UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

HEI-MUN CHRISTINA FAN and STEPHEN **QUAKE**
Junior Party
(Patent 8,195,415),

v.

YUK-MING DENNIS **LO**, ROSSA WAI KWUN CHIU, and KWAN CHEE CHAN
Senior Party
(Application 13/070,266).

Patent Interference No. 105,922 (DK)
(Technology Center 1600)

DECLARATION OF STACEY BOLK GABRIEL, PH.D.

STANFORD EXHIBIT 2115
SEQUENOM v. STANFORD

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I, Stacey Bolk Gabriel, declare as follows:

I. Introduction

1. I have been retained by Party Lo as an independent expert consultant in this proceeding before the United States Patent and Trademark Office. Although I am being compensated at a rate of $500 per hour for the time I spend on this matter, no part of my compensation is dependent on the outcome of this proceeding, and I have no other interest in this proceeding.

2. I have been told that this proceeding is a patent interference between Fan's U.S. Patent No. 8,195,415 ("the '415 patent") (**2011**) and Lo's Application No. 13/070,266 ("the '266 application") (**2016**).

3. I have been told that the '415 patent issued on June 5, 2012, from Application No. 12/696,509, filed on January 29, 2010.

4. I have been told the '266 application was filed on March 23, 2011, as a continuation of Application No. 12/614,350 ("the '350 application") (**2008**), filed on November 6, 2009, which is a continuation-in-part of Application No. 12/178,181 ("the '181 application") (**2009**), filed on July 23, 2008, which in turn claims priority to Provisional Application No. 60/951,438, filed July 23, 2007. I understand that the disclosure of the '266 application is identical to that of the '350 application. I also understand that, in comparison to the '181 application, the '350 application contains additional disclosure.

5. I previously provided declarations in three related patent interferences, that is, Interference Nos. 105,920, 105,923, and 105,924.

6. In this proceeding, I have been asked to provide my opinion as to whether a feature of the claims in the ’266 application reciting “using a number of windows of defined length within normally and abnormally distributed chromosome portions” (“the claim element” or “the claimed feature”) is described and enabled by the ’266 application.

7. I have been also asked to provide my opinion on whether the ’350 and ’181 applications describe and enable an embodiment of Count 1 (“the Count”) of this interference containing the claimed feature.

8. In addition, I have been asked to provide my opinion on whether claim 14 of the ’415 patent would have been obvious to a person of ordinary skill in the art in view of the subject matter of the Count of this interference and the knowledge in the state of the art as of September 20, 2008.

9. My opinions on these issues are set forth below.

II. Personal Background

10. I received a Bachelor of Sciences degree from Carnegie Mellon University in Molecular Biology in 1993. I received a Ph.D. in Genetics in 1998 from Case Western Reserve University. I conducted my thesis research projects under the direction of Dr. Aravinda Chakravarti using genomic mapping techniques and linkage analysis to identify genes involved in genetic diseases. My graduate research focused on characterizing genes involved in idiopathic congenital central hypoventilation syndrome, a rare disorder of respiratory control, and Hirschsprung (HSCR) disease, the most common cause of congenital intestinal obstruction.

11. My graduate research involved searching for sequence mutations in DNA by using techniques such as polymerase chain reaction (PCR), microsatellite genotyping, and DNA sequencing. I conducted genotyping on members from 61 families containing individuals with and without HSCR to study the inheritance pattern of the disease. I performed fluorescent dye-terminator cycle sequencing (based on the first generation Sanger dideoxy sequencing method) using PCR with genomic DNA in a primer extension sequencing reaction. The PCR products were run out (electrophoresed) on a slab gel and an automated ABI 377 DNA Sequencer was used for data collection. I then performed linkage analyses of the data by comparing DNA sequences from HSCR affected and non-affected individuals to search for differences (polymorphisms) in the sequences. This study identified three important regions of the genome to explain the inheritance of HSCR (only one of these regions was previously known). It also showed that some of these mutations are in non-protein coding regions, suggesting the importance of noncoding variation. This experiment was an early example of complete genetic dissection of a multifactorial disorder.

12. From November 1998 to February 2002, I was a Research Scientist in the Functional Genomics Program of the Whitehead Institute Center for Genome Research, now referred to as the Medical and Population Genetics Program of the Broad Institute of Harvard and MIT ("Broad Institute"). My responsibilities included laboratory work involving technology development for Single Nucleotide Polymorphism (SNP) genotyping, supervising technicians, and creating assays for SNP genotyping. During that time, I worked on the technical development and implementation of the first genotyping platforms to be used at our institute for high throughput SNP genotyping. All

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