Genome Scan

Chip | Longreads | Methyl arrays | Targeted | WES | WGBS | WGS

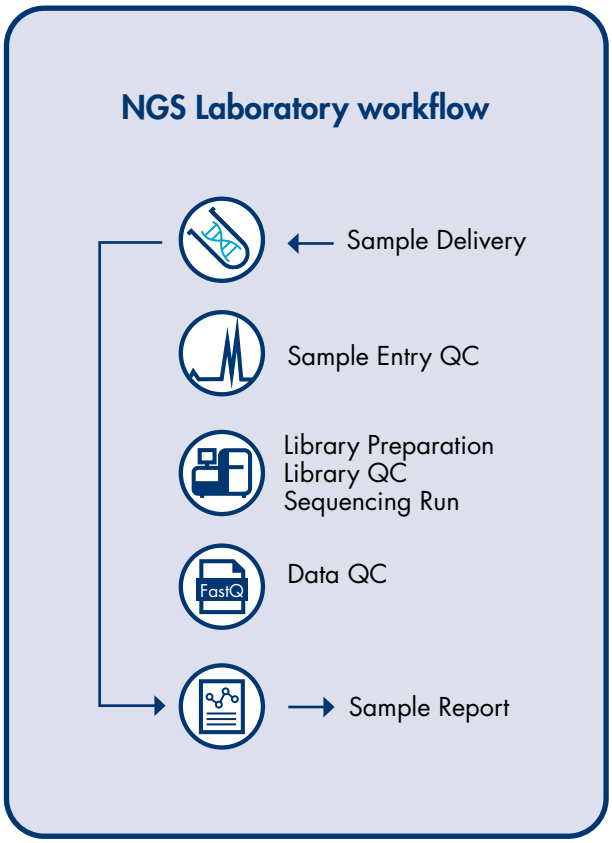
Long Read Sequencing

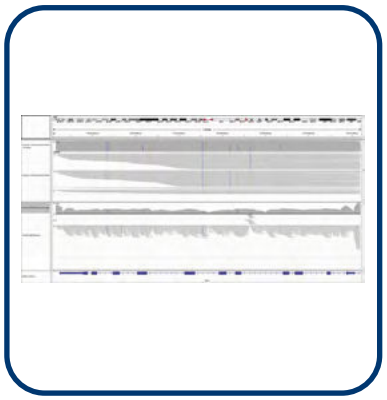
Genomic, transcriptomic and epigenetic characterization with high precision

In contrast to short-read NGS solutions, which only sequence a few hundred bases, long-read technology generally can generate highly accurate long reads (median consensus accuracy of > 99.9%) up to 30 kb. Beside the length, long read sequencing eliminates the PCR-amplification step utilized by short read platforms. Opposed to the large number of parallel reactions capturing short sequences, long read sequencing technology employs single molecules of circular templates immobilized on a surface. Nucleotide incorporation is then detected in real-time for the generation of long reads.

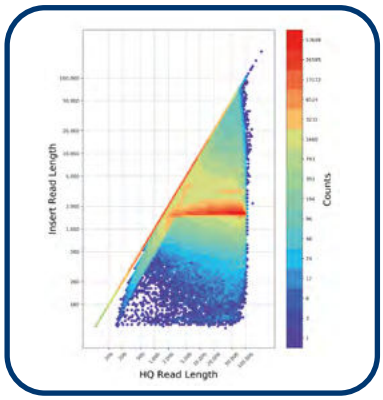
Long read sequencing is rapidly becoming popular for studying complex and repetitive regions of the genome, structural variants, and epigenetic heterogeneity. It is especially well adapted for *de-novo* genome assembly, for identifying complex transcripts and study the role of epigenetic modifications on certain disease conditions. It can particularly benefit researchers working on less characterized organisms.

GenomeScan has extensive experience with this technology and is one of the first companies to provide long-read sequencing as a service for *de novo* assembly, structural variant calling, targeted, (Long)Amplicon or RNA-sequencing. Our scientists are ready to help you define the parameters of your long read sequencing project, ensuring the correct applications are used to answer your questions.





Long-read gene phasing



Sequencing read lengths

de novo assembly

Committed to your project

Data quality guarantee:
Sequence quality control is an essential step in our workflow. We track, identify and exclude potential errors that could impact the interpretation of your results.

Long read sequencing:
With single molecule, real-time (SMRT) sequencing technology, we provide highly accurate long reads and are able to drive discoveries in different life sciences fields.

Reporting/Publication ready results:
We deliver comprehensive, consistent and transparent NGS data. Furthermore, we offer different visualization options to make your results ready for publication.

Data analysis options

In order to provide you easily comprehensible and ready-to-publish results, our workflow covers several steps that lead to insightful data visualizations (see frame). Depending on the application and your research question, we care for optimal interpretation of the data. Our highly experienced bio-informatics team has an arsenal of tools for either *de novo* assemblies, genome mapping and transcriptome analysis to facilitate a custom approach when needed to make fully use of the long read application.

Biological Insights

The biological insights that can be inferred from your data include:

- *de novo* genome assembly
- Role of structural variants in human diseases
- Epigenetic modifications
- Haplotype phasing information
- Variable number tandem repeat analysis
- Long amplicon analysis
- Full-length transcriptome analysis
- Metagenomics

Custom Solutions

At GenomeScan, we continuously improve our services and validate new solutions. Take advantage of our pilot program in which bioinformatics pipelines can be tailored to your specific needs, allowing more in-depth mining of your data set. In addition to that, we offer various customizable publication grade visualization options to present your results.

About GenomeScan

As an ISO-accredited leading Dutch Next Generation Sequencing service provider, GenomeScan develops customizable NGS solutions for pharmaceutical and biotech companies, healthcare providers and academic institutions. By providing state-of-the-art tools to analyze genetic disorders fast, affordably, and effectively, GenomeScan fosters innovation through partnership with medical centers and research laboratories.

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