

General rules for the use of the CeNT UW Genomics Core Facility

I. General provisions

1. The equipment is localized in room 03.231 and 05.101-05.115 in the CeNT I building.
2. Genomics Core Facility personnel:

Jeffrey Palatini (head) (e-mail: j.palatini@cent.uw.edu.pl);

Sample Processing Section:

Dorota Adamska (e-mail: d.adamska@cent.uw.edu.pl);

Michał Szelaąg (e-mail: m.szelaag@cent.uw.edu.pl);

Bioinformatics Section:

dr Krzysztof Goryca (e-mail: k.goryca@cent.uw.edu.pl);

3. Direct use of the equipment is restricted to the personnel of the Genomics Core Facility.
4. Users are requested to submit a brief description of the planned experiment and/or data analysis proposal by filling an electronic form. The project description is the basis for consultations scheduling, obtaining acceptance for the experiment from the Sample Processing Section and/or Bioinformatics Section, and enables them to plan sequencing and data analysis, respectively.
5. Users are requested to accept the preliminary cost estimate before starting the sample processing or data analysis.
6. Users are obliged to familiarize themselves with these rules.

II. Project submission

1. The submissions of experiment and data analysis proposals are made through the Genomics Core Facility website: "<https://cent.uw.edu.pl/en/core-facilities/genomics-core-facility/>"
2. By accepting the terms and conditions the Users declare that the samples and data provided have not been obtained in violation of applicable law, as well as their further processing requested by the Genomics Core Facility personnel is fully legal.

III. Sample preparation

1. Users submitting DNA/RNA samples must provide nucleic acid quality and quantity data or request such an analysis to be carried out by the Genomics Core Facility. Samples that do not meet quality requirements as specified by the selected sequencing library preparation protocol will be processed only upon written consent, wherein the User agrees that no guarantee is given for the successful library construction and the full costs of the library construction attempts (including the unsuccessful ones) are to be fully covered by the User.
2. Users submitting DNA libraries are required to follow sample preparation protocol approved by the head of the Sample Processing Section. They must also present data on the quality of the libraries delivered (results from Agilent Bioanalyzer or equivalent instrument) or request the quality analysis to be carried out by the Genomics Core Facility. Any modification (e.g. resulted from a human error) should be reported before the libraries are handed over for sequencing. The Genomics Core Facility bears no responsibility for the quality of results obtained, based on sequencing User-delivered libraries.
3. Users submitting sequencing data for analysis should deliver data in BCL, FASTQ, or BAM format.

IV. Provided services

1. The services are rendered, based on the initial consultation (see Collaboration Guide) and according to the written cost estimate provided to and accepted by the User.
2. The Genomics Core Facility personnel is responsible for scheduling the services. Generally, User requests are being processed on a first come, first served basis. However, the personnel reserves the right to queue the samples provided, according to the availability of measurement time and sequencing consumables, unless the User agrees to bear the full costs of the sequencing process, as estimated by the Genomics Core Facility personnel.
3. The general services offered by the Genomics Core Facility include:
 - Consulting services (help with designing the experiment, customizing sample preparation protocols, data interpretation);
 - Sample processing (eg. DNA/RNA quality assessment, DNA library preparation);
 - Sequencing run set up and raw data preprocessing (FASTQ generation, demultiplexing and basic quality report);
 - Data analysis (basic processing as well as tailored analysis and data visualization are available).
4. The services rendered are described on the Genomics Core Facility website and individually adjusted in accordance with experiment-specific modifications of the standard protocols and additional services requested (e.g. sample quality control, data analysis).
5. A consultation is expected to precede any sample processing and/or data analysis (see Collaboration Guide). As a result of the consultation, an optimal analytical

strategy is agreed upon and the estimated cost of services (calculated based on the Pricelist) is provided in a written form and explained.

6. The Genomics Core Facility personnel reserves the right to reject requests for the provision of services in objectively justified cases. In the event of a refusal, a constructive feedback will be provided to both the User who had requested the service, and to the appropriate head of the respective laboratory (where applicable).

V. Libraries storage, data storage & security

1. The results will be made available to the User in an adequate form::
 - o Report on the methodology and work results (for Sample processing service);
 - o Raw, demultiplexed data with basic quality report (for Sequencing service);
 - o Full report with a summary addressing the User's expectancies (for data analysis service).
2. Users are expected to collect data within 14 days from the time the results became available to them. After that time, access to the data will require intervention of the head of the lab, from which the project originated.
3. The samples and libraries remained will be stored for 6 months and provided to the User on demand or may be subjected to further sequencing on separate sequencing request.
4. Raw data will be stored on a server for a duration of 6 months. On request, they will be made available to the User.
5. Additional storage time of libraries or raw data requires written request from the User within 6 months from making results available to them and may result in storage cost covering by the User.

VI. Publication of data

1. Acknowledgment: For basic analyses, where a minimal intellectual contribution from the Genomics Core Facility personnel has been requested, their work should be clearly identified in the acknowledgments section of resulting publications with marked Research Resources ID (RRID:SCR_022718). Sequences and data analysis reports will be provided along with a generic statement about the instrumentation and the software utilized.
2. Co-authorship: When a significant intellectual contribution from the Genomics Core Facility personnel has been requested and delivered, their work must be acknowledged by naming them as co-authors of resulting publications. This is a default mode of agreement for projects involving the development of new sequencing and data analysis approaches and methods or projects requiring complex data processing and/or mining. A selection of publication-ready figures and an input into writing of the relevant sections of the paper will be provided by the Genomics Core Facility personnel.