



Intended Use

FoundationOne Liquid CDx is a qualitative next generation sequencing based in vitro diagnostic test that uses targeted high throughput hybridization-based capture technology to detect and report substitutions, insertions and deletions (indels) in 311 genes, including rearrangements and copy number losses only in *BRCA1* and *BRCA2*. FoundationOne Liquid CDx utilizes circulating cell-free DNA (cfDNA) isolated from plasma derived from anti-coagulated peripheral whole blood of cancer patients collected in FoundationOne Liquid CDx cfDNA blood collection tubes included in the FoundationOne Liquid CDx Blood Sample Collection Kit. The test is intended to be used as a companion diagnostic to identify patients who may benefit from treatment with the targeted therapies listed in Table 1 in accordance with the approved therapeutic product labeling. Additionally, FoundationOne Liquid CDx is intended to provide tumor mutation profiling for substitutions and indels to be used by qualified health care professionals in accordance with professional guidelines in oncology for patients with solid malignant neoplasms.

Table 1: Companion diagnostic indications

TUMOR TYPE	BIOMARKER(S) DETECTED	THERAPY
Non-Small Cell Lung Cancer (NSCLC)	<i>EGFR</i> exon 19 deletions and <i>EGFR</i> exon 21 L858R substitution	IRESSA® (gefitinib), TAGRISSO® (osimertinib) or TARCEVA® (erlotinib)
Prostate Cancer	<i>BRCA1</i> , <i>BRCA2</i> alterations	Rubraca® (rucaparib)

A negative result from a plasma specimen does not mean that the patient's tumor is negative for genomic findings. Patients who are negative for the mutations listed in Table 1 should be reflexed to routine biopsy and their tumor mutation status confirmed using an FDA-approved tumor tissue test, if feasible.

Genomic findings other than those listed in Table 1 are not prescriptive or conclusive for labeled use of any specific therapeutic product.

FoundationOne Liquid CDx is a single-site assay performed at Foundation Medicine, Inc. in Cambridge, MA.



Summary of Analytical Sensitivity and Specificity for FDA-Approved Content

Results from our Limit of Detection (LoD) study are shown below, indicating the median variant allele frequency or tumor fraction at which the test has shown 95% probability of detection.<sup>1</sup> Results are also included from the Limit of Blank (LoB) study, which evaluated variant calling in healthy donors. Please refer to our product labeling for a list of the 75 genes baited for enhanced sensitivity and complete product specifications.

ALTERATION TYPE	BAIT SET REGION	MEDIAN LIMIT OF DETECTION (LOD)	LOD RANGE QUARTILE 1-3	LIMIT OF BLANK (VARIANT DETECTION RATE IN HEALTHY DONORS) <sup>1</sup>
Short Variants	Enhanced Sensitivity	0.40% VAF	0.33% - 0.50% VAF	0.82%
	Standard Sensitivity	0.82% VAF	0.70% - 0.98% VAF	
Rearrangements	Enhanced Sensitivity	0.37% VAF	0.26% - 0.47% VAF	0%
	Standard Sensitivity	0.90% VAF	NA	
Copy Number Losses	NA	30.4% TF	NA	0%

VAF = variant allele frequency; TF = tumor fraction

\* The accuracy of %VAF / %TF have not been analytically validated

<sup>1</sup> Calculated as the number of unique variants detected at least once across all replicates divided by the total number of unique variants included in the analysis



## FoundationOne Liquid CDx FDA-Approved Gene List<sup>†</sup>

As part of its FDA-approved intended use, FoundationOne Liquid CDx interrogates 311 genes, including 309 genes with complete exonic (coding) coverage and 2 genes with only select non-coding coverage (indicated with \*). **Select genes and select exons (indicated in bold)** are captured with increased sensitivity.

