

The Leader in Whole Human Genome Sequencing

March 2012





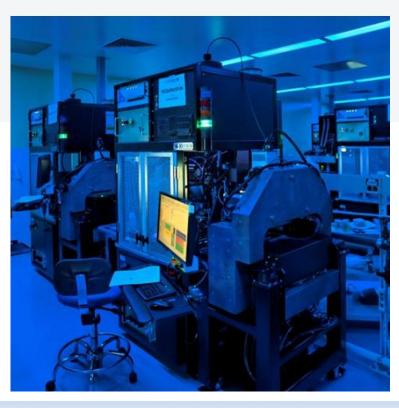
This presentation contains forward-looking statements about Complete Genomics, Inc. including, with respect to our future genome sequencing capacity, future market size, and number of genomes sequenced. Our actual results could differ materially from those discussed due to a number of factors, including but not limited to the ability of our technology to achieve and sustain sufficient market acceptance, the growth of markets for analysis of genetic variation and biological function, the shift of these markets to whole human genome sequencing, our ability to significantly increase the production capabilities of our genome sequencing service, our ability to convert backlog orders into revenue, and our ability to manage our rapid growth. Additional risks and uncertainties are described more fully in the Risk Factors in our Form 10-K and Form 10-Q filed with the Securities and Exchange Commission. We are providing this information as of the date of this presentation and do not undertake any obligation to update any forward-looking statements contained in this document as a result of new information, future events or otherwise.

The Leader in Whole Human Genome Sequencing



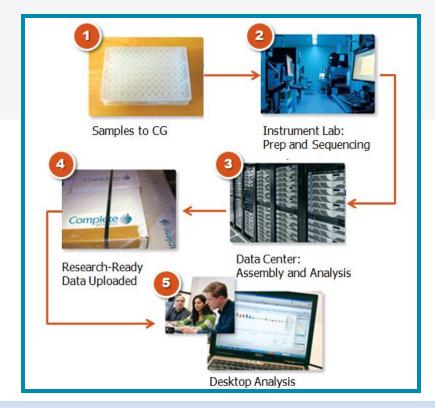
Proprietary Sequencing Technology

Designed and Optimized for Whole Human Genome Sequencing Quality, Cost and Scale



Outsourced Business Model

A Turnkey Service Enabling Customers to **Outsource** WGS – Samples In, **Research Ready Data** Out



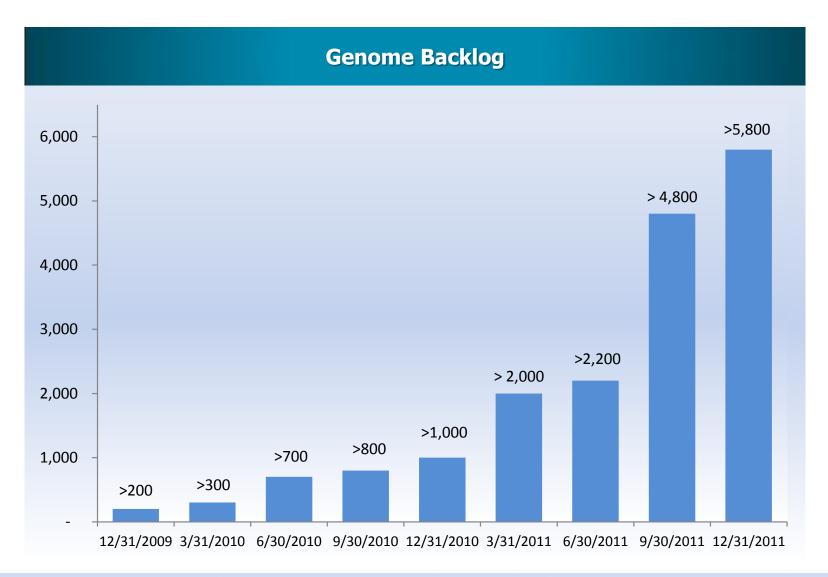




Year Ending December 31, 2011		
Revenue	\$19.3M	
Operating Loss	\$69.3M	
Cash	\$83.1M	
Debt	\$23.3M	

