COMPLETE GENOMICS INC Form 424B5 March 12, 2012 Table of Contents

Filed Pursuant to Rule 424(b)(5)

Commission File No. 333-178728

PROSPECTUS SUPPLEMENT

(To Prospectus dated January 24, 2012)

\$30,000,000

Complete Genomics, Inc.

Common Stock

We have entered into a sales agreement with MLV & Co. LLC, or MLV, relating to shares of our common stock offered by this prospectus supplement and the accompanying prospectus. In accordance with the terms of the sales agreement, we may offer and sell shares of our common stock, \$0.001 par value per share, having an aggregate offering price of up to \$30 million from time to time on The NASDAQ Global Market or other market for our common stock in the U.S. through MLV acting as our agent.

Our common stock is listed on The NASDAQ Global Market under the symbol GNOM . On March 8, 2012, the last reported sale price of our common stock on The NASDAQ Global Market was \$3.83 per share.

Sales of our common stock, if any, under this prospectus supplement and the accompanying prospectus may be made in sales deemed to be at-the-market offerings as defined in Rule 415 promulgated under the Securities Act of 1933, as amended, or the Securities Act, including sales made directly on or through The NASDAQ Global Market or other market for our common stock in the U.S., sales made to or through a market maker other than on an exchange or otherwise, in negotiated transactions at market prices prevailing at the time of sale or at prices related to such prevailing market prices, and/or any other method permitted by law. MLV will act as sales agent on a commercially reasonable efforts basis consistent with its normal trading and sales practices. There is no arrangement for funds to be received in any escrow, trust or similar arrangement.

MLV will be entitled to compensation at a commission rate of up to 3% of the gross sales price per share sold. In connection with the sale of the our common stock on our behalf, MLV may be deemed to be an underwriter within the meaning of the Securities Act, and the compensation of MLV may be deemed to be underwriting commissions or discounts.

Before buying shares of our common stock, you should carefully consider the risk factors described in <u>Risk Factors</u> beginning on page S-10 of this prospectus supplement and the risk factors described in the documents incorporated by reference herein.

Neither the Securities and Exchange Commission nor any state securities commission has approved or disapproved these securities or determined if this prospectus supplement and the accompanying prospectus are truthful or complete. Any representation to the contrary is a criminal offense.

The date of this prospectus supplement is March 9, 2012.

Table of Contents

	Page
Prospectus Supplement	
About this Prospectus Supplement	S-i
Prospectus Supplement Summary	S-1
Risk Factors	S-10
Forward-Looking Statements	S-11
Use of Proceeds	S-12
Dilution	S-13
Plan of Distribution	S-14
Legal Matters	S-15
Experts	S-15
Where You Can Find More Information	S-15
Incorporation by Reference	S-15
Prospectus	
About this Prospectus	1
About Complete Genomics	1
Where You Can Find More Information	2
Incorporation by Reference	2
Forward-Looking Statements	3
<u>Risk Factors</u>	4
Ratio of Earnings to Fixed Charges	4
<u>Use of Proceeds</u>	4
Description of Common Stock	5
Description of Preferred Stock	8
Description of Debt Securities	10
Description of Warrants	17
<u>Global Securities</u>	18
<u>Plan of Distribution</u>	21
Certain Provisions of Delaware Law and of the Company s Certificate of Incorporation and Bylaws	23
Legal Matters	24
Experts	24

About this Prospectus Supplement

You should rely only on the information contained in or incorporated by reference in this prospectus supplement, the accompanying prospectus and any free writing prospectus that we have authorized for use in connection with this offering. We have not, and MLV has not, authorized anyone to provide you with different information. If anyone provides you with different or inconsistent information, you should not rely on it. We are not, and MLV is not, making an offer to sell these securities in any jurisdiction where the offer or sale is not permitted or in which the person making that offer or solicitation is not qualified to do so or to anyone to whom it is unlawful to make an offer or solicitation. You should assume that the information appearing in this prospectus supplement, the accompanying prospectus, the documents incorporated by reference in this offering, is accurate only as of the date of those respective documents. Our business, financial condition, results of operations and prospects may have changed since those dates. You should read this prospectus supplement, the accompanying prospectus, and any free writing prospectus, the documents incorporated by reference in this prospectus supplement and the accompanying prospectus supplement, the accompanying prospectus, the documents incorporated by reference in this prospectus supplement and the accompanying prospectus, and any free writing prospectus, the documents incorporated by reference in this prospectus supplement and the accompanying prospectus, and any free writing prospectus, the documents incorporated by reference in this prospectus supplement and the accompanying prospectus, and any free writing prospectus, the documents incorporated by reference in this prospectus supplement and the accompanying prospectus, and any free writing prospectus, the documents incorporated by reference in this prospectus supplement and the accompanying prospectus, and any

This document is in two parts. The first part is this prospectus supplement, which describes the terms of this offering and also adds to and updates information contained in the accompanying prospectus and the documents incorporated by reference in this prospectus supplement and the accompanying prospectus. The second part, the

S-i

accompanying prospectus dated January 24, 2012, including the documents incorporated by reference therein, provides more general information, some of which may not apply to this offering. Generally, when we refer to this prospectus, we are referring to both parts of this document combined. To the extent there is a conflict between the information contained in this prospectus supplement, on the one hand, and the information contained in the accompanying prospectus or in any document incorporated by reference that was filed with the Securities and Exchange Commission, or SEC, before the date of this prospectus supplement, on the other hand, you should rely on the information in this prospectus supplement. If any statement in one of these documents is inconsistent with a statement in another document having a later date for example, a document incorporated by reference in the accompanying prospectus the statement in the document having the later date modifies or supersedes the earlier statement.

