

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

FORESIGHT DIAGNOSTICS INC.,
Petitioner,

v.

PERSONALIS, INC.,
Patent Owner.

Case No. IPR2023-00545
U.S. Patent No. 11,299,783

PETITIONER'S UPDATED EXHIBIT LIST

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<u>PETITIONER’S UPDATED EXHIBIT LIST</u>	
EX1001	U.S. Patent No. 11,299,783 to West <i>et al.</i>
EX1002	Rebecca J. Leary <i>et al.</i> , “Development of Personalized Tumor Biomarkers Using Massively Parallel Sequencing,” <i>Science Translational Medicine</i> (2010) (Leary)
EX1003	Quake <i>et al.</i> , WO 2011/057061 (Quake)
EX1004	Matthew W. Anderson & Iris Schrijver, “Next Generation DNA Sequencing and the Future of Genomic Medicine,” <i>Genes</i> (2010) (Anderson)
EX1005	Andreas Gnirke <i>et al.</i> , “Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing,” <i>Nature Biotechnology</i> (2009) (Gnirke)
EX1006	Florian Mertes <i>et al.</i> , “Targeted enrichment of genomic DNA regions for next-generation sequencing, Briefings in Functional Genomics,” <i>Briefings in Functional Genomics</i> (2011) (Mertes)
EX1007	Lira Mamanova <i>et al.</i> , “Target-enrichment strategies for next-generation sequencing,” <i>Nature</i> (2010) (Mamanova)
EX1008	K.C. Allen Chan <i>et al.</i> , “Cancer Genome Scanning in Plasma: Detection of Tumor-Associated Copy Number Aberrations, Single-Nucleotide Variants, and Tumoral Heterogeneity by Massively Parallel Sequencing,” <i>Clinical Chemistry</i> (2013) (Chan)
EX1009	Gary J.W. Liao <i>et al.</i> , “Targeted Massively Parallel Sequencing of Maternal Plasma DNA Permits Efficient and Unbiased Detection of Fetal Alleles,” <i>Clinical Chemistry</i> (2011) (Liao)
EX1010	<i>Personalis v. Foresight</i> , First Amended Complaint, D. Colo., Case No. 1:22-v-01913, Dkt. 9, filed August, 17, 2022 (“FAC”)
EX1011	Reserved

<u>PETITIONER’S UPDATED EXHIBIT LIST</u>	
EX1012	Timothy J. Ley <i>et al.</i> , “DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome,” <i>Nature</i> (2008) (Ley)
EX1013	Jay Shendure & Hanlee Ji, “Next-generation DNA sequencing,” <i>Nature Biotechnology</i> (2008) (Shendure)
EX1014	Jeffrey S. Ross and Maureen Cronin, “Whole Cancer Genome Sequencing by Next-Generation Methods,” <i>American Journal of Clinical Pathology</i> (2011) (Ross)
EX1015	David J. McBride, et al., “Use of Cancer-Specific Genomic Rearrangements to Quantify Disease Burden in Plasma from Patients with Solid Tumors,” <i>Genes, Chromosomes & Cancer</i> (2010) (McBride)
EX1016	David M. Kurtz, et al., “Enhanced detection of minimal residual disease by targeted sequencing of phased variants in circulating tumor DNA,” <i>Nature Biotechnology</i> (2021) (Kurtz) (EX J to FAC)
EX1017	https://www.aacc.org/science-and-research/clinical-chemistry/clinical-chemistry-podcasts/2013/cancer-genome-scanning-in-plasma-detection-of-tumor-associated-copy-number-aberrations
EX1018	NIH Spreadsheet Regarding DNA Sequencing Costs
EX1019	https://www.genome.gov/about-genomics/fact-sheets/DNA-Sequencing-Costs-Data
EX1020	Declaration of John Quackenbush, Ph.D.
EX1021	Reserved
EX1022	Reserved
EX1023	<i>Curriculum Vitae</i> of John Quackenbush

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EX1024	https://www.garvan.org.au/research/kinghorn-centre-for-clinical-genomics/learn-about-genomics/for-gp/genetics-refresher-1/types-of-variants
EX1025	Seo Young Oh, et al., “Improved DNA Extraction Method for Molecular Diagnosis from Smaller numbers of Cells,” <i>Korean Jornal of Clinical Laboratory Science</i> (2014) (Oh)
EX1026	Leary Supplemental Information
EX1027	Hugo Lam, et al., “Performance comparison of whole-genome sequencing platforms,” <i>Nature Biotechnology</i> (2012) (Lam)
EX1028	Illumina, Technical Note: Sequencing
EX1029	Illumina, Specification Sheet: Illumina Sequencing
EX1030	Tim Forshew, et al., “Noninvasive Identification and Monitoring of Cancer Mutations by Targeted Deep Sequencing of Plasma DNA,” <i>Science Translational Medicine</i> (2012) (Forshew)
EX1031	Matthew Meyerson, et al., “Advances in understanding cancer genomes through second-generation sequencing,” <i>Nature Reviews</i> (2010) (Meyerson)
EX1032	Reserved
EX1033	Reserved
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EX1036	Reserved
EX1037	Reserved
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<u>PETITIONER’S UPDATED EXHIBIT LIST</u>	
EX1040	D. Sims <i>et al.</i> , “Sequencing depth and coverage: key considerations in genomic analyses,” Nature Reviews: Genetics (2014) (<i>Sims</i>)
EX1041	H. Li, “Mapping short DNA sequencing reads and calling variants using mapping quality scores,” Genome Res. (2008) (<i>Li</i>)
EX1042	Ley Supplemental Information
EX1043	A. Newman <i>et al.</i> , “Integrated digital error suppression for improved detection of circulating tumor DNA,” Nature Biotechnology (2016) (<i>Newman</i>)
EX1044	A. Newman <i>et al.</i> , “An ultrasensitive method for quantitating circulating tumor DNA with broad patient coverage,” Nature Medicine (2014) (<i>Newman 2014</i>)
EX1045	Newman Supplementary Excel Spreadsheet
EX1046	M. Clark <i>et al.</i> , “Performance comparison of exome DNA sequencing technologies,” Nature Biotechnology (2011) (<i>Clark</i>)
EX1047	Illumina MiSeq Worksheet (2015)
EX1048	Genbank Record for CDH24
EX1049	Genbank Record for SLC15A1
EX1050	Genbank Record for KNDC1
EX1051	Genbank Record for PTPRT
EX1052	Genbank Record for GRINL1B
EX1053	Genbank Record for ADGRA1 (GPR123)
EX1054	Genbank Record for GPR183 (EBI2)
EX1055	Genbank Record for CDHR2 (PCLKC)

