Research Core Unit Genomics (RCUG)

Hannover Medical School, Carl-Neuberg Str.1, 30625 Hannover, www.mh-hannover.de/genomics.html

Introduction and Overall Organization

The RCUG is a research-driven service unit. Since its formation in January 2017, the RCUG is open to all departments at the MHH and selected external institutions for the realization of sequencing- and microarray-based projects. The extensive expertise of the personnel (six permanent employees) in the fields of planning, technical execution, analysis and publication of genome- and transcriptome-wide studies has been acquired during many years of research in their respective fields. To date, (April 2022) more than 160 groups from more than 55 different MHH departments have employed the services of the RCUG or its predecessors. The offered services are dedicated to all methodical aspects of data generation, raw data processing and quality control, supplemented by comprehensive overall support (project planning, analysis strategy, analysis workshops). Co-authorships are not a mandatory prerequisite for collaboration unless extensive methodological or analytical modifications are required or otherwise agreed.

Facilities

The RCUG is equipped with state of the art Illumina (**NextSeq 550**) sequencing technology. A **Sequel** machine for long-read analysis (Pacific Biosciences), one additional **NextSeq 500**, and three **MiSeqs** constitute so called 'decentralized sequencers'. These sequencers are operated by other groups at the MHH but are also available for use by the RCUG. A close cooperation in-house furthermore enables access to a production scale Illumina sequencer (**NovaSeq6000**). A **Chromium™ Single Cell Controller** (10x Genomics) located at the central sorter facility of the MHH is available for single cell RNA-seq experiments. Two decentralized **pipetting robots** are also on premises for large projects. Two **2100 Bioanalyzers** (Agilent Technologies), two **Qubit fluorometers** (Thermo), a **BluePippin system** (Sage science) and a **Nanodrop** spectrophotometer (Thermo) are present for quantification and fragment length analysis of generated cDNA libraries for sequencing applications. The RCUG is additionally equipped with an **Agilent microarray scanner** G2565C which allows automated scanning of up to 48 slides per run.

Personnel

The core personnel of the RCUG consist of two scientists who are in charge of overall coordination, experimental design, quality control and technical supervision. Two bioinformaticians are responsible for data management processes, data analysis and further development of data analysis strategies. Two technicians execute all wet chemistry work and maintain our laboratories.

Offered Services

Genomics: DNA QC, Sequencing of whole genomes (external sequencing because for economic reasons), Exomes, Amplicons, Target Enrichment-Seq, Metagenomics, ChIP-Seq, Epigenomics applications; *Transcriptomics:* RNA QC, mRNA-Microarrays, RNA-Seq, mRNA-Seq, single cell mRNA-Seq (incl. Cite-seq, Cell hashing, B/T cell repertoire), smallRNA-Seq, microRNA-Seq; *General Services:* Consultations (study design, data analysis), integration of data from public databases, deposition of data to public databases, provision of computing power, custom bioinformatics services, teaching (bioinformatics and data analysis).

Specific focus: Comprehensive support for data analyses and visualization

One of the main objectives of the RCUG is to advise clients and cooperation partners on the best way to extract meaningful information from generated data. Hence, a huge variety of open source bioinformatics software is hosted on the HPC-seq cluster, which has been designed and configured by RCUG scientists together with ZIMt. Software is available via Bioconda and Gitlab and documented with examples on an open Wiki website. A number of Galaxy flavours are hosted for point and click execution of NGS workflows. Visualization is also available via the web-based JBrowse or commercial software and further data analysis via the web-based RStudio environment. The RCUG also provides access to several user-friendly commercial software applications bookable by Microsoft Outlook calendars. We currently offer Qlucore Omics Explorer v3.7, Agilent GeneSpring v13.1.1, Qiagen Ingenuity Pathway Analysis (IPA) and Avadis StrandNGS v4.0. Regular practical training courses are provided. These courses cover RNA-seq, DNA-seq, mutation analysis and, in future, long read analysis.