

## Oral Program

### Sunday, February 24, 2019

**12:30-14:00 Registration** | Room: Breakthrough, Discovery, Exploration and Creation Foyer

Room | Breakthrough and Discovery Theatres

**14:00-17:00 Session 1: Atlasing Cell Types**

Session Chair: Huck Hui Ng, A\*STAR Genome Institute of Singapore

**14:00-14:15 Opening remarks: Robert Kruger**, Deputy Editor, Cell and **Shyam Prabhakar**, A\*STAR Genome Institute of Singapore

**14:15-14:45 J. Marioni**, European Molecular Biology Laboratory, European Bioinformatics Institute/Wellcome Sanger Institute, UK

Using single-cell RNA sequencing to provide insight into cell fate **[INV01]**

**14:45-15:15 I. Amit**, Weizmann Institute of Science, Israel

The power of ONE: Immunology in the age of single-cell genomics **[INV02]**

**15:15-15:30 A.M. Hockenberry\***, G. Takacs, M. Ackermann, ETH Zurich, Switzerland

Short-chain fatty acids destabilize *Salmonella enterica* virulent subpopulation development **[ST01]**

**15:30-16:00 Refreshment Break** | Room: Breakthrough, Discovery, Exploration and Creation Foyer

**16:00-16:30 N. Rajewsky**, Max Delbrück Center for Molecular Medicine in the Helmholtz Association, Germany

Function of RNA **[INV03]**

**16:30-17:00** Meet the Editors Session

**17:00-17:15** Poster Teasers

**17:15-19:00 Welcome Drinks Reception & Poster session 1** | Room: Breakthrough, Discovery, Exploration and Creation Foyer

### Monday, February 25, 2019

**08:30-09:00 Refreshment Break** | Room: Breakthrough, Discovery, Exploration and Creation Foyer

Room | Breakthrough and Discovery Theatres

**09:00-11:45 Session 2: Perturbing and Recording Single Cells**

Session Chair: Miao-Chih Tsai, Scientific Editor, Molecular Cell

**09:00-09:30 F. Watt**, King's College London, UK

Cellular heterogeneity in adult human skin **[INV04]**

**09:30-10:00 J. Lundeberg**, SciLifeLab/KTH, Sweden

Tissue expression anatomy by spatial transcriptomics **[INV05]**

**10:00-10:15 J. Ouyang\*<sup>1</sup>, X. Liu<sup>2</sup>, F. Rossello<sup>2</sup>, O. Rackham<sup>1</sup>, J. Polo<sup>2</sup>**

<sup>1</sup>Duke NUS Medical School, Singapore, <sup>2</sup>Monash University, Australia

Single-cell transcriptomics unravels the differences in human reprogramming for primed and naive pluripotency **[ST02]**

**10:15-10:45 Refreshment Break** | Room: Breakthrough, Discovery, Exploration and Creation Foyer

**10:45-11:15 J W. Shin**, Division of Genomic Medicine, Japan

Decoding neuronal diversity by single-cell Convert-seq **[INV06]**

**11:15-11:30 X. Jin\*<sup>1,2</sup>, S. Simmons<sup>2</sup>, A. Guo<sup>2</sup>, M. Ko<sup>3</sup>, J. Levin<sup>2</sup>, A. Regev<sup>2</sup>, P. Arlotta<sup>3</sup>, F. Zhang<sup>2</sup>**

<sup>1</sup>Harvard Society of Fellows, USA, <sup>2</sup>Broad Institute/MIT, USA, <sup>3</sup>Harvard Stem Cell and Regenerative Biology, USA

In vivo Perturb-Seq: Glial contribution to heterogeneous genetic variants in autism spectrum disorder **[ST03]**

**11:30-11:45** Poster Teasers

**11:45-12:45 Lunch** | Room: Breakthrough, Discovery, Exploration and Creation Foyer

**12:45-14:30 Poster Session 2** | Room: Breakthrough and Discovery Foyer

Room | Breakthrough and Discovery Theatres

**14:30-17:30 Session 3: Spatial and Temporal Profiling**

Session Chair: Matthew Pavlovich, *Editor, Trends in Biotechnology*

**14:30-15:00 E. Furlong**, *EMBL, Germany*

Understanding enhancer usage during embryonic development at a single-cell level [INV07]

**15:00-15:30 A. Forrest**, *Harry Perkins Institute of Medical Research/University of Western Australia, Australia*

The Western Australian cancer cell initiative [INV08]

**15:30-15:45 S. Ishikawa\*<sup>1,2</sup>, D. Komura<sup>1</sup>, R. Suzuki<sup>1</sup>, H. Katoh<sup>1,2</sup>** *<sup>1</sup>University of Tokyo, Japan, <sup>2</sup>Tokyo Medical and Dental University, Japan*

Interactome analysis of gastric cancer microenvironment by single-cell transcriptome sequencing [ST04]

**15:45-16:15 Refreshment Break** | *Room: Breakthrough, Discovery, Exploration and Creation Foyer*

**16:15-16:45 E. Lundberg**, *SciLifeLab/KTH, Sweden*

Dissecting spatiotemporal variations of the human proteome [INV09]

**16:45-17:00 J. Wang\*, R. Huber, Y. Wan**, *Genome Institute of Singapore, Singapore*

Single-cell mRNA secondary structure analysis reveals cell heterogeneity and dynamics [ST05]

