March 16, 2011

HEALTHCARE/LIFE SCIENCE TOOLS & DIAGNOSTICS

Stock Rating:

OUTPERFORM

12-18 mo. Price Target	$13.00
GNOM - NASDAQ	$7.14

3-5 Yr. EPS Gr. Rate	NM
52-Wk Range	$9.00-$6.60
Shares Outstanding	25.9M
Float	17.0M
Market Capitalization	$185.0M
Avg. Daily Trading Volume	91,731
Dividend/Div Yield	NM/NM
Fiscal Year Ends	Dec
Book Value	NM
2011E ROE	NM
LT Debt	$0.2M
Preferred	NM
Common Equity	$74M
Convertible Available	No

EPS Diluted	Q1	Q2	Q3	Q4	Year	Mult.
2010A	--	--	(21.87)	(0.69)	(13.60)	NM
2010A	--	--	(21.87)	(0.69)	(13.60)	NM
2011E	(0.56)	(0.56)	(0.51)	(0.33)	(1.95)	NM
2012E	--	--	--	--	(0.70)	NM

Revenue ($/mil)	Q1	Q2	Q3	Q4	Year	Mult.
2010E	--	--	--	--	9.4	13.0x
2010E	--	--	--	--	9.4	13.0x
2011E	5.0	5.7	9.4	13.1	33.2	3.7x
2012E	--	--	--	--	90.0	1.4x

Complete Genomics, Inc.

We Believe in the Service Model; Initiating at Outperform

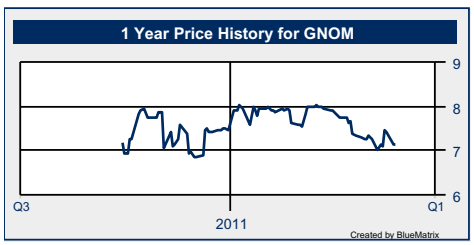
SUMMARY

We are initiating coverage of GNOM with an Outperform rating and $13 price target. GNOM has developed a proprietary, innovative sequencing platform including robust bioinformatics tools in order to provide researchers with a complete, outsourced human genome sequencing service. Despite a rapidly expanding installed base of NGS instruments, we believe demand from the research community and later from the clinical community will continue to outpace the total market sequencing capacity, thus creating an important niche for service providers like GNOM. Our $13 target price assumes no terminal growth on an estimated EBITDA of $109M in 2022.

KEY POINTS

- **High quality sequence delivered.** Initial data provided by GNOM and early users have demonstrated the company has produced high quality sequence data, validating the platform. For data driven scientists, we believe quality supersedes cost. Thus, we believe GNOM has the tools in hand to drive utilization.
- **The NGS market needs service providers.** We believe demand will outpace NGS capacity for these reasons: 1) despite rapid expansion, the NGS market is capacity constrained; 2) the fully loaded sequencing cost for a genome is estimated to be ~$30,000 (NHGRI.gov); and 3) informatics remain a bottleneck at all but the most advanced genome centers.
- **Clinical potential a call option.** NGS is applicable in almost any clinical setting. We believe service providers that specialize in decoding human genomes will be more appropriately positioned to capture this market when it develops in terms of volume and data consistency. Clinical expansion is not included in our estimates.
- **Risks Include:** 1) competition from the high throughput NGS installed base, 2) uncertainty over research funding, 3) technology obsolescence, 4) competition from other service providers, 5) clinical market perhaps taking time to develop, and 6) financing risk.

Stock Price Performance



Company Description

Complete Genomics is a life sciences tools company that has developed and commercialized what is arguably the most powerful DNA sequencing platform in the industry. GNOM operates on a service model, offering its NGS technology as an innovative, end-to-end, outsourced service to provide customers with data that is immediately ready to be used for genome-based research.

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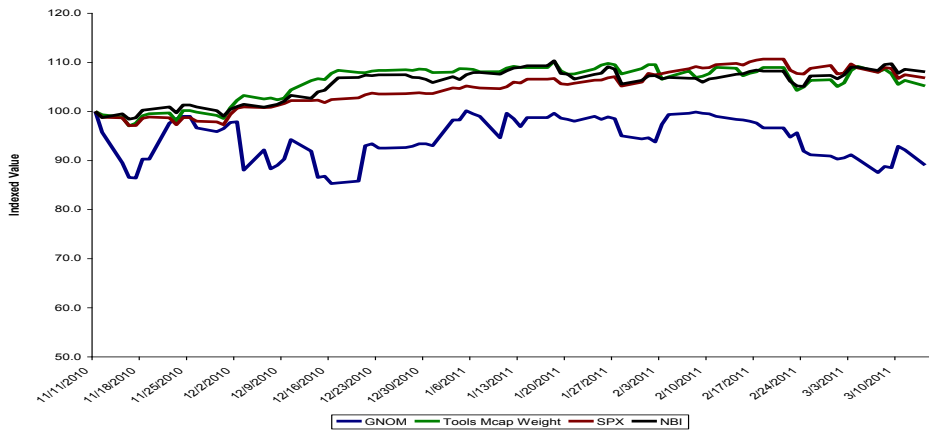
Investment Overview

We are initiating coverage of GNOM with an Outperform rating and $13 price target. GNOM has developed a proprietary, innovative sequencing platform including robust bioinformatics tools in order to provide researchers with a complete outsourced human genome sequencing service. Initial data provided by GNOM and early users have demonstrated the company has produced high quality sequence data, validating the platform. Despite a rapidly expanding installed base of NGS instruments, we believe demand from the research community and later from the clinical community will continue to outpace total market sequencing capacity, thus creating an important niche for service providers like GNOM. Our $13 target price assumes no terminal growth on an estimated EBITDA of $109M in 2022.

Exhibit 1: GNOM Performance Since IPO vs Tools Index



Source: FactSet Data, Oppenheimer & Co. estimates
Note: These results cannot and should not be viewed as an indicator of future performance.

With this report, we are expanding our coverage of medical devices, tools and diagnostics. See our initiations of Gen-Probe, Sequenom, Myriad Genetics, Cepheid, Affymetrix and Pacific Biosiences, also released today.

Investment Positives

The Proof Is in the Pudding: GNOM Delivers High Quality Genomes

Miller Syndrome Study. Scientists from the Institute for Systems Biology led by sequencing star Leroy Hood published results (April 2010) in the journal *Science* from sequencing a family of four, of whom the two offspring have Miller Syndrome (a rare genetic condition characterized by craniofacial malformations) and primary ciliary dyskinesia (an inherited disorder that affects the respiratory system). In comparison to whole genome sequencing of a single person, sequencing a family allows for the identification of recombination events as well as inheritance analysis. The family of four was sequenced at an average coverage of 40x with a call rate of between 85% and 92%. The use of inheritance analysis allowed researchers to narrow the list of potential causative genes for both disorders. The strength of the GNOM sequencing platform enabled this study and illustrates the future potential of family sequencing to help elucidate discovery of the genetic causation of disease inheritance. In January 2011, the Institute for Systems Biology signed a new agreement calling for the sequencing of 615 complete human genomes, further validating the strength of the data.

Genentech Lung Cancer Study. In May 2010, Genentech researchers published results in the journal *Nature,* from a study comparing paired genomes sequenced from a lung cancer patient (tumor and normal tissue). Both genomes were sequenced at high coverage (60x tumor, 46x normal tissue) and exhibited a substantial degree of variation including more than 50,000 SNPs (single-nucleotide polymorphisms),. The researchers validated 530 of the variants which included a well known mutation in the KRAS gene and 43 large scale structural rearrangements. The authors noted a mutational pattern which appeared to select for mutations in non expressed genes and against those within expressed genes as well as mutations in the promoter regions of genes. This study and similar studies have begun to illustrate the complexity of the variation in tumor genomes and also how continued investigation of tumor normal pairs is necessary to uncover mutational patterns and hopefully disease biomarkers.

AGBT 2011. Dr. Tim Yu (Harvard Medical School) presented data from his experience with Complete Genomics sequencing service at the 2011 Advances in **Genome** Biology and Technology (AGBT) meeting. Dr. Yu's research has focused on autism. Initial work to discover a genetic link used GWAS arrays with 500,000 SNPs and then the group moved to targeted sequencing. Targeted sequencing evolved into whole genome sequencing at which point they commissioned GNOM for 40 genomes. The major selling point for Dr. Yu's group was the fact GNOM provides ready to use data. On average, GNOM delivered genomes at 63x coverage with nearly 96% of bases called. In the end, Dr. Yu did not discover **the** autism gene; however, the whole genome sequencing studies gave a better picture of the genetic causes of the disease and even identified some common mutations among family members with autism.

60 Genome Data Release. To further illustrate the level of data quality GNOM provides, the company announced in conjunction with the 2011 AGBT meeting, the release of 60 high quality human genomes to the research community. On average, the genomes have 55x coverage with more than 12.2 terabases of total data with a call rate of 97%, including 96% of each exome. SNPs were detected with 00.93% concordance to the Infinium HapMap data subset. The company believes this will complement the most recent 1000 genome project data release which includes 6 high coverage and 179 low coverage genomes. Currently, 40 genomes are available for download via the BioNimbus cloud with the remaining 20 to be made available by the end of March 2011. On the 4Q10 earnings call, GNOM indicated that data from this release has been downloaded by 350 researchers already. We believe that this level of interest is extremely positive for GNOM and are hopeful will translate into new customers.

