# Validation of a Comprehensive Next-generation Sequencing Liquid Biopsy Assay for **Clinical Diagnostics and Clinical Trial Applications**

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## Introduction

**Background:** Next-generation sequencing of cell-free circulating solid tumor nucleic acid from blood samples, known as "liquid biopsy", provides a powerful non-invasive approach to detect solid tumor derived somatic variants in a massively parallel manner. It has rapidly become an invaluable choice of testing technologies for cancer diagnosis and therapy decisions when invasive tissue biopsy is inaccessible and/or inadequate for molecular characterization. This testing method is now being used to aid data collection for prospective clinical trials when tissue samples may be challenging to obtain.

**Methods:** In this study, we present the NGS-based NeoLAB<sup>®</sup> Solid Tumor Liquid Biopsy assay that was designed and validated specifically for liquid biopsy characterization. The assay was designed to test cell free DNA and cell free RNA from blood plasma for detection of single nucleotide variants (SNV), insertion/deletion (Indel), copy number variants (CNV), and gene fusions present in 52 most commonly mutated genes in cancers. The NeoLAB<sup>®</sup> Solid Tumor Liquid Biopsy assay comprehensively covers all actionable markers currently supported by evidence from FDA and EMAapproved drug labels, National Comprehensive Cancer Network (NCCN) and European Society for Medical Oncology (ESMO) Guidelines, and global clinical trials.

**Results:** To implement this assay for clinical utility, we performed an analytical and clinical assay validation to establish the assay accuracy, specificity, sensitivity, repeatability, and reproducibility, with including pre-characterized reference controls, retrospective plasma samples from cancer patients, and prospectively-collected clinic blood specimen. Triplicates were included and testing was performed at different times and by different operators to assess the assay precision. Over 100 clinic blood specimens were collected in Streck cfDNA tubes from multiple trial centers, including treatment naïve phase III-IV patients with various solid tumor types (lung cancer, breast cancer, brain cancer, prostate cancer, kidney cancer, melanoma, etc) as well as heathy donors, processed within 7 days for plasma separation and total nucleotide acid (TNA) extraction, and assessed by the NGS assay for mutation detection. The identified mutations and wild-types were verified with orthogonal ddPCR. Assay sensitivity as low as 0.1% for SNV and Indel, 1.3 fold change for CNV, and 10 copies for gene fusion were observed, with near-perfect assay specificity (>99.99%) at these sensitivity levels.

**Conclusion:** A targeted NGS liquid biopsy assay was analytically and clinically validated under medical oversight, with a demonstrated rigor of the test by its high sensitivity/specificity and robust reproducibility. The validated assay has been utilized for clinical diagnostics and to support research and development efforts in clinical trials.

### Suppressor Genes Copy Number Gene Fusions Hotspot Genes Variants AKT1 KRAS APC CCND1 FGFR1 RET ALK ALK MAP2K1 ROS1 FBXW7 CCND2 BRAF FGFR2 PTEN CCND3 AR FGFR3 MAP2K2 SF3B1 ERG ARAF ETV1 FGFR4 MET SMAD4 TP53 CDK4 BRAF FLT3 MTOR SMO CDK6 FGFR1 EGFR FGFR2 CHEK2 GNA11 NRAS NTRK1 ERBB2 FGFR3 CTNNB1 GNAQ NTRK3 FGFR1 MET DDR2 GNAS EGFR HRAS PDGFRA FGFR2 NTRK1 FGFR3 ERBB2 IDH1 PIK3CA NTRK3 ERBB3 IDH2 PTEN MET3 RET ESR1 KIT RAF1 MYC ROS1 Liquid Biopsy NGS Testing Specifications 12 CNVs Extended coverage of TP53 52 genes 272 amplicons >900 hotspots, MET exon 14 Single library from DNA and RNA 96 fusions SNVs and indels skipping Lab created Oncomi Templating cfDNA or Single blood cfNA report -Sequencing cfTNA\* Library pre Oncomine tube CHEF-S5 Knowledge extraction Annotation & Reporting 1 II 💿 🛋. Telefore for SAL particular accountinger Custom Report **Blood Sample** 3 Day Turn Around

**Assay Gene Content & Workflow** 

Table 1. Gene content of the NeoLAB<sup>®</sup> Solid Tumor Liquid **Biopsy assay.** It covers all the actionable markers supported by drug labels and clinical guidelines for Hotspot, CNV and gene fusion

Relevant evidence for genes on the panel: • Approved labels (FDA, EMA)

• Guidelines (NCCN, ESMO) • Clinical Trials (global)

Bladder	Esophageal
Brain and CNS	Gastric
Breast	Head and Neck
Cervical	Kidney
Colorectal	Liver
Endometrial	Lung

Table 2. Sample cancer types covered by the NeoLAB<sup>®</sup> Solid **Tumor Liquid Biopsy assay** 

Figure 1. Workflow of the NeoLAB<sup>®</sup> Solid Tumor Liquid **Biopsy assay**. Human whole blood specimen went though plasma preparation, cfTNA extraction, library preparation using the Oncomine cfTNA library prep kit, and sequenced on Ion S5 with the 550 chip. Raw sequencing data was then analyzed for variants calling and reporting...

