EUROPEAN UNION

Interreg
Austria-Czech Republic
European Regional Development Fund

Genomics Core Facility

What we do

Parasitology – Worms, are you there?

Screening for specific nematoda parasites in primates. Researchers from Veterinary university Brno (Dept. of Parasitology) and Czech Academy of Science (Institute of Vertebrate Biology) collected in central Africa gorilla, bonobo and human fecal samples. In cooperation with CF Genomics they employed NGS based metagenomic method for analysis of several DNA markers. This method involves PCR amplification of marker sequences (16S for bacteria, 18S, ITS and Cytochrome C oxidase for eukaryota), sample barcoding (up to 384 samples) and sequencing on Illumina MiSeq.

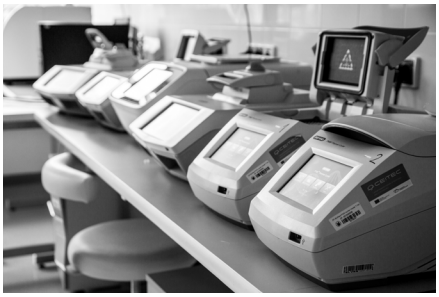
Inherited cancer – Unwanted heritage

Screening for disease associated genes in families with high incidence of early-onset cancer. Researchers from CEITEC Medical genomics are currently running a project that aims to identify possible causative genes in families suspected of hereditary (hematology) cancer. In this case whole exome sequencing of both affected and unaffected family members was selected and found genetic variants are analyzed in conjunction with pedigree.

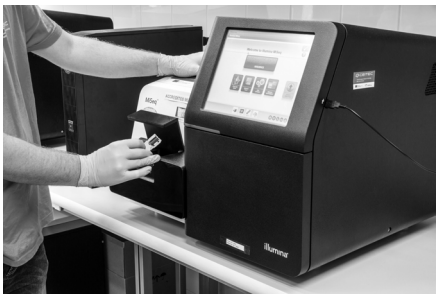
Cancer cells – Evolution in real time

Ultrasensitive screening for subclonal somatic variants. Researchers from CEITEC Medical genomics in cooperation with CF Genomics established method for detecting subclonal mutations in TP53 gene. Impaired function of the TP53 gene has huge negative impact on the prognosis of Chronic lymphocytic leukemia (CLL). Deep sequencing using massively parallel sequencers is currently the only available method to screen whole gene for mutations present in only a very small fraction of tumor cells. It is important to monitor mutated subclones as they may have different response to therapy and may become refractory to immuno-chemotherapy.

CEITEC
Kamenice 753/5, Brno, 625 00
University Campus Bohunice
Building A35
Czech Republic
www.ceitec.eu/genomics-core-facility
genomics@ceitec.muni.cz



PCR lab
We have capacity to allow users perform many simultaneous experiments.



Illumina MiSeq
One of our sequencers, can be used for almost all NGS experiments, for others we have Illumina NextSeq or Oxford Nanopore MINIon.

QuantStudio 12k
We operate several qPCR instruments including ThermoFisher QuantStudio 12k, Roche LightCycler 480 or Qiagen RotorGene Q5.

QuantStudio 12k
Most of our instrumentation is 384-well compatible.

Services and Methodologies Provided

We will help you with experiments involving any SERVICE or METHODOLOGY listed bellow. For NGS we can help you with library preparation and sequencing or for standardized applications like RNA-seq or exome sequencing we can prepare the libraries ourselves. We also offer complementary services to library preparation - sample/library quality control or library size selection. You can also use software and hardware installed in core facility to analyze NGS data.

- NextGen Sequencing on Illumina NextSeq and MiSeq and Oxford Nanopore MinION
- Library QC - electrophoresis, qPCR
- Library preparation - RNA-seq, whole exome sequencing

Equipment

- Illumina NextSeq and MiSeq
- Pippin Prep, TapeStation
- qPCR Roche, ThermoFisher, Wafergen

Contact and Location

CEITEC
Kamenice 753/5, Brno, 625 00, Czech Republic
University Campus Bohunice
Building A35
www.ceitec.eu/genomics-core-facility
genomics@ceitec.muni.cz

MUNI | CEITEC