PACIFIC BIOSCIENCES OF CALIFORNIA INC
Form 10-K
March 23, 2011
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UNITED STATES

SECURITIES AND EXCHANGE COMMISSION

Washington, D.C. 20549

Form 10-K

(Mark One)

x **ANNUAL REPORT PURSUANT TO SECTION 13 OR 15(d) OF THE SECURITIES EXCHANGE ACT OF 1934**
For the fiscal year ended December 31, 2010

Or

¨ **TRANSITION REPORT PURSUANT TO SECTION 13 OR 15(d) OF THE SECURITIES EXCHANGE ACT OF 1934**
For the transition period from to

Commission File Number 001-34899

Pacific Biosciences of California, Inc.

(Exact name of registrant as specified in its charter)

Delaware	16-1590339
(State or other jurisdiction of incorporation or organization)	(I.R.S. Employer Identification No.)
1380 Willow Road Menlo Park, CA 94025	94025
(Address of principal executive offices)	(Zip Code)

(Registrant s telephone number, including area code)

(650) 521-8000

Securities registered pursuant to Section 12(b) of the Act:

Title of Each Class	Name of Each Exchange on Which Registered
Common Stock, par value $0.001 per share	The NASDAQ Stock Market LLC

Securities registered pursuant to Section 12(g) of the Act:

None

Indicate by check mark if the registrant is a well-known, seasoned issuer, as defined in Rule 405 of the Securities Act. Yes ¨ No x

Indicate by check mark if the registrant is not required to file reports pursuant to Section 13 or Section 15(d) of the Act. Yes ¨ No x

Indicate by check mark whether the registrant (1) has filed all reports required to be filed by Section 13 or 15(d) of the Securities Exchange Act of 1934 during the preceding 12 months (or for such shorter period that the registrant was required to file such reports), and (2) has been subject to such filing requirements for the past 90 days. Yes x No ¨

Indicate by check mark whether the registrant has submitted electronically and posted on its corporate Web site, if any, every Interactive Data File required to be submitted and posted pursuant to Rule 405 of Regulation S-T (§232.405 of this chapter) during the preceding 12 months (or for such shorter period that the registrant was required to submit and post such files). Yes ¨ No ¨

Indicate by check mark if disclosure of delinquent filers pursuant to Item 405 of Regulation S-K is not contained herein, and will not be contained, to the best of registrant s knowledge, in definitive proxy or information statements incorporated by reference in Part III of this Form 10-K or any amendment to this Form 10-K. x

Indicate by check mark whether the registrant is a large accelerated filer, an accelerated filer, a non-accelerated filer, or a smaller reporting company. See the definitions of large accelerated filer, accelerated filer and smaller reporting company in Rule 12b-2 of the Exchange Act. (Check one):

Large accelerated filer ¨	Accelerated filer ¨
Non-accelerated filer x (Do not check if a smaller reporting company)	Smaller reporting company ¨

Indicate by check mark whether the registrant is a shell company (as defined in Rule 12b-2 of the Exchange Act). Yes ¨ No x

As of June 30, 2010, the last business day of the registrant s most recently completed second fiscal quarter, the registrant s common stock was not publicly traded. The registrant s common stock began trading on the NASDAQ Global Select Market on October 27, 2010. As of December 31, 2010, the aggregate market value of the voting stock held by non-affiliates of the registrant was approximately $472.6 million, based on the

closing price of the registrant s common stock on the NASDAQ Global Select Market on December 31, 2010.

Number of shares outstanding of the issuer s common stock as of February 28, 2011: 52,895,638

DOCUMENTS INCORPORATED BY REFERENCE:

Portions of the registrant s definitive Proxy Statement relating to its 2011 Annual Meeting of Stockholders to be held on June 23, 2011 are incorporated by reference into Part III of this Form 10-K where indicated. Such Proxy Statement will be filed with the U.S. Securities and Exchange Commission within 120 days after the end of the fiscal year to which this report relates.

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Pacific Biosciences of California, Inc.

Annual Report on Form 10-K

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SPECIAL NOTE REGARDING FORWARD LOOKING STATEMENTS

Discussions under the captions Business, Risk Factors, and Management s Discussion and Analysis of Financial Condition and Results of Operations contain or may contain forward-looking statements that are based on our management s beliefs and assumptions and on information currently available to our management. The statements contained in this Annual Report on Form 10-K that are not purely historical are forward-looking statements within the meaning of Section 27A of the Securities Act of 1933, as amended, and Section 21E of the Securities Exchange Act of 1934, as amended (the Exchange Act). Such statements may be signified by terms such as anticipates, believes, could, seeks estimates, expects, intends, may, plans, potential, predicts, projects, should, will, would or similar expressions and the neg Forward-looking statements involve known and unknown risks, uncertainties and other factors that may cause our actual results, performance or achievements to be materially different from any future results, performance or achievements expressed or implied by the forward-looking statements. Factors that could cause or contribute to such differences include, but are not limited to, those discussed under the heading Risk Factors in this report and in other documents we file with the Securities and Exchange Commission (SEC). Given these risks and uncertainties, you should not place undue reliance on these forward-looking statements. Also, forward-looking statements represent our management s beliefs and assumptions only as of the date of this report. Except as required by law, we assume no obligation to update these forward-looking statements publicly, or to update the reasons actual results could differ materially from those anticipated in these forward-looking statements, even if new information becomes available in the future.

PART I

ITEM 1. BUSINESS

Overview

We develop, manufacture and market an integrated platform for genetic analysis. We have developed a technology to study the synthesis and regulation of DNA. Combining recent advances in nanofabrication, biochemistry, molecular biology, surface chemistry and optics, we created a technology platform using our proprietary single molecule, real-time, or SMRT, technology. Our SMRT technology uses the natural processing power of enzymes, combined with specially designed reagents and detection systems, to record individual biochemical events as they occur. The ability to observe single molecule events in real time provides the scientific community with an advanced tool for investigating basic biochemical processes such as DNA synthesis. Our SMRT technology has the potential to advance scientific understanding by providing a window into biological processes that has not previously been open.

Our initial focus is on the DNA sequencing market where we have developed and introduced a third generation sequencing platform using our proprietary SMRT technology, the PacBio *RS*. The PacBio *RS* maintains many of the key attributes of currently available sequencing technologies while solving many of the inherent limitations of the first and second generation technologies, including short readlengths, limited flexibility, long time to result, complex sample preparation and risk of amplification bias. Our system provides long readlengths, flexibility in experimental design, fast time to result, and ease of use. The PacBio *RS* consists of an instrument platform that uses our proprietary consumables, which are currently comprised of our SMRT Cells and several chemical reagent kits used to format and sequence DNA samples. Our system is designed to be integrated into existing laboratory workflows and information systems. We have not yet generated revenue from our products and plan to commercially launch our first products during the second quarter of 2011.

