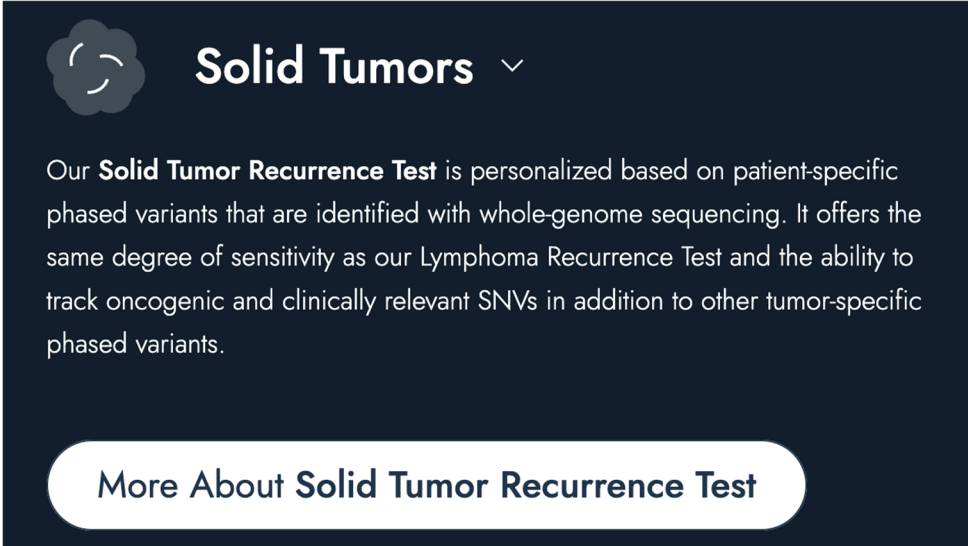
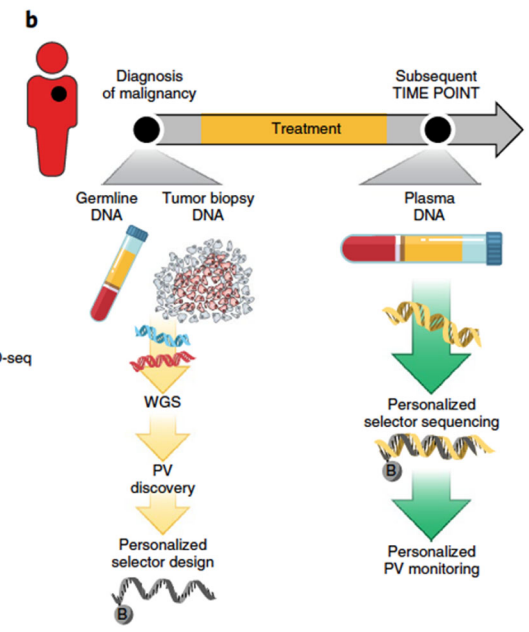
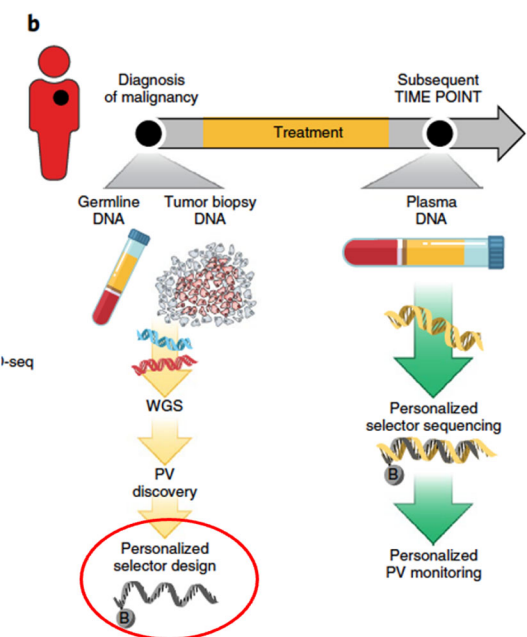