We further note that the representations, warranties and covenants made by us in any agreement that is filed as an exhibit to any document that is incorporated by reference into the accompanying prospectus were made solely for the benefit of the parties to such agreement, including, in some cases, for the purpose of allocating risk among the parties to such agreement, and should not be deemed to be a representation, warranty or covenant to you. Moreover, such representations, warranties or covenants were accurate only as of the date when made. Accordingly, such representations, warranties and covenants should not be relied on as accurately representing the current state of our affairs.

All references in this prospectus supplement and the accompanying prospectus to Complete Genomics, the Company, we, us, our, or similar references refer to Complete Genomics, Inc., except where the context otherwise requires or as otherwise indicated.

This prospectus supplement, the accompanying prospectus, and the information incorporated herein and therein by reference, include trademarks, service marks and trade names owned by us (including but not limited to our logo, Complete Genomics, Complete Genomics Analysis Platform, CGA Platform, CGATools, cPAL and DNB) or other companies. All trademarks, service marks and trade names included incorporated by reference into this prospectus supplement or the accompanying prospectus are the property of their respective owners.

S-ii

PROSPECTUS SUPPLEMENT SUMMARY

This summary highlights certain information about us, this offering and selected information contained elsewhere in or incorporated by reference into this prospectus supplement and the accompanying prospectus. This summary is not complete and does not contain all of the information that you should consider before deciding whether to invest in our common stock. For a more complete understanding of our company and this offering, we encourage you to read and consider carefully the more detailed information in this prospectus supplement and the accompanying prospectus, including the information incorporated by reference in this prospectus supplement and the accompanying prospectus, the information included in any free writing prospectus that we have authorized for use in connection with this offering, and the information referred to under the heading Risk Factors in this prospectus supplement on page S-10, in the accompanying prospectus and in the documents incorporated by reference into this prospectus supplement.

Our Company

We are a life sciences company that has developed and commercialized an innovative DNA sequencing platform. Our goal is to become the preferred solution for whole human genome sequencing and analysis. Our Complete Genomics Analysis Platform, or CGATM Platform, combines our proprietary human genome sequencing technology with our advanced informatics and data management software and our innovative, end-to-end, outsourced service model to provide our customers with data that is immediately ready to be used for genome-based research. We believe that our solution can provide academic, biopharmaceutical and translational medicine researchers with whole human genome data and analysis at an unprecedented combination of quality, cost and scale without requiring them to invest in in-house sequencing instruments, high-performance computing resources and specialized personnel. By removing these constraints and broadly enabling researchers to conduct large-scale whole human genome studies, we believe that our solution has the potential to significantly advance medical research and expand understanding of the basis, treatment and prevention of complex diseases.

We believe that our whole human genome sequencing technology, which is based on our proprietary DNA arrays and ligation-based read technology provides a superior combination of quality, costs and scale when compared to existing commercially available whole human genome sequencing platforms. In the DNA sequencing industry, whole human genome sequencing is generally deemed to be coverage of at least 90% of the nucleotides in the genome. Because we have optimized our technology platform and our operations for the unique requirements of high-throughput whole human genome sequencing, we are able to achieve accuracy levels in excess of 99.999% at a total cost that is significantly less than the total cost of purchasing and using commercially available DNA sequencing instruments and information process technology and then performing all the required sequence data assembly and analysis. We believe that we will be able to further improve our accuracy levels and reduce the total cost of sequencing and analysis, enabling us to maintain significant competitive advantages over the next several years. Because our technology resides only in our centralized facilities, we can quickly and easily implement enhancements and provide their benefits to our entire customer base. Our goal is to be the first company to sequence and analyze high-quality whole human genomes, at scale, for a total cost of under \$1,000 per genome.

From the earliest days of the field of genomic sequencing to the present, companies and organizations that have achieved sequencing milestones in quality, cost and scale have immediately announced and/or published these sequencing results. We regularly and actively monitor publications and have compared the parameters of our sequencing process and the sequencing results of competitive commercially available technologies announced in these various publications. We are currently unaware of any scientific publications by competitors publicly announcing superior sequencing results. Based on the above, we believe that our complete human genome sequencing technology provides a superior combination of quality, cost and scale when compared to existing commercially available complete genome sequencing methods, when taking into consideration the total cost of purchasing, operating and maintaining the instruments and information systems necessary for complete human genome sequencing.

While our competitors primarily sell DNA sequencing instruments and reagents that produce raw sequenced data, requiring their customers to invest significant additional resources to process that raw data into a form usable for research, we offer our customers an end-to-end, outsourced solution that delivers research-ready genomic data. As

the cost of complete human genome sequencing continues to decline, we believe the basis of competition in our industry will shift from the cost of sequencing to the value of the entire sequencing solution, including time to delivery, data accuracy and data management solutions. We believe that our integrated advanced informatics and data management services will emerge as a key competitive advantage as this shift occurs.

Our genome sequencing center, which began commercial operations in May 2010, combines a high-throughput sample preparation facility, a collection of our proprietary high-throughput sequencing instruments and a large-scale data center. Our customers ship us their samples via common carrier services such as Federal Express and United Parcel Service. We then sequence and analyze these samples and provide our customers with finished, research-ready data, enabling them to focus exclusively on their single highest priority, discovery.

