



A G B T 2017™

ADVANCES IN GENOME BIOLOGY AND TECHNOLOGY 2017 GENERAL MEETING

The Diplomat
Beach Resort
Hollywood Beach, Florida

MONDAY, FEBRUARY 13TH

11:00 AM – 8:00 PM

MEETING REGISTRATION

Great Hall Registration Desk

PLENARY SESSION:

GENOMICS I (ERIC GREEN, NHGRI, CHAIR)

Great Hall 4-6

5:00 PM – 5:30 PM

EIMEAR KENNY, PhD, Icahn School of Medicine at Mount Sinai
“Embracing global diversity for improving genomic medicine”

5:30 PM – 6:00 PM

ANDREW KUNG, MD, PhD, Memorial Sloan Kettering Cancer Center
“Clinical impact of next generation sequencing in pediatric oncology”

6:00 PM – 6:30 PM

STIRLING CHURCHMAN, PhD, Harvard Medical School
“Gene expression at high resolution, from the nuclear and mitochondrial genomes”

6:30 PM – 7:00 PM

WILLIAM GREENLEAF, PhD, Stanford University School of Medicine
“ATAC-ing’ single cell regulatory variation”

7:00 PM – 10:00 PM

WELCOME RECEPTION, Lagoon Lower Pool Decks

TUESDAY, FEBRUARY 14TH, MORNING

7:30 AM – 9:00 AM

BREAKFAST

South Palm Court

8:00 AM – 3:00 PM

MEETING REGISTRATION

Great Hall Registration Desk

PLENARY SESSION:

GENOMICS II: (BETH SHAPIRO, UNIVERSITY OF CALIFORNIA, SANTA CRUZ, CHAIR) Great Hall 4 – 6

9:00 AM – 9:30 AM

DANIEL DE CARVALHO, PhD, Princess Margaret Cancer Centre, University of Toronto
“Highly sensitive tumor detection and classification using Methylome Analysis of plasma DNA”

9:30 AM – 10:00 AM

OLIVER PYBUS, DPhil, BSc, MSc, University of Oxford
“Genomic evolution and epidemiology of Zika virus in the Americas”

- 10:00 AM – 10:30 AM **MARTIN JONES, PhD**, BC Cancer Agency Genome Sciences Centre
“Taking whole genomics to the cancer clinic: Integrative analysis for interpretation and communication of whole genome and transcriptome analysis at a tumour board”
- 10:30 AM – 11:00 AM **COFFEE BREAK**
 Great Hall 3
- * Denotes abstract selected talk
- 11:00 AM – 11:20 AM ***EDDY RUBIN, MD, PhD**, Metabiota
“The Global Virome Project”
- 11:20 AM – 11:40 AM ***RITA COLWELL, PhD**, University of Maryland and CosmosID
“Metagenomics of hospitalized diarrheal patients and healthy individuals in Kolkata, India”
- 11:40 AM – 12:00 PM ***FEDERICA DI PALMA, PhD**, Earlham Institute
“Evolution of tissue specific regulatory programs in Cichlid fishes”

TUESDAY, FEBRUARY 14TH, AFTERNOON

- 12:00 PM – 1:00 PM **BD SPONSOR WORKSHOP**
 Grand Ballroom, Complimentary Lunch Provided
 Rainer Blaesius, PhD, Manager R&D, Genomic Sciences, BD Technologies
“Single cell gene expression from solid tumor samples: Overcoming challenges in tumor dissociation and single cell analysis of heterogeneous samples”
- 12:00 PM – 1:00 PM **AGBT LUNCH**
 South Palm Court
- 1:00 PM – 2:30 PM **POSTER SESSION WITH COFFEE & DESSERT**
 Great Hall 3
- PLENARY SESSION:** **EVOLUTIONARY GENOMICS (LEN PENNACCHIO, LAWRENCE BERKELEY NATIONAL LABORATORY, CHAIR)**
 Great Hall 4 – 6
- 2:30 PM – 3:00 PM **LEIF ANDERSSON, PhD**, Uppsala University
“Detecting signatures of selection in natural populations using whole genome sequencing”
- 3:00 PM – 3:30 PM **DORIS BACHTROG, PhD, MSc**, The University of California, Berkeley
“Chromatin sinks & sex-specific aging in Drosophila: a role for the Y chromosome?”
- 3:30 PM – 3:50 PM ***EDWIN CUPPEN, PhD**, University Medical Center Utrecht
“Tissue-specific mutation accumulation in human adult stem cells during life”
- 3:50 PM – 4:10 PM ***ALEXANDER HOISCHEN, PhD**, Radboud University Medical Center
“Ultra-sensitive mosaic mutation detection in blood DNA of healthy individuals – new insights into age-related clonal hematopoiesis”

