Filed Pursuant to Rule 433 of the Securities Act of 1933
Issuer Free Writing Prospectus dated April 23, 2019
Relating to Preliminary Prospectus dated April 22, 2019
Registration No. 333-230985

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Opportunity

- Unique, proprietary sequencing platform (tSMS) for rapid growth billion dollar market
- $5.3B addressable market for DNA and RNA sequencing by 2025
- Proven technology (10+ years R&D) across diverse genomic applications
- Currently engaged in multiple research projects for scientific discoveries
- Company primed for broad market commercialization

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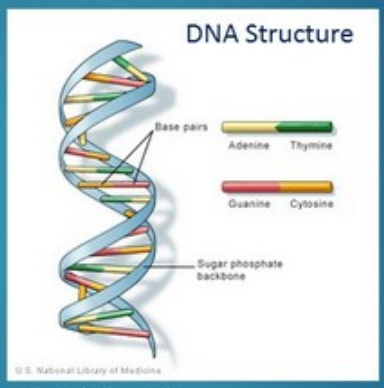
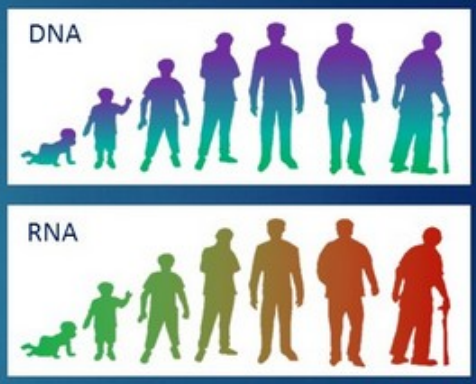
Next Generation Sequencing (NGS)

- DNA stores hereditary information, static in nature
  - ✓ May provide information about susceptibility to disease
- RNA stores cellular information, dynamic in nature
  - ✓ RNA sequencing delivers "real-time" information to advance the understanding of biology



Credit: U. S. National Library of Medicine



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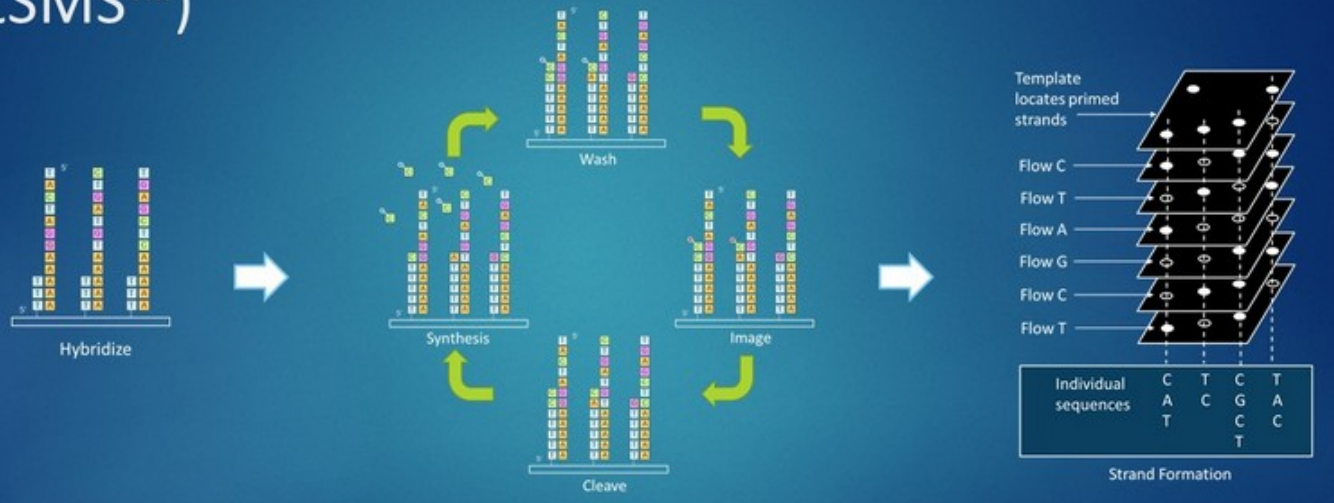
SeqLL's True Single Molecule Sequencing (tSMS™)



