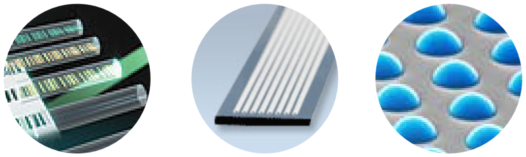
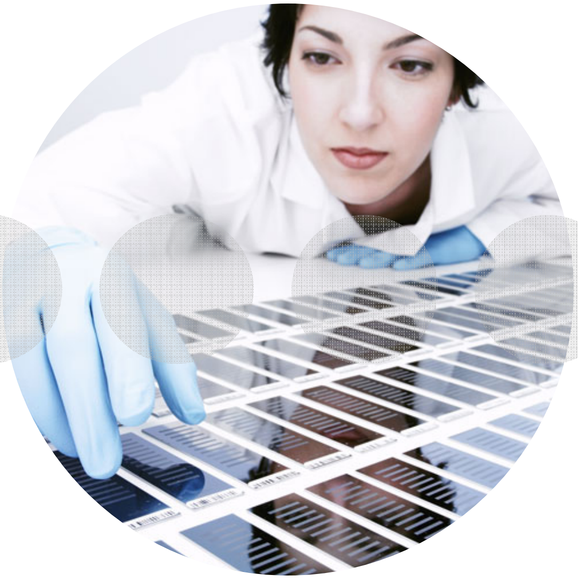


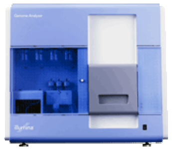


VeraCode Technology

From Research to Diagnostics

June 22, 2009

Most Complete Genomics Assay Portfolio

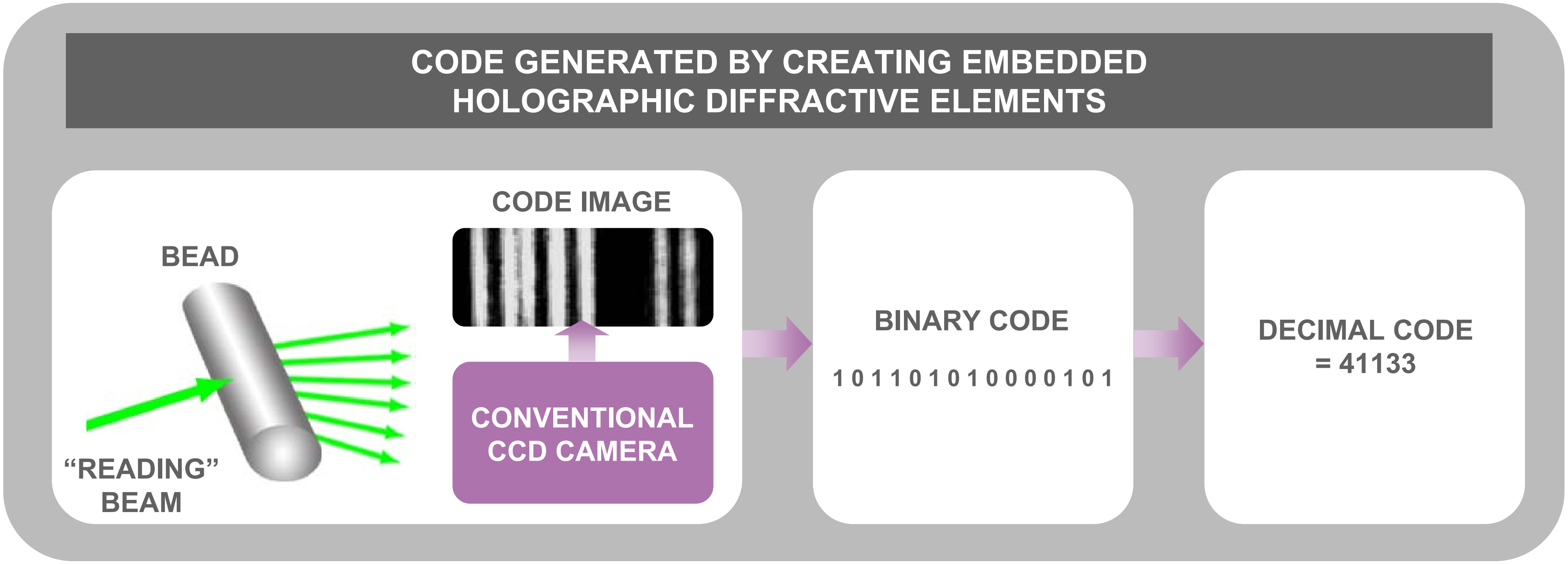
APPLICATION	Sequence-Based Discovery	Whole-Genome	Targeted Analysis		Validation, Screening & Standard Tests
TECHNOLOGY	Solexa Sequencing	BeadArray	BeadArray		VeraCode
PLATFORM	 Genome Analyzer	 iScan	 iScan		 BeadXpress
ASSAY	Sequencing by Synthesis	Infinium Assay Direct Hyb	Infinium Assay GoldenGate & DASL Assay		GoldenGate & DASL Assay
MARKER DENSITY	1base to >15GB	240K to 1M	6K to 60K (iSelect) 96 to 1536 (GoldenGate) Custom	Standard	1 to 384-plex Custom
PRODUCT 2008 Release	Resequencing SNP & CNV Discovery De novo Sequencing Tag Expression Transcript Profiling ChIP Sequencing MeDIP Sequencing BiSulfite CpG	Human1M-Duo HumanHap650Y Human610-Quad Exon510-Duo HumanCNV370-Duo Human 6/Ref-8 Gex Mouse 6/Ref-8 Gex Rat Ref-12 Gex Genome-wide Methylation27	Infinium iSelect Genotyping Panels 6K-60K GoldenGate Genotyping Panels 96-1536 DASL Expression Panels 384-1536 GoldenGate Methylation Panels 384-1536	Linkage-12 CNV-12 MHC GG African American Admixture GG CanineSNP20 BovineSNP50 Micro RNA Methylation Cancer Panel I	VeraCode GoldenGate 96- & 384-plex DASL Expression Methylation Carboxyl - Protein Universal Capture

Illumina's Solution for Diverse Applications

VeraCode® Technology

- Cylindrical glass microbeads
- 240 µm length x 28 µm diameter

VeraCode Technology



CODE GENERATED BY CREATING EMBEDDED HOLOGRAPHIC DIFFRACTIVE ELEMENTS

BEAD

"READING" BEAM

CODE IMAGE

CONVENTIONAL CCD CAMERA

BINARY CODE

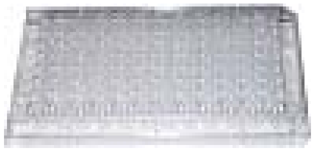
1 0 1 1 0 1 0 1 0 0 0 0 1 0 1

DECIMAL CODE
= 41133

- High Density Codes Easily Imprinted (24 bit)
- Virtually Unlimited Unique Bead Codes Available – 626 unique codes used in launched products
- Glass Surface of Beads Ideal for Bioassays – numerous surface chemistries available
- Specific panels created easily with addition or removal of specific bead types

Easily adaptable to changing content requirements

**VeraCode Beads
Pre-plated into standard
product**



Beads Pooled in
96-well Plates

(48 to 384-plex/well)

+

**Individual Tubes of
VeraCode Beads**

Customized panels
created by pooling
different tubes of beads

BeadXpress™ Reader

ASSAY
BEAD KIT

SAMPLE PLATE

ASSAY
CODE
LIBRARY

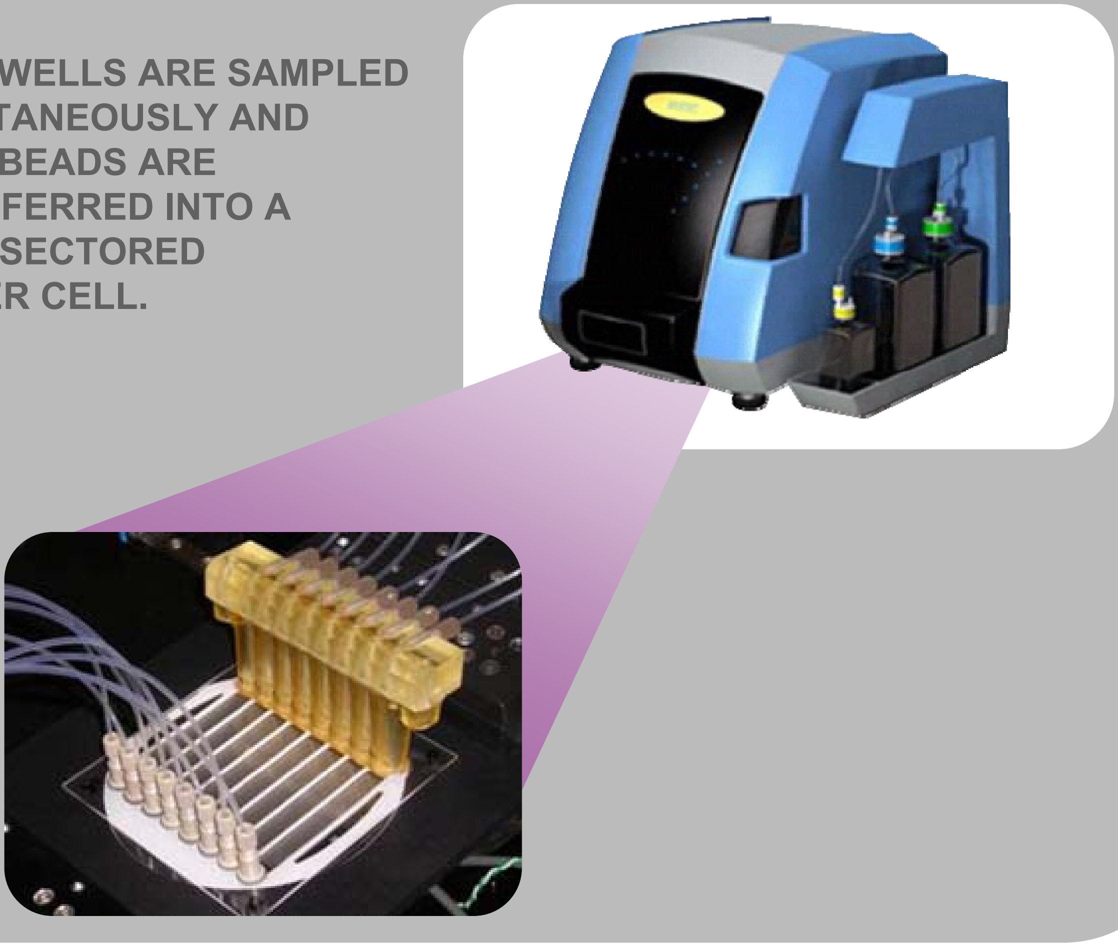
DATA &
LOG FILES

INSTRUMENT SPECIFICATIONS

SAMPLE DELIVERY FORMAT	● Standard 96-well plate & Stripwell Plates
MULTIPLEXING PER SINGLE WELL	● 1 to 384
THROUGHPUT	● 120 samples/hr at 10-plex (two-color detection) ● 80 samples/hr at 96-plex (two-color detection)
DETECTION	● Optional 1 or 2 color detection
REGULATORY	● Regulatory Design Control

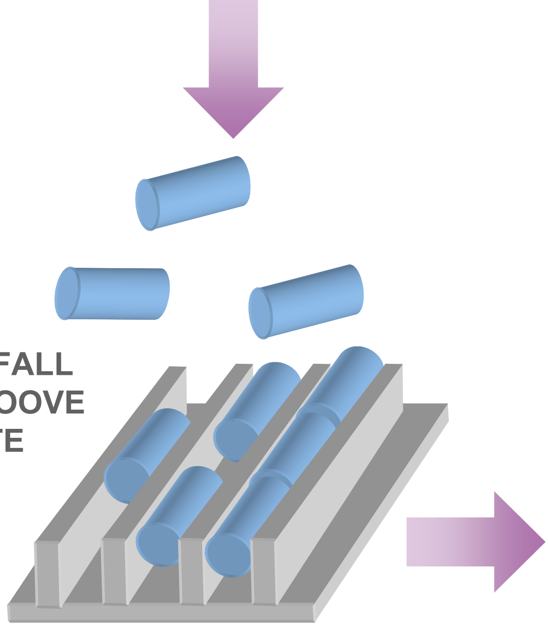
VeraCode Technology

EIGHT WELLS ARE SAMPLED SIMULTANEOUSLY AND MICROBEADS ARE TRANSFERRED INTO A MULTI-SECTORED READER CELL.

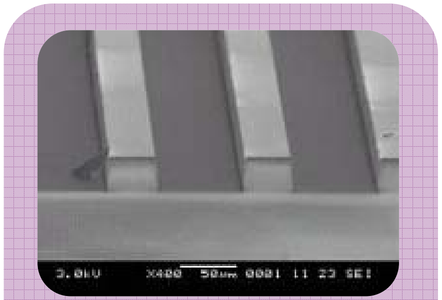


VeraCode Technology

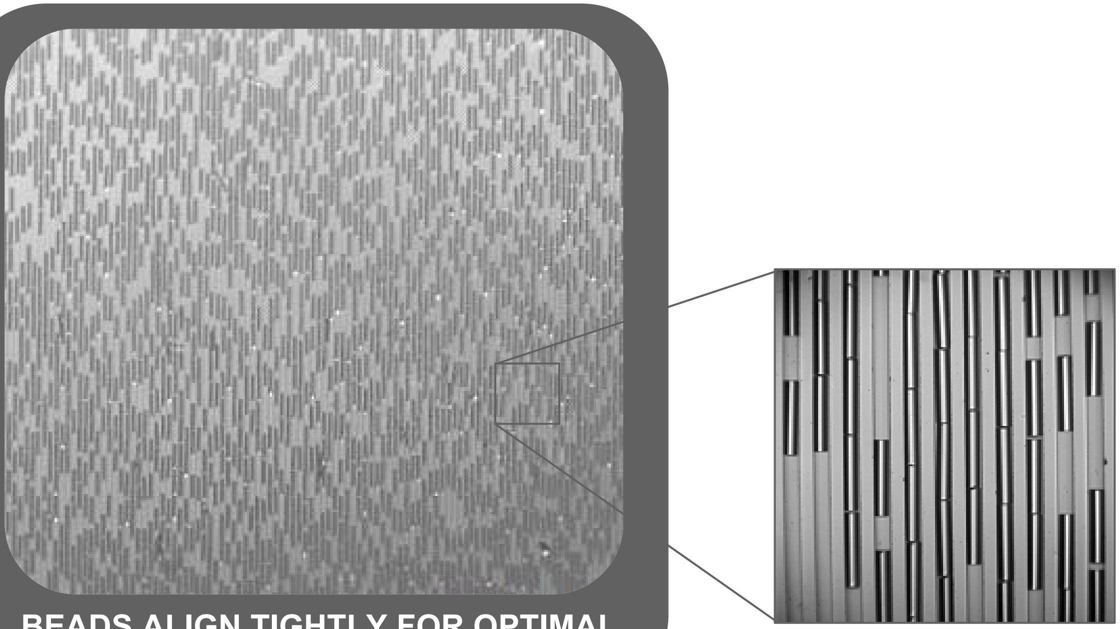
CAPILLARY FORCE ATTRACTS BEADS INTO GROOVES