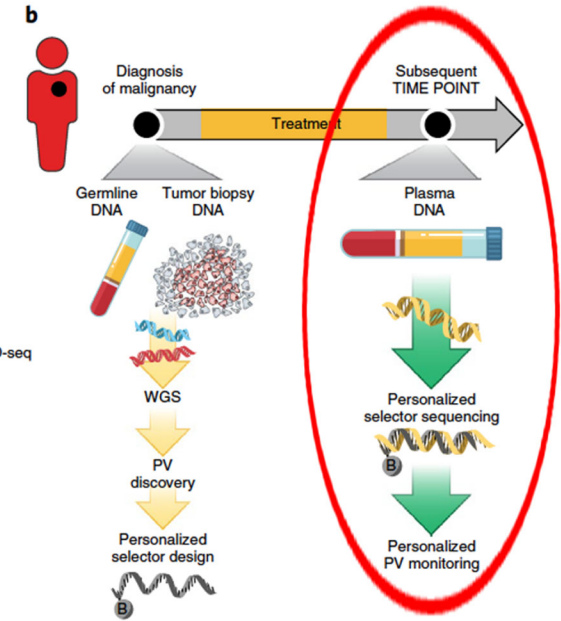
EXHIBIT D

Infringement Of U.S. Patent No. 10,450,611 Patent By Foresight's Solid Tumor Recurrence Test

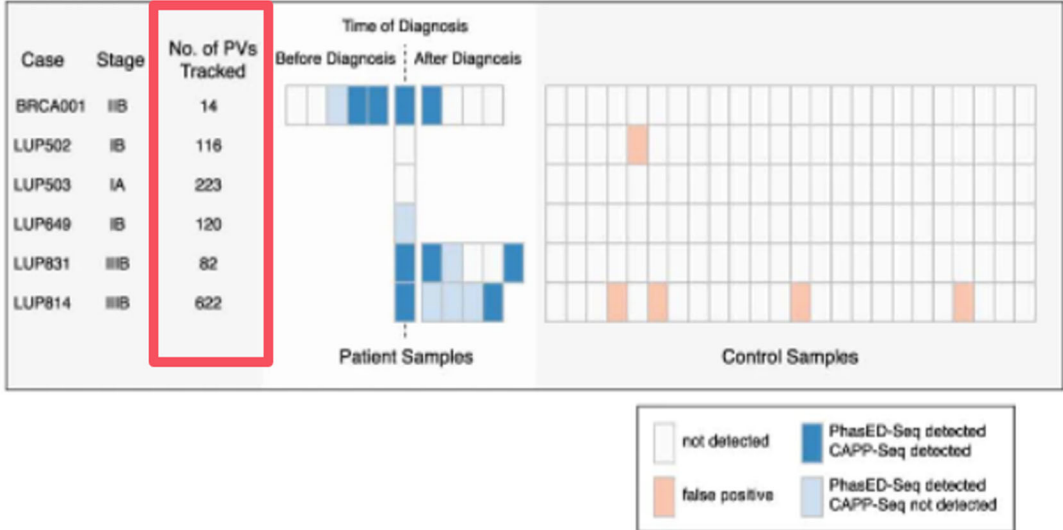
'611 Patent Claim Language	Infringement Support
1. A method for personalized genetic testing, comprising:	The Foresight Diagnostics Solid Tumor Recurrence Test performs a method for personalized genetic testing.  Source: https://foresight-dx.com/partnership
(a) sequencing nucleic acid molecules from at least one biological sample of a subject to generate sequencing data, wherein said sequencing data comprises sequencing 12 gigabases (GB) or more;	The Foresight Diagnostics Solid Tumor Recurrence test utilizes whole genome sequencing of a patient's tumor to generate sequencing data that comprises sequencing 12 GB or more. The application of PhasED-Seq to solid tumors sequenced lung adenocarcinoma samples at a coverage of between 21x - 44x for tumor thereby generating between 69GB - 145GB of sequencing data, respectively.