NGS Is the Fastest-Growing Life Science Tools Market

We estimate the next-generation sequencing market produced sales of ~$740M (+50% year/year) in 2010 and that it will grow at a 28% CAGR to more than $2.5B in 2015. Near-term growth is being led by a steady stream of new technology launches for the core labs like the PacBio RS as well as the gradual push of NGS into non-core labs by lower priced offerings currently available through Life Technologies (Ion Torrent) and Roche (GS Junior) and in 2H11 from Illumina (MiSeq).

Exhibit 2: NGS Market Expectations Snapshot

	2010	2015E	Growth ('10-'15)
High Throughput Installed Base	2,173	4,307	**14.7%**
% of Market	*95.6%*	*31.4%*	
High Throughput Revenue (000s)	**$718,172**	**$1,225,148**	**11.3%**
% of Revenue	*97.4%*	*48.3%*	
Mid-Low Throughput Installed Base	100	8,801	**144.9%**
% of Market	*4.4%*	*64.2%*	
Mid-Low Throughput Revenue (000s)	**$19,510**	**$1,022,260**	**120.7%**
% of Revenue	*2.6%*	*40.3%*	
3rd Gen Installed Base	0	621	
% of Market	*0.0%*	*4.5%*	
3rd Gen Revenue (000s)	**$0**	**$274,515**	
% of Revenue	*0.0%*	*10.8%*	
NGS Installed Base	**2,273**	**13,699**	**43.2%**
Estimated Penetration into High Throughput Labs	*15.2%*	*91.3%*	
Estimated Penetration into all Labs	*3.5%*	*21.1%*	
LIFE Market Share	*16.0%*	*46.1%*	
ILMN Market Share	*54.3%*	*35.9%*	
PACB Market Share	*0.0%*	*4.5%*	
Other Market Share	*29.7%*	*13.5%*	
Total NGS Revenue (000s)	**$737,682**	**$2,538,163**	**28.0%**

Source: Oppenheimer & Co. estimates

We expect the NGS installed base to grow robustly (a 43% CAGR) between 2010 and 2015, driven by further expansion into high throughput sequencing labs as well as into non-core labs with medium to low throughput sequencing needs. The non-core molecular biology labs (about 50,000 labs globally) represent a completely unpenetrated market opportunity that should greatly accelerate market growth. More important, as the NGS market continues to grow, we believe that the demand for sequencing related services will also grow. Thus, we believe continued growth in the base NGS market will correlate to growth in demand for GNOM's service.

There Is Ample Room for a Service Provider

Despite a rapidly expanding installed base, we believe demand from the research community and later from the clinical community will continue to outpace the total market sequencing capacity. We estimate that the total global whole genome sequencing capacity was ~75,000 genomes on an annual basis exiting 2010. With upcoming technologic improvements and another strong year of system placements at the high end, we expect the total whole genome sequencing capacity to exceed 300,000 genomes exiting 2011.

Exhibit 3: Estimated High Throughput Whole Genome Sequencing Capacity

	2009	2010	2011E	2012E	2013E	2014E	2015E	2016E
System Capacity (Genomes/yr)								
SOLiD 5500 XL	10,429	18,928	80,404	96,047	107,779	111,690	119,511	119,511
SOLiD 5500	0	0	2,764	6,674	9,281	10,585	10,585	10,585
HiSeq 2000	0	33,763	194,363	483,625	631,906	768,781	894,250	1,008,313
HiSeq 1000	0	0	9,581	38,781	55,891	67,297	73,000	78,703
GAIIx	20,205	21,770	20,596	17,338	13,427	9,516	5,605	2,998
Total 1 Year Fwd Capacity	**30,634**	**74,460**	**307,708**	**642,465**	**818,284**	**967,869**	**1,102,952**	**1,220,110**

Source: Oppenheimer & Co. estimates

While there will exist tremendous sequencing capacity, not all NGS machines will be used to sequence whole human genomes all of the time. We assume that only 50% of the existing sequencing capacity will be used to sequence human samples, and we estimate that only approximately 18% of that capacity will be used to sequence whole human genomes in 2011.

Exhibit 4: Estimated Total Genomes Sequenced (ex-GNOM)

	2009	2010	2011E	2012E	2013E	2014E	2015E	2016E
% Human	50%	50%	50%	50%	50%	50%	50%	50%
% WGS	5%	8%	18%	20%	25%	30%	35%	35%
Installed Base Genomes Sequenced	**766**	**2,978**	**27,694**	**64,247**	**102,286**	**145,180**	**193,017**	**213,519**

Source: Oppenheimer & Co. estimates

We believe there is ample room for service providers within the NGS market, specifically for those dedicated to whole human genome sequencing, for a few reasons: 1) despite rapid NGS growth, the market is still capacity constrained as many core facilities have lengthy wait lists; 2) the fully loaded sequencing cost for a genome is estimated to be ~$30,000 (NHGRI.gov), more than 3x the cost of GNOM sequencing now; and 3) informatics remain a bottleneck at all but the most advanced genome centers.

Exhibit 5: Complete Genomics Revenue Build

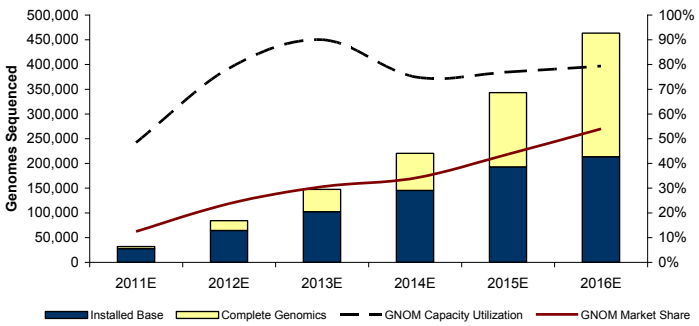
	2010E	2011E	2012E	2013E	2014E	2015E	2016E
Genomes Sequenced	900	3,950	20,000	45,000	75,000	150,000	250,000
Cost per Genome	$10.9	$8.4	$4.5	$3.0	$2.5	$1.5	$1.0
Total Service Revenue ($000s)	$9,786	$33,175	$90,000	$135,000	$187,500	$225,000	$250,000
Growth			*171.3%*	*50.0%*	*38.9%*	*20.0%*	*11.1%*

Source: Oppenheimer & Co. estimates

We believe that the Complete Genomics Sequencing solution solves a number of the issues that researchers that want to sequence whole human genomes face today. From a raw data perspective, we believe GNOM is providing a superior product as the consensus accuracy for delivered genomes is the highest in the industry at 99.999%. On the expense side, the pure cost of the GNOM sequencing service on a per genome basis is more comparable to the cost of the sequencing consumables if researchers were to do the work themselves on today's high throughput NGS platforms. Not to mention, the standard data analysis GNOM provides with completed genomes is the most challenging hurdle to overcome for researchers and also one of the largest cost components. As such, we expect that the task of sequencing genomes, especially more challenging ones such as in tumor samples, will be increasingly outsourced when cost and difficulty is weighed.

We forecast that in 2011, approximately 31,500 whole human genomes will be sequenced and that GNOM will capture 12% of that market. We expect both the number of whole genomes sequenced and the share captured by GNOM to grow substantially along with the rest of the NGS market. Ultimately, the reduction of the cost per genome will drive market expansion. We believe that GNOM will be able to consistently lower the ASP/genome and consequently drive sequencing volume. Our model calls for an ASP of $1,000 per genome in 2016 through the GNOM sequencing service, which we believe drive capture of ~50% of the whole genome sequencing (WGS) market.

Exhibit 6: Total WGS Market (2011E-2016E)



Source: Oppenheimer & Co. estimates

We believe that GNOM has exhibited great progress and most recently indicated that it can deliver 400 genomes per month. In addition, the company has reduced the turnaround time to less than 73 days with the goal of reducing that to less than 60 days by the end of 2011. In addition, the company should substantially expand sequencing capacity with its next generation of instruments which should be in production in 2010. These instruments will be capable of completing 10 genomes per day compared to the 1 per day of current instruments. GNOM has indicated its goal of exiting the year with a $5,000/genome ASP.

Future Potential in the Clinic

NGS is a research tool now. However, the power of the technology clearly expands the scope of utility into the clinic. We point to the growing body of evidence that suggests the evolution of NGS into a clinical tool is happening at a very rapid pace.

1. **LIFE starts First NGS Clinical Trial.** LIFE has an ongoing collaboration with the Translational Genomics Research Institute (TGen) and US Oncology to use NGS in clinical trials to help design new treatment strategies for 14 triple-negative breast cancer patients that have progressed despite multiple treatments.

2. **Prominence at ASCO 2010.** Dr. Daniel Von Hoff, the physician in chief of TGen, won the society's most prestigious award, the David A. Karnofsky Memorial Award and Lecture. During his Karnofsky Lecture, he highlighted his recent work with NGS and how he is using it at TGen to guide diagnosis and treatment plans in order to improve patient outcomes.

3. **GPRO investment in PACB.** In June 2010, GPRO made a $50M strategic investment into then private PACB. The goal of the agreement is for the companies to work collaboratively to develop a diagnostic system based on PACB's single molecule technology.