BEADS FALL INTO GROOVE PLATE

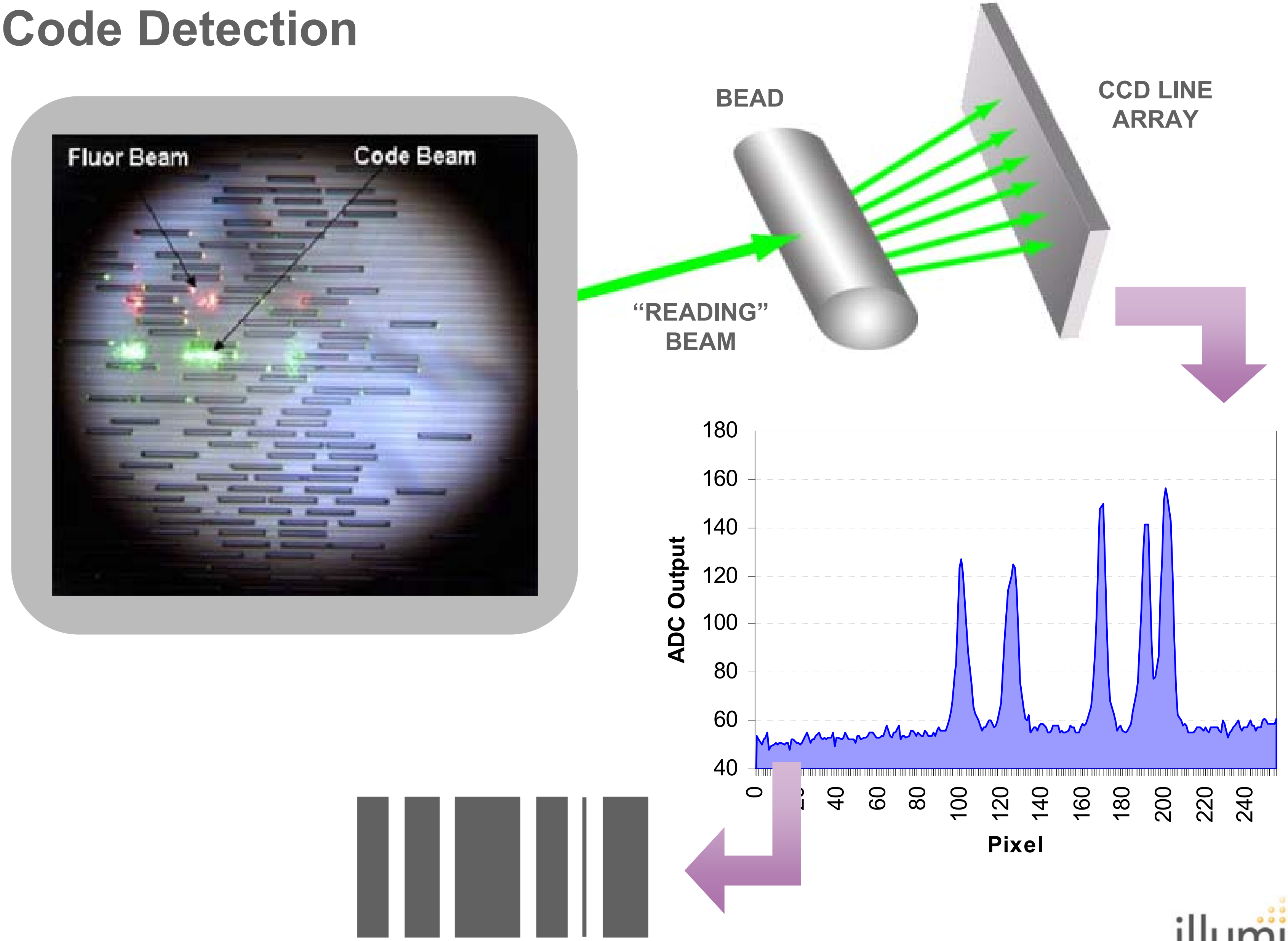


GROOVE PLATE CROSS-SECTION



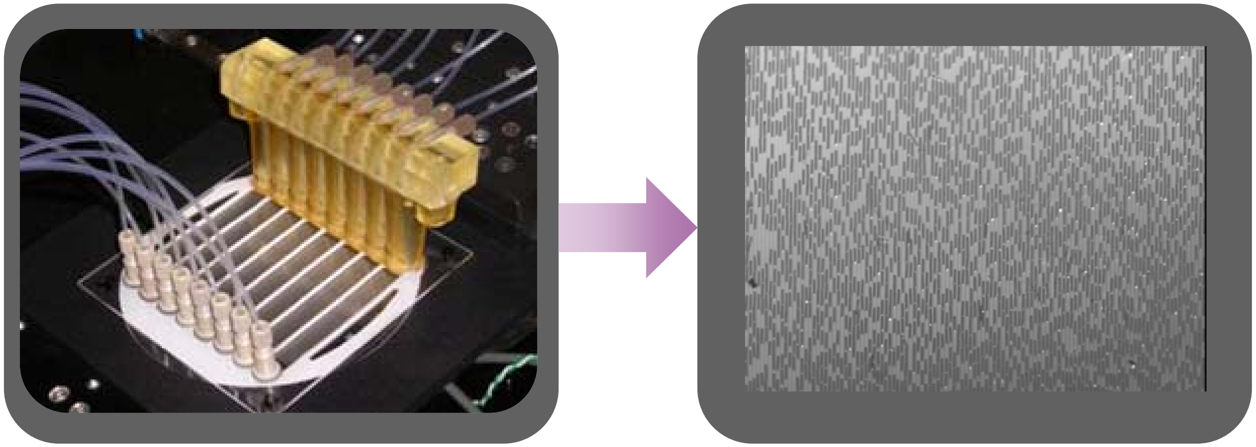
BEADS ALIGN TIGHTLY FOR OPTIMAL SCANNING EFFICIENCY

Code Detection

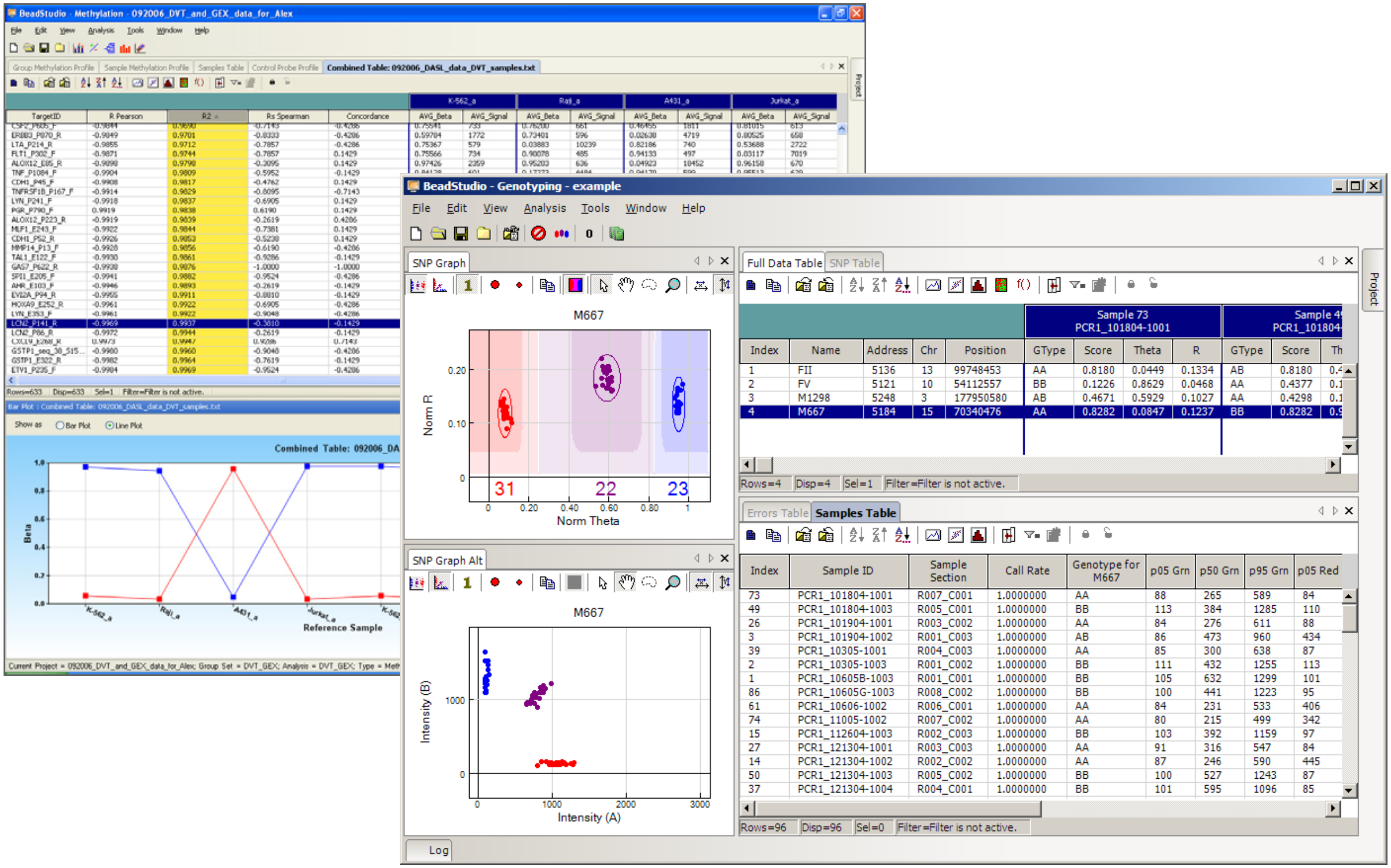


VeraCode Technology

FOLLOWING READOUT, THE BEADS ARE FLUSHED FROM THE READER CELL USING A SECOND ACTUATION PRESSURE CYCLE.



Data Analysis Streamlined with BeadStudio



TargetID	R Pearson	R2	Rs Spearman	Concordance
ERBB3_P870_R	-0.9849	0.9701	-0.8333	-0.4286
LTA_P214_R	-0.9855	0.9712	-0.7857	-0.4286
FLT1_P302_F	-0.9871	0.9744	-0.7857	0.1429
ALOX12_E85_R	-0.9898	0.9798	-0.3095	0.1429
TNF_P1084_F	-0.9904	0.9809	-0.5952	-0.1429
CDH1_P45_F	-0.9908	0.9817	-0.4762	0.1429
TNFRSF1B_P167_F	-0.9914	0.9829	-0.8095	-0.7143
LYN_P241_F	-0.9918	0.9837	-0.6905	0.1429
PGR_P790_F	0.9919	0.9838	0.6190	0.1429
ALOX12_P223_R	-0.9919	0.9839	-0.2619	0.4286
MLF1_E243_F	-0.9922	0.9844	-0.7381	0.1429
CDH1_P52_R	-0.9926	0.9853	-0.5238	0.1429
MMP14_P13_F	-0.9928	0.9856	-0.6190	-0.4286
TAL1_E122_F	-0.9930	0.9861	-0.9286	-0.1429
GAS7_P622_R	-0.9938	0.9876	-1.0000	-1.0000
SPI1_E205_F	-0.9941	0.9882	-0.9524	-0.4286
AHR_E103_F	-0.9946	0.9893	-0.2619	-0.1429
EVI2A_P94_R	-0.9955	0.9911	-0.8810	-0.1429
HOXA9_E252_R	-0.9961	0.9922	-0.6905	-0.4286
LYN_E353_F	-0.9961	0.9922	-0.9048	-0.4286
LCN2_P141_R	-0.9969	0.9937	-0.3810	-0.1429
LCN2_P86_R	-0.9972	0.9944	-0.2619	-0.1429
CXCL9_E268_R	0.9973	0.9947	0.9286	0.7143
GSTP1_seq_38_S15...	-0.9980	0.9960	-0.9048	-0.4286
GSTP1_E322_R	-0.9982	0.9964	-0.7619	-0.1429
ETV1_P235_F	-0.9984	0.9969	-0.9524	-0.4286

Rows=633 Disp=633 Sel=1 Filter=Filter is not active.

K-562_a AVG_Beta	K-562_a AVG_Signal	Raji_a AVG_Beta	Raji_a AVG_Signal	A431_a AVG_Beta	A431_a AVG_Signal	Jurkat_a AVG_Beta	Jurkat_a AVG_Signal
0.59704	1772	0.73401	596	0.02630	4719	0.00525	658
0.75367	579	0.03883	10239	0.82186	740	0.53688	2722
0.75566	734	0.90078	485	0.94133	497	0.03117	7019
0.97426	2359	0.95203	636	0.04923	10452	0.96158	670

					Sample 73 PCR1_101804-1001				Sample 4	
Index	Name	Address	Chr	Position	GType	Score	Theta	R	GType	Score
1	FII	5136	13	99748453	AA	0.8180	0.0449	0.1334	AB	0.8180
2	FV	5121	10	54112557	BB	0.1226	0.8629	0.0468	AA	0.4377
3	M1298	5248	3	177950580	AB	0.4671	0.5929	0.1027	AA	0.4298
4	M667	5184	15	70340476	AA	0.8282	0.0847	0.1237	BB	0.8282

Rows=4 Disp=4 Sel=1 Filter=Filter is not active.

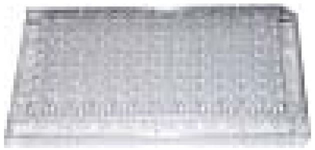
Index	Sample ID	Sample Section	Call Rate	Genotype for M667	p05 Grn	p50 Grn	p95 Grn	p05 Red
73	PCR1_101804-1001	R007_C001	1.0000000	AA	88	265	589	84
49	PCR1_101804-1003	R005_C001	1.0000000	BB	113	384	1285	110
26	PCR1_101904-1001	R003_C002	1.0000000	AA	84	276	611	88
3	PCR1_101904-1002	R001_C003	1.0000000	AB	86	473	960	434
39	PCR1_10305-1001	R004_C003	1.0000000	AA	85	300	638	87
2	PCR1_10305-1003	R001_C002	1.0000000	BB	111	432	1255	113
1	PCR1_10605B-1003	R001_C001	1.0000000	BB	105	632	1299	101
86	PCR1_10605G-1003	R008_C002	1.0000000	BB	100	441	1223	95
61	PCR1_10606-1002	R006_C001	1.0000000	AA	84	231	533	406
74	PCR1_11005-1002	R007_C002	1.0000000	AA	80	215	499	342
15	PCR1_112604-1003	R002_C003	1.0000000	BB	103	392	1159	97
27	PCR1_121304-1001	R003_C003	1.0000000	AA	91	316	547	84
14	PCR1_121304-1002	R002_C002	1.0000000	AA	87	246	590	445
50	PCR1_121304-1003	R005_C002	1.0000000	BB	100	527	1243	87
37	PCR1_121304-1004	R004_C001	1.0000000	BB	101	595	1096	85

Rows=96 Disp=96 Sel=0 Filter=Filter is not active.