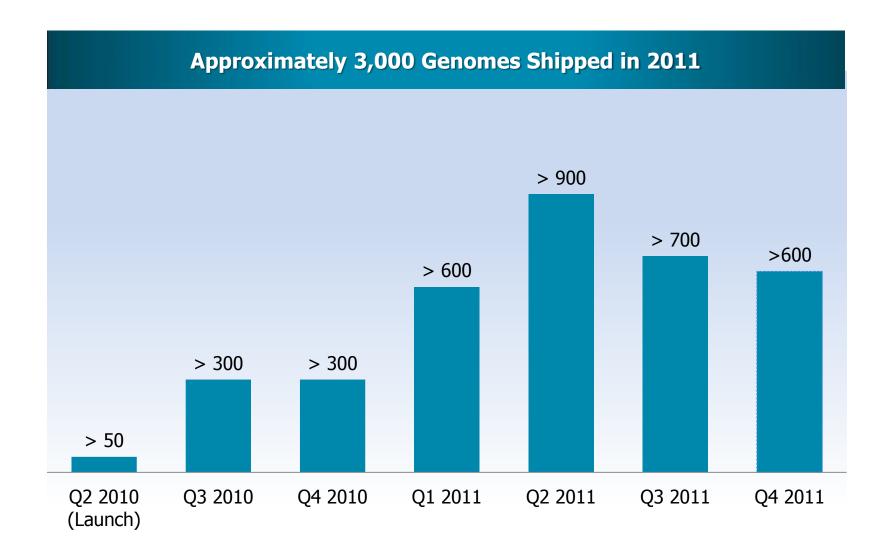












Diverse Base of 125+ Customers



Academic/ Government

























Academisch Medisch Centrum

Universiteit van Amsterdam







































Cancer

- NCI: pediatric cancer (TARGET)
- Genentech: Hepatitis B Virus (HBV) infection and HCC
- AMC: Neuroblastoma

Mendelian Diseases/ De Novo Mutations

- ISB: Miller's Syndrome
- U of Arizona: Infantile Epileptic Encephalopathy
- Erasmus: Craniosynostosis

Genomic Variation and Disease

- T2D GENES: Type II Diabetes risk in families
- Stanford: Genetic Determinants of Diabetes Risk
- Scripps Health: Clinical Annotation of Novel Variants (Cypher)

Translational Medicine

- Inova Health System: Pre-term Delivery Study
- Mayo Clinic: Translational genomics for guiding patient care
- USTW: Hypercholesterolimia





Accuracy	99.999%
Median Genome Read Coverage >10X	>98%
% of Genome called	>96%
% of Exome called	>97%

Note: Data for genomes shipped in Q42011.

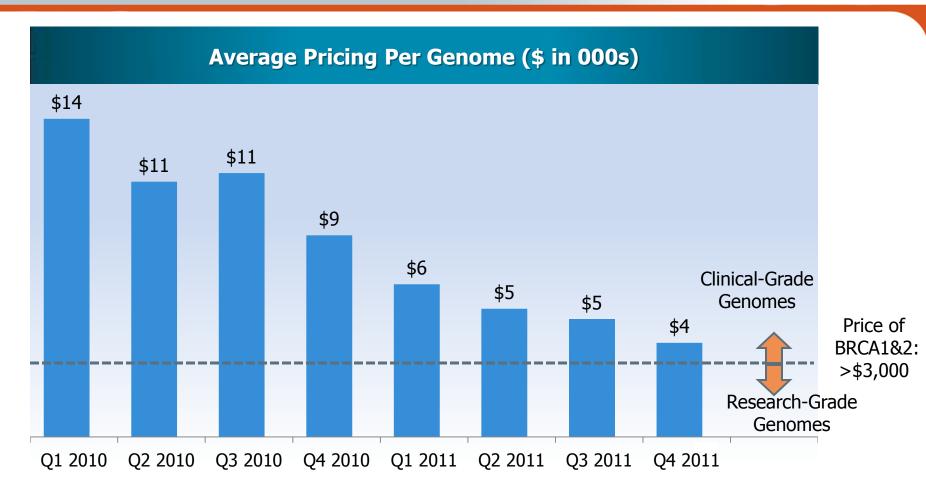




Q4 2011 Median Turn-Around Time	72 days
End Q1 2012 Capacity	~1000 Genomes Per Month
End Q4 2012 Capacity	~2000 Genomes Per Month