4. **PACB NEJM Cholera Publication.** In December 2010, PACB scientists along with collaborators from Harvard published a paper in the *New England Journal of Medicine* detailing the use of the PacBio RS to identify the Hatian Cholera outbreak strain.

Collectively, we believe the signs are pointing to the more rapid than expected evolution of NGS into a clinical tool. The next logical step, before NGS becomes a routine clinical diagnostic, would be the incorporation of the technology into the clinical development of drugs and devices. Ultimately, NGS could prove useful in almost any clinical setting, whether it be to help characterize an infective agent or to genotype a malignancy. Using cancer as an example, there are currently ~800 agents in clinical development to treat cancer. This would likely size the clinical trial sequencing market in the $100M range. Looking beyond the clinical trial market and toward cancer diagnosis and treatment, the opportunity is substantially larger. With an incidence of more than 1.5M cancer cases in the US annually and assuming a conservative $1,000 ASP per genome, with two samples per patient needed (tumor and normal tissue), at face value the market for NGS in cancer diagnostics is $3B. Extrapolating the cancer example out to all diseases with a genetic basis expands the clinical NGS market logarithmically. In addition, based on the complexity of the analysis and the difficulty in performing the procedure, we believe service providers that specialize in decoding human genomes will be more appropriately positioned to capture the market from in terms of handling high volume and providing consistent results.

Investment Risks

Competition from the Existing High-Throughput Installed Base

Illumina has dominated the high end of the NGS market and solidified its leadership position with the launch of the HiSeq 2000 in January 2010. Demand for the HiSeq 2000 was consistent through 2010 and appears to be continuing into 2011. We expect that the company's recent investment in manufacturing capacity expansion will lead to continued growth in the installed base. We forecast that the installed base of high-throughput NGS instruments will grow 30% in 2011 and continue to exhibit double digit growth for the next 3 years led primarily by ILMN.

Exhibit 7: High-End Sequencing System Comparison

	ILMN HiSeq 2000	LIFE SOLiD 5500xl	PACB PacBio RS
Cost	$690k	$595k	$695k
Throughput	600Gb/Run*	300 Gb/Run**	35-45Mb/chip****
Cost per Genome	$5,000*	$3,000**	NA
Raw Accuracy	>99%	99.99%***	85-90%
Read Length	100bp x 100bp	75bp x 35bp	~1000bp
Sample Prep	Bridge PCR	Emulsion PCR	SMRTbell Prep/Non-PCR
Sequencing Reaction	Synthesis	Ligation	Single Molecule Synthesis

*2Q11, **2H11, ***with ECC Chemistry, ****run time ~1 hour

Source: Company reports, Oppenheimer & Co. estimates.

ILMN has announced increases to the throughput of the systems to about 600G/run (300G/run, HiSeq 1000) by the spring of 2011 and has indicated the system has the headroom to go beyond 1T/run, which the company has achieved internally. Meanwhile, Life Technologies has not sat on the sidelines and has recently retooled its NGS product portfolio (November 2010). LIFE introduced the 5500 and 5500xl SOLiD Sequencers which are capable of producing 10-15 gb/day and 20-30 gb/day, respectively. In 2H11, LIFE plans to introduce a new chemistry using high density nano-beads that will increase the throughput of the 5500xl to 30-45gb/day. We estimate that the expansion of the installed base and chemistry improvements will increase the annual human genome sequencing capacity of the worldwide installed base to beyond 300,000 genomes. With continued growth in the installed base, we expect this capacity to top 1.2M genomes per year which will compete with service providers in the whole genome sequencing market.

Exhibit 8: Estimated High Throughput Whole Genome Sequencing Capacity

	2009	2010	2011E	2012E	2013E	2014E	2015E	2016E
System Capacity (Genomes/yr)								
SOLiD 5500 XL	10,429	18,928	80,404	96,047	107,779	111,690	119,511	119,511
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We believe there is ample room for service providers within the NGS market as the existing installed base will continue to be used for a variety of sequencing projects and not just whole genome sequencing. Additionally, informatics and cost remain bottlenecks. Complete Genomics has optimized its service precisely for sequencing human genomes including cost structure and informatics which we believe will lead to the most efficient and reliable product.

Democratization of NGS May Obviate the Service Model

While the continued expansion of high throughput systems into core labs and genome centers was the theme for the NGS market over the past few years, it seems there has been a sea change for manufacturers that are now looking to expand into noncore settings with lower cost systems. In fact, at the AGBT 2011 the new systems from LIFE

(Ion Torrent) and Illumina (ILMN) were prominently displayed, leading us to believe the next leg of growth will come from the democratization of sequencing. We believe low throughput or decentralized sequencing will comprise a large portion of the NGS revenue by 2015 (41%) and account for the majority of growth over the next 5 years.

Exhibit 9: NGS Market Revenue Breakdown by Segment

	2009	2010	2011E	2012E	2013E	2014E	2015E	Five-Year CAGR 2010-2015
3rd Gen Revenues	$0	$0	$31,319	$87,097	$155,597	$229,605	$274,515	
Growth		*NM*	*NM*	*178.1%*	*78.6%*	*47.6%*	*19.6%*	
Market Share	***0.0%***	***0.0%***	***2.9%***	***6.1%***	***8.8%***	***10.5%***	***10.8%***	
Mid/Low Throughput Revenue	$0	$19,510	$90,438	$240,445	$468,787	$741,985	$1,022,260	**120.7%**
Growth		*NM*	*363.5%*	*165.9%*	*95.0%*	*58.3%*	*37.8%*	
Market Share	***0.0%***	***2.6%***	***8.4%***	***16.8%***	***26.4%***	***34.0%***	***40.3%***	
High Throughput Revenue	$489,470	$718,172	$929,077	$1,072,342	$1,124,775	$1,186,593	$1,225,148	**11.3%**
Growth		*46.7%*	*29.4%*	*15.4%*	*4.9%*	*5.5%*	*3.2%*	
Market Share	***100.0%***	***97.4%***	***86.7%***	***74.9%***	***63.3%***	***54.4%***	***48.3%***	
Total NGS Revenue	**$489,470**	**$737,682**	**$1,071,490**	**$1,431,499**	**$1,776,399**	**$2,180,548**	**$2,538,163**	**28.0%**
Growth		*50.7%*	*45.3%*	*33.6%*	*24.1%*	*22.8%*	*16.4%*	

Source: Company reports, Oppenheimer & Co. estimates.

While we believe non-core NGS systems will ultimately represent a substantial portion of the market, as the systems stand right now they are more appropriately suited for smaller projects. Both the MiSeq and Ion Torrent will produce approximately 1G of data per run as compared to the ~100G of data needed to sequence a human genome at 30x coverage. Ultimately between the two systems, we believe the Ion Torrent will represent the greatest potential challenge to the service model as the cost and scalability of the system will approach the HiSeq 2000's (assuming consistent consumable improvements). However, the challenges of sequencing a genome remain (as described above); therefore, we expect large scale projects to continue to favor service providers.

Uncertainty over Research Budgets

As with all life science tools manufacturers, a major component of GNOM's revenue will be tied to US academic research that is primarily funded by the National Institutes of Health (NIH). Recently, debate over both the unresolved FY2011 budget and next year's federal budget has heated up substantially.

The FY2011 base NIH budget, excluding stimulus, was to receive a 3.2% increase over the prior year as outlined in the 2011 White House budget proposal. However, the 2011 budget has not yet been ratified by Congress. Instead, Congress has passed a series of continuing resolutions to keep the government operational, effectively holding governmental budgets flat from FY2010 numbers. The most recent continuing resolution signed into law by President Obama was to remain in effect until March 2011. Most recently, the House approved another continuing resolution that would remain in effect until April 8th that would include $6B of funding cuts. Prior to the continuing resolution, the Senate was debating an omnibus bill that would have issued a $750M funding bump to the NIH, a 2.4% increase.

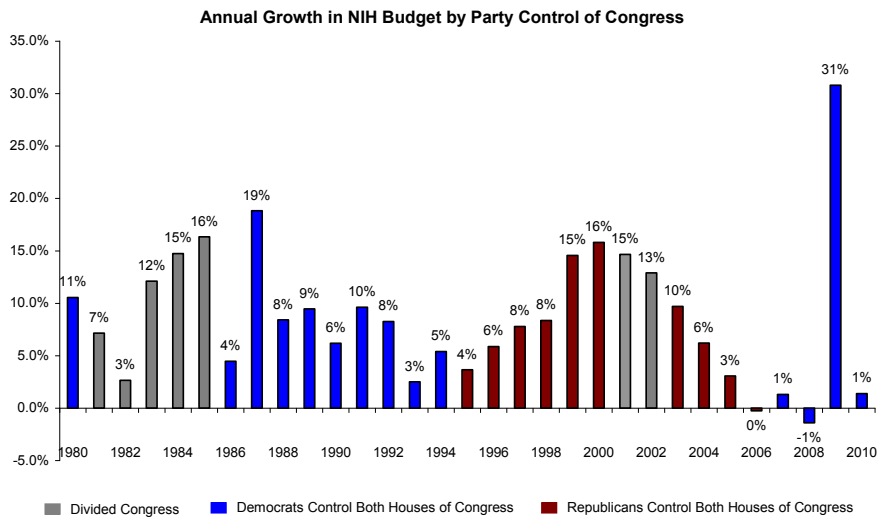
In the 2011 State of the Union address, President Obama called for the protection of research and education funding amid broader budget cuts. The Republican's first response called for $74B of total budget cuts to the President's original proposal. The original proposal called for a 4% cut to the Health and Human Services and Education Subcommittee, which funds the NIH. Within that proposal was a $1B reduction in the NIH budget for FY11 that was pegged to the President's proposal and not to the FY10 budget. President Obama had originally called for a $1B increase in NIH funding for FY11; thus, the Republicans had essentially called for a flat NIH budget for FY2011.