**17:00-17:30 P. Kharchenko**, *Harvard Medical School, USA*

Analysis of transcriptional dynamics with single-cell RNA-seq data [INV10]

**18:15-22:30 Meet the Speaker Dinner | Singapore Zoo (buses to depart promptly at 18:15)**

**Tuesday, February 26, 2019**

**08:30-09:00 Refreshment Break** | *Room: Breakthrough, Discovery, Exploration and Creation Foyer*

Room | Breakthrough and Discovery Theatres

**09:00-12:15 Session 4: Epigenetics and Multimodal Profiling**

Session Chair: Robert Kruger, *Deputy Editor, Cell*

**09:00-09:30 F. Tang**, *Peking University, China*

Decoding the gene regulation network in human germline cells by single-cell functional genomics approaches [INV11]

**09:30-10:00 F. Theis**, *Helmholtz Zentrum München, Germany*

Modeling differentiation and stimulation response in single-cell genomics [INV12]

**10:00-10:15 G. Zheng\*, D. Jhutti, Y. Yin, S. Ziraldo, L. Montesclaros, J. Lau, J. Wang**, *10x Genomics, USA*

High-throughput profiling of immune systems using integrated single-cell multiomics methods [ST06]

**10:15-10:30 H. Li\*<sup>1</sup>, A. Leun<sup>2</sup>, I. Yofe<sup>1</sup>, Y. Lubling<sup>1</sup>, D. Solodkin<sup>1</sup>, A. Akkooi<sup>2</sup>, H. Horlings<sup>2</sup>, T. Schumacher<sup>2</sup>, A. Tanay<sup>1</sup>, I. Amit<sup>1</sup> et al.**, *<sup>1</sup>Weizmann Institute, Israel, <sup>2</sup>Netherlands Cancer Institute, the Netherlands*

Dysfunctional CD8+ cells form a proliferative, dynamically regulated compartment within human melanoma [ST07]

**10:30-11:00 Refreshment Break** | *Room: Breakthrough, Discovery, Exploration and Creation Foyer*

**11:00-11:30 R. Satija**, *New York Genome Center/NYU, USA*

Comprehensive integration of single-cell data [INV13]

**11:30-12:00 S. Prabhakar**, *A\*STAR Genome Institute of Singapore, Singapore*

The Importance of Feature Selection for Clustering Single Cell Transcriptomes [INV14]

**12:00-12:15 G. Shull<sup>1</sup>, C. Haffner<sup>2</sup>, W. Huttner<sup>2</sup>, E. Taverna\*<sup>3</sup>, S.B. Kodandaramaiah<sup>1</sup>**

*<sup>1</sup>University of Minnesota Twin Cities, USA, <sup>2</sup>Max Planck Institute of Molecular Cell Biology and Genetics, Germany, <sup>3</sup>Max Planck Institute for Evolutionary Anthropology, Germany*  
Robotic platform for microinjection into single cells in intact tissue [ST08]

**12:15-13:15 Lunch** | *Room: Breakthrough, Discovery, Exploration and Creation Foyer*

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**13:15-17:00 Session 5: Toward Precision Medicine**

Session Chair: Shyam Prabhakar, *A\*STAR Genome Institute of Singapore*

**13:15-13:45 B. Tasic**, *Allen Institute for Brain Science, USA*

Defining transcriptomic cell types across neocortical areas of the mouse brain [INV15]

- 13:45-14:15** **W. Y. Park**, *Samsung Genome Institute/Sungkyunkwan University School of Medicine, South Korea*  
Investigating intercellular network in colon cancer **[INV16]**
- 14:15-14:30** **Y. Xue<sup>\*1</sup>, S. Rastogi<sup>1</sup>, T. Theisen<sup>1</sup>, A. Ferrel<sup>1</sup>, J.C. Boothroyd<sup>1</sup>, S.R. Quake<sup>1,2</sup>**  
<sup>1</sup>Stanford University, USA, <sup>2</sup>Chan Zuckerberg Biohub, USA  
Building a single-cell co-transcriptomic atlas of the toxoplasma interactome **[ST09]**
- 14:30-14:45** **J. Scolnick<sup>\*1,4</sup>, S. Hoon<sup>2,4</sup>, Y. Wang<sup>1</sup>, G. Yeo<sup>1,3</sup>**  
<sup>1</sup>National University of Singapore, Singapore, <sup>2</sup>Agency of Science Technology and Research, Singapore, <sup>3</sup>University of California, USA, <sup>4</sup>Proteona, Singapore  
Escape RNA sequencing: Simultaneous single-cell protein, gene expression and mutation analysis to profile the tumors **[ST10]**
- 14:45-15:15** **Refreshment Break** | Room: Breakthrough, Discovery, Exploration and Creation Foyer
- 15:15-15:45** **C. Eaves**, *University of British Columbia, Canada*  
Heterogeneity of individually assessed primitive human hematopoietic cells **[INV17]**
- 15:45-16:15** **Y. S. Ju**, *KAIST, South Korea*  
Single genome sequencing of normal cells reveals developmental lineage tree of early human embryogenesis **[INV18]**
- 16:15-16:45** **F. Ginhoux**, *A\*STAR Genome Institute of Singapore, Singapore*  
Macrophage and dendritic cell biology **[INV19]**
- 16:45-17:00** **Closing remarks: Miao-Chih Tsai**, *Scientific Editor, Molecular Cell*