

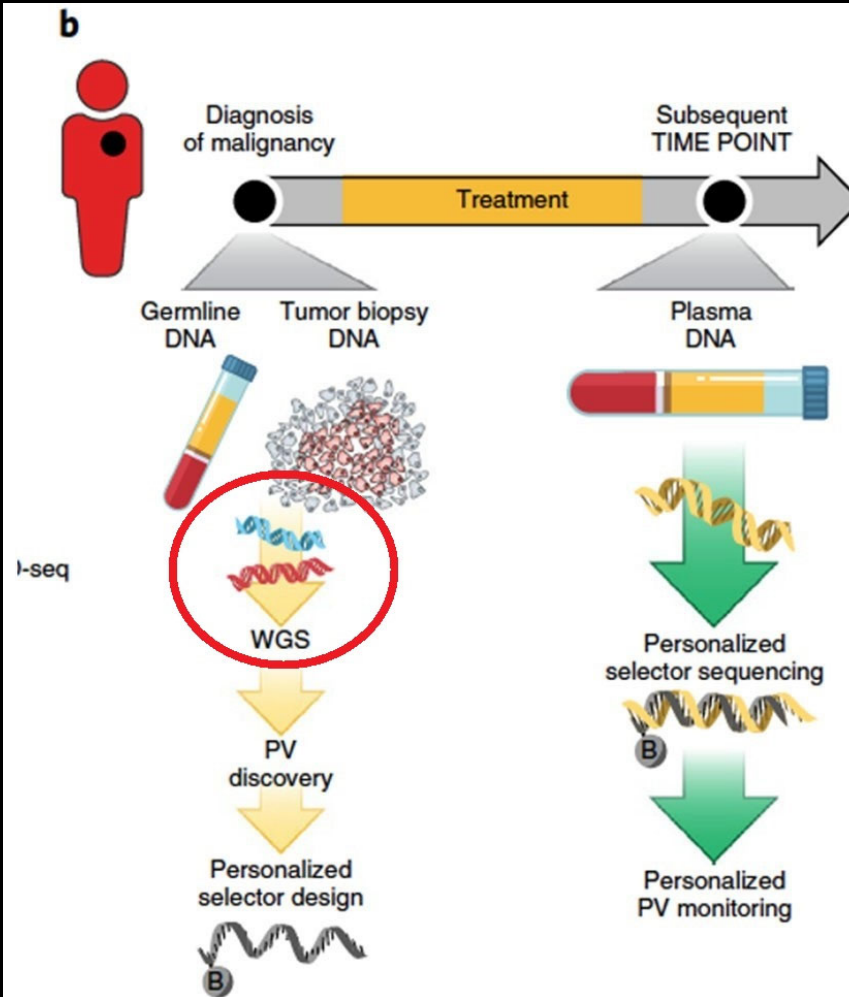
EXHIBIT F

Infringement Of U.S. Patent No. 11,584,968 Patent By Foresight's Solid Tumor Recurrence Test

'968 Patent Claim Language	Infringement Support
1. A method of analyzing a biological sample obtained from a subject being screened for a cancer, wherein the biological sample is from a non-fetal source, the method comprising:	The Foresight Diagnostics Solid Tumor Recurrence Test performs a method of analyzing a biological sample obtained from a subject being screened for a cancer, wherein the biological sample is from a non-fetal source.  Solid Tumors ▾ Our Solid Tumor Recurrence Test is personalized based on patient-specific phased variants that are identified with whole-genome sequencing. It offers the same degree of sensitivity as our Lymphoma Recurrence Test and the ability to track oncogenic and clinically relevant SNVs in addition to other tumor-specific phased variants. More About Solid Tumor Recurrence Test Source: https://foresight-dx.com/partnership “We compared the background profile and recovery of input genomes from plasma cfDNA samples from 12 healthy adults.”