In response to the President, the House Appropriations Committee introduced a new budget proposal to fund the government for the balance of the fiscal year. This new

budget proposed a $100B cut to the President's budget request. Specifically, the proposal called for an 11% reduction in the Health and Human Services and Education Subcommittee's budget (-22% to the President's request). The NIH budget fared slightly better with a proposed ~5% reduction. Specifically targeted for cuts within the NIH budget are a global AIDS program, Project BioShield, the Director's Common Fund, and building and facility spending. In addition, the proposal sought to halt inflationary increases to non-competing grant renewals. While the NIH was spared the same magnitude of cut that was proposed for the funding subcommittee, the proposed NIH budget would come in at a level just slightly above the enacted NIH budget for FY2008.

The split Congress prevents either side from steamrolling its agenda through. As such, we would expect some compromise, with a flattish NIH budget the obvious middle ground. Research was noted as a key area of investment in the President's State of the Union address in January.

Exhibit 10: NIH Budget Growth (with Stimulus) vs Congressional Control (1980-2010)



Source: Company reports, Oppenheimer & Co.

The White House's recently released FY2012 budget proposal requested an approximate 3% increase (+2% including transfers) in NIH funding to $31.8B. Overall, the FY2012 budget calls for $148B in total R&D funding with particularly strong support for the NSF, the DOE's Office of Science, and the NIST (clean energy, manufacturing, and cybersecurity research). The NIH retains support remains steadfast with increased focus on translational research.

Regardless of the outcome, we believe tools names, including GNOM, could be volatile as Federal budgets continue to be debated.

Potential Competition from New Technologies

The speed at which the sequencing market has evolved is astounding. In fact, it has most often been compared to the long term trend in computing hardware. Gordon Moore, co-founder of Intel, postulated that the number of transistors on a circuit would double every two years, which correlates with performance increases. In reality, over the past 4 years, the pace of innovation in sequencing has exceeded Moore's Law and is not displaying any

signs of slowing down. One of the greatest potential risks for GNOM will be to stay ahead of the innovation curve in NGS. We believe that the company's NGS technology is the most powerful and currently the most appropriately suited for sequencing whole genomes. However, competition currently looms on the horizon especially from third generation sequencing systems.

Pacific Biosciences. Currently, PACB has the only commercial-ready single-molecule sequencing platform. However, the current system specifications are hardly suited for whole genome sequencing. On the positive side, the average read length of the commercial system will be ~1000 bases. Raw read accuracy has hovered around 85-90% for beta users, as presented by beta users at the 2011 AGBT meeting. Moreover, throughput has been thus far on the low side with the beta chip falling in the 15Mb/run range. PACB has indicated that the technology is still in the infant stage with substantial room for improvement. To that end, PACB has indicated they will make technical improvements every 6 months which will have substantial impact on the systems capabilities.

Oxford Nanopore. Illumina invested in Oxford Nanopore to develop a sequencing system based on the nanopore. Led by Hagen Bayley (University of Oxford), Oxford Nanopore has made significant progress using *Staphylococcus aureus* toxin, α-hemolysin, as the nanopore for sequencing. Oxford Nanopore revealed a platform on its website, GridION, ahead of the 2011 AGBT meeting. The system is a rack-mount/node based platform that can be constructed in arrays of systems (like a server cluster). The implication is that power can be added through the addition of machines. A working demonstration was absent from the meeting; however, based on the website the system is compelling. We are unsure, though, of the ultimate throughput capacity and how well suited this system will be for sequencing human genomes.

NABsys. NABsys (private) aims to develop a solid state, electrical DNA sequencing platform utilizing nanopores that eliminates both amplification and labeling from the workflow. While short on data, Dr. John Oliver, VP of Research and Development, detailed the approach in a talk at the 2011 AGBT meeting. This system is likely years away from competing with high throughput systems.

Ion Torrent? The Ion Torrent PGM remains the cheapest platform option in NGS. Moreover, the technology has already demonstrated tremendous headroom. In addition, LIFE management has openly speculated about the potential to convert this system into a single molecule platform. The versatility, cost, and scalability of the Ion Torrent may potentially present the greatest long term competition to the service model. However, the same general hurdles to sequencing a genome will remain in place; thus, we do not expect this or any other system to ultimately displace the need for a service model.

Competing with Two 800-Pound Gorillas

Clearly, Complete Genomics was on to something with its whole genome sequencing service model, as shortly after commencement of commercial activities two additional service providers appeared. Both BGI, one of the world's largest genome centers, and Illumina have announced service businesses which will directly compete with GNOM.

Illumina. ILMN announced the creation of the Illumina Genome Network in July 2010. The network was created as a partnership to harness the excess sequencing capacity that ILMN customers may have. In order to become a member of the network, the participating institutions must complete Illumina's Certified Service Provider certification. ILMN will take orders from customers and match them with service providers in their network. Currently, two groups have signed on as partners and include Macrogen (Seoul National University) and the National Center for Genome Resources. Currently, the price per genome is around $10,000 with discounts for higher volume orders. As of the 4Q10

conference call, ILMN had over 1,000 genomes in backlog and had just booked an order in the hundreds of genomes range from a large pharmaceutical company.

BGI. BGI (formerly Beijing Genomics Institute) is one of the largest genome centers in the world. Currently, BGI claims to have 137 installed HiSeq 2000 systems and an additional 27 SOLiD 4 systems. We estimate this equates to whole genome sequencing capacity of between 35,000 and 60,000 genomes per year (current ILMN chemistry vs. midyear improvements). In order to expand its presence, BGI has opened a US office in Boston. Currently, BGI offers the range of genomics services from NGS to microarray as well as proteomic services. The BGI estimates that it will have completed between 10,000 and 20,000 genomes by the end of 2011. While the BGI represents a formidable competitor, it is not solely focused on sequencing genomes. Not to mention it is not completely focused on human genetics with projects to sequence 1,000 plants and animals and also a 10,000 microbial genome project.

Clinical Market May Take Time to Develop

Next generation sequencing is almost entirely a research technology today. In fact, very few diagnostics tests use first generation sequencing as the method of choice (BRCAnalysis being the best example). In order for NGS generally to progress into the clinic, a very clear line needs to be drawn between treatment outcome and the results of an NGS based test. As researchers are still grappling with the sheer volume of data produced in NGS runs, a substantial amount of improvement needs to be made on the informatics side in order to begin to make the technology ready for the clinic. In addition, as the technology is evolving so rapidly, with multiple players contributing, the data output has yet to be truly standardized. We believe a service provider like GNOM has the best chance to influence the transition as GNOM simplifies the informatics and provides a standardized solution.

Financing Risk

GNOM is not profitable, and there is no certainty that the company will become profitable. Thus, shareholders are at risk for a dilutive financing until the company can demonstrate the ability to attain profitability.

Business Overview

Complete Genomics was founded in 2005 with the goal of facilitating large whole human genome studies. To do so, GNOM developed a proprietary, innovative sequencing platform including robust bioinformatics tools in order to provide researchers with a complete outsourced human genome sequencing service. GNOM began offering its commercial sequencing service in May 2010 and in their first full quarter of operations, sequenced over 300 human genomes.

Complete Genomics NGS Technology

The Complete Genomics NGS platform was developed with the aim of producing the most cost efficient, highest throughput sequencing system for the human genome.

Library Preparation. The GNOM library prep involves a number of innovations. Genomic DNA is fragmented into 500bp fragments and circularized with the addition of adaptors spaced at regular intervals through the template (4 per template). The adaptors are ligated together to create a circular DNA template. The adapters serve as the initiation point for sequencing which occurs in 35 base paired end reads.

Template Amplification. The circular DNA templates are amplified in solution in a single reaction chamber. The resulting concatemers are the resultant of the circular template amplified more than 200 times. The concatemers are then assembled into DNA nano-balls (DNB). The efficiency of the amplification process allows for more than 10B DNBs to be generated in a one milliliter reaction volume.

DNA Array Formation. GNOM uses a silicon substrate for array formation. The first patterned array substrate is the size of a microscope slide and has the capacity to hold over one billion DNBs. The current arrays have the capacity to house nearly 3B DNBs. When DNBs are introduced to the array, they are only able to adhere to the sticky spots on the slide. In addition, once a DNB adheres to a spot, it repels other DNBs. The three-dimensional nature of the DNBs results in bright spots during sequencing and less material usage during the sequencing reaction. Currently, occupancy of the array exceeds 90%, making the process highly efficient.