4:10 PM – 5:10 PM

ILLUMINA SPONSOR WORKSHOP

Grand Ballroom, Complimentary Refreshments Provided
“The next era of sequencing starts now”

TUESDAY, FEBRUARY 14TH, EVENING

5:15 PM – 7:15 PM

DINNER ON YOUR OWN

5:30 PM – 7:15 PM

WOMEN’S NETWORKING EVENT

South Palm Court

**CONCURRENT
SESSION:**

**GENOME TECHNOLOGY (KEN DEWAR, MCGILL UNIVERSITY AND
GÉNOME QUÉBEC INNOVATION CENTRE, CHAIR)**

Great Hall 4 – 6

7:30 PM – 7:50 PM

VIVEK BHALLA, Stanford University Medical Center

“Single cell resolution of highly diverse subpopulations in the mammalian kidney achieved with high throughput single cell RNA-sequencing”

7:50 PM – 8:10 PM

ANDREW ADEY, Oregon Health & Science University

“Construction of thousands of single cell genome sequencing libraries using combinatorial indexing”

8:10 PM – 8:30 PM

JOCHEN WEILE, University of Toronto

“Building a functional atlas of all possible human disease gene variants”

8:30 PM – 8:50 PM

YUSUKE GOTO, Hitachi Ltd., Research & Development Group

“Solid-state Nanopore DNA sequencing: Single-nucleotide discrimination and bidirectional DNA translocation”

8:50 PM – 9:10 PM

CHRISTOPHER WHELAN, Stanley Center for Psychiatric Research, Broad Institute

“Exploring 50 whole genomes with linked read technology”

9:10 PM – 9:30 PM

ERIC VILAIN, University of California, Los Angeles

“Use of next generation mapping in undiagnosed genetic disorders”

**CONCURRENT
SESSION:**

**HUMAN GENETICS, (PAUL FLICEK, EUROPEAN BIOINFORMATICS
INSTITUTE, CHAIR) Great Hall 1**

7:30 PM – 7:50 PM

CATHERINE COTTRELL, Institute for Genomic Medicine, Nationwide Children’s Hospital, St. Louis, MO

“Clinical application of next-generation sequencing for detection of somatic mosaicism”

7:50 PM – 8:10 PM

YOSHIHIKO SUZUKI, The University of Tokyo

“Metagenome, metamobilome and meta-methylome of the human gut flora”

8:10 PM – 8:30 PM

DEANNA CHURCH, 10X Genomics

“More complete genome analysis”

8:30 PM – 8:50 PM	SHAWN LEVY , HudsonAlpha Institute for Biotechnology <i>“From Olympians to Muscular Dystrophies: Advancements in variant detection and de novo assembly for the analysis of complex human phenotypes”</i>
8:50 PM – 9:10 PM	TAYLOR JENSEN , Sequenom <i>“Genome-wide sequencing of cell-free DNA identifies copy number alterations that can be used for prediction and monitoring response to immunotherapy in cancer patients”</i>
9:10 PM – 9:30 PM	CHRISTINA FAN , BD <i>“Application of high throughput single cell transcriptomics for analysis of rare populations present in bronchoalveolar lavage samples”</i>
CONCURRENT SESSION:	GENERAL BIOLOGY (BETH SHAPIRO, UNIVERSITY OF CALIFORNIA SANTA CRUZ, CHAIR) Great Hall 2
7:30 PM – 7:50 PM	JASON UNDERWOOD , Pacific Biosciences/University of Washington <i>“Long-read genome assembly and full-length transcript profiling of stem cells from great apes”</i>
7:50 PM – 8:10 PM	DANIEL NEAFSEY , Broad Institute of MIT and Harvard <i>“A community effort using multiple technologies to produce a dramatically improved genome assembly of the Zika virus mosquito vector”</i>
8:10 PM – 8:30 PM	CHRISTIAN MATRANGA , Broad Institute of Harvard and MIT <i>“Genomic survey of origin and transmission of Zika virus in the Americas”</i>
8:30 PM – 8:50 PM	DAWN THOMPSON , Ginkgo Bioworks <i>“The synergy of rational design and natural genetic variation in a high throughput biological foundry for industrial strain improvement”</i>
8:50 PM – 9:10 PM	STEPHANIE HAO , Johns Hopkins University <i>“Antimicrobial resistance detection in Illumina and Nanopore Sequencing”</i>
9:10 PM – 9:30 PM	CARLOS CRUCHAGA , Washington University School of Medicine <i>“Novel rare variants in known genes, a look into the Familiar Alzheimer Sequencing (FASe) project”</i>
9:30 PM	PASSPORT PARTY Sponsors’ Promenade—South Tower

