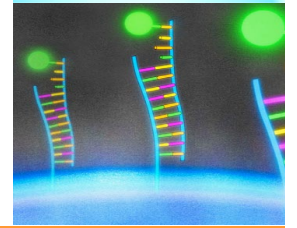
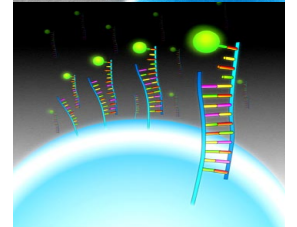
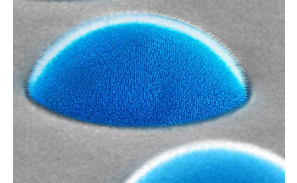
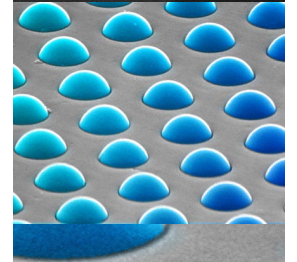
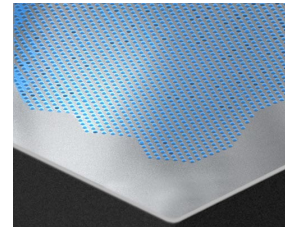


illumina®

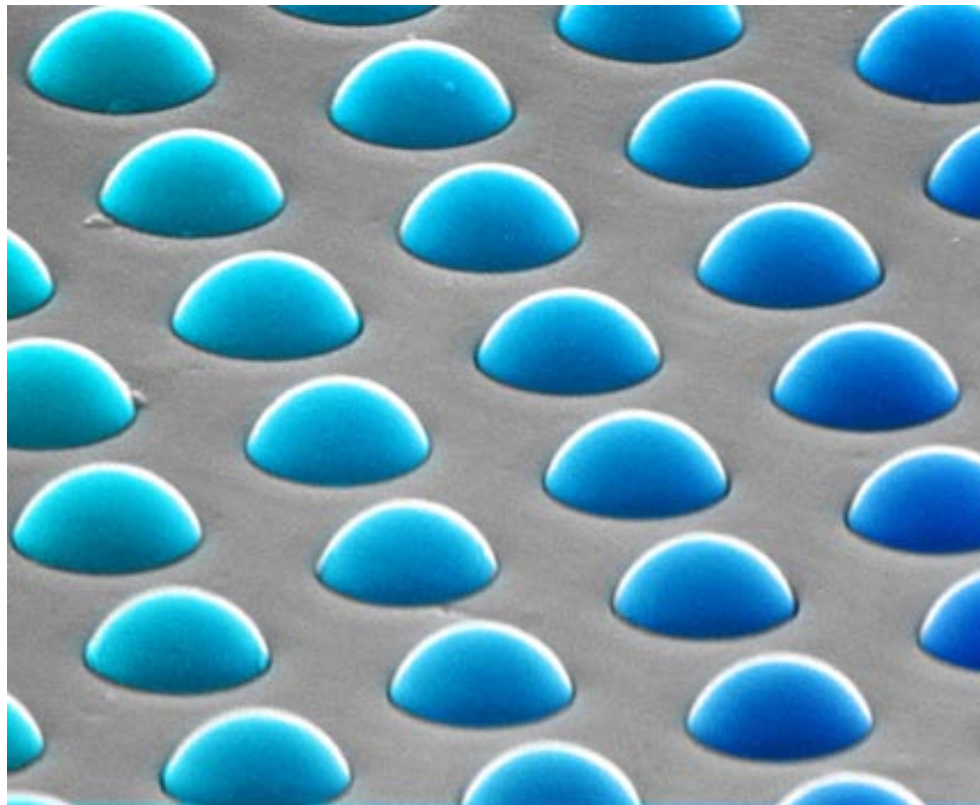
Genotyping and Gene Expression Using Illumina BeadArray® Technology

Tristan Orpin
VP Worldwide Sales, Illumina, Inc.