Sequencing. The GNOM sequencing assay, combinatorial Probe-Anchor Ligation (cPAL), is extraordinarily efficient and utilizes a combination of NGS technologies including ligation and sequencing by hybridization. The method retains the advantages of the sequencing-by-hybridization approach such as massively parallel reactions, the ability to read multiple bases per reaction, and base reading in a non-iterative manner. In addition, some of the previous shortcomings of the approach, such as the inability to sequence through simple repeats and the need for advanced computing techniques to call bases, are removed. The cPAL approach uses pools of probes with dyes specific to each base to read ten consecutive bases on either end of the adaptor. Ligation and subsequent fluorescent detection only occurs if the interrogated nucleotide is complementary to the probe. The raw error rate of this approach has been found to be less than 0.1%.

Instruments. Complete Genomics has constructed the most powerful NGS sequencing systems available from standard off the shelf imaging and robotics components. Current instruments are capable of running between 2 and 16 slides in parallel (one slide imaged at a time). GNOM's current systems are capable of sequencing up to 10 human genomes a day (instruments are capable of over 1.6T/run). Currently, the company has 16 installed systems which it plans to expand to 24 in 2011. In addition, GNOM will upgrade the platform by improving the optics. Management has indicated that there is considerable headroom from a technology standpoint to continue to increase the throughput and efficiency of the instruments.

Informatics. GNOM has built a computing center that contains 5,000 core processors within a Class Three computing facility. In addition, the company has spent more than $30M on the development of base calling, mapping, assembly, and analysis software. To call bases, 4 images are taken at each position corresponding to each potential base, and then the software is used to call the base with an accompanying quality score by determining dye intensity. The mapping software takes advantage of the massively parallel array of processors that GNOM has built and maps the reads to a reference genome. The software is able to accommodate genetic variation, read errors, and skipped bases. A separate mapping program using mate paired constructs is used to detect large scale rearrangements. The assembly program is capable of calling SNPs, insertions/deletions, substitutions (up to 50bp). A fully annotated genome is uploaded to the company's offsite storage location.

Financial Overview

2011 Sales and Earnings Outlook

We forecast $33.2M in revenue in 2011. We anticipate that GNOM will recognize revenue on the sequencing of 3,950 genomes on the year at an average ASP of $8,400 per genome. We expect the year to be back end-loaded for GNOM as it becomes more efficient in its genome sequencing and delivery as well as through expansion of the installed base of instruments. We anticipate the fully loaded average cost of sequencing a genome to average ~$6,000 in 2011. Meanwhile, we forecast GNOM will expand capacity throughout the year and end 2011 with the ability to sequence over 2,500 genomes per quarter. We expect that exiting the year, the ASP for newly ordered genomes will be substantially lower as evidenced by our ASP expectation for 2012.

We are comfortable with our revenue projections as GNOM had over 1,000 genomes in the backlog at the end of 2010 for more than $10M in revenue. In addition, at the time of its 4Q10 call, the company had already received an additional 1,400 genomes to add to backlog which did not include the 615 genome order from the Institute for Systems Biology. Therefore, more than 60% of our 2011 assumption for the number of genomes delivered is in the current backlog.

GNOM will continue to incur significant expense as it progresses through their first full year as a commercial entity. We expect that the company will make significant strides toward turning a gross profit through 2011. Our model calls for a dramatic reduction in the fully loaded cost of sequencing a genome from $11,000 in 1Q11 to less than $4,000 per genome in 4Q11. We model $29M of SG&A expense in 2011 which includes expansion of the commercial team throughout the year. R&D will continue to be a significant expense as GNOM further refines the sequencing technology and informatics. We model $31M in R&D expense in 2011. We estimate GNOM will lose $1.95 per share in 2011. Our model contemplates the need for a financing heading into 2012.

Exhibit 11: 2011 Earnings Snapshot

	2010	Margin	2011E	Growth	Margin
Sales	9.4		33.2		
Total Revenue	**9.4**		**33.2**	**NM**	
COGS	19.9	211.9%	26.3		79.3%
General and Administrative	9.3	99.5%	13.1		39.4%
Sales and Marketing	6.1	65.1%	16.1		48.6%
R&D	21.7	231.0%	30.6		92.1%
Operating Income	**($47.7)**	**NM**	**($52.9)**	**NM**	**NM**
Interest expense	(2.8)		(1.6)		
Other Income	(7.6)		0.2		
Pre-Tax Income	**($58.1)**	**NM**	**($54.3)**	**NM**	**NM**
Taxes	0.0		0		
Tax Rate	NM		NM		
Net Income	**($58.1)**	**NM**	**($54.1)**	**NM**	**NM**
EPS	**($13.60)**		**($1.95)**	**NM**	
Avg. Shares Out. - Fully Dil.	4.3		28.6		

Source: Company reports, Oppenheimer & Co.

2012 Sales and Earnings Outlook

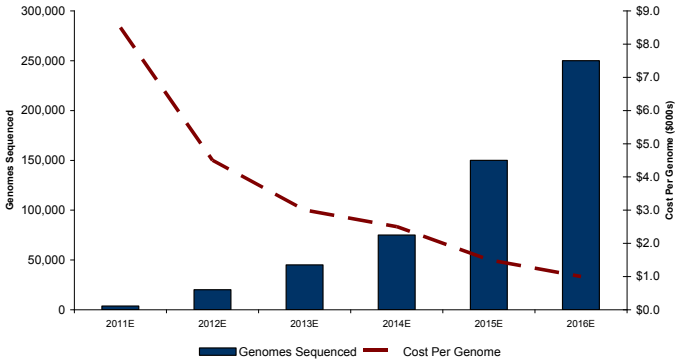
We project substantial revenue growth in 2012 and forecast sales of $90M for the year. Our revenue model calls for GNOM to sequence 20,000 human genomes in 2012 at an average cost of $4,500 per genome. We do not believe the demand for sequencing will exhibit a linear relationship with the average cost per genome. We anticipate that reductions in price will relate to substantially greater increases in demand.

We forecast that GNOM's gross margin will top 50% for the full year if the company meets our revenue prediction. We model $48M in SG&A expense as the company continues to expand its commercial organization. Our R&D expense estimate is $32M as we believe the company will have to continue to invest in technology development to remain the class leader in human genome sequencing. Finally, we anticipate a loss of $0.70 per share as GNOM makes significant strides towards profitability. Based on our projections, we do not expect GNOM to require an additional refinancing heading into 2013.

Long-Term Outlook

Our 5-year sales CAGR (2011-2016) is 50% and reflects our belief that the outsourced whole genome sequencing will grow alongside of the broader NGS market. We forecast GNOM will sequence 250,000 human genomes in 2016 at an ASP of $1,000 per genome.

Exhibit 12: GNOM Genomes Sequenced vs ASP/Genome (2011E-2015E)



Source: Company reports, Oppenheimer & Co.

We anticipate that GNOM will turn profitable in 2014. Our forecasts do not assume widespread clinical usage of whole genome sequencing. Should sequencing migrate faster than we expect into the clinical setting, we believe our estimates will prove extremely conservative.

Exhibit 13: GNOM Annual Sales and Earnings Model

	2009	2010	2011E	2012E	2013E	2014E	2015E	2016E
Sales	0.6	9.4	33.2	90.0	135.0	187.5	225.0	250.0
Total Revenue	**0.6**	**9.4**	**33.2**	**90.0**	**135.0**	**187.5**	**225.0**	**250.0**
COGS	5.0	19.9	26.3	38.4	42.6	46.1	68.5	70.5
General and Administrative	5.0	9.3	13.1	16.2	20.3	22.5	24.8	25.0
Sales and Marketing	1.8	6.1	16.1	31.5	40.5	46.9	49.5	50.0
R&D	22.4	21.7	30.6	31.5	33.8	37.5	40.5	42.5
Operating Income	**(33.6)**	**(47.7)**	**(52.9)**	**(27.6)**	**(2.1)**	**34.6**	**41.8**	**62.0**
Interest expense	(3.5)	(2.8)	(1.6)	(0.5)	(0.5)	(0.5)	(0.5)	(0.5)
Other Income	1.1	(7.6)	0.2	1.0	1.0	1.0	1.0	1.0
Pre-Tax Income	**(35.9)**	**(58.1)**	**(54.3)**	**(27.1)**	**(1.6)**	**35.1**	**42.3**	**62.5**
Taxes	0.0	0.0	0.0	0.0	0.0	0.0	4.2	21.9
Tax Rate	NM	NM	0.0%	0.0%	0.0%	0.0%	10.0%	35.0%
Net Income	**(35.9)**	**(58.1)**	**(54.1)**	**(27.1)**	**(1.6)**	**35.1**	**38.0**	**40.6**
EPS	**($6.40)**	**($13.60)**	**($1.95)**	**($0.70)**	**($0.04)**	**$0.86**	**$0.91**	**$0.95**
Avg. Shares Out. - Fully Dil.	5.6	4.3	28.6	38.6	39.6	40.6	41.6	42.6

Margin Analysis	**2009**	**2010E**	**2011E**	**2012E**	**2013E**	**2014E**	**2015E**	**2016E**
COGS	NM	NM	79.3%	42.6%	31.6%	24.6%	30.4%	28.2%
Gross Margin	NM	NM	20.7%	57.4%	68.4%	75.4%	69.6%	71.8%
General and Administrative	NM	NM	39.4%	18.0%	15.0%	12.0%	11.0%	10.0%
Sales and Marketing	NM	NM	48.6%	35.0%	30.0%	25.0%	22.0%	20.0%
R&D	NM	NM	92.1%	35.0%	25.0%	20.0%	18.0%	17.0%
Operating Margin	NM	NM	NM	NM	NM	18.4%	18.6%	24.8%
Net Margin	NM	NM	NM	NM	NM	18.7%	16.9%	16.3%

Growth Analysis	**2009**	**2010E**	**2011E**	**2012E**	**2013E**	**2014E**	**2015E**	**2016E**
Revenue	NM	NM	253.3%	171.3%	50.0%	38.9%	20.0%	11.1%
COGS	NM	NM	32.3%	45.8%	11.1%	8.0%	48.8%	2.9%
General and Administrative	NM	NM	39.9%	23.9%	25.0%	11.1%	10.0%	1.0%
Sales and Marketing	NM	NM	163.7%	95.5%	28.6%	15.7%	5.6%	1.0%
R&D	NM	NM	40.9%	3.1%	7.1%	11.1%	8.0%	4.9%
Operating Income	NM	NM	NM	NM	NM	NM	20.8%	48.5%
EPS	NM	NM	NM	NM	NM	NM	5.8%	4.3%

Source: Company reports, Oppenheimer & Co.