We were incorporated in the State of Delaware in 2000. Our executive offices are located at 1380 Willow Road, Menlo Park, California 94025, and our telephone number is (650) 521-8000.

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The Underlying Science

Genetic inheritance in living systems is conveyed through a naturally occurring information storage system known as deoxyribonucleic acid, or DNA. DNA stores information in linear chains of the chemical bases adenine, cytosine, guanine and thymine, represented by the symbols, A, C, G and T. Inside living cells, these chains usually exist in pairs bound together in a double helix by complementary bases, with A of one strand always binding to a T of the other strand and C always binding to G.

In humans, there are approximately three billion DNA base-pairs in the molecular blueprint of life, called the genome. These three billion bases are divided into 23 chromosomes ranging in size from 50 million to 250 million bases. Normally, there are two complete copies of the genome contained in each cell, one of maternal origin and the other of paternal origin. When cells divide, the genomes are replicated by an enzyme called the DNA polymerase, which visits each base in the sequence, creating a complementary copy of each chromosome using building blocks called nucleotides. Contained within these chromosomes are approximately 23,000 smaller regions, called genes, each one containing the recipe for a protein or group of related proteins. The natural process of protein production takes place in steps. In a simplified model, the first step is transcription, a process in which an enzyme called the RNA polymerase converts the DNA strand base for base into messenger RNA, or mRNA. The mRNA are then translated into proteins by ribosomes. The resulting proteins go on to play crucial roles in cellular structure and function and thus the operation of biological systems.

Numerous scientific approaches have evolved to adapt to the emerging awareness of the magnitude of complexity embedded in biological systems. The field of genomics developed to study the interactions among components in the genome and the massive quantities of associated data. Subsequently, proteomics, transcriptomics and a number of other related fields emerged.

Advances in biology over the next decade are expected to be shaped by a more detailed understanding of the fundamental complexity of biological systems. These systems vary among individuals in previously unrecognized ways and are influenced by factors including time, molecular interactions, and cell type.

Importantly for the future of genomics, the first few whole-genome sequencing studies of disease have shown that rare mutations play a critical role in human disease. These mutations would not have been detected in earlier studies because too few people, or perhaps only one person, carry the specific mutation. In addition, it is now understood that structural changes to the genome in which whole sections are deleted, inverted, copied or moved may be responsible for a significant fraction of variation among individuals. The scope of these structural changes challenges the very idea of a reference genome.

Recent discoveries have highlighted additional complexities in the building blocks of DNA and RNA, including the presence of additional bases. It has long been known that in humans and many other multicellular organisms, the cytosine bases can be chemically modified through the addition of a methyl group in a process called methylation. These chemical modifications have been shown to play a role in embryonic development, have important impacts on diseases such as cancer and can even affect the characteristics of offspring for multiple generations. More recently, it has been discovered that other bases, such as hydroxymethylcytosine, or hmC, 8-Oxoguanine and many others, play important physiological roles. In RNA, dozens of chemical modifications play important roles in cellular function.

Another source of complexity derives from the processing of RNA molecules after being transcribed from the genome. The majority of all genes have different forms of the protein that can be made depending on the structure of the RNA molecule, referred to as splice variants. A detailed understanding of both the expression pattern and regulation of these variants is believed to play an important role in a number of critical biological processes.

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Recent advances in our understanding of biological complexity have highlighted the need for new tools to study DNA, RNA and proteins. In the field of DNA sequencing incremental technological advances have provided novel insights into the structure and function of the genome. Despite these advances, researchers have not been able to fully characterize the human genome because of inherent limitations in these tools.

Evolution of Sequencing

In order to understand the limitations of current DNA sequencing technologies, it is important to understand the sequencing process. This consists of three phases: sample preparation, physical sequencing, and re-assembly. The first step of sample preparation is to break the target genome into multiple small fragments. Depending on the amount of sample DNA, the resulting fragments may be amplified into multiple copies using a variety of molecular methods. In the physical sequencing phase, the individual bases in each fragment are identified in order, creating individual reads. The number of individual bases identified contiguously is defined as readlength. In the re-assembly phase, bioinformatics software is used to align overlapping reads, which allows the original genome to be assembled into contiguous sequence. The longer the readlength the easier it is to reassemble the genome.

First Generation Sequencing

First generation sequencing, also referred to as Sanger sequencing, was originally developed by Frederick Sanger in 1977. With this technology, during sample preparation, scientists first make different sized fragments of DNA each starting from the same location. Each fragment ends with a particular base that is labeled with one of four fluorescent dyes corresponding to that particular base. Then all of the fragments are distributed in order of their length by driving them through a gel. Information regarding the last base is used to determine the original sequence. Under standard conditions, this method results in a readlength that is approximately 700 bases on average, but may be extended to 1,000 bases. These are relatively long readlengths compared with other sequencing methods. However, first generation sequencing is limited by the small amounts of data that can be processed per unit of time, referred to as throughput.

Second Generation Sequencing

Commercial second generation DNA sequencing tools emerged in 2005 in response to the low throughput of first generation methods. To address this problem, second generation sequencing tools achieve much higher throughput by sequencing a large number of DNA molecules in parallel. In order to generate this large number of DNA molecules, a copying method called PCR amplification is required. In addition to adding time and complexity to the sample preparation process, the amplification process can introduce errors known as amplification bias. The effect of this bias is that the resulting copies are not uniformly representative of the original template DNA.

In most second generation tools, tens of thousands of identical strands are anchored to a given location to be read in a process consisting of successive flushing and scanning operations. The flush and scan sequencing process involves sequentially flushing in reagents, such as labeled nucleotides, incorporating nucleotides into the DNA strands, stopping the incorporation reaction, washing out the excess reagent, scanning to identify the incorporated base and finally treating that base so that the strand is ready for the next flush and scan cycle. This cycle is repeated until the reaction is no longer viable.

Due to the large number of flushing, scanning and washing cycles required, the time to result for second generation methods is generally long, usually taking days. This repetitive process also limits the average readlength produced by most second generation systems under standard sequencing conditions to approximately 35 to 400 bases. The array of DNA anchor locations can have a high density of DNA fragments, leading to extremely high overall throughput and a resultant low cost per identified base when the machine is run at high capacity. However, the disadvantages of second generation sequencing include short readlength, complex sample

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preparation, the need for amplification, long time to result, the need for many samples to justify machine operation and significant data storage and interpretation requirements.

First and second generation sequencing technologies have led to a number of scientific advances. However, given the inherent limitations of these technologies, researchers still have not been able to unravel the complexity of genomes.