WEDNESDAY, FEBRUARY 15TH, MORNING

7:30 AM – 9:00 AM

BREAKFAST
South Palm Court

PLENARY SESSION:

TECHNOLOGY I (ELAINE MARDIS, THE INSTITUTE FOR GENOMIC MEDICINE AT NATIONWIDE CHILDREN'S HOSPITAL, CHAIR)
Great Hall 4 – 6

9:00 AM – 9:30 AM

NADA JABADO, MD, PhD, McGill University Health Center
"Oncohistones: Professional hijackers of the epigenome?"

9:30 AM – 10:00 AM

EMMA TEELING, PhD, MSc, BSc, University College Dublin
"Comparative genomics of bats: the secret of extended longevity?"

10:00 AM – 10:20 AM

***JOSHUA LEVIN, PhD**, Broad Institute of MIT and Harvard
"Single cell profiling the thalamic reticular nucleus (TRN) to understand a brain region strongly implicated in schizophrenia and autism"

10:20 AM – 10:55 AM

COFFEE BREAK
Sponsors' Promenade—South Tower

11:00 AM – 11:20 AM

***JUSTIN CHU, PhD**, BC Cancer Agency Genome Sciences Centre
"10x genomics chromium fragment assembly and scaffolding"

11:20 AM – 11:40 AM

***A. MCGARRY HOUGHTON, MD**, Fred Hutchinson Cancer Research Center
"3D Biology™ view of cancer: Simultaneous detection of somatic DNA mutations and expressed fusion transcripts plus expression profiling of phospho and total signaling proteins from lung-tumor FFPE samples"

11:40 AM – 12:00 PM

***BENJAMIN RUBIN**, University of California San Diego
"The Essential Gene Set of a Photosynthetic Organism"

WEDNESDAY, FEBRUARY 15TH, AFTERNOON

12:00 AM – 2:00 PM

NANOSTRING SPONSOR WORKSHOP
Grand Ballroom, Complimentary Lunch Provided

TRANSLATING NGS INSIGHTS INTO CLINICAL IMPACT

HYB & SEQ TECHNOLOGY: A NO AMP, NO LIBRARY, SINGLE MOLECULE SEQUENCER DESIGNED FOR THE CLINIC
Joseph Beechem, PhD, SVP R&D Nanostring.

THE FUTURE-HISTORY OF NEXT-GEN SEQUENCING
Chad Nusbaum, PhD, Director of the Broad Technology Labs.

NEXT GENERATION SEQUENCING FOR BIOMARKER DISCOVERY AND COMPANION DIAGNOSTICS DEVELOPMENT
Hirdesh Uppal, PhD, Head of Companion Diagnostics, Pfizer.

12:00 PM – 2:00 PM	AGBT LUNCH South Palm Court
PLENARY SESSION:	GENETICS (JOHN MCPHERSON, UNIVERSITY OF CALIFORNIA, DAVIS, CHAIR) Great Hall 4 – 6
2:00 PM – 2:30 PM	GONCALO ABECASIS, DPhil , University of Michigan
2:30 PM – 3:00 PM	DANIEL MACARTHUR, PhD , Harvard Medical School <i>“Leveraging massive-scale frequency databases to improve variant interpretation”</i>
3:00 PM – 3:30 PM	JOHN MARIONI, PhD , CRUK Cambridge Institute <i>“Using single-cell transcriptomics to understand cell fate decisions”</i>
3:40 PM – 4:40 PM	PACBIO SPONSOR WORKSHOP Grand Ballroom, Complimentary Coffee and Snack Provided <i>“The Sequel™ System: Covering all the Bases with SMRT® Sequencing”</i>
4:45 PM – 6:10 PM	POSTER SESSION AND SOFTWARE DEMO WITH WINE RECEPTION Great Hall 3

