Sample Submission Guidelines

Human Whole Genome Sequencing

Service	Sample Type	Sample Source	Optimum Input Amount	Volume	Concentration	Purity and Quality
hWGS (PCR-free)	gDNA	Fresh frozen tissue, cell line, saliva, blood	≥ 1.5 µg	≥ 20 µl	≥ 20 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 1.7
hWGS (PCR-based)	gDNA	Fresh frozen tissue, cell line, saliva, blood	≥ 500 ng	≥ 20 µl	≥ 20 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 1.7 DIN ≥ 7
	gDNA	FFPE	≥ 800 ng	≥ 20 µl	≥ 20 ng/µl	Main band of > 1,500 bp (Q Score > 0.5) DIN ≥ 4

Recommended suspension buffer: TE buffer or Nuclease-free water

Human Whole Exome Sequencing

Service	Sample Type	Sample Source	Optimum Input Amount	Volume	Concentration	Purity and Quality
hWES	gDNA	Fresh frozen tissue, cell line, saliva, blood	≥ 500 ng	≥ 20 µl	≥ 10 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 1.7 DIN ≥ 7
	gDNA	FFPE	≥ 500 ng	≥ 20 µl	≥ 10 ng/µl	Main band of > 1,500 bp (Q Score > 0.5) DIN ≥ 4

Recommended suspension buffer: TE buffer or Nuclease-free water

RNA Sequencing

Service	Sample Type	Sample Source	Optimum Input Amount	Volume	Concentration	Purity and Quality
RNA-Seq	Total RNA	Fresh frozen tissue, cell line, saliva, blood	≥ 500 ng	≥ 20 µl	≥ 25 ng/µl	OD260/280 = 1.8 - 2.1 OD 260/230 ≥ 2.0 RIN ≥ 6
	Total RNA	FFPE	≥ 500 ng	≥ 20 µl	≥ 25 ng/µl	OD260/280 = 1.8 - 2.1 OD 260/230 ≥ 2.0 DV200 ≥ 50% RIN ≥ 2
RNA-Seq (Directional)	Total RNA	Fresh frozen tissue, cell line, saliva, blood	≥ 1 µg	≥ 20 µl	≥ 25 ng/µl	OD260/280 = 1.8 - 2.1 OD 260/230 ≥ 2.0 RIN ≥ 6
	Total RNA	FFPE	≥ 1 µg	≥ 20 µl	≥ 25 ng/µl	OD260/280 = 1.8 - 2.1 OD 260/230 ≥ 2.0 DV200 ≥ 50% RIN ≥ 2

Recommended suspension buffer: Nuclease-free water

Human Whole Genome Methylation Sequencing

Service	Sample Type	Sample Source	Optimum Input Amount	Volume	Concentration	Purity and Quality
hWGMS	gDNA	Fresh frozen tissue, cell line, saliva, blood	≥ 1 µg	≥ 20 µl	≥ 20 ng/µl	OD260/280 = 1.8 - 2.0 OD 260/230 ≥ 1.7 DIN ≥ 7

Recommended suspension buffer: TE buffer or Nuclease-free water

Shotgun Metagenomics Sequencing

Service	Sample Type (pre-extraction)	Optimal Input Amount
Shotgun metagenomics	Human skin (skin swab or tape)	Variable depending on sampling method, please contact us with the specific request so that we may advise accordingly (Please submit only 1 skin swab or tape per tube)
	Human saliva	≥ 2 ml

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

Pre-made Library Sequencing Service

Service	Library Concentration (measured by Qubit)	Total Amount	Total Volume	Library Size
Pre-made library sequencing	≥ 2 ng/µl	≥ 200 ng	≥ 20 µl	200-700 bp

Stereo-seq Library Sequencing Service

Service	Library Type	Total Library Amount	Total Library Volume	Library Peak Fragment Size (bp)	Other QC Criteria
Stereo-seq FF library sequencing	Stereo-seq FF V1.3	≥ 300 ng (per 1B reads output)	≥ 15 µl	200-600	RIN ≥ 6 cDNA peak fragment size: 200-2000 bp
Stereo-CITE FF library sequencing	Stereo-CITE V1.1 ADT library	≥ 300 ng (per 1B reads output)	≥ 15 µl	200-250	RIN ≥ 6 cDNA peak fragment size: 180-230 bp
	Stereo-CITE V1.1 cDNA library	≥ 300 ng (per 1B reads output)	≥ 15 µl	200-600	RIN ≥ 6 cDNA peak fragment size: 200-2000 bp
Stereo-seq FFPE library sequencing	Stereo-seq FFPE V1.1	≥ 350 ng (per 3B reads output)	≥ 20 µl	200-1000	DV200 ≥ 30 cDNA peak fragment size: 150-350 bp
	Stereo-seq FFPE V1.0	≥ 350 ng (per 3B reads output)	≥ 20 µl	100-1000	DV200 ≥ 30 cDNA peak fragment size: 150-350 bp

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.

Shipping Information FAQ

1. How do I prepare and pack my samples for shipping?

Your MiRXES representative will provide you a Service Order Form and please fill in the required information, and then return it to us by both emailing a soft copy and attaching a printed copy in your sample package.

a) Ensure all tubes or plates are clearly labelled per your descriptions in the Service Order Form
b) Ensure all tubes or plates are tightly sealed to prevent leakage of samples
c) Attach a copy of the printed Service Order Form
d) Ensure adequate dry ice is used for the specimen storage & transport
e) For Singapore customers: Inform your MiRXES representative to come collect the package
For non-Singapore customers: Ship your sealed package with your preferred courier to the address below.

2. Where do I send my samples to?

Please send your samples to MiRXES Genomics Lab at:
Address: 8 Biomedical Grove #02-01 Neuros, Singapore 138665
Attention: Mr Noel Wong