Sample Preparation

Sequencing-By-Synthesis

Image Analysis

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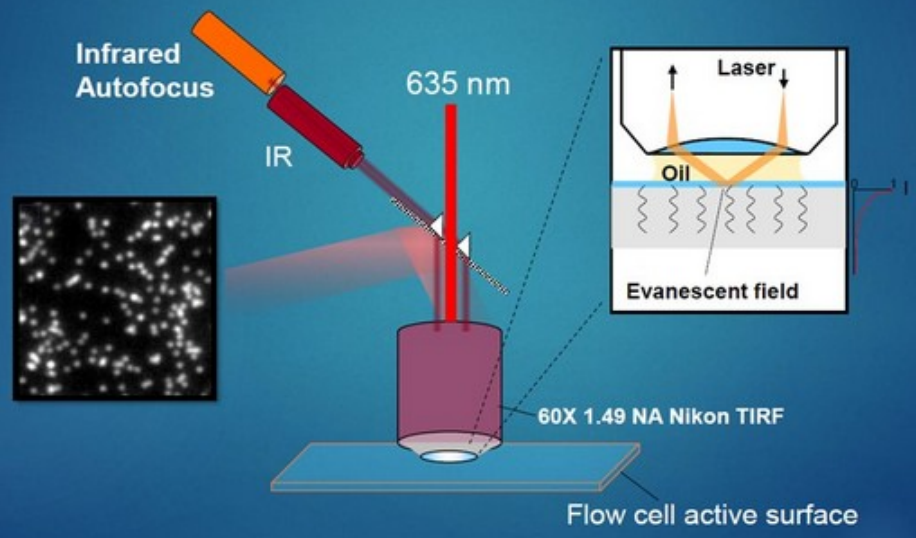
TIRF Illumination Enables Single Molecule Resolution Imaging



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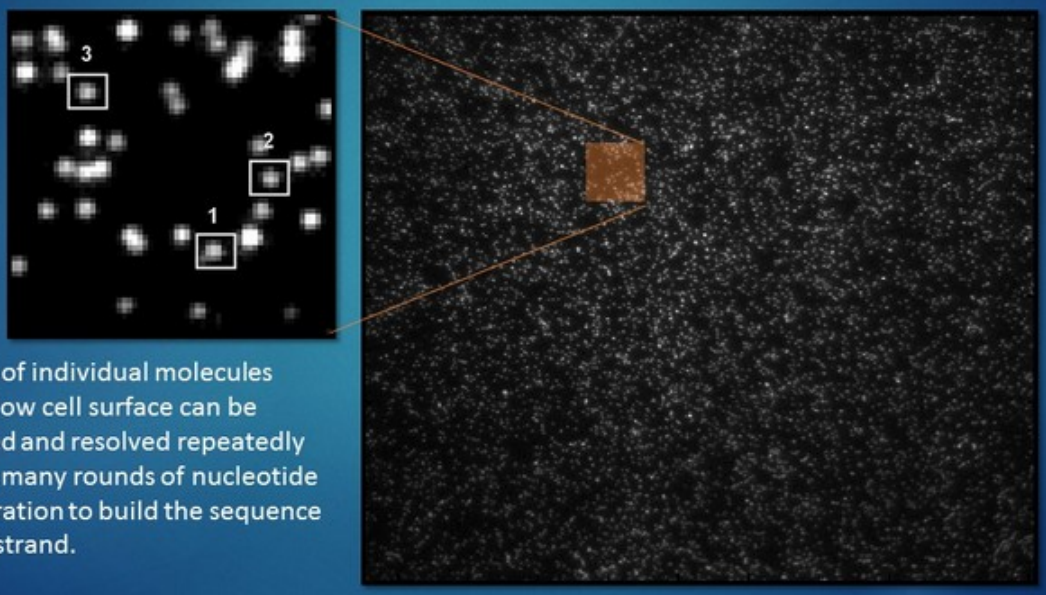
Massive Parallel Sequencing by Synthesis – a tSMS Advantage



Millions of individual molecules on the flow cell surface can be identified and resolved repeatedly through many rounds of nucleotide Incorporation to build the sequence of each strand.

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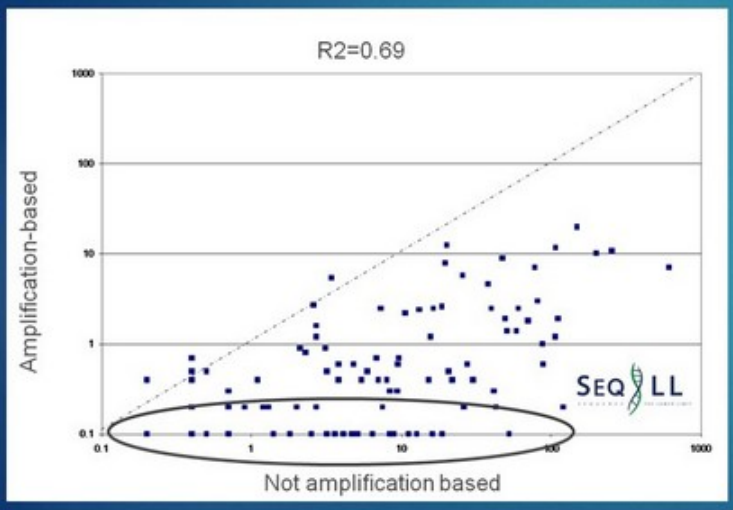
tSMS Captures Data Lost by Other NGS Platforms



Amplified vs Non-amplified miRNAs

- SeqLL tSMS efficiently sequences molecules of any length
- Short or degraded DNA/RNA
  - miRNAs
  - FFPE material
  - Forensic samples
- Micro RNAs are challenging to sequence due to their short length
- More complete analysis and greater depth of coverage