Pacific Biosciences Solution The Third Generation of Sequencing Technology

We have developed a technology platform that enables single molecule, real-time, or SMRT, detection of biological processes. Based on our platform SMRT technology we have introduced a third generation DNA sequencing system, the PacBio *RS*, that addresses many of the limitations of the first and second generation technologies, by providing longer readlengths, increased flexibility, reduced time to result, high throughput, simplified sample preparation and elimination of amplification bias, and may also enable additional biological research, including kinetic detection, RNA transcription monitoring, RNA sequencing, protein translation and ligand binding. We refer to this new paradigm of study as SMRT Biology.

Pacific Biosciences SMRT Technology

Our SMRT technology enables the observation of DNA synthesis as it occurs in real time by harnessing the natural process of DNA replication, which in nature is a highly efficient and accurate process actuated by the DNA polymerase. The DNA polymerase attaches itself to a strand of DNA to be replicated, examines the individual base at the point it is attached, and then determines which of four building blocks, or nucleotides, is required to replicate that individual base. After determining which nucleotide is required, the polymerase incorporates that nucleotide into the growing strand that is being produced. After incorporation, the enzyme advances to the next base to be replicated and the process is repeated.

To overcome the challenges inherent in observing the natural activity of the DNA polymerase, an enzyme that is 15 nanometers (nm) in diameter running in real time, we introduced three key innovations:

The SMRT Cell

Phospholinked nucleotides

The PacBio *RS*

The SMRT Cell

One of the fundamental challenges with observing a DNA polymerase working in real time is the ability to detect the incorporation of a single nucleotide, taken from a large pool of potential nucleotides, during DNA synthesis. To resolve this problem, we utilize our nanoscale innovation, the zero-mode waveguide, or ZMW.

A ZMW is a hole, tens of nanometers in diameter. The small size of the ZMW prevents visible laser light, which has a wavelength of approximately 600nm, from passing entirely through the ZMW. Rather than passing through, the light decays as it enters the ZMW. Therefore, by shining a laser into the ZMW, only the bottom 30nm of the ZMW becomes illuminated. Within each ZMW, a single DNA polymerase molecule is anchored to the bottom of the glass surface of the ZMW using a proprietary technique. Nucleotides, each type labeled with a different colored fluorophore, are then flooded above an array of ZMWs at the required concentration. As no laser light penetrates up through the holes to excite the fluorescent labels, the labeled nucleotides above the ZMWs are dark. Only when they diffuse through the bottom 30nm of the ZMW do they fluoresce. When the correct nucleotide is detected by the polymerase, it is incorporated into the growing DNA strand in a process that takes milliseconds in contrast to simple diffusion which takes microseconds. This difference in time results in higher signal intensity for incorporated versus unincorporated nucleotides, which creates a high signal-to-noise ratio. Thus, the ZMW has the ability to detect a single incorporation event against the background of fluorescently labeled nucleotides at biologically relevant concentrations.

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Our DNA sequencing is performed on proprietary SMRT Cells, each having an array of approximately 150,000 ZMWs. Each ZMW is capable of containing a DNA polymerase loaded with a different strand of DNA sample. Currently, our system can monitor 75,000 ZMWs simultaneously. The system can be set up to monitor the first set of 75,000 ZMWs on a SMRT Cell, then immediately shift to monitoring the second set of 75,000 ZMWs on the same SMRT Cell. As a result, the SMRT Cell enables the potential detection of approximately 150,000 single molecule sequencing reactions. Currently, our immobilization process randomly distributes polymerases into ZMWs across the SMRT Cell, resulting in approximately one-third of the ZMWs being available for use.

Phospholinked Nucleotides

Our proprietary phospholinked nucleotides have a fluorescent dye attached to the phosphate chain of the nucleotide rather than to the base. As a natural step in the synthesis process, the phosphate chain is cleaved when the nucleotide is incorporated into the DNA strand. Thus, upon incorporation of a phospholinked nucleotide, the DNA polymerase naturally frees the dye molecule from the nucleotide when it cleaves the phosphate chain. Upon cleaving, the label quickly diffuses away, leaving a completely natural piece of DNA with no evidence of labeling remaining.

The PacBio RS

The PacBio *RS* is an instrument that conducts, monitors, and analyzes single molecule biochemical reactions in real time. The PacBio *RS* uses a high numerical aperture objective lens and four single-photon sensitive cameras to collect the light pulses emitted by fluorescent reagents allowing the observation of biological processes. An optimized set of algorithms is used to translate the information that is captured by the optics system. Using the recorded information, light pulses are converted into either an A, C, G or T base call with associated quality metrics. Once sequencing is started, the real-time data is delivered to the system s primary analysis pipeline, which outputs base identity and quality values, or QVs. To generate a consensus sequence from the data, an assembly process aligns the different fragments from each ZMW based on common sequences.

SMRT Sequencing Advantages

Sequencing based on our SMRT technology offers the following key benefits:

***Single molecule, real-time analysis*.** The ability to observe single molecules in real time combined with long readlength allows our system to observe structural and cell type variation that present challenges for existing short-read technologies. Unlike many other sequencing platforms, minimal amounts of reagent and sample preparation are required and there are no time-consuming flushing, scanning and washing steps.

Longer readlengths. Our SMRT technology is designed to produce a distribution of readlengths with greater than 1,000 base pairs on average and instances of over 10,000 base pairs, which facilitates mapping and assembly. Longer readlengths require the sequencing of fewer overlapping segments, referred to as coverage, to efficiently assemble the underlying genomic structure. Long readlengths are an important factor in enabling a comprehensive view of the genome, as they can reveal multiple types of genetic variation, such as large-scale rearrangements observed in cancer.

Faster time to result. With the PacBio *RS*, sample preparation to sequencing results can take less than one day. A typical sequencing run can require as little as 30 minutes of instrument time, with target polymerase speeds of one to three bases per second, compared to existing technologies which often take multiple days to produce results. This fast time to result may have important implications for applications where speed is of critical importance such as infectious disease monitoring and molecular pathology.

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Ease of use. Our system is easy to use and adopt because it is compatible with existing lab workflows and informatics infrastructures. Our SMRTbell sample preparation protocol is designed to be simple and fast. It can be used with a variety of sample types and can output a range of DNA lengths. The PacBio *RS* is equipped with a touchscreen interface that requires minimal user intervention. The data format has been designed to be compatible with standard informatics systems. We believe that these attributes will allow for easy training and rapid adoption at customer sites.

Flexibility and granularity. The PacBio *RS* system offers multiple protocols, including standard, circular consensus, and strobe sequencing, enabling the user to optimize performance based on the needs for a particular project. The system also has the ability to scale the throughput and cost of sequencing across a range of small and large projects.

