

Actionable. Accessible. Affordable.

# Shotgun Metagenomic Sequencing

## Discover the diversity and functional potential of your sample microbiome

Shotgun metagenomic sequencing involves untargeted sequencing of all microbial genomes in each sample, enabling unbiased characterisation and in-depth study of microbial communities in their living environments.

The human microbiota plays a major role in health and disease, and we are just beginning to understand its impact and tap into its vast potential.

Mirxes offers high throughput shotgun metagenomic sequencing, complete with bioinformatics analysis, tailor-made to suit your project needs.



### High Quality Data

Q30 score of >80% for PE150 and >85% for PE100



### Both host and microbial genomes are sequenced

Enabling detailed study of host-microbiome interactions



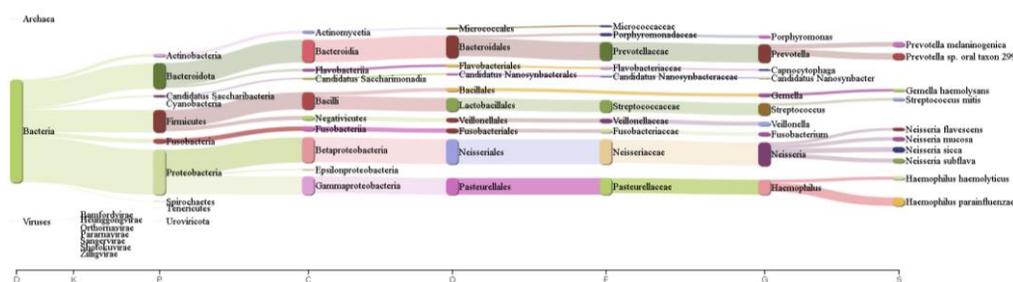
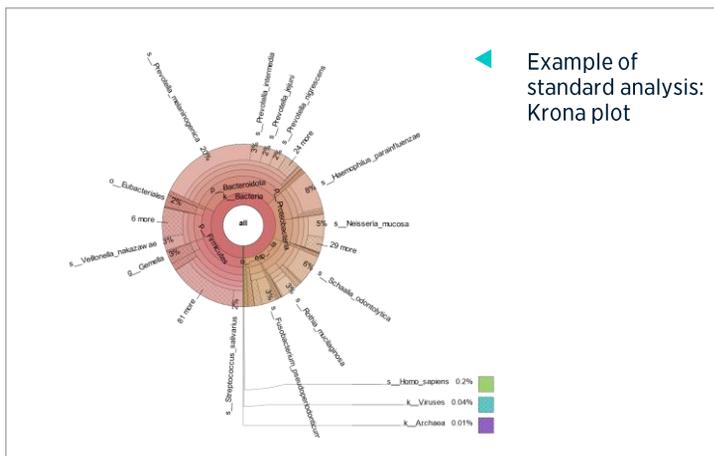
### Expert Bioinformatics Service

Experienced team providing customised analysis



### Reliable Service and Turnaround Time

All operations based in Singapore, using certified manufacturers' workflows



## Shotgun Metagenomic Service Workflow



\*Mirxes currently supports DNA extraction for human skin (swab or tape) and saliva only.

Minimum Data Quantity (before host genome exclusion)	Sequencing Platforms	Turnaround Time
Saliva: ≥ 10 Gb raw data	DNBSEQ-T7	2-4 weeks from successful sample QC* to data delivery
Skin: ≥ 10 Gb raw data		
gDNA from other sources e.g. Stool: ≥ 6 Gb raw data		

\*The sample QC requirement for this assay is dependent on the assay type.

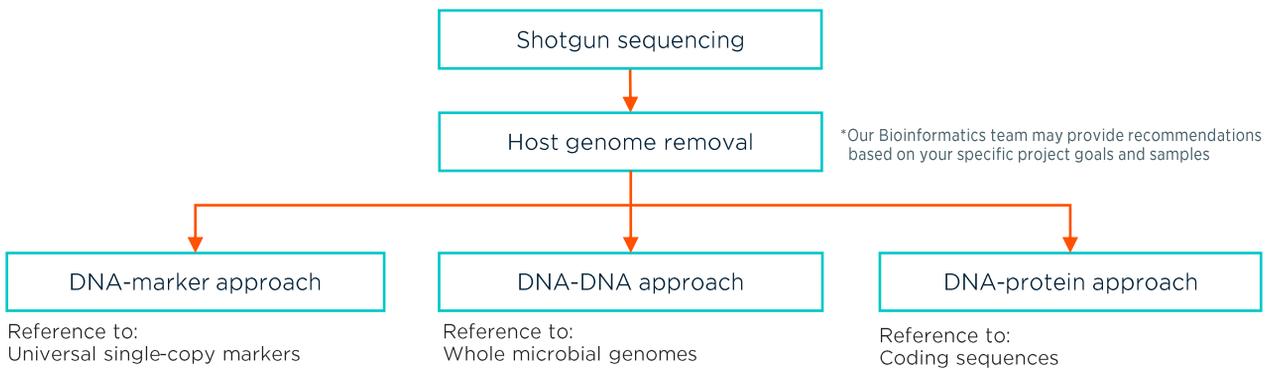
Note: Minimum data quantity required may vary depending on the source of the gDNA, and the purpose of the sequencing project. Please contact us for further recommendations of sequencing data quantity.

Sample Type (pre-extraction)	Optimal Input Amount
Human skin (skin swab or tape)	Variable depending on sampling method, please contact us with the specific request so that we may advise accordingly
Human saliva	≥ 2 ml

Sample Type (post-extraction)	Optimal Input Amount	Volume	Concentration	Purity and Quality
Human gDNA	≥ 100 ng	≥ 20 µl	≥ 5 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 1.7 DIN ≥ 7

Please note that these requirements serve only as a guide. Please contact us for further assessment if your samples do not meet the requested amounts.

## Bioinformatics Analysis and Support



### Standard analysis

- Data Quality Control: Filtering reads with adapter or low-quality sequence data
- Removal of host genome
- Taxonomy and abundance
- Gene function annotation
- Pathway analysis for different taxa identified

### Additional Tertiary Analysis

- Linkage between microbial taxa and specific variations in human genome
- Variation calling from whole genome
- Antibiotic Resistance Gene Annotation
- Other options available upon request

## Contact Us

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