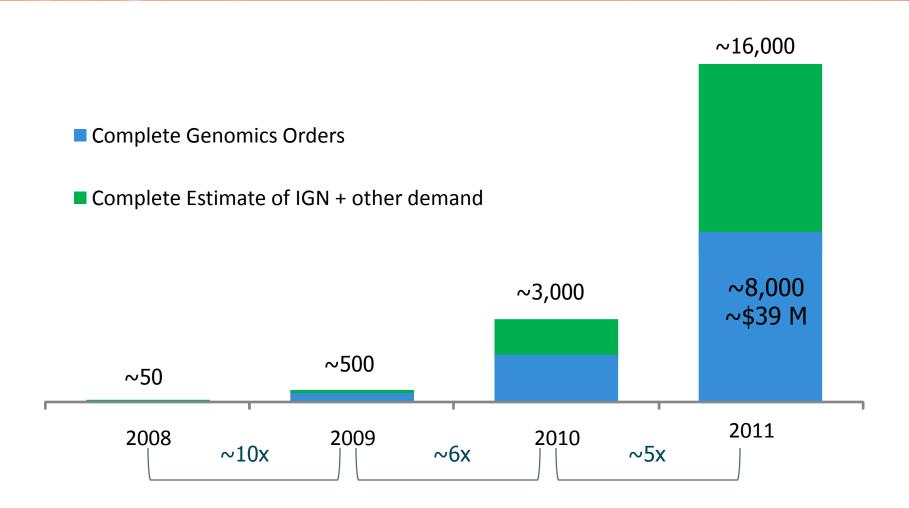




^{* \$5}K for orders less than 50, \$4K for orders greater than 50, with further discounts for large orders



Estimated Whole Human Genome Demand



Sources: Company estimates, Illumina press releases, Nature: "The Genome at Ten", Nature: "Genomes by the Thousands"

Emergence of the Outsourced Whole Genome Sequencing Market



Small Projects and **Small** Infrastructure

Thousands of academic cores & commercial labs worldwide

 Growing market, wellserved by new and existing instruments









Large Projects but **Small** Infrastructure

Targeting ~1,000 top human disease research labs

- Not served by instrument vendors
- Genome center collaborations or inferior research methods (SNPs, exomes, ...) are unattractive
- Three Key Requirements: Low Cost, High Quality and Fast Delivery at Large Scale







Large Projects and **Large** Infrastructure

Large Genome Centers: Broad, WashU, Baylor, Sanger, ...

 Traditional leaders, now shrinking (NHGRI funding)



illumına*/HiSeq

Uniquely Positioned Among CHGS Outsourced Service Providers



Defining Characteristics

Commercial Implications



Proprietary Platform

- Only focused and optimized WGS technology
- Only automated factory production model

 Achieves superior performance (quality, cost and scale) for WGS



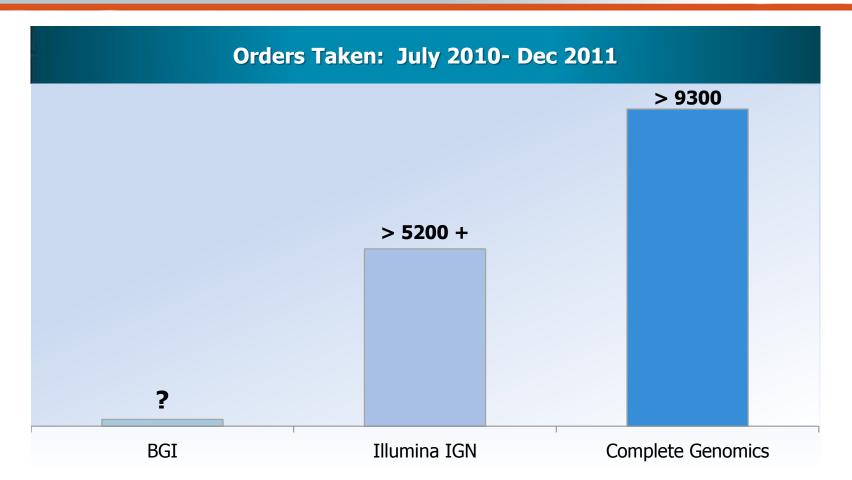
 General purpose instruments designed for wide range of sequencing applications Lower performance for WGS than optimized offering



 Low-cost labor and third-party general-purpose instruments Margin stacking severe competitive disadvantage

Capturing Significant Share of the Outsourced WGS Market





Source: Illumina announcements from 05/09/11, 7/26/11, 8/3/11, and 10/25/11 and 1/10/12

Published Comparison Paper: "Complete More Accurate Than Illumina"



nature biotechnology (18 Dec 2011)

