Introducing HiSeq™ 2000

Redefining the trajectory of sequencing.

What if you could:

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- Perform gene expression profiling on 200 samples?
- Sequence a genome on one flow cell and its epigenome and transcriptome on the other flow cell?

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The University of Miami, Nature Publishing Group and Scripps Florida present

miami 2011 winter symposium
a nature conference

MIAMI 2011 WINTER SYMPOSIUM
Epigenetics in Development and Disease

Recent years have witnessed rapid progress in elucidating the role of epigenetic modifications in nuclear organization and chromosome packaging, profoundly impacting our understanding of development, disease and natural variation. An increasingly diverse picture is emerging of the range of epigenetic mechanisms involved in regulating these processes, from DNA methylation and histone modification to non-coding RNAs, chromatin remodeling and interactions of higher order chromosome structures. Concurrently, rapid progress is being made in the development of technologies that facilitate the analysis of genome-wide epigenetic changes as well as the genetic and chemical means for experimentally manipulating cellular reprogramming and epigenetic modifications in stem and somatic cells. The 44th Miami Winter Symposium will bring together leaders in the field to address key aspects of the mechanisms of epigenetic regulation, cellular reprogramming, development and disease.

February 6-9, 2011
JW Marriott Marquis Hotel Miami
Miami, FL, USA

SYMPOSIUM AWARDEES

Distinguished Service Award:
Peter Jones (University of Southern California, USA)

Lynen Lecture:
Andrew Feinberg (Johns Hopkins School of Medicine, USA)

Lifetime Achievement Award:
Rudolf Jaenisch (Massachusetts Institute of Technology, USA)

Special Achievement Award:
Danesh Moazed (Harvard Medical School, USA)

CONFIRMED SPEAKERS

Asifa Akhtar (Max-Planck-Institute of Immunobiology, Germany)
Robin Allshire (The University of Edinburgh, UK)
Shelly Berger (University of Pennsylvania School of Medicine, USA)
Howard Cedar (Hebrew University of Jerusalem, Israel)
Manel Esteller (Bellvitge Biomedical Research Institute, Spain)
Tan Ince (Harvard Medical School, USA)
Tony Kouzarides (University of Cambridge, UK)
Jeannie Lee (Massachusetts General Hospital, USA)
Jason Lieb (University of North Carolina at Chapel Hill, USA)
Rolf Ohlsson (Karolinska Institutet, Sweden)
Renato Paro (ETH Zurich, Switzerland)
Wolf Reik (The Babraham Institute, UK)
Bing Ren (University of California, San Diego, USA)
Miguel Ramalho Santos (University of California, San Francisco, USA)
Paolo Sassone-Corsi (University of California, Irvine, USA)
Ramin Shiekhattar (The Wistar Institute, USA)
John Stamatoyannopoulos (University of Washington, USA)
Patrick Trojer (Constellation Pharma, USA)
Claes Wahlestedt (Scripps Florida, USA)
Chia-Lin Wei (Genome Institute of Singapore, Singapore)
Emma Whitelaw (Queensland Institute for Medical Research, Australia)
Yi Zhang (University of North Carolina at Chapel Hill, USA)

Image: Chromatin Iznik chini by Tayfun Özçelik

Abstract Submission and Early Registration Deadline — November 18, 2010. For more information and to register visit:

www.nature.com/natureconferences/miami/MWS2011

a nature conference

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Make Directional RNA-Seq Libraries in Less Than 3 Hours

EPICENTRE's new ScriptSeq™ mRNA-Seq Library Preparation Kit (Illumina-compatible) uses a unique terminal-tagging technology that simplifies the preparation of mRNA-Seq libraries from any animal, plant, or bacterial species.

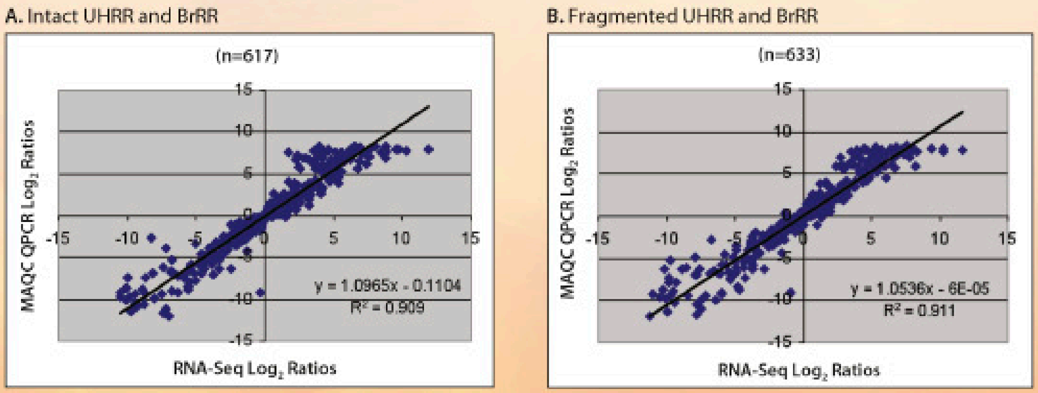
ScriptSeq Illumina-compatible libraries:

