myReads®

Long-read whole genome sequencing services

Resolve complex genomes with highly accurate long-read sequencing

Access high-accuracy HiFi long-read WGS without the hassle

Leverage industry-leading long-read technology

- PacBio® Vega™ system
- ~60 Gbp per flow cell
- HiFi data generation with 99.9% accuracy per read
- Methylation calling without bisulfite treatment

Deploy the tools to fit your data goals

- For projects ranging from a single sample to hundreds
- Receive exactly the right data for your research
- Save time on downstream analysis

Benefit from expert execution and review

- Dedicated laboratory experts
- Decades of combined experience across diverse research areas

Rest easy with secure data delivery

- Data generated during your project is stored securely and available on our online portal
- Control who has access to your data

Find your perfect fit.

Our service model is designed around your project, not the other way around. We work with you to generate precisely the data your study requires—no more, no less—at a budget aligned with your goals.

Customize and optimize your sequencing pipeline.

We operate as an extension of your laboratory, providing seamless integration into your research workflow. Our myReads NGS service packages offer a modular, flexible approach to project execution, designed to adapt efficiently and reliably to your project's unique needs.

Working on a timeline? We work with you.

From clear project planning and transparent workflow overviews to reliable turnaround times—with options to expedite when needed—we keep your project moving forward. You'll receive proactive, frequent communication on status and milestones (including sample arrival and condition, QC report, data delivery), along with high-touch support during critical moments.

Contact us to get a project started.

Choose the support you need – from single steps to end-to-end execution

High molecular weight DNA extraction

Sample types:
Tissue, blood, cells, saliva, and FFPE

Sample categories:
Plant, animal, insect, invertebrate, fungi, and bacteria

SMRTbell® library preparation

Specialized protocols for long-read sequencing samples.

Barcoded SMRTbell prep allows for multiplexed sequencing runs.

Vega sequencing

HiFi data generation with 99.9% accuracy per read.

Methylation calling with every run.

Analysis

Directly download FASTQ and BAM files with demultiplexed CCS HiFi reads and QC reports that include median read length, quality score, and duplication results.

Your science, our expertise: packages that meet your needs

Long-read whole genome sequencing

- SMRTbell library preparation
- Vega SMRT® cell

Additional libraries and cells available upon request

High molecular weight DNA extraction

- Ordered by sample
- We accept a wide variety of sample types. Contact us for guidelines and recommendations.

Bioinformatics analysis

- Methylation profiling, variant calling, and basic de novo genome assembly for microbes and haploid/diploid eukaryotes.
- Choose the package based on the amount of sequencing data.

Genome size restrictions apply

Pair with our short-read DNA sequencing services for de novo assembly polishing or our short-read RNA sequencing services for genome annotation!

Need a reference-quality assembly with Hi-C data? We can connect you with a service team. Contact us to get started.

Questions? Contact us via the methods listed below. Our team is happy to assist you!

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