<b>ABL1</b> [Exons 4-9]	CD70	FANCG	<b>JAK3</b> [Exons 5,11,12,13,15,16]	NKX2-1	RAD51D	WHSC1
ACVR1B	CD79A	FANCL	JUN	NOTCH1	RAD52	WT1
<b>AKT1</b> [Exon 3]	CD79B	FAS	KDM5A	NOTCH2	RAD54L	XPO1
AKT2	CDC73	FBXW7	KDM5C	NOTCH3	<b>RAF1</b> [Exons 3,4,6,7,10,14,15,17]	XRCC2
AKT3	<b>CDH1</b>	FGF10	KDM6A	<b>NPM1</b> [Exons 4-6,8,10]	RARA	ZNF217
<b>ALK</b> [Exons 20-29]	<b>CDK12</b>	FGF12	KDR	<b>NRAS</b> [Exons 2,3]		ZNF703
ALOX12B	<b>CDK4</b>	FGF14	KEAP1	NSD3 (WHSC1L1)	<b>RB1</b>	
AMER1 (FAM123B)	<b>CDK6</b>	FGF19	KEL	NT5C2	RBM10	
<b>APC</b>	CDK8	FGF23	<b>KIT</b> [Exons 8,9,11,12,13,17]	<b>NTRK1</b> [Exons 14,15]	REL	
<b>AR</b>	CDKN1A	FGF3	KLHL6	NTRK2	<b>RET</b> [Exons 11,13-16]	
<b>ARAF</b> [Exons 4,5,7, 11,13,15,16]	CDKN1B	FGF4	KMT2A (MLL)		RICTOR	
ARFRP1	<b>CDKN2A</b>	FGF6	KMT2D (MLL2)	<b>NTRK3</b> [Exons 16,17]	RNF43	
ARID1A	CDKN2B	<b>FGFR1</b>	<b>KRAS</b>	P2RY8	<b>ROS1</b> [Exons 31,36-38,40]	
ASXL1	CDKN2C	<b>FGFR2</b>	LTK	<b>PALB2</b>	RPTOR	
<b>ATM</b>	CEBPA	<b>FGFR3</b> [Exons 7, 9 (alternative designation exon 10), 14, 18]	LYN	PARK2	SDHA	
<b>ATR</b>	CHEK1	FGFR4	MAF	PARP1	SDHB	
ATRX	<b>CHEK2</b>	FH	<b>MAP2K1 (MEK1)</b> [Exons 2,3]	PARP2	SDHC	
AURKA	CIC	FLCN	<b>MAP2K2 (MEK2)</b> [Exons 2-4,6,7]	PARP3	SDHD	
AURKB	CREBBP	FLT1	MAP2K4	PAX5	SETD2	
AXIN1	<b>CRKL</b>	<b>FLT3</b> [Exons 14,15,20]	MAP3K1	PBRM1	SF3B1	
AXL	CSF1R	<b>FOXL2</b>	MAP3K13	PDCD1 (PD-1)	SGK1	
BAP1	CTCF	FUBP1	MAPK1	<b>PDCD1LG2 (PD-L2)</b>	SMAD2	
BARD1	CTNNA1	GABRA6	MCL1	<b>PDGFRA</b> [Exons 12,18]	SMAD4	
BCL2	<b>CTNNB1</b> [Exon 3]	GATA3	<b>MDM2</b>	<b>PDGFRB</b> [Exons 12-21,23]	SMARCA4	
BCL2L1	CUL3	GATA4	MDM4		SMARCB1	
BCL2L2	CUL4A	GATA6	MED12	PIK1	<b>SMO</b>	
BCL6	CXCR4	<b>GNA11</b> [Exons 4,5]	MEF2B	PIK3C2B	SNCAIP	
BCOR	CYP17A1	GNA13	MEN1	PIK3C2G	SOCS1	
BCORL1	DAXX	<b>GNAQ</b> [Exons 4,5]	MERTK	<b>PIK3CA</b> [Exons 2,3,5-8,10,14,19,21] (Coding Exons 1, 2, 4-7, 9, 13, 18, 20)	SOX2	
<b>BRAF</b> [Exons 11-18]	DDR1	<b>GNAS</b> [Exons 1,8]	<b>MET</b>	PIK3CB	SOX9	
<b>BRCA1</b> (Introns 2, 7, 8, 12, 16, 19, 20)	<b>DDR2</b> [Exons 5,17,18]	GRM3	MITF	PIK3R1	SPEN	
<b>BRCA2</b> (Intron 2)	DIS3	GSK3B	MKNK1	PIM1	SPOP	
BRD4	DNMT3A	H3F3A	MLH1	PMS2	SRC	
BRIP1	DOTIL	HDAC1	<b>MPL</b> [Exon 10]	POLD1	STAG2	
BTG1	EED	HGF	MRE11A	POLE	STAT3	
BTG2	<b>EGFR</b>	HNF1A	MSH2	PPARG	<b>STK11</b>	
<b>BTK</b> [Exons 2,15]	EP300	<b>HRAS</b> [Exons 2,3]	MSH3	PPP2R1A	SUFU	
C11orf30 (EMSY)	EPHA3	HSD3B1	MSH6	PPP2R2A	SYK	
C17orf39 (GID4)	EPHB1	ID3	MST1R	PRDM1	TBX3	
CALR	EPHB4	<b>IDH1</b> [Exon 4]	MTAP	PRKAR1A	TEK	
CARD11	<b>ERBB2</b>	<b>IDH2</b> [Exon 4]	<b>MTOR</b> [Exons 19,30,39,40, 43-45,47,48,53,56]	PRKCI	TERC* {ncRNA}	
CASP8	ERBB3 [Exons 3,6,7,8,10,12,20, 21,23,24,25]	IGF1R	MUTYH	PTCH1	<b>TERT* {Promoter}</b>	
CBFB	ERBB4	IKBKE	<b>MYC</b>	<b>PTEN</b>	TET2	
CBL	ERCC4	IKZF1	MYCL (MYCL1)	<b>PTPN11</b>	TGFBR2	
<b>CCND1</b>	ERG	INPP4B	<b>MYCN</b>	PTPRO	TIPARP	
CCND2	<b>ERF1</b> [Exons 4-8]	IRF2	<b>MYD88</b> [Exon 4]	QKI	TNFAIP3	
CCND3	<b>EZH2</b> [Exons 4,16,17,18]	IRF4	NBN	RAC1	TNFRSF14	
CCNE1	FAM46C	IRS2	<b>NF1</b>	RAD21	<b>TP53</b>	
CD22	FANCA	JAK1	NFE2L2	RAD51	TSC1	
<b>CD274 (PD-L1)</b>	FANCC	<b>JAK2</b> [Exons 14]	NFKBIA	RAD51B	TSC2	
				RAD51C	TYRO3	
					U2AF1	
					<b>VEGFA</b>	
					VHL	