Our customers include some of the leading academic research centers, government research centers, biopharmaceutical companies, and healthcare providers. At present, our facility has the capacity to sequence and analyze approximately 1,000 whole human genomes per month at 40x coverage. We expect this capacity to approximately double by year-end 2012 as we deploy additional sequencers and increase the throughput of our facility through process improvements. In future years, we plan to construct additional genome centers in the United States and other international strategic markets to accommodate an expected growing global demand for whole human genome sequencing on a large scale.

Our Industry

Studying how genes and proteins differ between species and among individuals within a species, or genetic variations, helps scientists determine their functions and roles in health and disease and, we expect, will continue to drive advancements in medical research and diagnostics. Genetic analysis products comprise instruments and consumables, as well as associated hardware, software and services directly involved in the study of DNA and RNA. Scientia Advisors, a third-party research firm, estimated genomic revenue in 2009 to be approximately \$5.8 billion and projects the market to grow to approximately \$9.0 billion by 2014. Scientia Advisors further estimates that human genomics research will grow from \$4.6 billion in 2009 to \$7.3 billion in 2014.

The primary genetic analysis methods traditionally used by genetic researchers fall into three categories: DNA sequencing, genotyping and gene expression analysis. DNA sequencing is the process of determining the exact order, or sequence, of the individual nucleotides in a DNA strand so that this information can be correlated to the genetic activity influenced by that segment of DNA. Genotyping is the process of examining certain known mutations or variations in the DNA sequence of genes to determine whether the particular variant can be associated with a specific disease susceptibility or drug response. Gene expression analysis is the process of examining the molecules that are produced when a gene is activated, or expressed, to determine whether a particular gene is expressed in a specific biological tissue.

The Importance of Whole Human Genome Sequencing and the Limitations of Existing Technologies

One of the most difficult challenges facing the genetic research and analysis industry is improving our understanding of how genes contribute to diseases that have a complex pattern of inheritance. For many diseases, multiple genes each make a subtle contribution to a person s predisposition or susceptibility to a disease or response to a drug treatment protocol. Accordingly, we believe that unraveling this complex network will be critical to understanding human health and disease. We believe that sequencing whole human genomes is the most comprehensive and accurate method by which to achieve these objectives and improve our understanding of human disease. However, the cost and complexity associated with whole human genome sequencing have been prohibitively high for researchers and have slowed our progress in understanding the genetic underpinnings of disease.

Innovations in DNA sequencing have led to the development of high-throughput sequencing technologies, commonly referred to as next-generation or second-generation sequencing, which produce thousands to millions of sequences at once. Although second-generation sequencing technologies have led to dramatic reductions in cost and improvements in quality and throughput for complete human genome sequencing, they were designed as general-

purpose instruments for sequencing the DNA or RNA of plants, animals, bacteria and viruses. We believe the key limitations of the model of purchasing and using second-generation technologies for sequencing large numbers of complete human genomes include the following:

High Cost. Laboratories using commercially available DNA sequencing instruments cannot sequence complete human genomes at a price low enough to make large-scale projects affordable to researchers.

Insufficient Scale and Speed. Laboratories using commercially available DNA sequencing instruments typically require months to sequence all of the genomes for large projects.

Difficulty of Data Management. Many users of commercially available DNA sequencing instruments lack the costly computing resources, storage capacity, network bandwidth and specialized personnel to process and analyze the massive data sets generated by sequencing complete human genomes.

Our Solution

We have developed a novel approach focused on whole human genome sequencing. We combine our proprietary human genome sequencing technology, which achieves accuracy levels in excess of 99.999%, with our advanced informatics and data management software and our innovative, end-to-end service model, to deliver research-ready genomic data at a total cost that is significantly less than the total cost of purchasing and using commercially available DNA sequencing instruments and the required information management hardware and software.

Proprietary Sequencing Technology

There are two primary components of our proprietary human genome sequencing technology: DNA nanoball, or DNB, arrays and combinatorial probe-anchor ligation, or cPAL, reads. Our patterned DNB arrays, due to their small size and biochemical characteristics, enable us to pack DNA very efficiently on a silicon chip. We have developed a proprietary process that causes the DNA to adhere to desired spots on the chip, while conversely preventing the DNA from adhering to the area between these spots. This enables us to affix individual particles of DNA to over 90% of these spots. In addition, we have developed a highly accurate cPAL read technology, which enables us to read the DNA fragments efficiently using small concentrations of low-cost reagents while retaining extremely high single-read accuracy. As reported in the January 2010 edition of *Science*, we sequenced a whole human genome with a consensus accuracy of 99.999% and a consumables cost of approximately \$1,800. To our knowledge, based on our review of scientific publications in the genome sequencing field, there are no commercially available technologies that have achieved the accuracy comparable to our sequencing results. Our accuracy was further validated by the Institute for Systems Biology, or ISB, as published in *Science Express* in March 2010. We have identified and are developing additional performance enhancements to our core technologies that we believe will enable us to maintain a significant competitive advantage in terms of our combination of quality, cost and scale.

Advanced Informatics and Data Management Software

Sequencing whole human genomes generates substantial amounts of data that must be managed, stored and analyzed. While many users of instrument-based sequencing systems have historically conducted their own in-house data analysis on a limited number of genomes, many of these users lack the computing, storage and network bandwidth necessary to manage the massive data sets generated by larger scale whole human genome studies. In response to this need by our customers, we have built a genomic data processing facility with computing infrastructure for managing both small- and large-scale genomic sequencing projects.