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## **Analytical Assay Validation**

able 3. How Analvtical Acc	uracv Results v	were calculated	k				SNV/Indel	Indels	CNVs	Gene Fusions
Annotated variant Libraries (n=25) prepared		' <b>Indel</b> 0	5	CNV 5	Gene Fusion	Cohort of previously	Annotated mutations at allele frequencies	Annotated mutations at allele frequencies	Copies of 7.0, 6.4, 5.9, 3.25,	Copies of 40, 20, 10, an
between 2 operators		0	CNV (n=12)	CNV (n=12)	Gene fusions (n=99)	characterized samples	of 1%, 0.5%, 0.25%, and 0.1%	of 1%, 0.5%, 0.25%, and 0.1%	3.0, and 2.75	Copies 01 40, 20, 10, 6
# Positions queried	SNVs (n=79)	ndels (n=6)	CNV-positive (n=2), CNV- negative (n=10)	CNV-positive (n=2), CNV- negative (n=10)	(gene fusion- positive (n=1) gene fusion- negative (n=98)	Concordance criteria with reference for	Lowest variant allele frequency that consistently identified expected	Lowest variant allele frequency that consistently identified expected mutations	Lowest copy number that consistently identified expected mutations with a	Lowest gene fusion that consistently iden expected mutations
Concordance if expected ariant or wildtype detected (VAF cutoff = 0.065% 1.2 ratio)	3 copies	3 copies		3 copies	3 copies	each sample	mutations with a concordance percentage of 80%	with a concordance percentage of 80%	concordance percentage of 80%	concordance percer of 80%
ccuracy acceptance criteria	≥95%		≥95%	≥95%	≥95%	LOD	0.1%-0.25% (0.15, estimated by linear interpolation), 0.1% indels	0.1%	2.75 copies	10 copies
Concordance achieved	10	0%	95%	100%	100%					

Table 3. Analytical assay accuracy. The analytical accuracy of the NeoLAB® Solid Tumor Liquid Biopsy panel was assessed for all of the gene targets by testing a total of 25 libraries of pre-characterized reference cell-free DNA and cell-free RNA samples (10 for SNV/indel, 5 for CNV, and 10 for gene fusion) with annotated mutation status on at least one variant position.

able 4. Analytical Assay Specificity			Category	Acceptance Criteria	Percentage Concordance		
Specificity	SNV/Indel	CNV	Gene Fusion				
Acceptance criteria	≥95%	≥95%	≥95%	Clinical Accuracy	≥95%	98.02%	
Analytical	100%	100%	100%	Clinical Specificity	≥95%	98.76%	
specificity Clinical				Clinical Sensitivity	≥95%	95.12%	
pecificity (tumor patients and healthy donors)	s and 100% 100% 100%		100%	Clinical Repeatability	≥95%	99.95%	
<b>ible 4. Analytical assay specificity.</b> The analytical specificity of the NeoLAB <sup>®</sup> Solid Tumor Liquid Biopsy panel was determined by testing both ild-type and annotated reference samples to determine concordance for each annotated position in every sample. The SNV, indel, CNV, and gene sion specificity rate of 100% achieved the specificity acceptance rate of ≥95%.			Clinical Across-Time Reproducibility	≥95%	99.97%		
able 5. Analytical Assay Sensitivity			Clinical Across-Operator Reproducibility	≥95%	99.94%		

Sensitivity	Acceptance Criteria	Variant Sensitivity Results	PPV Acceptance Criteria	Variant PPV Results
SNVs	≥97%	100%	≥99%	100%
Indels	≥90%	90.00%	≥95%	100%
CNVs	≥90%	100%	≥95%	100%
Gene Fusions	≥90%	100%	≥95%	100%

Table 5. Analytical assay sensitivity. The analytical sensitivity of the NeoLAB® Solid Tumor Liquid Biopsy panel was determined by testing previously characterized samples, each containing annotated mutations at known allele frequencies. Concordance of reference genes with each annotated mutation in every sample, including SNVs, indels, CNVs and gene fusions, achieved the acceptance criteria for sensitivity and positive predictive value (PPV)

Melanoma Ovarian Pancreatic Prostate Sarcoma Thyroid



# 5038

### Table 6. How limit of detection (LOD) was determined

# **Clinical Assay Validation & Clinical Utility**

### Table 7. Clinical Assay Validation

## Figure 2. Applications in Clinical Diagnosis and Clinical Trials



= Non-Small Cell Lung Cente Cholangiocarcinoma ovarian cancer \* Thy rold Cancer Liver Cancer Diffuse Large B-Cell Lymphom a = Mesothelisma Undifferentiated/Unclassified: Angiosarcoma . Embryonal Rhabdomyosa room Lymphema Skin Basal Gell Carcinoma Prostate Cancer Rectal Cance Colorectal Cancer Bladder Cancer Bladder Urothelial Carcinoma Non-Hodgkin's Lymphoma Small Cell Lung Cancer Thyroid Gland Medullary Carcine B-CellNon-Hodgkin's Lymphoma Endometrial Carcinoma Marginal Zane Lymphoma

Table 7. Clinical assay validation. Clinical accuracy, specificity, and sensitivity were calculated using the same formula and acceptance metrics as analytical validation. Blood samples from late stage (III/IV) patients with various types of solid tumors were procured from 11 different clinical centers in USA and Europe and were included in the validation.

Figure 2. Applications in clinical diagnosis and clinical trials. Over 40 types of solid tumor were tested with NeoLAB<sup>®</sup> Solid Tumor Liquid Biopsy assay. Over 75% of patients with actionable mutation detected by NeoLAB<sup>®</sup> Solid Tumor Liquid Biopsy assay.