## Summary of Analytical Sensitivity and Specificity for Professional Services Content

Results from our Limit of Detection (LoD) study are shown below, indicating the median variant allele frequency, tumor fraction or unstable loci at which the test has shown 95% probability of detection.<sup>2</sup> Please refer to our product labeling for a list of the 75 genes baited for enhanced sensitivity and complete product specifications.

ALTERATION TYPE	BAIT SET REGION	MEDIAN LIMIT OF DETECTION (LOD)
Copy Number Amplification	NA	21.7% TF
MSI	NA	0.8% Unstable loci
bTMB (component indels)	NA	1.00% VAF
bTMB (component subs)	NA	1.00% VAF

VAF = variant allele frequency; TF = tumor fraction

\* The accuracy of %VAF / %TF have not been analytically validated

In our Limit of Blank study, which evaluated variant calling in healthy donors, 1,735 unique variants were included in the analysis for a total of 137,065 data points. A total of 18 false positives were observed across 4 unique short variants. The LoB was determined to be the ideal value of zero for short variants, rearrangements and CNAs. The false positive rate was shown to be 0% for rearrangements and CNAs and 0.013% (~1 in 8,000) for short variants (substitutions and indels).<sup>2</sup>



## Information Provided as a Professional Service

As a professional service, FoundationOne Liquid CDx interrogates 324 genes, including 309 genes with complete exonic (coding) coverage and 15 genes with only select non-coding coverage (indicated with an \*); **75 genes (indicated in bold)** are captured with increased sensitivity and have complete exonic (coding) coverage unless otherwise noted. The test also detects tumor fraction and the genomic signatures blood mutational burden (bTMB) and microsaetellite instability high (MSI-H) status.

