

BMFZ Core Labs Newsletter

#03-2023

Dear Reader,
Please feel free to contact the Genomics and Transcriptomics Laboratory (GTL) for any questions regarding DNA or RNA analyses and the Molecular Proteomics Laboratory (MPL) for any protein-related questions. We look forward to supporting you and appreciate your feedback!
Yours,
The GTL and MPL Teams

New team members



New Team members are helping in all parts of the sequencing process, from QC of high-molecular weight DNA to starting new NGS workflows. The help is welcome in our lab given the amount of complex sample preparation and indeed rising sequencing demand.

WGGC:

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UMIs are now default for 3' mRNA assays

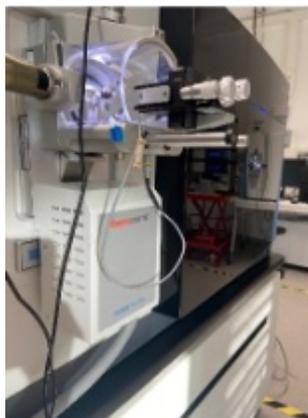


For NGS short-read transcriptome projects, technical duplicates are now a remainder of the past! More precise quantification of your RNA is now another reason to sequence RNA at the GTL. If you need help with the additional steps introduced by UMIs in the post-processing we can help you as well.

Source of the picture: <https://faqs.lexogen.com/faq/quantseq-umi-module>

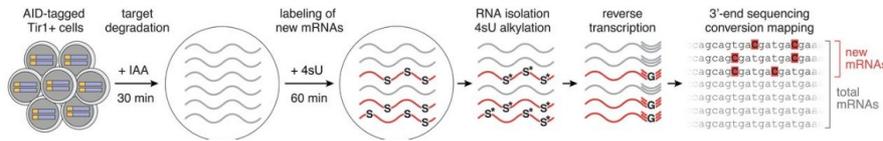
Contact Daniel.Rickert@hhu.de or
Thorsten.Wachtmeister@hhu.de

Ion mobility supports MPL in deeper proteomics



With the support of the BMFZ steering board, the MPL gets access to the newest ion mobility technology. The Thermo Scientific FAIMS Pro Duo interface extends differential ion mobility to address analytical challenges for a broad range of qualitative and quantitative applications. The benefits of the new device are better signal-to-noise ratios, higher sample throughput and coverage for LC-MS applications.

SLAM-Seq Pilot Experiments



In 2022, first SLAM-Seq samples arrived at the GTL. In SLAM-Seq experiments (<https://doi.org/10.1038/nmeth.4435>, also source of the picture) the total RNA fraction is metabolically labelled and transcriptional changes can be detected after a treatment/pulse/change in environment, by differentiating old and newly transcribed RNA.

RNA SLAM-Seq samples are sequenced on Illumina short-read platforms, very similar to regular mRNA samples. In order to detect the dynamic changes in gene expression, a dedicated data analysis pipeline (<https://github.com/t-neumann/slamdunk>) was implemented at the GTL.

Contact Daniel.Rickert@hhu.de or
Thorsten.Wachtmeister@hhu.de

Betz Foundation supports MPL in lab automation



Opentron ©



ANTON-BETZ-STIFTUNG
DER RHEINISCHEN POST E.V.

As quantitative proteomics experiments increase in scale and complexity, greater consistency and precision are required, which is best delivered by automation. Therefore, the MPL is supported by a grant of the Anton-Betz foundation for acquiring a liquid handling system. The liquid handling system will be used to automatize the recently established sample preparation method SP3 which is used for ultra-low input proteomics.

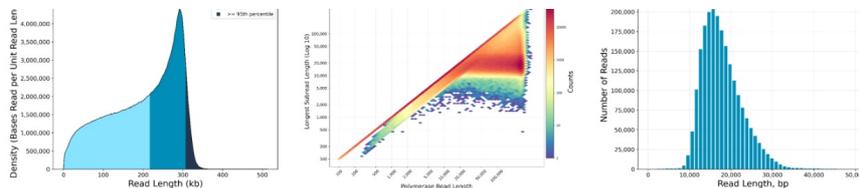
Extended scope in quality management



Recertification of the GTL according to DIN EN 9001:2015 was due in 2022 and is now valid until 2025. During the recertification process, we extended the scope to single-cell transcriptome analysis. Last year we participated also successfully in five external quality assessments to assure the performance and quality of our work

Contact
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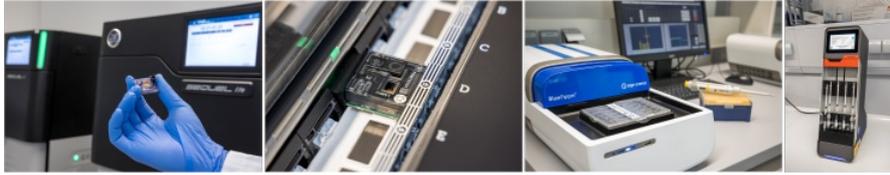
PacBio upgrades



Our sequencing machines from Pacific Biosciences received upgrades in chemistry and new workflows. The HiFi reads can now be delivered in combination with 5mC methylation data. In the future you will also have the possibility to start a single-cell isoform RNA sequencing (MAS-Seq) project, combining 10XGenomics and PacBio long-read sequencing.

Contact Tassilo.Wollenweber@hhu.de or
Francy.Perez.Llanos@hhu.de

Long-Read Sequencing is elected by Nature as Method of the Year 2022!



The journal Nature has elected 'long-read sequencing' as Method of the year 2022. Oxford Nanopore Technologies' and Pacific Biosciences' long-read sequencing techniques have their advantages and disadvantages, and both are offered at the GTL! So let us know if you need help. Source: doi.org/10.1038/s41592-022-01759-x

Data Output in long-read sequencing has more than doubled (**138%**) in 2022

“Bio Data Science Evenings” going regular



The West German Genome Center invites you to “Bio Data Science Evenings” with following opportunity to talk to fellow scientists and try some snacks. The meetings are open to everyone interested, but you are asked to register for each talk beforehand.

Contact Iuliia.Novoselova@hhu.de

Save the dates!

BMFZ.de

Biologisch-Medizinisches Forschungszentrum

06.03.2023	14:30, Geb. 22.07.U1, R. 25	BMFZ Colloquium
08.03.2023	17:00, O.A.S.E.	Bio Data Science
Evening		
13.06.2023	14:30, O.A.S.E.	30th BMFZ
Anniversary		
25.-26.09.2023	Kardinal-Schulte Haus Bergisch-Gladbach	BMFZ Retreat
2023		

Need anything?

Please contact us if you have any suggestions, feedback, questions or would like to work with us on a project!

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