There are two major components of our data management solution: assembly software and analysis software. Assembly is the process of using computers to organize all of the overlapping 70-base nucleotide sequences to reconstruct the complete human genome. Our proprietary assembly software uses advanced data analysis algorithms and statistical modeling techniques to make high confidence calls of an average of over 97% of the genome and over 96% of the exome from approximately two billion 70-base reads. After assembling the genomic data, we use our analysis software to identify and annotate key differences, or variants, in each genome.

By using our analytical tools and data management software, our customers can significantly reduce their investments in computing infrastructure. Our customers are provided with reliable access to assembled and annotated sequence data in multiple formats to ease data sharing and comparative analyses. In addition, our data storage options provide flexibility and allow customers to customize their data management strategy based on their particular business and scientific requirements. We have also developed a suite of open source analytical tools, called CGATM Tools, designed to enable our customers to rapidly analyze the data we generate from their samples. As the reagent cost of sequencing declines, we believe that the cost and complexity of data analysis and management will emerge as the primary limiting factor for conducting whole human genome analysis.

Innovative, End-to-End, Outsourced Solution

While our competitors primarily sell DNA sequencing instruments and reagents that produce raw sequenced data, requiring their customers to invest significant additional resources to process that raw data into a form usable for research, we offer our customers an end-to-end, outsourced solution that delivers research-ready genomic data. Our genome sequencing center combines a high-throughput sample preparation facility, a collection of our proprietary high-throughput sequencing instruments and a large-scale data center. Our customers ship us their samples via common carrier services such as Federal Express and United Parcel Service. We then sequence and analyze these samples and provide our customers with finished, research-ready genomic data, enabling them to focus exclusively on their single highest priority, discovery.

Our customers are not required to purchase expensive sequencing instruments and high-performance computing resources to sequence and analyze large sets of whole human genomes. Our outsourced service model enables our customers to offload to us the complex processes of sample preparation, sequencing, computing and data storage and management. We believe our services will expand the potential addressable market by enabling a broad base of researchers who may lack sufficient capital and the specialized personnel necessary to build and operate a sequencing laboratory, or who have historically been constrained by the high total cost of sequencing, to conduct large-scale whole human genome studies.

We believe our end-to-end solution provides the following advantages to our customers:

High-Quality Data. Our technology delivers what we believe is the industry s highest accuracy whole human genome data.

Cost-Savings. Our customers are not required to purchase expensive sequencing instruments and high-performance computing resources or hire the necessary specialized personnel to sequence and analyze large sets of whole human genome data.

Speed at Scale. Our customers can often complete their large-scale projects more quickly by using our services than by purchasing and operating commercially available sequencing instruments.

Ease of Use. We believe our customers can avoid the difficulty and time-consuming process of purchasing and operating their own sequencing instruments and can outsource the entire process to us, from sample preparation to delivery of research-ready data.

Operational Flexibility. By outsourcing their large-scale whole human genome sequencing projects to us, our customers can free up the capacity of in-house instruments to run smaller or more targeted sequencing projects and applications.

Technological Flexibility. As DNA sequencing technology improves, our customers have available to them the latest technology that we have developed, and they avoid the risk of their expensive instruments becoming technologically obsolete.

Enables Customers to Focus on Discovery. Outsourcing offloads the operational burdens of managing large-scale genome sequencing projects and enables our customers to focus their resources on research, which can reduce the time to discovery. We have more than 125 past and current customers, which include some of the leading global academic and government research centers and biopharmaceutical companies. Our project with SAIC-Frederick, Inc., the prime contractor for the National Cancer Institute s research and development facility in Frederick, Maryland, involves sequencing and analyzing more than 600 tumor-normal pairs, comprising over 1,200 whole human genomes, to identify patterns relating to the genesis of cancerous tumors in children. This study may potentially lead to improved diagnosis and treatment of pediatric cancers. This project forms part of the National Cancer Institute s Therapeutically Applicable Research to Generate Effective Treatments, or TARGET, Initiative. TARGET seeks to use genomic technologies to rapidly identify valid therapeutic targets in childhood cancers so that new, more effective treatments can be developed. It is currently focusing on five childhood cancers: acute lymphoblastic leukemia, acute myeloid leukemia, neuroblastoma, osteosarcoma and Wilms tumor. Our project with the Inova Health System, a not-for-profit- health care system based in Northern Virginia, involves sequencing 1,500 genomes from 500 babies and their parents. The goal of this project is to identify prognostic, diagnostic and therapeutic targets for pre-term delivery and potentially other obstetrics associated abnormalities. The study may also help provide the framework to enable Inova to begin to use genomic data to customize care within Inova s hospital network. Data from Inova Health System s electronic medical record system will support outcomes-based research on this cohort.

Applications for Our Sequencing Service

Potential applications for our whole human genome sequencing service include:

Cancer Research. Researchers are sequencing cancer genomes and comparing them to normal genomes, which are referred to as tumor-normal pairs, to identify the mutations in cancer genomes. We believe understanding these mutations will guide development of new cancer therapeutics and diagnostics and enable doctors to select the best course of therapy based on the specific mutations found in a tumor.

Mendelian Disease Research. There are thousands of Mendelian inherited diseases that have been found to run in families, and are accordingly likely to have a significant genetic component. However, the genetic cause of most of these diseases is currently unknown. By sequencing the whole genomes of the affected families, we believe the genetic causes of these Mendelian diseases can be discovered, which could lead to the development of novel diagnostics and therapeutics.

