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Genomics-Core Facility

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Next Generation Sequencing Sample Submission Form

Sample Input Recommendations (Input DNA Quantity & Quality):

The success or failure of a library preparation strongly depends on an optimal quantity and quality of input DNA/RNA.:

- We recommend an optimal quantity of
  - **500 ng input DNA for Exome Enrichment**
  - **2 µg WG Sequencing**
  - **2 µg RNA**.

  (please contact the core facility for lower quantities)
- It is necessary to quantify samples by fluorimetric measurement. This can be done at the core facility.
- Genomic DNA samples should be carefully collected to ensure that they are high molecular weight and free of contaminants (RNA or small nucleic acid fragments such as nucleotides).
- Gel electrophoresis is suitable for revealing the condition of the DNA.
- Impurities, such as detergents or proteins, can be revealed by smearing of DNA bands. RNA, which interferes with 260 nm readings, is often visible at the bottom of a gel. A ladder or smear below a band of interest may indicate nicking or other damage to DNA.
- **For DNA please provide a digital image of a gel for each sample with clearly indicated sample identity and size standard (give band sizes).**
- **RNA will be checked by Bioanalyzer. RNA samples with a RIN < 7 will only be processes at the risk of the customer**
- **DNA/RNA stocks and libraries will be discarded after two month without further notice**

PI Name:

Institution: **Department:**

Email: **Phone:**

Sample Type:

☐ gDNA ☐ ChIP DNA ☐ small RNA ☐ total RNA ☐ shRNA library

Isolation Method:

Elution Buffer:

Please note that DNA/RNA isolated by Phenol/Chloroform/Trizol can only be processed at the risk of the customer, as it can interfere with the library construction.

Type of Sequencing:

DNA:

☐ Whole genome ☐ Exome enrichment (37 Mb)

☐ Expanded Ex.Enr.(incl. UTRs and miRNAs, 67 Mb) ☐ ChIP ☐ shRNA screen

RNA:

☐ Counting ☐ Counting and alternative splicing ☐ poly-A RNA

☐ Total RNA (including ncRNA but not miRNA) ☐ miRNA

Mean Sequencing Depth:

☐ 30x ☐ 50x ☐ 100x ☐ ultra deep specify (reads):

Please note that it is not possible to guarantee the sequencing depth.

Sequencing length:

☐ SR 50bp ☐ PE 100bp ☐ other (specify):

Primary Bioinformatics Analysis:

☐ Base calling and demultiplexing ☐ Alignment to reference genome:

Please contact PD Dr. H. Kestler for further bioinformatics analysis

Additional information required for shRNA library screen[1]:

Due to high number of variables in shRNA screens, PIs are requested to give a brief description of their project. Points of emphasis are suggested below.

		Description here
Library description:	**Type of virus**	
Library source:	**Commercial (specify)**	
	Custom made (requires further discussion)	
	Total number of shRNA in library	
Target organism/species:		
Multiplicity of Infection (MOI):		
Number of cells used:		
Desired read:		
Barcode information:		
shRNA Reference library:		

[1] For other variants of shRNA or RNAi based sequencing, further discussion would be advisable

Please fill in the form and submit it with your samples

Delivery date:

	Sample Name	Organism	Conc.(ng/µl)	260/280 Ratio	Volume (µl)	Qubit Measurement (ng/µl)
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2						
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