Illumina Technology Updates

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Genomics Specialist
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Illumina’s Mission

Innovating for the Future of Genetic Analysis

To be the leading provider of integrated solutions that advance the understanding of genetics and health
A Sequencer for Every Need. Every Budget. Every Lab.

Redefining the trajectory of sequencing.


Two proven technologies. One powerful platform.

The most widely cited platform, now at half the price

My Samples. My Study. MiSeq

HiSeq 2000  HiSeq 1000  HiScanSQ  GA\textsubscript{IIx}  MiSeq
Evolution of Instrument Performance

*From &lt;1Gb to &gt;1Tb in 4 Years*

Internally we have completed multiple runs generating &gt;1Tb of data per run

Greater than 80Gb per day!
Greater than 7.5B PE reads!

**Sequencing Run Parameters**

- **Run format**: 2x150 bp
- **Output full run**: 1.13 Tb
- **Output per day**: 81 Gb
- **Data passing filter**: 88.9%

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**Graph**

- **2008**: 400 Gb/run
- **2011**: 1200 Gb/run

**Legend**

- **GA**
- **HiSeq 2000**
HiSeq 2000
Redefining the trajectory of sequencing

HIGHEST OUTPUT
Initially capable of up to 200 Gb per run

FASTEST DATA RATE
~25 Gb/day
7-8 days for 2 x 100 bp

HIGHEST NUMBER OF READS
One billion single-end reads*
Two billion paired-end reads*

*Based on one billion clusters passing filter
HiSeq System Performance – Spring 2011

Continuing to redefine the trajectory of sequencing

HiSeq 2000 PERFORMANCE*
500 - 600 Gb per run
Up to 3 billion single-end reads
Up to 6 billion paired-end reads

HiSeq 1000 PERFORMANCE *
250 - 300 Gb per run*
Up to 1.5 billion single-end reads
Up to 3 billion paired-end reads

*Anticipated performance based on reagents and software to be released in Spring 2011
Delivering on the Scalability of HiSeq

*Significantly scaled output, lower priced genome and highest data quality*

**EXPECT PERFORMANCE OF 500 – 600GB PER RUN**

(Up to 300Gb on HiSeq 1000)

- Available Now!
- 2 x 100bp reads
- New reagents and software; No hardware changes
- 2 – 2.5x Reduction in price per genome
  - Reagent list price <$5000 USD

**NEW CHEMISTRY ENABLES HIGHEST COVERAGE UNIFORMITY**

- Significant reduction in GC bias
- Enables significant increase in cluster density
- Lowest number of gaps
  - Lowest risk of missing variants
What Can You Do with 600G in a Single Run?

ULTRA-DEEP SEQUENCING OF MANY LARGE, COMPLEX GENOMES AND TRANSCRIPTOMES
Cancer progression studies
  • 5–6 cancer genomes in a single run
Ultra-deep sequencing of tumors
Population-level genome and exome studies
100 sample exome studies in a single run

LARGE-SCALE, HIGH-THROUGHPUT SCREENING OF EXPRESSION PROFILES
Crops and livestock
Drug responses and pathways

MAKE ROUTINE WHOLE-GENOME SEQUENCING POSSIBLE
Humans, crops, livestock, consumer genomics
Launched TruSeq sample prep and sequencing reagents
  – Ease of sample prep:
    ▪ Over 50% reduction in steps and tubes
  – Reduced costs by up to 80%
  – Enhanced quality controls

Launched TruSeq Exome Enrichment Kits
  – Enriches for entire Exome
  – Most comprehensive coverage, highest uniformity, and lowest DNA input
  – Pooling of samples yields pricing as low as $150/sample

Co-marketing agreements with Caliper, Sage and Covaris
  – Easy integration of peripherals into Illumina workflow
TruSeq Sample Prep Kits for RNA & DNA