Rare Variant Disease Research. Diseases such as central nervous system disorders, cardiac disease, certain metabolic disorders, and other diseases that appear broadly in the population are thought to be caused by rare variants. Large-scale studies of affected individuals may help to identify the disrupted pathways and lead to the development of novel diagnostics and therapeutics.

Translational Research. We believe that over time, healthcare systems will use genomic data to direct an individual s medical care. Leading institutions are beginning to conduct research aimed at identifying how best to use the knowledge of the genome to improve patient healthcare and achieve cost savings in the delivery of healthcare.

Clinical Trial Optimization. We believe that selecting or stratifying patients on the basis of their genetic profiles could enable the preferential admission of high responders into a clinical trial. This stratification could enable the trial to reach its conclusion with fewer patients and lower costs and result in faster clinical trials and drug commercialization.

Companion Diagnostic Discovery. We believe that therapeutics that are not first-line treatments for the general population may be elevated to first-line treatments or used in combination therapies for subsets of the population that share a common genetic profile. Whole human genome studies may unlock new market opportunities for these therapies or combination therapies.

In addition to these research applications, we expect future clinical applications to include:

Idiopathic Disease Pediatric Diagnostics. We believe that sequencing the whole genome of idiopathic sick children, or children the cause of whose sickness is unknown, could identify genomic mutations as well as complex interaction pathways that cannot be discovered by only analyzing selected areas of the genome. This approach may result in more rapid diagnosis and better patient care.

Cancer Pathology. We believe that whole human genome sequencing will be the most reliable and economic way to analyze complex cancer genomes that involve large and unpredictable structural changes. In the United Sates alone, there are approximately 1.5 million new cases of cancer diagnosed each year according to the National Cancer Institute.

Universal Diagnostics. As medical records technology and public health policy advance, we believe that large numbers of people will have their whole human genomes sequenced and stored for use by their physicians in managing their health care decisions. Competitive Strengths

We believe that our competitive strengths are as follows:

Proprietary Human Genome Sequencing Technology. Our proprietary sequencing technology achieves accuracy levels of 99.999% at a total cost that is significantly less than the total cost of purchasing and operating commercially available DNA sequencing instruments and the necessary information processing technology, and then performing all the required sequence data assembly and analysis.

Fully Integrated Advanced Informatics and Data Management Software. Our solution enables our customers to manage and gain useful information from the massive data sets generated in complete human genome sequencing.

Highly Scalable and Capital-Efficient Business Model. Consolidating volume across our entire customer base enables us to sequence large numbers of genomes while avoiding the cost and complexity of employing a large field installation and support organization. By implementing a high degree of automation, we have reduced the possibility of human errors that could adversely affect quality and increase costs.

Unique Insight Into Customer Needs. We interact directly with our customers on their discovery projects, which enables us to develop and enhance our analysis software to meet our customers specific needs while expanding our understanding of variation in the human genome.

Fast and Efficient Deployment of Operational and Technological Enhancements. Because our sequencing operations and data center are centralized, we can rapidly upgrade our technology and deliver the benefits to our customers. In addition, our access to genomic data allows our software engineers to continually refine and improve our software with each genome we sequence.

Expanded Market Opportunity. We believe our outsourced model will expand the potential addressable market by providing academic and biopharmaceutical researchers who lack sufficient budgets or the specialized personnel necessary to build and operate a sequencing laboratory with access to high-quality, low-cost complete human genome data.

Our Strategy

Our goal is to improve human health by providing genomic information to understand, prevent, diagnose and treat diseases and conditions. We intend to become the preferred solution for whole human genome sequencing and analysis by:

Continuing to Deliver the Highest Quality Genomic Data and Analysis at a Low Total Cost. By continuing to deliver the highest quality research-ready data and by enabling our customers to avoid the cost, complexity and risks associated with purchasing and operating the instruments and computing resources required to undertake whole human genome sequencing, our goal is to become the preferred solution for our customers.

Maintaining and Strengthening our Technology. We plan to continue to conduct research and product development activities to further improve quality, reduce costs, increase throughput and reduce our turnaround time. We plan to further develop the biochemistry, informatics, instrumentation and software that we believe together make up the industry s most robust solution. We will also seek to continually improve our operational processes and analysis software.

Capitalizing on our Scalable Model. Due to the highly scalable nature of our service model, we believe we are well positioned to serve customers looking to sequence a small number of genomes as well as customers who are looking to rapidly sequence a very large number of genomes.

Establishing Ourselves as the Leader in Outsourced Whole Human Genome Sequencing. We intend to continue to focus exclusively on whole human genome sequencing. We believe that this focus will put us in a strong position to become the preferred platform for whole human genome sequencing.

Developing Clinical Applications for the Use of our Technology. While our current focus is on providing whole human genome solutions primarily to academic, biopharmaceutical, and translational medicine researchers, we expect to develop clinical applications for whole genome sequencing for use in idiopathic pediatric disease diagnosis, cancer pathology, and ultimately, as a universal diagnostic.

Exploring Strategic Partnerships and Collaborations. We expect to establish strategic partnerships and collaborations with commercial and research organizations to leverage our genome sequencing technology with the strengths of these organizations to further develop and expand the applications for our sequencing technology.

Expanding Globally to Increase Capacity and Reach New Markets. We expect to enter into partnership agreements with domestic and international organizations to build additional genome sequencing centers around the world. These genome sequencing centers will increase our sequencing capacity, provide us with improved access to global markets and expand our revenue opportunities. Risks Associated with our Business

Our business is subject to numerous risks, as discussed more fully in the section entitled Risk Factors immediately following this prospectus supplement summary. These risks include the following, among others:

We are an early, commercial-stage company and have a limited operating history, which may make it difficult to evaluate our current business and predict our future performance.