<b>ABL1</b> [Exons 4-9]	<b>BRAF</b> [Exons 11-18, Introns 7-10]	CDK8	EPHB4	<b>FGFR1</b> [Introns 1, 5, Intron 17]	<b>IDH1</b> [Exon 4]	<b>MAP2K2 (MEK2)</b> [Exons 2-4, 6, 7]
ACVR1B		CDKN1A	<b>ERBB2</b>		<b>IDH2</b> [Exon 4]	MAP2K4
<b>AKT1</b> [Exon 3]	<b>BRCA1</b> [Introns 2, 7, 8, 12, 16, 19, 20]	CDKN1B	<b>ERBB3</b> [Exons 3, 6, 7, 8, 10, 12, 20, 21, 23, 24, 25]	<b>FGFR2</b> [Intron 1, Intron 17]	IGF1R	MAP3K1
AKT2	<b>BRCA2</b> [Intron 2]	CDKN2B	ERBB4	<b>FGFR3</b> [Exons 7, 9 (alternative designation exon 10), 14, 18, Intron 17]	IKBKE	MAP3K13
AKT3	BRD4	CDKN2C	ERCC4	FGFR4	IKZF1	MAPK1
ALK	BRIP1	CEBPA	ERG	FH	INPP4B	MCL1
[Exons 20-29 Introns 18,19]	BTG1	CHEK1	<b>ERRFI1</b>	FLCN	IRF2	<b>MDM2</b>
ALOX12B	BTG2	<b>CHEK2</b>	<b>ESR1</b> [Exons 4-8]	FLT1	IRF4	MDM4
AMER1 (FAM123B)	<b>BTK</b> [Exons 2, 15]	CIC	ETV4* [Intron 8]	FLT3	IRS2	MED12
<b>APC</b>		CREBBP	ETV5* [Introns 6,7]	<b>FOXL2</b>	JAK1	MEF2B
<b>AR</b>	CT1orF30 (EMSY)	<b>CRKL</b>	<b>ETV6*</b> [Introns 5,6]	FUBP1	<b>JAK2</b> [Exon 14]	MEN1
<b>ARAF</b> [Exons 4, 5, 7, 11, 13, 15, 16]	CT1orF39 (GID4)	CSF1R	EWSR1* [Introns 7-13]	GABRA6	<b>JAK3</b> [Exons 5, 11, 12, 13, 15, 16]	MERTK
ARFRP1	CARD11	CSF3R	<b>EZH2</b> [Exons 4, 16, 17, 18]	GATA3	JUN	<b>MET</b>
ARID1A	CASP8	CTCF	EZR* [Introns 9-11]	GATA4	KDM5A	MITF
ASXL1	CBFB	CTNNA1		GATA6	KDM5C	MKNK1
<b>ATM</b>	CBL	<b>CTNNB1</b> [Exon 3]		GATA6	KDM6A	MLH1
<b>ATR</b>	<b>CCND1</b>	CUL3		<b>GNA11</b> [Exons 4, 5]	KDR	<b>MPL</b> [Exon 10]
ATRX	CCND2	CUL4A	FAM46C	GNA13	KEAP1	MRE11A
AURKA	CCND3	CXCR4	FANCA	<b>GNAQ</b> [Exons 4, 5]	KEL	MSH2 [Intron 5]
AURKB	CCNE1	CYP17A1	FANCC	<b>GNAS</b> [Exons 1, 8]	KIT [Exons 8, 9, 11, 12, 13, 17, Intron 16]	MSH3
AXIN1	CD22	DAXX	FANCG	GRM3	KLHL6	MSH6
AXL	CD70	DDR1	FANCL	GSK3B	KMT2A (MLL) [Introns 6, 8-11, Intron 7]	MST1R
BAP1	CD74* [Introns 6-8]	DDR2 [Exons 5, 17, 18]	FAS	H3F3A	KMT2D (MLL2)	MTAP
BARD1	CD79A	DIS3	FBXW7	HDAC1	<b>KRAS</b>	<b>MTOR</b> [Exons 19, 30, 39, 40, 43-45, 47, 48, 53, 56]
BCL2	CD79B	DNMT3A	FGF10	HGF	LTK	MUTYH
BCL2L1	<b>CD274 (PD-L1)</b>	DOT1L	FGF12	HNFA	LYN	MYB* [Intron 14]
BCL2L2	CDC73	EED	FGF14	<b>HRAS</b> [Exons 2, 3]	MAF	<b>MYC</b> [Intron 1]
BCL6	<b>CDH1</b>	<b>EGFR</b> [Introns 7, 15, 24-27]	FGF19	HSD3B1	<b>MAP2K1 (MEK1)</b> [Exons 2, 3]	MYCL (MYCL1)
BCOR	<b>CDK12</b>	EP300	FGF23	ID3		<b>MYCN</b>
BCORL1	<b>CDK4</b>	EPHA3	FGF3			<b>MYD88</b> [Exon 4]
BCR* [Introns 8, 13, 14]	<b>CDK6</b>	EPHB1	FGF4			
			FGF6			