Simple, scalable, cost-effective

- **Master mixed formulations & gel-free RNA protocol**
  - Simple workflow with minimal pipetting and clean-up steps

- **Universal adapter design with embedded index**
  - Flexibility - single kit for SR, PE, MP
  - Robust indexing solution

- **Plate-based processing up to 96 samples; volumes optimized for liquid handling**
  - High throughput and automation friendly

- **Low price, all-inclusive kit**
  - Convenient, one-stop shop
  - Enables economical large scale studies

- **Internal quality controls**
  - Monitor sample prep success with software support
TruSeq Small RNA Sample Prep
*Simplified, higher throughput, unbiased*

- **Superior design with 48 Indexes**
  - No compromise on data quality
  - Multiplexed sequencing for economical high throughput small RNA solution

- **Hypothesis-free Small RNA Sequencing**
  - Target all microRNAs including iso-mirs
  - Access all small RNAs from any species

- **Pre-gel sample pooling**
  - Simple, high throughput workflow with minimum hands on time

- **Optimized, flexible kit design**
  - Enables extended applications including strand specific RNA, RIP-, CLIP, Ribo-Seq
**Illumina TruSeq Targeted Resequencing**
*A broad suite of tools for discovery or validation experiments*

<table>
<thead>
<tr>
<th>Option</th>
<th>Amount of sequence</th>
<th>Best for</th>
<th>Availability</th>
</tr>
</thead>
<tbody>
<tr>
<td>TruSeq Exome Enrichment</td>
<td>~62Mb</td>
<td>Study of Mendelian disease; case-control exome studies, exome-wide linkage</td>
<td>Now!</td>
</tr>
<tr>
<td>TruSeq Custom Enrichment</td>
<td>~1 to ~10Mb</td>
<td>GWAS follow-up; validation of variants, variant discovery</td>
<td>Mid-2011</td>
</tr>
<tr>
<td>TruSeq Custom Amplicon</td>
<td>Sub-500Kb</td>
<td>Amplicon sequencing; high-throughput CE experiments, ultra deep seq, variant disc, screening</td>
<td>2H2011</td>
</tr>
</tbody>
</table>
Exome Sequencing

- Targeted Resequencing focuses on a subset of the genome
  - Harness the power of NGS
  - Cost-effective and enables larger studies

- Exome (protein coding genome) is ~1-2% of total genome
  - Discover causal variants in protein coding sequence
  - Discover rare variants in complex diseases
  - Use for linkage studies, complement GWAS

2010 has seen rapid adoption of exome sequencing
TruSeq Custom Enrichment Kits
Same Proven Technology Deployed in TruSeq Exome Enrichment Kits

TARGET 1 – 10 MB OF DNA PER SAMPLE
Highest enrichment efficiency and coverage uniformity

INTELLIGENT PROBE DESIGN FOR ANY REGION
Interactive online design software
High coverage of targeted regions

PRE-ENRICHMENT SAMPLE POOLING
Up to 12 samples per enrichment reaction
Reduce hands-on time; increase throughput

INTEGRATED WITH TRUSEQ DNA SAMPLE PREP KITS
Fully optimized workflow
Most cost-effective solution available
TruSeq Custom Amplicon Sequencing
Highly Multiplexed Targeted Amplicon Resequencing

FULLY CUSTOMIZED TARGET PROBES AND CAPTURE
Based upon GoldenGate Technology

INTERACTIVE PROBE DESIGN AND ORDERING
Streamlined user interface
Rapid probe turnaround

RAPID & ECONOMICAL AMPlicON SEQUENCING
Up to 384 amplicons per sample
Plate based processing; 96 samples per plate
Assay time <8 hours
No additional hardware requirements

UP TO 10X MORE COST EFFECTIVE THAN CURRENT CE TECHNOLOGY
Epicentre Nextera Technology for Library Prep
Single Tube, Rapid Library Prep