- Enable directional sequencing.
- Are made in 3 hours without the need for adaptor ligation.
- Are barcode-capable. Easily incorporate Illumina-compatible barcodes (available separately) or user-defined barcodes.
- Demonstrate high concordance with MAQC qPCR results.

**Covered by issued and/or pending patents.*

ScriptSeq™ mRNA-Seq Library Preparation Kit (Illumina-compatible) generates libraries for directional sequencing in less than 3 hours. Times for each step are shown in hours:minutes.

Conventional mRNA-Seq Method		ScriptSeq™ Method	
Fragment RNA	(1:00)	Fragment RNA and synthesize di-tagged cDNA	(1:40)*
Synthesize cDNA	(4:30)		
Ligate adaptors	(2:00)	Clean up cDNA	(0:10)
Size-select from gel	(1:30)	—	
Enrich library by PCR	(1:00)	Enrich library by PCR	(1:00)
Total Time:	10:00	Total Time: **single-tube reaction*	~3:00


A. Intact UHRR and BrRR

B. Fragmented UHRR and BrRR

Correlation of gene expression between EPICENTRE ScriptSeq™ libraries and corresponding MAQC data. A) Libraries prepared from rRNA-depleted, intact UHRR and BrRR. B) Libraries prepared from partially fragmented, rRNA-depleted UHRR and BrRR. UHRR, Universal Human Reference RNA; BrRR, Brain Reference RNA.

ScriptSeq™ mRNA-Seq Library Preparation Kit (Roche Titanium-compatible) and ScriptMiner™ Small RNA-Seq Library Preparation Kit (Illumina-compatible) are also available. For more information, visit: **www.EpiBio.com/rnaseq**

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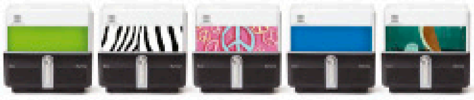

