

## MONDAY 09-10-2023

### Time

11.30-13.00 Registration and welcoming lunch @Kursaal

13.00-13.15 Welcome address

### Session Titlis chair: Barbara Treutlein

13.15-13.40 **Dana Pe'er** | Memorial Sloan Kettering Cancer Center, New York, USA

*Celebrating a decade: Musing on manifolds and pondering plasticity*

13.40-14.05 **Maria Brbic** | EPFL, Lausanne, Switzerland

*Bridging AI and Single-Cell Genomics: Towards AI-driven Discoveries*

14.05-14.20 **Gioele La Manno** | EPFL, Lausanne, Switzerland

*A 3D High-resolution Lipidomic Atlas of the Adult Mouse Brain*

14.20-14.35 **Verena Volf** | Harvard Medical School, Boston, USA

*DNA cryptography in living cells through multi-site base editing*

14.35-15:00 **Alexander van Oudenaarden** | Hubrecht Institute, Utrecht, Netherlands

*Novel sequencing tools to explore translation in individual cells*

15.00-15.40 Coffee break

### Session Matterhorn chair: Alexander van Oudenaarden

15.40-16:05 **Ed Boyden** | MIT and Howard Hughes Medical Institute, Boston, Cambridge, USA

*Precision Multiplexed Imaging of Molecules and Signals Throughout Biological Systems*

16.05-16:30 **Amos Tanay** | Weizmann Institute of Science, Rehovot, Israel

*Canonical spatio-temporal models from snapshots of single cells and single tissues*

16.30-16.45 **Fides Zenk** | EPFL, Lausanne, Switzerland

*Single-cell epigenomic reconstruction of developmental trajectories in human neural organoid systems*

16.45-17.10 **Nir Yosef** | Weizmann Institute of Science, Rehovot, Israel

*Analysis in multi-donor settings*

17.10-17.25 Sponsor Talk: **George Emanuel** | Vizgen

*MERSCOPE: Highly-multiplexed, multiomic tissue mapping with single-cell resolution*

17.30-17.55 **Poster Flashtalks**

*Rohit Agarwal, Leonard Hartmanis, Akanksha Jain, Dominik Klein, Samuel Marsh, Cameron Park, Ofir Raz, Antonio Santinha, Lisa McGinnis, Hannah Katharina Dickmänken, Jasper Janssens*

18.00-21.00 Dinner & Poster viewing @Bellevue

## TUESDAY 10-10-2023

### Time

#### Session Jungfrau chair: Rickard Sandberg

- 09.00-09.25 **Xiaowei Zhuang** | Harvard University and Howard Hughes Medical Institute, Cambridge, USA  
*Spatially resolved single-cell genomics & cell atlas of the brain*
- 09.25-09.50 **Kikuë Tachibana** | Max Planck Institute for Biochemistry, Martinsried, Germany  
*Mechanisms of zygotic genome activation at the start of life*
- 09.50-10.05 **Jonas Fleck** | Institute of Human Biology, Basel, Switzerland  
*Dissecting disease and development with multiplexed perturbations in human organoids*
- 10.05-10.30 **John Marioni** | Genentech, South San Francisco, USA  
*Adventures in space and time*
- 10.40-11.10 *Coffee break*

#### Session Finsteraarhorn chair: Amos Tanay

- 11.10-11.35 **Sten Linnarsson** | Karolinska Institute, Stockholm, Sweden  
*Gene regulation during early human brain development, and cell state and identity in human glioblastoma*
- 11.35-11.50 **Tanja Stadler** | ETH Zurich, Basel, Switzerland  
*Trees in cell biology*
- 11.50-12.05 **Dominic Grün** | Julius-Maximilians-Universität Würzburg, Würzburg, Germany  
*Understanding spatial driving forces of cell state variability in local tissue niches*
- 12.05-12.30 **Sanja Vickovic** | Columbia University and New York Genome Center, New York, USA  
*Spatial host-microbiome sequencing*
- 12.30-14.30 *Lunch break @Bellevue | Speakers lunch @Kempinski*

#### Session Monte Rosa chair: Aviv Regev

- 14.30-14.55 **Fabian Theis** | Helmholtz Center and Technical University Munich, Munich, Germany  
*Learning single-cell dynamics across time and space*
- 14.55-15.20 **Gray Camp** | Institute of Human Biology, Basel, Switzerland  
*Exploring multicellular interactions in engineered models of the human gut*
- 15.20-15.35 **Lea Jopp-Saile** | Deutsches Krebsforschungszentrum (DKFZ) and HI-STEM, Heidelberg, Germany  
*Combined single-cell and spatially-resolved mapping of lymph node ecosystems reveals fundamental principles of lymphoma tissue organization*
- 15:35-16:00 **Evan Macosko** | Broad Institute of MIT and Harvard, Cambridge, USA  
*Slide-tags: a unifying platform for spatial genomics*
- 16:00-16.15 **Merja Heinäniemi** | University of Eastern Finland, Kuopio, Finland  
*Cell-type-specific characterization of microRNA gene dynamics in immune cell subpopulations during aging and atherosclerosis disease development at single-cell resolution*
- 16.15-16.45 *Coffee break*

