

Introducing EPI2ME

Data analysis for all levels of expertise



EPI2ME – an extensible product for applied bioinformatics to make sense of your sequencing

EPI2ME™* delivers an actively maintained portfolio of Nexflow-based bioinformatics pipelines. These provide ‘one-click’ solutions for scientific applications that span technical domains from plasmid assembly to whole human genome analysis

More information can be found at: epi2me.nanoporetech.com

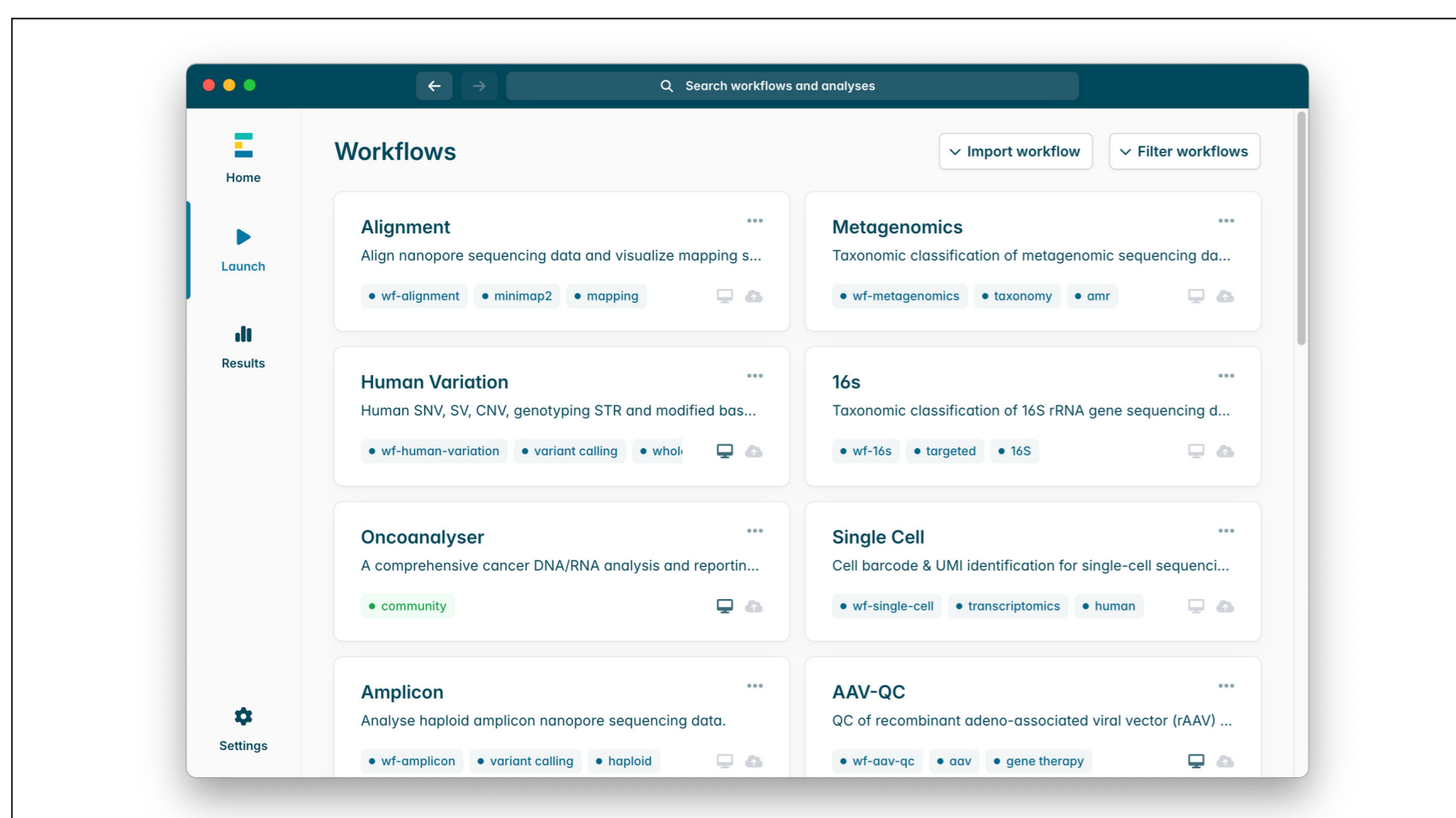


Fig. 1 Screenshot of EPI2ME Desktop Application showing available workflows.

