

EXHIBIT A

U.S. Patent No. 11,319,596 (“’596 Patent”)			
No.	Proposed Term	Natera’s Proposed Construction and Supporting Intrinsic and Extrinsic Evidence	NeoGenomics’ Proposed Construction and Supporting Intrinsic and Extrinsic Evidence
1	“the isolated cell-free DNA” (Claim 1)	<u>Claim Construction:</u> Plain and ordinary meaning, which includes cell-free DNA isolated from any of the plurality of biological samples obtained from the subject at different time points. <u>Intrinsic Evidence</u> <u>Claims/Specification</u> ’596 Patent at 15:10-42, 16:12-45, 16:49-17:8, 17:13-36, 18:10-16, 19:23-20:65, 21:6-33, 24:14-25:29, 27:59-28:6, 28:11-44, 28:30-62, 30:41-31:6, 34:31-35:17, 36:53-37:8, 44:26-45:43, 52:26-53:2, 58:32-59, 59:13-63, 62:20-30, 63:50-63, 65:64-67, 66:28-53, 67:54-64, 79:29-49, 88:60-90:4, 93:56-95:12, 95:27-46, 95:59-98:46, 98:52-99:41, 103:17-105:66, 109:23-111:17, 114:43-115:8, 120:6-28, 123:41-61, 137:51-140:67; 147:41-67, Examples 1, 4, 6-9, 12-14, Figs. 43A1, 47A, 48A, 63A; Claims 1, 2, 10, 11, 17. <u>File History</u> 07/01/2019 Preliminary Amendment	<u>Claim Construction:</u> Plain and ordinary meaning, which is cell-free DNA isolated from a plurality of biological samples obtained from the subject. <u>Intrinsic Evidence</u> <u>Claims/Specification</u> ’596 Patent at 95:31-37, Claim 1 <u>’596 Patent File History</u> 4/22/2020 Restriction Requirement 5/4/2020 Applicant Response to Restriction Requirement 6/18/2020 Non-Final Office Action 10/16/2020 Examiner Interview Summary 11/16/2020 Applicant Argument/Remarks Made in an Amendment 12/30/2020 Final Office Action 6/1/2021 Applicant Argument/Remarks Made in an Amendment 9/15/2021 Notice of Allowance 3/14/2022 Notice of Allowance

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		04/22/2020 Restriction Requirement 05/04/2020 Response to Restriction Requirement 06/18/2020 Non-Final Office Action 10/26/2020 Examiner Interview Summary 11/16/2020 Response to Non-Final Office Action 12/30/2020 Final Office Action 06/01/2020 Response to Final Office Action 09/15/2021 Notice of Allowance 03/14/2022 Notice of Allowance U.S. Patent Application No. 14/692,703, issued as U.S. Patent No. 10,179,937	<u>Extrinsic Evidence:</u> • <i>Markman</i> ruling (Doc. 280) • NeoGenomics’ prior claim construction briefing and supporting evidence (Docs. 264, 264-5, 271), and any exhibits to any of the foregoing. • Natera’s prior claim construction briefing and supporting evidence (Docs. 262, 263, 272, 273), and any exhibits to any of the foregoing. • Additional written and/or live expert testimony regarding the meaning of this term as understood by a person of ordinary skill in the art, read in light of the specification and the prosecution history.

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		<u>Extrinsic Evidence:</u> • <i>Markman</i> ruling (Doc. 280) • Natera’s prior claim construction briefing and supporting evidence (Docs. 262, 263, 272, 273) • NeoGenomics’ prior claim construction briefing and supporting evidence (Docs. 264, 264-5, 271) • Opening Declaration of Dr. Michael Metzker in support of Natera’s Preliminary Injunction (“PI”) Motion dated July 31, 2023 (Doc. 17) • Rebuttal Declaration of Dr. Brian Van Ness in support of NeoGenomics’ PI Opposition dated October 19, 2023 (Doc. 116) • Reply Declaration of Dr. Michael Metzker in support of Natera’s PI Motion dated November 6, 2023 (Doc. 145)	

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		• Opening Expert Report of Dr. Michael Metzker dated August 2, 2024 • Opening Expert Report of Dr. Niall Lennon dated August 2, 2024 • September 26, 2023 Deposition testimony of Dr. Metzker (Doc. 116-6) • October 4, 2023 Deposition testimony of Dr. Bernhard Zimmermann (Doc. 144-4) • October 25, 2023 Deposition testimony of Dr. Brian Van Ness (Doc. 145-1) • November 14, 2023 Deposition testimony of Dr. Metzker (Doc. 163-1) • November 27, 2023 PI Hearing testimony of Dr. Metzker • July 9, 2024 Deposition testimony of Dr. George Gemelos	