Valuation

We value GNOM by a discounted cash flow (DCF) analysis. Our $13 target price assumes a WACC of 11% and no terminal growth on an estimated EBITDA of $109M in 2022 (after two stages of revenue growth—about 50% in 2011 to 2016 and 5% in 2017-2022). GNOM trades at a higher 2011 EV/sales multiple than either life science tools peers (3.5x vs. 2.9x for tools companies) or CRO peers (3.5x vs. 1.6x for contract research organizations). However, as the company has less than a full year as a commercial entity, it is difficult to make peer group comparisons.

Exhibit 14: GNOM DCF Valuation

Revenue Growth (2011-2016)	49.8%
Revenue Growth (2017-2022)	5.0%
FCF Growth (2011-2016)	NM
FCF Growth (2017-2022)	0.7%
Terminal FCF Growth	0.0%
NPV FCF (2011-2022)	$132.6
Terminal FCF Value	$135.3
Total PV FCF	**$267.8**
Add Cash	$67.8
Less BV of Debt	$0.2
Equity Value	$335.4
Shares Oustanding	26.0
12 Month Fwd Value	**$13.23**

Source: Company reports, Oppenheimer & Co. estimates

Next Generation Sequencing Background

DNA sequencing has become increasingly visible to the public beginning with the race to sequence the human genome during the Human Genome Project. Despite the remarkable feat, the Human Genome Project failed to live up to its hype as the driver of the next medical revolution. Next generation sequencing technologies have advanced so rapidly that scientists are once again hopeful for a genomic revolution.

DNA sequencing is the method by which the genetic code can be deciphered. Recent advances in sequencing technology have enabled significant leaps in both data generation and speed over the previous sequencing standard. Concomitant with the increase in speed and data generation has been a reduction in cost. Moreover, NGS systems are not confined to DNA sequencing but can also determine gene expression and DNA/protein interactions.

Traditional sequencing, or Sanger Sequencing (capillary electrophoresis, CE) was first described in 1977 by two separate groups, Maxam & Gilbert and Sanger. CE has evolved to be able to achieve read lengths of up to 1000 base pairs (DNA bases, bp). However, for large scale projects the technology remains expensive and slow as the Human Genome Project took 13 years to complete at a cost of $2.7B.

NGS Advantages – Despite considerable advances in throughput, CE sequencers cannot handle the ever increasing demands of genomic biologists. The most powerful CE machine (the 3730xl DNA Analyzer from LIFE) is capable of 96 simultaneous capillary reactions, which is still roughly 6 logs of data output behind NGS platforms. While the cost of sequencing one kilobase of DNA can be as low as $0.50 on a CE machine, when scaled up to the size of the human genome, the cost would balloon to over $1.5M. In comparison, today's NGS platforms can accomplish the same task at less than $10,000 ($3,00 on SOLiD 4 Hq, reagents only 4Q10E). An additional benefit of NGS is the initial template amplification (SOLiD, Genome Analyzer, 454) or the elimination of the step completely with single molecule platforms (HeliScope, Starlight, Pacific Biosciences). NGS platforms are also capable of detecting minor alleles and quantifying copy number, both of which can be overlooked by CE methodology. Beyond DNA sequencing, NGS platforms can also analyze epigenetic changes, gene expression (whole transcriptome), and protein/DNA interaction mapping at the whole genome scale.

NGS Disadvantages – The major drawback to NGS platforms is that they are far more error-prone than Sanger sequencing. Accuracy is improved through increasing the sequencing runs, thus correcting errors through redundant sequencing. Both Sanger and NGS platforms are subject to errors created by template amplification. Single molecule platforms will not be subject to amplification errors since this step is eliminated. Another disadvantage of NGS platforms is the challenge of de novo genome assembly due to short read lengths (less of a problem with PACB). Genome assembly is an extremely computer-intensive process and is currently the rate limiting step in data generation in many large scale projects. Finally, the IT commitment for NGS platforms is immense. Not only is an incredible amount of processing power needed to analyze the data, but also an incredible amount of storage space is needed to store the raw data prior to analyzing. The decrease in the cost of solid state hard drives as well as the increase in capacity, which are both fast and space efficient, should positively impact NGS.

Stock prices of other companies mentioned in this report (as of 3/14/11)
Helicos (HLCS-PINK, $0.16, Not Rated)

Roche Holding Ltd. (RHHBY(ADR)-PINK, $35.48. Not Rated)

GNOM Comparables Analysis vs Tools (EV/Sales)

Company (Symbol)	Rating	Price 3/14/11	Mkt Cap ($ in millions)	Sales 2010	Sales 2011E	Sales 2012E	Sales Growth 2010	Sales Growth 2011E	Sales Growth 2012E	Sales Growth ('10-'12)	EV/Sales 2010	EV/Sales 2011E	EV/Sales 2012E
Pacific BioSciences (PACB)	P	$14.26	753.3	1.7	32.3	87.1	NM	NM	169.5%	NM	280.5	14.5	5.4
Affymetrix (AFFX)	P	$4.77	337.2	310.7	298.2	291.8	-5.0%	-4.0%	-2.1%	-3.1%	1.1	1.1	1.1
Life Technologies (LIFE)	OP	$51.27	9,344.1	3,594.3	3,822.5	4,052.3	8.8%	6.3%	6.0%	6.2%	3.2	3.0	2.9
Illumina (ILMN)	P	$64.27	8,137.1	902.7	1,127.9	1,384.8	35.5%	24.9%	22.8%	23.9%	9.1	7.3	5.9
Caliper Life Sciences (CALP)*	NR	$6.30	316.8	123.7	141.3	155.9	-5.1%	14.2%	10.4%	12.3%	2.4	2.1	1.9
Bio-Rad Laboratories (BIO)*	NR	$115.60	3,213.6	1,927.1	2,057.3	2,178.4	8.0%	6.8%	5.9%	6.3%	1.6	1.5	1.4
Agilent (A)*	NR	$44.84	15,469.8	5,605.9	6,481.5	6,916.9	20.8%	15.6%	6.7%	11.1%	2.7	2.3	2.2
Group Average				**1,780.9**	**1,994.4**	**2,152.5**	**10.5%**	**10.6%**	**31.3%**	**9.9%**	**3.3**	**2.9**	**2.6**
Complete Genomics (GNOM)	**OP**	**$7.15**	**185.3**	**9.4**	**33.2**	**90.0**	**NM**	**NM**	**171.3%**	**NM**	**12.5**	**3.5**	**1.3**

* Reuters Consensus

Source: Oppenheimer & Co. estimates for all OPCO covered companies; Bloomberg, FactSet, Reuters for all non-OPCO covered companies

Results presented cannot and should not be viewed as an indicator of future performance. NR = Not Rated; O = Outperform; P = Perform; U = Underperform.

GNOM Comparables Analysis vs CROs (EV/Sales)

Company (Symbol)	Rating	Price 3/14/11	Mkt Cap ($ in millions)	Sales 2010	Sales 2011E	Sales 2012E	Sales Growth 2010	Sales Growth 2011E	Sales Growth 2012E	Sales Growth ('10-'12)	EV/Sales 2010	EV/Sales 2011E	EV/Sales 2012E
PPDI, Inc (PPDI)*	NR	$27.97	3,329.7	1,470.6	1,530.4	1,687.1	3.8%	4.1%	10.2%	7.1%	1.9	1.8	1.6
Charles River Laboratories (CRL)*	NR	$38.11	2,151.0	1,133.4	1,134.1	1,174.4	-5.7%	0.1%	3.6%	1.8%	2.3	2.3	2.3
Parexel (PRXL)*	NR	$23.90	1,400.0	1,179.2	1,281.0	1,411.7	8.1%	8.6%	10.2%	9.4%	1.4	1.2	1.1
Covance (CVD)*	NR	$56.28	3,647.2	2,038.5	2,040.4	2,171.3	3.9%	0.1%	6.4%	3.2%	1.7	1.7	1.6
Kendle International (KNDL)*	NR	$9.02	134.5	333.8	333.2	359.0	-19.9%	-0.2%	7.7%	3.7%	0.7	0.7	0.7
Group Average				**1,231.1**	**1,263.8**	**1,360.7**	**-2.0%**	**2.5%**	**7.6%**	**5.1%**	**1.6**	**1.6**	**1.5**
Complete Genomics (GNOM)	**OP**	**$7.15**	**185.3**	**9.4**	**33.2**	**90.0**	**NM**	**NM**	**171.3%**	**NM**	**12.5**	**3.5**	**1.3**

* Reuters Consensus

Source: Oppenheimer & Co. estimates for all OPCO covered companies; Bloomberg, FactSet, Reuters for all non-OPCO covered companies

Results presented cannot and should not be viewed as an indicator of future performance. NR = Not Rated; O = Outperform; P = Perform; U = Underperform.