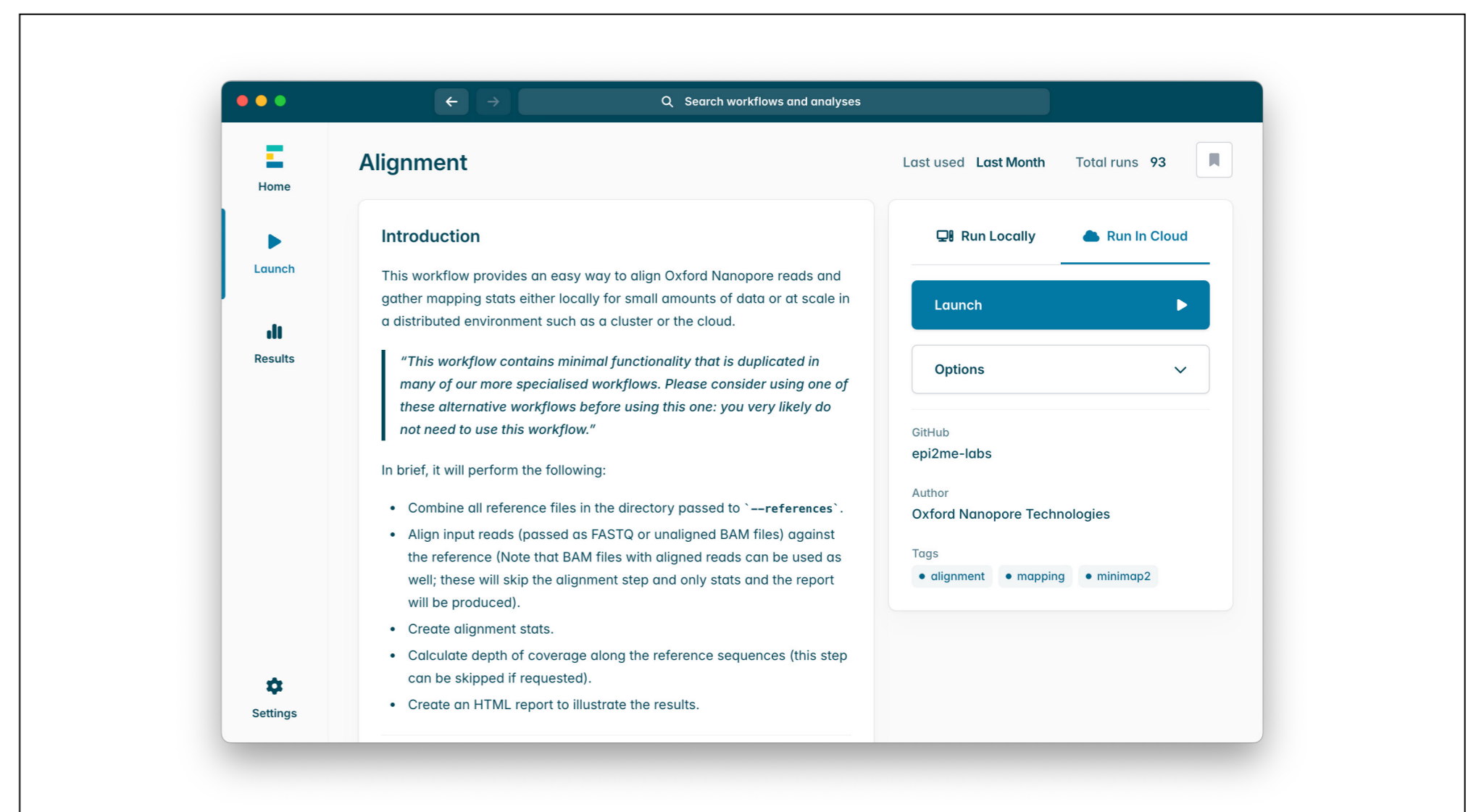


Fig. 2 Screenshot illustrating setup of an EPI2ME cloud workflow.

From laptop-based lambda DNA analyses to cluster computing of massive datasets

The EPI2ME Desktop Application provides a graphical user interface (GUI) to simplify setting up routine bioinformatics analyses. It can be run on Windows, macOS, or Linux computers and provides access to our collection of over 15 bioinformatics workflows. The EPI2ME workflows are all open source. They are implemented using Nextflow and are distributed from the product's GitHub pages. The software used by the workflows, and code for producing interactive reports, have been packaged into containers to provide isolation of the required software and ensure the analysis is reproducible. These containers are distributed through DockerHub. The workflows are versioned and can be scheduled to run on compute clusters.

Computer needs more power! Running bioinformatics analyses in the EPI2ME cloud

The EPI2ME cloud provides a key expansion of our bioinformatics ecosystem. Whether you are constrained by compute resources, struggling with local environment setup, or working from a shared device, the EPI2ME cloud can help. This AWS-based solution is secure and scalable, with most of our workflows. Analyses have access to compute resources to ensure speedy turnaround times and are limited only by network speed.