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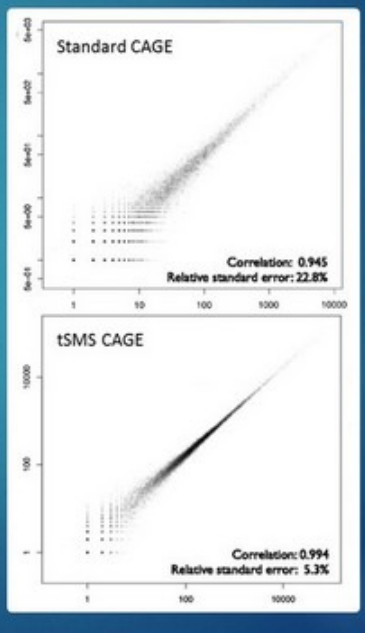
tSMS Offers Superior Signal-to-Noise for Detection of Subtle Changes

- Cap Analysis of Gene Expression (CAGE) captures mature, capped RNA species
- SeqLL (tSMS CAGE) measures full transcriptome with **high accuracy, reproducibility** and **minimal bias**
- Greatly improved signal-to-noise ratio compared to standard CAGE protocol
- Unprecedented detection of low-fold changes in gene expression
- Ability to correlate subtle changes in gene expression with health status for **biomarker discovery, patient stratification** and **disease monitoring**



Direct comparison of SeqLL tSMS CAGE protocol to standard CAGE protocol demonstrates higher correlation and lower standard error on the SeqLL platform

Reference:
Kawaji, et al (2014) Genome Research (24)708-717

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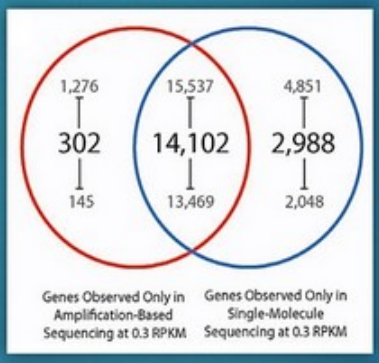
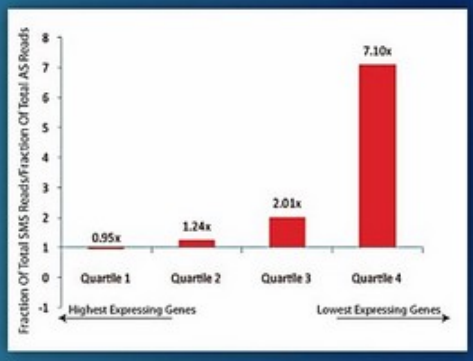
tSMS Yields Greater Sensitivity and More Information

- SeqLL tSMS™ identifies very low-expression transcripts **missed by the PCR-based method**
- **7-fold better detection** of low abundance transcripts
- 5-log linear dynamic range
- Superior tool for biomarker discovery and diagnosis





OPEN ACCESS Freely available online PLoS one

A Comparison of Single Molecule and Amplification Based Sequencing of Cancer Transcriptomes

Lee T. Sam[1,2,3], Doron Lipson[4], Tal Raz[4], Xuhong Cao[1,5,6], John Thompson[4], Patrice M. Milos[4], Dan Robinson[1,5], Arul M. Chinnaiyan[1,5,6,7,8]*, Chandan Kumar-Sinha[1,5]*, Christopher A. Maher[1,2,5]*

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tSMS requires Simple Sample Preparation

- Streamlines workflow to minimize manipulation bias and sample loss
  - ✓ Does not utilize PCR amplification
  - ✓ Avoids complex library prep
  - ✓ Less restrictive nucleic acid quality requirements and no spec for GC content
- Molecules of DNA or RNA are prepared for sequencing by:
  - ✓ Standard nucleic acid isolation from any sample type
  - ✓ Shearing/cleaving to appropriate length (20-500bp)
  - ✓ Addition of Poly-A tail
  - ✓ Hybridization to flow cell surface
  - ✓ Sequencing individual strands by synthesis

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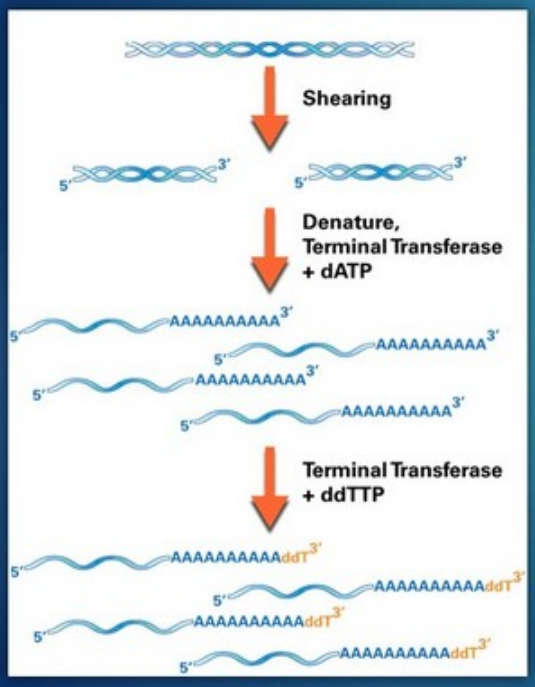
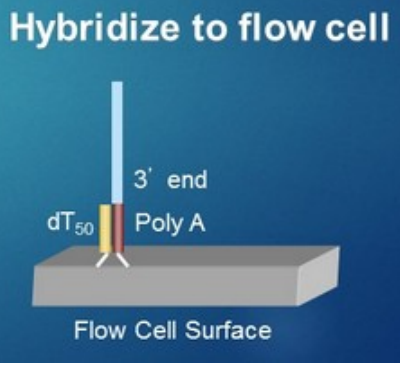
Simple Sample Preparation – DNA