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EX1056	Genbank Record for FLT3
EX1057	Genbank Record for NPM1
EX1058	Genbank Record for BRCA2
EX1059	Genbank Record for TP53
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EX1063	Reserved
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EX1067	Reserved
EX1068	Reserved
EX1069	Reserved
EX1070	S. Dawson, <i>et al.</i> , “Analysis of Circulating Tumor DNA to Monitor Metastatic Breast Cancer,” New England Journal of Medicine (2013) (<i>Dawson</i>)
EX1071	R. Burrell, <i>et al.</i> , “The causes and consequences of genetic heterogeneity in cancer evolution,” Nature (2013) (<i>Burrell</i>)
EX1072	Plaintiff Personalis’ Infringement Contentions for United States Patent 11,299,783

<u>PETITIONER’S UPDATED EXHIBIT LIST</u>	
EX1073	C. Haferlach, <i>et al.</i> , “Mutations of the TP53 gene in acute myeloid leukemia are strongly associated with a complex aberrant karyotype,” <i>Leukemia</i> (2008)
EX1074	S. Misawa, <i>et al.</i> , “Significance of chromosomal alterations and mutations of the N-RAS and TP53 genes in relation to leukemogenesis of acute myeloid leukemia,” <i>Leukemia Research</i> (1998) (<i>Misawa</i>)
EX1075	S. Davies, <i>et al.</i> , “Indications for Hematopoietic Cell Transplantation in Acute Leukemia,” <i>Biology of Blood and Marrow Transplantation</i> (2008) (<i>Davies</i>)
EX1076	B. Alter, <i>et al.</i> , “Clinical and molecular features associated with biallelic mutations in <i>FANCD1/BRCA2</i> ,” <i>Journal of Medical Genetics</i> (2007) (<i>Alter</i>)
EX1077	D. Bentley, <i>et al.</i> , “Accurate whole human genome sequencing using reversible terminator chemistry,” <i>Nature</i> (2008) (<i>Bentley</i>)
EX1078	Deposition of Henry Morrice Furneaux, January 26, 2024, IPR2023-00545/IPR2023-00546
EX1079	Patent Owner’s Preliminary Response, IPR2023-00224, U.S. Patent No. 11,384,394
EX1080	<i>Neogenomics Labs., Inc. v. Natera, Inc.</i> , IPR2024-00346, Petition for <i>Inter Partes</i> Review of U.S. Patent No. 11,530,454
EX1081	U.S. Patent No. 11,384,394
EX1082	<i>Neogenomics Labs., Inc. v. Natera, Inc.</i> , IPR2024-00346, Expert Declaration of Niall Lennon, Ph.D in Support of Petition for <i>Inter Partes</i> Review of U.S. Patent No. 11,530,454
EX1083	Deposition of Henry Morrice Furneaux, Ph.D., December 12, 2023, IPR2023-00224/IPR2023-00317
EX1084	Declaration for Pro Hac Vice Admission of Alan J. Heinrich

<u>PETITIONER'S UPDATED EXHIBIT LIST</u>	
EX1085	Petitioner's Oral Hearing Demonstratives

Dated: May 3, 2024

Respectfully submitted,

/Andrew E. Krause/

Andrew E. Krause, Reg. No. 76,276
Abigail Sellers, (Reg. 80,391)
Alan J. Heinrich (*pro hac vice*)
IRELL & MANELLA LLP
1800 Avenue of the Stars, Ste. 900
Los Angeles, CA 90067
(310) 203-7668
akrause@irell.com

Amir Naini, Reg. No. 45,770
NAINI P.C.
2632 Wilshire Blvd., Suite 268
Santa Monica, CA 90403
(310) 592-3030
amir@nainipc.com

Attorneys for Petitioner
Foresight Diagnostics Inc.

CERTIFICATE OF SERVICE

I hereby certify, pursuant to 37 C.F.R. section 42.6, that on May 3, 2024, a complete copy of the foregoing document **PETITIONER'S UPDATED EXHIBIT LIST** and **EX1085** (Petitioner's Oral Hearing Demonstratives) were served upon the following, by ELECTRONIC MAIL:

WEIL, GOTSHAL & MANGES LLP

Derek C. Walter, Lead Counsel
Derek.walter@weil.com

Adrian Percer, Backup Counsel
Adrian.percer@weil.com

Personalis.Foresight@weil.com

KNOBBE, MARTENS, OLSON, & BEAR, LLP

Nathanael Luman, Backup Counsel
2nrl@knobbe.com

BoxPersonalis783@knobbe.com

/Pia S. Kamath/
Pia S. Kamath