BeadArray

Optically Wired Beads in Wells



June 05

High Throughput Genotyping Solutions

GoldenGate™ Assay

- Multiplexed from 384 to 1536 (and multiples thereof)
- For custom and standard SNP projects
 - Linkage projects (5800 loci)
 - MHC/HLA (2400 loci)
- Industry standard for completeness & quality
- 250ng DNA input

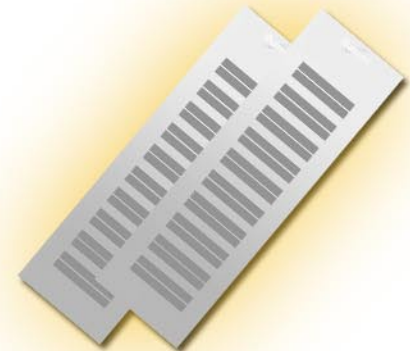
Infinium™ Whole Genome Genotyping Assay

- Multiplexed from 10,000 to 1,000,000+ loci
- For standard panel SNP projects (custom on 2006)
- Ability to select SNPs for best content
 - No complexity reduction
- Single tube amplification – no PCR
- Accuracy >99.95%
- Automation and LIMS support
- 250-750ng DNA input

1 Million SNPs – 2 Chips



100K SNPs
Human - 1



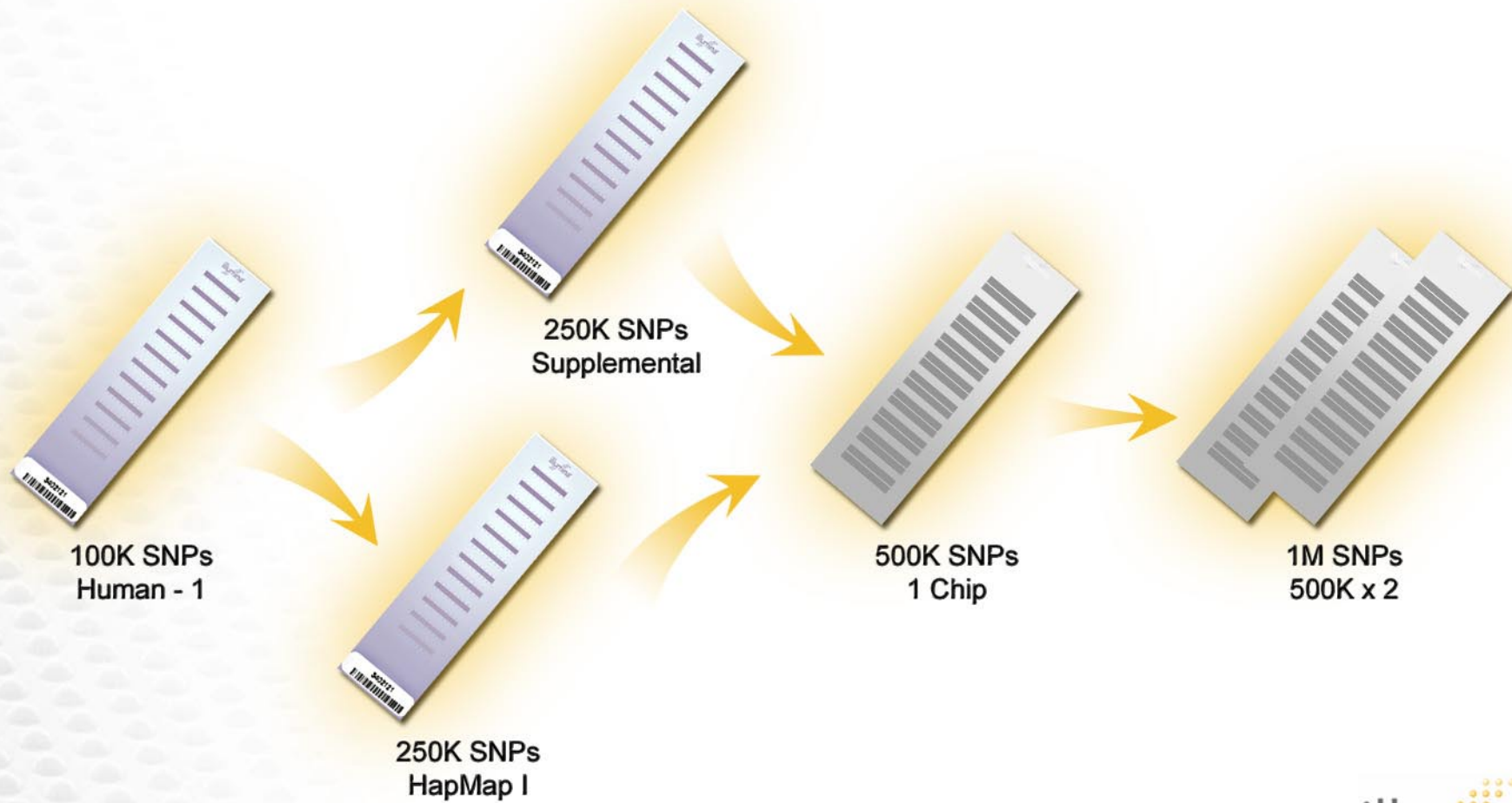
1M SNPs
500K x 2



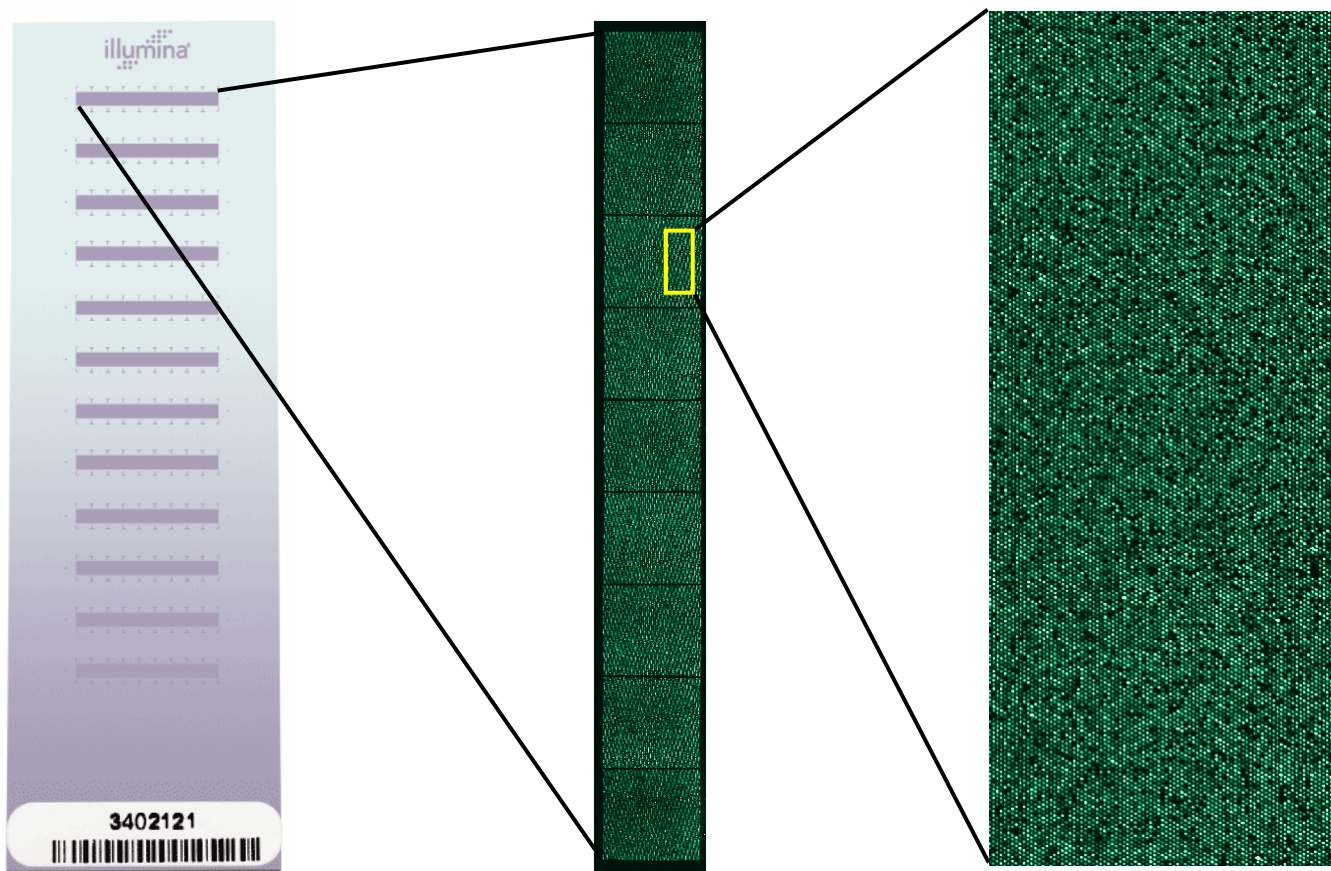
Q205 ...