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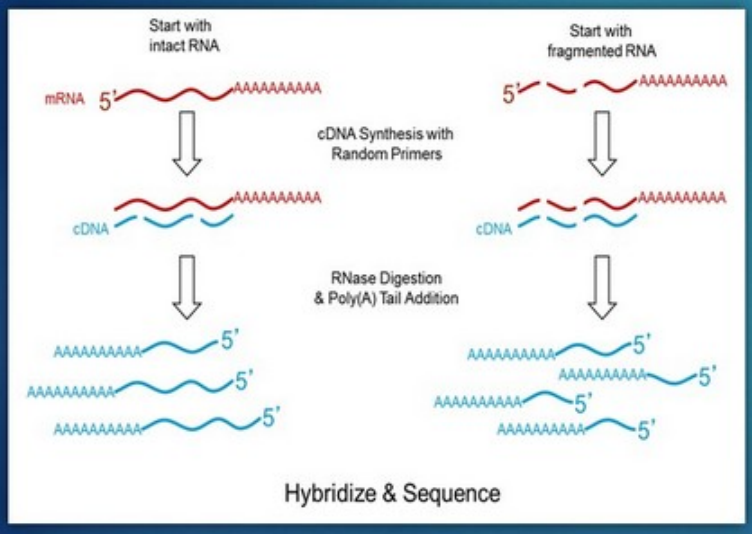
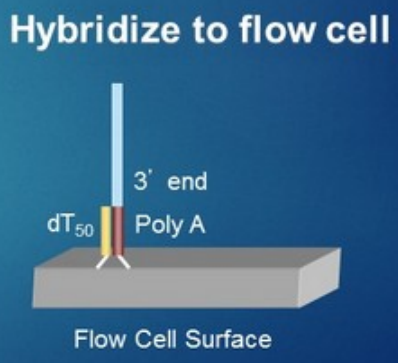
Simple Sample Preparation – RNA





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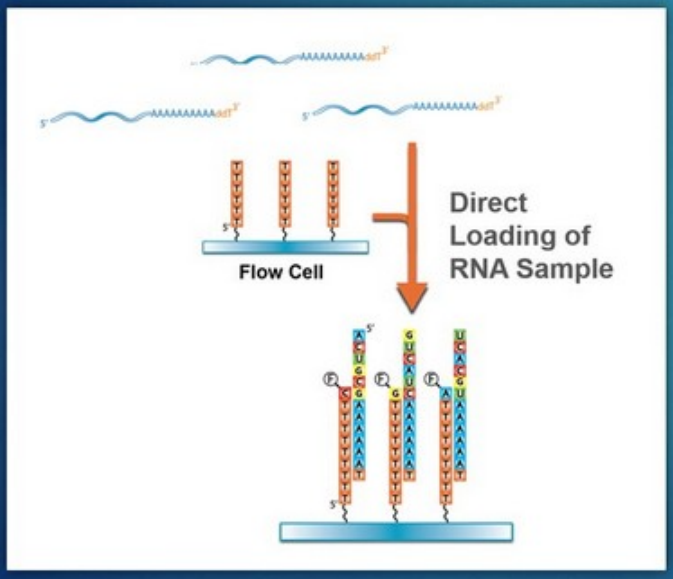
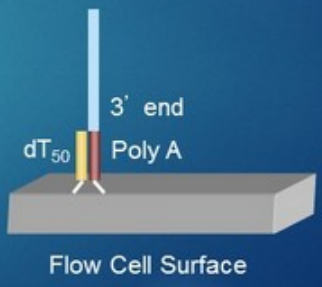
Simple Sample Preparation – Direct RNA Sequencing (DRS®)



Hybridize to flow cell



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tSMS Requires Few Steps During Sample Prep

- SeqLL technology

- Other NGS Options

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The tSMS Advantages – More Accurate, Sensitive & Cost-Effective

- **Rapid**, **scalable**, **low cost** sample preparation
- No amplification step means **higher accuracy, sensitivity** and **predictive value**
- **Picogram** DNA/RNA material yields millions of sequence reads
- **Direct RNA sequencing** is first developed on SeqLL platform
- **Direct capture** allows analysis of a set of target genes with minimal sample prep and high depth of coverage

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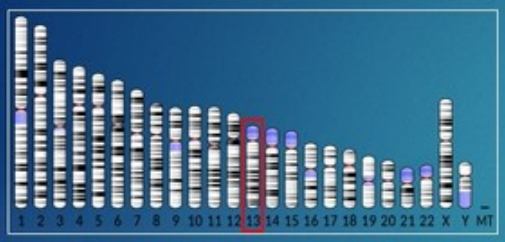
tSMS Application Areas and Customers