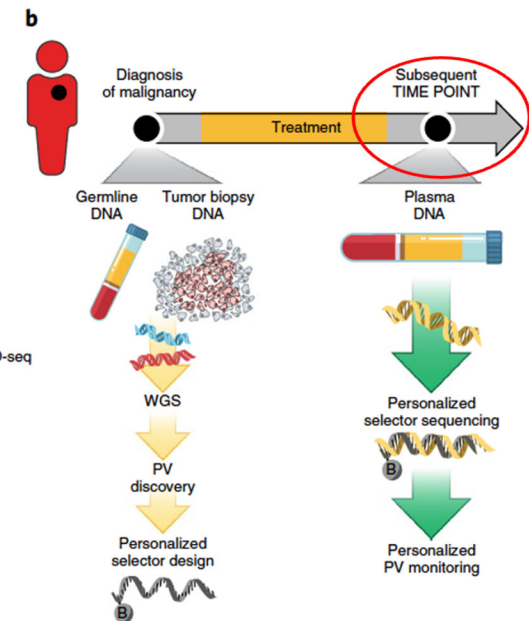
'611 Patent Claim Language	Infringement Support
	Source: Kurtz, et. al., Enhanced detection of minimal residual disease by targeted sequencing of phased variants in circulating tumor DNA, Nature Biotechnology, June 2021 (hereinafter "Kurtz," attached hereto as Exhibit J), Supplementary Table 9.
(b) computer processing said sequencing data to identify a plurality of nucleic acid sequences having a set of genetic variants, wherein said set of genetic variants are identified with respect to a reference	The Foresight Diagnostics Solid Tumor Recurrence test utilizes computer processing to identify a plurality of genetic variants that are identified with respect to a reference. The test sequences both tumor and germline DNA (to provide a reference) in order to identify phased variants that are present in the tumor sample.  The diagram, labeled 'b', illustrates the workflow of the Foresight Diagnostics Solid Tumor Recurrence test. It begins with a patient (red figure) undergoing a 'Diagnosis of malignancy' (black dot) and 'Treatment' (orange bar). Following treatment, a 'Subsequent TIME POINT' is reached (black dot). The workflow then branches into two paths: one for 'Germline DNA' and 'Tumor biopsy DNA' (left), and another for 'Plasma DNA' (right). The left path involves 'I-seq' (represented by a test tube), 'WGS' (represented by a DNA helix), 'PV discovery' (represented by a DNA helix with a red dot), and 'Personalized selector design' (represented by a DNA helix with a red dot). The right path involves 'Personalized selector sequencing' (represented by a DNA helix with a red dot) and 'Personalized PV monitoring' (represented by a DNA helix with a red dot). The diagram uses various symbols to represent different stages: a red figure for the patient, a black dot for diagnosis, an orange bar for treatment, a black dot for subsequent time point, a test tube for I-seq, a DNA helix for WGS, a DNA helix with a red dot for PV discovery, a DNA helix with a red dot for personalized selector design, a DNA helix with a red dot for personalized selector sequencing, and a DNA helix with a red dot for personalized PV monitoring. Source: Kurtz, Figure 7b.
(c) obtaining a probe set comprising a plurality of nucleic acid probe molecules having said plurality of nucleic acid	The Foresight Diagnostics Solid Tumor Recurrence test utilizes a probe set to selectively enrich or amplify sequences comprising genetic variants over other sequences in a biological sample. For example, The Foresight Diagnostics Solid

