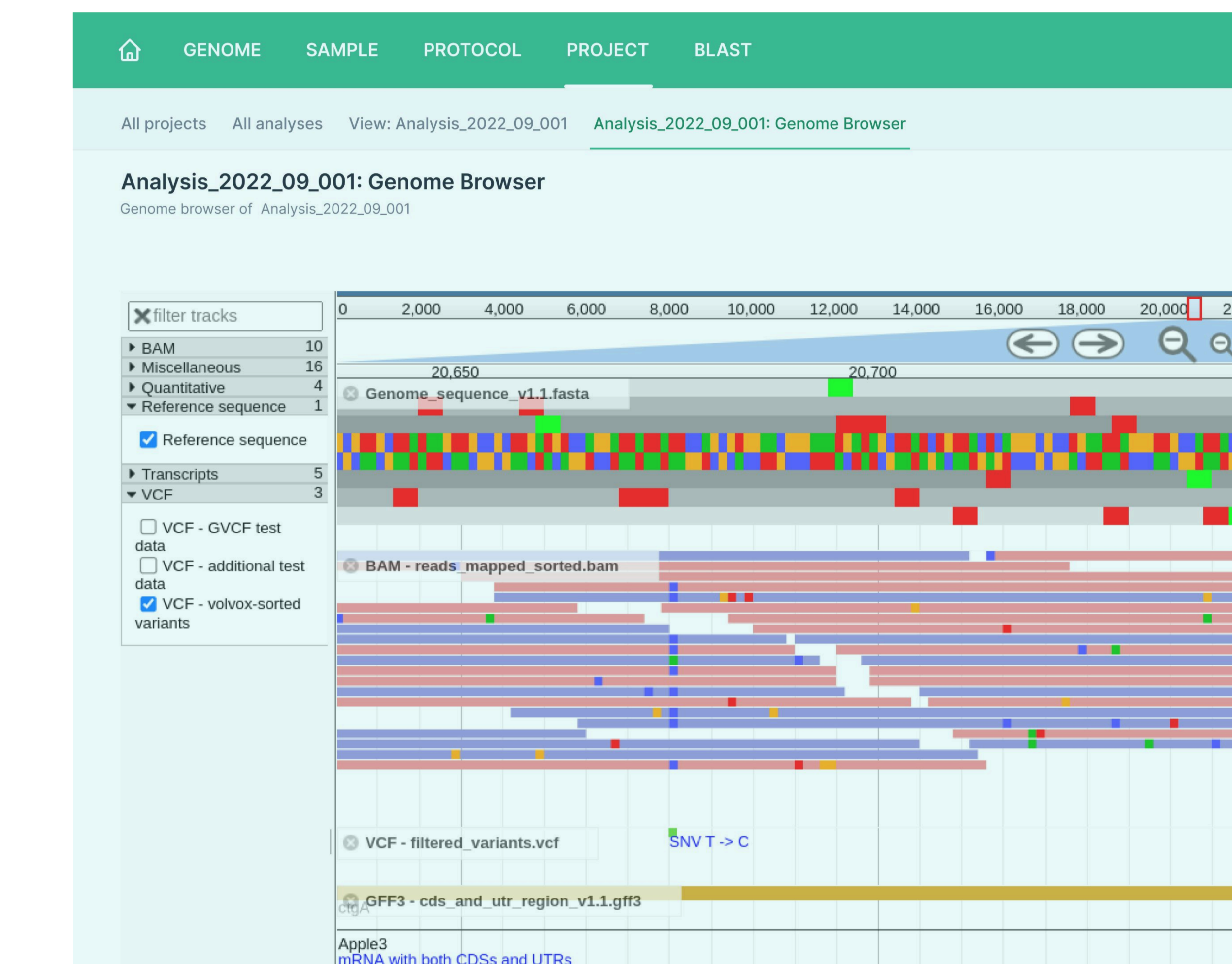
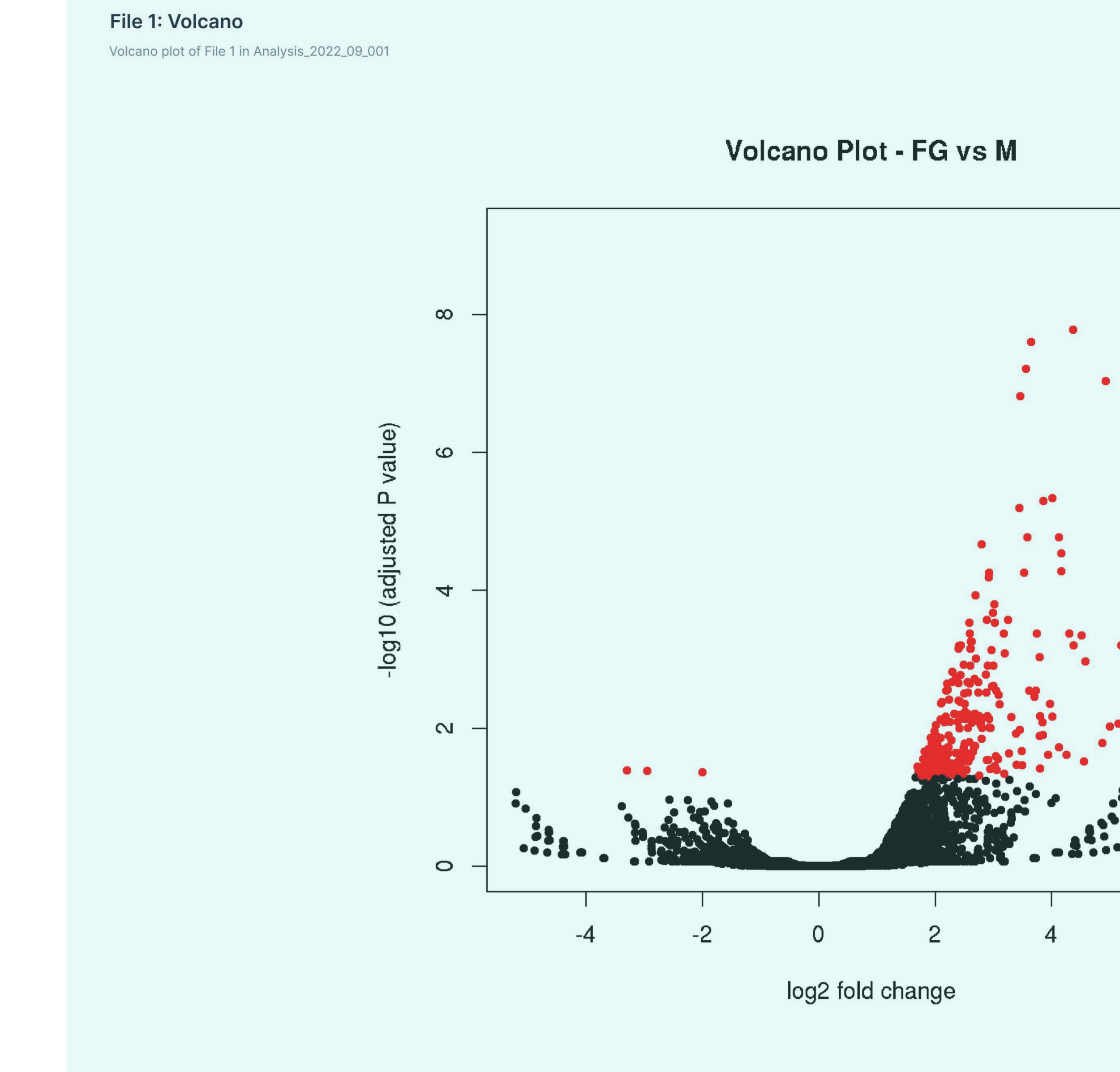
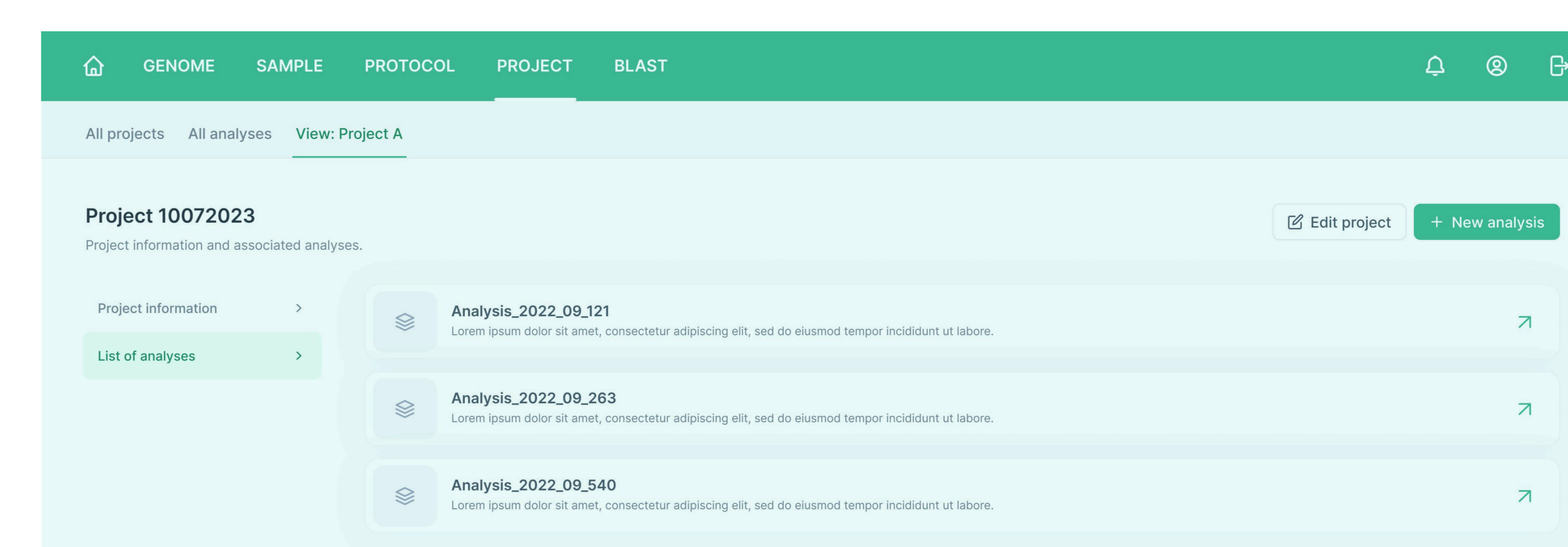
