# Amsterdam UMC
### University Medical Centers

# *Core Facility Genomics*

News Flash - April 2023

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**18th**

***Core Facility Genomics (CFG)***

***user webinar***

2nd of May 16:00-17:00

**"Nanostring GeoMX DSP, designing my experiment and data processing and analysis"**

To join: Teams link

For more info: CFG website

cfg.amsterdamumc.nl

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**nanoString GeoMx DSP Grandopening @ Amsterdam UMC, AMC location**

31st of May 10:00-14:00

Save the date for the nanoString GeoMx DSP grand-opening @ Amsterdam UMC, to celebrate the arrival of the GeoMx DSP in the imaging core of Eric Reits. If you are interested in using the machine, please email the CFG.

Soon the speakers will be announced and flyer will be send around.

## *CFG goes Spatial!*

Dear CFG users, we are excited and happy to inform you about our latest achievement on acquiring spatial technology of Nanostring.

Spatial technology allows molecular analysis, i.e. at transcriptome or protein level, or multi-omic level within a morphological context. The GeoMX Digital Spatial Profiler (DSP) of Nanostring allows to perform genome wide, panel or custom based transcriptomic and proteomic analysis.
Moreover, this technology can be applied on fresh frozen and FFPE preserved tissues that opens the door for further molecular analyses on the huge amount of samples stored in our institute.

In brief, the workflow of the GeoMX is rather simple and flexible.
Slides with whole mount or tissue microarray (TMA) are prepped with UV cleavable antibodies or hybridization probes. Moreover, slides are stained with morphology markers, enabling proper selection of your regions of interest (ROIs; UV illuminated). The UV cleavage releases reporter molecules for which read out can be achieved using Illumina next generation sequencing or the Nanostring nCounter (CEMM).

Standard bioinformatic processing merge the molecular and image readout. Subsequently differential analyses can be performed.

*Publications*
A number of (company selected) peer reviewed publications of studies that have applied and implanted GeoMX DSP technology can be found here.

*GeoMX DSP in AmsterdamUMC*
The achievement of the GeoMX DSP was a joined effort of many groups in the Amsterdam UMC, of which the cart was pulled by two Amsterdam UMC core facilities, namely the Core Facility Genomics (CFG) and the Core Facility Flow and Microscopy (location AMC). In our next upcoming webinar (18th), scheduled for the 2nd of May 2023, both the CFG and CFI will talk about the ins and outs of this spatial application, as well as the financial aspects of GeoMX experiments. Moreover, this webinar will also touch on the bioinformatics that this technology obviously involves. We hope that you will join and participate this webinar. If you can't wait, please contact us by email, we will be happy to answer all your questions!
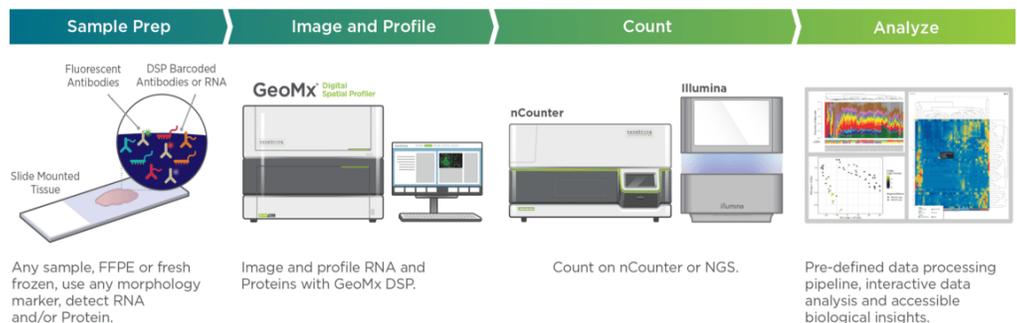


## *CFG LIMS*

As most of our customers know, over 2 years ago our old LIMS system went offline. The application was old and presented security risks for the AUMC. A temporary application was built in Excel, which made sure we could continue operations in the short term. In the meantime, we have been working hard on a new long-term solution, called "CFG LIMS".

CFG LIMS is a web based application, completely build in-house, which aims to support our wet-lab work for the foreseeable future and presenting a modern and easy-to-use interface for all users.