Professional Service Gene List continued



## (Information Provided as a Professional Service Continued)

NBN	P2RY8	PIM1	RAD52	SDHC	SUFU	XPO1
NF1	<b>PALB2</b>	PMS2	RAD54L	SDHD	SYK	XRCC2
NF2	PARK2	POLD1	<b>RAF1</b> [Exons 3, 4, 6, 7, 10, 14, 15, 17, Introns 4-8]	SETD2	TBX3	ZNF217
NFE2L2	PARP1	POLE		SF3B1	TEK	ZNF703
NFKBIA	PARP2	PPARG		SGK1	TERC* {ncRNA}	
NKX2-1	PARP3	PPP2R1A	RARA [Intron 2]	SLC34A2* [Intron 4]	<b>TERT* {Promoter}</b>	
NOTCH1	PAX5	PPP2R2A	<b>RB1</b>	SMAD2	TET2	
NOTCH2 [Intron 26]	PBRM1	PRDM1	RBM10	SMAD4	TGFBR2	
NOTCH3	PDCD1 (PD-1)	PRKARIA	REL	SMARCA4	TIPARP	
<b>NPM1</b> [Exons 4-6, 8, 10]	<b>PDCD1LG2 (PD-L2)</b>	PRKCI	RET [Introns 7, 8, Exons 11, 13-16, Introns 9-11]	SMARCB1	TMPRSS2* [Introns 1-3]	
<b>NRAS</b> [Exons 2, 3]	<b>PDGFRA</b> [Exons 12, 18, Introns 7, 9, 11]	<b>PTEN</b>	RICTOR	<b>SMO</b>	TNFAIP3	
NSD3 (WHSC1L1)	<b>PDGFRB</b> [Exons 12-21, 23]	<b>PTPN11</b>	RNF43	SNCAIP	TNFRSF14	
NT5C2	PK1	PTPRO	<b>ROS1</b> [Exons 31, 36-38, 40, Introns 31-35]	SOCS1	<b>TP53</b>	
<b>NTRK1</b> [Exons 14, 15, Introns 8-11]	PIK3C2B	QKI	RPTOR	SOX2	TSC1	
	PIK3C2G	RAC1		SOX9	TSC2	
NTRK2 [Intron 12]	<b>PIK3CA</b> Exons 2, 3, 5-8, 10, 14, 19, 21 (Coding Exons 1, 2, 4-7, 9, 13, 18, 20)	RAD21	RSPO2* [Intron 1]	SPEN	TYRO3	
<b>NTRK3</b> [Exons 16, 17]		RAD51	SDC4* [Intron 2]	SPOP	U2AF1	
NUTM1* [Intron 1]	PIK3CB	RAD51B	SDHA	SRC	<b>VEGFA</b>	
	PIK3R1	RAD51C	SDHB	STAG2	VHL	
		RAD51D		STAT3	WHSC1	
				<b>STK11</b>	WT1	

\* Visit [foundationmedicine.com](http://foundationmedicine.com) to create an online account. ‡ Current as of August 2020. Please visit [foundationmedicine.com](http://foundationmedicine.com) for the most up-to-date gene list.

### References:

1. FoundationOne Liquid CDx Technical Information. For full label refer to [www.F1LCDxLabel.com](http://www.F1LCDxLabel.com)
2. Data on File, Foundation Medicine, Inc., 2020

FoundationOne® Liquid CDx is for prescription use only and is a qualitative next-generation sequencing based *in vitro* diagnostic test for advanced cancer patients with solid tumors. The test analyzes 324 genes utilizing circulating cell-free DNA and is FDA-approved to report short variants in 311 genes and as a companion diagnostic to identify patients who may benefit from treatment with specific therapies (listed in Table 1 of the Intended Use) in accordance with the approved therapeutic product labeling. Additional genomic findings may be reported and are not prescriptive or conclusive for labeled use of any specific therapeutic product. Use of the test does not guarantee a patient will be matched to a treatment. A negative result does not rule out the presence of an alteration. Patients who are negative for companion diagnostic mutations should be reflexed to tumor tissue testing and mutation status confirmed using an FDA-approved tumor tissue test, if feasible. For the complete label, including companion diagnostic indications and complete risk information, please visit [www.F1LCDxLabel.com](http://www.F1LCDxLabel.com).