Biomarker Discovery

Drug Discovery

Precision Medicine

MASSACHUSETTS GENERAL HOSPITAL

GW School of Medicine & Health Sciences

華僑大學 HUAQIAO UNIVERSITY

VE RI TAS

RIKEN Institute 理化学研究所 RIKEN

מכון ויצמן למדע WEIZMANN INSTITUTE OF SCIENCE

The Jackson Laboratory

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NGS Market Opportunity

DNA

CAGR 21.7%

RNA

CAGR 20.4%

Addressable Market Opportunity

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Representative NGS Market Landscape

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SeqLL Revenue Generation

- Sequencing Systems
- Custom Solutions
- Consumables

- Sequencing Services
- Custom Applications
- Bioinformatics Services

- R&D Grants
- Research Projects
- Strategic Partnerships

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Management Team

- **Daniel Jones – CEO, President & Co-Founder** – 15 years in biotechnology sector, including 7 years at Helicos BioSciences developing applications for the tSMS technology platform. Co-inventor of Direct RNA Sequencing (Nature, 2009) and Single-Molecule Decoding of Combinatorially Modified Nucleosomes (Science, 2016). Mr. Jones has worked at U.S. Genomics on the development of their Trilogy 2020 Single Molecule Analyzer and Direct miRNA assays and at Exact Sciences on ColoGuard, a non-invasive, FDA-approved molecular diagnostic for colorectal cancer. Mr. Jones serves on the Board of Directors.
- **John W. Kennedy, MBA – CFO** – Finance executive with 34 years experience in finance and management. Worked at The Federal Reserve Board, Peat Marwick Mitchell (KPMG), Morgan Stanley & Co., and D.H. Blair & Co. Extensive investment banking expertise especially in small-caps, including roles as CFO & COO, and Managing Principal for US Broker-Dealers.
- **Erik Volke – Director of Operations** – Expertise in Manufacturing, Quality Assurance, and R&D. He has over 16 years' experience in manufacturing biotechnology and medical device instrumentation at Affymetrix, Helicos Biosciences, Life Technologies and T2 Biosystems where he has held manufacturing and quality management positions at both start-up and established FDA regulated ISO 13485 environments.
- **Abhijeet Shinde, MS – Director of Engineering** – Brings over 12 years' experience in developing biotechnology and medical device instrumentation, and developing products from concept to commercialization in FDA regulated ISO 13485 environments. More than 7 years of direct experience with single molecule sequencing at Helicos Biosciences where he lead system integration efforts.
- **William St. Laurent, Chairman , Investor and Co-Founder** – Founder of numerous companies in diverse economic sectors. Mr. St. Laurent has over thirty years of experience in leading growth companies, developing and executing strategy, including building businesses from the ground up. Serves on the Board of Directors of the St. Laurent Institute and Genomic Diagnostic Technologies, both focusing on technologies in Systems Biology. Mr. St. Laurent is the Chairman of the Board of Directors.

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Case Studies – Summary of tSMS Applications

- Identified biomarkers used as a gene panel for pancreatic cancer screen test
- Identified biomarkers used as a gene panel for CAD Risk Assessment
- Custom implementation of BRCA1 mutation detection and identification
- Effective information generation from degraded FFPE samples
- Pathway changes identified by high-sensitivity differential gene expression analysis

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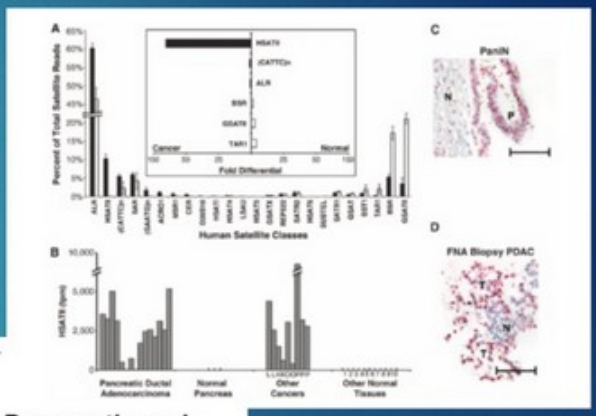
Case Study #1 – Screen Test for Pancreatic Cancer

- HSATII Satellite Overexpression for early detection of Pancreatic Cancer
- Discovered using tSMS technology
- Detectable ONLY with single molecule sequencing technology



PNAS

CrossMark

Pericentromeric satellite repeat expansions through RNA-derived DNA intermediates in cancer

Science. 2011 February 4; 331(6017): 593–596. doi:10.1126/science.1200801.

Aberrant Overexpression of Satellite Repeats in Pancreatic and Other Epithelial Cancers

David T. Ting[1,*], Doron Lipson[2], Suchismita Paul[1], Brian W. Brannigan[1], Sara Akhavanfard[1], Erik J. Coffman[1], Gianmarco Contino[1], Vikram Deshpande[1], A. John Iafrate[1], Stan Letovsky[2], Miguel N. Rivera[1], Nabeel Bardeesy[1], Shyamala Maheswaran[1], and Daniel A. Haber[1,†]

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Case Study #2 – Diagnosis of Coronary Artery Disease

Heart Attack?
Acid Reflux?
Pulmonary?
Neurological?
Muscular?