Complete Genomics Quarterly Income Statement ($MMs except per share data)

	2009	3Q10	4Q10	2010E	1Q11	2Q11	3Q11	4Q11	2011E
System Sales	0.62	4.16	3.80	9.39	5.00	5.70	9.35	13.13	33.18
Total Revenue	**0.62**	**4.16**	**3.80**	**9.39**	**5.00**	**5.70**	**9.35**	**13.13**	**33.18**
COGS	5.03	6.01	4.90	19.90	7.50	5.99	5.94	6.90	26.32
General and Administrative	4.95	2.33	2.15	9.35	2.55	2.85	3.74	3.94	13.08
Sales and Marketing	1.80	1.59	1.98	6.11	2.40	3.14	4.68	5.91	16.12
R&D	22.42	4.95	5.64	21.69	6.75	7.98	7.95	7.88	30.55
Operating Income	**(33.59)**	**(10.72)**	**(10.87)**	**(47.65)**	**(14.20)**	**(14.25)**	**(12.95)**	**(11.49)**	**(52.89)**
Interest Expense	(3.47)	(0.91)	(0.78)	(2.83)	(0.50)	(0.40)	(0.40)	(0.30)	(1.60)
Other, net	1.10	(9.23)	1.39	(7.61)	0.20	0.10	0.10	0.00	0.20
Pre-Tax Income	**(35.95)**	**(20.86)**	**(10.26)**	**(58.09)**	**(14.50)**	**(14.55)**	**(13.25)**	**(11.79)**	**(54.09)**
Taxes	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Tax Rate	NM	NM	NM	NM	NM	NM	NM	NM	0.0%
Net Income	**(35.95)**	**(20.86)**	**(10.26)**	**(58.09)**	**(14.50)**	**(14.55)**	**(13.25)**	**(11.79)**	**(54.09)**
Non-GAAP EPS	**($386.56)**	**($21.87)**	**($0.69)**	**($13.60)**	**($0.56)**	**($0.56)**	**($0.51)**	**($0.33)**	**($1.95)**
Avg. Shares Out. - Fully Dil.	0.1	1.0	14.8	4.3	26.0	26.1	26.2	36.2	28.6

Margin Analysis	**2009**	**3Q10**	**4Q10**	**2010E**	**1Q11**	**2Q11**	**3Q11**	**4Q11**	**2011E**
COGS	**NM**	144.4%	128.9%	**NM**	150.0%	105.0%	63.5%	52.5%	**79.3%**
Gross Margin	**NM**	-44.4%	-28.9%	**NM**	-50.0%	-5.0%	36.5%	47.5%	**20.7%**
General and Administrative	**NM**	NM	NM	**NM**	51.0%	50.0%	40.0%	30.0%	**39.4%**
Sales and Marketing	**NM**	NM	NM	**NM**	48.0%	55.0%	50.0%	45.0%	**48.6%**
R&D	**NM**	NM	NM	**NM**	135.0%	140.0%	85.0%	60.0%	**92.1%**
Operating Margin	**NM**	NM	NM	**NM**	NM	NM	NM	NM	**NM**
Net Margin	**NM**	NM	NM	**NM**	NM	NM	NM	NM	**NM**

Growth Analysis	**2009**	**3Q10**	**4Q10**	**2010E**	**1Q11**	**2Q11**	**3Q11**	**4Q11**	**2011E**
Revenue	**NM**	NM	NM	**NM**	NM	NM	124.7%	245.1%	**253.3%**
COGS	**NM**	NM	NM	**NM**	NM	NM	-1.1%	40.6%	**32.3%**
Selling and Marketing	**NM**	NM	NM	**NM**	NM	NM	60.5%	82.9%	**39.9%**
Selling, General and Administrative	**NM**	NM	NM	**NM**	NM	NM	60.4%	39.6%	**40.9%**
Operating Income	**NM**	NM	NM	**NM**	NM	NM	NM	NM	**NM**
EPS	**NM**	NM	NM	**NM**	NM	NM	NM	NM	**NM**

Source: Oppenheimer Estimates, Company Reports

Complete Genomics Balance Sheet ($MMs)

	2008	2009	2010E	2011E	2012E	2013E
Assets						
Cash and Equivalents	6.2	7.8	67.8	68.9	53.4	49.3
Accounts Receivable	0.0	1.3	2.7	9.4	16.1	33.5
Inventories	0.0	0.4	6.9	9.7	13.4	16.1
Prepaid expenses	0.5	5.2	0.4	1.1	1.6	1.9
Other	0.6	0.5	0.3	0.3	0.3	0.3
Total Current Assets	**7.2**	**15.0**	**78.1**	**89.3**	**84.8**	**101.1**
Property, Plant, & Equipment	8.0	14.9	27.4	50.0	59.5	74.4
Other	0.5	0.4	2.3	2.3	2.3	2.3
Total Assets	**15.8**	**30.3**	**107.8**	**141.6**	**146.6**	**177.8**
Liabilities						
Accounts Payable	0.7	4.3	10.0	5.6	7.8	9.3
Accrued Liabilities	1.7	2.0	1.9	3.9	5.4	5.6
Notes Payable	4.0	4.4	4.6	4.6	4.6	4.6
Deferred Revenue	0.0	1.3	3.4	1.1	1.5	1.5
Total Current Liabilities	**6.5**	**12.1**	**19.9**	**15.2**	**19.3**	**21.1**
Notes Payable	7.7	3.5	0.2	0.2	0.2	0.2
Deferred Rent	0.0	5.0	4.5	4.5	4.5	4.5
Convertible preferred stock	1.1	1.6	0.0	0.0	0.0	0.0
Total Liabilities	**15.3**	**22.1**	**24.6**	**19.9**	**24.0**	**25.7**
Shareholders' Equity	**0.5**	**8.1**	**83.2**	**121.7**	**122.6**	**152.1**
Total Liabilities & Equity	**15.8**	**30.3**	**107.8**	**141.6**	**146.6**	**177.8**

Source: Oppenheimer Estimates, Company Reports

Complete Genomics Statement of Cash Flows ($MMs)

	2007	2008	2009	2010	2011	2012	2013
Cash Flow from Operating Activities							
Net Income (Loss)	(12.3)	(28.4)	(35.9)	(57.7)	(54.1)	(27.1)	(1.6)
Depreciation and Amortization	0.8	2.8	5.2	7.1	10.7	12.6	13.1
Amortization of debt issuance	0.1	0.2	0.3	0.3	0.3	0.0	0.0
Issuance of common stock for IP	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Issuacne of common stock to founders	0.0	0.0	0.0	1.8	0.0	0.0	0.0
Change in Convertible Preferred Stock liability	0.2	(0.1)	(1.1)	8.6	0.0	0.0	0.0
Stock Based Comp	0.1	0.3	1.4	3.8	6.6	13.5	16.2
Noncash interest expense related to promissory notes	0.0	0.0	2.1	2.0	0.0	0.0	0.0
(Gain) loss on disposal of PP&E	0.0	0.5	0.0	0.0	0.0	0.0	0.0
Total Operating Sources	**(11.1)**	**(24.6)**	**(28.0)**	**(34.1)**	**(36.5)**	**(1.0)**	**27.7**
Operating Uses							
Accounts Receivable	0.0	0.0	(1.3)	(1.4)	(6.7)	(6.7)	(17.4)
Inventories	0.0	0.0	(0.4)	(6.5)	(2.8)	(3.8)	(2.7)
Prepaid Expenses	(0.2)	(0.2)	(4.7)	4.7	(0.6)	(0.5)	(0.3)
Other Current Assets	(0.1)	(0.2)	0.1	0.1	0.0	0.0	0.0
Other Assets	(0.1)	0.0	(0.1)	(0.6)	0.0	0.0	0.0
Accounts Payable	0.6	(0.0)	1.1	6.3	(4.4)	2.2	1.6
Accrued liabiliites	0.8	0.7	0.3	(0.1)	2.0	1.5	0.2
Deferred revenue	0.0	0.0	1.3	2.1	(2.3)	0.4	0.0
Deferred rent	0.0	0.0	5.0	(0.5)	0.0	0.0	0.0
Total Operating Uses	**1.1**	**0.3**	**1.3**	**4.1**	**(14.8)**	**(6.9)**	**(18.6)**
Operating Cash Flow	**(10.0)**	**(24.3)**	**(26.7)**	**(30.0)**	**(51.3)**	**(7.9)**	**9.1**
Investing							
Purchase of PP&E	(3.7)	(7.4)	(9.7)	(20.2)	(22.6)	(9.5)	(14.9)
Other	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Net Cash Flow from Investing	**(3.7)**	**(7.4)**	**(9.7)**	**(20.2)**	**(22.6)**	**(9.5)**	**(14.9)**
Cash Flow from Financing							
Proceeds from promissory notes	1.0	0.0	14.7	22.2	0.0	0.0	0.0
Proceeds from Notes Payable	2.8	13.2	0.0	0.0	0.0	0.5	0.4
Repayments of Notes Payable	(0.3)	(5.0)	(4.0)	(3.3)	0.0	0.5	0.6
Proceeds from issuance of preferred	12.9	25.4	27.2	27.0	1.1	0.9	0.8
Proceeds from Stock Issuance	0.0	0.0	0.0	64.0	75.0		0.0
Exercise of Stock Options	0.0	0.0	0.0	0.1	0.0	0.0	0.0
Net Cash Flow from Financing	**16.3**	**33.6**	**37.9**	**110.1**	**76.1**	**1.9**	**1.8**
Effect of Exchange Rates	0.0	0.0	0.0	0.0	0	0	0
Beginning Cash	1.6	4.3	6.2	7.8	67.8	68.9	53.4
Net Increase (Decrease) in Cash	2.6	1.9	1.6	60.0	1.2	(15.5)	(4.1)
Ending Cash	**4.3**	**6.2**	**7.8**	**67.8**	**68.9**	**53.4**	**49.3**