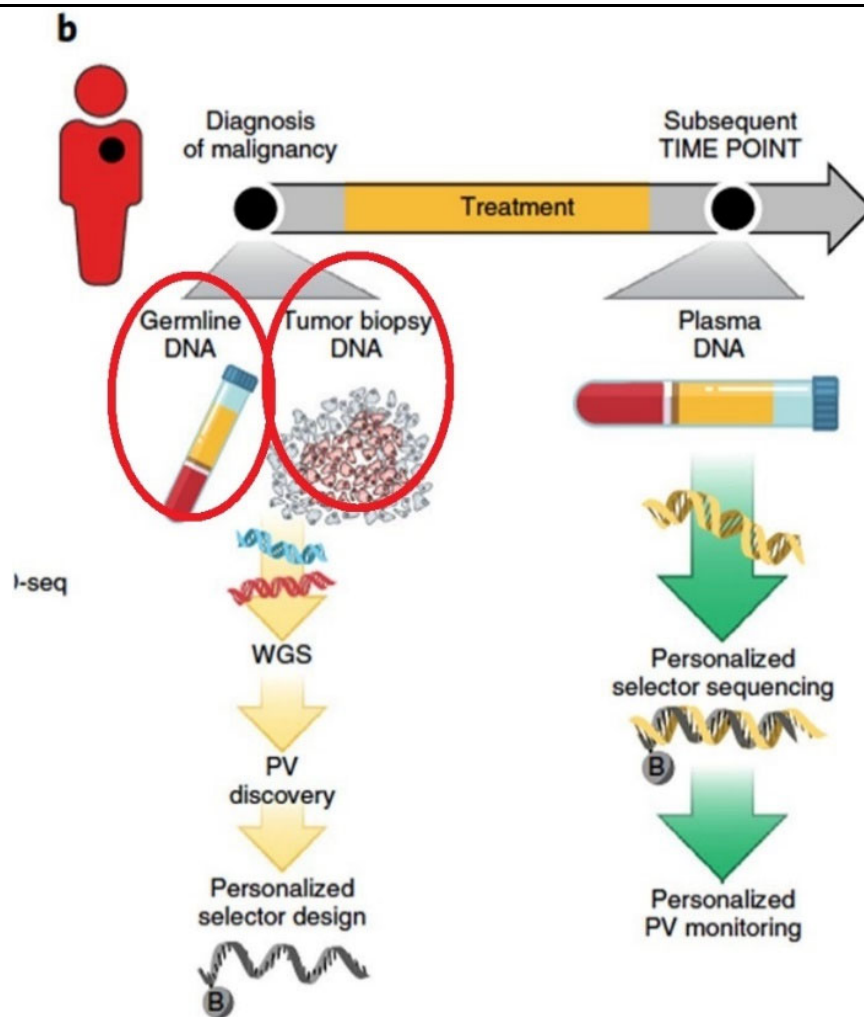
	Source: Kurtz, et. al., Enhanced detection of minimal residual disease by targeted sequencing of phased variants in circulating tumor DNA, Nature Biotechnology, June 2021 (hereinafter “Kurtz,” attached hereto as Exhibit D), at 5.
(a) obtaining a first set of sequence reads and a second set of sequence reads by sequencing nucleic acid molecules derived from a first set of nucleic acid molecules and a second set of nucleic acid molecules, wherein said first set of sequence reads corresponds to said first set of nucleic acid molecules and said second set of sequence reads corresponds to said second set of nucleic acid molecules, wherein said first set of sequence reads and said second set of sequence reads are generated using	The Foresight Diagnostics Solid Tumor Recurrence test obtains a first and second set of sequence reads, corresponding to sequencing a first and second set of nucleic acid molecules. The Foresight Diagnostics Solid Tumor Recurrence test generates the first and second set of sequence reads using whole genome sequencing.

whole genome sequencing, and wherein (i) said first set of nucleic acid molecules is extracted from tissue sample of said subject, and (ii) said second set of nucleic acid molecules is extracted from leukocytes from a blood sample;



Source: Kurtz, Fig. 7b.

