**Guidelines for the use of the NGS platform of CF-Genomics**

The Core Facility Genomics (CFG) offers high-quality, state-of-the-art services individualized to your project needs. All available NGS services are provided by core facility personnel only. A self-service option is available for the operation of some core instruments by trained users.

It is mandatory to contact us before the start of a project to arrange for an in-depth consultation session ([CF-Genomics@helmholtz-munich.de](mailto:CF-Genomics@helmholtz-munich.de)). In our experience users achieve best results when involving us at the earliest stages of a project, but in any case, before starting with sample preparation. NGS experiments must be carefully designed and have special requirements in terms of sample preparation, data generation and statistical validity.

For automated DNA and RNA isolation we accept a broad range of human and non-human sample types such as whole blood (also in Pax tubes), cells, various tissues etc. All tissue material delivered to CF-Genomics can be up to Biosafety grade 2 (BSL-2). If you are working with samples above BSL-2 you must contact head of CF-Genomics (inti.velazquez@helmholtz-munich.de) to discuss if they can potentially be processed after thorough fixation and obtain prior written permission before sending such specimen by the head of CF-Genomics ([inti.velazquez@helmholtz-munich.de](mailto:inti.velazquez@helmholtz-munich.de%20) ).

When submitting already isolated DNA, RNA or prepared libraries CF-Genomics will perform sample QC (QuBIT, Bioanalyzer, Gel-electrophoresis for DNA) as a mandatory first step. If any samples fail QC user can opt to include these for further processing at their own risk and expense.

All sample material must arrive at the core in a fully anonymized manner. The core facility will store sample material only for the duration of the project. Any leftover material will be discarded or shipped back at the user’s expense upon request.

Users are responsible for ensuring that any scientific experiment carried out at CF-Genomics fulfills the relevant ethical and legal specifications.

Furthermore, every user is responsible to provide a valid source of payment for the work ordered and as outlined in the quote provided by CF-Genomics. This has to be confirmed in writing on the project proposal form by the head of the research team.

Data are stored for a maximum of 90 days after completion of the user’s project, long-term storage is in the user’s responsibility. We typically provide our users with basic processed data (FASTQ files), other formats are available upon request. Please note that mixing of different barcode length or single indices and dual indices in a single lane is not supported and if applied only RAW data can be provided. If you wish to include bioinformatics analysis of your data please contact the team of our bioinformatics platform ([thomas.walzthoeni@helmholtz-munich.de](mailto:thomas.walzthoeni@helmholtz-munich.de)). While internal customers can download their data via a dedicated server, external clients will agree on a data delivery path during the initial project discussion.

Please follow the procedure outlined below to guarantee efficient completion of your project.

1. Initial project meeting at an early stage:

Please arrange for a mandatory project discussion on your NGS or Single-Cell experiment ([CF-Genomics@helmholtz-munich.de](mailto:CF-Genomics@helmholtz-munich.de)). Sample preparation, suitable protocols, project planning and more details will be discussed in the meeting. Please also consider the downstream data analysis path, we are experts at qualitative and quantitative analysis and data interpretation of NGS and single cell data sets.

1. Project proposal form:

A further prerequisite is the submission of a project proposal. Please include any information needed to provide a clear and solid understanding of your goals and expectations.

Please download the [Project Proposal Template](https://www.helmholtz-muenchen.de/fileadmin/MPC/FILES/ProjectProposal_template_w_DATA_PROTECTION_STATEMENT.docx) for NGS and complete all requested information. This project proposal will contain the results of the discussions from the previous meeting (step 1) and needs to be sent in Word file format (.docx) to the scientist in charge of your project who will add the prospective effort for the facility and provide a quote and time estimate to complete the work. After mutual agreement, please sign the document and send as .pdf. Work will commence only after receiving the signed project proposal with valid funding source.

1. Sample submission

Please download the appropriate submission form and sample list files from our webpage and submit the completed documents to: [CF-Genomics@helmholtz-munich.de](mailto:CF-Genomics@helmholtz-munich.de):

* For library prep from customer DNA or RNA samples and sequencing on the Novaseq6000
  + - CFG\_Sample\_List\_template\_DNA\_RNA\_submission.xlsx
    - CFG-Sequencing\_submission\_form\_for\_DNA-RNA\_samples\_NovaSeq.docx
* For sequencing of customer prepared libraries/pools for sequencing on the Novaseq 6000 or Miseq
  + - CFG\_Sample\_List\_template\_libraries\_submission.xlsx
    - CFG-Sequencing\_submission\_form\_for\_Libraries\_NovaSeq.docx
* For submission of samples for DNA or RNA isolation (cells, tissues, blood, etc).
  + - CFG-Submission form\_for\_Nucleic\_Acid\_isolation.docx
    - CFG\_Sample\_List\_template\_Nucleic\_Acid\_isolation.xlsx
* For special services (sample QC, qubit or bioanalyzer measurement, or any request not covered in previous forms)
  + - CFG­ Submission\_form\_for\_Special\_Services.docx
    - CFG\_Sample\_List\_template\_Special\_service.xlsx

Users must complete a new sample submission sheet for each new order with a unique identifier for each tube or plate. Please remember that we can only accept fully anonymized samples. Also, it is relevant to think about the order or grouping of your samples before you submit them. Samples can be submitted in tubes or 96 well plates, depending on the type and number. Please mark samples clearly using permanent markers/labels! We strongly encourage you to get advice on these aspects from the scientist in charge for your project at the Core Facility.

RNA samples are to be sent on dry ice. DNA and library pool samples can be sent on dry ice or ICE packs. Samples can be delivered in person or shipped using a commercial service at the user’s expense. Please always contact us prior to bringing or shipping samples to us ([CF-Genomics@helmholtz-munich.de](mailto:CF-Genomics@helmholtz-munich.de)). For sample safety avoid shipment over the weekend and close to bank holidays.

Delivery address:

Helmholtz Zentrum München  
Campus Neuherberg  
Core Facility Genomics – NGS Platform  
Attn: Dr. Inti Velazquez/ Dr Gertrud Eckstein   
Building 34 Room 019  
Ingolstaedter Landstr.1

85764 Neuherberg, Germany