UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

FOUNDATION MEDICINE, INC.,
Petitioner,

v.

GUARDANT HEALTH, INC.,
Patent Owner.

Case No. IPR2019-00637
U.S. Patent No. 9,902,992

EXHIBIT LIST

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Exhibit No.	Description
1001	U.S. Patent No. 9,902,992 ("the '992 patent")
1002	Declaration of Dr. Stacey Gabriel ("Gabriel Declaration")
1003	*Curriculum Vitae* of Dr. Stacey Gabriel
1004	Forshew et al., "Noninvasive Identification and Monitoring of Cancer Mutations by Targeted Deep Sequencing of Plasma DNA," Science Translational Medicine, 2012, 4(136) ("Forshew")
1005	Meyerson et al., "Advances in understanding cancer genomes through second-generation sequencing," Nature Review Genetics, Vol. 11 (2010), 685-696 ("Meyerson")
1006	Williford and Betrán, "Gene Fusion," eLS 2013, 1-8 ("Williford")
1007	Ding et al., "Analysis of next-generation genomic data in cancer: accomplishments and challenges," Hum. Mol. Genet. 2010 19(R2), R188-R196 ("Ding")
1008	Sehnert et al., "Optimal Detection of Fetal Chromosomal Abnormalities by Massively Parallel DNA Sequencing of Cell-free Fetal DNA from Maternal Blood," Clinical Chemistry 2011, 57:7, 1042-1049 ("Sehnert")
1009	Redon et al., "Global variation in copy number in the human genome," Nature 2006 444(7118), 444-454 ("Redon")
1010	Gordon et al., "Causes and consequences of aneuploidy in cancer," Nat. Rev. Genet. 2012 13(3), 189-203 ("Gordon")
1011	U.S. Patent No. 9,752,188 ("Schmitt")
1012	U.S. Provisional Application 61/613,413 ("Schmitt '413 provisional")
1013	Duncan and Patel, Diagnostic Molecular Pathology: A Guide to Applied Molecular Testing 25-33 (Coleman and Tsongalis eds., 1st ed. 2016)

1014	Nielsen et al., "Genotype and SNP calling from next-generation sequencing data," Nat. Rev. Genet. 2011 12(6), 443-451 ("Nielsen")
1015	Shendure and Ji, "Next-generation DNA sequencing," Nat. Biotechnol. 2008 26(10), 1135-1145 ("Shendure")
1016	Kao et al., "BayesCall: A model-based base-calling algorithm for high-throughput short-read sequencing," Genome Res. 2009 19(10), 1884-1895 ("Kao")
1017	Quinlan et al., "Pyrobayes: an improved base caller for SNP discovery in pyrosequences," Nat. Methods 2008 5(2), 179-181 ("Quinlan")
1018	Liang et al., "Bayesian basecalling for DNA sequence analysis using hidden Markov models," IEE/ACM Trans. Comput. Biol. Bioinform. 2007 4(3), 430-440 ("Liang")
1019	Ledergerber and Dessimoz, "Base-calling for next-generation sequencing platforms," Brief Bioinform. 2011 12(5), 489-497 ("Ledergerber")
1020	Kircher et al., "Improved base calling for the Illumina Genome Analyzer using machine learning strategies," Genome Biol. 2009, 10(8), R83 ("Kircher")
1021	U.S. Patent No. 6,582,908 ("Fodor")
1022	U.S. Patent No. 9,476,095 ("Kinde")
1023	Metzker, "Sequencing technologies - the next generation," 2010 11(1), 31-46 ("Metzker")
1024	Lo et al., "Quantitative analysis of fetal DNA in maternal plasma and serum: implications for noninvasive prenatal diagnosis," Am. J. Hum. Genet. 1998, 62(4), 768-775 ("Lo")
1025	Narayan et al., "Ultrasensitive Measurement of Hotspot Mutations in Tumor DNA in Blood Using Error-Suppressed Multiplexed Deep Sequencing," Cancer Res. 2012 72(14), 3492-3498 (published July 15, 2012) ("Narayan")
1026	International Publication No. WO 2012/042374 A2 ("Taipale")

1027	U.S. Patent Application No. 15/076,565 (the "'565 application")
1028	U.S. Patent Application No. 15/076,565 March 21, 2016 TrackOne Request
1029	U.S. Patent Application No. 15/076,565 April 29, 2016 Application Data Sheet
1030	U.S. Patent Application No. 15/076,565 June 10, 2016 TrackOne Request Granted
1031	U.S. Patent Application No. 15/076,565 June 15, 2017 Notice of Allowance
1032	U.S. Patent Application No. 15/076,565 February 9, 2017 Non-Final Rejection
1033	U.S. Patent Application No. 15/076,565 February 9, 2017 List of References Cited by Examiner
1034	U.S. Patent Application No. 15/076,565 February 9, 2017 List of References Cited by Applicant and Considered by Examiner
1035	U.S. Patent Application No. 15/076,565 May 9, 2017 Amendment and Response to Non-Final Office Action
1036	U.S. Provisional 61/696,734
1037	U.S. Provisional 61/704,400
1038	U.S. Provisional 61/793,997
1039	U.S. Provisional 61/845,987
1040	PCT/US2013/058061
1041	U.S. Patent Application No. 13/969,260
1042	U.S. Provisional 61/948,530
1043	Sparks et al., "Selective analysis of cell-free DNA in maternal blood for evaluation of fetal trisomy," Prenat. Diagn. 2012, 32(1), 3-9 ("Sparks")

1044	U.S. Patent No. 8,209,130 ("Kennedy")
1045	April 5, 2018 Memorandum from Deputy Commissioner for Patent Examination Policy to Patent Examining Corps
1046	Mertes et al., "Targeted enrichment of genomic DNA regions for next-generation sequencing," Brief Funct. Genomics 2011, 10(6), 374-386 ("Mertes")
1047	Schmitt et al., "Detection of ultra-rare mutations by next-generation sequencing," Proc. Natl. Acad. Sci. USA 2012, 109(36), 14508-14513 ("Schmitt 2012")
1048	Fan et al., "Noninvasive diagnosis of fetal aneuploidy by shotgun sequencing DNA from maternal blood," Proc. Natl. Acad. Sci. USA 2008, 105(42), 16266-16271 ("Fan")
1049	Kinde et al., "Detection and quantification of rare mutations with massively parallel sequencing," Proc. Natl. Acad. Sci. USA 2011, 108(23), 9530-9535 ("Kinde 2011")
1050	Chiu et al., "Non-invasive prenatal assessment of trisomy 21 by multiplexed maternal plasma DNA sequencing: large scale validity study", BMJ 2011;342, c7401 ("Chiu")
1051	Diehl et al., "Detection and quantification of mutations in the plasma of patients with colorectal tumors," Proc. Natl. Acad. Sci. USA 2005, 102(45), 16368-16373 ("Diehl")
1052	Liao et al., "Targeted massively parallel sequencing of maternal plasma DNA permits efficient and unbiased detection of fetal alleles," Clin. Chem. 2011, 57(1), 92-101 ("Liao")
1053	5 Vasyukhin et al., Challenges of Modern Medicine, 141-150 (Verna and Shamoo eds, 1994) ("Vasyukhin")
1054	Schwarzenbach et al., "Cell-free nucleic acids as biomarkers in cancer patients," Nat. Rev. Cancer 2011, 11(6), 426-437 ("Schwarzenbach")
1055	Koboldt et al., "The next-generation sequencing revolution and its impact on genomics," Cell 2013, 155(1), 27-38 ("Koboldt")

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