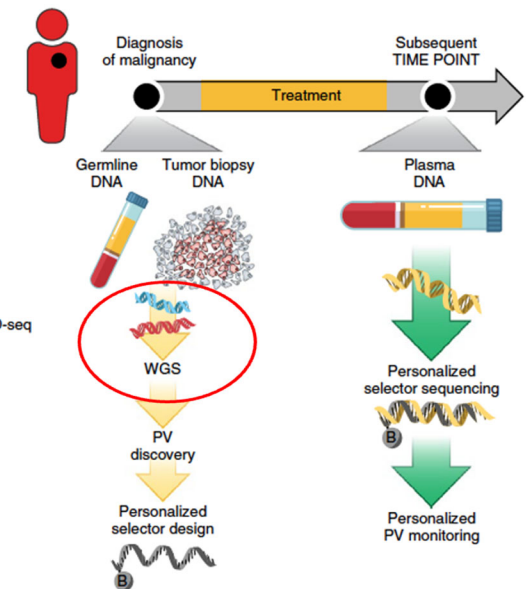
'611 Patent Claim Language	Infringement Support						
sequences or complements thereof, wherein said plurality of nucleic acid probe molecules are configured to selectively enrich or amplify sequences comprising said set of genetic variants over other sequences in said at least one biological sample;	Tumor Recurrence test designs personalized probes directed to the particular phased variants detected in the tumor sample.  The diagram illustrates a workflow for tumor recurrence testing. It begins with a patient (red figure) undergoing 'Diagnosis of malignancy' and 'Treatment'. At the 'Diagnosis of malignancy' stage, 'Germline DNA' and 'Tumor biopsy DNA' are collected. 'Germline DNA' is processed via 'WGS' (Whole Genome Sequencing) for 'PV discovery' (Phased Variant discovery), leading to 'Personalized selector design' (highlighted with a red circle). 'Tumor biopsy DNA' is processed via 'WGS' for 'PV discovery', leading to 'Personalized selector design' (highlighted with a red circle). At the 'Subsequent TIME POINT' stage, 'Plasma DNA' is collected and processed via 'Personalized selector sequencing' (highlighted with a green arrow) to perform 'Personalized PV monitoring' (highlighted with a green arrow). The diagram also shows a 'Phased variant' (PV) being tracked over time. Source: Kurtz, Fig. 7b <table><tr><td>PhasED-Seq (Foresight Diagnostics)</td><td>Hybrid capture-based NGS</td><td>PVs, SNVs</td><td>Baseline: tumor or plasma MRD/monitoring: plasma</td><td>Tumor-informed</td><td>< 0.0001% TF</td></tr></table> Chen K et al., MolDiag&Ther 2021 Source: BloodPac annual meeting slides (attached hereto as Exhibit L); Chen, et al., Commercial ctDNA Assays for Minimal Residual Disease Detection of Solid Tumors, MolDiag&Ther (2021) at Table 1 (hereinafter "Chen," attached hereto as Exhibit M).	PhasED-Seq (Foresight Diagnostics)	Hybrid capture-based NGS	PVs, SNVs	Baseline: tumor or plasma MRD/monitoring: plasma	Tumor-informed	< 0.0001% TF
PhasED-Seq (Foresight Diagnostics)	Hybrid capture-based NGS	PVs, SNVs	Baseline: tumor or plasma MRD/monitoring: plasma	Tumor-informed	< 0.0001% TF		

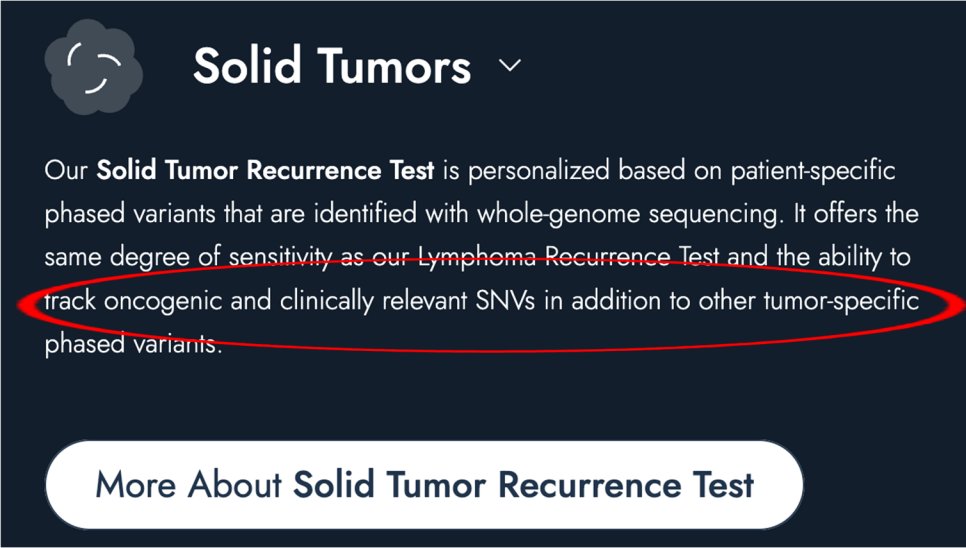
'611 Patent Claim Language	Infringement Support
(d) using said probe set to selectively enrich or amplify sequences comprising said set of genetic variants over other sequences in an additional biological sample from said subject or at least one biological relative of said subject, to generate a sequencing library; and	The Foresight Diagnostics Solid Tumor Recurrence test utilizes the probe set to selectively enrich or amplify sequences comprising the set of genetic variants (phased variants) over other sequences in an additional biological sample from the subject.  Source: Kurtz, Fig. 7b
(e) subjecting said sequencing library to sequencing at a coverage of 175 kilobases (kb) or less to identify a presence or absence of at least a subset of said set of genetic variants in said additional biological sample from said subject or said at least one biological relative, wherein a sequencing of (e) is	The Foresight Diagnostics Solid Tumor Recurrence test sequences the sequencing library at a coverage of 175kb or less to identify the presence or absence of at least a subset of genetic variants in the additional biological sample. For example, the Foresight Diagnostics Solid Tumor Recurrence test tracks a subset of phased variants in plasma.