#### Session Dent Blanche chair: Ido Amit

- 16.45-17.05 **Nikolaus Rajewsky** | Max Delbrück Center BIMS, Berlin, Germany  
*Spacial Omics in 3-D*
- 17:05-17:20 **Basak Eraslan** | Genentech, South San Francisco, USA  
*PerturbDecode, a probabilistic analysis framework to recover regulatory circuits and predict genetic interactions from large-scale perturbation screens*
- 17:20-17:35 **Denis Jabaudon** | Geneva University, Geneva, Switzerland  
*Developmental molecular controls over arealization of descending corticofugal pathways*
- 17:35-17.55 **Rickard Sandberg** | Karolinska Institute, Stockholm, Sweden  
*New single-cell analyses of transcriptional and post-transcriptional gene regulation*
- 17.55-18.05 Sponsor Talk: **Melanie Masuda** | Scale Biosciences  
*Single Cell Biology at Scale: Unlock single cell genomics on 100s of thousands of cells with ScaleBio*
- 18:05-18:30 **Poster Flashtalks**  
*Michael Vaninsberghe, Pierre Bost, Hechen Li, Daniel Kunz, Anna Pascual Reguant, Zhisong He, Yanay Rosen, Anita Térmeg, Elin Vinsland*
- 18.30-21.30 *Dinner & Poster viewing @Bellevue*

## WEDNESDAY 11-10-2023

### Time

**Session Schreckhorn** chair: **Sten Linnarsson**

09.00-09.25	<b>Hongkui Zeng</b>   Allen Institute for Brain Science, Seattle, USA <i>Cell type organization across the mouse brain</i>
09.25-09.50	<b>Stein Aerts</b>   KU Leuven, Leuven, Belgium <i>Cell type evolution through the lens of enhancer logic</i>
09.50-10.05	<b>Spyros Darmanis</b>   Genentech, South San Francisco, USA <i>Overloading And unpacking (OAK) enables ultra-high throughput single cell multiomic profiling</i>
10.05-10.20	<b>Akhiad Bercovich</b>   Weizmann Institute of Science, Rehovot, Israel <i>Quantitative modeling of chromosomal accessibility and inference of de-novo motif binding energy models for accessibility regression</i>
10.20-10.45	<b>Barbara Treutlein</b>   ETH Zurich, Basel, Switzerland <i>Charting human neural fates through single-cell morphogen perturbation screens</i>
10.45-11.15	Coffee break

**Session Dom** chair: **John Marioni**

11.15-11.40	<b>Aviv Regev</b>   Genentech, South San Francisco, USA <i>Deciphering causal cell circuits: design and randomness</i>
11.40-11.55	<b>Daniel Kirschenbaum</b>   Weizmann Institute of Science, Rehovot, Israel <i>Temporally resolved single-cell transcriptomics defines immune dysfunction trajectories and checkpoints in the glioblastoma microenvironment</i>
11.55-12.20	<b>Xiao Wang</b>   Broad Institute of MIT and Harvard, Cambridge, USA <i>Translating spatial cell atlas to tissue function</i>
12.20-12.45	<b>Alex Schier</b>   University of Basel, Basel, Switzerland <i>Reconstructing Differentiation</i>
12.45-13.00	<b>Vitalii Kleshchevnikov</b>   Wellcome Sanger Institute, Cambridge, UK <i>Cell2state: a mechanistic end-to-end model of how transcription factors regulate DNA accessibility and cell plasticity</i>
13.00-14.30	Lunch break @Bellevue

**Session Weissshorn** chair: **Barbara Treutlein**

14.30-14.55	<b>Prisca Liberali</b>   Friedrich Miescher Institute, Basel, Switzerland <i>Symmetry breaking and a default mode of intestinal differentiation</i>
14.55-15.10	<b>Ozgun Gokce</b>   University of Bonn, Bonn, Germany <i>Spatial Transcriptomics-Correlated Electron Microscopy maps transcriptional and ultrastructural responses to brain injury</i>
15.10-15.35	<b>Jean Fan</b>   John Hopkins University, Baltimore, USA <i>Multi-scale characterization of cell-type spatial relationships in spatially resolved omics data</i>
15.35-15.50	<b>Andreas Moor</b>   ETH Zurich, Basel, Switzerland <i>Systematic perturbation of cellular interactions in the tumor microenvironment</i>
15.50-16.05	<b>Marloes Blotenburg</b>   Hubrecht Institute, Utrecht, Netherlands <i>Profiling of single-cell histone mark distributions and full-length transcriptome during in vitro gastrulation identifies rapid epigenetic rearrangements at the onset of lineage commitment</i>
16.05-16.30	<b>Ido Amit</b>   Weizmann Institute of Science, Rehovot, Israel <i>The power of ONE: Immunology in the age of spatial and single cell genomics</i>
16:30-16:35	Concluding remarks   End of scientific meeting
18.30-22.00	Dinner @Kursaal