**Guidelines for the use of the Genotyping of CF-Genomics**

The Core Facility Genomics (CF-GEN) offers high-quality, state-of-the-art services individualized to your project needs. All available genotyping services are provided by core facility personnel only. A self-service option is available for the operation of some core instruments to 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-muenchen.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. Genotyping 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 must be of 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 for genotyping workflows CF-Genomics strongly recommends that users will opt for sample QC (QuBIT, Bioanalyzer, Gel-electrophoresis for DNA) as a first step, for large numbers of samples we recommend a minimum of check of concentration and spot checks on sample integrity. If any samples will fail QC or are provided at sub-standard amounts 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 users 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 users project. We typically provide our users with raw data files (e.g. idat files ) or basic processed data, other formats are available upon request.

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 your proteomics 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 genotyping data.

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 Genotyping 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 for your 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 sourceSample submission

1. Sample submission:

Please download the appropriate sample submission sheet and submit the completed document to [CF-Genomics@helmholtz-munich.de](mailto:CF-Genomics@helmholtz-munich.de).

* Sample submission DNA or RNA isolation
* Sample submission form for Genotyping
* Sample submission form for Sanger Sequencing
* Sample submission form for Fragment Analysis

Users must complete a new sample submission sheet for each new submission with a unique identifier for each tube. 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. We strongly encourage you to get advice on these aspects from the scientist in charge for your project at the Core Facility ([CF-Genomics@helmholtz-munich.de](mailto:CF-Genomics@helmholtz-munich.de)).

RNA samples are to be stored on dry ice and 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 ([CF-Genomics@helmholtz-munich.de](mailto:CF-Genomics@helmholtz-munich.de)). For (sample safety,please avoid shipment over the weekend and close to bank holidays.

Delivery address:

Helmholtz Zentrum München  
Campus Neuherberg  
Core Facility Genomics – NGS Platform  
Attn: Dr. Peter Lichtner/ Dr Gertrud Eckstein   
Building 34  
Ingolstaedter Landstr.1

85764 Neuherberg, Germany