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GENOMICS CTU SERVICE LIST 2022-2023

PROJECT QUOTATION SUBMISSION GUIDELINES

- All requests should be submitted via our online Project Request Form.
- Once this has been reviewed, you will be issued with a Quotation for the work requested.
- If you wish to proceed with the work, please sign the quotation, complete with grant code/PO number for charging and return to genomics@qub.ac.uk.
- You will then be issued with a Project Number and your project scheduled.
- Samples may then be left to the Genomics CTU and should be labelled with the relevant Project number.
- **NOTE** samples should not be left for testing prior to a Project number being assigned.

TASK REQUEST SUBMISSION GUIDELINES

- All requests should be submitted via our online Project Request Form.
- Once this has been reviewed, you will be issued with a Task number.
- Samples may then be left to the Genomics CTU and should be labelled with the relevant Task number.
- **NOTE** samples should not be left for testing prior to a task number being assigned.

Our estimated turnaround time is 8 weeks for projects and 2 days for tasks.

Projects (for which samples have been received) are scheduled at a weekly Monday meeting.

Service	Costing Summary
Individual Sample QC Tasks	
Fragment Analyser	Per row (≤66 samples) Per plate (67-88 samples)
TapeStation	Per sample
Qubit/Quant-IT	Per sample
Equipment Use Only	
Echo	Per 15 min slot
MagNA Pure 96	Per hour
Automated Nucleic Acid Extraction - MagnaPure	
RNA from FFPE Tissue	≤ 24 samples 25 - 48 samples 49 - 96 samples
RNA from Cells/Whole Blood	
DNA from FFPE Tissue	
DNA from Cells/Whole Blood	
Library Preparation – Single Cell	
10x Genomics GEX	Per sample
10x Genomics ATAC	Per sample
10x Genomics Multiome	Per sample
Parse Evercode™ Whole Transcriptome Mini	≤ 12 samples
Parse Evercode™ Whole Transcriptome WT	≤ 48 samples
Parse Evercode™ Whole Transcriptome Mega	≤ 96 samples
Library Preparation – DNA/RNA	
KAPA RNA HyperPrep Kit with RiboErase (Human, Mouse, Rat)	Per sample
KAPA RNA HyperPrep Kit (without RiboErase)	Per sample
KAPA mRNA HyperPrep Kit with Poly A enrichment	Per sample
KAPA DNA HyperPlus	Per sample
Illumina RNA Prep with Exome Enrichment	Per sample
QIAseq miRNA Prep (Small RNA library processing)	Per sample

