7th NGS Symposium
14th April – 16th April 2026

	Tuesday 14th April	
	12:00 – 12:30	**Arrival and Coffee**
Opening session	12:30 – 12:40	**Lars Feuerbach** *Welcome and Overview*
	12:40 – 13:15	**Lars Feuerbach** *Characterizing telomeres by single-cell and long-read sequencing*
	13:15 – 13:40	**David Wissel** *Benchmarking long-read RNA-seq for transcript quantification across modalities, methods, and sequencing depths*
	13:40 – 14:05	**Mathias Boulanger** *Molecular co-accessibility identifies coordinated regulation between distant cis-regulatory elements*
	14:05 – 14:30	**Break**
Single molecule & Single cell	14:30 – 14:55	**Philippe Hupé** *Deployment practices with nextflow and apptainer for production-ready bioinformatics pipelines: example at the Institut Curie*
	14:55 – 15:20	**Michela Palamin** *ChromSMF: integrated profiling of histone modifications, protein–DNA interactions and DNA methylation on multi-kilobase DNA molecules*
	15:20 – 15:45	**Mark Hartmann** *scIGMT-seq: A single-cell multi-omics framework for simultaneous profiling of immunophenotype, genotype, methylome, and transcriptome*
	15:45 – 16:10	**Break**
Spatial-omics	16:10 – 16:35	**Martin Emons** *Quantification and multi-sample comparison of spatial omics data using spatial statistics*
	16:35 – 17:00	**Rémi Montagne** *Through spatial transcriptomics and proteomics data analysis*
	17:00 – 17:25	**Gianni Zanardelli** *Spatio temporal regulation of cell cycle states in tumor microenvironments using spatial transcriptomics*
	TBA	**Pub Crawl or restaurant visit**

Please note that the program is susceptible to change and will be continuously updated

7th NGS Symposium
14th April – 16th April 2026

	Wednesday 15th April	
Epigenomics and TFs	9:30 – 9:55	**Martina Capriati** *Essential genes are dominantly activated by single transcription factors*
	9:55 – 10:20	**Lukas Burger** *Using deep learning to infer the chromatin sensitivity of transcription factors from ChIP-seq data*
	10:20 – 10:45	**Daniel Lipka** *Rapid Multi-Omics Leukemia Diagnostics using Nanopore-Sequencing*
	10:45 – 11:10	**Yahia Hadj-Arab** *Neuronal epigenetic plasticity in polyaddictions*
	11:10 – 11:30	**Break**
AI and ML	11:30 – 11:55	**Ilia Kats** *MOFA-FLEX: One factor model to rule them all*
	11:55 – 12:20	**Ferdinand Popp** *ML-guided TMM diagnostics in precision oncology programs*
	12:20 – 12:45	**Emma Engel / Oscar Gonzales Velasco** *Machine Learning Approaches to Infer the Primary Site from Cancers of Unknown Primary (CUP) Using Spatial Transcriptomics*
	12:45 – 14:00	**Lunch break**
Cancer and Precision med.	14:00 – 14:25	**Robert Autry** *INFORM Bioinformatics: From Impact to Innovation through Collaboration and Data Sharing*
	14:25 – 14:50	**Kendra Maaß** *Liquid biopsy in early diagnosis, therapy monitoring and surveillance*
	14:50 – 15:15	**Frank Westermann** *TBA*
	15:15 – 16:00	**Priya Chudasama** *ALTernative architecture of chromosomal-instable sarcoma*
	16:00 – 16:30	**Break**
	16:30	*Panel discussion „Genomics in the Clouds“*

Please note that the program is susceptible to change and will be continuously updated

7th NGS Symposium
14th April – 16th April 2026

	Thursday 16th April	
Frameworks & Workflows	9:00 – 9:25	**Charlotte Soneson** *A computational framework for representation and analysis of single molecule genomics data*
	9:25 – 9:50	**Daniel Hübschmann** *Assessment of cellular interactions at ultra-high throughput*
	9:50 – 10:15	**Wolfgang Maier** *Reproducible data analysis integrated with research data management with Galaxy*
	10:15 – 10:40	**Jan Eufinger** *The German Human Genome-Phenome Archive (GHGA): A national resource for the reuse of human Omics data*
	10:40 – 11:00	**Break**
Latest breakthroughs	11:00 – 11:25	**Anne Friedrich** *A thousand near telomere-to-telomere yeast genome assemblies help to decipher the genotype-phenotype relationship*
	11:25 – 11:50	**Daria Doncevic** *PELICAN: Conditional Wasserstein Adversarial Learning Enables Unpaired and Batch-Integrated Translation Across Single-Cell Modalities.*
	11:50 – 12:15	**Juan Caballero Perez** *Early experiences with AVITI sequencing technology*
	12:15 – 12:30	**Break**
	12:30 – 12:55	**Cihan Erkut** *Integrative analysis of the TBXT-driven transcriptome and proteome in chordoma*
Keynote	12:55 – 13:40	**Tobias Rausch** *Discovery of structural variants with long-read genomics*

Please note that the program is susceptible to change and will be continuously updated