SIMPLE, FAST LIBRARY PREP IN LESS THAN 2 HOURS
Closed tube DNA fragmentation
Transposon-mediated library preparation
Ultra-low input requirements (50 ng)

ENABLES A RANGE OF CE AND NGS APPLICATIONS

VALIDATED BY LEADING RESEARCHERS

“Comparison to conventional methods of library preparation, relying on mechanical or endonuclease fragmentation, finds that although transposase-catalyzed adaptor insertion demonstrates a slightly greater insertion bias, this has little impact at the level of genomic coverage, and is offset by large advantages with respect to speed, simplicity, and low input requirements.”
MiSeq™ System

My Samples. My Study. MiSeq
MiSeq
The World’s Most Widely Adopted Sequencing Technology Just Got Personal

UNPRECEDEDNTED PERFORMANCE
Complete workflow for some applications in a single day
Throughput up to 1-1.5 Gb
Scalable run time vs. output: 36bp to 2x150bp

UNMATCHED COST EFFECTIVENESS
<$125,000 list price “all in”
$400-$750 per run (amplification + sequencing)

EASIEST TO USE WORKFLOW
On-board cluster generation and data analysis
Plug and play reagents with RFID

MOST ACCURATE SEQUENCING
Uses proven TruSeq SBS reversible terminator chemistry

CE AND NGS APPLICATIONS
MiSeq
Next-Gen Made Simple: Load & Go

INTUITIVE HUMAN INTERACTION DESIGN
Preloaded single use reagent cartridge
  • Contains cluster generation, SBS &
RFID based reagents & flowcell tracking
On-board cluster generation & PE fluidics
Auto flow cell positioning
Walkaway automation
MiSeq
On-Instrument Alignment & Variant Calling

SIMPLE & INTUITIVE DATA ANALYSIS
Analysis complete in <2 hours
Base calling, quality values & variant reporting
Output in industry standard formats
Real time run monitoring
MiSeq

Evolving Cycle Time with SBS

SBS cycle times (2007-HiSeq)

31 min to 21 min (chemistry)
47 min to 25 min (imaging)
78 min to 46 min (total)

MiSeq innovations

- Further chemistry improvements
  - Reagents, formulations, protocols
- Optimized fluidics
  - flow-rate, volumes, flow cell
- Scan less area
  - New flow cell
MiSeq

Application Flexibility for Every Lab

CAPILLARY ELECTROPHORESIS AND NEXT-GEN APPLICATIONS ON A SINGLE INSTRUMENT

FLEXIBLE AND SCALABLE AMPLICON SEQUENCING ASSAYS

SEQUENCE BACTERIAL GENOMES IN ANY LAB

MAKE SCREENING ROUTINE

Infectious diseases
Vaccine QC
Clone checking
Library QC
Tissue typing

FAST CHIP-SEQ OR SMALL RNA SEQUENCING
MiSeq – Prep, Run, Analyze
Sample to Data in as Little as Eight Hours*

MiSeq is the Only Personal Sequencing System Capable of
an 8 Hour Sample to Data Workflow

Amplicons
Clones
gDNA

Library Prep
1.5 hours
(15-30 min hands on)

Prepped Library thru Sequencing
4.5 hours
(20 minutes hands on)

Alignment and Variant Calling
2 hours
(fully automated)

*1x36bp run – 3 hr sequencing
**MiSeq Applications**

*Amplicon Sequencing*

- Multiplexed amplicon sequencing of KRAS and BRAF in a single workday
- 165,000x average coverage of 4 amplicons
- All basecalls concordant with previous whole genome sequencing data

![Amplicons to Library Prep](1.5 hours (15-30 min hands on))

![Clustering + Sequencing](4.5 hours (20 min hands on))

![Demultiplex + Coverage Analysis](1 hour (On instrument))

*1x36bp*
MiSeq Applications

Plasmid Sequencing

- Sequencing 8 kb pET11a-PRO217 plasmid and four mutated versions in a single workday
- De novo assembly yielded single 8 kb contig for each plasmid
- 100% concordance with previous Sanger sequencing results confirming mutations
### MiSeq - Comparison to CE Sequencing