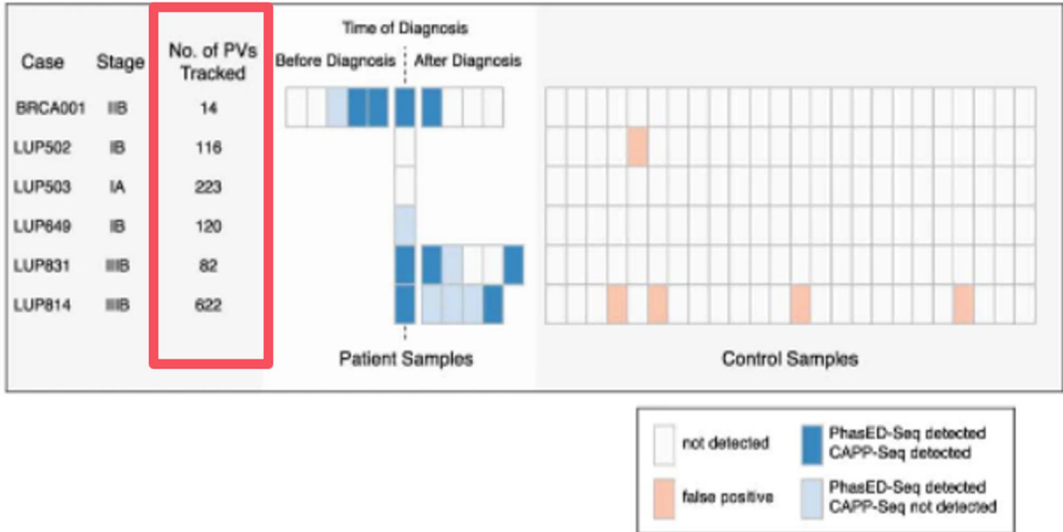
'611 Patent Claim Language	Infringement Support																					
greater than a sequencing depth of said sequencing of (a).	d <table><thead><tr><th>Case</th><th>Stage</th><th>No. of PVs Tracked</th></tr></thead><tbody><tr><td>BRCA001</td><td>IIIB</td><td>14</td></tr><tr><td>LUP502</td><td>IB</td><td>116</td></tr><tr><td>LUP503</td><td>IA</td><td>223</td></tr><tr><td>LUP649</td><td>IB</td><td>120</td></tr><tr><td>LUP831</td><td>IIIB</td><td>82</td></tr><tr><td>LUP814</td><td>IIIB</td><td>622</td></tr></tbody></table> The timeline shows 'Time of Diagnosis' with 'Before Diagnosis' and 'After Diagnosis' periods. The 'Patient Samples' section shows a grid of results for each case, with blue bars indicating 'PhasED-Seq detected' and orange bars indicating 'false positive'. The 'Control Samples' section shows a grid of results for each case, with blue bars indicating 'PhasED-Seq detected' and orange bars indicating 'false positive'. Source: Kurtz, Extended Fig. 10d.	Case	Stage	No. of PVs Tracked	BRCA001	IIIB	14	LUP502	IB	116	LUP503	IA	223	LUP649	IB	120	LUP831	IIIB	82	LUP814	IIIB	622
Case	Stage	No. of PVs Tracked																				
BRCA001	IIIB	14																				
LUP502	IB	116																				
LUP503	IA	223																				
LUP649	IB	120																				
LUP831	IIIB	82																				
LUP814	IIIB	622																				
2. The method of claim 1, further comprising outputting a report that is generated at least based on comparison of results from said sequencing of (a) with results from at least said subjecting said sequencing library to said sequencing of (e).	The Foresight Diagnostics Solid Tumor Recurrence test issues a report regarding the patient's MRD status that is based on a comparison of the sequencing results of the WGS sequencing of the tumor and the sequencing of the phased variants detected in the subsequent plasma sample. For example, the Foresight Diagnostics Solid Tumor Recurrence test reports on the presence or absence of the specific phased variants identified both prior to and after diagnosis.																					