... Q206

1 Million SNPs – 2 Chips



Human-1 BeadChip (100K Exon Centric Content)



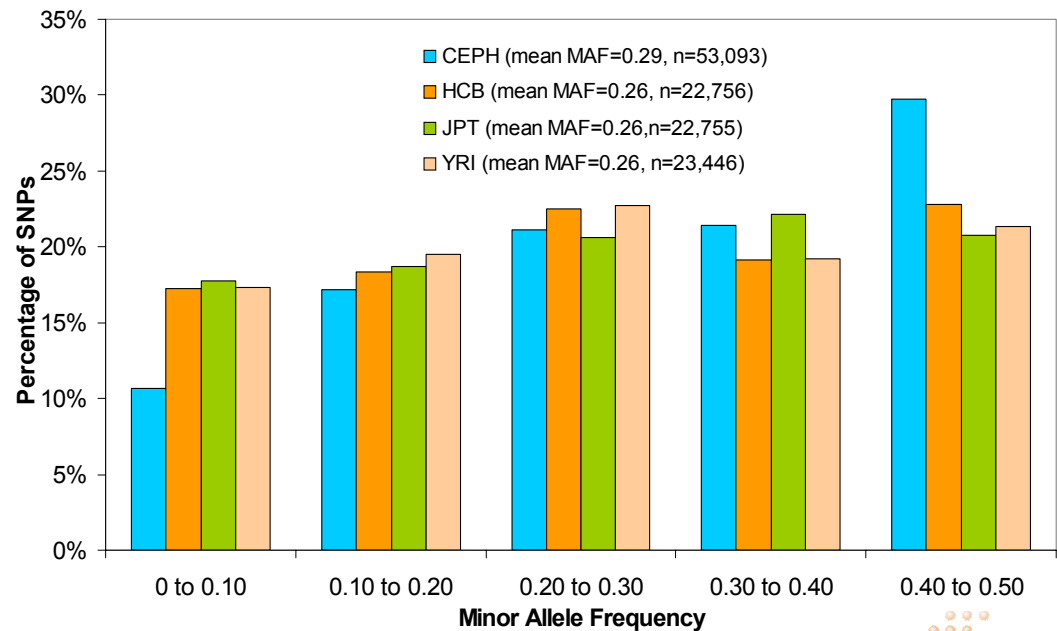
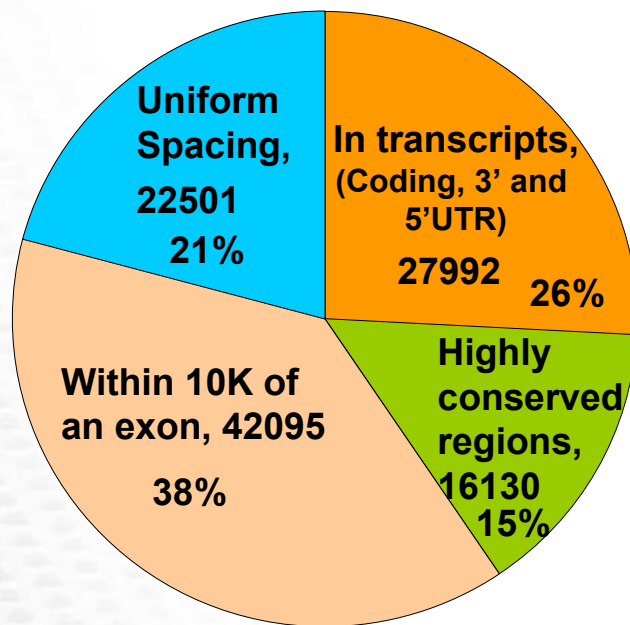
12 Sections
(max 288K beadtypes, 144K loci)

>890,000 features
per section

Average 30 fold
redundancy

Content of 100K Genotyping BeadChip

- Intelligent SNP selection
- Exon-centric focus: 90% of exons have ≥ 1 SNP within 10Kb
- Uniform spacing: average distance between SNPs is ~ 30 Kb



Infinium Assay Performance

Parameter	Value
Call Rate (3814 not called/ 713,564 possible genotypes)	99.49%
Reproducibility (213779 concordant genotypes/213,786 genotypes called in 6 replicated DNAs)	99.997%
Trios Heritability (10 trios, 51 errors/356,928 genotypes)	99.986%