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		• July 12, 2024 Deposition testimony of Dr. Bernhard Zimmermann • August 7, 2024 Deposition testimony of Dr. Matthew Rabinowitz • IPR2024-00346 (NeoGenomics’ Petition for IPR of the ’454 Patent and evidence cited in support of its Petition, Natera’s Preliminary Patent Owner Response, and the Decision Denying Institution) • IPR2024-00812 (NeoGenomics’ Petition for IPR of the ’035 Patent and evidence cited in support of its Petition, Natera’s Preliminary Patent Owner Response, and the Decision Denying Institution) • Additional written and/or live expert testimony regarding the meaning of this term as understood by a person of ordinary skill in the art. • Metzker & Caskey, <i>Polymerase Chain Reaction</i>, <i>ENCYCLOPEDIA OF MEDICAL</i>	

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		DEVICES AND INSTRUMENTATION, Second Edition, Volume 5, pp. 380-387 (2006). • Meyer & Kircher, Illumina sequencing library preparation for highly multiplexed target capture and sequencing, COLD SPRING HARBOR PROTOCOLS, pdb.prot5448 pp. 1-10 (2010). • Glenn, <i>Field guide to next-generation DNA sequencers</i>, MOLECULAR ECOLOGY RESOURCES, 11:759–769 (2011). • William Strunk, Jr. & E.B . White, <i>The Elements of Style</i> 27 (4th ed. 2000) • Oxford Modern English Grammar (2011) • Oxford Dictionary of English Grammar (2nd edition 2014)	

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2	“performing high-throughput sequencing of the amplified DNA comprising the plurality of target loci to obtain sequence reads, wherein an SNV mutation that is present in less than or equal to 0.015% of the cell-free DNA having the	<u>Claim Construction:</u> Plain and ordinary meaning, which means that the terms are part of the “performing high-throughput sequencing . . . to obtain sequence reads” step and the “wherein” clause informs the mechanics of how the high-throughput sequencing is performed. <u>Intrinsic Evidence</u> <u>Claims/Specification</u> ’596 Patent at 6:16-21, 31:16-24, 44:6-25, 44:44-64, 58:32-45, 62:1-13, 63:50-63, 65:16-20, 67:54-64, 68:6-12, 68:31-44, 93:8-55, 96:36-40, 98:57-59, 99:42-100:48; 101:28-35, 135:25-38, 147:41-67, Examples 1, 6, 9, 11-14; Claims 1, 12. <u>File History</u> 07/01/2019 Preliminary Amendment 04/22/2020 Restriction Requirement 05/04/2020 Response to Restriction Requirement	<u>Claim Construction:</u> Plain and ordinary meaning, no construction necessary beyond the constructions of Terms 3 and 4 below. <u>Intrinsic Evidence</u> <i>See</i> terms 3 and 4. <u>Extrinsic Evidence:</u> <i>See</i> terms 3 and 4.

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	SNV locus is detected from the sequence reads” (Claim 1)	06/18/2020 Non-Final Office Action 10/26/2020 Examiner Interview Summary 11/16/2020 Response to Non-Final Office Action 12/30/2020 Final Office Action 06/01/2020 Response to Final Office Action 09/15/2021 Notice of Allowance 03/14/2022 Notice of Allowance U.S. Patent Application No. 14/692,703, issued as U.S. Patent No. 10,179,937 <u>Extrinsic Evidence:</u> Same as above. Illumina, "HiSeq 2500 Sequencing System", System Specification Sheet: Sequencing,	

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		available via URL https://www.illumina.com/documents/products/datasheets/datasheet_hiseq2500.pdf , 2015, 4 pgs.	
3	“performing high-throughput sequencing of the amplified DNA” (Claim 1)	<u>Claim Construction:</u> Plain and ordinary meaning, which permits intermediate steps after multiplex amplification but before sequencing. <u>Intrinsic Evidence:</u> Same as above. <u>Extrinsic Evidence:</u> Same as Term No. 2.	<u>Claim Construction:</u> Plain and ordinary meaning, which is performing high-throughput sequencing of the amplified DNA obtained from the targeted multiplex PCR amplification step. <u>Intrinsic Evidence</u> <u>Claims/Specification</u> ’596 Patent at 20:2–8, 20:26–28, 33:61–63, 58:32–39, 62:1–11, 66:39-51, 86:56-58, 96:23-47, 98:47–99:41, 99:66-100:8, 103:46-104:5, 106:3-10, 116:11-21, 116:57-67, 123:50-67, 125:48–52, 152:65-67, Examples 1, 3, 5, 7, 9, and 14, Claim 1 <u>’596 Patent File History</u>