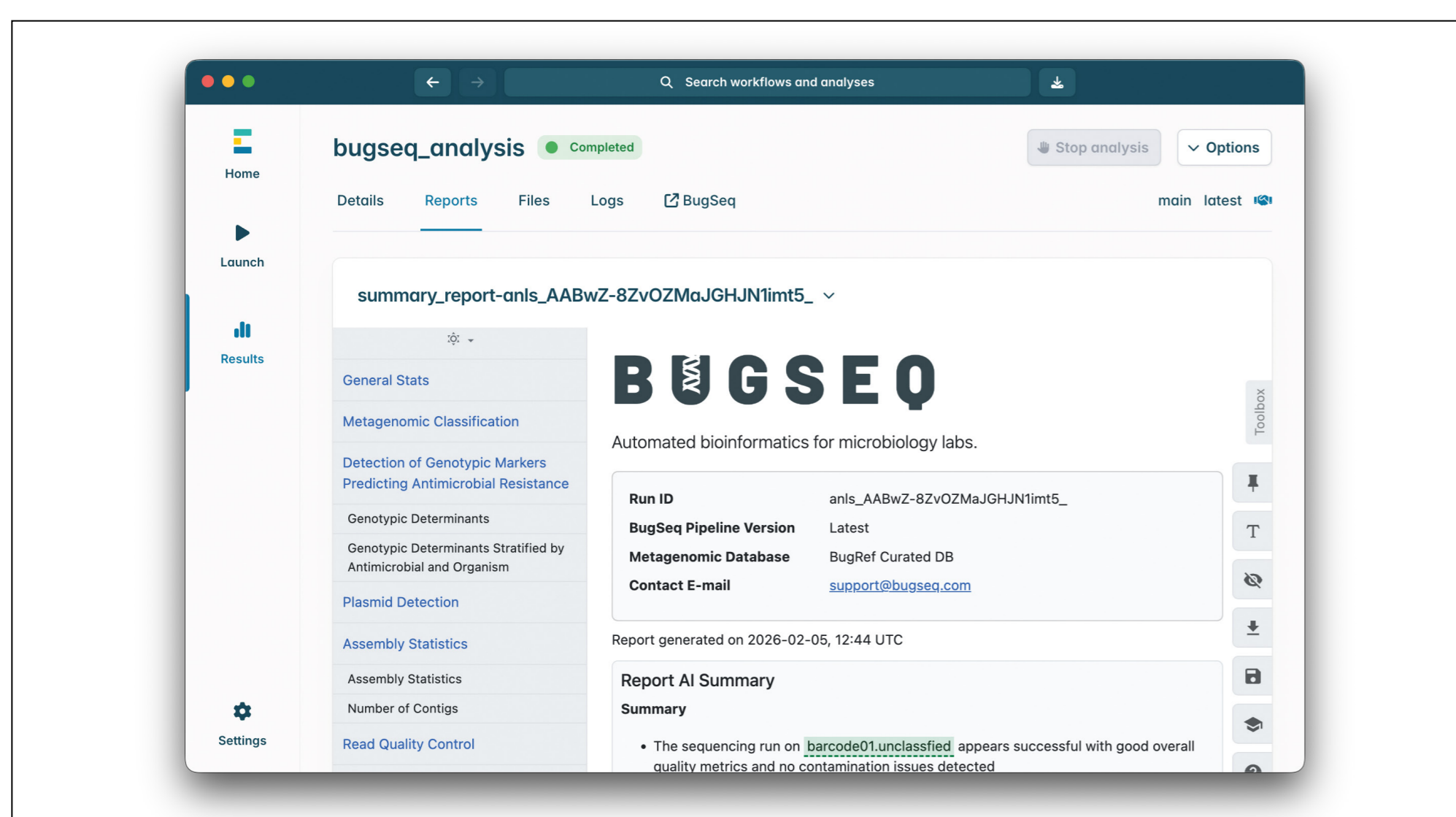


Fig. 3 The EPI2ME Desktop Application, showing integration with BugSeq.