Twist Epigenome Library Prep with Enzymatic C-T Conversion	Per sample
16S/ITS Metagenomic Library Prep (other regions on request)	Per sample
PacBio 16S Metagenome Seq	Per 96 samples
PacBio 16S Metagenome Seq	Per 192 samples
PacBio WGS - 1 sample per SMRT cell	Per sample
PacBio WGS - 2 samples per SMRT cell	Per 2 samples
PacBio WGS - 4 samples per SMRT cell	Per 4 samples
PacBio Iso-Seq RNA seq - 1 sample per SMRT cell	Per sample
PacBio Iso-Seq RNA seq - 2 samples per SMRT cell	Per 2 samples
PacBio Iso-Seq RNA seq - 4 samples per SMRT cell	Per 4 samples
Other Library Prep kits	Custom quote
Illumina Sequencing – MiSeq	
MiSeq Reagent Kit v3 (150-cycle, 22-25M RPF)	Per run
MiSeq Reagent Kit v3 (600-cycle, 22-25M RPF)	Per run
MiSeq Reagent Kit v2 (50-cycles, 12-15M RPF)	Per run
MiSeq Reagent Kit v2 (300-cycles, 12-15M RPF)	Per run
MiSeq Reagent Kit v2 (500-cycles, 12-15M RPF)	Per run
MiSeq Reagent Micro Kit v2 (300-cycles, 4M RPF)	Per run
MiSeq Reagent Nano Kit v2 (300-cycles, 1M RPF)	Per run
MiSeq Reagent Nano Kit v2 (500-cycle, 1M RPF)	Per run
Illumina Sequencing – NextSeq	
NextSeq 1000/2000 P1 Reagents (300 Cycles, 100M RPF)	Per run
NextSeq 1000/2000 P2 Reagents v3 (100 Cycles, 400M RPF)	Per run
NextSeq 1000/2000 P2 Reagents v3 (200 Cycles, 400M RPF)	Per run
NextSeq 1000/2000 P2 Reagents v3 (300 Cycles, 400M RPF)	Per run
NextSeq 2000 P3 Reagents (100 Cycles, 1.2B RPF)	Per run
NextSeq 2000 P3 Reagents (200 Cycles, 1.2B RPF)	Per run
NextSeq 2000 P3 Reagents (300 Cycles, 1.2B RPF)	Per run
Illumina Sequencing – NovaSeq	
NovaSeq 6000 SP Reagent Kit v1.5 (100 cycles, 650-800M RPF)	Per run
NovaSeq 6000 SP Reagent Kit v1.5 (200 cycles, 650-800M RPF)	Per run
NovaSeq 6000 SP Reagent Kit v1.5 (300 cycles, 650-800M RPF)	Per run
NovaSeq 6000 SP Reagent Kit v1.5 (500 cycles, 650-800M RPF)	Per run
NovaSeq 6000 S1 Reagent Kit v1.5 (100 cycles, 1.3-1.6B RPF)	Per run
NovaSeq 6000 S2 Reagent Kit v1.5 (100 cycles, 3.3-4.1B RPF)	Per run
NovaSeq 6000 S2 Reagent Kit v1.5 (100 cycles, 3.3-4.1B RPF) – XP	Per run
NovaSeq 6000 S2 Reagent Kit v1.5 (200 cycles, 3-4.1B RPF)	Per run
NovaSeq 6000 S2 Reagent Kit v1.5 (200 cycles, 3-4.1B RPF) – XP	Per run
NovaSeq 6000 S2 Reagent Kit v1.5 (300 cycles, 3-4.1B RPF)	Per run
NovaSeq 6000 S2 Reagent Kit v1.5 (300 cycles, 3-4.1B RPF) – XP	Per run
NovaSeq 6000 S4 Reagent Kit v1.5 (200 cycles, 8-10B RPF)	Per run
NovaSeq 6000 S4 Reagent Kit v1.5 (200 cycles, 8-10B RPF) – XP	Per run
NovaSeq 6000 S4 Reagent Kit v1.5 (300 cycles, 10B RPF)	Per run
NovaSeq 6000 S4 Reagent Kit v1.5 (300 cycles, 10B RPF) – XP	Per run
PacBio Sequencing - Sequel IIe	
Sequel IIe – Run Only	Per run
8M SMRT Cell	Per SMRT cell
Data Management (FASTQC generation, Data Transfer and 1-Year Data Storage)	
>500Gb	Per run
>100Gb - <500Gb	Per run
>20 - <100Gb	Per run
<20Gb	Per run
Bioinformatic Analysis - Additional Services that must be requested.	
Primary Alignment (Human & Mouse Only)	Per sample
Counts (RNA-Seq Only)	Per sample
RNA Exome Analysis	Per sample

Differential Gene Expression Analysis (DGEA)	1-6 comparisons
	>6 comparisons – Custom Quote
Pathway Analysis (Human Only)	1-6 comparisons
	>6 comparisons – Custom Quote
Other Services	
Oxford Nanopore Technology GridION long read sequencing	Contact for further information
10X Genomics Visium Spatial Transcriptomics	Contact for further information

RPF = Reads Passing Filter

STANDARD GENOMICS CTU WORKFLOWS (Exemplar workflows - may differ based on specific protocol)

RNA-Seq
- o Sample QC on TapeStation 4200 or Fragment Analyser for small RNA and NanoDrop
- o Library Preparation (including sample normalisation)
- o Library QC on TapeStation 4200 & Qubit
- o Libraries normalised and pooled
- o Pool run on TapeStation & Qubit
- o *For NextSeq P3 and NovaSeq runs only* – normalised libraries are QC-ed on MiSeq V2 Nano cart to ensure indexes are balanced
- o Sample Sequencing
- o Data Management – FASTQC, FASTQ generation, Data Transfer and 1-Year Data Storage

DNA-Seq
- o Sample QC on Fragment Analyser & Qubit
- o Library Preparation (including sample normalisation)
- o Library QC on TapeStation 4200 & Qubit
- o Libraries normalised and pooled
- o Pool run on TapeStation & Qubit
- o *For NextSeq P3 and NovaSeq runs only* – normalised libraries are QC-ed on MiSeq V2 Nano cart to ensure indexes are balanced
- o Sample Sequencing
- o Data Management – FASTQC, FASTQ generation, Data Transfer and 1-Year Data Storage

Metagenomics
- o Amplicon PCR and clean up
- o Amplicon PCR QC on Fragment Analyser
- o Index PCR and clean up
- o Index PCR QC on Fragment analyser and Quant-it
- o Libraries normalised and pooled
- o Pool run on TapeStation & Qubit
- o Sample Sequencing
- o Data Management – FASTQC, FASTQ generation, Data Transfer and 1-Year Data Storage