**Example: TruSeq Custom Amplicon with 96 Samples x 96 Targets**

<table>
<thead>
<tr>
<th>CE</th>
<th>TruSeq Amplicon</th>
<th>MiSeq 1 day</th>
<th>Cost/Target</th>
</tr>
</thead>
<tbody>
<tr>
<td>Each well contains DNA + oligos for 1 target</td>
<td>Each well contains DNA + oligos for 96 targets and indices for sample pooling</td>
<td>Assay biochemistry</td>
<td>1 plate</td>
</tr>
<tr>
<td>2 rounds of PCR &amp; cleanup</td>
<td></td>
<td></td>
<td>96 plates</td>
</tr>
<tr>
<td>3730xl</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Each well contains DNA + oligos for 1 target.
- Each well contains DNA + oligos for 96 targets and indices for sample pooling.
- Assay biochemistry.
- 1 plate.
- MiSeq 1 day.
- <$0.50/target.
- ~$3/target.
- 3730xl in 5 days.
MiSeq Applications
Small Genome Resequencing

- Resequencing of 5.2Mb *B. cereus* in a single workday
- 5.4 million reads yielded 175Mb of data which aligned to ATCC10987 with mismatch rate of 0.06%
- >98% of genome with average coverage of 30x

![Diagram showing the workflow of gDNA Prep, Library, Clustering + Sequencing, and Align to reference/Call SNPs.]

*1x36bp*
## Of MiSeq, Microbes, and Man

<table>
<thead>
<tr>
<th>Organism</th>
<th>Genome size</th>
<th>n</th>
<th>depth</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Staphylococcus aureus</em> (MRSA)</td>
<td>2.8 Mb</td>
<td>6</td>
<td>40x</td>
</tr>
<tr>
<td><em>Mycobacterium tuberculosis</em> (TB)</td>
<td>4.4 Mb</td>
<td>4</td>
<td>40x</td>
</tr>
<tr>
<td><em>Escherichia coli</em></td>
<td>4.6 Mb</td>
<td>4</td>
<td>40x</td>
</tr>
<tr>
<td><em>Plasmodium falciparum</em></td>
<td>22.9 Mb</td>
<td>1</td>
<td>30x</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Human</th>
<th>Target size</th>
<th>n</th>
<th>depth</th>
</tr>
</thead>
<tbody>
<tr>
<td>20 exons</td>
<td>3 kb</td>
<td>250</td>
<td>1000x</td>
</tr>
<tr>
<td>Targeted region</td>
<td>0.5 Mb</td>
<td>40</td>
<td>50x</td>
</tr>
<tr>
<td>All coding exons</td>
<td>25 Mb</td>
<td>1</td>
<td>30x</td>
</tr>
<tr>
<td>RNA, miRNA, ChIP-Seq, etc</td>
<td>5M tags</td>
<td>1</td>
<td>n.a.</td>
</tr>
</tbody>
</table>
From HiSeq to MiSeq

HiSeq:
- High yield
- High throughput
- High data quality

MiSeq:
- Fast run time
- Low cost device
- Same data quality
  (lower table shows equivalent runs)

<table>
<thead>
<tr>
<th></th>
<th>HiSeq</th>
<th>MiSeq¹</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reads</td>
<td>2 x 100</td>
<td>2 x 100</td>
</tr>
<tr>
<td>Yield</td>
<td>600 Gb</td>
<td>1 Gb</td>
</tr>
<tr>
<td>Run time</td>
<td>10 days</td>
<td>&lt;1 day</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>HiSeq</th>
<th>MiSeq¹</th>
</tr>
</thead>
<tbody>
<tr>
<td>Density</td>
<td>961,000</td>
<td>944,000</td>
</tr>
<tr>
<td>PF (%)</td>
<td>90.4</td>
<td>91.6</td>
</tr>
<tr>
<td>Bases &gt;Q30 (%)</td>
<td>85.5</td>
<td>87.7</td>
</tr>
</tbody>
</table>
MiSeq Instrument
Next-Gen Sequencing Just Got Personal