Performance comparison of whole-genome sequencing platforms

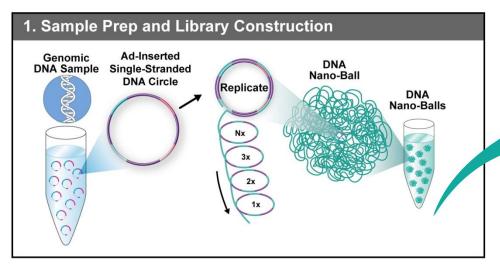
Hugo Y K Lam^{1,8}, Michael J Clark¹, Rui Chen¹, Rong Chen^{2,8}, Georges Natsoulis³, Maeve O'Huallachain¹, Frederick E Dewey⁴, Lukas Habegger⁵, Euan A Ashley⁴, Mark B Gerstein^{5–7}, Atul J Butte², Hanlee P Ji³ & Michael Snyder¹

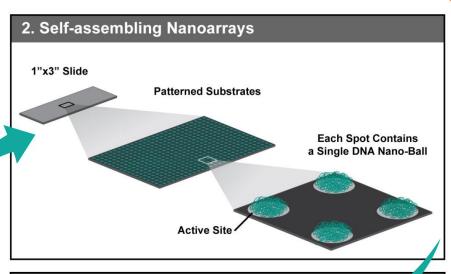
Lam/Snyder: "Based on the transition/ transversion ratio and Sanger sequencing,CG appears to be more accurate, but also slightly less sensitive."

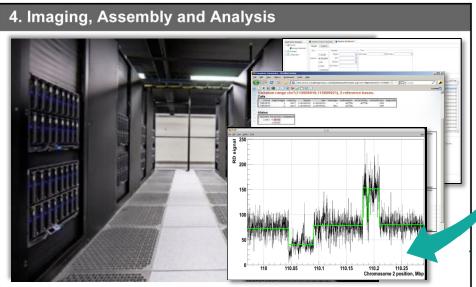
Complete: Based on Sanger validation, Complete has **1/50th as many errors** as Illumina, and is **more sensitive** (finds ~48,000 more true SNPs) than Illumina

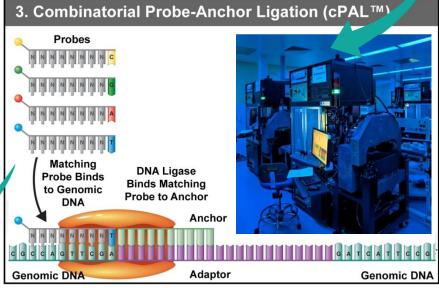
Technology: Highly Scalable WGS and Cloud-Based Delivery





