MHTP
Monash Health
Translation Precinct
Medical Genomics Facility

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NGS Sample Submission Requirements.

Below are details for standard procedures. Please contact us if your requirements are not listed or your samples fail any given criteria.

Note that amounts required/available will vary according to method of processing. Note that lower amounts will nearly always result in less complex libraries and thus less complex data.

General Criteria.

Provide as much information as possible about the samples e.g. Source tissue/cells and amounts; any fixation; how they have been processed etc. DNA should be resuspended in Water or Low TE and RNA in Water.
DNA should be free of RNA contamination and RNA should be free of DNA contamination.
Absorbance readings should have 260:280 and 260:230 ratios >1.8. Also note that for low concentrations of nucleotides Nanodrop often overestimates the concentration.
Samples will be assessed for integrity upon receipt and extensively degraded material will not be processed.

DNA-Sequencing.

PCR-free DNA Sequencing provide 5ug in not more than 50ul.
Standard DNA sequencing provide >100ng in not more than 50ul.

Exome Sequencing.

300ng - 3ug in not more than 50ul.

ChIP-Seq.

>2ng in not more than 50ul.
Please also provide size range of IP'd DNA (200-600bp) and details of how the sample has been purified post-capture. We have best results using the Diagenode iPure cleanup kit. Where suitable targets are known, we recommend validating IP by qPCR before performing ChIP-Seq.

RNA-Sequencing.

RNA should be purified and treated with on-column DNase during the purification procedure. Please provide 2 tubes for each sample on dry ice, one with 2-3ul for sample QC and the other with the stock required for processing.

PolyA-RNA-Seq.

50ng-3ug of Total RNA in less than 50ul

Ribodepletion RNA-Seq.

100ng-500ng of Total RNA in less than 10ul

Low input RNA-Seq.

2-50ng of Total RNA in less than 10ul.