Ability to observe and capture kinetic information. The ability to observe the activity of a DNA polymerase in real time enables the PacBio *RS* to collect, measure and assess the dynamics and timing of nucleotides being added to a growing DNA strand, referred to as kinetics. It is well established in the scientific community that chemical modification of DNA such as the addition of a methyl group, known as methylation, can alter the biological activity of the affected nucleotide. The PacBio *RS* detects changes in kinetics automatically by capturing and recording changes in the duration of, and distances between, each of the fluorescent pulses during a typical sequencing analysis. First and second generation sequencing systems are unable to accurately record this type of kinetic data because the flush and scan sequencing process disrupts the timing of the natural incorporation process.

Our Products

We are preparing to enter the market with our first product, the PacBio *RS*, a third generation sequencing instrument that provides real-time information at the single molecule level. The initial application for the system is DNA sequencing, and the architectural design of the system will enable a broader range of applications over time. The instrument is designed for expandable capability to permit performance improvements and new applications to be delivered through chemistry and software enhancements without necessitating changes to the hardware.

Our sequencing system includes the PacBio *RS* instrument and proprietary consumables, including SMRT Cells and reagent kits, providing a complete solution to the customer.

The PacBio RS

The PacBio *RS* is an instrument that conducts, monitors and analyzes biochemical sequencing reactions. The instrument is an integrated unit that includes high performance optics, automated liquid handling, a touchscreen control interface, a computational Blade Center and software. The instrument s high performance optics monitor the thousands of ZMWs in real time. The automated liquid handling robotics perform reagent mixing and prepare SMRT Cells. The instrument s touchscreen control interface, the *RS* Touch, is the user s primary control center to design and monitor experiments as they occur in real time. The Blade Center is the computational brain of the PacBio *RS,* responsible for the secondary processing of the sequencing data being produced on the SMRT Cells. The PacBio *RS* has been designed to allow for performance improvements without an upgrade or replacement of the instrument hardware.

Consumables

To run our PacBio *RS*, our customers must purchase our proprietary consumable products. Our consumable products include our proprietary SMRT Cells and reagent kits. One SMRT Cell is consumed per sequencing reaction on the PacBio *RS*. Eight SMRT Cells are individually hermetically sealed and packaged together into a streamlined 8Pac format. This enables a researcher to use one or more SMRT Cells per run.

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We offer several reagent kits, each designed to address a specific step in the workflow. The Template Preparation Kit is used to convert DNA into our SMRTbell double-stranded DNA library format and therefore includes typical molecular biology reagents, such as ligase and restriction enzymes. The Binding Kit, which includes our modified DNA polymerase, is then used to bind this library to the polymerase in preparation for sequencing. The Sequencing Kit contains the reagents required for on-instrument, real-time sequencing, including the phospholinked nucleotides. Each sample can be sequenced in a single SMRT Cell or across many SMRT Cells depending on the needs of the project. As a result, the price per reaction is dependent on the experiment design.

Market Opportunity

The market for sequencing products is large and is expected to grow significantly. In 2009, the sequencing market was estimated to be $1.2 billion, which is comprised of $600 million and $600 million for first and second generation sequencing, respectively, and is expected to grow to more than $3.6 billion by 2014 according to a report commissioned on our behalf and conducted by Scientia Advisors, a life sciences consulting firm. The growth in this market is expected to be driven by increases in the demand for sequencing products from both research institutions and commercial companies, including academic institutions, reference labs and genomics service providers, pharmaceutical companies and agriculture biology, or AgBio, companies.

The primary areas of market growth are expected to be genomics, increasing from approximately $700 million in 2009 to $1.9 billion by 2014, and AgBio, increasing from approximately $200 million in 2009 to $1.3 billion by 2014. Historically, improvements in tools have driven growth in demand. We believe the emergence of third generation sequencing products, including our products, along with improvements in existing second generation products, will contribute to and comprise an important facet of this growth.

There are a number of emerging markets for sequencing-based tests, including molecular diagnostics, which represent significant potential opportunities for our products. For example, the market for sequence-based molecular diagnostics is estimated to be $1.6 billion in 2014 according to Scientia Advisors.

Pacific Biosciences Strategy

We plan to execute the following strategy:

Contribute to the future of biological analysis by offering differentiated products based on our proprietary SMRT technology. Our SMRT technology provides a window into biological processes that has not previously been available. The combination of our products and underlying SMRT technology s ability to deliver long read lengths, high throughput and short time to result afford the scientific community a new tool to conduct research not possible with first and second generation sequencing instruments.

Focus initially on the DNA sequencing market. We will initially sell our products into the rapidly growing DNA sequencing market. We believe our third generation sequencing technology will address most of the limitations in current sequencing technologies and enable a wide range of experiments and applications. We believe that the introduction of the PacBio *RS* will expand the market for genetic analysis tools.

Continually enhance product performance to increase market share. The design of the PacBio *RS* will allow for significant performance improvements without an upgrade or replacement of the instrument hardware. Our flexible platform is designed to generate a recurring revenue stream through the sale of proprietary SMRT Cells and reagent kits. Our research and development efforts are focused on product enhancements to reduce DNA sequencing cost and time as well as expand capabilities.

Leverage platform to develop and launch additional applications. We plan to leverage our SMRT technology platform to develop new applications targeting kinetic detection, RNA transcription

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monitoring, RNA sequencing, protein translation and ligand binding. We believe these applications will create substantial new markets for our technology.

Create a global community of users to enhance informatics capabilities and drive adoption of our products. We have worked closely with members of the informatics community to develop and define standards for working with single molecule, real-time sequence data. We have launched the PacBio DevNet, a software developer s open network to support academic informatics developers, life scientists and independent software vendors interested in creating tools to work with our third generation sequencing data. This gives the user flexibility to perform further analysis of the sequencing data through third-party software or share data with collaborators. To maximize the flexibility and functionality for all users, all of our secondary analysis algorithms are open source.

Marketing and Sales

We market our products through a direct sales force in North America and Europe and recently established a presence in Asia to service the Asia Pacific market. Our sales strategy involves the use of a combination of sales managers, sales representatives and field application specialists. As of December 31, 2010, we had eleven sales managers and sales representatives and ten field application specialists. We expect to increase our sales force as we expand our business.

The role of our sales managers and sales representatives is to educate customers on the advantages of SMRT technology and the applications that our technology makes possible. The role of our field application specialists is to provide on-site training and scientific technical support to prospective and existing customers. Our field application specialists are technical experts with advanced degrees, and generally have extensive experience in academic research and core sequencing lab experience.

