**Sequencing Submission Form for Libraries on the MiSeq Platform**

Almost all existing Illumina sequencing libraries can be sequenced on the MiSeq system.

Libraries generated for Illumina platforms with recent kits from major suppliers (e.g. Bioo, Kapa, NEB, Nugen, Qiagen) will give high quality sequencing results. Please assess the quality and quantity of your library/pool via the Bioanalyzer (Agilent) or equivalent and Qubit or equivalent and consider the following exclusion criteria prior a submission of libraries or pools for sequencing on the MiSeq system:

Exclusion criteria:

* A lot of adapter dimers (if present, these should constitute less than 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 acceptable.
* Single-end adapters.

Sample submission:

|  |  |  |
| --- | --- | --- |
| Please submit at least 5 nM libraries/pools in clearly labeled “**low bind**” tubes.  | Miseq Flow cell Type | required Volume [µl] |
| Nano | 5 |
| Micro | 5 |
| V2/V3 | 5 |

Together with the library/pool please provide the Bioanalyzer trace as **.xad** and **.pdf** file (sample labeling as is in the sample list and on the tube) as well as the filled sample list and library submission information form. Processing of your library/pool starts with the complete and properly filled submission of requested documents as well as the samples and MiSeq reagents.

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:**

* Library/pool fulfill all requirements
* Submitted library/pool is in a low bind tube
* Bioanalyzer trace as xad file provided (TapeStation trace as pdf)
* Sample List completely and properly filled
* Sample submission information form completely filled
* 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

General Information:

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

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

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

Finance:

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

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

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

# Requested Sequencing Configuration

* MiSeq reagent kits are ordered directly by the users, please specify the kit to be used: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_
* Read length: R1/\_\_\_\_\_\_\_\_\_\_i7/\_\_\_\_\_\_\_\_\_\_i5/\_\_\_\_\_\_\_\_\_\_R2/\_\_\_\_\_\_\_\_\_\_

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. 34, room 019) or use the following address:

Genomics Core Facility

Gertrud Eckstein/Peter Lichtner

Building 34/ Room 019

Helmholtz München

Ingolstaedter Landstraße 185764 Neuherberg, Germany

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: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Contact**

**Genomics Core Facility, NGS Platform**

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| --- | --- |
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