Source: Oppenheimer Estimates, Company Reports

Investment Thesis

We are initiating coverage of GNOM with an Outperform rating and $13 price target. GNOM has developed a proprietary, innovative sequencing platform including robust bioinformatics tools in order to provide researchers with a complete outsourced human genome sequencing service. Initial data provided by GNOM and early users have demonstrated the company has produced high quality sequence data, validating the platform. Despite a rapidly expanding installed base of NGS instruments we believe demand from the research community and later from the clinical community will continue to outpace the total market sequencing capacity, thus creating an important niche for service providers like GNOM. Our $13 target price assumes no terminal growth on an estimated EBITDA of $99M in 2022.

Price Target Calculation

We value GNOM by a discounted cash flow (DCF) analysis. Our $13 target price assumes a WACC of 11% and no terminal growth on an estimated EBITDA of $109M in 2022 (after two stages of revenue growth—about 50% in 2011 to 2016 and 5% in 2017-2022).

Key Risks to Price Target

These include: 1) competition from the high throughput NGS installed base, 2) uncertainty over research funding, 3) technology obsolescence, 4) competition from other service providers, 5) the clinical market perhaps taking time to develop, and 6) financing risk.

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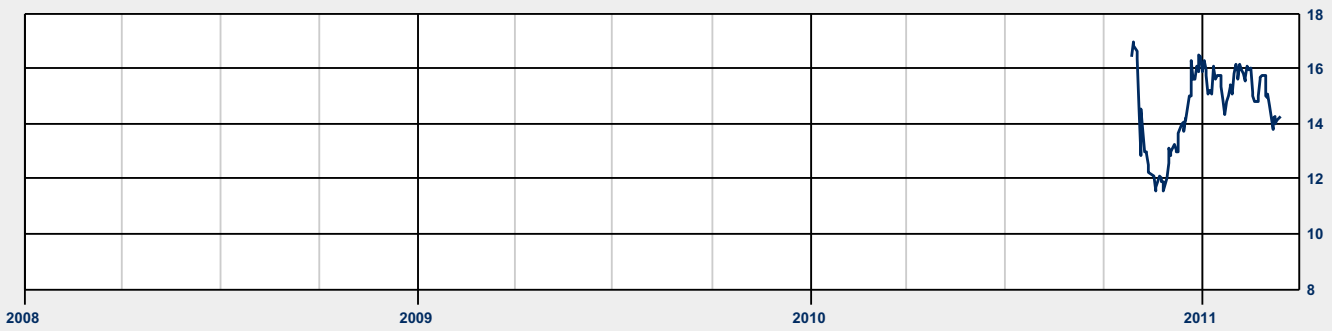
Stock Prices as of March 16, 2011

Pacific Biosciences of California (PACB - Nasdaq, 14.24, PERFORM)
Life Technologies, Inc. (LIFE - Nasdaq, 50.96, OUTPERFORM)

Rating and Price Target History for: Pacific Biosciences of California (PACB) as of 03-15-2011



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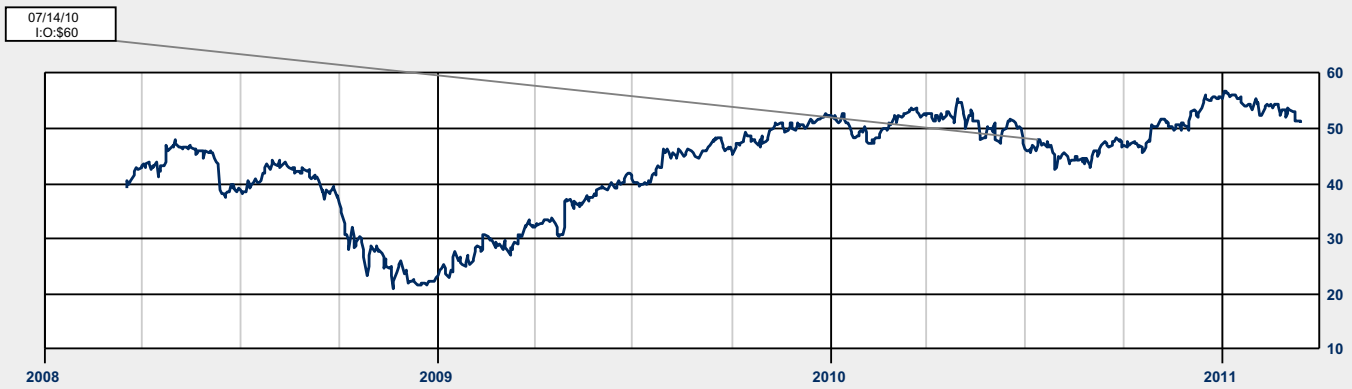
Rating and Price Target History for: Life Technologies, Inc. (LIFE) as of 03-15-2011



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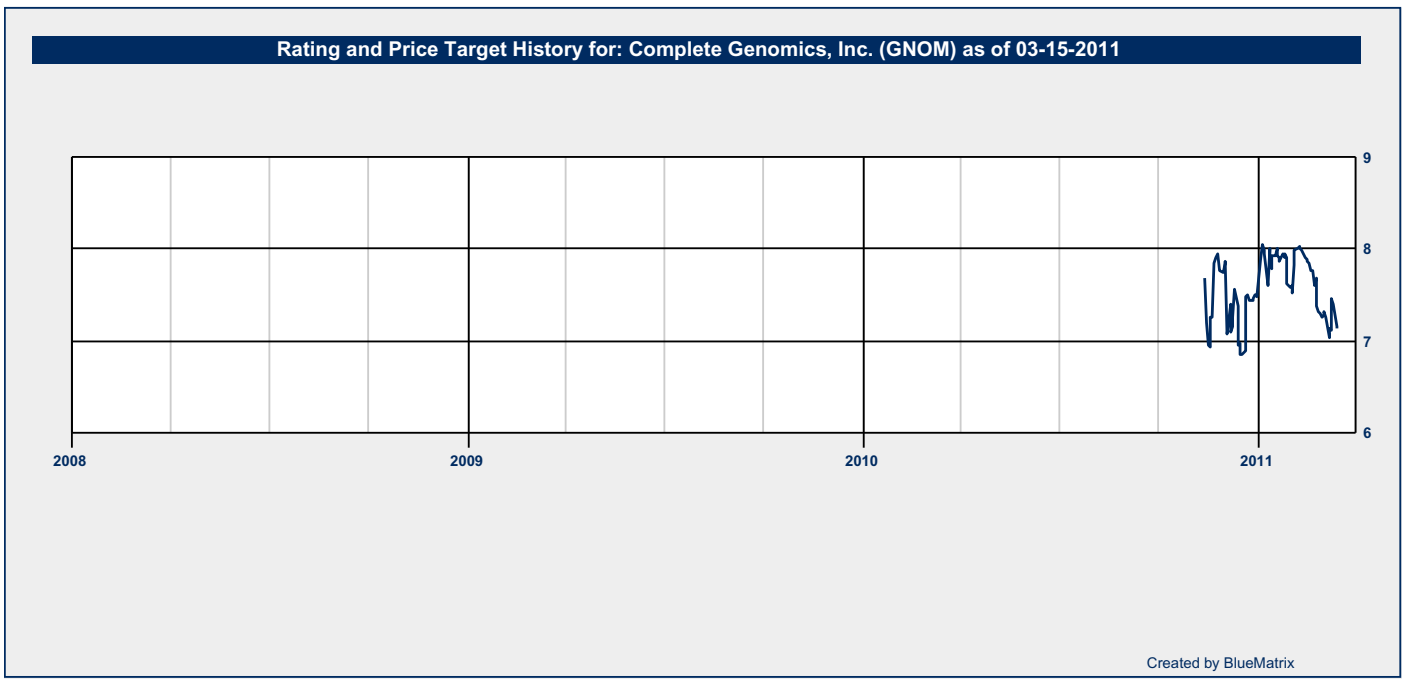

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			IB Serv/Past 12 Mos.	
Rating	Count	Percent	Count	Percent
OUTPERFORM [O]	293	53.10	128	43.69
PERFORM [P]	248	44.90	79	31.85
UNDERPERFORM [U]	11	2.00	2	18.18

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