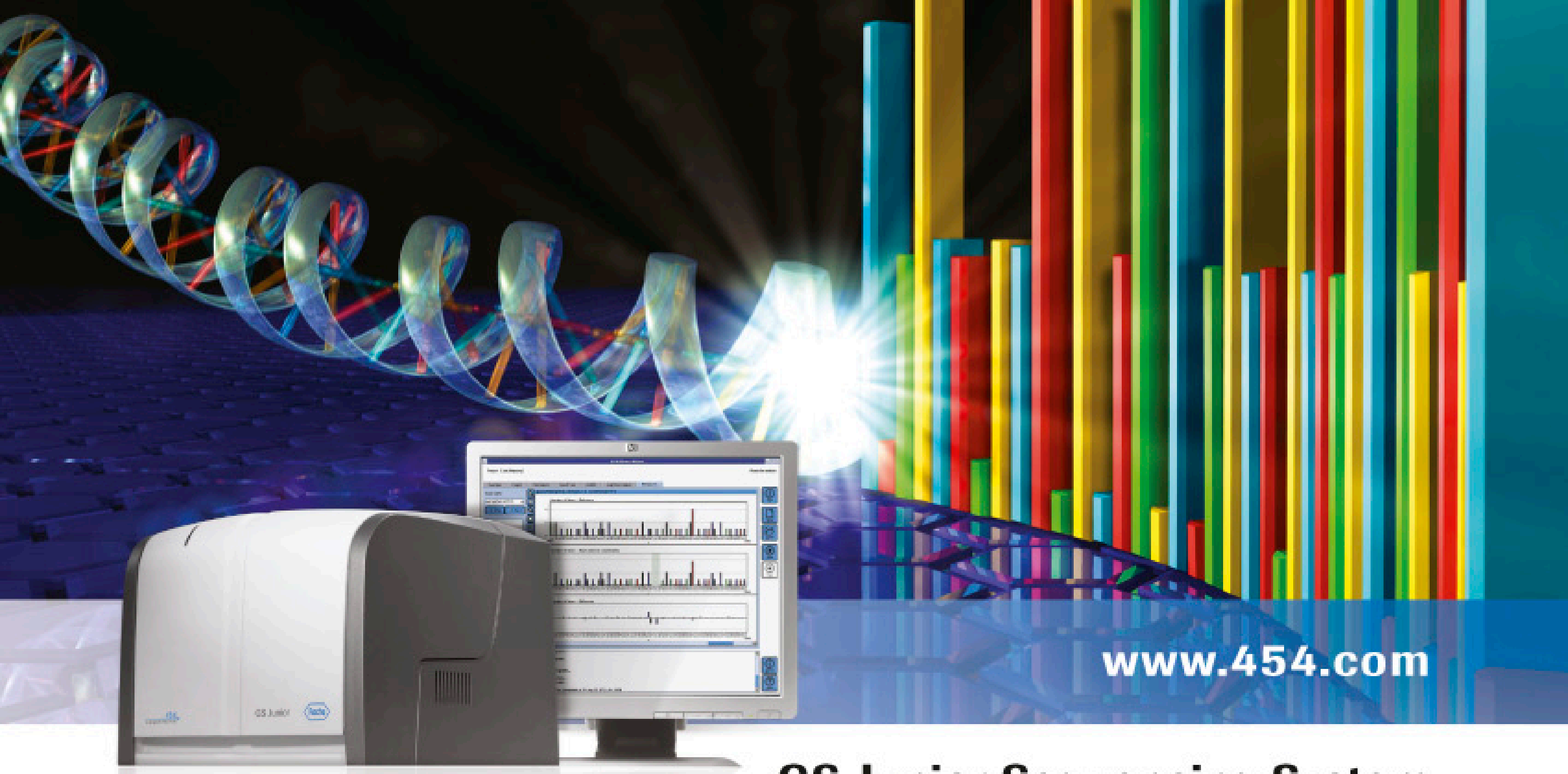

GS Junior Sequencing System

A *NEW* Scale of Sequencing –

Amplicon Sequencing on Your Benchtop

Amplicon Assay	Samples per Run
HIV Drug Targets (*e.g.*, 16 amplicons covering 5 regions at 1500X [Protease, RT, Integrase, Envelope V3, gp41 heptad repeats])	8
Gene Sequencing (*e.g.*, CFTR, 34 amplicons covering 27 exons at 50X)	48
HLA Sequencing (*e.g.*, high-resolution genotyping at 7 loci)	16
VDJ Sequencing (*e.g.*, for vaccine response or minimal residue detection for known clonality)	8

Figure 1: Get the right depth and coverage for your amplicon project. You can customize your experimental design to maximize data throughput for optimal sample coverage per sequencing run. Examples of various applications and optimum sample number per run are shown for the GS Junior System.

Bring the power of 454 pyrosequencing to your amplicon projects. Now available, the new small-footprint **GS Junior System** generates 70,000 reads per run, and delivers the performance and long reads (up to 500 base pairs) of the GS FLX Titanium chemistry to your benchtop.

- **Detect SNPs, insertions, and deletions.**
- **Discover rare somatic mutations in complex samples based on ultra-deep sequencing of amplicons.**
- **Sequence and analyze collections of human exons for identifications of rare alleles.**
- **Find viral quasispecies present within infected populations.**
- **Identify rare alleles associated with diseases.**

For complete information on the GS Junior System and all of the Roche sequencing solutions, visit ***www.454.com*** or contact your local Roche representative today.

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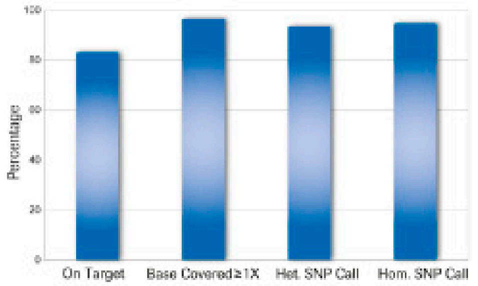

Exome Capture Performance With Single Lane Sequencing: The exome from HapMap sample NA12762 was captured and sequenced with a single 2x75 paired-end lane, generating 18.8 ± 1.9 million reads (n = 16) and providing 50.6 ± 4.8 fold average coverage of the target regions. SNP calls from single lane data were compared to HapMap SNPs.