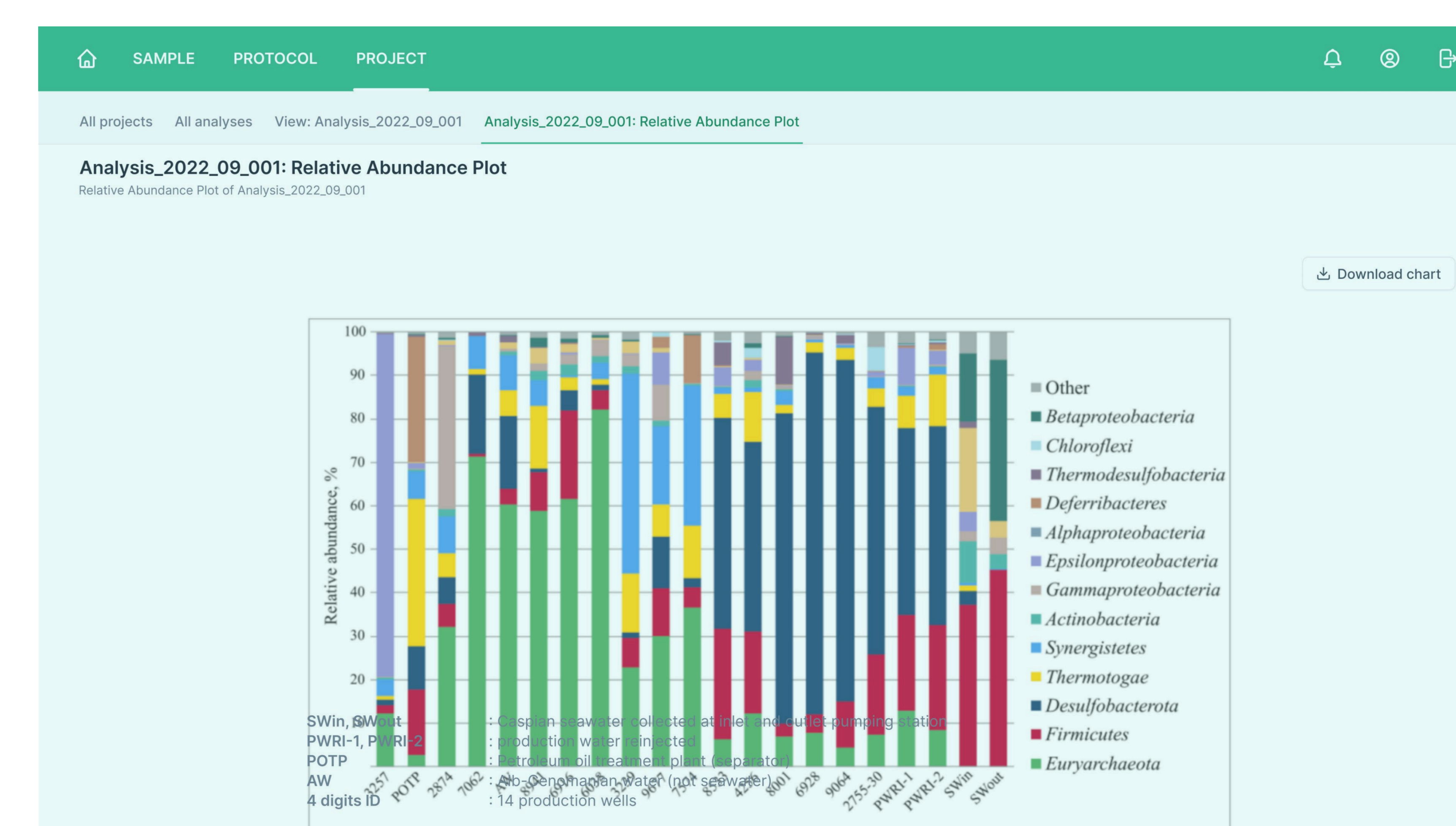
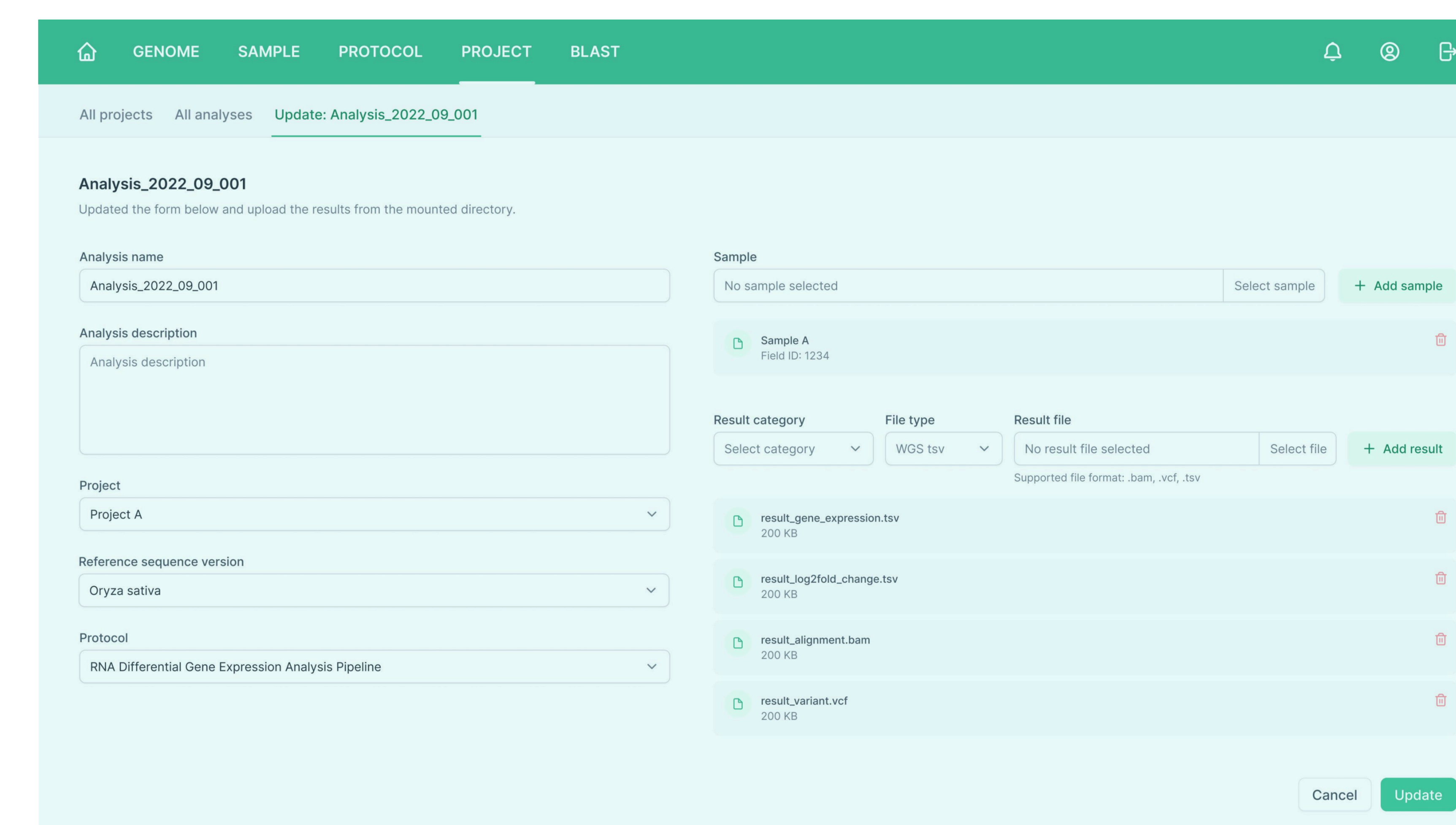
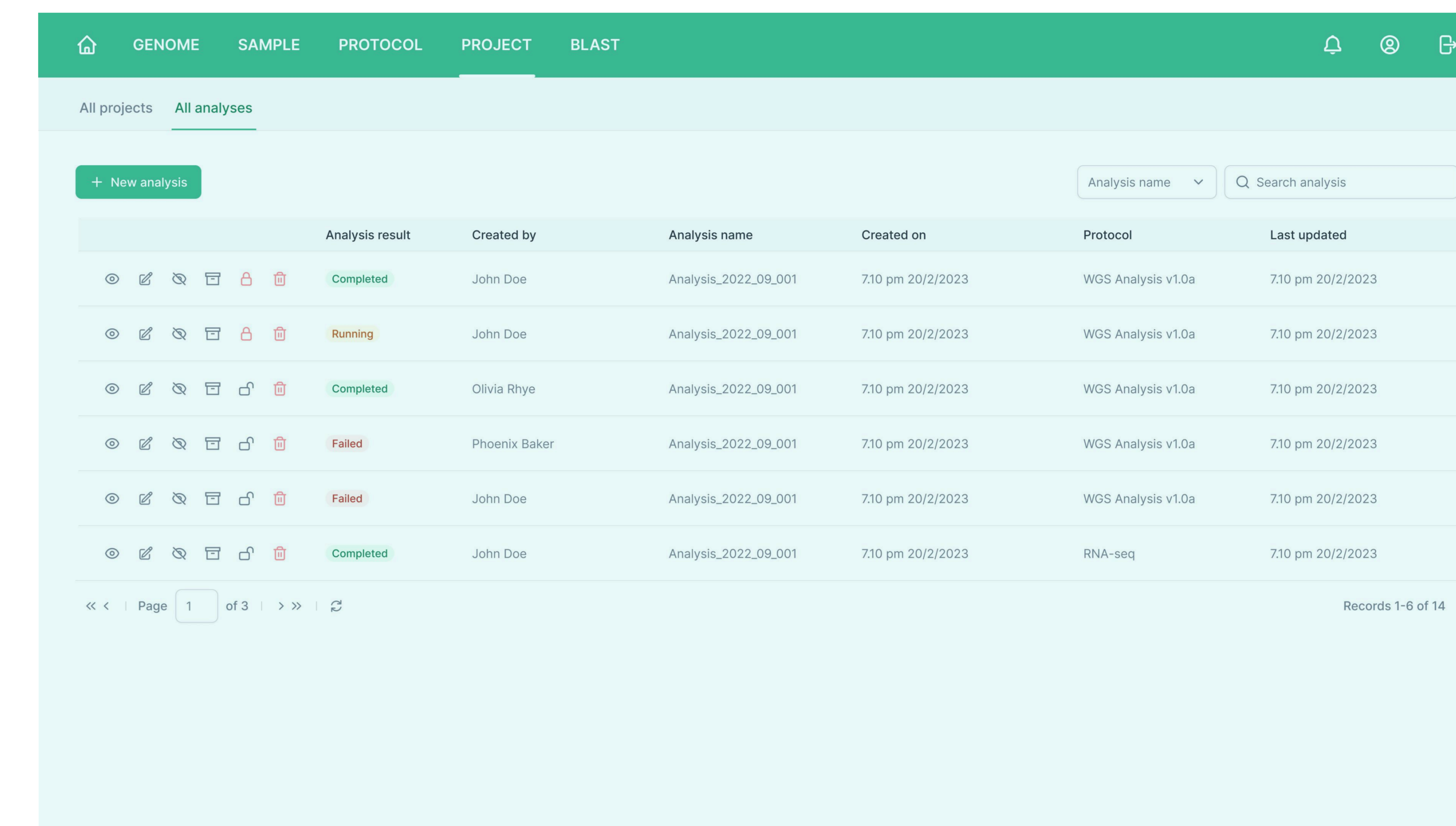