Edgar Filing: COMPLETE GENOMICS INC - Form 424B5

We will require substantial additional funding and may be unable to raise capital when needed, which could force us to delay, reduce or cancel certain business objectives or we may be unable to continue as a going concern.

We have a history of losses, and we may not achieve or sustain profitability in the future, on a quarterly or annual basis.

Our only source of revenue is our human genome sequencing service, which is a new business model in an emerging industry, and failure to achieve market acceptance will harm our business.

Our order backlog may never be completed, and we may never earn revenue on backlogged contracts to sequence genomes. In addition, the timing of the conversion of our order backlog into revenue is dependent on the timing of receipt of samples from our customers.

The presence or absence in a specific quarter of one or more new large orders, our ability to process orders or the cancellation of previous orders, may cause our results of operations and backlog to fluctuate significantly on a quarterly basis.

Our success depends on the growth of markets for analysis of genetic variation and biological function, and the shift of these markets to whole human genome sequencing.

We face significant competition. Our failure to compete effectively could adversely affect our sales and results of operations.

We must significantly increase our production capabilities in order to achieve profitability.

If our Mountain View genome sequencing facility becomes inoperable, we will be unable to perform our genome sequencing services and our business will be harmed.

We currently are, and could in the future be, subject to litigation regarding patent and other proprietary rights that could harm our business.

Corporate Information

We were incorporated in the state of Delaware on June 14, 2005. The address of our principal executive offices is 2071 Stierlin Court, Mountain View, California 94043, and our telephone number is (650) 943-2800. Our website address is <u>www.completegenomics.com</u>. We do not incorporate the information on, or that can be accessed through, our website into this prospectus supplement or the accompanying prospectus, and you should not consider it part of this prospectus supplement or the accompanying prospectus.

The Offering

Common stock offered by us in this offering Shares of our common stock, par value \$0.001 per share, having an aggregate offering price of up to \$30 million. Manner of offering At-the-market offering that may be made from time to time on The NASDAQ Global Market or other market for our common stock in the U.S. through our agent, MLV & Co. LLC. See the section entitled Plan of Distribution in this prospectus supplement. Use of proceeds from this offering We intend to use the net proceeds from this offering for general corporate purposes, which may include funding research and development, increasing our working capital, reducing indebtedness, acquisitions or investments in businesses, products or technologies that are complementary to our own, and capital expenditures. Pending these uses, we intend to invest the net proceeds in short-term, investment-grade, interest-bearing securities. See the section entitled Use of Proceeds in this prospectus supplement. Risk factors You should read the Risk Factors section of this prospectus supplement, in the accompanying prospectus and in the documents incorporated by reference in this prospectus supplement for a discussion of factors to consider before deciding to purchase shares of our common stock. NASDAQ Global Market symbol GNOM

RISK FACTORS

An investment in our common stock involves a high degree of risk. Before deciding whether to invest in our common stock, you should consider carefully the risks described below and discussed under the section captioned Risk Factors contained in our Annual Report on Form 10-K for the year ended December 31, 2011, which is incorporated by reference in this prospectus supplement in its entirety, together with other information in this prospectus supplement, the accompanying prospectus and the information and documents incorporated herein and therein by reference, and any free writing prospectus that we have authorized for use in connection with this offering. If any of these risks actually occurs, our business, financial condition, results of operations or cash flow could be seriously harmed. This could cause the trading price of our common stock to decline, resulting in a loss of all or part of your investment.

Risks Related to This Offering

Management will have broad discretion as to the use of the proceeds from this offering, and we may not use the proceeds effectively.

Our management will have broad discretion in the application of the net proceeds from this offering and could spend the proceeds in ways that you do not agree with or that do not improve our results of operations or enhance the value of our common stock. Our failure to apply these funds effectively could have a material adverse effect on our business and cause the price of our common stock to decline.

You will experience immediate and substantial dilution in the net tangible book value per share of the common stock you purchase.

The price per share of our common stock being offered may be higher than the net tangible book value per share of our common stock outstanding prior to this offering. Assuming that an aggregate of 7,832,898 shares are sold at a price of \$3.83 per share, the last reported sale price of our common stock on The NASDAQ Global Market on March 8, 2012, for aggregate proceeds of \$30 million in this offering, and after deducting commissions and estimated aggregate offering expenses payable by us, you will suffer immediate and substantial dilution of \$1.12 per share, representing the difference between the as adjusted net tangible book value per share of our common stock as of December 31, 2011 after giving effect to this offering and the assumed offering price. See the section entitled Dilution below for a more detailed discussion of the dilution you will incur if you purchase common stock in this offering.

You may experience future dilution as a result of future equity offerings.

In order to raise additional capital, we may in the future offer additional shares of our common stock or other securities convertible into or exchangeable for our common stock. We cannot assure you that we will be able to sell shares or other securities in any other offering at a price per share that is equal to or greater than the price per share paid by investors in this offering, and investors purchasing shares or other securities in the future could have rights superior to existing stockholders. The price per share at which we sell additional shares of our common stock or other securities convertible into or exchangeable for our common stock in future transactions may be higher or lower than the price per share in this offering. As of December 31, 2011, 3,422,336 shares of common stock were reserved for future issuance under our 2006 Equity Incentive Award Plan, as amended, or the 2006 Plan, our 2010 Equity Incentive Plan, or the 2010 Plan, and our Employee Stock Purchase Plan, or ESPP, and 15,003 shares of common stock and 1,533,823 warrants outstanding to purchase shares of our common stock. You will incur additional dilution upon the grant of any shares under the 2006 Plan or the 2010 Plan, upon vesting of any outstanding restricted stock units, or upon exercise of any outstanding stock options or warrants.