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			4/22/2020 Restriction Requirement 5/4/2020 Applicant Response to Restriction Requirement 6/18/2020 Non-Final Office Action 10/16/2020 Examiner Interview Summary 11/16/2020 Applicant Argument/Remarks Made in an Amendment 12/30/2020 Final Office Action 6/1/2021 Applicant Argument/Remarks Made in an Amendment 9/15/2021 Notice of Allowance 3/14/2022 Notice of Allowance <u>File History of Related Patent US 11,486,008</u> 1/8/2021 Applicant Argument/Remarks Made in an Amendment 5/22/2020 Applicant Initiated Interview Summary • IPR2024-00346 (NeoGenomics’ Petition for IPR of the ’454 Patent and evidence cited in support of its Petition, Natera’s Preliminary Patent Owner Response, the Decision Denying Institution, and any exhibits to any of the foregoing)

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			<u>Extrinsic Evidence:</u> • <i>Markman</i> ruling (Doc. 280) • NeoGenomics’ prior claim construction briefing and supporting evidence (Docs. 264, 264-5, 271), and any exhibits to any of the foregoing. • Natera’s prior claim construction briefing and supporting evidence (Docs. 262, 263, 272, 273), and any exhibits to any of the foregoing. Additional written and/or live expert testimony regarding the meaning of this term as understood by a person of ordinary skill in the art, read in light of the specification and the prosecution history.
4	“wherein an SNV mutation . . . is detected from the sequence reads”	<u>Claim Construction:</u> Plain and ordinary meaning, which means that the terms are part of the “performing high-throughput sequencing . . . to obtain sequence reads” step and the “wherein” clause informs the mechanics of how the high-throughput sequencing is performed.	<u>Claim Construction:</u> Plain and ordinary meaning, which is wherein an SNV mutation is determined to be present from the sequence reads. <u>Intrinsic Evidence</u> <u>Claims/Specification</u>

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	(Claim 1)	<u>Intrinsic Evidence:</u> Same as above. <u>Extrinsic Evidence:</u> Same as Term No. 2.	’596 Patent at 5:4-6:15, 27:1-39, 65:14-67, 66:1-27, 66:39-46, 67:11-24, 67:30-64, 67:65-68:30, 93:18-33, 96:40-47, 98:65-99:9, 100:1-4, 100:37-60, 136:1-6, 158:6-58, 158:62-66, 159:40-41, 160:4-15, 165:19-167:26, 167:47-48, 167:63-66, 169:3-5, Claim 1 <u>’596 Patent File History</u> 4/22/2020 Restriction Requirement 5/4/2020 Applicant Response to Restriction Requirement 6/18/2020 Non-Final Office Action 10/16/2020 Examiner Interview Summary 11/16/2020 Applicant Argument/Remarks Made in an Amendment 12/30/2020 Final Office Action 6/1/2021 Applicant Argument/Remarks Made in an Amendment 9/15/2021 Notice of Allowance 3/14/2022 Notice of Allowance <u>File History of Related Patent US 11,486,008</u> 10/09/2020 Non-Final Rejection

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			5/22/2020 Applicant Initiated Interview Summary 1/8/2021 Applicant Argument/Remarks Made in an Amendment 3/8/2021 Notice of Allowance <u>Extrinsic Evidence:</u> • <i>Markman</i> ruling (Doc. 280) • NeoGenomics’ prior claim construction briefing and supporting evidence (Docs. 264, 264-5, 271), and any exhibits to any of the foregoing. • Natera’s prior claim construction briefing and supporting evidence (Docs. 262, 263, 272, 273), and any exhibits to any of the foregoing. • Additional written and/or live expert testimony regarding the meaning of this term as understood by a person of ordinary skill in the art, read in light of the specification and the prosecution history.