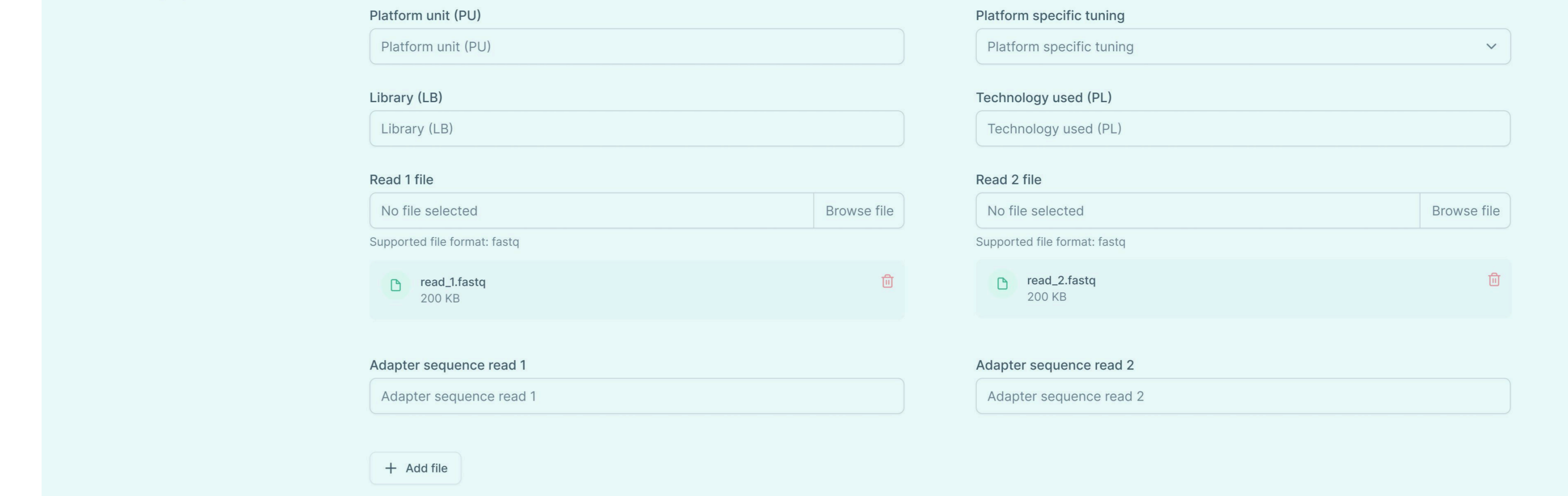
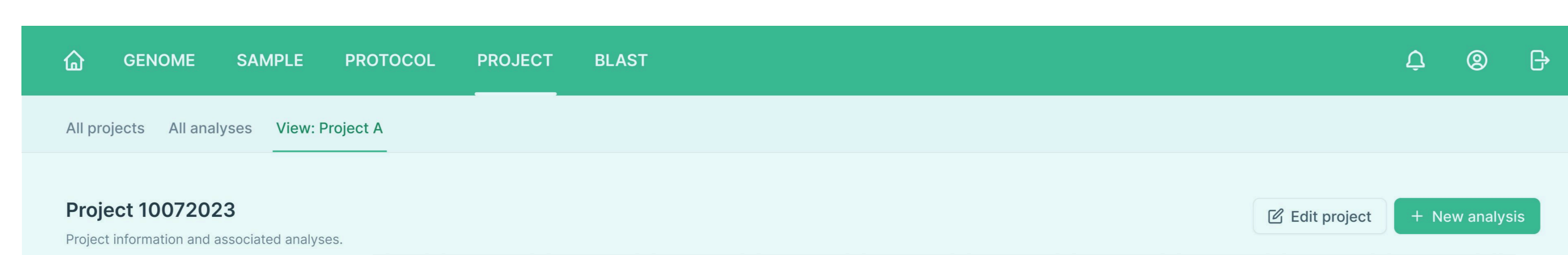
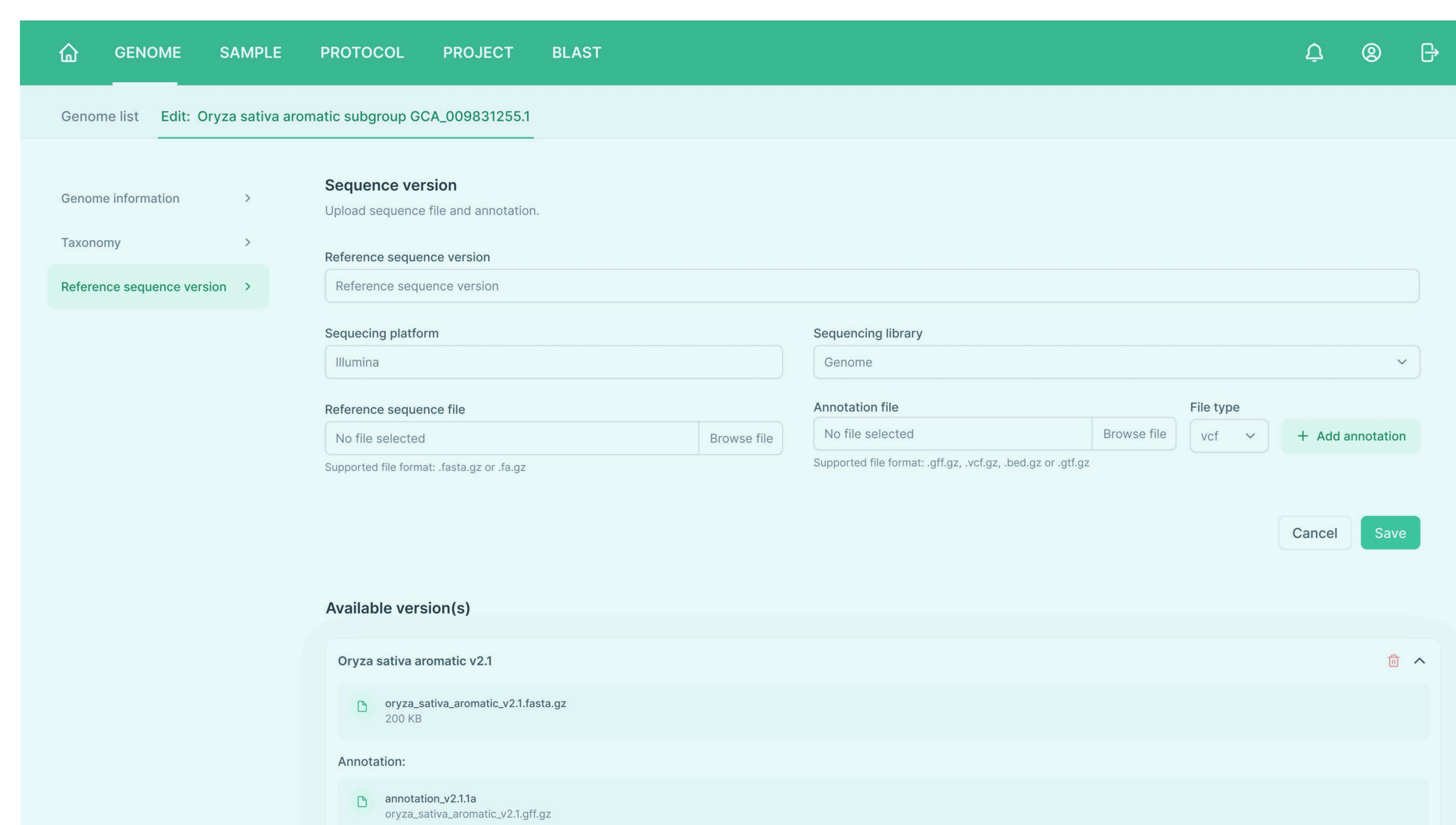