VeraCode Custom Products

Easily adaptable to changing content requirements

VeraCode Beads Pre-plated into standard product



Beads Pooled in 96-well Plates

(48 to 384-plex/well)

\+

Individual Tubes of VeraCode Beads

Customized panels created by pooling different tubes of beads

Comprehensive VeraCode product portfolio

- VeraCode Carboxyl Bead Sets
- VeraCode Universal Capture Bead Sets
- Custom GoldenGate Genotyping, 48 to 384-plex
- DASL Custom Gene Expression, 96 & 384-plex
- Custom GoldenGate Methylation, 96 & 384-plex

Available Products

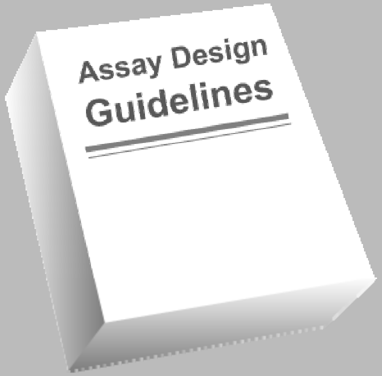
CARBOXYL BEAD SETS (PROTEIN BASED ASSAYS)

PRODUCT

Unique Bead Code Types in Tubes

+

GUIDELINES



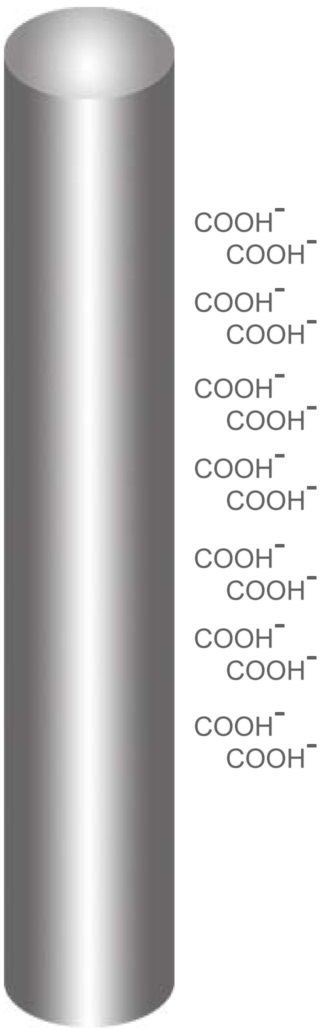
Assay Design Guidelines (RUO)

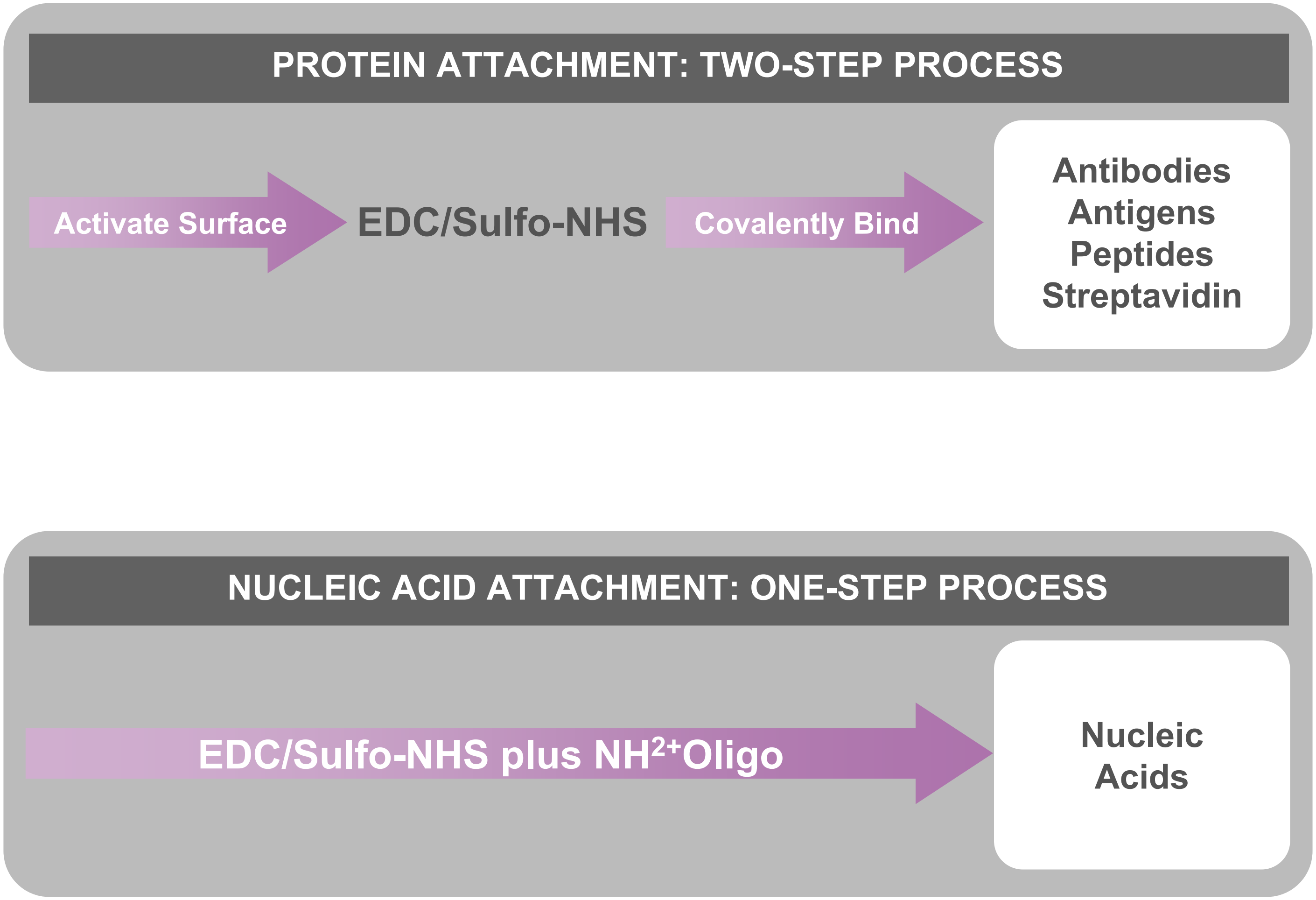
→

CUSTOMER DEVELOPED ASSAY

Customer controls level of multiplexing and number of samples

Carboxyl Beads: Chemistry of Attachment





PROTEIN ATTACHMENT: TWO-STEP PROCESS

Activate Surface → EDC/Sulfo-NHS → Covalently Bind →

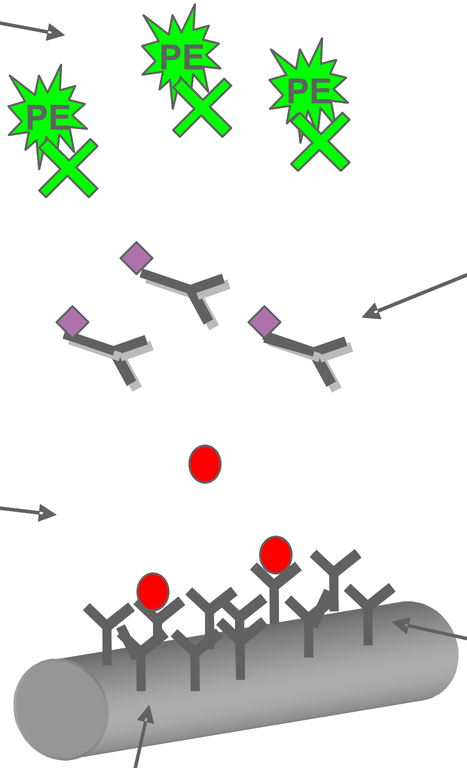
Antibodies
Antigens
Peptides
Streptavidin

NUCLEIC ACID ATTACHMENT: ONE-STEP PROCESS

EDC/Sulfo-NHS plus NH^{2+}Oligo →

Nucleic Acids

Cytokine Sandwich Assay Overview



Streptavidin
Phycoerythrin

Biotinylated
Secondary
Antibody

Cytokine
Antigens

Antibodies immobilized
via COOH surface and EDC
linker chemistry

VeraCode Bead

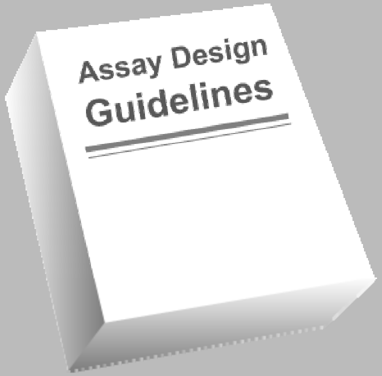
Available Products

UNIVERSAL CAPTURE BEAD SETS

PRODUCT

Unique Bead Code Types in Tubes

GUIDELINES



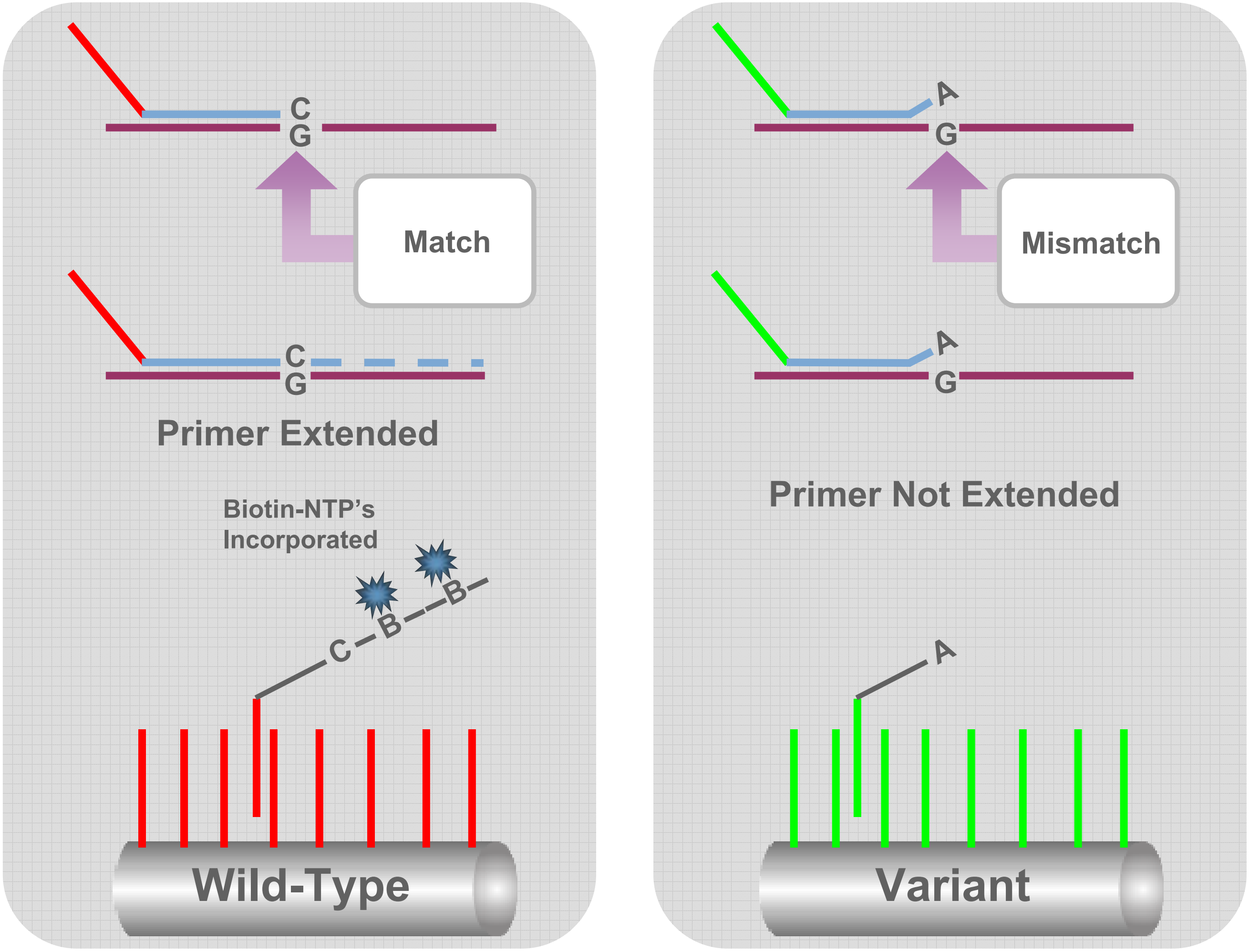
Assay Design Guidelines (RUO)

VeraCode Primer Design Software

CUSTOMER DEVELOPED ASSAYS

Customer controls level of multiplexing and number of samples

Allele-Specific Primer Extension (ASPE)



Match

Primer Extended

Biotin-NTP's
Incorporated

Wild-Type

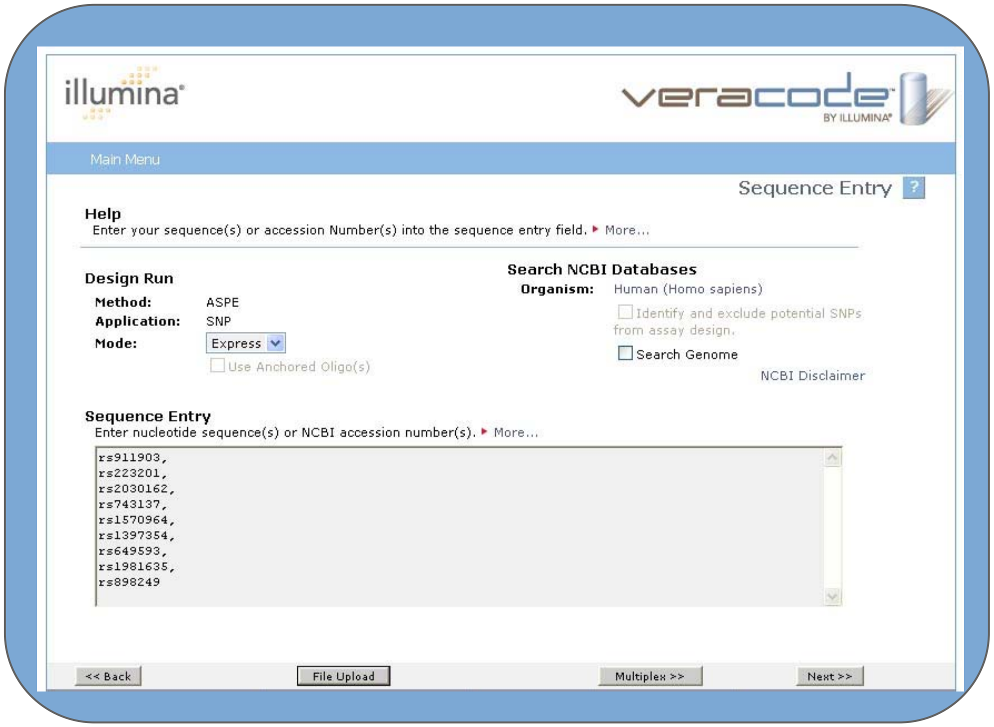
Mismatch

Primer Not Extended

Variant

The VeraCode Assay Designer Solution

- Access user-specific accounts
- Input SNP targets
- Choose workflow option
- Customize design parameters
- Select among possible assay designs
- Download detailed ordering information



Help
Enter your sequence(s) or accession Number(s) into the sequence entry field. ▸ More...