For now the application will handle our Sanger sequencing submissions and equipment reservations, while we work on adding additional features, like support for TapeStation and Next Generation Sequencing workflows.

At this moment we have started processing samples using CFG LIMS with a select group of users from within the Human Genetics department. We hope to finalize our testing and present the application to all users soon, aiming for a public release in Q2 2023.

## News from the lab

**New version NGS sequencing submission (Illumina Sequencing)**

We have updated our **NGS Sequencing submission form**. This form need to be used when you want to submit samples directly for Illumina sequencing (NovaSeq6000, NextSeq2000 or iSeq).

**Submissions for library preparation did not change.**

The form was already used by users who submitted directly to VUmc. Now users who hand in samples at location AMC need to use this form too.

For **all** users it is necessary that they use the most up to date version of the form, which can be found in **K2**.

When using the form for the first time, you might need some help. Please email NGS-KlinGen.

### Consumables

Because of the robotics used at the CFG it is important that the samples are in the correct type of disposable.
The CFG is updating all the procedures with the allowed disposables that can be used to hand in samples. In **K2** you can find all the allowed disposables. Some techniques require more specific disposables, you can find them in the procedures specific for the technique.

**Visit our website!**
cfg.amsterdamumc.nl

E-MAIL
cfg@amsterdamumc.nl

## HPC cluster

At the end of last year, the Core Facility Genomics initiated the open use of the HPC cluster. This cluster is a collection of computers which is now accessible to users from different departments within the Amsterdam UMC network. The purpose of the project is to have a cluster that functions as a central point for in-house data storage and processing. In this way, we want to achieve sharing of knowledge and resources, more data security, easier for users to adhere to data FAIR principles, and all of this in a cost-efficient manner. Currently, the cluster consists of 12 calculation nodes (computers), a fast storage system for fast writing and a slower storage system for archival purposes. We also have GPU nodes available which can be used for image processing and machine learning projects.

We asked two of our users about their experiences so far with the cluster:

*"The HPC cluster maintained by the Genomics facility team is an amazing resource and vital to my research. We perform high-dimensional cytometry and multiplexed imaging, which generate large amounts of data that need to be analysed in one go. With easy-to-follow documentation and excellent support, the facility enables convenient access to the cluster. It is very flexible in its use, allowing me to run predetermined scripts, as well as more exploratory analyses through Rstudio. I highly recommend any researcher at the AmsterdamUMC with an interest in R to work on the HPC clusters."*
Jan Verhoeff – Postdoctoral researcher at the Tytgat Institute for Liver & Intestinal Research

*"HPC Genomics has offered the HPC cluster, which has been a crucial resource for our bioinformatics activity within the Tumor Genome Analysis Core (TGAC). They provide us with sufficient storage, CPU power, and security within the AUMC firewall that suits our needs in NGS data analysis and bioinformatics research. I highly appreciate that such an infrastructure is available within AUMC."*
Yongsoo Kim, Assistant professor in Bioinformatics/Oncogenomics, Department of Pathology

These user reviews mean a lot to us. We are now a group of four bioinformaticians members (Rick, Adri, Reinier and Daoud), and we spend a lot of time to support users on the cluster as best we can next to our own day to day bioinformatics projects at the Lab of Genome Analysis. We hope to see more users join the community we have set up. Additionally, we are expanding the cluster with more computing power and storage to meet the increasing demand of our own department and external users. We are very excited to see results of many interesting projects produced on the cluster!

## Windows10 updates

Making sure equipment software is up-to-date with the latest, secure versions is a continuous process, which requires close collaboration between users, operators, IT and the equipment supplier.

In the last couple of weeks we have performed several windows 10 updates to machines such as the ABI37030 sequencers and the Illumina MiSeq sequencers, while the update of the LightCycler 480 is still being scheduled.

For machines that already received the updates, we were able to gradually update one machine at a time. This gave all users time to test their experiments with the new software, while minimizing impact on the regular flow. We would like to thank all users that participated in testing these new software updates.

## CFG costs

Twice a year, in March and September, the CFG updates the prices. Our prices are based on the costs we make incur at our suppliers. Since the various suppliers have recently implemented huge price increases, this has an effect on our rates. In addition to this effect, we also see the effect of the structural CAO wage increase of our employees. All in all, this results in an increase in our rates. Current prices can be found at our CFG website.