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			• Li, <i>et al.</i> The Sequence Alignment/Map format and SAMtools, <i>Bioinformatics</i>, 25(16):2078-79 (2009) • Larson, <i>et al.</i> SomaticSniper: identification of somatic point mutations in whole genome sequencing data, <i>Bioinformatics</i>, 28(3):311-17 (2012) • Koboldt, <i>et al.</i> VarSacan: variant detection in massively parallel sequencing of individual and pooled samples, <i>Bioinformatics</i> 25(17):2283-85 (2009) • Illumina Technical Note: Systems and Software, <i>Complete Secondary Analysis Workflow for the Genome Analyzer</i> (2009). • Nielsen, <i>et al.</i> Genotype and SNP calling from next-generation sequencing data, <i>Nat Rev Genet.</i> 12(6):443-51 (2011) • Saunders, <i>et al.</i> Strelka: accurate somatic small-variant calling from sequenced tumor-normal

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			sample pairs, <i>Bioinformatics</i>, 28(14):1811-17 (2012) • A map of human genome variation from population scale sequencing, <i>Nature</i> 467(7319):1061-73 (2010) • Oxford English Dictionary, Twelfth Edition (2011). • Collins English Dictionary, Eleventh Edition (2011). • Illumina Application Note: Sequencing, <i>Amplicon Sequencing from FFPE tissues on the MiSeq™ System</i> (2011). • Illumina Technical Note: Sequencing, <i>Quality Scores for Next-Generation Sequencing</i> (2011). • O’Rawe J, Low concordance of multiple variant-calling pipelines: practical implications for exome and genome sequencing. <i>Genome Med.</i> 5(3):28 (2013)

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			- Forster M, et al., From next-generation sequencing alignments to accurate comparison and validation of single-nucleotide variants: the pibase software. <i>Nucleic Acids Res.</i> 41(1):e16 (2013) - Cibulskis <i>et al.</i>, Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples, 31 <i>Nat. Biotech.</i> 213-219 (2013) - Daber <i>et al.</i>, Understanding the limitations of next generation sequencing informatics, an approach to clinical pipeline validation using artificial data sets, 206 <i>Cancer Genetics</i> 441-448 (2014) - Metzker, Sequencing technologies – the next generation, <i>Nature Reviews Genetics</i>, 11:31-46 (2010). - Bentley, et al., Accurate whole human genome sequencing using reversible terminator chemistry. <i>Nature</i> 456:53-59 (2008).

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			• Li, et al., Mapping short DNA sequencing reads and calling variants using mapping quality scores, <i>Genome Res.</i> 18:1851-58 (2008). • Frazer, et al., Human genetic variation and its contribution to complex traits. <i>Nature Rev. Genet.</i> 10:241-51 (2009). • Ley, et al., DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. <i>Nature</i> 456:66-72 (2008). • Sarin, et al., <i>Caenorhabditis elegans</i> mutant allele identification by whole-genome sequencing. <i>Nature Methods</i> 5:865-67 (2008). • Mardis, <i>Next-Generation Sequencing Methods</i>, <i>Annu. Rev. Genomics Hum. Genet.</i> 9:387, 388 (2008) • Narayan <i>et al.</i>, Ultrasensitive Measurement of Hotspot Mutations in Tumor DNA in Blood Using Error-Suppressed Multiplexed Deep Sequencing, <i>72 Cancer Res.</i> 3492 (2012)

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			• Kennedy <i>et al.</i>, Detecting ultralow-frequency mutations by Duplex Sequencing. Nat Protoc 9, 2586–2606 (2014) • U.S. Patent Publication No. 2016/0032396 • U.S. Patent Publication No. 2014/0066317 • Broad Institute, <i>BroadE: Introduction to data processing and variant detection for next-generation DNA sequencing</i>, YouTube (March 4, 2013), https://www.youtube.com/watch?v=1m0ZiEvzDKI • Broad Institute, <i>BroadE: Calling variants</i>, YouTube (Sept. 30, 2013), https://www.youtube.com/watch?v=JENHDFqYteg • Broad Institute, <i>BroadE: Variant quality score recalibration</i>, YouTube (Sept. 30, 2013), https://www.youtube.com/watch?v=nIIMr1kWr5Q • Broad Institute, <i>BroadE: GATK/Introduction to High-Throughput Sequencing data formats and methods (2015)</i>, YouTube (Jan. 11, 2016), https://www.youtube.com/watch?v=kCeV8qjW6fM

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			• Illumina, <i>Intro to Sequencing by Synthesis: Industry-leading Data Quality</i>, YouTube (Apr. 2, 2014), https://www.youtube.com/watch?v=HMyCqWhwB8E • Illumina, <i>Illumina Sequencing Technology</i>, YouTube (Oct. 23, 2013), https://www.youtube.com/watch?v=womKfikWlXM