Design Run
Method: ASPE
Application: SNP
Mode: Express
☐ Use Anchored Oligo(s)

Search NCBI Databases
Organism: Human (Homo sapiens)
☐ Identify and exclude potential SNPs from assay design.
☐ Search Genome

Sequence Entry
Enter nucleotide sequence(s) or NCBI accession number(s). ▸ More...

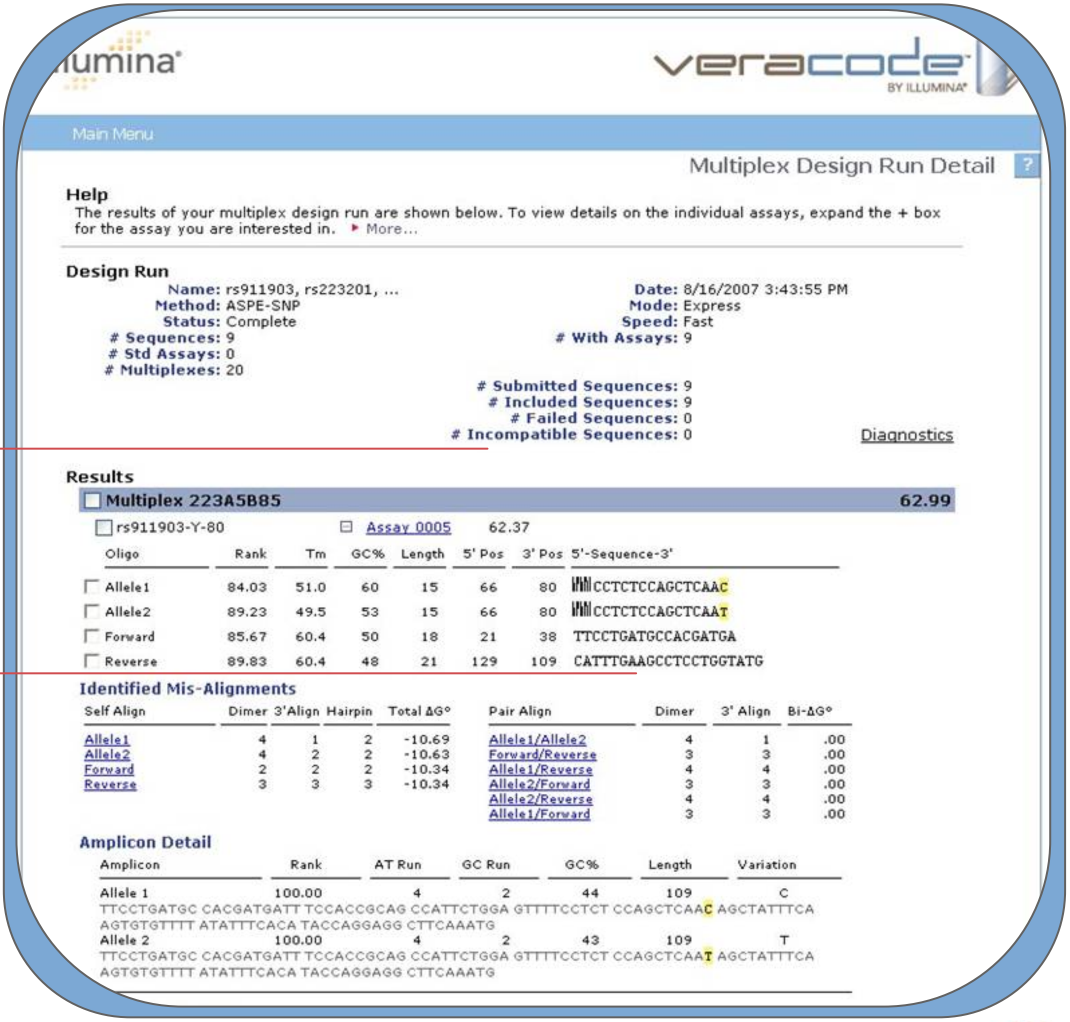
```
rs911903,
rs223201,
rs2030162,
rs743137,
rs1570964,
rs1397354,
rs649593,
rs1981635,
rs898249
```

Assay Design Results

- Example output of an assay design run

Summary Results

Primer Designs



Multiplex Design Run Detail

Help

The results of your multiplex design run are shown below. To view details on the individual assays, expand the + box for the assay you are interested in. ▸ More...

Design Run

Name: rs911903, rs223201, ...
Method: ASPE-SNP
Status: Complete
 # Sequences: 9
 # Std Assays: 0
 # Multiplexes: 20

Date: 8/16/2007 3:43:55 PM
Mode: Express
Speed: Fast
 # With Assays: 9

 # Submitted Sequences: 9
 # Included Sequences: 9
 # Failed Sequences: 0
 # Incompatible Sequences: 0

Diagnostics

Results

☐ **Multiplex 223A5B85** **62.99**

☐ rs911903-Y-80 ⊟ Assay 0005 62.37

	Oligo	Rank	Tm	GC%	Length	5' Pos	3' Pos	5'-Sequence-3'
☐	Allele1	84.03	51.0	60	15	66	80	CCTCTCCAGCTCAAC
☐	Allele2	89.23	49.5	53	15	66	80	CCTCTCCAGCTCAAT
☐	Forward	85.67	60.4	50	18	21	38	TTCCTGATGCCACGATGA
☐	Reverse	89.83	60.4	48	21	129	109	CATTTGAAGCCTCCTGGTATG

Identified Mis-Alignments

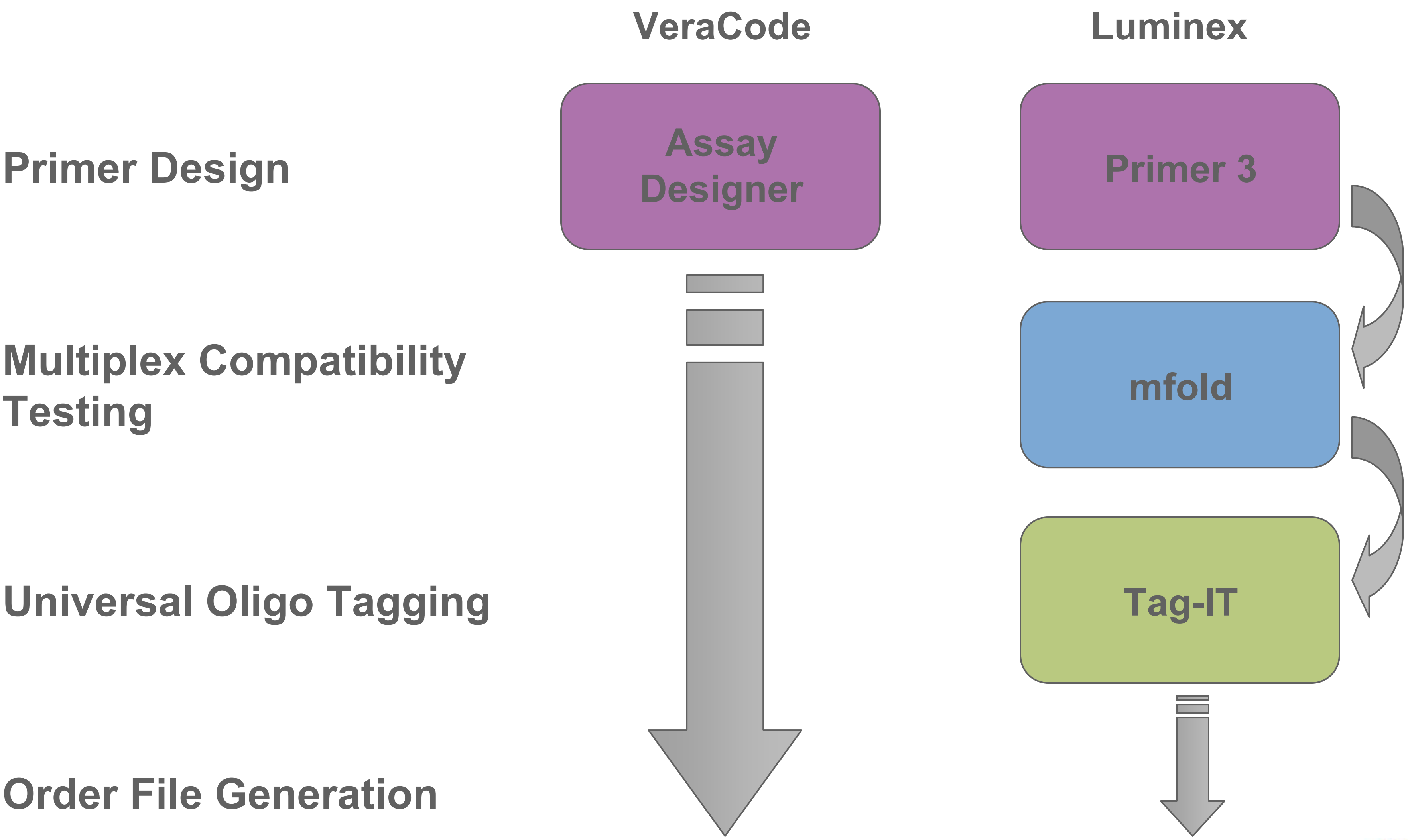
Self Align	Dimer	3'Align	Hairpin	Total ΔG°
Allele1	4	1	2	-10.69
Allele2	4	2	2	-10.63
Forward	2	2	2	-10.34
Reverse	3	3	3	-10.34

Pair Align	Dimer	3' Align	Bi-ΔG°
Allele1/Allele2	4	1	.00
Forward/Reverse	3	3	.00
Allele1/Reverse	4	4	.00
Allele2/Forward	3	3	.00
Allele2/Reverse	4	4	.00
Allele1/Forward	3	3	.00

Amplicon Detail

Amplicon	Rank	AT Run	GC Run	GC%	Length	Variation
Allele 1	100.00	4	2	44	109	C
TTCCTGATGC CACGATGATT TCCACCGCAG CCATTCTGGA GTTTTCCTCT CCAGCTCAAC AGCTATTTCA AGTGTGTTTT ATATTTCACA TACCAGGAGG CTTCAAATG						
Allele 2	100.00	4	2	43	109	T
TTCCTGATGC CACGATGATT TCCACCGCAG CCATTCTGGA GTTTTCCTCT CCAGCTCAAT AGCTATTTCA AGTGTGTTTT ATATTTCACA TACCAGGAGG CTTCAAATG						