High Throughput Gene Expression Solutions

Direct Hybridization Assay

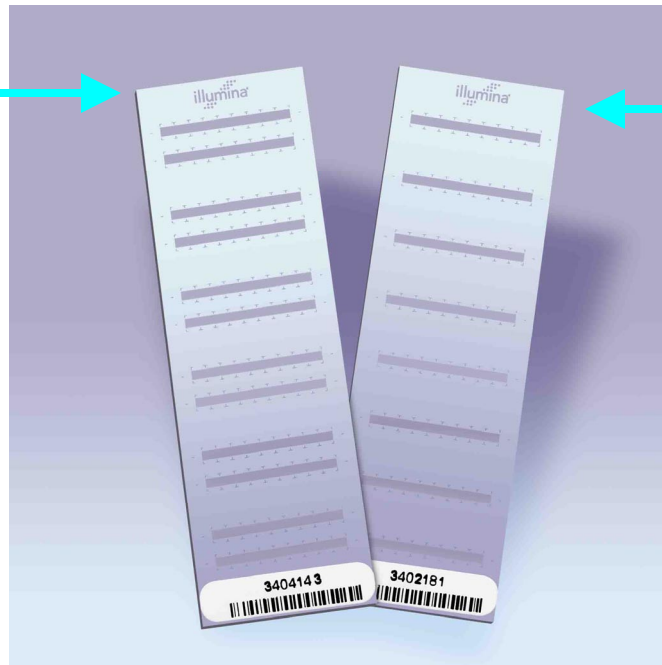
- Whole Genome Human versions
 - Mouse, Rat and Yeast soon
- Exceptional sensitivity (50mers), LDR and reproducibility
- 50-100ng total RNA input (single round IVT)
- Multi-sample processing for significantly increased throughput
- All probes functionally screened
- Utilizes latest content and RefSeq builds
- Focused set Direct Hyb products available
 - Custom or standard content
 - 1500 targets

Direct Hyb: Whole Genome Expression Arrays

Human-6

Whole Genome
BeadChip

- 6 samples per slide
- 48,000 sequences
- >10 million features

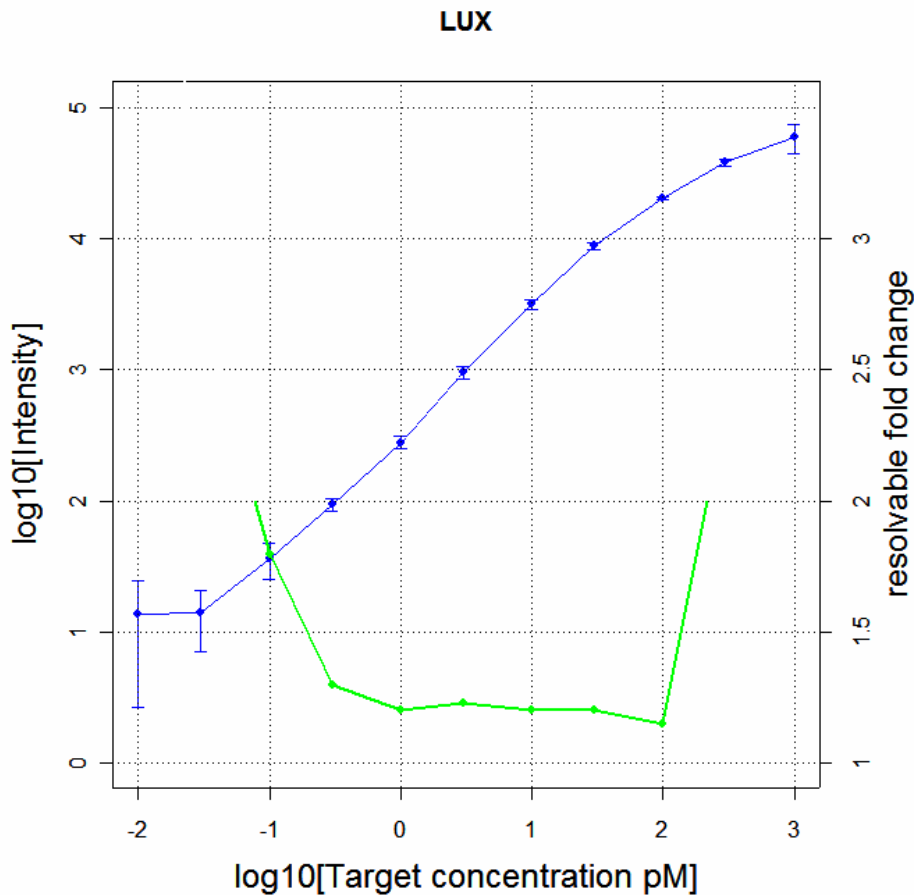


Human-8

RefSeq
BeadChip

- 8 samples per slide
- 24,000 sequences

Dose-Response Experiment Results

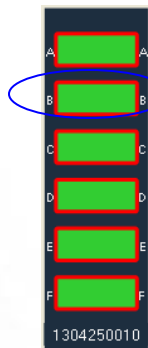
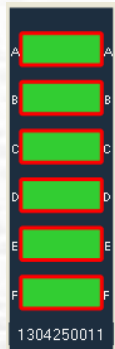