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	d  Source: Kurtz, Extended Fig. 10d.
3. The method of claim 1, wherein in said sequencing of (a), said at least one biological sample is obtained from said subject at a first time point, and wherein said additional biological sample is obtained from said subject or said at least one biological relative at a second time point subsequent to said first time point.	The Foresight Diagnostics Solid Tumor Recurrence test sequences a tumor sample obtained from a first time point and a plasma sample that is obtained at a subsequent time point (i.e., after surgery).

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	 The diagram, labeled 'b', illustrates a clinical workflow. It begins with a red human figure. A horizontal timeline shows 'Diagnosis of malignancy' (black dot), 'Treatment' (yellow bar), and 'Subsequent TIME POINT' (black dot, circled in red). Below the timeline, 'Germline DNA' is represented by a test tube and 'Tumor biopsy DNA' by a cluster of cells. A vertical arrow labeled 'I-seq' points down from the DNA samples to 'WGS' (Whole Genome Sequencing), represented by a DNA double helix. This leads to 'PV discovery' (Pathway Discovery), then 'Personalized selector design' (represented by a DNA helix with a 'B' marker). On the right, 'Plasma DNA' is shown in a test tube. A vertical arrow labeled 'Personalized selector sequencing' points down to 'Personalized PV monitoring' (represented by a DNA helix with a 'B' marker). Source: Kurtz, Fig. 7b.
4. The method of claim 1, wherein said sequencing of (a) comprises (i) exome sequencing, (ii) sequencing a panel of genes, (iii) whole genome sequencing, and/or (iv) sequencing a population of complementary deoxyribonucleic acid molecules derived from ribonucleic acid molecules.	The Foresight Diagnostics Solid Tumor Recurrence test sequences the tumor using whole genome sequencing.

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	b  The diagram illustrates a personalized medicine workflow. It begins with a patient (red figure) undergoing 'Diagnosis of malignancy'. This leads to 'Germline DNA' and 'Tumor biopsy DNA'. The 'Tumor biopsy DNA' is processed through 'WGS' (Whole Genome Sequencing), which is highlighted with a red circle. This step leads to 'PV discovery' (Pathogenic Variant discovery) and 'Personalized selector design'. The 'Personalized selector design' leads to 'Personalized selector sequencing'. This step leads to 'Personalized PV monitoring'. The workflow also includes a 'Treatment' phase, which leads to a 'Subsequent TIME POINT' where 'Plasma DNA' is analyzed. The 'Plasma DNA' is then processed through 'Personalized selector sequencing' and 'Personalized PV monitoring'. Source: Kurtz, Fig. 7b.
5. The method of claim 1, wherein each of said plurality of nucleic acid probe molecules includes oligonucleotide-directed genomic content comprising (i) at least one variable portion from a result of said sequencing of (a) and (ii) at least one fixed portion independent of said result of said sequencing of (a).	The Foresight Diagnostics Solid Tumor Recurrence test includes both variable portions based upon the prior whole genome sequencing as well as fixed content that is related to genes with known oncogenic or clinically relevant variants.