In addition, we maintain an applications lab team in Menlo Park, California composed of scientific experts who can transfer knowledge from the research and development team to the field application specialists. The applications lab team also runs foundational scientific collaborations and proof of principle studies, which help demonstrate the value of our product offering to prospective customers.

Customers

We are targeting customers that include genome centers, clinical, government and academic institutions, genomics service providers and agricultural companies. In general, our customers will isolate, prepare and analyze genetic samples using the PacBio *RS* in their own research labs to address their specific applications and scientific questions. For example, customers in academic research institutions may have DNA samples isolated from human cancer patients while AgBio companies may have DNA samples isolated from different strains of corn or other crops.

We instituted a limited production release program pursuant to which we received orders for eleven limited production release instruments from entities such as genome centers, clinical, government and academic institutions and agricultural companies. This program was designed to help us garner quality feedback on the product prior to our full commercial launch. We received orders for our limited production release instrument from Baylor College of Medicine, the Broad Institute of MIT and Harvard, Cold Spring Harbor Laboratory, the U.S. Department of Energy Joint Genome Institute, The Genome Center at Washington University, Monsanto Company, the National Cancer Institute/SAIC-Frederick, the National Center for Genome Resources, the Ontario Institute for Cancer Research, Stanford University and Wellcome Trust Sanger Institute. During 2010, we shipped all eleven PacBio *RS* limited production release instruments During the LPR testing period, which we expect to last through the first quarter of 2011, we will work with these customers to obtain feedback and plan to incorporate relevant improvements into the commercial release version of the PacBio *RS*.

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Backlog

As of December 31, 2010, our backlog was approximately $24.0 million, comprised of 38 systems, including PacBio *RS* limited production release instruments shipped in 2010. We define backlog as purchase orders or signed contracts from our customers which we believe are firm and for which we have not yet recognized revenue. We expect to deliver all orders in our backlog by December 31, 2011.

Manufacturing

Our principal manufacturing facilities are located at our headquarters in Menlo Park, California. We currently manufacture our instruments in-house. Over time, we intend to outsource various sub-assemblies to third-party manufacturers, but we expect to continue to conduct the final assembly in-house. With respect to the manufacture of SMRT Cells, we subcontract wafer fabrication and processing to semiconductor processing facilities, but conduct critical surface treatment processes internally. In addition, we currently manufacture critical reagents in-house, including our phospholinked nucleotides and our DNA polymerase.

We purchase both custom and off-the-shelf components from a large number of suppliers and subject them to significant quality specifications. We periodically conduct quality audits of suppliers and have established a supplier certification program. We purchase components through purchase orders and generally do not maintain large volumes of inventory. Some of the components required in our instruments are currently either sole sourced or single sourced.

Service and Support

Service for our instruments is performed by our field service engineers. As of December 31, 2010, we employed fourteen field service engineers, and we intend to hire additional field service engineers as we grow our business. Our field service engineers are trained in-house, building, testing and troubleshooting instruments on our factory floor before being qualified to service instruments installed at customer sites.

Research and Development

Our SMRT technology requires the blending of a number of unique disciplines, namely nanofabrication, physics, photonics, optics, molecular biology, engineering, signal processing, high performance computing, and bioinformatics. Our research and development team is a blend of these disciplines creating a single, cross-functional operational unit. We have also established productive working relationships with technology industry leaders, as well as leading academic centers, to augment and complement our internal research and development efforts. Research and development expense incurred for these activities was $111.8 million, $75.9 million and $38.0 million during 2010, 2009, and 2008, respectively.

We plan to continue investment in research and development to support the ongoing development of chemistry components and protocols to enhance overall system performance. Our goals are to continuously improve sequencing readlength, raw read accuracy and the number of reactions on each SMRT Cell, as well as to develop and introduce into the marketplace new applications that will take full advantage of our single molecule, real-time detection technology. In addition, our engineering teams will continue their focus on increasing instrument component and system reliability, reducing costs, increasing sample throughput, and implementing additional system flexibility and versatility.

Intellectual Property

Developing and maintaining a strong intellectual property position is an important element of our business. We have sought patent protection for our SMRT technology, and may seek patent protection for improvements and ancillary technology conceived in developing our SMRT technology if we believe such protection will give us an advantage over competitors or potential competitors.

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Our current patent portfolio, including patents exclusively licensed by us, is directed to various technologies, including SMRT nucleic acid sequencing and other methods for analyzing biological samples, ZMW arrays, surface treatments for such ZMW arrays, reagents for use in nucleic acid sequencing, including phospholinked nucleotides, and other methods for analyzing biological samples, optical components and systems, processes for identifying nucleotides within nucleic acid sequences and processes for analysis and comparison of nucleic acid sequence data. Some of the patents and applications that we own, as well as some of the patents and applications that we have licensed, are subject to U.S. government march-in rights, whereby the U.S. government may disregard our exclusive patent rights on its own behalf or on behalf of third parties by imposing licenses in certain circumstances, such as if we fail to achieve practical application of the U.S. government funded technology, because action is necessary to alleviate health or safety needs, to meet requirements of federal regulations, or to give preference to U.S. industry. In addition, U.S. government funded inventions must be reported to the government and U.S. government funding must be disclosed in any resulting patent applications.

As of December 31, 2010, we own or hold exclusive licenses to 55 issued U.S. patents, 135 pending U.S. patent applications, six granted foreign patents and 158 pending foreign patent applications, including foreign counterparts of U.S. patent and patent applications. The full term of these issued U.S. patents will expire between April 17, 2016 and May 9, 2028

Of these patents and patent applications, 19 issued U.S. patents, seven pending U.S. patent applications, one granted foreign patent and six pending foreign patent applications are licensed to us by the Cornell Research Foundation, which manages technology transfers on behalf of Cornell University, collectively referred to as Cornell. These patents and patent applications are directed to the core SMRT sequencing methods and systems and other analysis methods, and to ZMW arrays used in our current and planned products. The license agreement provides us with the exclusive right to make, use, sell, offer for sale, lease, import, export or otherwise dispose of products covered by the licensed patents in all fields of use. In exchange, we are obligated to make certain royalty payments to Cornell, including a minimum annual royalty payment, and meet certain reporting and other requirements to Cornell. We are also obligated to reimburse Cornell for the costs of prosecuting the patents and patent applications that are subject to the license. The research leading to the licensed technology was funded by the U.S. government and therefore our license from Cornell is subject to U.S. government march-in rights. Cornell may terminate its agreement with us if we are in default of our payment or reporting obligations, are in material breach of the agreement, or fail to fulfill our diligence obligations with respect to commercializing products using the licensed technology.