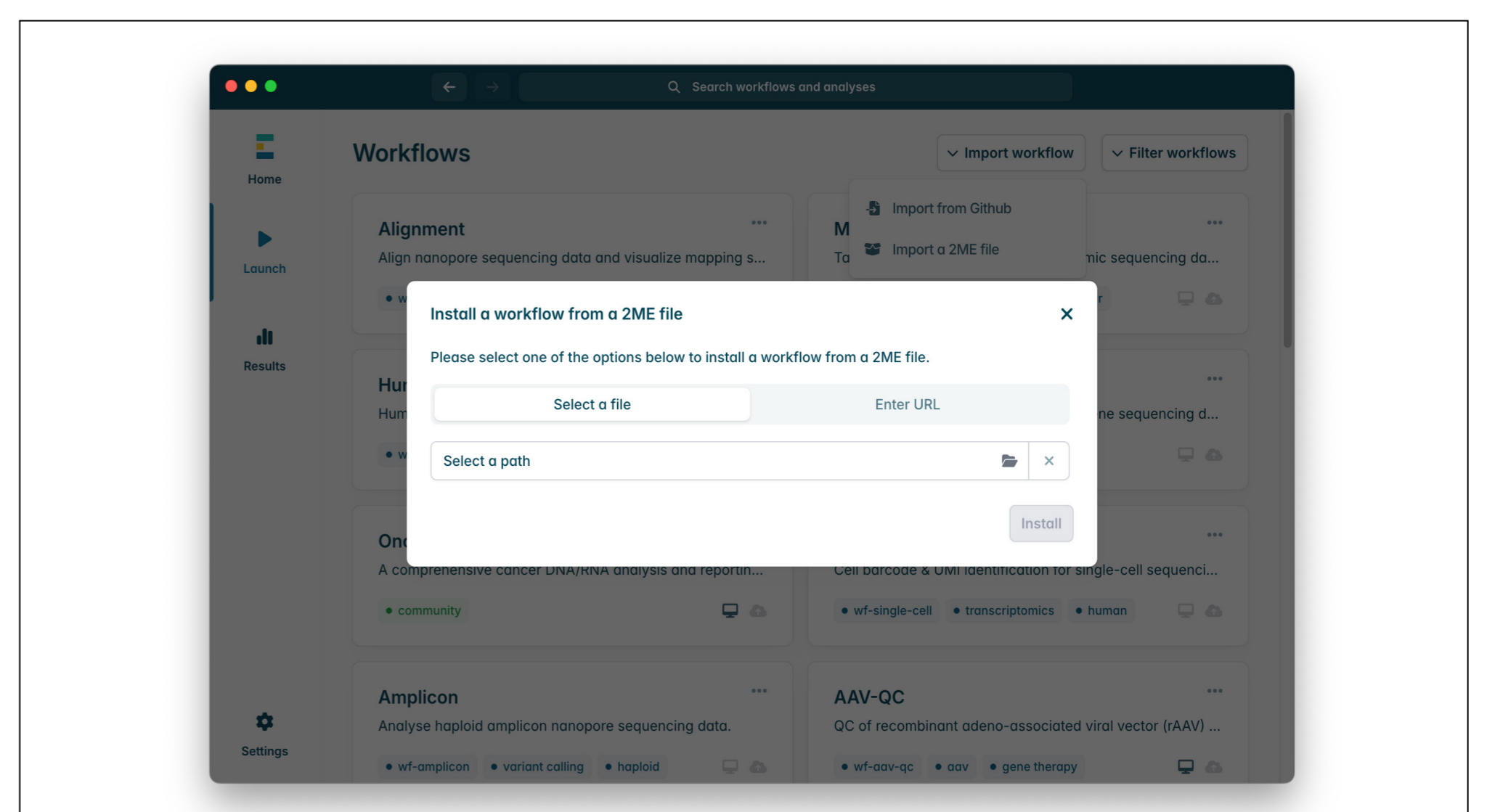


Fig. 4 Installation of a workflow offline via 2ME file format.

Third-party integration: expanding the EPI2ME ecosystem

The EPI2ME Desktop Application has been integrated with BugSeq, allowing for simple upload and automated analysis of Oxford Nanopore data. BugSeq is a bioinformatics platform that provides definitive microbial organism identification and antibiotic susceptibility and resistance profiling based on the genomic sequence of the pathogen. Oxford Nanopore Technologies has agreements with several third-party and tertiary analysis providers to seamlessly integrate with EPI2ME. We plan to expand the number of integrations in the EPI2ME Desktop Application in 2026.

2ME takeover: a standardised format for workflow distribution

2ME is a TAR archive format for the EPI2ME ecosystem that bundles the Nextflow code, Docker containers, and other workflow requirements into a single 2ME file for any given workflows. 2ME simplifies the distribution of workflows by reducing the number of cloud service contacts. 2ME files are distributed via EPI2ME cloud. 2ME also supports the installation of workflows offline via the EPI2ME Desktop Application, empowering customers who operate in heavily restricted environments.