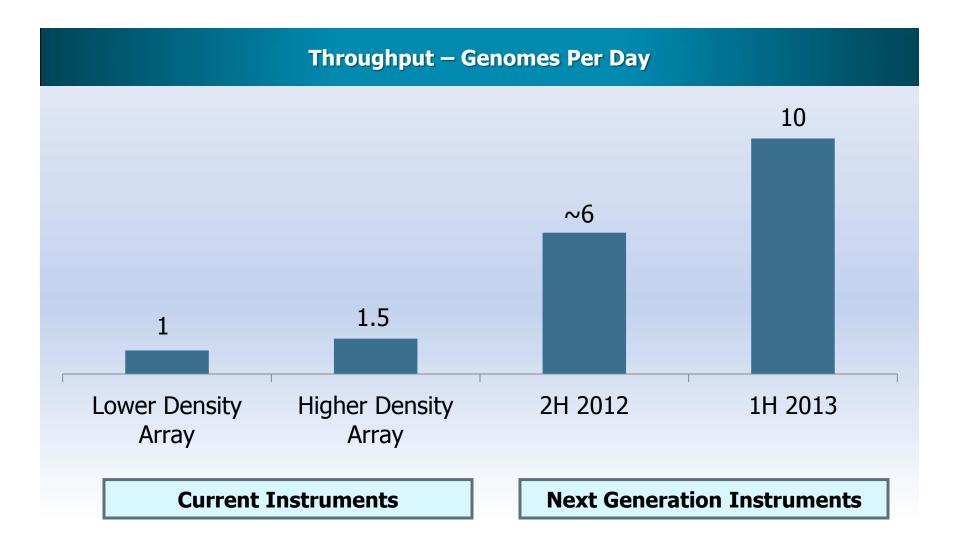






Driving Up Scale: Projected Instrument Throughput Increases

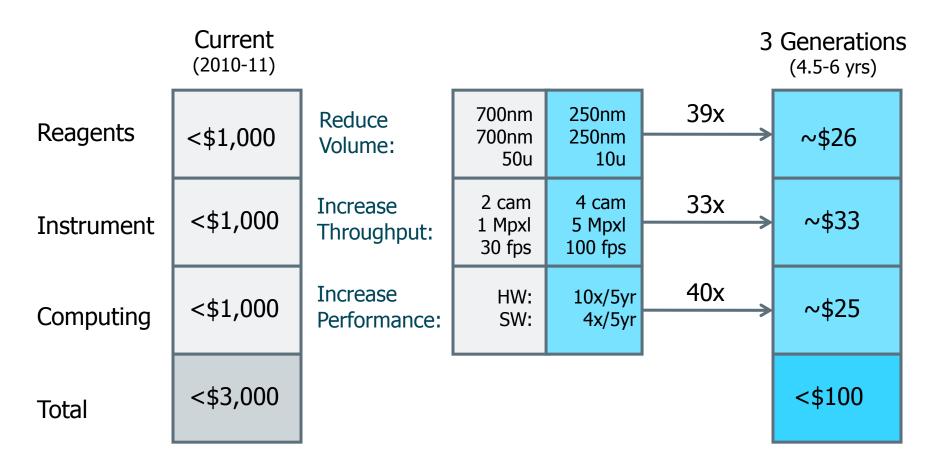




Driving Down Cost: Long-Term Cost of Core Technologies



Continued Engineering Improvements Reduce Sequencing Costs



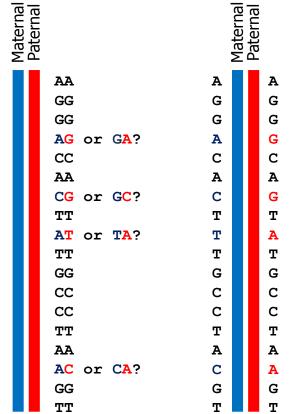
Sample Prep Costs Reduced by Automation and Multiplexing Large Batches Other Costs (QC, Validation, Sample Handling, Analysis) Will Dominate

Driving Up Quality: Long Fragment Read Technology









Patented Method

- Fragment to ~100,000 base fragments
- Tag (bar code) each fragment
- Chemistry: all fragments the same (low cost)
- Informatics: analyze each fragment separately

Advantages of Virtual 100Kb Reads

- Separates ("phases") maternal and paternal chromosomes
- Resolved distributed repeats (e.g. pseudogenes)

Achieves Clinical-Quality Genomes

 Clinical-quality genomes will be phased (required to understand multiple mutations)





Translational Medicine

- Large patient studies to validate clinical utility
- Save WGS data, analyze new variants as knowledge grows

Human Genomics Research

- \$4.6B (8.8% CAGR)
- \$700M Human "Next Gen"
- WGS Replaces Partial Methods

Pediatric Diagnostics

- >200K Newborns on "Diagnostic Odyssey"
- WGS as Complete Genomic Screen

Cancer Pathology

- 5M New Tumors Annually
- WGS to Select Therapies

Personalized Medicine

- 13M+ Newborns Annually
- WGS as Universal Diagnostic

Sources: Scientia Advisors 2009; CISCRP.org, BCC Cancer Profiling Report 2010; AACR Cancer Statistics, American Cancer Society: Global Cancer Facts & Figures 2007, US Census Bureau





Long-Term Business Model Target		
Gross Margins	65-70%	
R&D as % of Revenue	20-25%	
SG&A as % of Revenue	20-25%	
Operating Margins	20-25%	
Annualized Revenue Breakeven Targets		
Gross Margin	\$40-50M	
Operating Margin	\$140-160M	

Investment Highlights



Compelling Customer Value

 Combines Ease of Outsourcing with Quality, Cost, and Speed of Specialized Technology and Factory Automation

Proven Customer Adoption

 Approximately 8,000 Genomes Ordered in 2011 and Over 125 Customers Since Beginning Commercial Ops

Strong Competitive Position

 Leader in Outsourced WGS, Sustainable Through Focusing Strategy and Resources 100% on Outsourced WGS

Efficient Production Model

Deploying in 2012 new 6-10 genome/day instruments;
 50 Instruments @ 10 Genomes/Day = 150K Genomes/Yr

Large Expansion Opportunities

• Expand within \$4.6B Research Market and into Much Larger Clinical Markets, Including Cancer Pathology and Diagnostics

Sources: Scientia Advisors, 2009; BCC Cancer Profiling Report, 2010