We have also entered into a license agreement with Indiana University Research and Technology Corporation, or IURTC, for U.S. Patent No. 6,399,335, which relates to nucleoside triphosphates that include a labeling group attached through the terminal phosphate group in the triphosphate chain. Under the terms of this license agreement, we have exclusive rights to make, have made, sell, offer to sell, have sold, use, import and have imported, products that practice the invention claimed in the patent in certain sequencing-related fields. In exchange, we are obligated to make certain royalty and milestone payments to IURTC, and to meet certain reporting requirements to IURTC. We are also obligated to reimburse IURTC for the costs of prosecuting the patents and patent applications that are subject to the license. The research leading to the licensed technology was funded by the U.S. government and therefore our license from IURTC is subject to U.S. government march-in rights. IURTC may terminate its agreement with us if we are in default of our payment or record keeping obligations, are in material breach of the agreement, or fail to fulfill our diligence obligations with respect to commercializing products using the licensed technology.

In addition, we have entered into a license agreement with Stanford University, or Stanford, for U.S. Patent No. 7,297,532, referred to as the 532 patent, which relates to immobilized ribosomes for use in analysis of ribosomal activity. Under the terms of this license agreement, we have exclusive rights to make, have made, use, import, offer to sell and sell products that would practice the invention claimed in the patent in certain fields of use until June 8, 2018, after which the license will become non-exclusive until the 532 patent expires. In

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exchange, we are obligated to make certain royalty and license maintenance payments to Stanford, and to meet certain reporting and other obligations to Stanford. We are also obligated to reimburse Stanford for all patenting expenses associated with the 532 patent, including maintenance fees and costs associated with any interference or reexamination matters. The research leading to the 532 patent was funded by the U.S. government and therefore our license from Stanford is subject to U.S. government march-in rights. Stanford may terminate its agreement with us if we are in default of our payment or reporting obligations, are in breach of any provision of the agreement, or fail to fulfill our diligence obligations with respect to commercializing products relating to the 532 patent.

We have also entered into a license agreement with GE Healthcare Bio-Sciences Corp, or GE Healthcare, under several U.S. and foreign patents and pending patent applications related to labeled nucleoside polyphosphate compounds. Under the terms of the license, we have the non-exclusive right to make, have made, import, use, distribute, offer to sell and sell products that practice the inventions claimed in the patents. In exchange, we are obligated to make certain royalty and other payments to GE Healthcare. GE Healthcare may terminate its agreement with us if, among other things, we are in breach of the agreement.

In June 2010, we entered into a collaboration agreement with Gen-Probe Incorporated, or Gen-Probe, regarding the research and development of instruments integrating our SMRT technologies and Gen-Probe s sample preparation technologies for use in clinical diagnostics. Subject to customary termination rights, the initial term of the collaboration will end on the earlier of (i) December 15, 2012 and (ii) six months after we achieve certain development milestones. During the collaboration period, each party will be free to sell instrument systems that incorporate its own technology but, subject to limited exceptions, neither party may jointly develop integrated sequencing systems for clinical diagnostics with any third party nor license its technology to any third party for such use. In addition, the collaboration agreement provides each party with preferred access to certain products of the other party when commercially available, both during and after the collaboration period.

Where patent protection is difficult to obtain or difficult to enforce for a particular technological development or the technological development derives greater value from being maintained as confidential information, we seek to protect such information as a trade secret.

Competition

Given the market opportunity, there are a significant number of competing companies offering DNA sequencing equipment or consumables. These include Illumina Inc., Life Technologies Corporation and Roche Applied Science. Some of these companies have or will have greater financial, technical, research and other resources than us. They may also have larger and more established manufacturing capabilities and marketing, sales and support functions. We expect the competition to intensify within this market as there are also several companies in the process of developing new technologies, products and services. These emerging potential competitors include Complete Genomics, Inc. and Oxford Nanopore Technologies Ltd..

In order for us to successfully compete against these companies, we will need to demonstrate that our products deliver superior performance and value as a result of our key differentiators, including single molecule, real-time resolution, long readlength, fast time to result and flexibility, as well as the breadth and depth of current and future applications.

Employees

As of December 31, 2010, we had 431 full-time employees. Of these employees, 217 were in research and development, 104 were in operations, 64 were in sales, marketing and service, and 46 were in general and administration. With the exception of our field-based sales and service teams, all of our employees are located at our headquarters in Menlo Park, California. None of our employees are represented by labor unions or are

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covered by a collective bargaining agreement with respect to their employment. We have not experienced any work stoppages, and we consider our relationship with our employees to be good.

Available Information

Our web site is located at www.pacificbiosciences.com. The information posted on our web site is not incorporated into this Annual Report on Form 10-K. Our Annual Report on Form 10-K, Quarterly Reports on Form 10-Q, Current Reports on Form 8-K and amendments to reports filed or furnished pursuant to Sections 13(a) and 15(d) of the Securities Exchange Act of 1934, as amended, are available free of charge through the Investors section of our web site as soon as reasonably practicable after we electronically file such material with, or furnish it to, the SEC.

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ITEM 1A. RISK FACTORS

You should consider carefully the risks and uncertainties described below, together with all of the other information in this Annual Report on Form 10-K, which could materially affect our business, financial condition, results of operations and prospects. The risks described below are not the only risks facing us. Risks and uncertainties not currently known to us or that we currently deem to be immaterial also may materially affect our business, financial condition, results of operations and prospects.

Risks Related to Our Business

We are a development stage company with limited operating history.

We may never achieve commercial success and have not yet commercially launched our first product. We have no historical financial data upon which to base our projected revenue. We have limited historical financial data upon which to base our planned operating expense or upon which to evaluate us and our prospects. Based on our limited experience in developing and marketing new products, we may not be able to effectively:

drive adoption of our products;

attract and retain customers for our products;

comply with evolving regulatory requirements applicable to our products;

anticipate and adapt to changes in our market;

focus our research and development efforts in areas that generate returns on these efforts;

maintain and develop strategic relationships with vendors and manufacturers to acquire necessary materials for the production of our products;

implement an effective marketing strategy to promote awareness of our products;

scale our manufacturing activities to meet potential demand at a reasonable cost;

avoid infringement and misappropriation of third-party intellectual property;

obtain licenses on commercially reasonable terms to third-party intellectual property;

obtain valid and enforceable patents that give us a competitive advantage;

protect our proprietary technology;

provide appropriate levels of customer training and support for our products;

protect our products from any equipment or software-related system failures; and

attract, retain and motivate qualified personnel.

In addition, a high percentage of our expenses is and will continue to be fixed. Accordingly, if we do not generate revenue as and when anticipated, our losses may be greater than expected and our operating results will suffer.

We have incurred losses to date, and we expect to continue to incur significant losses as we develop our business and may never achieve profitability.

