



## Intended Use

FoundationOne® Liquid CDx is a next generation sequencing based in vitro diagnostic device that analyzes 324 genes. Substitutions and insertion and deletion alterations (indels) are reported in 311 genes, copy number alterations (CNAs) are reported in 310 genes, and gene rearrangements are reported in 324 genes. The test also detects tumor fraction and the genomic signatures blood tumor mutational burden (bTMB) and microsatellite instability high (MSI-H) status. FoundationOne® Liquid CDx utilizes circulating cell-free DNA (cfDNA) isolated from plasma derived from the anti-coagulated peripheral whole blood of cancer patients. The test is intended to be used as a companion diagnostic to identify patients who may benefit from treatment with targeted therapies in accordance with the approved therapeutic product labeling. Additionally, FoundationOne® Liquid CDx is intended to provide tumor mutation profiling to be used by qualified health care professionals in accordance with professional guidelines in oncology for patients with malignant neoplasms.

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 genomic findings should be reflexed to routine biopsy and their tumor mutation status confirmed using an FDA-approved tumor tissue test, if feasible.

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



## Summary of Analytical Sensitivity and Specificity<sup>1</sup>

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. 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)
Short Variants	Enhanced Sensitivity	0.40% VAF
	Standard Sensitivity	0.82% VAF
Rearrangements	Enhanced Sensitivity	0.37% VAF
	Standard Sensitivity	0.90% VAF
Copy Number Amplification	NA	21.7% TF
Copy Number Loss	NA	30.4% 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).



## FoundationOne® Liquid CDx Gene List<sup>1</sup>

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 microsatellite instability high (MSI-H) status.

<b>ABL1</b> [Exons 4-9]	ALOX12B	ASXL1	BAP1	BCR* [Introns 8, 13, 14]	BRIP1	CASP8
ACVR1B	AMER1 (FAM123B)	<b>ATM</b>	BARD1	<b>BRAF</b> [Exons 11-18, Introns 7-10]	BTG1	CBFB
<b>AKT1</b> [Exon 3]	<b>APC</b>	<b>ATR</b>	BCL2	<b>BRCA1</b> [Introns 2, 7, 8, 12, 16, 19, 20]	BTG2	CBL
AKT2	<b>AR</b>	ATRAX	BCL2L1	<b>BRCA2</b> [Intron 2]	<b>BTK</b> [Exons 2, 15]	<b>CCND1</b>
AKT3	<b>ARAF</b> [Exons 4, 5, 7, 11, 13, 15, 16]	AURKA	BCL2L2	BRD4	C11orf30 (EMSY)	CCND2
<b>ALK</b> [Exons 20-29 Introns 18,19]	ARFRP1	AURKB	BCL6		C17orf39 (GID4)	CCND3
	ARID1A	AXINI	BCOR		CALR	CCNE1
		AXL	BCORL1		CARD11	CD22

(FoundationOne® Liquid CDx Gene List continued)

