**Core Facility Genomics**

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# General Information
# Sample Submission

## Sample Input Recommendations (Input DNA Quantity & Quality):

The success of a Next Generation Sequencing or Microarray experiment strongly depends on an optimal quantity and quality of input DNA/RNA.:

- For standard applications we recommend an optimal quantity of
    - 200 - 500 ng input DNA for Exome Enrichment
    - 200 - 500 ng input DNA for WG Sequencing
    - 200 - 500 ng total RNA (RNA- as well as miRNA-Seq or Microarrays).
    - 100 pg–10 ng DNA for ChIP-Seq
    - For special applications (i.e. Single Cell RNA-Seq, Plasma-Seq or Exosomes) please contact the Core Facility Genomics

- All samples should be quantified by a photometric measurement (i.e. Nanodrop)
  260/280 Ratio should be ~ 2 for RNA and ~ 1.8 for DNA
  260/230 Ratio should be ~ 2 - 2,2

- Low 260/230 ratios might indicate a contamination with phenol which might inhibit later enzymatic reactions.

- Please note that RNA isolated by Phenol/Chloroform/Trizol can only be processed at the risk of the customer, as it even small traces can interfere with the library construction / Microarray labelling.

- All samples need to be quantified by fluorimetric measurement additionally, as a photometric measurement does not differentiate between DNA and RNA. This can be done at the Core Facility Genomics.

- For any miRNA Analysis, please make sure that your isolation method is suitable (not all are) and retains miRNAs.
- RNA samples should be stored at -80°C and transport to the Core Facility should be done on dry ice!
- For RNA-Seq experiments a DNAse treatment is recommended.
- For RNA Microarray experiments a DNAse treatment is usually not necessary.
- Genomic DNA samples should be carefully collected to ensure that they are of high molecular weight and free of contaminants (RNAase treatment is recommended).
- DNA fragmentation should be avoided and checked by Gel electrophoresis.
- RNA will be checked on a Agilent Tape Station. 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, so please collect any remaining sample rests after the analysis!**

For Next Generation Sequencing experiments it is highly recommended that customers contact the Core Unit Bioinfomatics and Datamanagement (https://cubi.medizin.uni-ulm.de/) **before** starting their experiments, to make sure that the design of the experiment is suitable for answering your scientific questions!

**If the project has not been paid in advance, all customers need to provide the signed document "CF Genomics Bestätigung Kostenstelle" as otherwise your samples can not be processed!**

**Please note that for any sequencing experiment you will also need to fill out the corresponding document of the Core Unit Bioinformatics and Data management, or you won't receive any Data!**