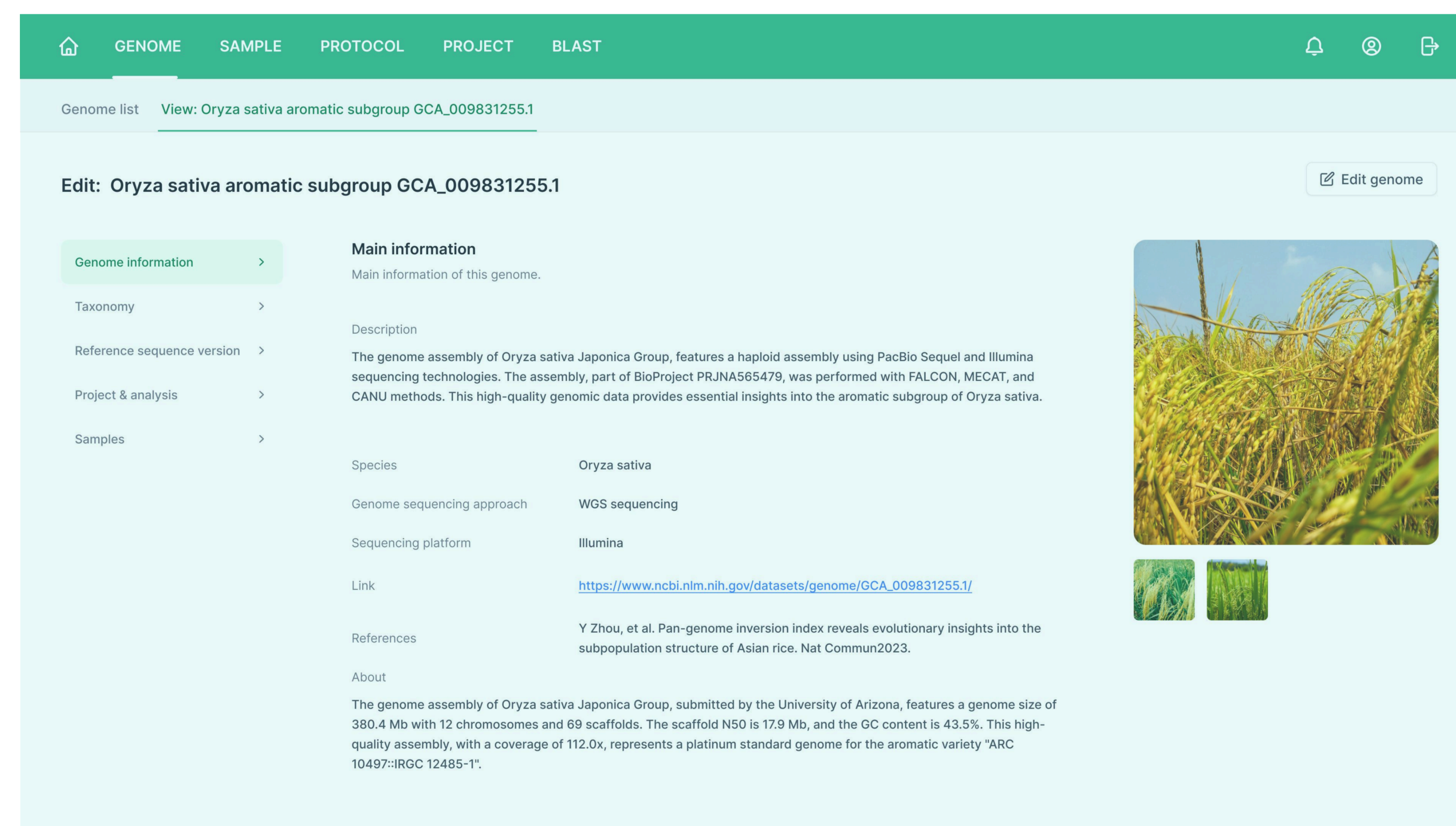
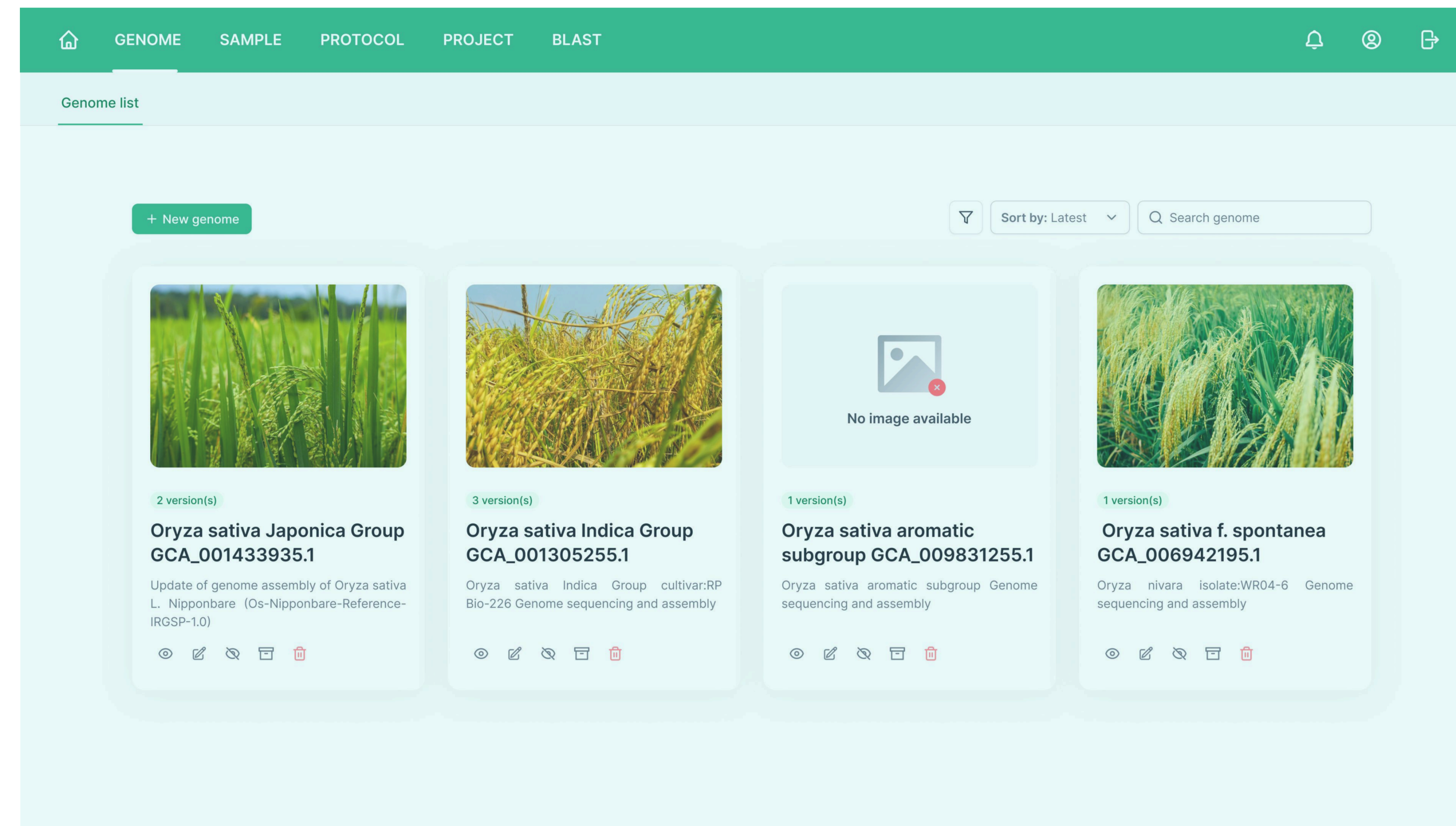
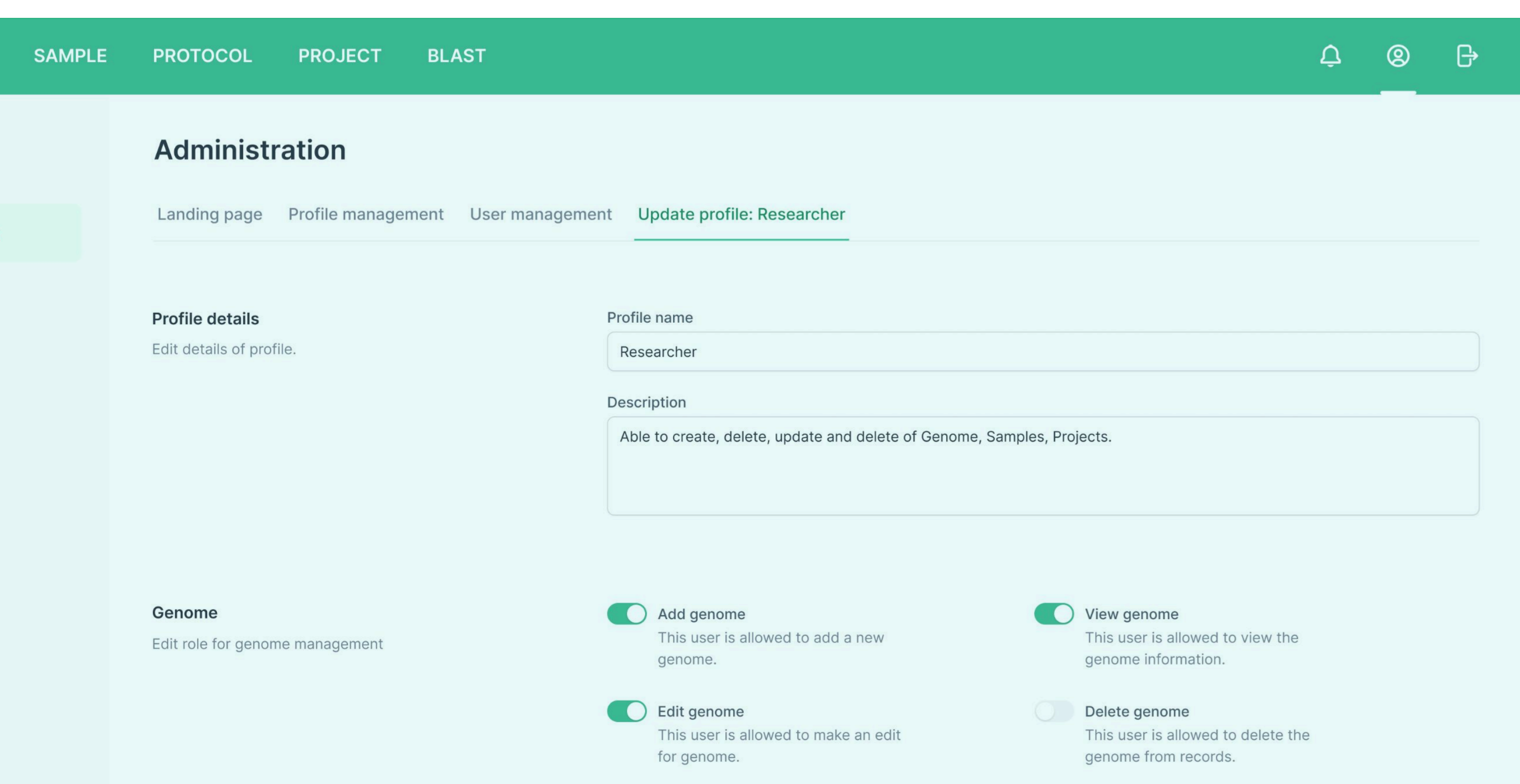