CT Angiogram or Nuclear Stress Test

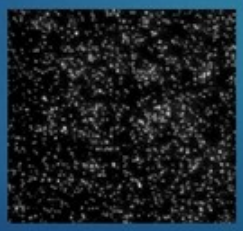
$$$

10%

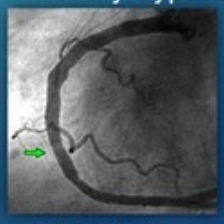
90%

Stent Placement or Coronary Bypass

Other diagnosis



Can we find gene expression changes that accurately predict CAD?



Blocked Artery

Open Artery

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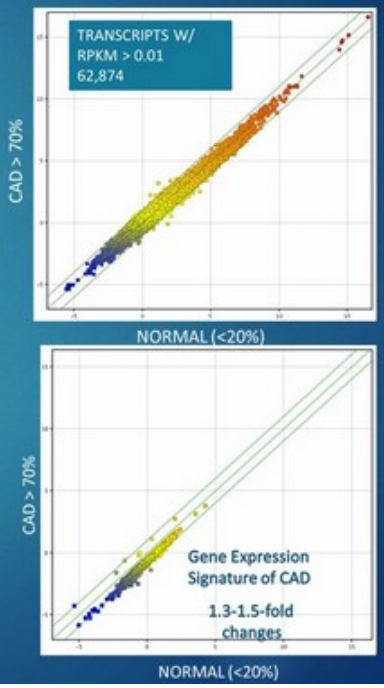
Discovery of Novel Biomarkers

Detect signals not resolved by other NGS platforms

- Genes with 1.3 to 1.5 fold change identified and investigated
- Panel of 7 transcripts identified as highly predictive risk markers
- Diagnostic assay for clinical use under development



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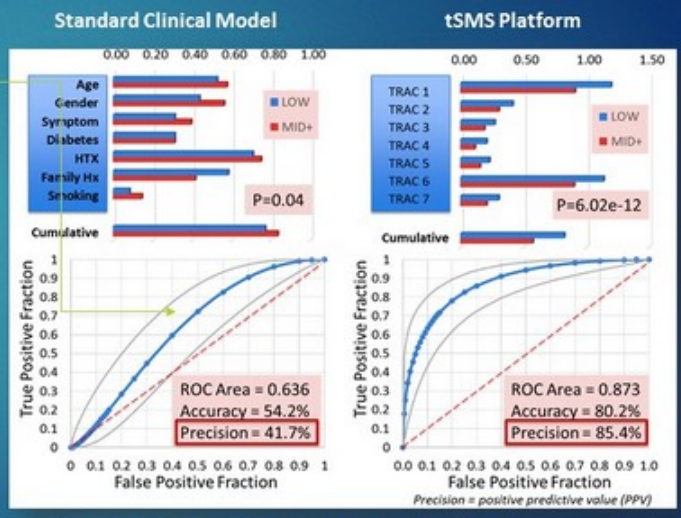
tSMS Outperforms the Clinical Model

- Standard of care clinical model based on 7 indicators has very low positive predictive value **(41.7%)**
- tSMS platform based on 7 transcripts has a far superior positive predictive value **(85.4%)**



Graphs courtesy of Dr. Timothy A. McCaffrey, George Washington University

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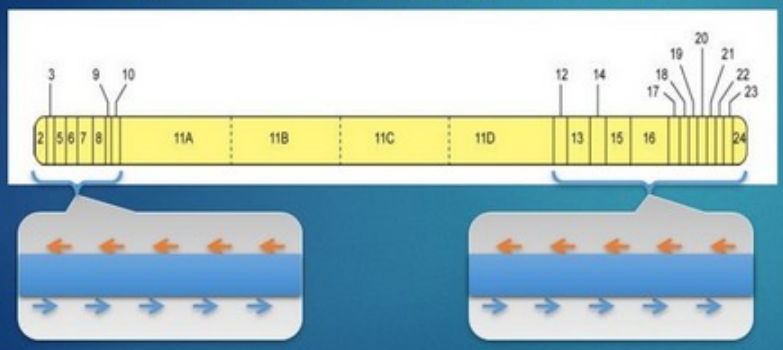
Case Study #3 – Direct Capture Sequencing (BRCA1)

Direct Capture Oligos Spanning BRCA1 Gene



- Capture primers are designed to span regions of interest in one or more genes
- Primers are deposited onto flow cell surface
- Isolated DNA/RNA is loaded directly onto flow cell without further manipulation
- Captured sequences are sequenced by synthesis

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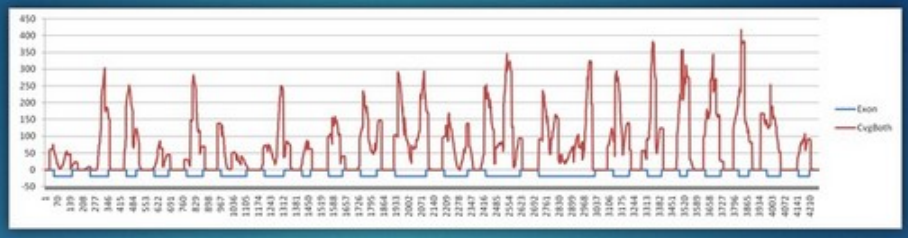
Direct Capture Sequencing – BRCA1