Customer Feedback: Software Required for Multiplex Assays



VeraCode

Luminex

Primer Design

Multiplex Compatibility Testing

Universal Oligo Tagging

Order File Generation

Assay Designer

Primer 3

mfold

Tag-IT

illumina

Multiplex ASPE Genotyping Protocol

Multiplex PCR

SAP/EXO

Multiplex ASPE

Prepare Microtitre Plate

User defined Kitting Options

Add ASPE Sample

Hybridize

Detection

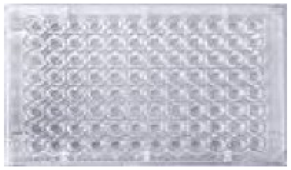
Scan

Total Hands On Time ~ 1.5 hr/plate
Total Time (Sample to Answer) ~ 6.5 hours

Bead Kitting Workflow – VeraCode vs. Luminex

Transfer to kit, add buffer & shake

Aspirate excess buffer, seal plate



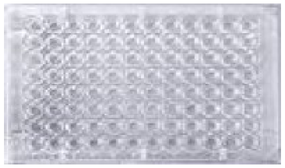
Light Sensitive

Centrifuge

Sonicate

Vortex

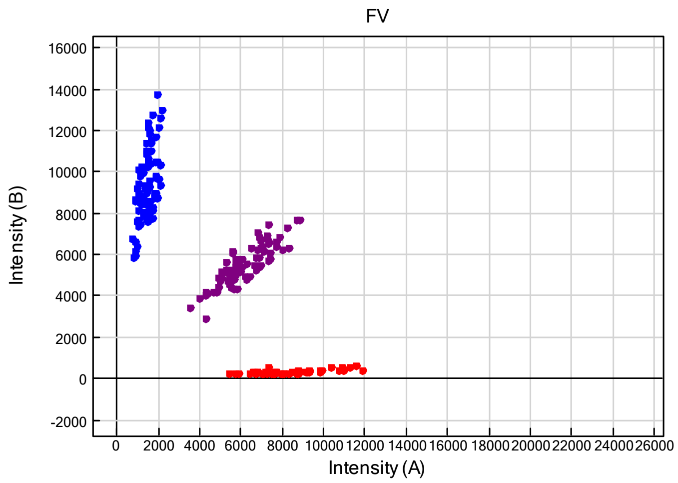
Transfer to plate

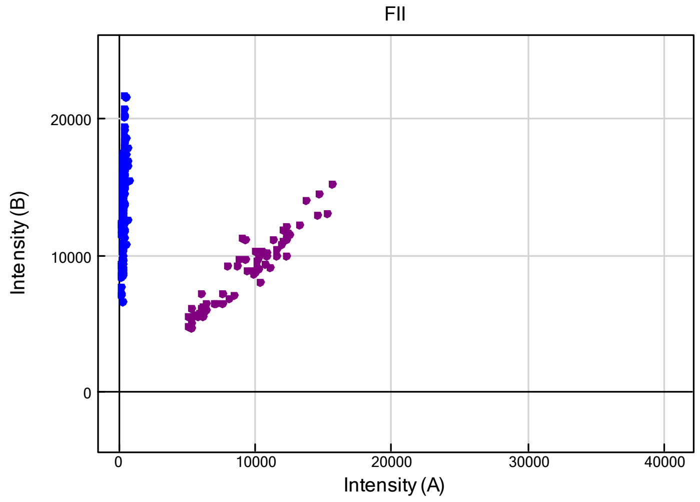


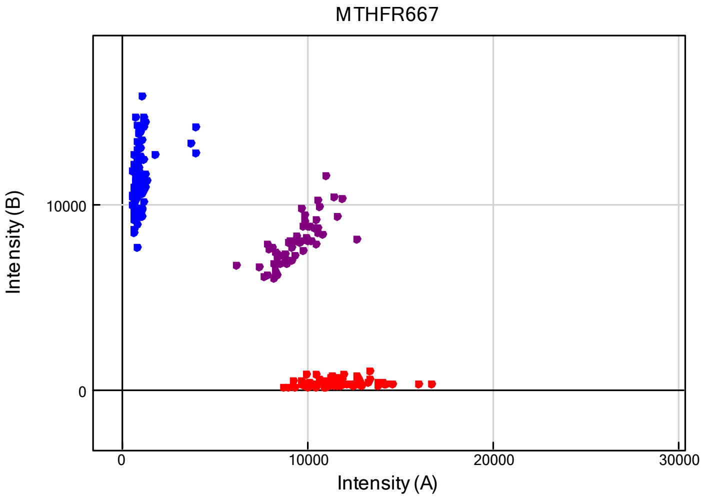
Centrifuge; remove supernatant

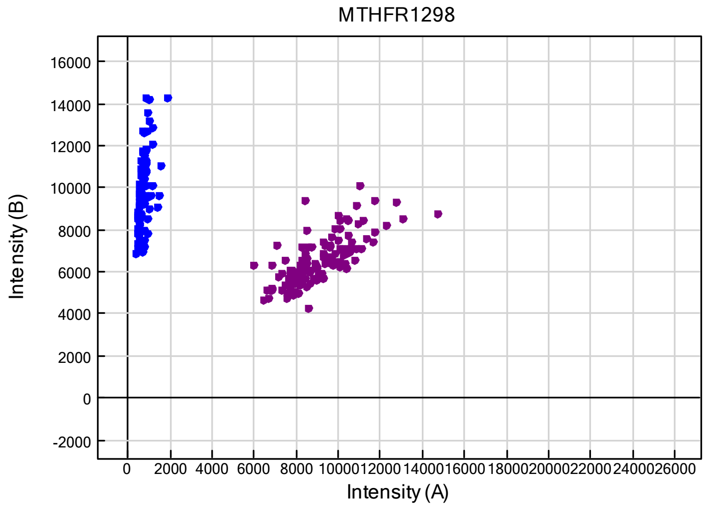
Wash: add buffer; vortex; repeat

Low Plex ASPE Genotyping Results









- **≥ 99.99% reproducibility**
- **100% concordant genotypes**

Customer Success

- Sciona – Health and Wellness company offering genetic testing and personalized exercise, diet and lifestyle recommendations
  - Validated assays presented in October 28, 2008 Webinar[1]
  - GSTM1: Deletion of GSTM1 associated with compromised detoxification
  - GSTT1: Deletion of GSTT1 associated with compromised detoxification
  - ALDH2: 487 G->A associated with alcohol intolerance
  - CYP1A1: 462 A->G associated with increased metabolism of carcinogens
- Children's Hospital of Eastern Ontario – Newborn screening laboratory testing 135,000 children per year
  - Assay development presented at 2008 Illumina Seminar Series[2]
  - HbC, HbE, HbSickle, HbO and HbF: Hemaglobinopathy panel
  - SMA – Spinal Muscular Atrophy assay looks at gene copy number variation associated with severity of muscular disease

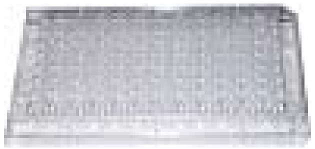
1: http://www.illumina.com/webinars/archives/archivesWebinars.ilmn?entry=50&w=20

2: http://www.illumina.com/seminars/archive/Crocker_0808_NewbornScreening.pdf

Available Products

GOLDENGATE GENOTYPING ASSAY (48, 144, 192 & 384-PLEX)

Custom GoldenGate



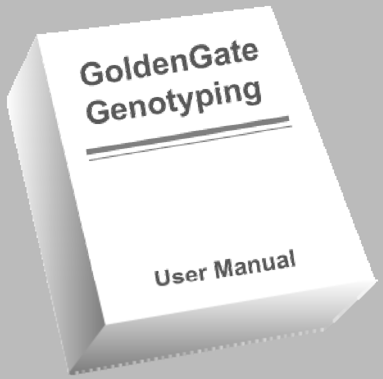
Beads Pooled in
96-well Plates

(48 to 384-plex/well)

Assay specific
oligos
+
Reagents

+

USER MANUAL



GoldenGate
Genotyping
User Manual
(RUO)

**GOLDENGATE
GENOTYPING**

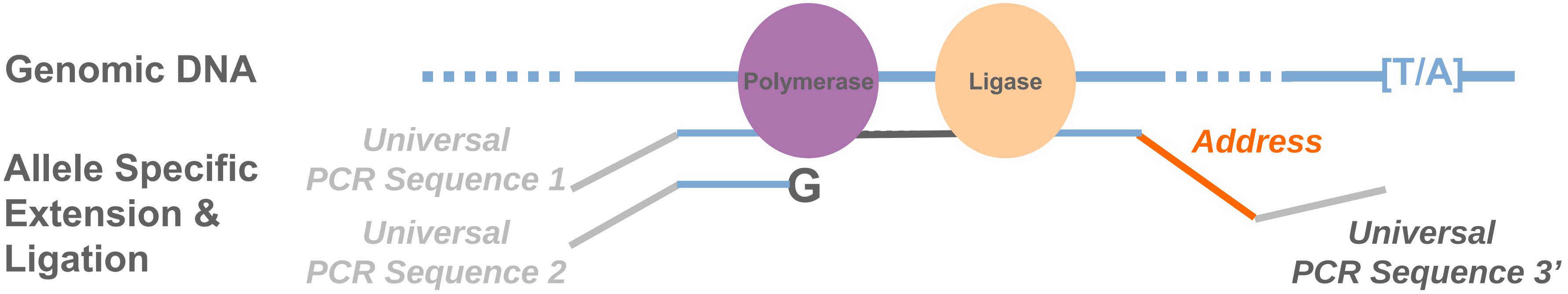
GoldenGate Assay Used for Majority of the International HapMap Project

Country	Research Group and Leaders	Chromosome Assignment	% of Genome
Japan	Yusuke Nakamura, RIKEN/University of Tokyo	5, 11, 14, 15, 16, 17, 19	25.1%
United Kingdom	David Bentley, Wellcome Trust Sanger Institute	1, 6, 10, 13, 20	24.0%
Canada	Thomas Hudson, McGill University	2, 4p	10.0%
China	The China HapMap Consortium	3, 8p, 21	10.0%
United States	Illumina	8q, 9, 18q, 22, X	15.5%
	Broad	4q, 7q, 18p, Y	9.1%
	Baylor	12	4.4%
	UCSF & Washington University	7p	1.9%

- >1,000,000 SNP assays developed
- 285,000,000 genotype calls made
- ~70% done with Illumina GoldenGate assay using the Sentrix BeadArray Reader

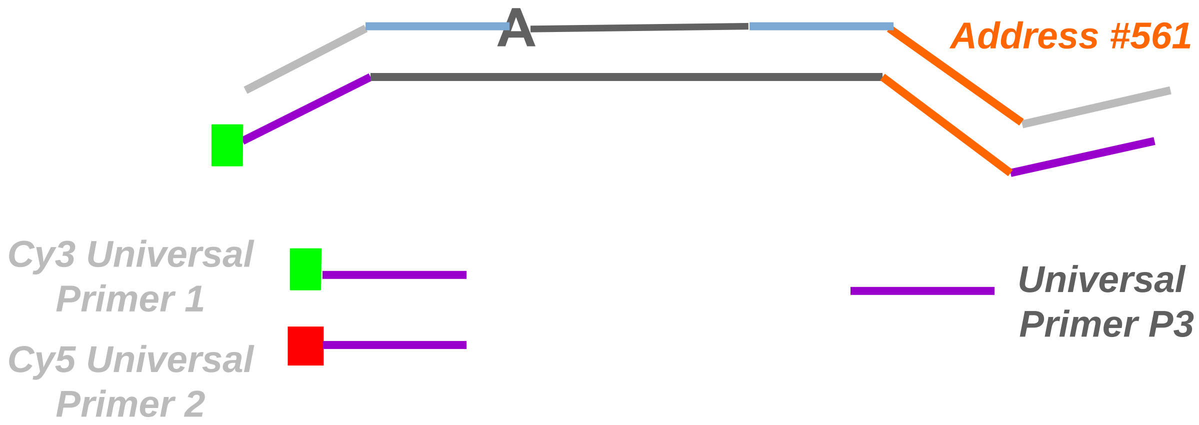
GoldenGate Genotyping Assay

Allele Specific Extension and Ligation



GoldenGate Genotyping Assay

Amplification

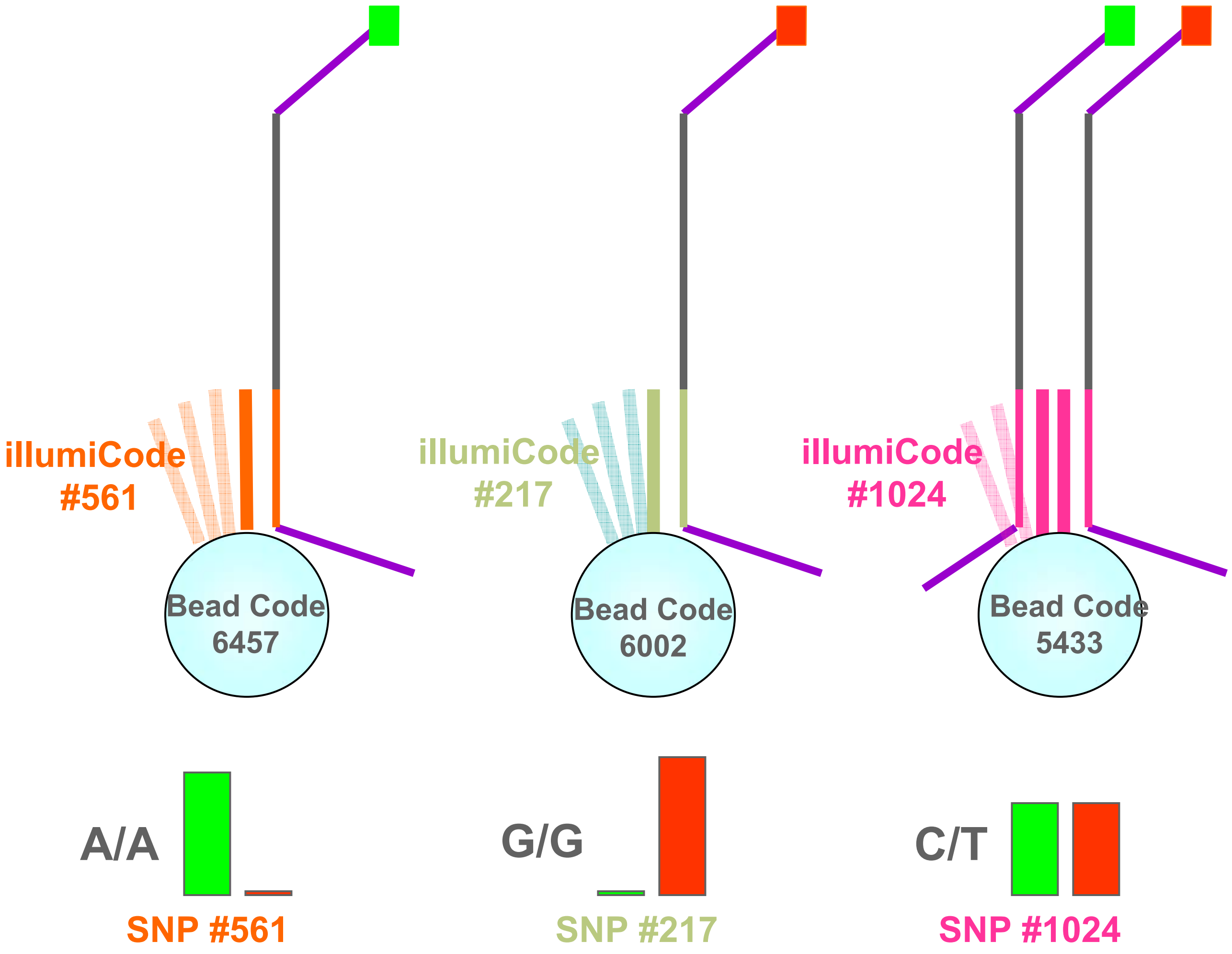


Amplification Template

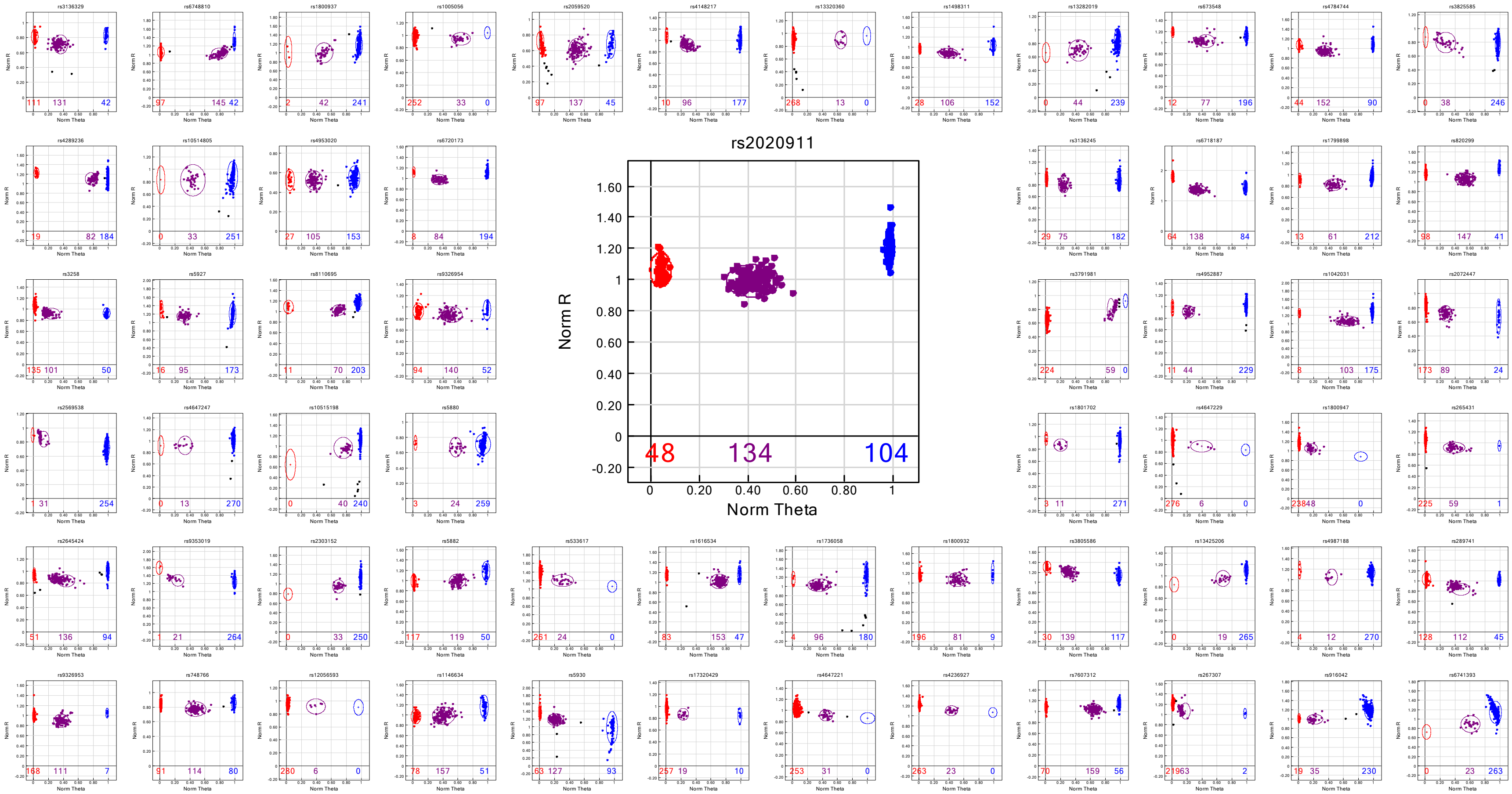
PCR with Common Primers

GoldenGate Assay – two color detection

- Hybridization to VeraCode Beads – one SNP per bead type



GoldenGate Assay Results



Reaction Multiplex	Samples Tested	Call Rate	Total # of Data Points	Reproducibility	Heritability
96	286	99.9%	41,184	100%	100%