WEDNESDAY, FEBRUARY 15TH, EVENING

6:15 PM – 7:25 PM	AGBT DINNER South Palm Court
CONCURRENT SESSION:	INFORMATICS (MICHAEL ZODY, NEW YORK GENOME CENTER, CHAIR) Great Hall 4 – 6/General Session Room
7:30 PM – 7:50 PM	MARK DEPRISTO , Verily Life Sciences <i>“Mastering variant calling of SNPs and small indels with deep neural networks”</i>
7:50 PM – 8:10 PM	EVAN MAXWELL , Regeneron Genetics Center, Regeneron Pharmaceuticals <i>“Detection and analysis of copy number variation and aneuploidy from 100,000 exomes”</i>
8:10 PM – 8:30 PM	MICHAEL SCHATZ , Cold Spring Harbor Laboratory and Johns Hopkins University <i>“Personalized phased diploid genomes of the EN-Tex samples”</i>
8:30 PM – 8:50 PM	PREYAS SHAH , 10x Genomics <i>“Local assemblies from one library drive completeness of diploid genomes”</i>
8:50 PM – 9:10 PM	GIUSEPPE NARZISI , New York Genome Center <i>“Lancet: somatic variant calling using localized colored DeBruijn graphs”</i>

9:10 PM – 9:30 PM

JIMMIE YE, University of California, San Francisco
*“Multiplexing droplet-based single cell RNA-seq using
“genetic barcodes”*

**CONCURRENT
SESSION:**

**CANCER (JOHN MCPHERSON, UNIVERSITY OF CALIFORNIA, DAVIS,
CHAIR)** Great Hall 1

7:30 PM – 7:50 PM

JOSEPH BEECHEM, NanoString Technologies
*“Library-free, targeted sequencing of native gDNA from FFPE
samples using Hyb & Seq™ technology – the hybridization based
single molecule sequencing system”*

7:50 PM – 8:10 PM

JOSEPH BOLAND, National Cancer Institute
*“A novel whole genome sequencing method to comprehensively
map all HPV16 integration events across multiple human genomes”*

8:10 PM – 8:30 PM

RANJAN PERERA, Sanford Burnham Prebys Medical Discovery Institute
*“Systems level investigation of urine enriched RNA and
metabolites, and their use as combinatorial biomarkers for
early prostate cancer detection”*

8:30 PM – 8:50 PM

JESSICA NORDLUND, Uppsala University
*“Dissection of the Heterogeneous Fusion Gene Landscape in
Pediatric Acute Lymphoblastic Leukemia”*

8:50 PM – 9:10 PM

ANN-CHRISTINE SYVÄNEN, Uppsala University
*“Deep-targeted sequencing in pediatric acute l lymphoblastic
leukemia unveils distinct mutational patterns between genetic
subtypes and novel relapse-associated genes”*

9:10 PM – 9:30 PM

GABOR MARTH, University of Utah
*“Tracking the evolution of a patient’s tumor across multiple time
points or multisite metastases”*

**CONCURRENT
SESSION:**

**TRANSCRIPTOME & EPIGENOMICS (ROBERT LYONS, UNIVERSITY
OF MICHIGAN, CHAIR)** Great Hall 2

7:30 PM – 7:50 PM

OSCAR HARARI, Washington University School of Medicine
*“Cell-type specific transcriptomic downstream events triggered by
Alzheimer Disease Mendelian mutations”*

7:50 PM – 8:10 PM

ANTHONY GRISWOLD, University of Miami
*“Identification of extracellular RNA biomarkers of osteoarthritis in
synovial fluid following traumatic knee l injury”*

8:10 PM – 8:30 PM

LI JIA, National Cancer Institute
*“Single-cell RNA-seq data analysis to discover gene expression
profiles involved in the persistence of T cells following cell transfer
cancer immunotherapy”*

8:30 PM – 8:50 PM

RAHUL SATIJA, New York Genome Center
“Drop-seq analysis of early fate decisions in human hematopoiesis”

8:50 PM – 9:10 PM

ZORA MODRUSAN, Genetech

“Advances in RNA-seq enable highly parallel transcriptional profiling of hundreds of single cells”

9:10 PM – 9:30 PM

THEODORE DAVIS, New England Biolabs

“APOBEC-Seq: An enzymatic method for methylome analysis at single-base resolution without bisulfite treatment”

THURSDAY, FEBRUARY 16TH, MORNING

7:30 AM – 9:00 AM

BREAKFAST

South Palm Court

BRONZE SPONSOR WORKSHOPS

Great Hall 4 - 6

9:00 AM – 9:20 AM

FLUIDIGM

Ramesh Ramakrishnan, PhD, Senior Director, R&D

“Scaling NGS library preparation with automated microfluidics to achieve significant cost efficiencies at production scale”