- Nine RNA targets spiked into 12 samples
- Concentrations from 0.01 to 1000 pM
- Quadruplicate hyb's
- Median responses of all 18 probes below

LOD	0.20 pM
Fold Change Detectable	1.22 fold
Dynamic Range	3.20 logs

Technical Replicates on Human-6 BeadChips

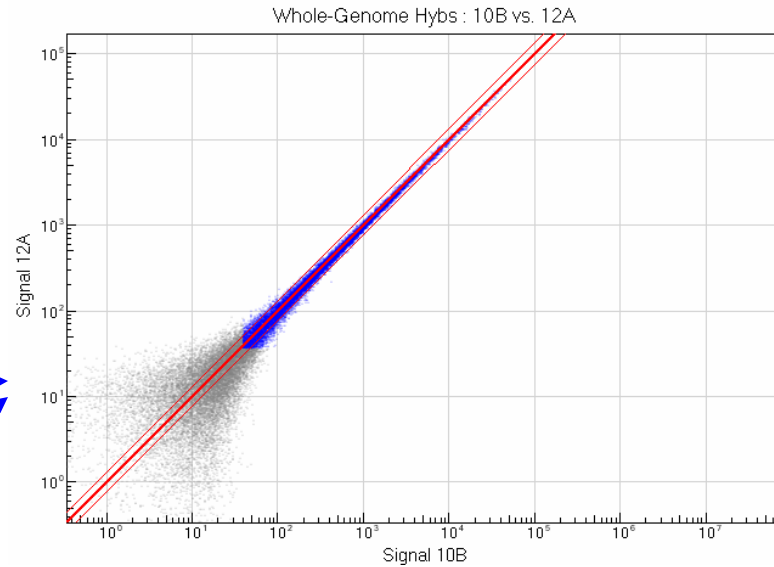
Hybridize the same sample to 3 whole-genome BeadChips



