UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE PATENT TRIAL AND APPEAL BOARD

TWINSTRAND BIOSCIENCES, INC. Petitioner,

v.

GUARDANT HEALTH, INC. Patent Owner.

Case IPR2022-01152 U.S. Patent No. 11,118,221

PETITION FOR *INTER PARTES* REVIEW OF U.S. PATENT NO. 11,118,221

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II.		ment of Precise Relief Requested and Reasons Therefor (37 C.F.R. 22(A))
III.	State	of the art before December 2013
	A.	Optimization techniques for DNA library preparation were well known
	B.	Cell-free DNA isolated from blood was widely used in NGS
		platforms51. The presence of cell-free tumor DNA in human blood
		was well known
		2. Isolating cfDNA from blood was routine with off-the- shelf kits
	C.	The prior art taught that Duplex Sequencing dramatically lowers NGS error rate
	D.	The prior art taught applying Duplex Sequencing to cfDNA
IV.	The '	221 patent and its prosecution history 15
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VI.	Clain	n construction
VII.	Ident	ification of the challenge (37 C.F.R. §42.104(b))
VIII.	The f	facts and law weigh against discretionary denial of institution
	А. В.	This Petition satisfies 35 U.S.C. §325(d)
IX.		nd 1: claims 1-4, 6-7, 9-15, 18-22, and 24-28 would have been obvious Narayan and Schmitt
	Α.	 Claim 1

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ends of a molecule of the plurality of the cfDNA "(c) amplifying a plurality of the tagged parent 3. polynucleotides to produce amplified progeny "(d) sequencing at least a subset of the amplified 4. progeny polynucleotides to produce a set of sequence "(e) reducing or tracking redundancy in the set of 5. sequence reads using at least sequence information from the molecular barcodes to generate a plurality of consensus sequences representative of original cfDNA molecules from among the tagged parent polynucleotides, wherein the plurality of consensus sequences is generated from (i) paired reads corresponding to sequence reads generated from a first tagged strand and a second tagged complementary strand derived from a cfDNA molecule from among the tagged parent polynucleotides, and (ii) unpaired reads corresponding to sequence reads generated from a first tagged strand having no second tagged complementary strand derived from a cfDNA molecule from among the 6. A POSA would have had a reason to combine Narayan A POSA would have had a reasonable expectation of 7. "A method, comprising: (a) providing a population of 1. double-stranded cell-free deoxyribonucleic acid (cfDNA) molecules having first and second "(b) non-uniquely tagging a plurality of the double-2. stranded cfDNA molecules of the population with a set of duplex tags comprising molecular barcodes from a set of molecular barcodes to produce non-uniquely tagged parent polynucleotides, wherein the doulestranded cfDNA molecules that map to a mappable base position of a reference sequence are tagged with a number of different molecular barcodes ranging from

B.

	1 atciit 11,110,221
	at least 2 to fewer than a number of the double-stranded
	cfDNA molecules that map to the mappable base
	position"
	3. "(c) amplifying a plurality of the non-uniquely tagged
	parent polynucleotides to produce amplified progeny
	polynucleotides"
	4. "(d) sequencing at least a subset of the amplified
	progeny polynucleotides to produce a set of sequence
	reads"
	5. "(e) reducing or tracking redundancy in the set of
	sequence reads using at least sequence information
	from the molecular barcodes"
	6. "(f) sorting the set of sequence reads into paired reads
	and unpaired reads, wherein (i) a paired read
	corresponds to sequence reads generated from a first
	tagged strand and a second tagged complementary
	strand derived from a double-stranded cfDNA
	molecule from among the non-uniquely tagged parent
	polynucleotides, and (ii) an unpaired read corresponds
	to sequence reads generated from a first tagged strand
	having no second tagged complementary strand
	derived from a double-stranded cfDNA molecule from
	among the non-uniquely tagged parent
	polynucleotides"
	1 ·
	7. "(g) determining, at one or more loci of a reference
	sequence, quantitative measures of at least two of (i)
	the paired reads, (ii) the unpaired reads, (iii) read depth
	of the paired reads, and (iv) read depth of the unpaired
	reads."
C.	Claims 2 and 19
D.	Claims 3 and 20
Е.	Claims 4 and 21
F.	Claim 6
G.	Claim 7
H.	Claim 22
I.	Claims 9-10 and 24-25
J.	Claims 11 and 26
K.	Claims 12 and 13
L.	Claim 14
M.	Claim 15
	-

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	N. Claims 27 and 2860
X.	Ground 2: claim 5 would have been obvious over Narayan, Schmitt, and Meyer
XI.	Ground 3: claims 8 and 23 would have been obvious over Narayan, Schmitt, and Craig
XII.	Ground 4: claims 16-17 and 29-30 would have been obvious over Narayan, Schmitt, and Kivioja
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