Single cell RNA Sequencing (10x 3' Gene Expression Libraries*)
- o Generation of barcoded single cells
- o cDNA generation and QC on Fragment Analyzer
- o Library Preparation (including sample normalisation)
- o Library QC on TapeStation & Qubit
- o Library normalisation and pooling
- o Pool QC on TapeStation and Qubit
- o MiSeq V2 Nano cart sequencing to determine mean reads per cell
- o Deeper sequencing (NextSeq 2000, NovaSeq 6000)
- o Data analysis – CellRanger
- o Data transfer and storage for 1 year

- o *Can accommodate other 10x workflows (e.g., multiome ATAC, immune profiling) and Parse*

PacBio Projects
- o Sample QC on TapeStation 4200 or Fragment Analyser and NanoDrop
- o Library Preparation (including sample normalisation)
- o Library QC on TapeStation 4200 or Fragment Analyser & Qubit
- o Diffusion loading
- o Sample Sequencing
- o Sequencing summary report & Demultiplexed HiFi FASTQ / BAM files
- o *Iso-Seq analysis (human only)*: Generation of transcript isoforms.

SAMPLE REQUIREMENTS

Please refer to table below for guidance on type, quantity, and concentration of sample to submit for different project types.

All samples should be of good quality with a 260:230 ratio of ~ 2.0-2 and 260:280 ratio of ~ 1.8-2.0.

Customers will be notified if sample quality following QC is suboptimal prior to proceeding with library preparation.

Library Prep Method	Type of Nucleic Acid	Sample Volume	Sample Conc.	Total Required	Format for 1-24 samples	Format for 25-96 samples
KAPA Stranded RNA HyperPrep with Riboerase HMR	Total RNA	15 μL	>50 ng/μL	750 ng	Single tubes or 96-well plate	96-well plate
KAPA Stranded RNA HyperPrep without Riboerase	mRNA, ribosomal-depleted RNA	15 μL	>10 ng/μL	100 ng	Single tubes or 96-well plate	96-well plate
KAPA mRNA HyperPrep (poly(A) mRNA capture)	Total RNA	15 μL	>50 ng/μL	750 ng	Single tubes or 96-well plate	96-well plate
Kapa HyperPlus for target capture enrichment or WGS	Genomic DNA	15 μL	20 ng/μL	200 ng	Single tubes or 96-well plate	96-well plate
QiaSeq miRNA	Total RNA	15 μL	20 ng/μL	100 – 500ng	Single tubes or 96-well plate	96-well plate
Sequencing on MiSeq	Pooled NGS Libraries	10 μL	10 nM	100 fmol	Single tube	Single tube
Sequencing on NextSeq 2000	Pooled NGS Libraries	10 μL	10 nM	100 fmol	Single tube	Single tube
Sequencing on NovaSeq 6000 – SP	Pooled NGS Libraries	30 μl	10 nM	300 fmol	Single tube	Single tube
Sequencing on NovaSeq 6000 – S1	Pooled NGS Libraries	30 μl	10 nM	300 fmol	Single tube	Single tube
Sequencing on NovaSeq 6000 – S2	Pooled NGS Libraries	40 μl	10 nM	400 fmol	Single tube	Single tube
Sequencing on NovaSeq 6000 – S4	Pooled NGS Libraries	70 μl	10 nM	700 fmol	Single tube	Single tube
*Sequencing on MiSeq	Individual NGS Library	10 μL	10 nM	100 fmol	Single tubes or 96-well plate	96-well plate
*Sequencing on NextSeq 2000	Individual NGS Library	10 μL	10 nM	100 fmol	Single tubes or 96-well plate	96-well plate
*Sequencing on NovaSeq 6000	Individual NGS Library	10 μL	10 nM	100 fmol	Single tubes or 96-well plate	96-well plate
10X Single cell suspensions	N/A	100-200 μL	800-1200 cells/μl	-	Single tube	Single tube
PacBio 16s rRNA gene sequencing	Genomic DNA	20 μL at 10 ng/ μL	10 ng/μL	200ng	96-well plate	96-well plate
PacBio Metagenome Shotgun sequencing	Genomic DNA with average mode size > 15Kb	60 μL at ~100 ng/μL	~ 100 ng/ μL	6 μg	Single tube	Single tube
PacBio Whole Genome Sequencing	Genomic DNA with average mode size of > 30Kb	60 μl at ~100ng/μL	~100 ng/ μl	6 μg	Single tube	Single tube
PacBio RNA-seq with Iso-Seq lib prep	Total RNA	25 μL at ~50 ng/ μL	>50 ng/ μL	~1000ng	Single tube	Single tube

*NOTE For sequencing only projects, if libraries are not provided pooled in a single tube, you will be charged for library QC (regardless of any completed prior to sample delivery) and staff time for normalisation and pooling. A MiSeq index run will be added to ensure balance before proceeding with sequencing.

If you have any questions or wish to discuss your project prior to submitting a request, please do not hesitate to contact us at genomics@qub.ac.uk.