CD70	<b>ERBB2</b>	<b>FOXL2</b>	KLHL6	<b>NF1</b>	PPARG	SMAD2
CD74* [Introns 6-8]	<b>ERBB3</b> [Exons 3, 6, 7, 8, 10, 12, 20, 21, 23, 24, 25]	FUBP1	KMT2A (MLL) [Introns 6, 8-11, Intron 7]	NF2	PPP2R1A	SMAD4
CD79A	ERBB4	GABRA6	NFE2L2	NFKBIA	PPP2R2A	SMARCA4
CD79B	ERCC4	GATA3	NFKB1	PRDM1	PRKAR1A	SMARCB1
<b>CD274 (PD-L1)</b>	ERG	GATA4	NKX2-1	PRKAR1A		<b>SMO</b>
CDC73	<b>ERRF1</b>	GATA6	NOTCH1	PRKCI		SNCAIP
<b>CDH1</b>	<b>ESR1</b> [Exons 4-8]	<b>GNA11</b> [Exons 4, 5]	LTK	PTCH1		SOCS1
<b>CDK12</b>		GNA13	LYN	<b>PTEN</b>		SOX2
<b>CDK4</b>	ETV4* [Intron 8]	<b>GNAQ</b> [Exons 4, 5]	MAF	NOTCH3	<b>PTPN11</b>	SOX9
<b>CDK6</b>	ETV5* [Introns 6,7]	<b>GNAS</b> [Exons 1, 8]	<b>MAP2K1 (MEK1)</b> [Exons 2, 3]	<b>NPM1</b> [Exons 4-6, 8, 10]	PTPRO	SPEN
CDK8	<b>ETV6*</b> [Introns 5,6]	GRM3	<b>MAP2K2 (MEK2)</b> [Exons 2-4, 6, 7]	<b>NRAS</b> [Exons 2, 3]	GKI	SPOP
CDKN1A	EWSR1* [Introns 7-13]	GSK3B	MAP2K4	NSD3 (WHSC1L1)	RAC1	SRC
CDKN1B	<b>EZH2</b> [Exons 4, 16, 17, 18]	H3F3A	MAP3K1	NT5C2	RAD21	STAG2
<b>CDKN2A</b>		HDAC1	MAP3K13	<b>NTRK1</b> [Exons 14, 15, Introns 8-11]	RAD51	STAT3
CDKN2B	EZR* [Introns 9-11]	HGF	MAPK1	NTRK2 [Intron 12]	RAD51B	<b>STK11</b>
CDKN2C	FAM46C	HNF1A	MCL1	<b>NTRK3</b> [Exons 16, 17]	RAD51C	SUFU
CEBPA	FANCA	HSD3B1	<b>MDM2</b>	NUTM1* [Intron 1]	RAD51D	SYK
CHEK1	FANCC	ID3	MDM4	P2RY8	RAD52	TBX3
<b>CHEK2</b>	FANCG	<b>IDH1</b> [Exon 4]	MEDI2	<b>PALB2</b>	RAD54L	TEK
CIC	FANCL	<b>IDH2</b> [Exon 4]	MEF2B	PARK2	<b>RAF1</b> [Exons 3, 4, 6, 7, 10, 14, 15, 17, Introns 4-8]	TERC* {ncRNA}
CREBBP	FAS	IGF1R	MEN1	PARP1	RARA [Intron 2]	<b>TERT* {Promoter}</b>
<b>CRKL</b>	FBXW7	IKBKE	MERTK	PARP2	RBM10	TET2
CSF1R	FGF10	IKZF1	<b>MET</b>	PARP3	<b>RB1</b>	TGFBR2
CSF3R	FGF12	INPP4B	MITF	PAX5	RBM10	TIPARP
CTCF	FGF14	IRF2	MKNK1	PBRM1	REL	TMPRSS2* [Introns 1-3]
CTNNA1	FGF19	IRF4	MLH1	PDCD1 (PD-1)	RET [Introns 7, 8, Exons 11, 13-16, Introns 9-11]	TNFAIP3
<b>CTNNB1</b> [Exon 3]	FGF23	IRS2	<b>MPL</b> [Exon 10]	<b>PDCD1LG2 (PD-L2)</b>	<b>TP53</b>	TNFRSF14
CUL3	FGF3	IRS4	MRE11A	<b>PDGFRA</b> [Exons 12, 18, Introns 7, 9, 11]	RICTOR	<b>TP53</b>
CUL4A	FGF4	JAK1	MSH2 [Intron 5]	<b>PDGFRB</b> [Exons 12-21, 23]	RNF43	TSC1
CXCR4	FGF6	<b>JAK2</b> [Exon 14]	MSH3	PDK1	<b>ROS1</b> [Exons 31, 36-38, 40, Introns 31-35]	TSC2
CYP17A1	<b>FGFR1</b> [Introns 1, 5, Intron 17]	<b>JAK3</b> [Exons 5, 11, 12, 13, 15, 16]	MSH6	PIK3C2B	RPTOR	TYRO3
DAXX	<b>FGFR2</b> [Intron 1, Intron 17]	<b>JUN</b>	MST1R	PIK3C2G	RSPO2* [Intron 1]	U2AF1
DDR1	<b>FGFR3</b> [Exons 7, 9 (alternative designation exon 10), 14, 18, Intron 17]	KDM5A	MTAP	<b>PIK3CA</b> Exons 2, 3, 5-8, 10, 14, 19, 21 (Coding Exons 1, 2, 4-7, 9, 13, 18, 20)	SDC4* [Intron 2]	<b>VEGFA</b>
<b>DDR2</b> [Exons 5, 17, 18]	FGFR4	KDM5C	<b>MTOR</b> [Exons 19, 30, 39, 40, 43-45, 47, 48, 53, 56]	PIK3CB	SDHA	VHL
DIS3	FH	KDM6A	MUTYH	PIK3R1	SDHB	WHSC1
DNMT3A	FLCN	KDR	MYB* [Intron 14]	PIM1	SDHC	WT1
DOT1L	FLT1	KEAP1	<b>MYC</b> [Intron 1]	PMS2	SDHD	XPO1
EED	<b>FLT3</b> [Exons 14, 15, 20]	KEL	MYCL (MYCL1)	POLD1	SDH	XRCC2
<b>EGFR</b> [Introns 7, 15, 24-27]		<b>KIT</b> [Exons 8, 9, 11, 12, 13, 17, Intron 16]	<b>MYCN</b>	POLE	SETD2	ZNF217
EP300			<b>MYD88</b> [Exon 4]		SF3B1	ZNF703
EPHA3					SGK1	
EPHB1					SLC34A2* [Intron 4]	
EPHB4			NBN			

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