- Input
  - Nanogram amounts of nucleic acid

- Library Preparation
  - As short as 90 minutes

- Output
  - Up to 1.5Gb

- Read Length
  - Up to 2x150bp

- Raw Accuracy
  - >75% bases >Q30 at 2x150bp

- Sample-to-Answer
  - Single working day

- Paired End Capability
  - On instrument

- Amplification Capability
  - On instrument in 1 hour

- Computer Hardware/Data Analysis
  - On instrument

- Instrument Price
  - $125K (all inclusive)

- Price per run
  - $400 - $750

- Price per Mb
  - $0.50
What is the Illumina Genome Network?

*Whole Genome Sequencing Services Without Compromise*

- An Illumina-run program that links researchers interested in running large whole human genome sequencing projects with leading institutes worldwide that provide access to Illumina sequencing.

  - Illumina is the primary point of contact
    - Connect customers with partners
    - Manage logistics

  - Sequencing for you
    - Expand your laboratory’s capabilities without the time and expense of acquiring equipment and training personnel

- Ideal solution for affordable, large sample-size human whole-genome sequencing studies
Synergies between Arrays and Sequencing

- Custom Arrays
  Evaluating & Validating Variants

- Next-Gen Sequencing
  Identifying Variants

- Targeted resequencing

- RNA-sequencing

- GWAS Arrays
  Confirming Variants

- Custom Validation Arrays
  Re-Confirming Variants, Fine Mapping

- Low Density Panels
  Barcoding & QCing Samples

- Low Density Arrays
  Deploying Variants
HiScanSQ.
Two proven technologies. One powerful platform.
Introducing HiScanSQ
Technologies merge. Opportunities emerge.

PROVEN PERFORMANCE
iScan-inspired optics provide industry leading array throughput and data quality
Most widely-adopted and proven sequencing chemistry

STREAMLINED SOLUTION
Simplest user experience
Minimize hands on time, maximize CapEx investment

EASILY EXPANDABLE
Start with a powerful configuration
Scale up with automation options
Add sequencing when you’re ready
Seamlessly Transition Between Technologies.  
*Go where the biology takes you.*

THE ABILITY TO EXPLORE THE GENOME, TRANSCRIPTOME AND EPIGENOME ON YOUR OWN TERMS OPENS A WORLD OF POSSIBILITIES.  
ADD NEXT-GEN SEQUENCING TO HISCAN WHEN YOU’RE READY.

<table>
<thead>
<tr>
<th>Whole-Genome Analysis</th>
<th>Whole-Genome SNP Genotyping</th>
<th>Whole-Genome SNP Discovery</th>
</tr>
</thead>
<tbody>
<tr>
<td>Copy Number Variation (CNV)</td>
<td>CNV Analysis</td>
<td>CNV Discovery</td>
</tr>
<tr>
<td>Targeted Genome Analysis</td>
<td>Custom and Focused SNP Genotyping</td>
<td>Targeted Resequencing</td>
</tr>
</tbody>
</table>
| Gene Regulation and Epigenetic Analysis | Whole-Genome DNA Methylation Profiling |  - Whole-Genome DNA Methylation Discovery and Analysis  
| | |  - Chromatin Immunoprecipitation (ChIP-Seq)  
| | |  - Small RNA Discovery and Analysis  |
| Gene Expression |  - Whole-Genome Gene Expression Analysis  
| |  - FFPE Sample Analysis | Transcriptome Discovery and Profiling |
| Cytogenetics | Cytogenetic Abnormalities | Digital Karyotyping |