FORWARD-LOOKING STATEMENTS

This prospectus supplement, the accompanying prospectus, the documents we have filed with the SEC that are incorporated by reference in this prospectus supplement or the accompanying prospectus and any free writing prospectus that we have authorized for use in connection with this offering contain forward-looking statements within the meaning of Section 27A of the Securities Act and within the meaning of Section 21E of the Securities Exchange Act of 1934, as amended, or the Exchange Act, that are subject to the safe harbor created by those sections. These forward-looking statements involve risks and uncertainties and are contained principally in the sections entitled Prospectus Supplement Summary, Risk Factors, and Business. These statements relate to future events or our future financial or operational performance and involve known and unknown risks, uncertainties and other factors that could cause our actual results, levels of activity, performance or achievement to differ materially from those expressed or implied by these forward-looking statements. These risks and uncertainties are contained principally in the section entitled Risk Factors.

Forward-looking statements include all statements that are not historical facts. In some cases, you can identify forward-looking statements by terms such as may, will, should, intend, could, would, continue, expect, plan, anticipate, believe, estimate, project, negative of those terms, and similar expressions and comparable terminology intended to identify forward-looking statements. These statements reflect our current views with respect to future events and are based on assumptions and subject to risks and uncertainties. Given these uncertainties, you should not place undue reliance on these forward-looking statements. These forward-looking statements represent our estimates and assumptions only as of the date of this prospectus, and, except as required by law, we undertake no obligation to update or revise publicly any forward-looking statements, whether as a result of new information, future events or otherwise after the date of this prospectus supplement or the accompanying prospectus, as applicable, or that any information incorporated by reference in this prospectus supplement or the accompanying prospectus is accurate as of any date other than the date of the document so incorporated by reference. Thus, you should not assume that our silence over time means that actual events are bearing out as expressed or implied in such forward-looking statements.

This prospectus supplement, the accompanying prospectus, the documents we have filed with the SEC that are incorporated by reference in this prospectus supplement or the accompanying prospectus and any free writing prospectus that we have authorized for use in connection with this offering also contain estimates and other information concerning our current and target markets that are based on industry publications, surveys and forecasts, including those generated by Scientia Advisors. These estimates and information involve a number of assumptions and limitations, and you are cautioned not to give undue weight to these estimates and information. These industry publications, surveys and forecasts generally indicate that their information has been obtained from sources believed to be reliable. The industry in which we operate is subject to a high degree of uncertainty and risk due to a variety of factors, including those described in Risk Factors. These and other factors could cause actual results to differ materially from those expressed in these publications, surveys and forecasts.

You should rely only on the information contained, or incorporated by reference, in this prospectus supplement, the accompanying prospectus and any free writing prospectus that we have authorized for use in connection with this offering. We and MLV have not authorized anyone to provide you with different information. The common stock offered under this prospectus supplement and the accompanying prospectus is not being offered in any state where the offer is not permitted.

USE OF PROCEEDS

The amount of proceeds from this offering will depend upon the number of shares of our common stock sold and the market price at which they are sold. There can be no assurance that we will be able to sell any shares under or fully utilize the sales agreement with MLV as a source of financing. We intend to use the net proceeds from this offering for general corporate purposes, which may include funding research and development, increasing our working capital, reducing indebtedness, acquisitions or investments in businesses, products or technologies that are complementary to our own, and capital expenditures. We may also use a portion of the net proceeds from this offering to acquire or invest in complementary businesses, technologies, product candidates or other intellectual property, although we have no present commitments or agreements to do so.

The amounts and timing of these expenditures will depend on a number of factors, such as the commercial success of our CGA Platform, as well as the amount of cash used in our operations. As of the date of this prospectus supplement, we cannot specify with certainty all of the particular uses of the proceeds from this offering. Accordingly, we will retain broad discretion over the use of such proceeds. Pending the use of the net proceeds from this offering as described above, we intend to invest the net proceeds in short-term, investment-grade, interest-bearing securities. We cannot predict whether the proceeds invested will yield a favorable return, if any.

DILUTION

Our net tangible book value as of December 31, 2011 was approximately \$82.4 million, or \$2.47 per share. Net tangible book value per share is determined by dividing our total tangible assets, less total liabilities, by the number of shares of our common stock outstanding as of December 31, 2011. Dilution in net tangible book value per share represents the difference between the amount per share paid by purchasers of shares of common stock in this offering and the as adjusted net tangible book value per share of our common stock immediately after giving effect to this offering.

