**Sequencing Submission starting from customer libraries on the NovaSeq 6000 Platform**

Almost all existing Illumina sequencing libraries can be sequenced as is on the NovaSeq 6000. Libraries generated for Illumina platforms with recent kits from major suppliers (e.g. Bioo, Kapa, NEB, Nugen, Qiagen) will also give high quality sequencing results. Please assess the quality of your library/pool via the Bioanalyzer (Agilent) or equivalent and consider the following exclusion criteria prior a submission of libraries or pools for sequencing on the NovaSeq 6000 system:

Exclusion criteria:

* A lot of adapter dimers (if present, these should constitute less than of 0.5% of the molecules).
* A considerable percentage of longer fragments (insert sizes over 550 bp, or total lengths over 670 bp). Minor “tails” of longer fragments are still suitable.
* Single-end adapters.
* Custom sequencing primers are not supported by Illumina on the NovaSeq 6000.

Sample submission requirements:

|  |  |  |
| --- | --- | --- |
| Please submit at least 5 nM of the libraries/pools in a clearly labeled **“low bind”** tube.  | NovaSeq Flow cell Type | required Volume [µl] |
| SP / S1 | 45 |
| S2 | 80 |
| S4 | 160 |

Together with the library/pool please provide the Bioanalyzer trace as **.xad** and **.pdf** file (sample labeling as is in the submission form and on the tube) as well as the filled library submission form. Processing of your library/pool starts once the Core Facility has accepted your complete and properly filled documents as well as the samples. Completion of services takes three weeks on average.

**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 Library submission form completely and properly filled (.xlsx)
File name:
* Submitted library/pool fulfill all requirements
* Submitted library/pool is in a low bind tube
* Bioanalyzer trace as .xad file provided (TapeStation trace as .pdf)
* All legal and ethical requirement are fulfilled to perform the ordered work
* Guarantee that sample material is not above BSL2 level

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

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:

Library Preparation Kit: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Requested Sequencing Configuration:

[ ]  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

[ ]  Transcriptome sequencing with ~35x10 reads per library – 150 bp paired-end⁶ reads per library – 150 bp paired-end

[ ]  ChIP sequencing with ~35x10 reads per library – 100 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:

Libraries/pools can be shipped in clearly labeled tubes. Cold packs (e.g. “blue ice”) are usually sufficient. 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

**Contact**

**Genomics Core Facility, NGS Platform**

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| --- | --- |
| CoordinatorDr. Inti A. De La Rosa VelázquezTel: +49 89 3187 3546Inti.velazquez@helmholtz-munich.de | Laboratory ManagerDr. Gertrud EcksteinTel: +49 89 3187 3525Eckstein@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