The speed of microarrays + The power of next-gen sequencing
Illumina’s GWAS Roadmap: next-generation genotyping studies in the post-1KGP era
Illumina’s Genotyping Product Portfolio

- **Options:**
  Illumina’s Genotyping toolbox provides an entire spectrum of plex ranges from 1 to 5M SNPs

- **Quality:**
  Robust assay technologies (GoldenGate and Infinium) provide industry-best data quality

- **Flexibility:**
  Interrogate virtually any SNP

- **Reliability:**
  Proven GG and Infinium platforms support researchers with effective and dependable tools
Enabling discoveries with the right technology
The 1,000 Genomes Project
Sequence 2,500 genomes to complete the picture of genetic variation

Achieve a nearly complete catalog of common human genetic variants with frequency 1% or higher.

Project Goals

1. Accelerate fine-mapping efforts in gene regions identified through genome-wide association studies or candidate gene studies.

2. Improve the power of future genetic association studies by enabling design of next-generation genotyping microarrays that more fully represent human genetic variation.

3. Enhance the analysis of ongoing and already completed association studies by improving our ability to “impute” or “predict” untyped genetic variants.
The Omni Family of Microarrays
*Powerful, flexible and additive arrays out to 5M markers per sample*

<table>
<thead>
<tr>
<th>Omni Express*</th>
<th>Omni1-Quad</th>
<th>Omni1S-8</th>
<th>Omni2.5-8</th>
<th>Omni2.5S-8*</th>
<th>Omni5-Quad*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Highest-throughput array with industry-proven quality at an exceptional price.</td>
<td>Optimal combination of common SNPs, CNVs, and content from 1kGP.</td>
<td>Takes researchers from Omni1/Express to 2.5M</td>
<td>The most optimal and comprehensive set of both common and rare SNP content from the 1kGP</td>
<td>~2.5M additional markers providing rare 1kGP content</td>
<td>The ultimate GWAS tool providing near complete coverage of common and rare variation</td>
</tr>
</tbody>
</table>

| MAF > 5% | MAF >2.5% | MAF > 1% |

* Available as semi-custom products
## Roadmap Paths

<table>
<thead>
<tr>
<th>Path</th>
<th>Step 1</th>
<th>Step 2</th>
<th>Step 3</th>
<th>Total Markers</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>OmniExpress</td>
<td>Omni1S</td>
<td>Omni2.5S</td>
<td>~4.4 Million</td>
</tr>
<tr>
<td>2</td>
<td>Omni1</td>
<td>Omni1S</td>
<td>Omni2.5S</td>
<td>~5 Million</td>
</tr>
<tr>
<td>3</td>
<td>Omni2.5</td>
<td>Omni2.5S</td>
<td></td>
<td>~5 Million</td>
</tr>
<tr>
<td>4</td>
<td>Omni5</td>
<td></td>
<td></td>
<td>~5 Million</td>
</tr>
</tbody>
</table>
# Custom Genotyping Family of Options

*Driving the Cycle of Discovery and Validation*

<table>
<thead>
<tr>
<th>VeraCode</th>
<th>GoldenGate Indexing</th>
<th>GoldenGate</th>
<th>iSelectHD 3k-90k</th>
<th>iSelectHD 90k-250k</th>
<th>iSelectHD 250k-1M</th>
<th>Semi-Custom OEx+</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image1" alt="VeraCode" /></td>
<td><img src="image2" alt="GoldenGate Indexing" /></td>
<td><img src="image3" alt="GoldenGate" /></td>
<td><img src="image4" alt="iSelectHD 3k-90k" /></td>
<td><img src="image5" alt="iSelectHD 90k-250k" /></td>
<td><img src="image6" alt="iSelectHD 250k-1M" /></td>
<td><img src="image7" alt="Semi-Custom OEx+" /></td>
</tr>
</tbody>
</table>