We have incurred net losses since inception and have not generated revenue from product sales to date. We expect to incur increasing costs as we grow our business. We cannot be certain if or when we will produce sufficient revenue from our operations to support our costs. Even if profitability is achieved, we may not be able to sustain profitability. We expect to incur substantial losses and negative cash flow for the foreseeable future.

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If our products fail to achieve and sustain sufficient market acceptance, we will not generate expected revenue and our business may not succeed.

Since we have not yet commercialized our products, we cannot be sure that they will gain acceptance in the marketplace. Our success depends, in part, on our ability to develop products that displace or supplement current technology, as well as to expand the market for genetic analysis to include new applications that are not practical with current technologies. To accomplish this, we must develop and successfully commercialize our SMRT technology for use in a variety of life science applications. There can be no assurance that we will be successful in securing customers for our products, in particular, our first product which is focused on DNA sequencing. Furthermore, we cannot guarantee that the design of our products, including the initial specifications and any enhancements or improvements to those specifications, will be satisfactory to potential customers in the markets we seek to reach. These markets are dynamic, and there can be no assurance that they will develop as quickly as we expect or that they will reach their full potential. As a result, we may be required to refocus our marketing efforts, and we may have to make changes to the specifications of our products to enhance our ability to enter particular markets more quickly. Even if we are able to implement our technology successfully, we may fail to achieve or sustain market acceptance of our products by academic and government research laboratories and pharmaceutical, biotechnology and agriculture companies, among others, across the full range of our intended life science applications. If the market for our products fails to develop or grows more slowly than anticipated, if competitors develop better or more cost-effective products or if we are unable to develop a significant customer base, our future sales and revenue would be materially harmed and our business may not succeed.

The products we expect to introduce are highly complex, with unknown support requirements.

In light of the highly complex technology involved in our products, there can be no assurance that we will be able to successfully complete the development or manufacture of our products or obtain sufficient reliability for commercial launch. In addition, there can be no assurance that we will be able to successfully provide adequate support for our products. If our products have reliability or other quality issues or require unexpected levels of support, our reputation and business could be harmed. We cannot estimate with any certainty the cost of service and support. We intend to ship our Pac Bio *RS* instruments with one year of service included in the purchase price with an option to purchase an additional year of service. If service and support costs are more than we anticipate, our business and operations may be adversely affected.

We may not be able to produce instruments with the specifications required by our customers.

We have developed performance standards for our commercial products that may not be achieved using our current design and manufacturing processes. If the actual performance of the commercial instrument deviates substantially from our target specifications or is below the performance mandated by our customers, customer demand may be negatively affected. Customers may refuse to accept our products in a timely manner or at all, which would adversely affect our revenue. Any inability to meet performance standards may materially impact the commercial viability of our products and harm our business.

We may be unable to manufacture our consumable kits, including SMRT Cells, to the specifications required by our customers or in quantities necessary to meet demand at an acceptable cost.

In order to successfully commercialize our products, we will need to supply our customers with consumable kits to be used with our instruments. We have limited experience manufacturing these consumable kits. For example, the manufacture of our SMRT Cells involves complex manufacturing processes. Since we are in an early phase of producing SMRT Cells, our current manufacturing yields are low and therefore the cost of manufacturing these products is high. There is no assurance that we will be able to manufacture our consumable kits or SMRT Cells so that they consistently achieve the product specifications and quality that our customers expect. There is also no assurance that we will be able to increase manufacturing yields and decrease costs. Furthermore, we may not be able to increase manufacturing capacity for our consumable kits or SMRT Cells to meet anticipated demand. An inability to manufacture consumable kits and SMRT Cells that consistently meet specifications, in necessary quantities and at commercially acceptable costs will have a negative material impact on our business.

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We may never earn revenue from our orders in backlog.

Our backlog represents product orders from our customers that we have confirmed and for which we have not yet recognized revenue. We may never ship products represented by this backlog or receive revenue from these orders, and the order backlog we report may not be indicative of our future revenue.

Many events can cause an order not to be completed or delayed, some of which may be out of our control. If we delay fulfilling customer orders, those customers may seek to cancel their orders with us. In addition, customers may otherwise seek to cancel or delay their orders even if we are prepared to fulfill them. If our orders in backlog do not result in sales, our operating results will suffer and we may have write-offs associated with excess or obsolete inventory.

Rapidly changing technology in life sciences could make the products we are developing obsolete unless we continue to develop and manufacture new and improved products and pursue new market opportunities.

Our industry is characterized by rapid and significant technological changes, frequent new product introductions and enhancements and evolving industry standards. Our future success will depend on our ability to continually improve our products, to develop and introduce new products that address the evolving needs of our customers on a timely and cost-effective basis and to pursue new market opportunities. These new market opportunities may be outside the scope of our proven expertise or in areas which have unproven market demand, and new products and services developed by us may not gain market acceptance. Our inability to gain market acceptance of new products could harm our future operating results. Our future success also depends on our ability to manufacture new and improved products to meet customer demand in a timely and cost-effective manner, including our ability to resolve manufacturing issues that may arise as we commence production of these complex products. Unanticipated difficulties or delays in replacing existing products with new products or in manufacturing improved or new products in sufficient quantities to meet customer demand could diminish future demand for our products and harm our future operating results.

We may be unable to develop our future commercial applications.

Our future business depends on our ability to execute on our plans to develop, manufacture, and market additional commercial applications of our SMRT technology, including SMRT Kinetic Detection, SMRT Transcription, SMRT RNA Sequencing, SMRT Translation and SMRT Ligand Binding. These future commercial applications will require significant investments of cash and resources and we may experience unexpected delays or difficulties that could postpone our ability to commercially launch these future applications, which could have a material adverse effect on our business, prospects, operating results and financial condition.

A significant portion of our potential sales depends on customers capital spending budgets that may be subject to significant and unexpected variation.

A substantial portion of our potential product sales represent significant capital purchases by customers. Our potential customers include academic and government institutions, medical research institutions, pharmaceutical, biotechnology and chemical companies, and their capital spending budgets can have a significant effect on the demand for our products. These budgets are based on a wide variety of factors, including the allocation of available resources to make purchases, funding from government sources, the spending priorities among various types of research equipment and policies regarding capital expenditures during recessionary periods. Any decrease in capital spending or change in spending priorities of our potential customers could significantly reduce the demand for our products. Moreover, we have no control over the timing and amount of purchases by these potential customers, and as a result, revenue from these sources may vary significantly due to factors that can be difficult to forecast. We may also have to write off excess or obsolete inventory if sales of our products are not consistent with our expectations or the market requirements for our products change due to technical innovations in the marketplace. Any delay or reduction in purchases by potential customers or our inability to forecast fluctuations in demand could harm our future operating results.

