



## 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.



## 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	PRKCI		<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>	<b>ETV4*</b> [Intron 8]	GNA13	LYN	<b>PTEN</b>		SOX2
<b>CDK4</b>	<b>ETV5*</b> [Introns 6, 7]	<b>GNAQ</b> [Exons 4, 5]	MAF	NOTCH3		SOX9
<b>CDK6</b>	<b>ETV6*</b> [Introns 5, 6]	<b>GNAS</b> [Exons 1, 8]	<b>MAP2K1 (MEK1)</b> [Exons 2, 3]	<b>NPM1</b> [Exons 4-6, 8, 10]		SPEN
CDK8	<b>EWSR1*</b> [Introns 7-13]	<b>GRM3</b>	<b>MAP2K2 (MEK2)</b> [Exons 2-4, 6, 7]	<b>NRAS</b> [Exons 2, 3]		SPOP
CDKN1A	<b>EZR*</b> [Introns 9-11]	GSK3B	MAP2K4	NSD3 (WHSC1L1)		SRC
CDKN1B	<b>FAM46C</b>	H3F3A	MAP3K1	RAD21		STAG2
<b>CDKN2A</b>	<b>EZH2</b> [Exons 4, 16, 17, 18]	HDAC1	MAP3K13	RAD51		STAT3
CDKN2C	<b>FANCA</b>	HGF	MAPK1	RAD51B		<b>STK11</b>
CEBPA	<b>FANCC</b>	HNF1A	MCL1	RAD51C		SUFU
CHEK1	<b>FANCG</b>	<b>HRAS</b> [Exons 2, 3]	<b>MDM2</b>	RAD51D		SYK
<b>CHEK2</b>	<b>FANCL</b>	HSD3B1	MDM4	RAD52		TBX3
CIC	<b>FAS</b>	ID3	MED12	RAD54L		TEK
CREBBP	<b>FANCC</b>	<b>IDH1</b> [Exon 4]	MEF2B	<b>RAF1</b> [Exons 3, 4, 6, 7, 10, 14, 15, 17, Introns 8-11]		TERC* {ncRNA}
<b>CRKL</b>	<b>FANCG</b>	<b>IDH2</b> [Exon 4]	MEN1	<b>TERT*</b> {Promoter}		TET2
CSF1R	<b>FANCL</b>	<b>IGF1R</b>	MERTK	<b>PALB2</b>		TGFBR2
CSF3R	<b>FAS</b>	IGF1R	<b>MET</b>	PARK2		TIPARP
CTCF	<b>FBXW7</b>	IKBKE	MITF	PARP1		RBM10
CTNNA1	<b>FGF10</b>	IKZF1	MKNK1	PARP2		<b>TMPRSS2*</b> [Introns 1-3]
<b>CTNNB1</b> [Exon 3]	<b>FGF12</b>	INPP4B	MLH1	PARP3		REL
CUL3	<b>FGF14</b>	IRF2	<b>MPL</b> [Exon 10]	PAX5		RET
CUL4A	<b>FGF19</b>	IRF4	MRE11A	PBRM1		<b>TP53</b>
CXCR4	<b>FGF23</b>	IRS2	MSH2 [Intron 5]	PDCD1 (PD-1)		RICTOR
CYP17A1	<b>FGF3</b>	IRS2	MSH3	<b>PDCD1LG2 (PD-L2)</b>		RNF43
DAXX	<b>FGF4</b>	JAK1	MSH6	<b>PDGFRA</b> [Exons 12, 18, Introns 7, 9, 11]		<b>ROS1</b> [Exons 31, 36-38, 40, Introns 31-35]
DDR1	<b>FGF6</b>	<b>JAK2</b> [Exon 14]	MST1R	<b>PDGFRB</b> [Exons 12-21, 23]		RPTOR
<b>DDR2</b> [Exons 5, 17, 18]	<b>FGFR1</b> [Introns 1, 5, Intron 17]	<b>JAK3</b> [Exons 5, 11, 12, 13, 15, 16]	MTAP	PDK1		RSPO2* [Intron 1]
DIS3	<b>FGFR2</b> [Intron 1, Intron 17]	JUN	<b>MTOR</b> [Exons 19, 30, 39, 40, 43-45, 47, 48, 53, 56]	PIK3C2B		SDC4* [Intron 2]
DNMT3A	<b>FGFR3</b> [Exons 7, 9 (alternative designation exon 10), 14, 18, Intron 17]	KDM5A	MUTYH	PIK3C2G		SDHA
DOT1L	<b>FGFR4</b>	KDM5C	MYB* [Intron 14]	<b>PIK3CA</b> Exons 2, 3, 5-8, 10, 14, 19, 21 (Coding Exons 1, 2, 4-7, 9, 13, 18, 20)		SDHB
EED	<b>FH</b>	KDM6A	<b>MYC</b> [Intron 1]	PIK3CB		SDHC
<b>EGFR</b> [Introns 7, 15, 24-27]	<b>FLCN</b>	KDR	MYCL (MYCL1)	PIK3R1		SDHD
EP300	<b>FLT1</b>	KEAP1	<b>MYCN</b>	PIM1		SETD2
EPHA3	<b>FLT3</b> [Exons 14, 15, 20]	KEL	<b>MYD88</b> [Exon 4]	PMS2		SF3B1
EPHB1		<b>KIT</b> [Exons 8, 9, 11, 12, 13, 17, Intron 16]	NBN	POLD1		SGK1
EPHB4				POLE		SLC34A2* [Intron 4]

1. Data on file M-GB-00001408



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