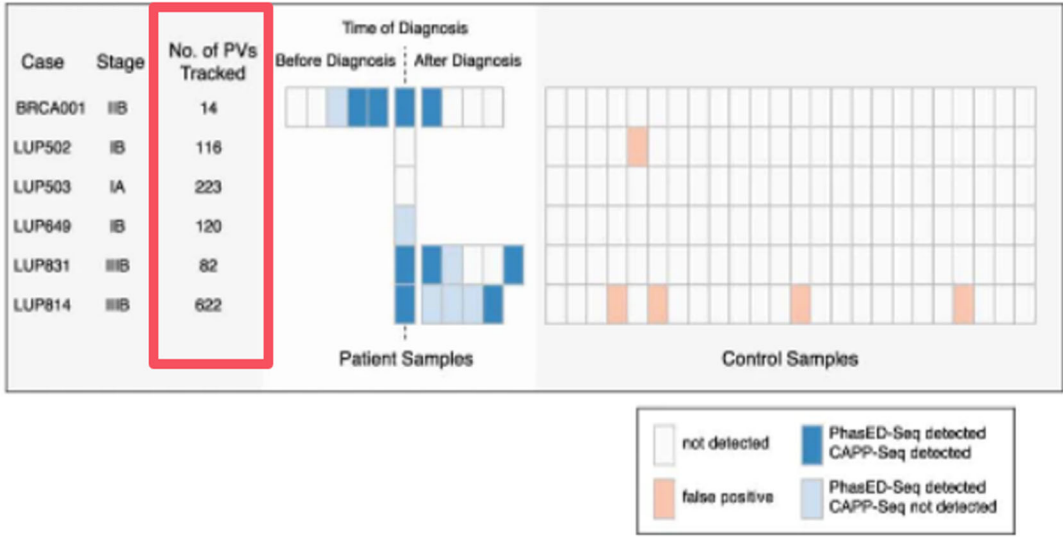
'611 Patent Claim Language	Infringement Support
	 Source: https://foresight-dx.com/partnership
9. The method of claim 1, further comprising outputting a report that identifies said presence or absence of said at least said subset of said genetic variants in said subject or said at least one biological relative.	The Foresight Diagnostics Solid Tumor Recurrence test issues a report regarding the patient's MRD status that is based on an identification of the presence or absence of the phased variants between the WGS sequencing of the tumor and the subsequent sequencing of the plasma sample. For example, the Foresight Diagnostics Solid Tumor Recurrence test reports on the presence or absence of the specific phased variants identified both prior to and after diagnosis.

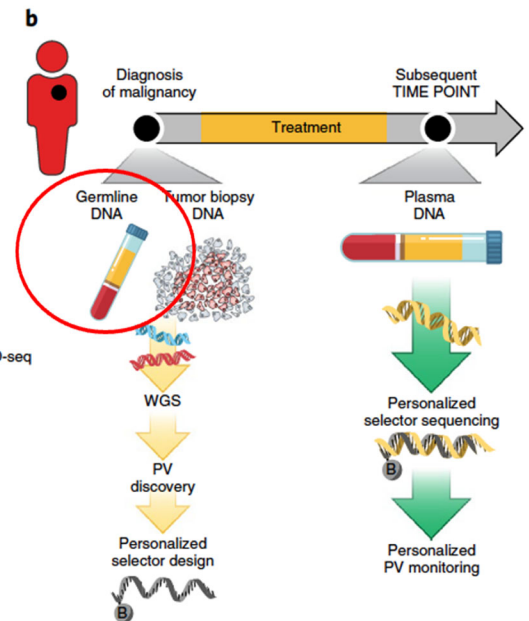
'611 Patent Claim Language	Infringement Support
	d  Source: Kurtz, Extended Fig. 10d.
10. The method of claim 1, further comprising providing a therapeutic intervention at least based on said presence or absence of said at least said subset of said genetic variants identified in (e).	The Foresight Diagnostics Solid Tumor Recurrence test issues a report regarding the identification of patients in need of additional therapy.

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	vs Foresight Diagnostics ✓ Best-in-class sensitivity at all time-points ✓ Detects relapse 200+ days prior to clinical relapse⁽⁴⁾ ✓ Identifies relapse when disease burden is low and probability of cure is higher ✓ Identifies the majority of patients in need of additional therapy Source: https://foresight-dx.com/technology
11. The method of claim 1, wherein said at least one biological sample includes a tumor sample and said nucleic acids molecules are from cells in said tumor sample.	The Foresight Diagnostics Solid Tumor Recurrence test utilizes a biological sample that is a tumor sample and sequences nucleic acid molecules from the tumor sample.