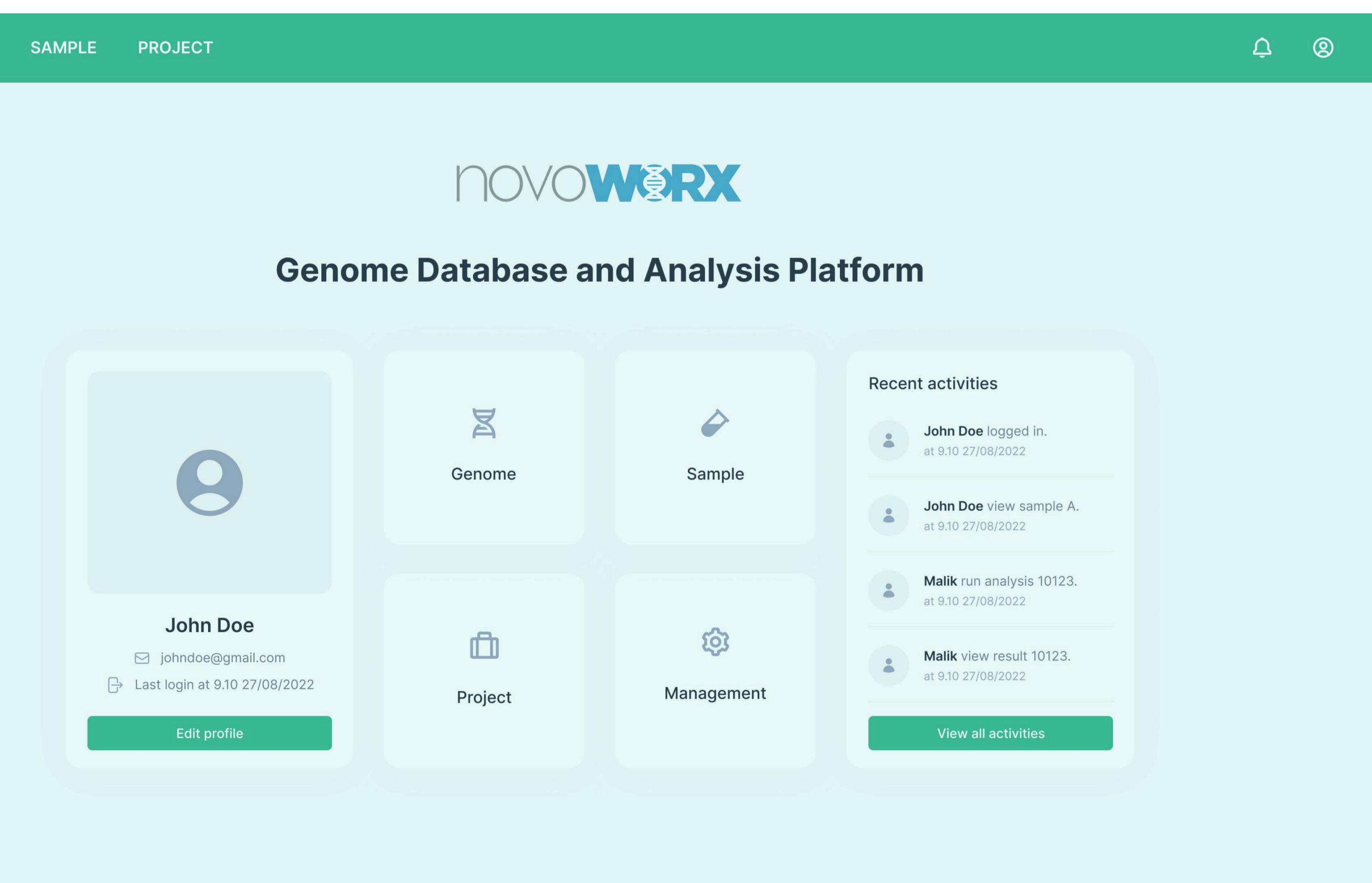
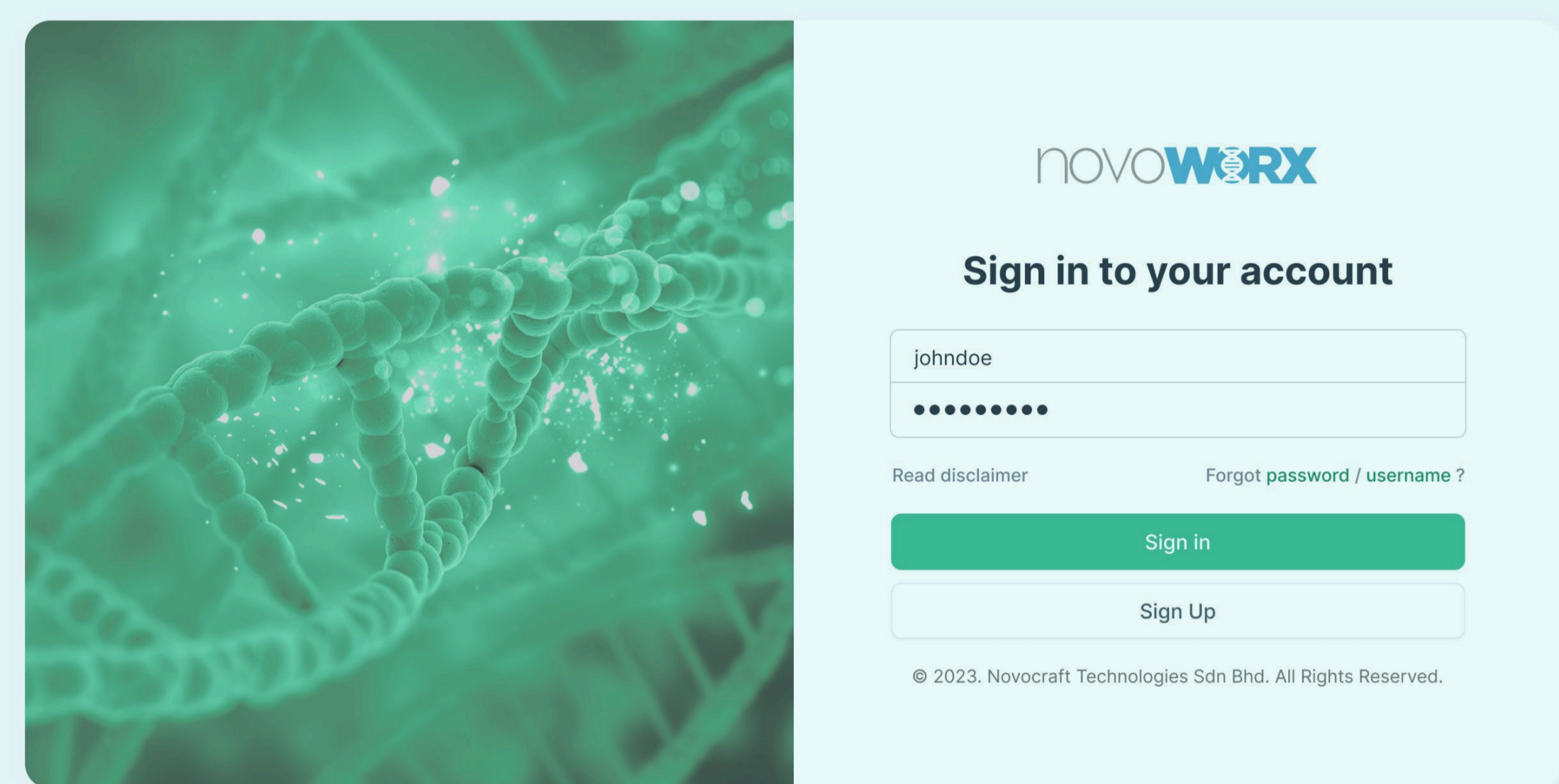
Performs the assembly of reference-based reads. The reads will be mapped to *E. coli* using novoAlign and novoSort.

● De Novo Assembly Pipeline

Performs reads assembly where in this analysis, references are not required.

Streamlined, user-friendly interface

- ✔ Interactive visual outputs
- ✔ Advanced and detail-rich results
- ✔ Integrated genome browser





For more information



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