

QUB Functional Genomics CTU

Project Request Form

The following pro forma is designed to capture all of the necessary information in order to design a genomic profiling experiment. This information will be used to:

1. design the most appropriate profiling
2. identify samples required for analysis
3. ensure sample tracking
4. provide a single document that encapsulates sufficient information to enable smooth running of the entire process

The successful running and outcome of each project is directly related to the advance planning steps. As such, capturing the requisite information prior to the instigation of the project is of paramount importance.

Client Details	
Name (user)	
P.I	
Institution	
Department	
Address	
Telephone	
Email	
PO / Project Code for charging	
Funding Body (UK or EU)	
Allocated Project Number if applicable	

Background

Please OUTLINE the biological question to be addressed, OR specify the metrics you want

Sample Processing Details:

Number of Samples Requested	
Has ethical approval and/or consent form been given for the sequencing?	
Are samples in your possession and ready to submit?	
Number of experimental groups	
Number of experimental replicates	
Additional details	

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Sample Type:

Total RNA	
Total DNA	
Blood	
Tissue (please indicate fresh or frozen)	
Formalin Fixed Paraffin Embedded tissue (FFPE)	
Additional details	

Species of Interest:

Human	
Rat	
Mouse	
Other	
Additional details (please include genome link if possible)	

Sample Extraction:

Extraction Method used by Client	
Type of solution sample dissolved in	
Does buffer contain EDTA	
Samples DNase treated	
Gel Image/ Bioanalyser traces available	
Additional details	

Project Type:

Extraction (MagnaPure)	
Sample QC Only	
mRNA Seq	
miRNA Seq	
Targeted/ custom RNA Seq	
DNA Seq Whole Exome	
DNA Seq targeted Hotspot	
Mitochondrial DNA	
Chip-Seq library prep	
Methylation Sequencing	
Instrument Run only (MiSeq / NextSeq)	
Fluidigm C1 (single cell lib prep)	
Genomics 10x (single cell lib prep)	
Sanger Sequencing Electrophoresis only	
Sanger Sequencing Cleanup & Electrophoresis	
Sanger Full Sequencing	
Informatics Only	
Other (please specify):	

Kit Preference (if Known)

Small RNA Library Prep	
Tru Seq Stranded mRNA Library Prep	
KAPA (Stranded) RNA HyperPrep with Riboerese HMR	
KAPA (Stranded) RNA HyperPrep without Riboerese	
Targeted Choice RNA Library Prep	
Exome/ Medexome Library Prep	

Nextera DNA Library Prep	
DNA Kapa HyperPlus/ HyperPrep	
Tru Seq Methyl Capture Library Prep	
Targeted DNA Library Prep Qiagen	
Diagenode ChIP Library Prep	
SeqCap Epi CpGiant Enrichment Kit	
SeqCap Epi Choice Enrichment Kit	
Other (Please Specify)	

NGS Run Specification Required (If Known):

Run Parameters	
Read Length (bp)	
SR	
PE	
No reads/ sample (M)	
Depth of Coverage	
<u>Additional Information</u>	

NB

Primary QC analysis will be provided with all sequencing runs performed within the GCTU.

We will provide raw sequencing quality metrics and first pass alignment/coverage metrics as standard for Human and Mouse alignments. Other species alignments need to be discussed and may cost extra.

Data will be returned as De-multiplexed FASTQ files standard.

Project Schedule:

Expected Date of sample delivery	
Action for samples at project close out (samples will be destroyed unless otherwise specified)	

<u>Additional Information</u>

	QUB GCTU Approval	Client Approval
Name	Julia Miskelly	
Title	GCTU Manager	
Signature		

Date		
PO / Project Code for charging For Project Codes please include start and end dates. *Projects will not be tracked until an active project code or P.O is provided		
Funding Body (UK or EU)		
Allocated Project Number		
Quoted Cost		

For further details contact
genomics@qub.ac.uk
028 90972193