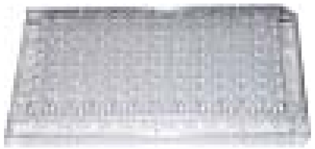
Inter-User Variability

	Specification	Target	User A	User B	User C
Setup	Number of DNA Samples	95	95		
	Bead Multiplex	144	144		
	OPA multiplex	96	96		
Results	Concordance	> 99.5%	99.96%	99.92%	100%
	Reproducibility	> 99.0%	100%	100%	100%
	Heritability (Parent/Parent/Child)	> 99.5%	100%	100%	100%
	Call Rate	> 99.0%	99.97%	99.74%	99.97%
	Sample Success Rate	> 95%	100%	98.94%	100%
	Locus Success Rate	> 90%	100%	100%	100%

Available Products

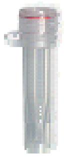
VERACODE DASL CUSTOM GENE EXPRESSION (32 to 384-transcripts)

Custom DASL



Beads Pooled in
96-well Plates

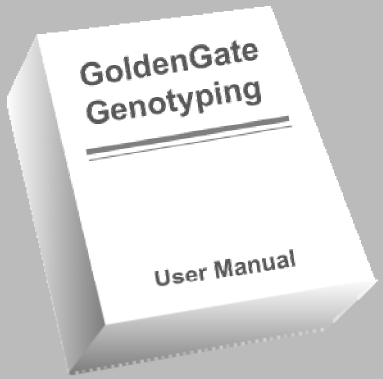
(96 & 384-plex/well)



Assay specific
oligos
+
Reagents

+

USER MANUAL



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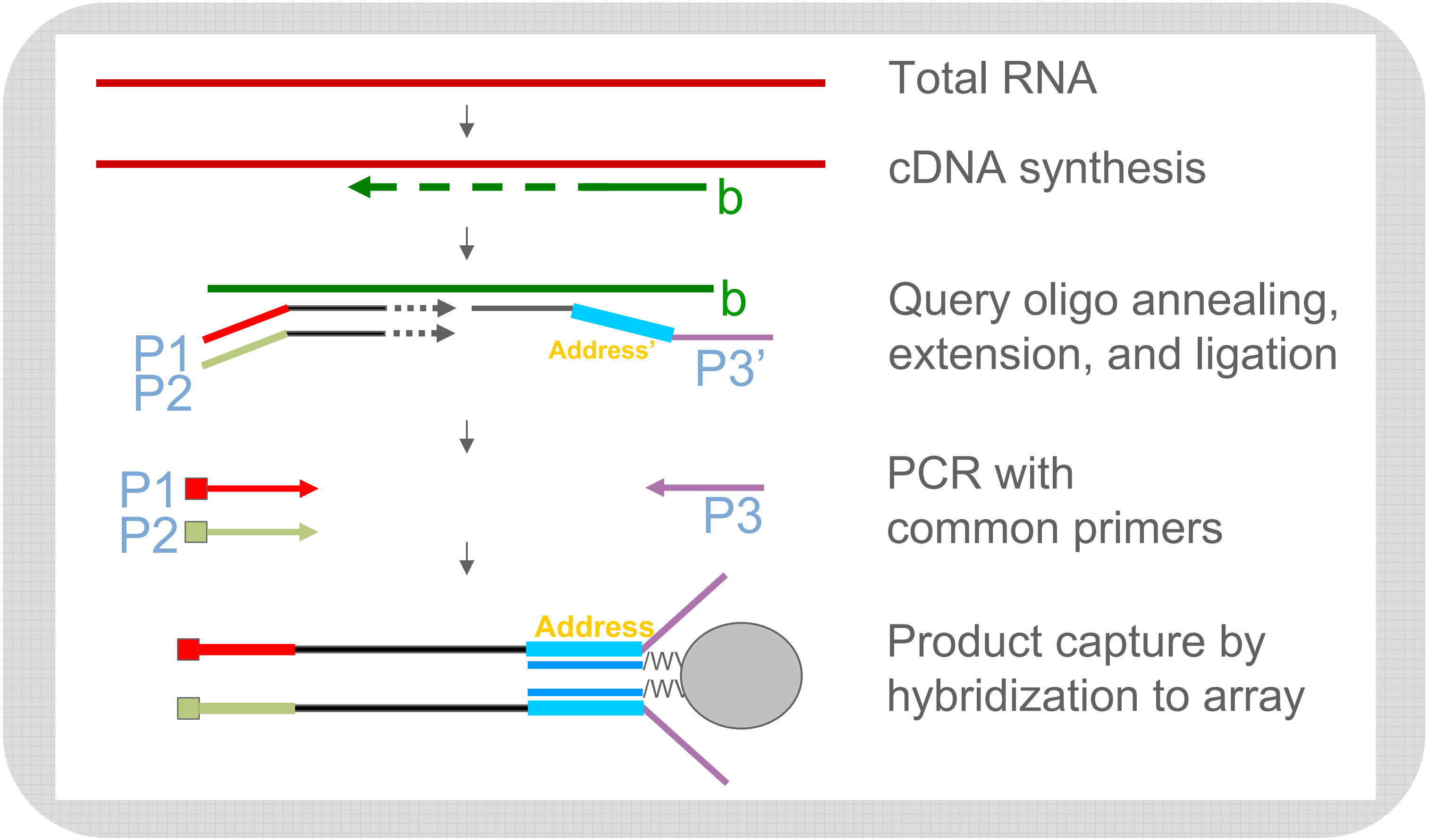
**DASL
GENE EXPRESSION**

The DASL Assay



Total RNA

cDNA synthesis

Query oligo annealing, extension, and ligation

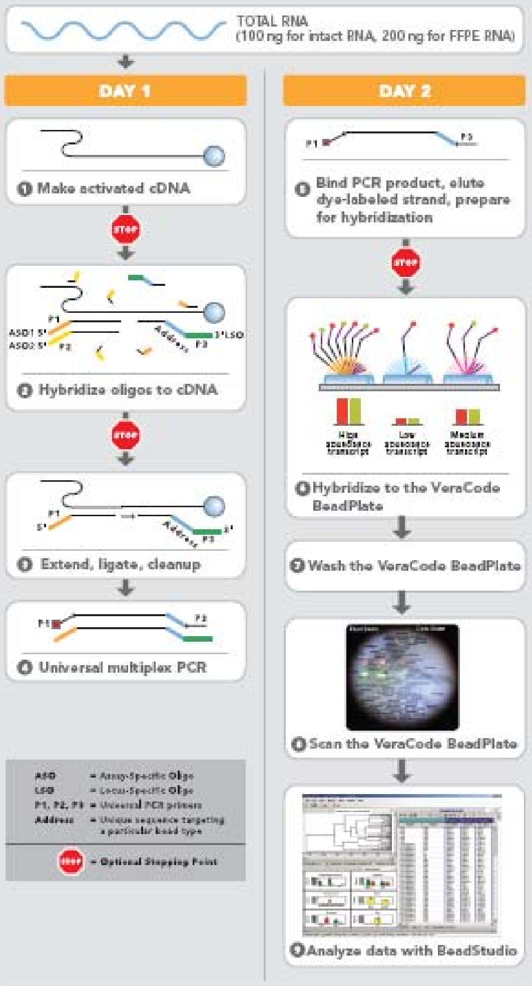
PCR with common primers

Product capture by hybridization to array

- cDNA synthesis includes random priming for fragmented RNAs.
- Sequences of ~ 50 nt are targeted for analysis by addressed query oligos.
- PCR primers are shared among all targets, and amplicons are a uniform size.
- Reproducible across a wide range of RNA degradation.

VeraCode DASL Assay Workflow

FIGURE 2: DASL ON VERACODE WORKFLOW

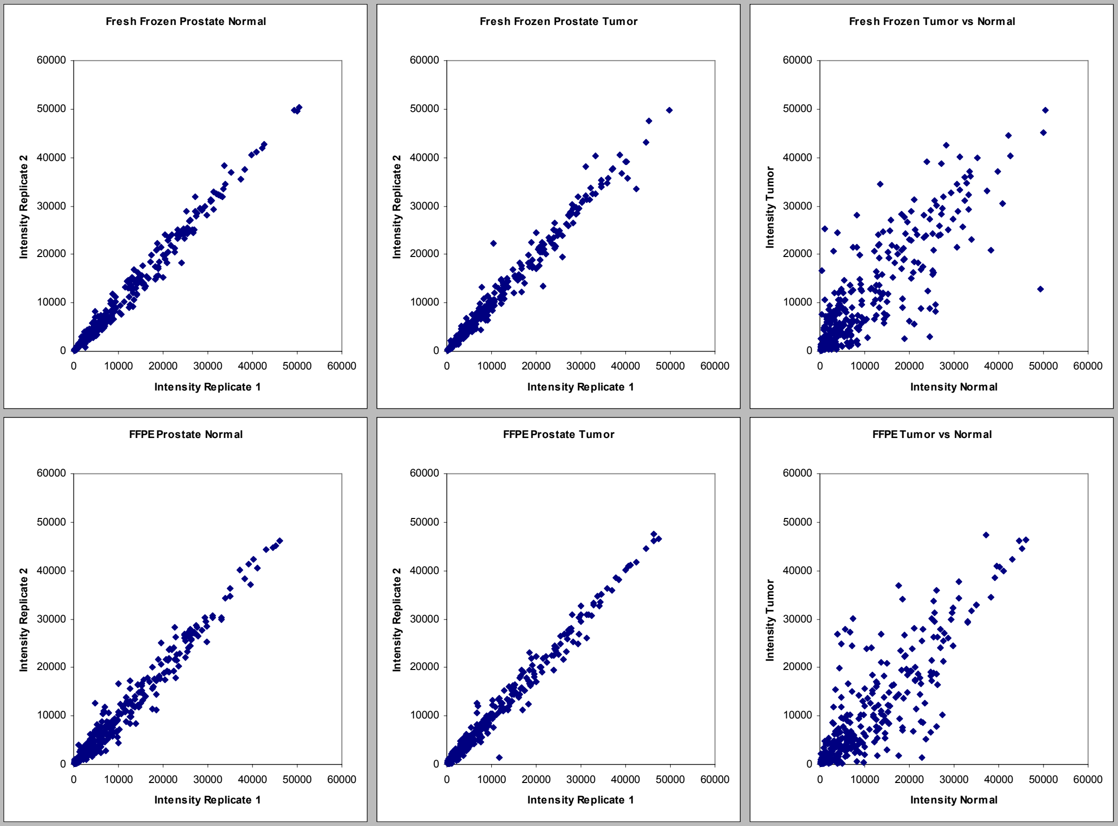


The two-day DASL Assay with readout on VeraCode technology begins with cDNA creation from total RNA. Specific hybridization, followed by enzymatic extention provides target specificity. Universal PCR with labeled primers generates a fluorescent product that is detected by the BeadXpress Reader to quantify gene expression levels. The inscribed code in VeraCode Beads identifies the assayed locus.

- 2-day assay from sample to answer
- 100 ng for intact RNA; 200 ng for FFPE RNA
- Pre-kitted VeraCode bead plates in 96 or 384-plex (32 to 384 transcripts)
- Same controls as found in DASL on BeadArray
- Each bead plate contains 30-fold redundancy for each unique VeraCode bead code
- Data Analysis performed on BeadStudio GX module

Fresh Frozen and FFPE RNA Reproducibility on VeraCode

- RNAs derived from fresh frozen or FFPE human tissues were analyzed.
- FFPE RNAs demonstrated nearly equivalent reproducibility compared to intact RNAs ($r^2 > 0.98$).



