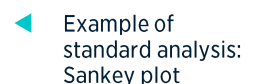
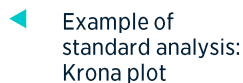
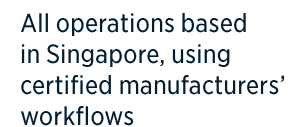


Shotgun Metagenomic Sequencing

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



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		

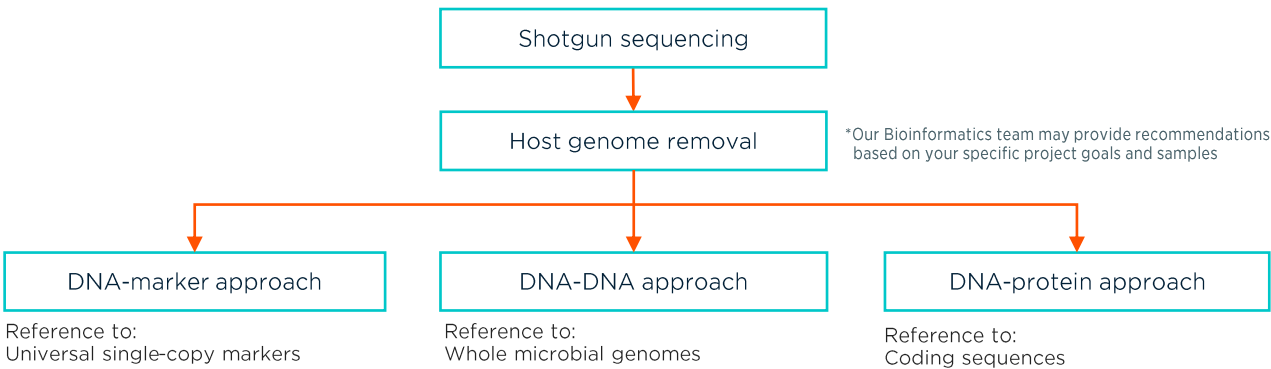
*The sample QC requirement for this assay is dependent on the assay type.
Note: Minimum data quantity required may vary depending on the source of the gDNA, and the purpose of the sequencing project. Please contact us for further recommendations of sequencing data quantity.

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

Email: genomics@mirxes.com

Phone: +65 6950 5864

Website: mirxes.com