**The power of the GoldenGate assay on a platform and at a price accessible to all labs.**

**Enhancement of the GoldenGate assay to deliver the highest throughput at industry leading value.**

**Pre-optimized design of customizable content using the most trusted assay with the highest quality data in the industry.**

**Validating genomic discoveries with the most robust, powerful data and flexible content design. 24-sample, 3k-90k plex.**

**Enabling more genomic discoveries with the most robust, powerful data and flexible content design. 12-sample, 90k-250k plex.**

**Enabling more genomic discoveries with the most robust, powerful data and flexible content design. 4-sample, 250k-1m plex.**

**Customizable GWAS array with industry proven quality at an exceptional price.**

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<table>
<thead>
<tr>
<th>1 – 384 Plex</th>
<th>96 – 384 Plex</th>
<th>96 – 3,072 Plex</th>
<th>3,072 – 1,000,000 Plex of Custom Content</th>
<th>200k Plex Custom</th>
</tr>
</thead>
</table>
Infinium 450K Methylation BeadChip
1. Interest in epigenetics is on the rise

The decoding of the human epigenome, nearly a decade ago fueled excitement that an understanding of all hereditary influences was within reach. But the connections between, say, disease turned out to be more complicated than imagined. What has since emerged is a new frontier: study of genetic signaling known as epigenetics, which holds that expression of genes can be modified by environmental influences and that changes can be passed down through generations. So people who smoke cigarettes in their youth, for example, sustain certain epigenetic changes, which may then increase the risk that their children's children will reach puberty early. In October, a team led by Joseph Ecker at the Salk Institute in La Jolla, Calif., studied human skin and stem cells to produce the first detailed map of the
Introducing: epigenome-wide association studies (EWAS)

“(This product) will enable studies to be done that would otherwise have been impossible.”

Devin Absher
HudsonAlpha
Member – HM450 Consortium

450K Infinium methylation array

- Genome-wide coverage
  - 99% RefSeq genes, 96% CpG islands
  - All content categories requested by an expert consortium
- High throughput
  - 12 sample per array format
  - Automation compatible
- Affordable price
  - $240 / sample USD w/ volume discount
Infinium HD FFPE Sample Solution
Illumina’s Infinium HD FFPE Sample Solution

Achieve high quality genotype calls from degraded FFPE samples

- **Fully-integrated QC kit**
  - Simple real-time PCR assay identifies recoverable samples

- **Novel restoration kit**
  - Rapid protocol with ILMN-developed reagents to restore degraded FFPE samples which pass QC test

- **Whole-genome analysis on FFPE optimized CytoSNP or OmniExpress BeadChips**
  - >250k to >650K genome-wide markers in a 12-sample array format for GT and CNV
  - Modified Infinium HD assay with optimized reagents for degraded samples

- **High-data quality**
  - Robust data for reliable genotyping and copy number variation analysis
Introducing Illumina’s Eco Real-Time PCR System

NEW PARADIGM OFFERING
• 5X better performance
• Industry-leading data quality
• Economical price ($13,900) provides access to individual researchers

BROAD APPLICATION OPTIONS
• 4-color multiplex, HRM
• Gene expression, genotyping, viral load
• Standard and FAST cycling protocols
• Supports ALL Real-Time PCR chemistries

SYSTEM OVERVIEW
• 48-well format for single users
• Includes instrument, netbook PC, dock
• Streamlined software for novices and experts
• Small footprint fits single-user bench top
Why Partner with Illumina?

SUPERIOR TECHNOLOGY AND PERFORMANCE
Output, data quality and coverage
Unmatched scaling opportunities
Simplest workflow and best user experience

ACCESS TO BROADEST RANGE OF APPLICATIONS
Unparalleled publications history and potential*

BROAD NETWORK OF CUSTOMERS AND 3RD PARTY SOFTWARE PROVIDERS
Preferred partner of large and small labs world wide

*5 fold more publications than closest competitor in the high throughput sequencing segment
Thank you!