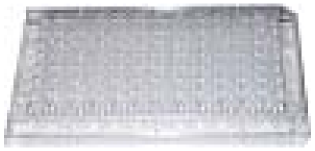
Performance Summary

Metric	Value
Overall reproducibility of technical replicates (intact RNA)	$r^2 > 0.99$
Overall reproducibility of technical replicates (FFPE RNA)	$r^2 > 0.98$
Reproducibility between operators	$r^2 > 0.98$
Reproducibility between VeraCode bead lots	$r^2 > 0.99$
Concordance with BeadArray for Number of Probes Detected	> 92%
False positive rate	< 1%

Available Products

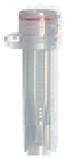
VERACODE GOLDENGATE METHYLATION (48 to 384-promoter regions)

Custom DASL



Beads Pooled in
96-well Plates

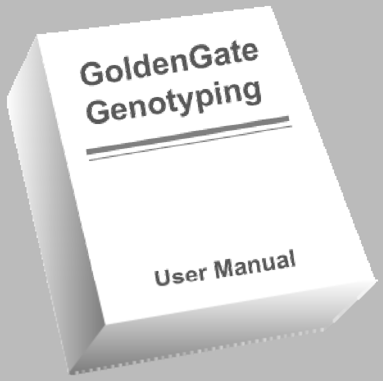
(96 & 384-plex/well)



Assay specific
oligos
+
Reagents

+

USER MANUAL



GoldenGate
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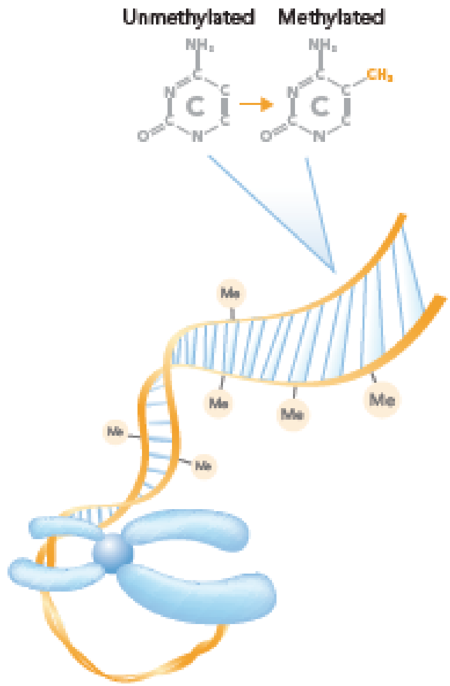
DASL
GENE EXPRESSION

GoldenGate Methylation Assay

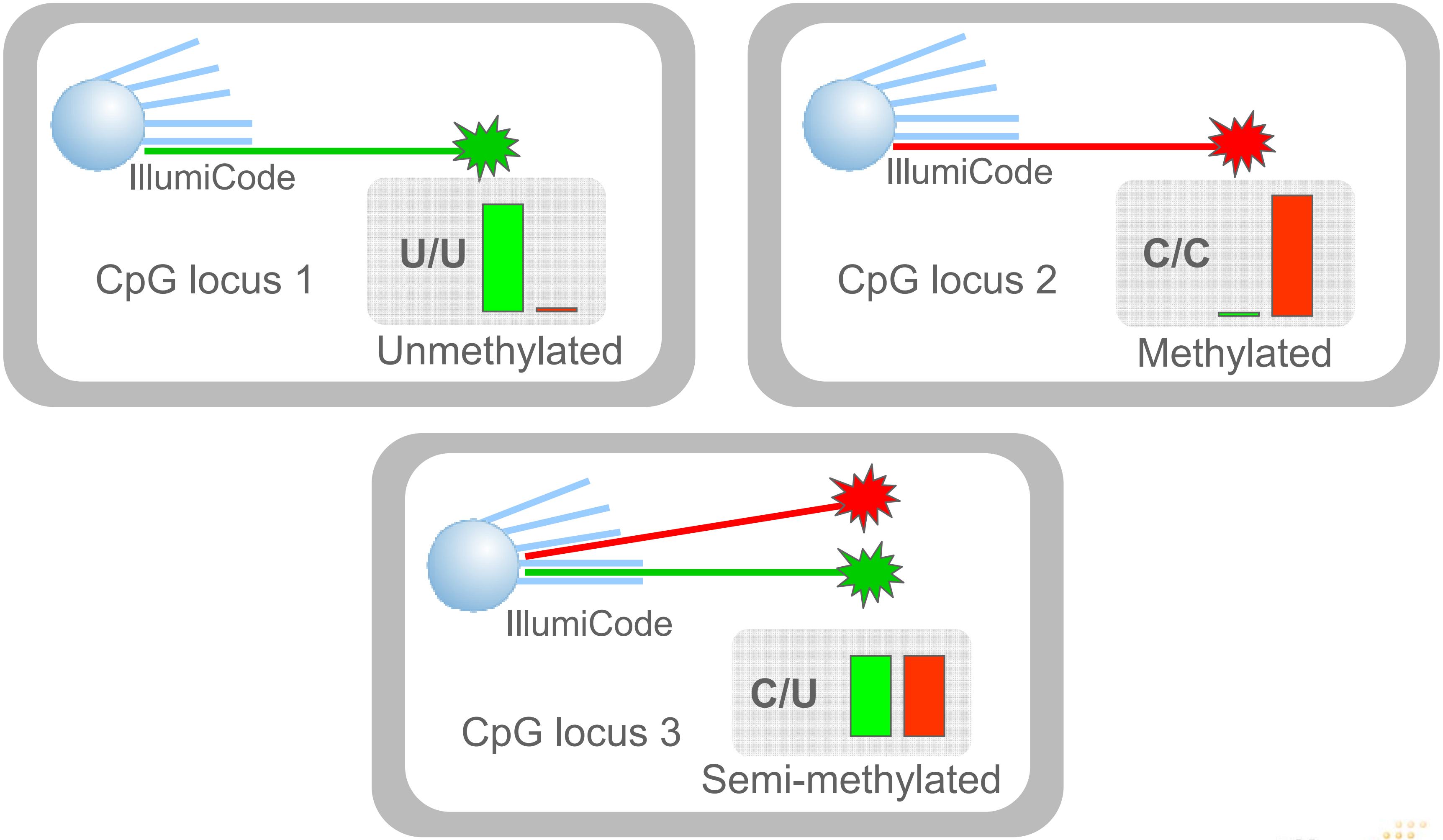


1. Bisulfite treatment of DNA
   - Convert unmethylated cytosine to uracil
2. GoldenGate Assay
   - DNA Activation
   - Allele-Specific Extension (ASE) & Ligation
   - PCR Amplification
   - Hybridize to Bead Substrate
   - Scan

illumina

GoldenGate Methylation Assay

Hybridization & Detection



IllumiCode

CpG locus 1

U/U

Unmethylated

IllumiCode

CpG locus 2

C/C

Methylated

IllumiCode

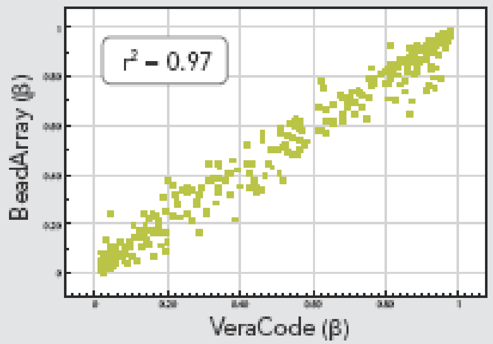
CpG locus 3

C/U

Semi-methylated

VeraCode Methylation Data Analysis

FIGURE 3: ASSAY CONSISTANCY ON BEADARRAY OR VERACODE PLATFORMS



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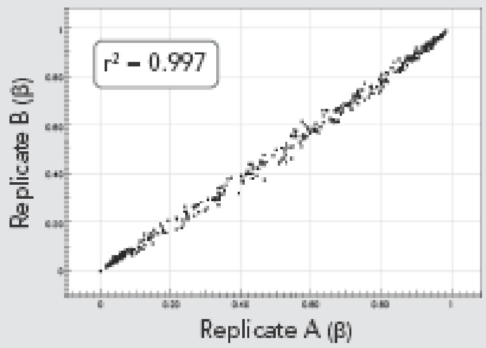
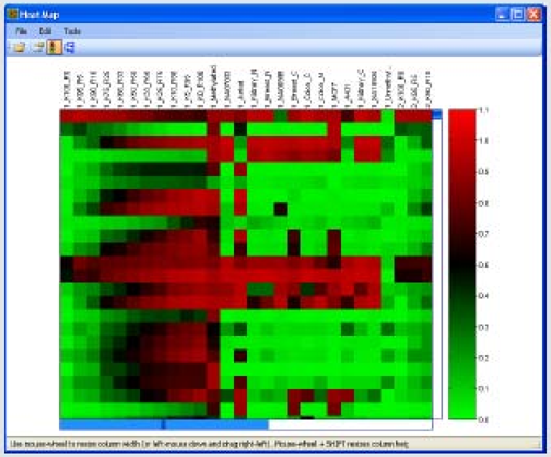
research
design.

FIGURE 4: HIGH ASSAY REPRODUCIBILITY



f robust
denGate
h VeraCode
ntative
has an r²

FIGURE 5: DATA ANALYSIS WITH ILLUMINA BEADSTUDIO SOFTWARE

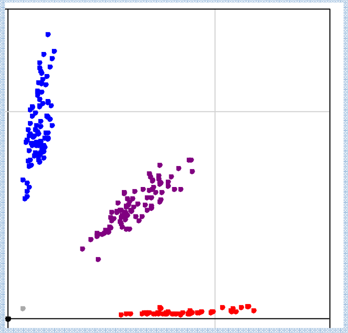


Methylation status (β) is shown for many loci (y-axis) across many samples (x-axis) in graphical heat map format to easily see trends and outliers.

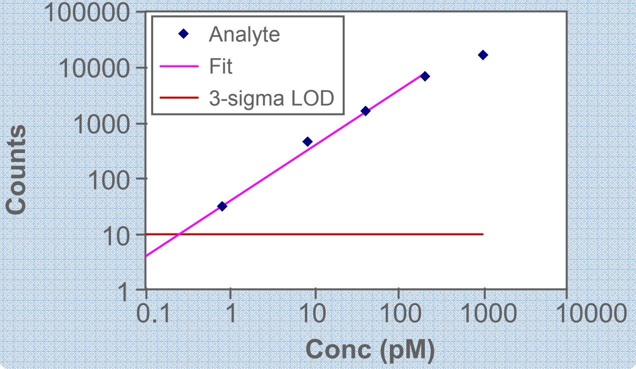
- Data analysis performed on BeadStudio Methylation module
- Internal replication experiments show an r^2 correlation of 0.997
- Experiments comparing methylation results for the same loci on BeadArray and VeraCode show high concordance (r^2 = 0.97)

Ability to Analyze Multiple Applications

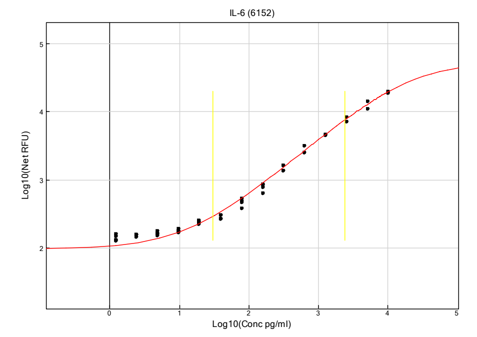
GENOTYPING



GENE REGULATION



PROTEIN EXPRESSION

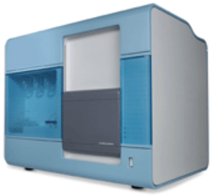


Bridging from the lab to the clinic

Laboratory

Translate

Clinic



Genome Analyzer

iScan

- Collaborative approach to research
- Constantly improving throughput
- Excellent cost position
- Highly multiplexed
- Multiple markers on one system

Services

BeadXpress

Illumina Diagnostics Strategy

To be the leader in cancer translational diagnostics

Oncology Discovery – Identify novel biomarkers

- Identify novel biomarkers for the early detection of ovarian cancer
- Identify novel biomarkers to indicate response to platinum therapy in late stage ovarian cancer

Sequencing Services – Utilize service lab for rapid translation

- Establish a CLIA laboratory
- Begin to offer services in the oncology area based on the ovarian biomarkers

Platform Partnering – Build a large installed base

- Partner with content providers
- Enable broad adoption with removal of royalty burden
- Internally develop products to create breadth of menu

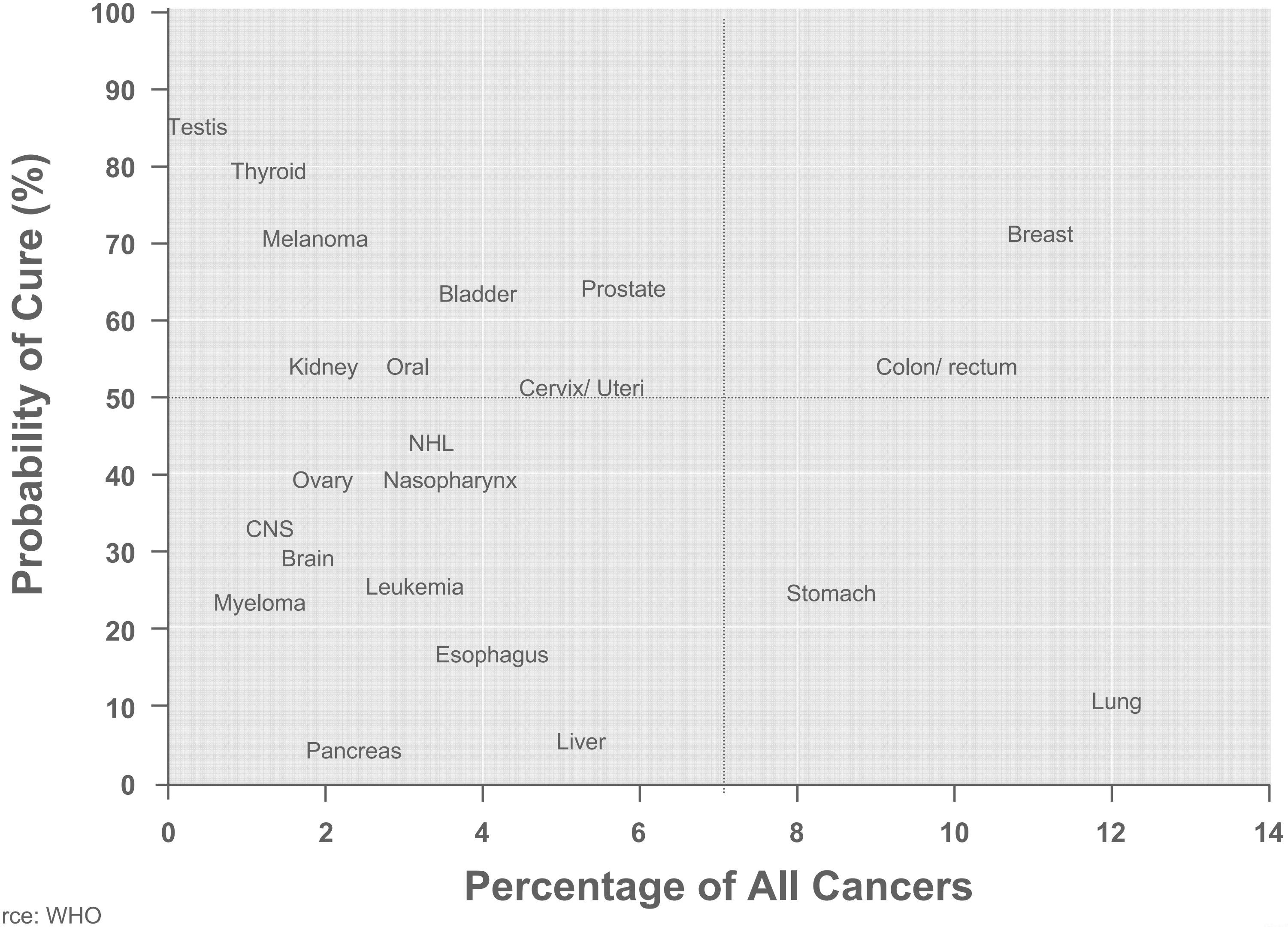
Illumina Diagnostics Vision

**To Be the Leader in
Cancer Translational Diagnostics**

Focus Core Technologies on Cancer

- Next Generation Sequencing
- Whole Transcriptome Analysis
- Methylation Profiling

Initial Targets



Source: WHO

Ovarian Cancer Will be Our Entry Point

Deadly

- Leading cause of death from gynecological cancer
- Fifth leading cause of cancer mortality in women
- Mortality: 15,520 (US Only)

