**Library preparation form starting from DNA/RNA Samples**

The Genomics Core Facility provides whole genome and whole exome library preparation for DNA (TruSeq PCR-free Genomic DNA library and Agilent V6 Exome) as well as mRNA and total RNA library preparation (TruSeq Stranded mRNA and TruSeq Stranded Total RNA). The input DNA and RNA quantities specified below apply if the samples are quantified by a fluorometric method (e.g. Qubit, PicoGreen, RiboGreen). If a spectrophotometer (e.g. Nanodrop) was used, we suggest submitting twice the requested amount of sample since this type of measurement is often unreliable. In any case, sample amounts higher than the minimum requirements will improve the library complexity and thus the quality of the data.

Sample submission requirements:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Library Type** | **Quality** | **Quantity** | **Concentration** | **Buffer** |
| TruSeq PCR-free Genomic DNA  Library/  DNA PCR-Free Prep, Tagmentation library | double-stranded non-degraded DNA A260/280 ratio > 1.8,  RNA-free | > 1.5 µg | > 20 ng/µl | EB\*, H2O |
| Agilent V6 Exome | double-stranded DNA non-degraded A260/280 ratio > 1.8,  RNA-free | > 3.5 µg | > 25 ng/µl | EB\*, H2O |
| Twist Exome/Panels | double-stranded DNA non-degraded A260/280 ratio > 1.8,  RNA-free | > 1 µg | > 10 ng/µl | EB\*, H2O |
| Stranded  mRNA | mRNA, RIN > 7 DNA-free | > 300 ng | In 50 µl | non-DEPC treated H2O |
| Stranded Total RNA | Total RNA, RIN > 7 DNA-free | > 300 ng | In 10 µl | non-DEPC treated H2O |

\*EB: Elution Buffer

If any expert advice beforehand is needed please contact the Genomics Core Facility: CF-Genomics@helmholtz-muenchen.de

**Before submitting your project to CF-Genomics ensure you have done and agreed to all on the checklist below:**

* GCF sequencing submission form completed, signed, submitted as .PDF  
  File name:
* GCF Sample submission form DNA/RNA completely and properly filled (.xlsx)  
  File name:
* Submitted DNA/RNA complies specified recommendations
* Bioanalyzer traces of total RNA for mRNA and total RNA sequencing submitted as **.xad** and **.pdf** file (sample labeling as is in the manifest and on the tube).
* All legal and ethical requirement are fulfilled to perform the ordered work
* Guarantee that sample material is not above BSL2 level

General Information:

User Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ PI Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Institution: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Department: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Email: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Phone: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Finances:

PSP-element for internal projects: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Offer number for external projects: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Date, Signature of Person responsible for payment:

**Requested Library prep and Sequencing Configuration**

Requested library prep and number of samples submitted:

Whole genome sequencing with 35-fold average coverage per library – 150 bp paired end

Exome sequencing with 120-fold average coverage per library – 100 bp paired end

mRNA sequencing with ~35x10 reads per library – 150 bp paired end⁶ reads per library – 150 bp paired end

Total RNA sequencing with ~35x10 reads per library – 150 bp paired end⁶ reads per library –   
 150 bp paired end

Other (please specify flow cell type, number of lanes, and any other option needed)   
 \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_   
 Read length: R1/\_\_\_\_\_\_\_\_\_\_i7/\_\_\_\_\_\_\_\_\_\_i5/\_\_\_\_\_\_\_\_\_\_R2/\_\_\_\_\_\_\_\_\_\_

Data transfer:

Please indicate the name and email of the person(s) who will receive the link to download the data:

Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ email: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ email: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Sample Shipment:

Submit your samples in clearly labeled tubes. For dsDNA shipment with cold packs (e.g. “blue ice”) is usually sufficient. RNAsamples should be shipped on dry ice. Please drop-off the samples in our lab (HMGU Bldg. 35/37, room 8131) or use the following shipping address:

Genomics Core Facility, NGS Platform

Gertrud Eckstein

Building 3537/ Room 8131

Helmholtz Zentrum Muenchen

Ingolstaedter Landstraße 1

85764 Neuherberg, Germany

**Contacts:**

**Genomics Core Facility, NGS Platform**

|  |  |
| --- | --- |
| Head  Dr. Inti A. De La Rosa Velázquez  Tel: +49 89 3187 3546  Inti.velazquez@helmholtz-munich.de | Laboratory Manager  Dr. Gertrud Eckstein  Tel: +49 89 3187 3525  Eckstein@helmholtz-munich.de |

Board of Directors: Prof. Dr. Matthias H. Tschöp, Kerstin Günther

Register of Societies: Amtsgericht München HRB 6466   
Value added tax identification number: DE 129521671