

# SINGLE CELL GENOMICS

sometimes the sum of the parts is greater than the whole

September 16-18, 2015  
Hubrecht Institute,  
Utrecht, The Netherlands



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- P002**                    **A controlled approach for measuring and modelling in vitro amplification noise of microsatellite from single cells**  
Ofir Raz, Weizmann  
Tamir Biezuner, Weizmann
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- P003**                    **Developing a rigorous quality control procedure for single cell transcriptomics data**  
Helen Lockstone, University of Oxford
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- P004**                    **Robust lineage reconstruction from high-dimensional single-cell data**  
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- P005**                    **Single cell transcriptomics analysis of induced pluripotent stem cell-derived cortical neurons reveals frequent dual layer identity**  
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- P006**                    **Multi-parameter RNA and protein data from the same single cell**  
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- P008**                    **Single-cell transcriptomes of fluorescent, ubiquitination-based cell cycle indicator cells**  
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Franziska Paul, Weizmann Institute of Science  
Yaara Arkin, Weizmann Institute of Science
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Gal Avital, Technion - Israel Institute of Technology
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Dominic Grün, Max Planck Institute of Immunobiology and Epigenetics
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Jiankui He, South University of Science and Technology of China
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Ewart Kuijk, Hubrecht Institute and University Medical Center Utrecht
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Hadas Keren-Shaul, Weizmann Institute of Science
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Armin Schneider, SYGNIS Bioscience GmbH & Co KG
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<b>P120</b>	<b>Identification of novel regulators of Th17 cell pathogenicity by single-cell genomics</b> Nir Yosef, UC Berkeley
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Sven Sagasser, Karolinska Institute
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Rory Nolan, University of Oxford
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Florian Buettner, European Bioinformatics Institute
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Alejandro Reyes, European Molecular Biology Laboratory
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