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	b Source: Kurtz, Fig. 7b.
13. The method of claim 1, wherein said plurality of nucleic acid sequences having said set of genetic variants comprises genetic variants in a germline sequence of said subject.	The Foresight Diagnostics Solid Tumor Recurrence test analyzes the germline sequence of the individual in order to identify the phased variants for tracking.

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	b Source: Kurtz, Fig. 7b.
18. The method of claim 1, wherein subjecting said sequencing library to sequencing in (e) comprises generating nucleic acid sequence data from said additional biological sample.	The Foresight Diagnostics Solid Tumor Recurrence test may be used on additional biological samples obtained from an individual for purposes of monitoring for disease recurrence over time. For example, certain samples were tracked over multiple time points after diagnosis.

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	d  Source: Kurtz, Supplemental Fig. 10d.
19. The method of claim 1, wherein computer processing of said sequence data comprises identifying one or more of (i) genetic variants of said nucleic acid sequence with respect to a germline sequence(s), (ii) alleles which match said reference sequence(s) and are correlated with a type of cancer or other disease, (iii) alleles which determine a human leukocyte antigen (HLA) type, (iv) metrics of gene expression or allele-specific expression, and (v) quantification of non-coding ribonucleic acid (RNA) molecules or micro-RNA	The Foresight Diagnostics Solid Tumor Recurrence test analyzes the germline sequence in comparison with the sequence of the tumor of the individual in order to identify the phased variants for tracking.

'611 Patent Claim Language	Infringement Support
molecules which are at least partially tissue-type specific or cancer-type specific.	 The diagram, labeled 'b', illustrates a personalized medicine workflow. It begins with a red human figure. A horizontal timeline shows 'Diagnosis of malignancy' (black dot), 'Treatment' (yellow bar), and 'Subsequent TIME POINT' (black dot). Below the timeline, two DNA samples are shown: 'Germline DNA' (circled in red) and 'Tumor biopsy DNA'. The 'Germline DNA' sample is processed through 'I-seq' (indicated by a blue arrow), 'WGS' (yellow arrow), 'PV discovery' (yellow arrow), and 'Personalized selector design' (yellow arrow), resulting in a 'Personalized selector' (represented by a blue and yellow wavy line with a 'B' in a circle). The 'Tumor biopsy DNA' sample is processed through 'Personalized selector sequencing' (green arrow) and 'Personalized PV monitoring' (green arrow), resulting in a 'Personalized PV monitoring' (represented by a blue and yellow wavy line with a 'B' in a circle). A 'Plasma DNA' sample is also shown, which is processed through 'Personalized selector sequencing' (green arrow) and 'Personalized PV monitoring' (green arrow), resulting in a 'Personalized PV monitoring' (represented by a blue and yellow wavy line with a 'B' in a circle). Source: Kurtz, Fig. 7b.
28. The method of claim 1, further comprising using said presence or absence of said at least said subset of said set of genetic variants identified in (e) to treat said subject or said at least one biological relative for a disorder.	The Foresight Diagnostics Solid Tumor Recurrence test uses the information including whether the presence or absence of PVs is detected to inform treatment of the individual.

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	 vs Foresight Diagnostics ✓ Best-in-class sensitivity at all time-points ✓ Detects relapse 200+ days prior to clinical relapse^(*) ✓ Identifies relapse when disease burden is low and probability of cure is higher ✓ Identifies the majority of patients in need of additional therapy Source: https://foresight-dx.com/technology
29. The method of claim 1, wherein said reference comprises a human reference sequence.	The Foresight Diagnostics Solid Tumor Recurrence test compares the sequencing information to a human reference sequence. For example, Kurtz states in the Methods section that “[s]equencing reads were aligned to hg19 and deduplicated with samtools markup, as described above.” Source: Kurtz, Methods
30. The method of claim 1, wherein said reference is a human reference sequence.	The Foresight Diagnostics Solid Tumor Recurrence test compares the sequencing information to a human reference sequence. For example, Kurtz states in the Methods section that “[s]equencing reads were aligned to hg19 and deduplicated with samtools markup, as described above.” Source: Kurtz, Methods