Incurable

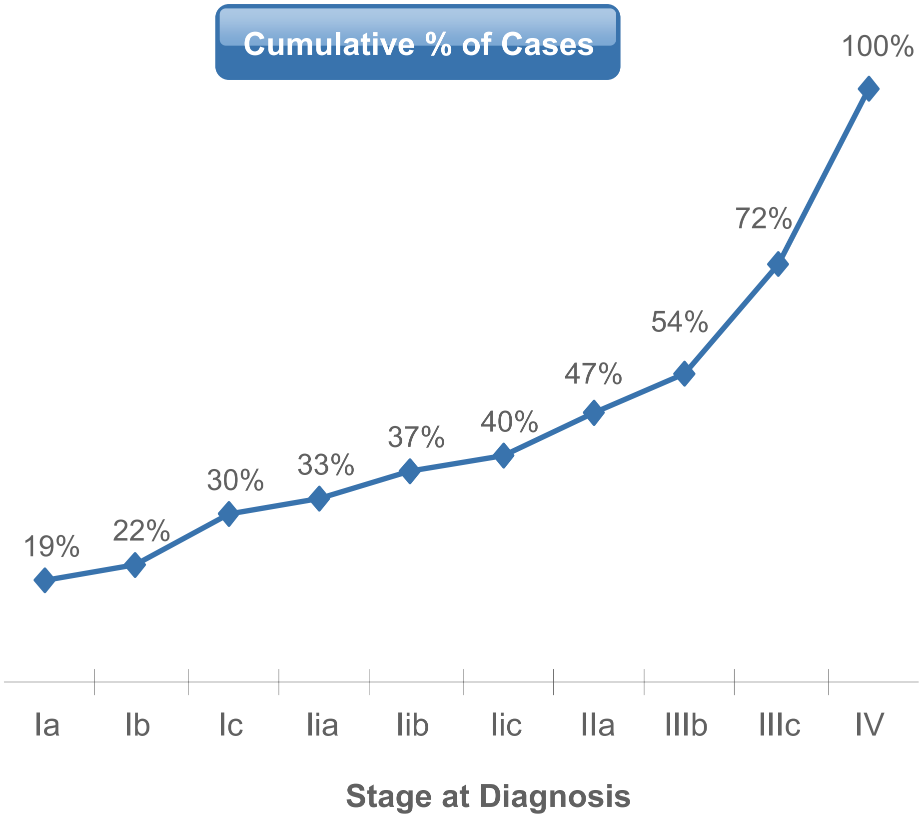
- Laparotomy/Hysterectomy/Remove ovaries
- Followed with six cycles of chemotherapy
- Less than 40% are cured

Difficult Dx

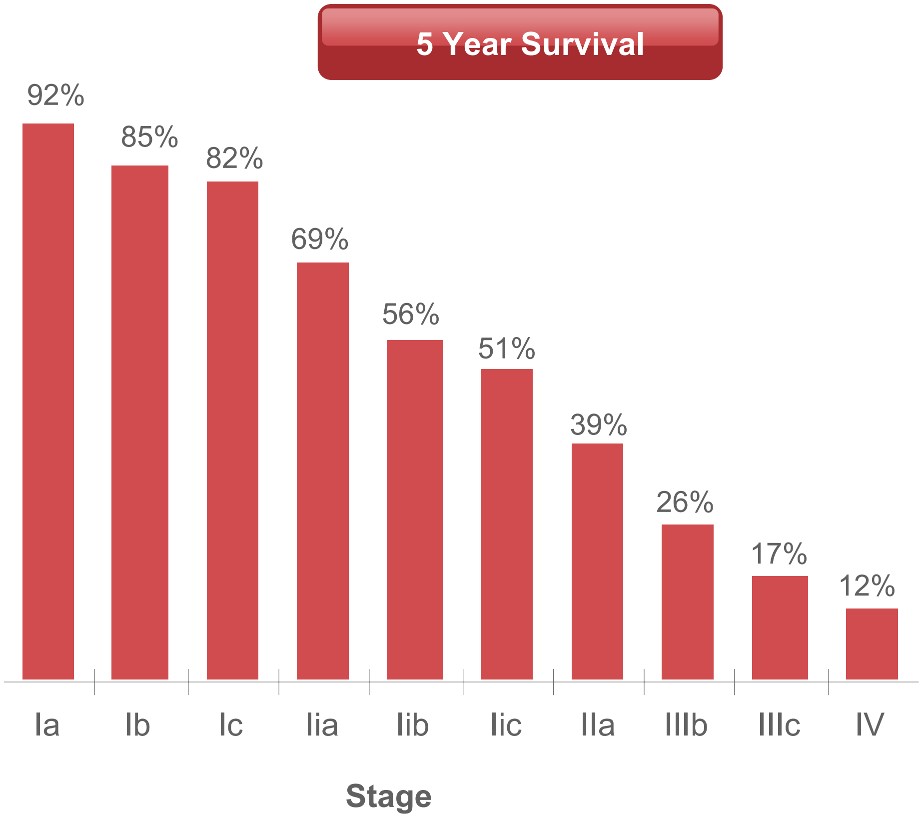
- Abdominal/pelvic exam, Ultrasound, CT, CA-125
- Patients present with a suspicious/palpable mass
- BRCA 1/2 positive in a limited number of cases

Early Detection for Ovarian Cancer is Critical

Late stage diagnosis …

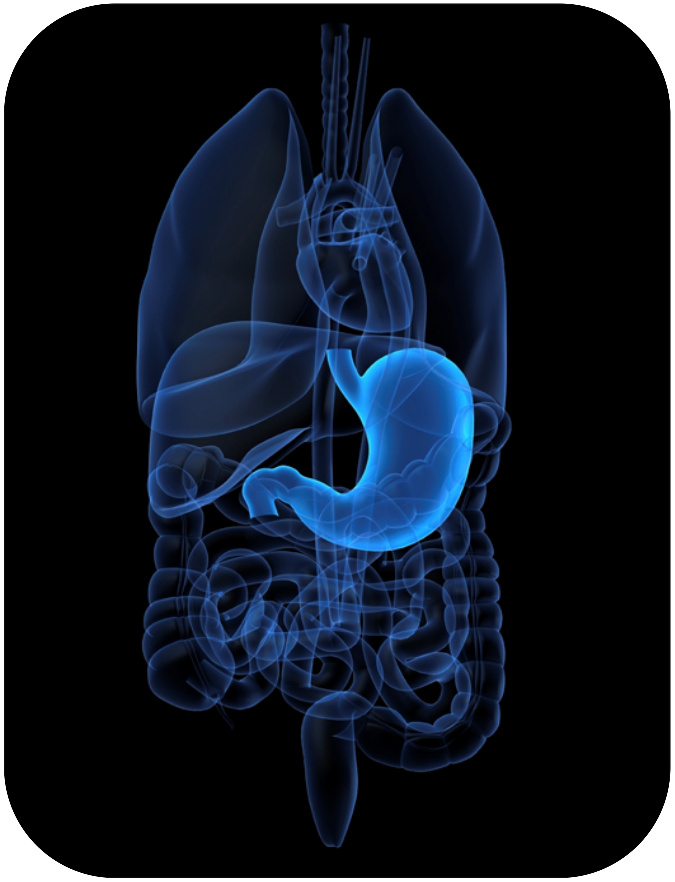


… results in poor prognosis

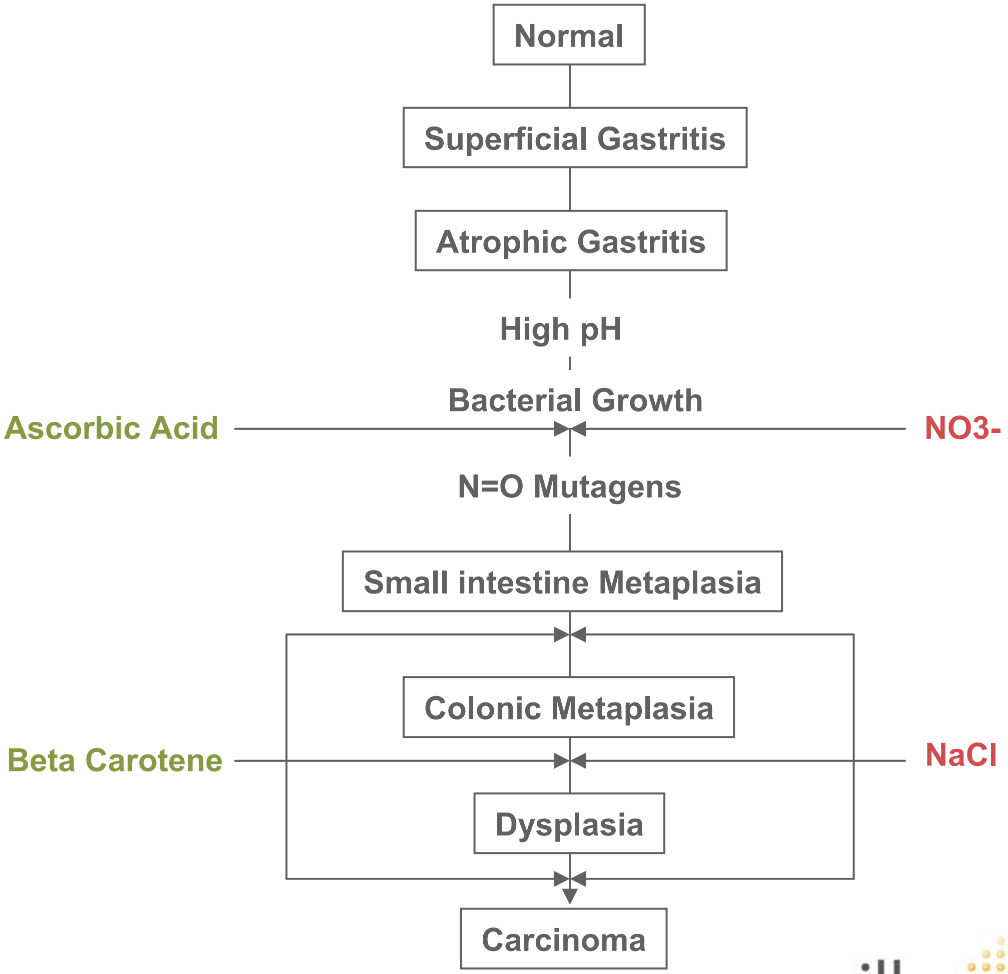


Gastric Cancer will be Our Second Target

Cardia 15% of Gastric Cancers
Increasing due to obesity



Gastric Carcinogenesis



Normal

Superficial Gastritis

Atrophic Gastritis

High pH

Bacterial Growth

Ascorbic Acid

NO3-

N=O Mutagens

Small intestine Metaplasia

Colonic Metaplasia

Beta Carotene

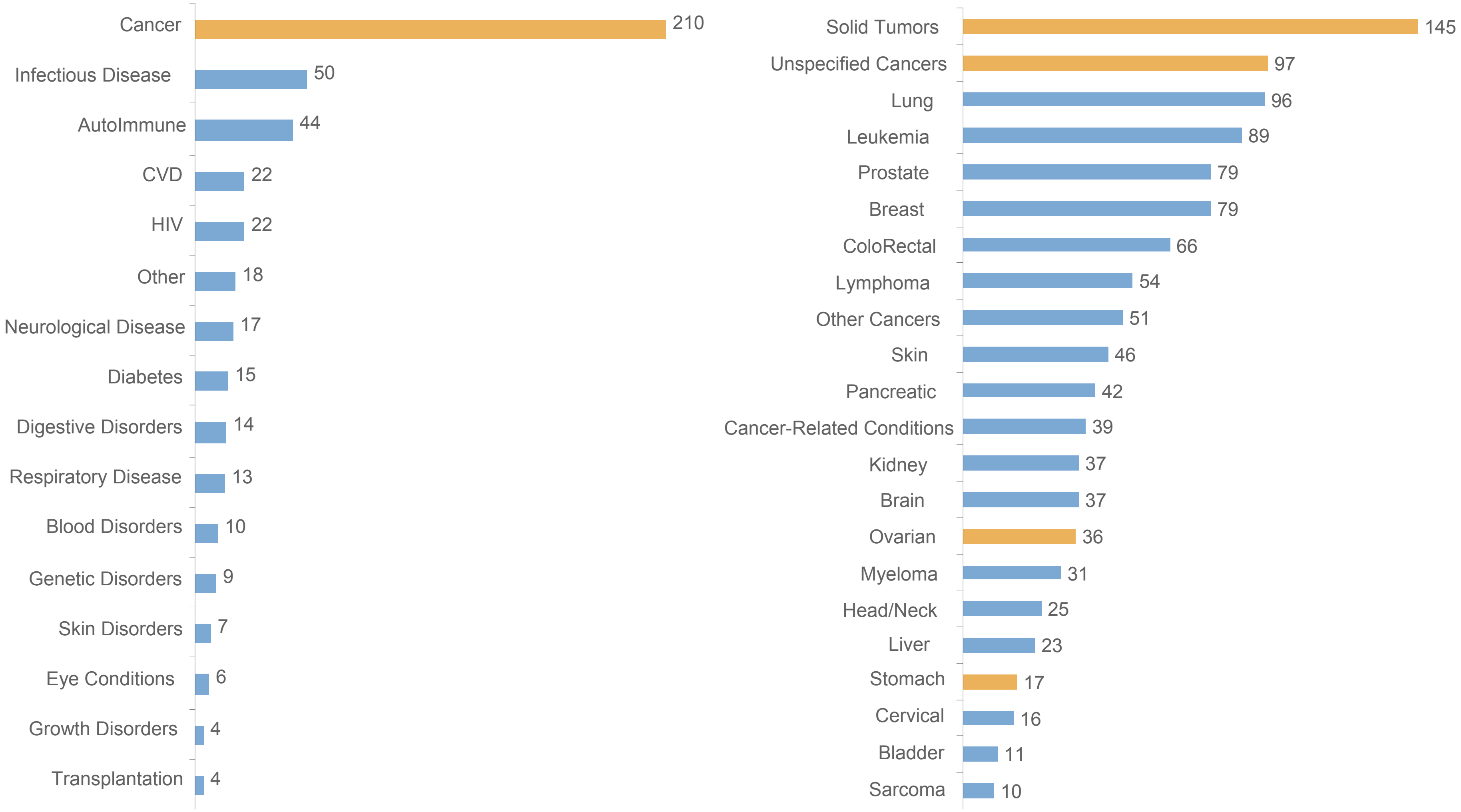
NaCl

Dysplasia

Carcinoma

More Therapies Means More Choices

Drug Pipeline



Source: PhRMA: 2006 Medicines in Development Biotechnology

Discovery, Strategy & Advantages

Focused Approach Addresses Unmet Medical Needs

Strategy

- Begin with 25 Tumor/Normal pairs
- Comprehensive genetic analysis
- Sequence to 30x coverage whole genome
- Analyze full methylome and transcriptome
- Validate findings on larger sample size
- Implement on flexible platform

Illumina Advantage

- Low cost internal sequencing
- Significant throughput improvements
  - Currently 1 genome/week internally
- Unique bioinformatics capability
  - Multiple genome analysis
- Capable of analyzing across methods
- Ability to deploy content on arrays
- BeadXpress optimal for multiple methods

Illumina's Diagnostic Division Branding

illuminaDx™