Best Correlation:
 $R^2 = 0.998$

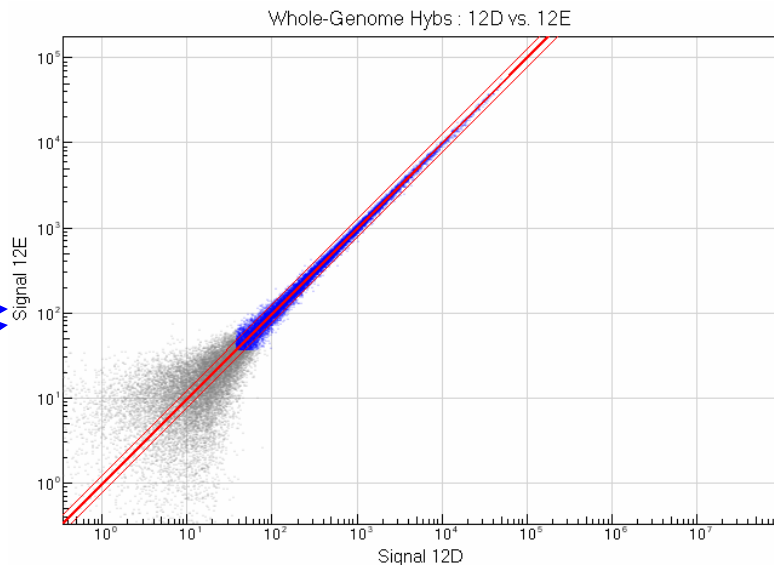


Worst Correlation:
 $R^2 = 0.996$



Blue points:
detected at
 $p < 0.01$

Red
lines:
1.3-fold
change
intervals

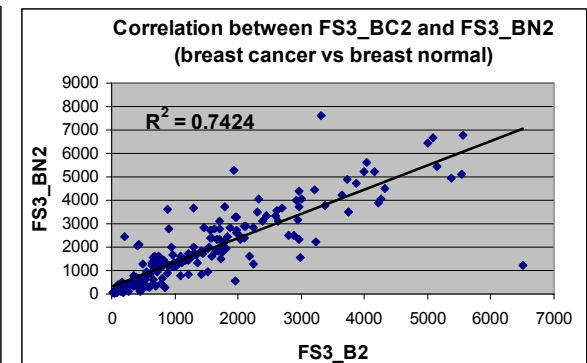
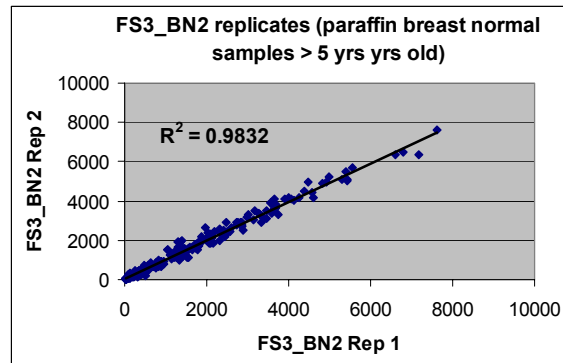
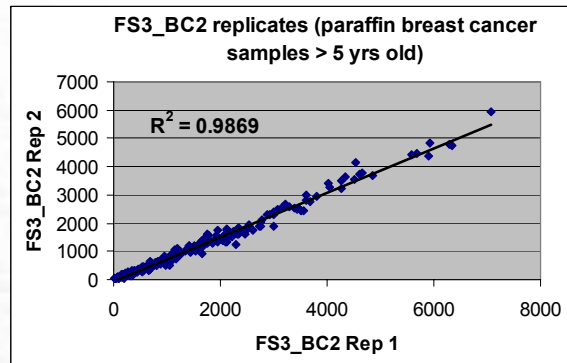
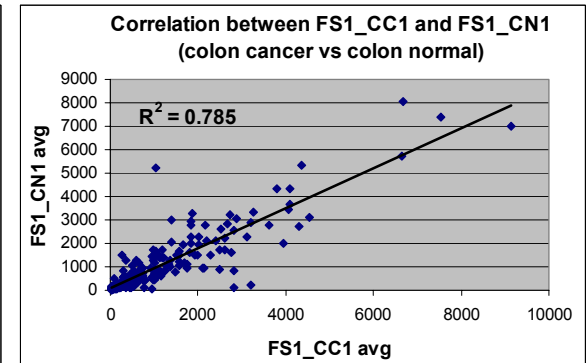
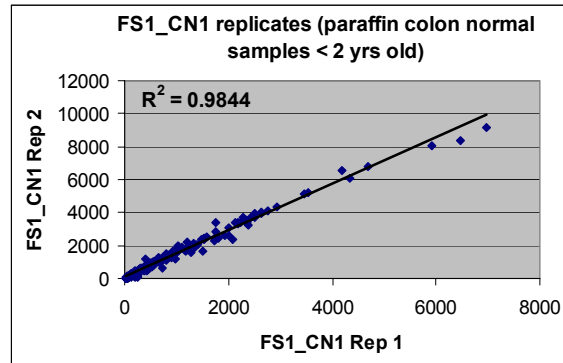
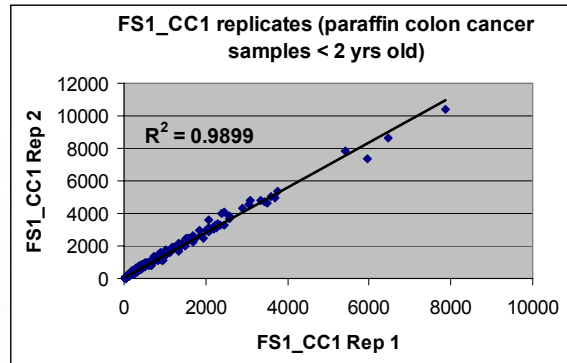