The Foresight Diagnostics Solid Tumor Recurrence test extracts (i) the first set of nucleic acid molecules from a tumor biopsy from the subject, and (ii) the second set of nucleic acid molecules from a germline DNA sample, obtained from Peripheral Blood Mononuclear Cells (PBMCs).



Source: Kurtz, Fig. 7b.

METHODS

Tumor tissues (n=46), PBMCs (n=46) and plasma samples (n=169) from 46 Stage I-III NSCLC patients treated with curative intent were prospectively collected at Memorial Sloan Kettering Cancer Center. Patients were selected such that a sufficient number of recurrences were included. Foresight Diagnostics was blinded to clinical outcomes during the performance of testing. All patients underwent resection and received either neoadjuvant +/- adjuvant therapy (n=14), adjuvant therapy without neoadjuvant (n=17), or neither (n=15).

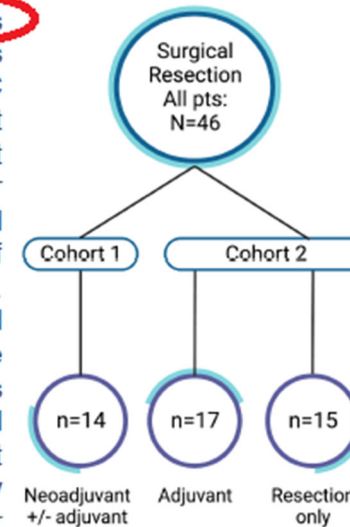
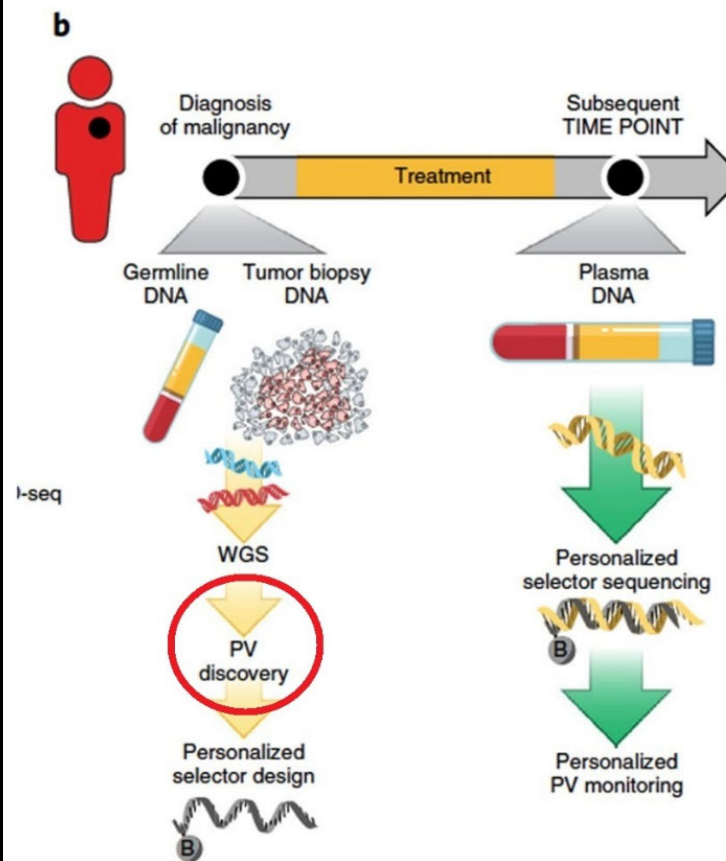


Fig. 2 – Breakdown of study cohorts

Abstract Number: 3375

Source: Isbell, et. al., Ultrasensitive ctDNA MRD Monitoring in Early Stage Lung Cancer with PhasED-Seq, Memorial Sloan Kettering Cancer Center, Abstract Number: 3375, <https://foresight-dx.com/Ultrasensitive%20ctDNA%20minimal%20residual%20disease%20monitoring%20in%20early%20NSCLC%20with%20PhasED-Seq.pdf> (hereinafter “Isbell,” attached hereto as Exhibit J).