Deep Coverage of Targeted Regions

BRCA1



- Deep coverage achieved in target regions (exons)
- Absence of intronic reads demonstrates specificity of capture
- Depth of coverage allows unambiguous SNP calling

Oligos

Reads

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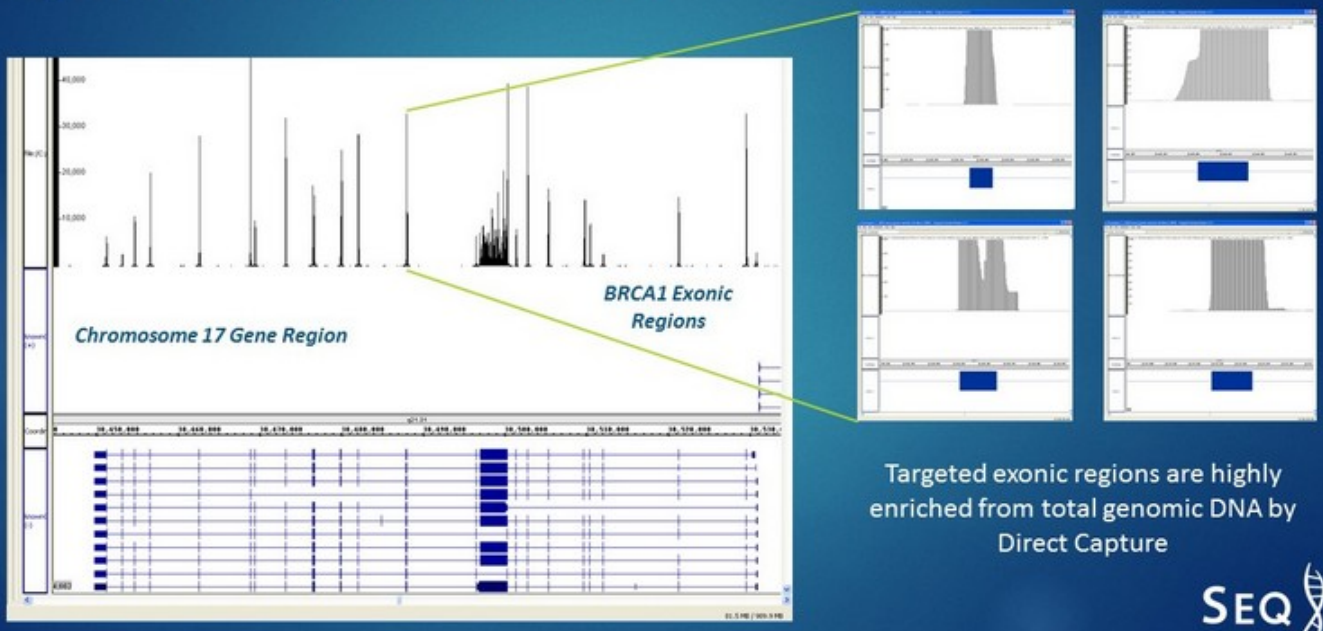
Direct Capture Sequencing – BRCA1

Target Enrichment from Genomic DNA



Targeted exonic regions are highly enriched from total genomic DNA by Direct Capture

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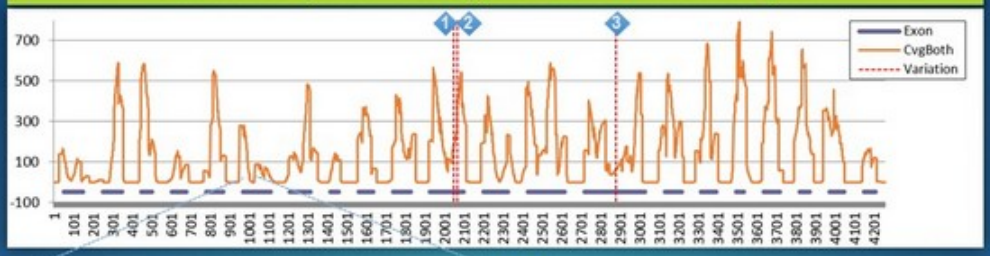
Direct Capture Sequencing – BRCA1

Successful Proof-of-Principle

Excellent Sequence Coverage Across BRCA1 Gene Regions



Accurate Sequence Readout

97% covered with 99.995% accuracy

Accurate Clinical Information

1. T → C Heterozygous Substitution
   Known benign polymorphism
2. C → G *BRCA1* Mutation
   Known disease causing mutation
3. A → G Heterozygous Substitution
   Known benign polymorphism

