

Dr. Peter K. Koo
LIST OF MATERIALS CONSIDERED

Ex. No.	Description
1001	U.S. Patent No. 11,091,794 to Lo (“the ’794 patent”)
1002	Declaration of Dr. Christophe Dessimoz
1003	Curriculum Vitae of Christophe Dessimoz, Ph.D.
1004	U.S. Patent Application No. 16/995,607 File History (focus on the office actions,
1005	U.S. Patent Application No. 17/379,544 File History
1006	Flusberg, et al., “Direct Detection of DNA Methylation During Singlemolecule, Real-Time Sequencing,” Nature Methods 7(6) (2010) (“Flusberg”)
1007	U.S. Patent No. 9,175,338 to Flusberg et al. (“Flusberg-338”)
1008	Clark, et al. “Direct Detection and Sequencing of Damaged DNA Bases” Genome Integrity 2 (2011) (“Clark”)
1009	Loomis et al., “Sequencing the Unsequenceable: Expanded CGG-repeat Alleles of the Fragile X Gene,” Genome Research 23(1) (2013) (“Loomis”)
1010	Schadt, et al., “Modeling Kinetic Rate Variation in Third Generation DNA Sequencing Data to Detect Putative Modifications to DNA Bases,” Genome Research 23(1) (2013) (“Schadt”)
1011	BAM Format Specification for PacBio, PacBioFileFormats 5.0 Documentation, http://web.archive.org/web/20170916112547/http://pacbiofileformats.readthedocs.io/en/5.0/BAM.html (archived Sep. 16, 2017) (“PacBio-BAM”)
1012	SAM/BAM Specification Working Group, Sequence Alignment/MapFormat Specification, http://web.archive.org/web/20180613134937/http://samtools.github.io/h

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	ts-specs/SAMv1.pdf (archived Jun. 13, 2018) (“SAM/BAM Specification”)
1014	Take2 Tech, Ltd. v. Pac. Biosciences of Cal., Inc., DDE-1-22-cv-01595, Infringement Claim Chart for U.S. Patent No. 11,091,794 (“Take2 Infringement Contentions”)
1015	Feng, et al, “Detecting DNA modifications from SMRT Sequencing Data by Modeling Sequence Context Dependence of Polymerase Kinetic,” PLoS Computational Biology, 9(3) (2013) (“Feng”)
1021	Pacific Biosciences kineticsTools Manual, http://web.archive.org/web/20170813085437/https://github.com/PacificBiosciences/kineticsTools/blob/master/doc/manual.rst (2018) (“kineticsTools manual”)
1022	Liu et al., “Detection of DNA Base Modifications by Deep Recurrent Neural Network on Oxford Nanopore Sequencing Data,” Nature Comms. 10(1) (Jun. 4, 2019) (“Q. Liu”)
1026	GenomeWeb, “PacBio Reveals Beta System Specs for RS; Says Commercial Release is on Track for First Half of 2011,” https://www.genomeweb.com/sequencing/pacbios-q3-losses-widen-itreadies-launch-rs-system (2010) (“GenomeWeb”)
1030	Tse et al., “Genome-wide Detection of Cytosine Methylation by Single Molecule Real-time Sequencing,” Proceedings of the National Academy of Sciences, 118(5) (2021) (“Tse”)
1033	Pacific Biosciences, PacBioFileFormats Documentation (Feb. 2022) (“PacBioFileFormats-2022”)
1038	Liu et al., “Accurate Detection of m6A RNA Modifications in Native RNA Sequences,” https://www.biorxiv.org/content/10.1101/525741v1 (Jan. 21, 2019) (“H. Liu”)
2001	Color Drawings of US 11,091,794 Downloaded from USPTO Patent Center

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2004	Li et al. and 1000 Genome Project Data Processing Subgroup. 2009. “The Sequence Alignment/Map format and SAMtools,” <i>Bioinformatics</i> 25(16): 2078-2079 (“Li”)
2005	Suzuki et al., “AgIn: measuring the landscape of CpG methylation of individual repetitive elements,” <i>Bioinformatics</i> , 32(19), 2016, 2911–2919 (“Suzuki”)
2006	Zheng and Casari, “Feature Engineering for Machine Learning,” First Edition, O’Reilly Media, Inc., Sebastopol, CA, 2018 (Excerpts)
2007	Web page (print friendly screen capture): Johns Hopkins University Center for Computational Biology, StringTie – Transcript assembly and quantification for RNA-Seq. URL: https://ccb.jhu.edu/software/stringtie/index.shtml . Web page visited January 23, 2024
2008	Web page (print friendly screen capture): Broad Institute Genome Analysis Toolkit. URL: https://gatk.broadinstitute.org/hc/en-us . Web page visited January 23, 2024
2009	Web page (print friendly screen capture): Broad Institute Genome Analysis Toolkit - HaplotypeCaller. March 4, 2020. URL: https://gatk.broadinstitute.org/hc/en-us/articles/360040096812-HaplotypeCaller . Web page visited January 23, 2024
2010	Web page: University of California at Santa Cruz, Genome Browser BAM Track Format. URL: https://genome.ucsc.edu/goldenPath/help/bam.html . Web page visited January 23, 2024
2011	Web page (print friendly screen capture): Git Hub HPC Training – Peak calling with MACS2. June 12, 2017. URL: https://hbctraining.github.io/Intro-to-ChIPseq/lessons/05_peak_calling_mac2.html . Web page visited January 23, 2024
2012	YouTube Video: PacBio Data Deep Dive: A Closer Look at HiFi Sequencing. PacBio May 24, 2021. URL: https://www.youtube.com/watch?v=1aqnLQ-nwYk . Downloaded January 22, 2024. (Also available at

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	https://www.pacb.com/videos/pacbio-data-deep-dive-a-closer-look-at-hifi-sequencing/)
2013	Screen Capture of Exhibit 2012 (YouTube) https://www.youtube.com/watch?v=1aqnLQ-nwYk
2014	Screen Capture of Exhibit 2012 (PacBio.com) https://www.pacb.com/videos/pacbio-data-deep-dive-a-closer-look-at-hifi-sequencing/
2015	Transcript of 9:50 – 11:45 of Exhibit 2012
2027	Web page: PacBio Sequencing 101: The SMRT Cell in PacBio long-read sequencing. URL: https://www.pacb.com/blog/smrt-cell/ . Web page visited January 23, 2024