(b) using said first set of sequence reads and said second set of sequence reads to identify mosaic variants specific to said tissue sample of said subject in said first set of sequence reads that is not present in said second set of sequence reads;	The Foresight Diagnostics Solid Tumor Recurrence test identifies mosaic variants when it identifies PVs (“multiple variants ‘in-phase’”), which are a subset of mosaic variants. See First Amended Complaint ¶¶ 43-44; see also Cohen Wilson & Trinh Ye, <i>Detecting Somatic Mosaicism: Considerations and Clinical Implications</i>, 87 CLINICAL GENETICS 554, at 555, 558 (2015) (attached hereto as Exhibit O). The Foresight Diagnostics Solid Tumor Recurrence test uses a first and second sequence read to identify PVs in the second nucleic acid sample obtained from the tumor biopsy. For example, Kurtz at Extended Fig. 10b shows the identification of the PVs via comparing (“aligning”) the germline and tumor biopsy nucleic acid sequences.
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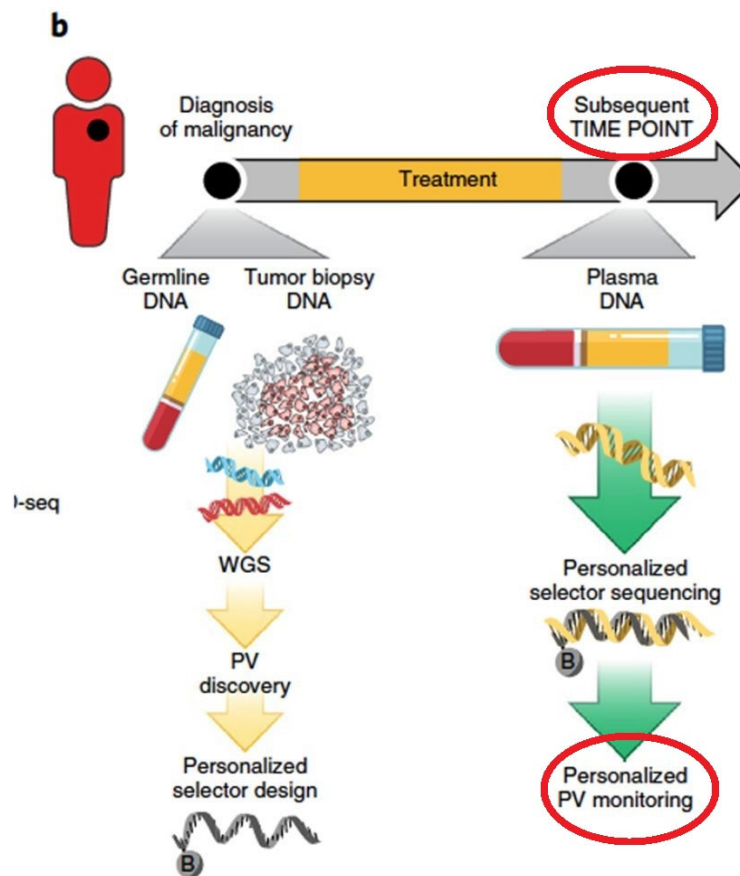
Source: Kurtz, Fig. 7b.

“Identification of phased variants

Identification of phased variants and allelic quantitation

After generating UMID error-suppressed alignment files (i.e., BAM files), we identified PVs from each sample as follows. **First, matched germ-line sequencing of uninvolved peripheral blood mononuclear cells (PBMCs) was performed to identify patient-specific constitutional single nucleotide polymorphisms (SNPs).** These were defined as non-reference positions with a variant allele fraction (VAF) above 40% with a depth of at least

