Microbiome
Service Specification Sheet

Genome Scan

Full Genome

16S

Whole Metagenome Shotgun Sequencing

Biodiversity studies from microbial populations (Insight into all genotypic features)

Rapid and accurate identification of complex microbial populations is a critical need for groups in clinical microbiology, veterinary research, biotech companies and the agro-industry. To distinguish between highly related species, microbial profiling through whole metagenomic analysis offers the ultimate solution. This analysis can provide high-resolution information including antibiotic resistance cassettes, pathogenicity genes and characterization of important genetic variants. A high-resolution analysis is also an excellent tool for comparative genomic studies that employ de novo sequencing or resequencing methods.

As part of GenomeScan's whole metagenome microbial profiling workflow, human or other eukaryotic host DNA can be selectively removed from your samples prior to sequencing (upon request). This prevents an increase in sequencing inefficiency and associated cost. We offer short (Illumina) or long-read (PacBio/ONT) sequencing options for fast and high throughput or highly accurate and sensitive analysis respectively. Our PCR-free library preparation eliminates PCR-induced bias and the use of unique dual-indexing enables the analysis of hundreds of samples in parallel.

Input material

Isolated genomic DNA

Isolated sample requirements

- Preferred minimal input: ≥ 50 ng / sample
- Minimal volume of 25 µl / sample
- HMW genomic DNA, column or bead purified

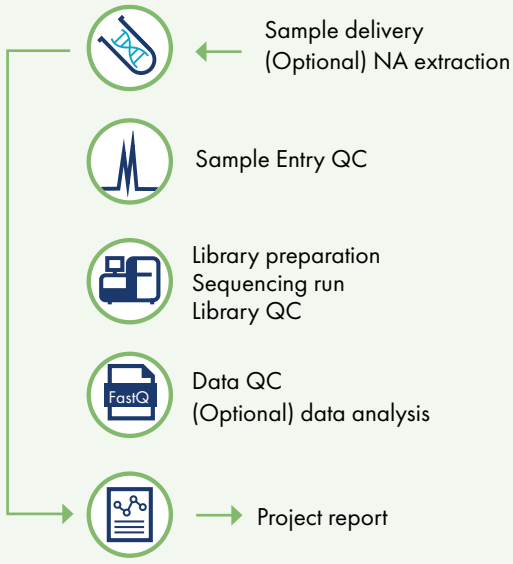
Sequencing on Illumina NovaSeq (PE 150)

- Standard read depth 7.5 Gb / sample or above if needed
- PCR-free library preparation possible
- Enrichment for prokaryotic DNA possible
- Unique dual indexing combined with unique molecular identifiers (for samples with PCR)

Deliverables

- FastQ files
- Quality score (Q30) ≥ 80%
- Project Report
- Optional data analysis with comprehensive report

NGS Laboratory workflow



Committed to your project

Data quality guarantee

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

Detecting unique molecules

Our service includes the use of unique molecular identifiers (UMIs), which ensures the removal of PCR artifacts and detection of identical reads that originate from different genomic regions.

Results

We deliver comprehensive, consistent and transparent NGS information. We offer different visualization options to present your results and/or comply with publisher's policies.

Data analysis options

To provide you with easily comprehensible and ready-to-publish results, our workflow covers several steps that lead to insightful data visualizations (see below). Sequential steps include data trimming and preparation for alignment to the NCBI reference database to determine the characteristics of different microbial populations.

Our data analysis report provides multiple visualization possibilities. A comprehensive list of all detected microorganisms, their taxonomic rank and the number of reads used for classifications are all displayed in an informative table. Furthermore, Sankey and krona-plots make visualizing sample compositions not only insightful, but also aesthetically pleasing. Finally, we apply gene prediction, functional annotation and/or de novo assembly completely in line with your specific needs and requirements.

Biological Insights

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

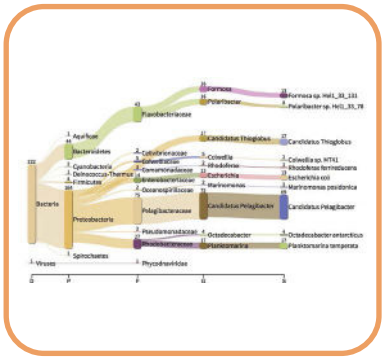
- Taxonomic classification down to species, subspecies and strain level
- Detailed insights into genotypic features
- *de novo* assembly or resequencing of the whole metagenome
- Clustering of samples based on similarity of microorganism abundance
- Prediction of capacity for antibiotic resistance
- Accurate detection of highly similar variants
- Identification of metagenomic biomarkers
- Compare relative microorganism abundances between pre-defined groups
- Gene prediction, functional annotation and metabolic pathway analysis for microbial consortia

Custom analysis

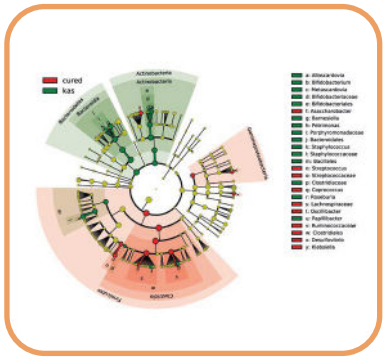
Whether you wish to type or characterize microbial isolates, monitor food-borne pathogens, or perform quality control on starter cultures, custom bioinformatics can be performed allowing more in-depth mining of your dataset. We generate reports that optimally address your research question.

About GenomeScan

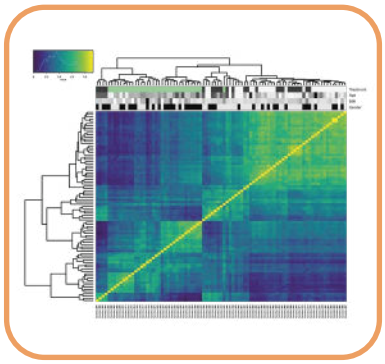
As an ISO-accredited leading Dutch Next Generation Sequencing service provider, GenomeScan develops customizable NGS solutions for pharmaceutical and biotech companies, healthcare providers and academic institutions. By providing state-of-the-art tools to analyze genetic disorders fast, affordably, and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



Interactive analysis of metagenomics data



Differential microbial abundance



Heatmap

genomescan.nl

+31 71 5681050

info@genomescan.nl

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