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We have limited experience in sales and marketing of our products and, as a result, may be unable to successfully commercialize our products.

Neither Ms. Fine nor Mr. Jozwiak have, during the last five years, been convicted in a criminal proceeding (excluding traffic violations or similar misdemeanors).

(e)
None of the Reporting Persons, or other persons with respect to whom information is given in response to this Item 2, has, during the last five years, been a party to a civil proceeding of a judicial or administrative body of competent jurisdiction and as a result of such proceeding was or is subject to a judgment, decree or final order enjoining future violations of, or prohibiting or mandating activities subject to, federal or state securities laws or finding any violation with respect to such laws.

Item 3. Source and Amount of Funds or Other Consideration.

The net investment costs (including commissions, if any) of the Shares directly owned by the private investment funds advised by FCP is approximately $31,691,617. Ms. Fine, FCP and FCA do not directly own any Shares.

Item 4. Purpose of Transaction.

The purpose of the acquisition of the Shares by the Reporting Persons is for investment, and the purchases of the Shares by the Reporting Persons were made in the ordinary course of business and were not made for acquiring control of the Issuer. The Reporting Persons, from time to time, will communicate with the Issuer and other holders of Shares. The Reporting Persons may in the future purchase additional Shares or dispose of some or all of their Shares in open-market transactions or privately negotiated transactions. The Reporting Persons do not currently have any plans or proposals that would result in any of the actions described in paragraphs (b) through (j) of Item 4 of the instructions to Schedule 13D.

Item 5. Interest in Securities of the Issuer.

(a) - (e) As of the date hereof, (i) FCP, FCA and Ms. Fine may be deemed to be the beneficial owners of 1,653,300 Shares, constituting 6.3% of the Shares, based upon 26,442,959* Shares outstanding as of the date hereof.

FCP has the sole power to vote or direct the vote of 0 Shares; has the shared power to vote or direct the vote of 1,653,300 Shares; has the sole power to dispose or direct the disposition of 0 Shares; and has the shared power to dispose or direct the disposition of 1,653,300 Shares.

FCA has the sole power to vote or direct the vote of 0 Shares; has the shared power to vote or direct the vote of 1,653,300 Shares; has the sole power to dispose or direct the disposition of 0 Shares; and has the shared power to dispose or direct the disposition of 1,653,300 Shares.

Ms. Fine has the sole power to vote or direct the vote of 0 Shares; has the shared power to vote or direct the vote of 1,653,300 Shares; has the sole power to dispose or direct the disposition of 0 Shares; and has the shared power to dispose or direct the disposition of 1,653,300 Shares.

The transactions by the Reporting Persons in the securities of the Issuer during the past sixty days are set forth in Exhibit B.

*This outstanding Shares figure reflects the number of outstanding Shares at June 30, 2010, as reported in the Issuer's Form 10-Q, filed on August 9, 2010.

Item 6. Contracts, Arrangements, Understandings or Relationships with Respect to Securities of the Issuer.

Not Applicable

Item 7. Material to be Filed as Exhibits.

Exhibit A: Joint Filing Agreement
Exhibit B: Schedule of Transactions in Shares

SIGNATURE

After reasonable inquiry and to the best of my knowledge and belief, I certify that the information set forth in this statement is true, complete and correct.

November 12, 2010
(Date)

Fine Capital Partners, L.P.
By: Fine Capital Advisors, LLC, its general partner

By: /s/ Debra Fine
Debra Fine, Manager

Fine Capital Advisors, LLC

By: /s/ Debra Fine
Debra Fine, Manager

By: /s/ Debra Fine
Debra Fine

Attention: Intentional misstatements or omissions of fact constitute Federal criminal violations (see 18 U.S.C. 1001).

Exhibit A

AGREEMENT

The undersigned agree that this Schedule 13D dated November 12, 2010, relating to the Common Stock, $0.01 par value of Hornbeck Offshore Services, Inc. shall be filed on behalf of the undersigned.

November 12, 2010
(Date)

Fine Capital Partners, L.P.
By: Fine Capital Advisors, LLC, its general partner

By: /s/ Debra Fine
Debra Fine, Manager

Fine Capital Advisors, LLC

By: /s/ Debra Fine
Debra Fine, Manager

By: /s/ Debra Fine
Debra Fine

Exhibit B

Transactions by the Reporting Persons during the past 60 Days

Date of Transaction	Title of Class	Number of Shares Purchased	Number of Shares Sold	Price Per Share
9/15/2010	Common Stock, $0.01 Par Value	39,200		15.6650
9/15/2010	Common Stock, $0.01 Par Value		40,000	17.2579
9/23/2010	Common Stock, $0.01 Par Value	24,000		18.1377
9/30/2010	Common Stock, $0.01 Par Value	22,400		19.5081
10/1/2010	Common Stock, $0.01 Par Value	5,100		19.6635
10/4/2010	Common Stock, $0.01 Par Value	23,400		18.9000
10/5/2010	Common Stock, $0.01 Par Value	22,900		19.2074
10/6/2010	Common Stock, $0.01 Par Value	22,700		19.7996
10/7/2010	Common Stock, $0.01 Par Value	22,500		19.7567
10/7/2010	Common Stock, $0.01 Par Value	22,800		19.7065
10/8/2010	Common Stock, $0.01 Par Value	20,000		19.9009
10/11/2010	Common Stock, $0.01 Par Value	22,000		20.4011
10/12/2010	Common Stock, $0.01 Par Value	16,900		20.0905
10/13/2010	Common Stock, $0.01 Par Value	32,500		20.7852
10/14/2010	Common Stock, $0.01 Par Value	22,400		20.4888
10/15/2010	Common Stock, $0.01 Par Value	23,400		20.4482
10/15/2010	Common Stock, $0.01 Par Value	23,000		20.5991
10/18/2010	Common Stock, $0.01 Par Value	15,200		20.3875
10/19/2010	Common Stock, $0.01 Par Value	23,200		20.4868
10/19/2010	Common Stock, $0.01 Par Value	35,500		19.9250
10/20/2010	Common Stock, $0.01 Par Value	46,700		20.0896
10/21/2010	Common Stock, $0.01 Par Value	46,500		20.0762
10/27/2010	Common Stock, $0.01 Par Value	21,800		21.4117
11/1/2010	Common Stock, $0.01 Par Value	227,000		22.7496
11/3/2010	Common Stock, $0.01 Par Value	25,800		22.3221
11/4/2010	Common Stock, $0.01 Par Value	134,400		21.4774
11/5/2010	Common Stock, $0.01 Par Value	75,000		20.7535

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