- **Enhanced uniformity by rebalancing 2.1 million probes** minimizing sequencing needs to only a single lane while maximizing exome coverage.
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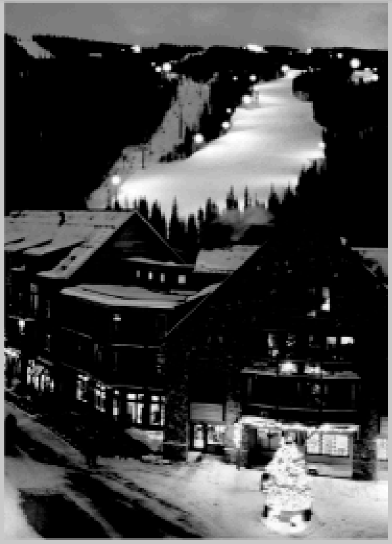
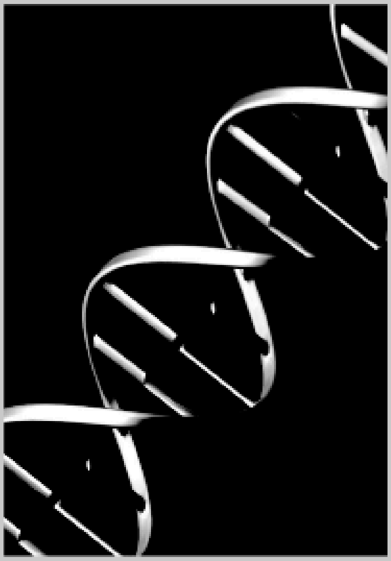


Functional Consequences of Structural Variation in the Genome
Scientific Organizers: Evan E. Eichler and Matthew Hurles
January 8–13, 2011
Sheraton Steamboat Resort • Steamboat Springs, Colorado • USA
Keynote Speaker: **James R. Lupski**, Baylor College of Medicine, USA
Late-Breaking Abstract Deadline – Oct 11, 2010 / Early Registration Deadline – Nov 8, 2010
www.keystonesymposia.org/11A1

Genomic Instability and DNA Repair
Scientific Organizers: Junjie Chen, Karlene A. Cimprich and Michael B. Yaffe
January 30–February 4, 2011
Keystone Resort • Keystone, Colorado • USA
Keynote Speakers: **David M. Livingston**, Dana-Farber Cancer Institute, USA
Stephen J. Elledge, Harvard-Partners Center for Genetics and Genomics, USA
Late-Breaking Abstract Deadline – Nov 2, 2010 / Early Registration Deadline – Nov 30, 2010
www.keystonesymposia.org/11B4

Environmental Genomics and Disease Susceptibility
Scientific Organizers: Randy L. Jirtle, Moshe Szyf and Frederick L. Tyson
March 27–April 1, 2011
Grove Park Inn Resort & Spa • Asheville, North Carolina • USA
Keynote Speaker: **Matt Ridley**, Blagdon Seaton Burn, UK
Abstract & Scholarship Deadline – Nov 30, 2010 / Late-Breaking Abstract Deadline – Dec 31, 2010 / Early Registration Deadline – Jan 28, 2011
www.keystonesymposia.org/11D3

Changing Landscape of the Cancer Genome
Scientific Organizers: Lynda Chin, Christoph Lengauer and Michael Stratton
June 20–25, 2011
Boston Park Plaza & Towers • Boston, Massachusetts • USA
Keynote Speaker: **Tom Hudson**, Ontario Institute for Cancer Research, Canada
Abstract & Scholarship Deadline – Feb 21, 2011 / Late-Breaking Abstract Deadline – Mar 21, 2011 / Early Registration Deadline – Apr 20, 2011
www.keystonesymposia.org/11F3

Programs subject to change. For the most up-to-date information on these and more than 50 other conferences in 2011, please visit ***www.keystonesymposia.org/2011meetings.***

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The International Conference on the Status of Plant & Animal Genome Research

January 15–19, 2011
Town & Country Hotel, San Diego, California

Speakers

Roger Beachy, USDA/Washington
Joe Ecker, Salk Institute
Ed Green, UC Santa Cruz
Dave Lipman, NCBI, NLM, NIH
Sharon Long, Stanford University
Michael Lynch, Indiana University
Pam Ronald, UC Davis