	10, or a VAF of above 0.25% with a depth of at least 100. Next, we identified PVs from read-level data for a sample of interest. Following UMID-mediated error suppression, we analyzed each individual paired-end (PE) read and identified all non-reference positions using ‘samtools calmd’. We used PE data rather than single reads to identify variants occurring on the same template DNA molecule, which could subsequently fall into either read 1 or read 2. Any read-pair containing ≥ 2 nonreference positions was considered to represent a possible somatic PV. For reads with >2 nonreference positions, each permutation of size ≥ 2 was considered independently: i.e., if 4 nonreference positions were identified in a read-pair, all combinations of 2 SNVs (i.e., ‘doublet’ phased variants) and all combinations of 3 SNVs (i.e., ‘triplet’ phased variants) were independently considered. PVs containing putative germ-line SNPs were also removed as follows: if in a given n-mer (i.e., n SNVs in phase on a given molecule) $\geq n-1$ of the component variants were identified as germ-line SNPs, the PV was redacted. This filtering strategy ensures that for any remaining PV, at least 2 of the component SNVs were not seen in the germ-line, as relevant for both sensitivity and specificity. Source: Kurtz, at 36 (Supplementary Methods).
(c) subsequent to (b), identifying said mosaic variants specific to said tissue sample of said subject in a first additional sample of said subject, wherein said first additional sample is obtained from a source that is different than said tissue sample and at a time point that is different than said tissue sample; and	The Foresight Diagnostics Solid Tumor Recurrence test, subsequent to identifying the PVs, identifies the PVs in a subsequent sample, specifically a plasma sample, from the subject.

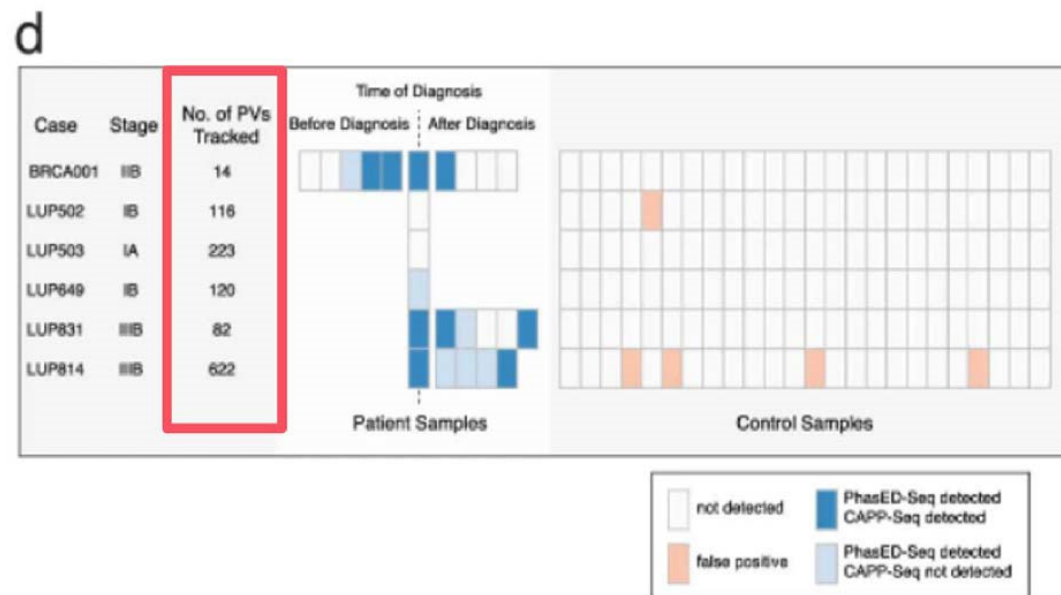


Source: Kurtz, Fig. 7b.

(d) providing a report based on an identification of said mosaic variants specific to said tissue sample of said subject in said first additional sample, wherein said report comprises predicting, diagnosing, and/or prognosing a status or outcome of a

The Foresight Diagnostics Solid Tumor Recurrence test issues a report regarding the identification of the presence or absence of the detected PVs in the second nucleic acid sample obtained from plasma for the purpose of predicting, diagnosing, and/or prognosing a status or outcome of a cancer. For example, Kurtz at Extended Fig. 10d shows the tracking and identification of the presence or absence of the PVs in subsequently obtained samples.

cancer in said subject.



Source: Kurtz, Extended Fig. 10d.