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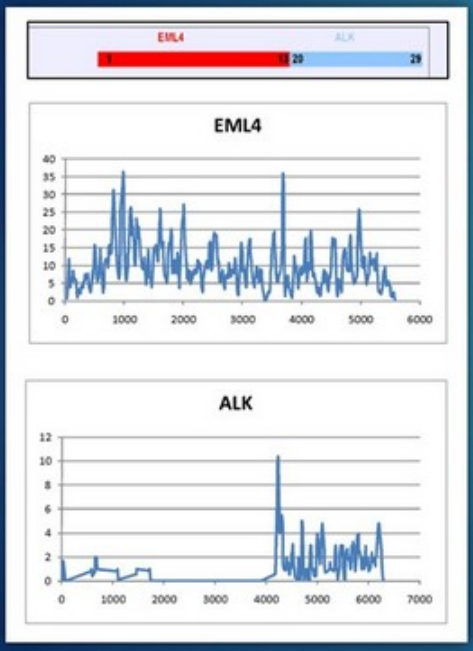
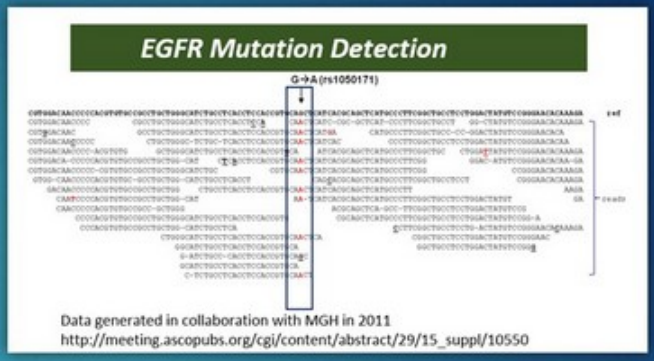
Case Study#4 – FFPE-RNA Cancer Diagnostics





- RNA-Seq detects known gene fusions, SNPs, and mutations in NSCLC.
- SeqLL short read platform is optimal for sequencing of degraded FFPE samples.
- Potential to unlock 1000s of clinical specimens for R&D and future diagnostics.

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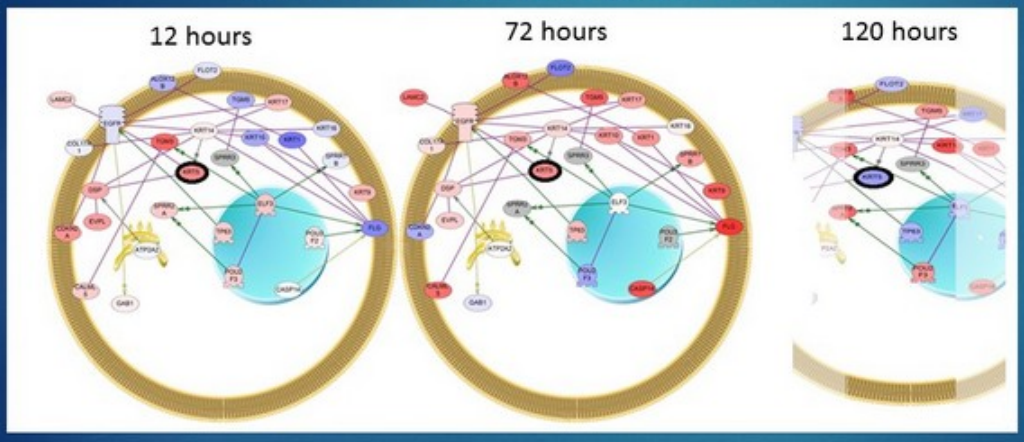
Case Study #5 – Drug Mechanism of Action Analysis

Epidermis development gene subnetwork



- Transcriptome profiling identified drug activity on genes and pathway(s) related to wound healing
- Time course demonstrated that cell motility is increased by drug, which facilitates wound healing

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Summary of Applications & Case Studies

Pharmacogenomics and Biomarker discovery

- Clinical Trial Screening Biomarkers
- Patient Stratification
- Companion Diagnostics

Microbial Analyses

- Microbiome Sequencing
- Antimicrobial Resistance Detection/Monitoring
- Food Safety Testing
- Forensics

Precision Medicine

- Early Disease Detection/Diagnosis
- Infection/Inflammation Differentiation
- Direct Capture Gene Sequencing
- FFPE Sample Analysis
- Cell-free DNA and RNA

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Summary of tSMS Technology

- A superior tool for biomarker discovery, diagnostic development and sample analysis
- Unique features open up new capabilities not possible with other NGS technologies
  - Unsurpassed accuracy and reproducibility of molecule counting
  - Enhanced signal to noise allows identification of subtle gene expression signatures detectable on other systems
  - Lack of amplification and library prep produce the most unbiased read of the sample available in the industry today
  - Low sample prep costs and simplified workflow save time and money
  - Capable of generating data from short and degraded samples
- Applications in a wide range of human disease areas, microbiome analysis, safety testing, forensics, clinical trial patient stratification and more

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Contact Info

WallachBeth Capital LLC
Harborside Financial Center Plaza 5
185 Hudson Street, Suite 1410
Jersey City, NJ 07311

T: 646.998.7602
F: 212.495.0270
cap-mkts@wallachbeth.com

SeqLL Inc
317 New Boston St
Suite 210
Woburn MA 01801

T: 781.460.6016
dan@seqll.com
jwkennedy@seqll.com