Workshops

- Abiotic Stress
- Allele Mining
- Animal Epigenetics
- Apomixis
- Aquaculture
- Arthropod Genomics
- Banana Genomics
- Barley
- Bioinformatics
- Brachypodium Genomics
- Brassicas
- Cacao Genome Sequencing
- Cassava Genomics
- Cattle/Sheep/Swine
- Citrus Genome
- Coffee
- Comparative Genomics
- Cool Season Legumes
- Cotton Genome Initiative
- Cucurbit
- Ecological Genomics
- Equine
- Evolution of Genome Size
- Forage & Turf Plants
- Forest Tree
- Fruit/Nuts
- Functional Genomics
- Fungal Genomics
- Gene Expression Analysis
- Genomics Assisted Breeding
- Genomics for Disease Resistance
- Grape Genome Initiative
- Grass Genome Initiative
- Host-Microbe Interactions
- Large Insert DNA Library
- Lolium Genome Initiative
- Maize
- Molecular Markers
- Mutation Screening
- Oats
- Ornamentals
- Phylogenomics
- Plant Cytogeneics
- Plant Interactions/Pests
- Plant Introgression
- Plant Reproductive Genomics
- Polyploidy
- Population & Conservation
- Poultry
- Proteomics
- QTL Cloning
- Rice Blast
- Rice Functiional Genomics
- Root Genomics
- Sex Chromosomes
- Solanaceae
- Somatic Genome
- Soybean Genomics
- Statistical Genomics
- Sugar Beet
- Sugar Cane
- Swine Genome Sequencing
- Transposable Element
- Weedy & Invasive Plant Genomics
- Wheat Genome Sequencing

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2010 COLD SPRING HARBOR ASIA

FALL MEETINGS

Suzhou Dushu Lake Conference Center, Suzhou, China

- Human Genetics & Genomics
  September 6-10, Abstracts due July 25
  Organizers: Paul Liu, Maynard Olson, Svante Pääbo, Huanming Yang
  Keynote speakers: Sydney Brenner, Edison Liu, Mathias Uhlen

- Molecular Switches and Genome Function in Stem Cells & Development
  September 21-25, Abstracts due July 25
  Organizers: Shin-ichi Nishikawa, Duanqing Pei, Patrick Tam
  Keynote speakers: Andras Nagy

- Computational Biology
  September 27-October 1, Abstracts due July 30
  Organizers: Satoru Miyano, Martin Vingron, Michael Zhang
  Keynote speakers: Richard Durbin, Minoru Kanehisa, Gary Stormo

- Emerging Infectious Diseases
  October 18-22, Abstracts due July 30
  Organizers: Yi Guan, Margaret Liu, Zihe Rao, Tianyi Wang
  Keynote speakers: Louise Chow, Zihe Rao

- From Plant Biology to Crop Biotechnology
  October 25-29, Abstracts due August 29
  Organizers: Nam-Hai Chua, David Jackson, Jiayang Li, Kazuo Shinozaki
  Keynote speakers: Cathie Martin, Marjori Matzke

- RNA Biology
  November 1-5, Abstracts due August 13
  Organizers: Xumei Chen, Soo-Chen Cheng, Masatoshi Hagiwara, Adrian Krainer
  Keynote speakers: Thomas Steitz

- Frontiers of Immunology in Health and Diseases
  November 7-10, Abstract due Augusts 20
  Organizers: Xuetao Cao, Richard Flavell, Tadatsugu Taniguchi
  Keynote speakers: Xuetao Cao, Richard Flavell

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Cancer Genetics & Epigenetics
January 23-28, 2011
Ventura, CA

Cell Biology of Megakaryocytes & Platelets (GRS)
Gordon-Kenan Research Seminar (a two-day seminar for graduate students & post docs)
Establishing a Research Career in Platelet Biology and Hemostasis/Thrombosis
March 19-20, 2011
Galveston, TX

-and-

Cell Biology of Megakaryocytes & Platelets
March 20-25, 2011
Galveston, TX

Cellular & Molecular Mechanisms of Toxicity
NEW!
Understanding Innovative Mechanistic Toxicologyin the Post-Genomic Era
August 7-12, 2011
Andover, NH

CO_2 Assimilation in Plants: Genome to Biome
May 29 - June 3, 2011
Les Diablerets, Switzerland

Ecological & Evolutionary Genomics
July 10-15, 2011
Biddeford, ME

Human Genetics & Genomics
July 17-22, 2011
Newport, RI

Mycotoxins & Phycotoxins (GRS)
Gordon-Kenan Research Seminar (a two-day seminar for graduate students & post docs)
Discovery and Risk Management of Harmful Biotoxins
June 11-12, 2011
Waterville, ME

-and-

Mycotoxins & Phycotoxins
June 12-17, 2011
Waterville, ME

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