After giving effect to the sale of our common stock in the aggregate amount of \$30 million in this offering at an assumed offering price of \$3.83, the last reported sale price of our common stock on The NASDAQ Global Market on March 8, 2012, and after deducting commissions and estimated aggregate offering expenses payable by us, our as adjusted net tangible book value as of December 31, 2011 would have been approximately \$111.7 million, or \$2.71 per share. This represents an immediate increase in net tangible book value of \$0.24 per share to existing stockholders and immediate dilution in net tangible book value of \$1.12 per share to new investors purchasing our common stock in this offering. The following table illustrates this dilution on a per share basis:

Assumed public offering price per share		\$ 3.83
Net tangible book value per share as of December 31, 2011	\$ 2.47	
Increase per share attributable to new investors	\$ 0.24	
As adjusted net tangible book value per share after this offering		\$ 2.71
Dilution per share to new investors		\$ 1.12

The shares sold in this offering, if any, will be sold from time to time at various prices. An increase of \$0.50 per share in the price at which the shares are sold from the assumed offering price of \$3.83 per share shown in the table above, assuming all of our common stock in the aggregate amount of \$30 million is sold at that price, would increase our as adjusted net tangible book value per share after the offering to \$2.77 per share and would increase the dilution in net tangible book value per share to new investors to \$1.56 per share, after deducting commissions and estimated aggregate offering expenses payable by us. A decrease of \$0.50 per share in the price at which the shares are sold from the assumed offering price of \$3.83 per share shown in the table above, assuming all of our common stock in the aggregate amount of \$30 million is sold at that price, would increase our as adjusted net tangible book value per share after the offering to \$2.63 per share and would decrease the dilution in net tangible book value per share after the offering to \$2.63 per share and would decrease the dilution in net tangible book value per share after the offering to \$2.63 per share and would decrease the dilution in net tangible book value per share after the offering to \$2.63 per share and would decrease the dilution in net tangible book value per share to new investors to \$0.70 per share, after deducting commissions and estimated aggregate offering expenses payable by us. This information is supplied for illustrative purposes only.

The above discussion and table are based on 33,409,638 shares of common stock outstanding as of December 31, 2011, and exclude as of that date:

4,101,953 shares of common stock issuable upon the exercise of outstanding options, at a weighted average exercise price of \$6.06 per share;

1,533,823 shares of common stock issuable upon the exercise of outstanding warrants, at a weighted average exercise price of \$2.29 per share;

15,003 shares of common stock issuable upon the vesting of outstanding restricted stock units; and

3,422,336 shares of common stock reserved for future issuance under the 2006 Plan, the 2010 Plan and the ESPP. To the extent that outstanding options or warrants are exercised or outstanding restricted stock units vest, investors purchasing our common stock in this offering will experience further dilution. In addition, we may choose to raise additional capital due to market conditions or strategic considerations even if we believe we have sufficient funds for our current or future operating plans. To the extent that additional capital is raised through the sale of equity or convertible debt securities, the issuance of these securities could result in further dilution to our stockholders.

PLAN OF DISTRIBUTION

We have entered into an At Market Issuance Sales Agreement, or the sales agreement, with MLV & Co. LLC, or MLV, under which we may issue and sell shares of our common stock having aggregate sales proceeds of up to \$30 million from time to time on The NASDAQ Global Market or other market for our common stock in the U.S. through MLV acting as agent. The sales agreement has been filed as an exhibit to a Current Report on Form 8-K filed under the Exchange Act and incorporated by reference in this prospectus supplement. MLV may sell the common stock by any method that is deemed to be an at-the-market equity offering as defined in Rule 415 promulgated under the Securities Act of 1933, as amended, or the Securities Act, including sales made directly on or through The NASDAQ Global Market or any other existing trading market for our common stock in the U.S. or to or through a market maker. MLV may also sell the common stock in privately negotiated transactions, subject to our prior approval. We may instruct MLV not to sell our common stock if the sales cannot be effected at or above the price designated by us from time to time. We or MLV may suspend the offering of our common stock upon notice and subject to other conditions. As an agent, MLV will not engage in any transactions that stabilize the price of our common stock.

We will pay MLV commissions for its services in acting as agent in the sale of our common stock. MLV will be entitled to compensation at a commission rate of up to 3% of the gross sales price per share sold. Because there is no minimum offering amount required as a condition to closing this offering, the actual total public offering amount, commissions and proceeds to us, if any, are not determinable at this time.

We estimate that the total expenses for the offering, excluding compensation payable to MLV under the terms of the sales agreement, will be approximately \$75,000.

Settlement for sales of our common stock will occur on the third business day following the date on which any sales are made, or on some other date that is agreed upon by us and MLV in connection with a particular transaction, in return for payment of the net proceeds to us. There is no arrangement for funds to be received in an escrow, trust or similar arrangement.

MLV will act as sales agent on a commercially reasonable efforts basis consistent with its normal trading and sales practices. In connection with the sale of the common stock on our behalf, MLV may, and will with respect to sales effected in an at-the-market offering, be deemed to be an underwriter within the meaning of the Securities Act, and the compensation of MLV may be deemed to be underwriting commissions or discounts. We have agreed to provide indemnification and contribution to MLV against certain civil liabilities, including liabilities under the Securities Act.

The offering pursuant to the sales agreement will terminate upon the earlier of (i) the issuance and sale of all shares of our common stock subject to the sales agreement, or (ii) the termination of the sales agreement as permitted therein. We may from time to time terminate the offering pursuant to the sales agreement in order to undertake other kinds of offerings, and accordingly may update this prospectus supplement to reflect any change in the amounts available for offerings pursuant to the sales agreement.

In compliance with guidelines of the Financial Industry Regulatory Authority, or FINRA, the maximum consideration or discount to be received by any FINRA member or independent broker dealer may not exceed 8% of the aggregate amount of the securities offered pursuant to this prospectus supplement and the accompanying prospectus.

MLV and its affiliates may in the future provide various investment banking and other financial services for us and our affiliates, for which services they may in the future receive customary fees. To the extent required by Regulation M, MLV will not engage in any market making activities involving our common stock while the offering is ongoing under this prospectus supplement.