9:20 AM – 9:40 AM

ROCHE

Maryke Appel, Sr. International Product Manager, Library Prep

“Roche Sequencing Solutions: An integrated approach to NGS sample prep”

9:40 AM – 10:00 AM

NEW ENGLAND BIOLABS

Peter Ellis, PhD, Wellcome Trust Sanger Institute, Cambridge, UK

“Next generation DNA library construction for high-throughput genomics”

10:00 AM – 10:20 AM

ADVANCED ANALYTICAL

Steve Siembieda, VP Commercialization

“FEMTO Pulse™ Automated Pulsed-Field CE Instrument for femtogram detection sensitivity with accurate HMW DNA sizing”

10:20 AM – 10:40 AM

PERKIN ELMER

“NEXTflex™ Spike-in Controls designed for assessing sample cross contamination and misidentification in sequencing workflows”

10:40 AM – 11:05 AM

COFFEE BREAK

Great Hall Foyer

11:05 AM – 11:20 AM

LEXOGEN

Lukas Paul, Lexogen

“Getting the most out of gene expression profiling with QuantSeq: high multiplexing, sensitivity, and reproducibility with lowest costs and efforts”

11:20 AM – 11:35 AM

THERMO FISHER

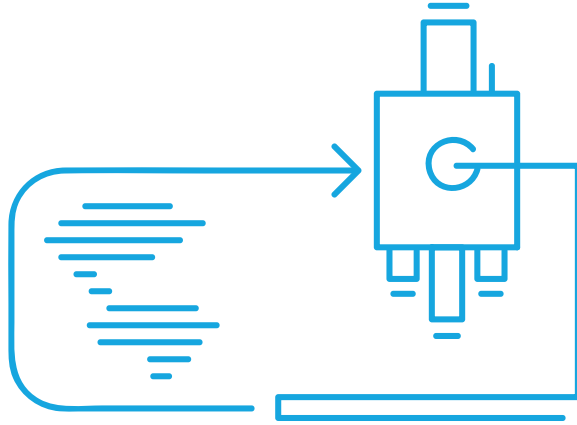
Simon Cawley, PhD, Senior Director, Software and Informatics
Clinical Sequencing Division, Thermo Fisher Scientific

“Advancing precision genomics using ion torrent technology”

- 11:35 AM – 11:50 AM **PROMEGA**
Thomas J. Livelli, Vice President Life Sciences, Promega Corporation
“Next generation integrative life science research: Looking into the future”
- 11:50 AM – 12:05 PM **DDN**
George Vacek, PhD, MBA, Global Director Life Sciences
“Managing Data Across the Genomics Research Data Lifecycle”
- 12:05 PM **PASSPORT GRAND PRIZE WINNER ANNOUNCED**

THURSDAY, FEBRUARY 16TH, AFTERNOON

- 12:05 PM – 1:15 PM **AGBT LUNCH**
South Palm Court
- PLENARY SESSION:** **TECHNOLOGY II (MARTIN HIRST, UNIVERSITY OF BRITISH COLUMBIA, CHAIR),** Great Hall 4 - 6
- 1:30 PM – 2:00 PM **IDO AMIT, PhD,** Weizmann Institute of Science
“The power of one: Immunology in the age of single cell genomics”
- 2:00 PM – 2:30 PM **JARED SIMPSON, PhD,** Ontario Institute for Cancer Research
“Nanopore sequencing of a human genome”
- 2:30 PM – 2:50 PM ***CHRISTOPHER MASON, PhD,** Weill Cornell Medicine
“DNA sequencing, genome assembly, and epigenetics on the international space station”
- 2:50 PM – 3:10 PM **COFFEE BREAK**
Great Hall Foyer
- 3:10 PM – 3:30 PM ***GARY NOLAN, PhD,** Stanford University School of Medicine
“Sequencers as Flow Cytometers: Ultra-High Throughput Single Cell Analysis of Proteins and RNAs by Split-pool Synthesis”
- 3:30 PM – 3:50 PM ***JEFFREY ROSENFELD, PhD,** Rutgers Cancer Institute of NJ
“Single-cell RNA sequencing in sperm from fathers of autistic children”
- 3:50 PM – 4:10 PM ***EVAN DAUGHARTHY, PhD,** Harvard University
“RNA sequencing in situ: A revolutionary new technology”
- 4:10 PM – 4:40 PM **CLOSING COMMENTS AND MEETING FEEDBACK**
- 7:00 PM – 12:00 AM **FAREWELL DINNER PARTY**
Great Hall 1-4



THE GENOME
PARTNERSHIP™