



Full Genome



16S

Whole Metagenome Shotgun Sequencing

Identification, quantitation and comparison of 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 and the agro-industry. For distinguishing 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 genomics 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. This prevents an increase in sequencing inefficiency and associated cost. We offer short (Illumina) or long-read (PacBio) sequencing options for fast and high throughput or highly accurate and sensitive analysis respectively. Our PCR-free library preparation eliminates PCR-induced biases and the use of unique dual-indexing enables the analysis of hundreds of samples in parallel.

Input material

Purified genomic DNA

- Validated input PCR free: ≥ 50 ng / sample
- Minimum volume: 15 μ l / sample
- Quality: HMW DNA, column or bead purified

Sequencing on Illumina NovaSeq 6000 (PE150)

- Standard PCR-free library preparation
- Unique dual indexing and unique molecular identifiers
- Standard read depth 7.5 Gb / sample

Deliverables

- **TAT: 2-3 weeks after successful sample QC**
- FastQ files via secured electronic transfer
- Quality score Q30 $\geq 80\%$ for PE150 reads
- Optional data analysis with comprehensive report

Laboratory workflow



Sample delivery



Sample Entry
QC



Library Preparation
Library QC
Sequencing Run



Data QC



Sample Report



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.

Publication ready results

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

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 below). Sequential steps include data trimming and preparation for alignment to the NCBI reference database to determine the characteristics of different microbial populations. We optimize these processes for short or long read sequencing to allow for the use of different instruments based on your specific needs. Our data analysis report provides multiple visualization possibilities. A comprehensive list of all detected microorganisms, their taxonomic rank, genome size, and the number of reads used for classifications are all displayed in an informative table. Furthermore, hierarchical clustering, Principal Component Analysis, heat maps 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:

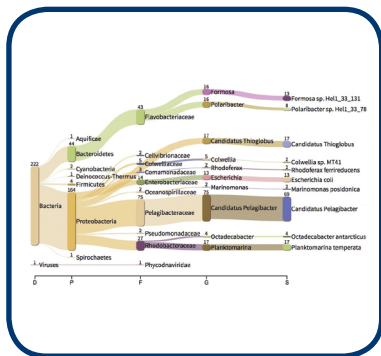
- Taxonomic classification down to species, subspecies and strain level
- Detailed insights into genotypic features
- *De novo* assembly or resequencing of the whole metagenome
- Clustering of samples based on similarity of microorganism abundance
- Prediction of capacity for antibiotic resistance
- 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

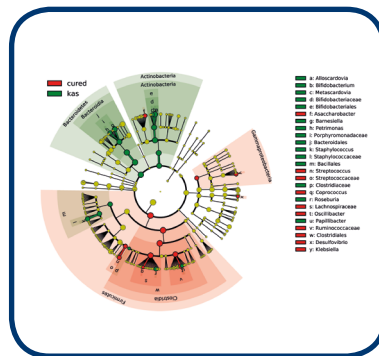
Whether you wish to type or characterize microbial isolates, monitor food-borne pathogens, or perform a quality control on starter cultures, custom bioinformatics can be performed allowing more in-depth mining of your dataset. We generate reports that optimally address your research question.

About GenomeScan

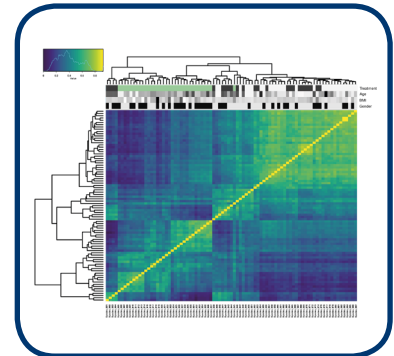
As an ISO-accredited leading Dutch Next Generation Sequencing service provider, GenomeScan develops customizable NGS solutions for pharmaceutical and biotech companies, health care providers and academic institutions. By providing new tools to analyze genetic disorders quicker, affordably and effectively,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



Interactive analysis of metagenomics data



Differential microbial abundance between sample groups



Heatmap