Dear Reader,

**EASI-Genomics** has come to an end and in this last issue of the news_trends we look back and reflect on the four and a half years of the project. We start with a word from Prof. Dr. Ivo Gut, our Project Coordinator.

Next, we provide our readers with summary of transnational access projects and present the final results of the user survey as well as a short report from the **EASI-Genomics Summit: Advanced Genomics in Science and Medicine** that took place in May in Berlin.

Moreover, as tradition dictates, we introduce suggestions for readings, recent publications of **EASI-Genomics** partners and TNA users and a feature article on a new exciting technological developments.

Last but not least, we would like to use this opportunity to thank Scientific Advisory Board, our reviewers, users, applicants and all other stakeholders for following and supporting us for the last four and a half years.

The authors of this news_trends confirm to have no conflict of interest.
from: Ivo Gut

"EASI-Genomics has been an excellent exhibition of the impact of advanced genomics technologies, of the diverse projects it has helped to realize, as well as on the positive influence EASI-Genomics had in boosting the careers of over 100 researchers."

TNA_calls_summary

- **EASI-Genomics** has provided support to **170 projects**.

- **EASI-Genomics** sequencing facilities produced a total of **185 Terabases** of sequencing data across all TNA projects and calls.

- A total of 467 tissue sections with an area of **128.8 cm²** were processed in twelve spatial transcriptomics and *in situ* sequencing projects.

- In 27 single cell projects, more than **1.8 Mio single cells** were analyzed.

- To date, **twenty-six articles and two pre-prints** were published that include data from TNA projects. Many of the TNA projects’ results appeared in high-impact journals such as *Science*, *Science Immunology*, *Nature* and *Nature Communications*. Three of the COVID Call projects, PID12342, PID12352 and PID12587, were particularly successful in publishing. Data from these three projects appeared in twenty-one publications so far.

- The sequencing data produced in EASI-Genomics projects are **archived in open and controlled repositories**, namely EGA for sensitive human data and ENA for non-human data.
user_feedback

A user output survey was conducted between April and July 2023 addressing all TNA call users. A total of 37 users participated.

- **Most of the users either is planning to publish or already published the data obtained in their TNA project**

![Bar Chart](image)

- **TNA projects are supporting grant application processes**

![Bar Chart](image)

**Testimonials:**

“*Besides grants and publications, EASI Genomics data gave us the opportunity to gain expertise in the analysis of sc multiomics data.*”

“I had an excellent collaboration with a highly professional facility, producing high quality sequencing data.”

“Please, continue to offer this kind of calls/projects, for me and my project has been a game changer allowing me to do a first-time biological observation in the interface microbiome-host epigenetics”

“For us it has been a great opportunity, with benefits that will last for years. I just hope that there will be more of this in the future!”
EASI-Genomics has carried out diverse research projects covering topics as de novo assembly, transcriptomic and epigenetic analysis, and has contributed during the COVID-19 pandemic to elucidating the genetic causes underlying severe Covid-related disease. EASI-Genomics is finishing at the end of July and the "EASI-Genomics Summit: Advanced Genomics in Science and Medicine" was the closing public event. At this event we highlighted some of the achievements of EASI-Genomics in the context of the needs of the research community.

A quote from Ivo Gut, Director of CNAG and EASI-Genomics Coordinator: "It has been an excellent showcase of the impact of advanced genomics technologies, of the diverse projects EASI-Genomics has helped to realize, as well as on the positive influence EASI-Genomics had in boosting the career of over 100 researchers."

Janine Altmüller, head of the Genomics Platform at MDC: "The exchange of best-practises with other genomic platforms led to the joint development and optimization of new genomics methods" - read the full interview here.

We were indeed honoured to have seven of our TNA-users present at this event and are pleased to see that our support made a difference in their research. Finally, we wish to thank all our consortium members for their considerable efforts in making this project a success story.
Members of the 'technology watch' team prepared a selection of the most influential papers published in the field of Next Generation Sequencing in recent months (see below).*


* This list of publications is biased by a limited number of researchers that participated in the process of publication selection and is by no means comprehensive.
** These publications have not been peer-reviewed.
latest_publications_by_EASI-Genomics


latest_publications_generated_by_TNA


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The reduction in DNA sequencing costs in the last 20 years is so rapid that it outpaces Moore's Law. (Figure). This leads to more and more sequencing data being generated every year. The National Human Genome Research Institute (NIH) estimates that genomics research will generate between 2 and 40 exabytes of data within the next decade.

![Cost per Human Genome](image)

*Figure. Decrease of sequencing costs 2001-2022 in comparison to Moore’s law (source: National Human Genome Research Institute).*

In fact, at the moment, sequencing data can be generated much faster than it can be processed and analysed. This calls for ever more powerful hardware, software and data storage infrastructures to be able to decipher the information the DNA sequences contain at the sufficient pace. Therefore, in the last issue of news_trends we feature **GPU-accelerated NVIDIA® Parabricks®**.

NVIDIA Parabricks is a suite of accelerated genomic analysis applications for high-throughput data, supporting end-to-end data analysis workflows for DNA and RNA applications. They deliver up to 107x acceleration over CPU-based tools. More information about the suite can be found in this [white paper](#).

An example of a Parabricks tool is **DeepVariant retraining tool**, that enables DeepVariant fine-tuning. DeepVariant is a convolutional-neural-network-based variant caller for germline workflows for short and long-read data. DeepVariant retraining tool allows to increase the accuracy of variant calling by re-training the model on custom data. A case study describing application of the DeepVariant retraining tool on Singular Genomics’ sequencing data can be read [here](#). To try it on your own data you can download a [Parabricks DeepVariant Retraining Notebook](#).