High Throughput Gene Expression Solutions

DASL Assay

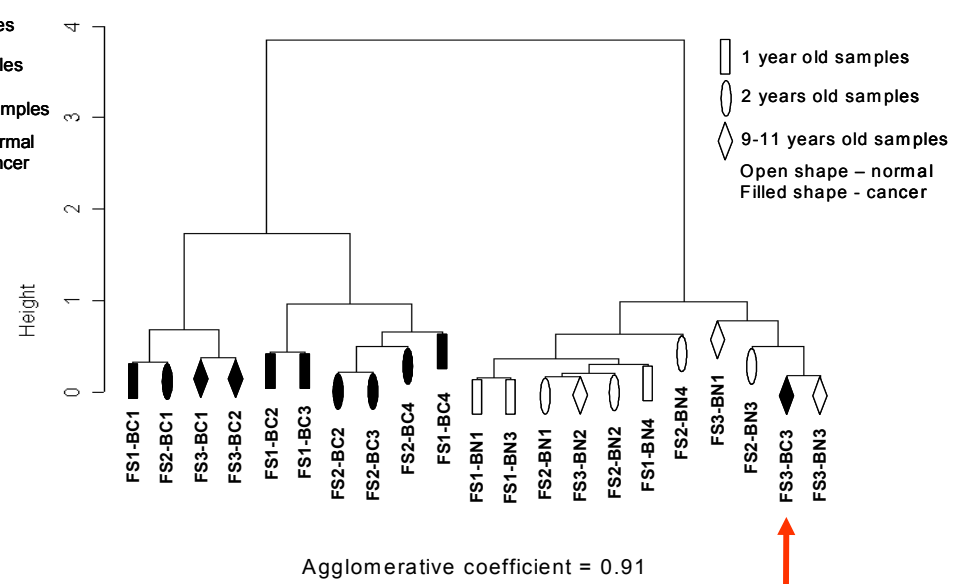
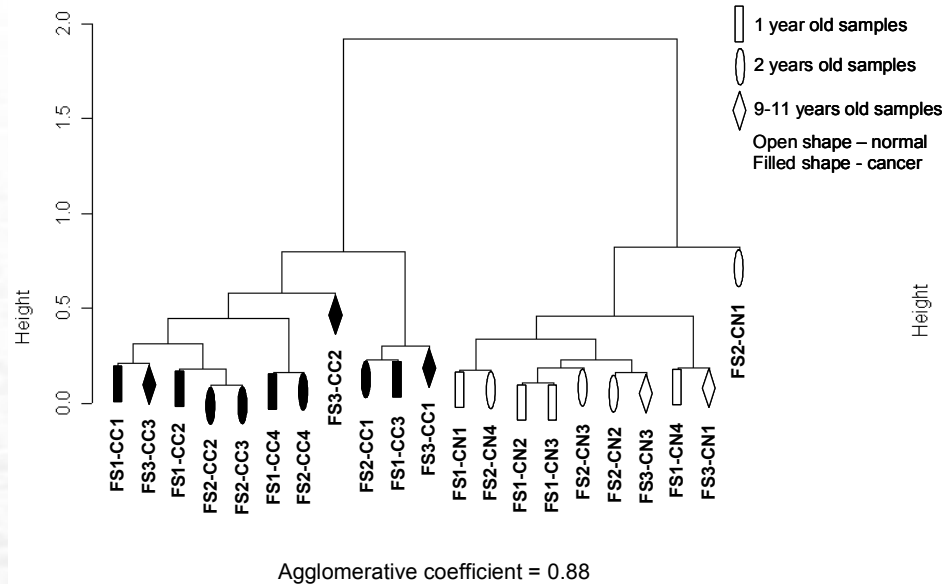
- High throughput gene expression profiling of FFPE samples
- Access millions of archived samples with clinical histories
- Automated process (from total RNA to data report)
- 200ng total RNA input
- Multiplex up to 500 genes (3-4 probes per gene)
- No 3' bias and ability to analyze splice variants
- Uses same Universal arrays as GoldenGate Genotyping
- Basis for exciting future applications:
 - Methylation, LOH, ASE, alternative splicing

Reproducibility and Comparative Data from Paraffin Samples



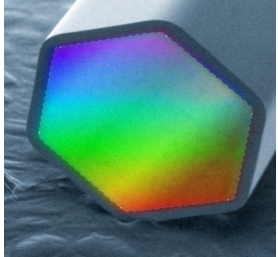
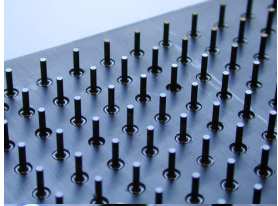
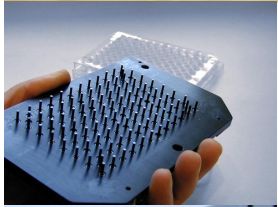
- Replicate analyses of RNA from formalin-fixed, paraffin-embedded tissues show good correlation
- Expression data show disease-related differences in samples over 5 years old

Cluster Analysis of Patient Samples



FS3-BC3:
ductal
carcinoma in-
situ

- DASL assay data were used to cluster FFPE breast or colon samples
- Normal samples were clearly distinguished from cancer samples with one exception: an 11 year old sample of an early stage breast tumor



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