FOUNDATION**ONE**®**HEME**

Technical Specifications

FoundationOne Heme is a laboratory developed test (LDT) that combines DNA and RNA sequencing for patients with hematologic malignancies, sarcomas, or solid tumors where RNA sequencing is desired.

Methods

- Uses hybrid capture-based next-generation sequencing.
- Identifies the four main classes of genomic alterations (base substitutions, insertions and deletions, copy number alterations, and rearrangements).
- Sequences RNA of 265 genes commonly rearranged in cancer to better identify known and novel gene fusions.
- Sequences DNA to a median depth of ~500X unique coverage and RNA to an average of ~6.9 million unique pairs.
- All specimens are reviewed by a hematopathologist or pathologist to ensure specimen viability and tumor content.

ACCURACY		
Sensitivity: Base Substitutions	At ≥ Minor Allele Frequency	>99.0%
Sensitivity: Insertions/Deletions (1-40bp)	At ≥ 10 Mutant Allele Frequency	98.0%
Sensitivity: Focal Copy Number Alterations (Homozygous Deletions or Amplifications)	At ≥ 8 copies	>95.0%
Sensitivity: Microsatellite status	At ≥ 20% tumor nuclei	97.0%
Sensitivity: Known Gene Fusions	>95.0%	
Specificity: Base Substitutions, Insertions/Deletions, and Focal Copy Number Alterations	Positive Predictive Value (PPV)	>99.0%
Specificity: Known Gene Fusions	Positive Predictive Value (PPV)	>95.0%
Specificity: Microsatellite status	Positive Predictive Value (PPV)	>95.0%
Accuracy: Tumor Mutation Burden	At ≥ 20% tumor nuclei	>90.0%
Reproducibility (average concordance between replicates)	97.0% Inter-batch precision 97.0% Intra-batch precision 95.0% microsatellite status precision 96.0% tumor mutation burden precision	

Assay specifications were determined for typical median exon coverage of approximately 500X. For more information regarding the validation of FoundationOne Heme, please refer to the article, He, J. et al. Integrated genomic DNA/RNA profiling of hematologic malignancies in the clinical setting. Blood. (2016 June 16).

Reporting

- Test results are provided in an interpretive report, curated by biomedical informatics scientists, and approved by on-site board-certified and licensed pathologists and hematopathologists.
- Genomic findings are listed with clinically relevant targeted therapies, immunotherapies, and clinical trial options.
- Reported alterations may indicate response or lack of response to therapy (FDA-approved or in clinical trials), or may be unambiguous drivers of oncogenesis based on reported scientific literature.
- Reports include tumor mutational burden (TMB) status and microsatellite instability (MSI) status, biomarkers that may help predict response to checkpoint inhibitors.

FoundationOne Heme Gene List →

FoundationOne Heme Gene List

Genes With Complete Exonic (Coding) Coverage[1]

- *ABL1*
- *ACTB*
- *AKT1*
- *AKT2*
- *AKT3*
- *ALK*
- *AMER1* (FAM123B or WTX)
- *APC*
- *APH1A*
- *AR*
- *ARAF*
- *ARFRP1*
- *ARHGAP26* (GRAF)
- *ARID1A*
- *ARID2*
- *ASMTL*
- *ASXL1*
- *ATM*
- *ATR*
- *ATRX*
- *AURKA*
- *AURKB*
- *AXIN1*
- *AXL*
- *B2M*
- *BAP1*
- *BARD1*
- *BCL10*
- *BCL11B*
- *BCL2*
- *BCL2L2*
- *BCL6*
- *BCL7A*
- *BCOR*
- *BCORL1*
- *BIRC3*
- *BLM*
- *BRAF*
- *BRCA1*
- *BRCA2*
- *BRD4*
- *BRIP1* (BACH1)
- *BRSK1*
- *BTG2*
- *BTK*
- *BTLA*
- *C11orf30* (EMSY)
- *CAD*
- *CALR*
- *CARD11*
- *CBFB*
- *CBL*
- *CCND1*
- *CCND2*
- *CCND3*
- *CCNE1*
- *CCT6B*
- *CD22*
- *CD274* (PD-L1)
- *CD36*
- *CD58*
- *CD70*
- *CD79A*
- *CD79B*
- *CDC73*
- *CDH1*
- *CDK12*
- *CDK4*
- *CDK6*
- *CDK8*
- *CDKN1B*
- *CDKN2A*
- *CDKN2B*
- *CDKN2C*
- *CEBPA*
- *CHD2*
- *CHEK1*
- *CHEK2*
- *CIC*
- *CIITA*
- *CKS1B*
- *CPS1*
- *CREBBP*
- *CRKL*
- *CRLF2*
- *CSF1R*
- *CSF3R*
- *CTCF*
- *CTNNA1*
- *CTNNB1*
- *CUX1*
- *CXCR4*
- *DAXX*
- *DDR2*
- *DDX3X*
- *DNM2*
- *DNMT3A*
- *DOT1L*
- *DTX1*
- *DUSP2*
- *DUSP9*
- *EBF1*
- *ECT2L*
- *EED*
- *EGFR*
- *ELP2*
- *EP300*
- *EPHA3*
- *EPHA5*
- *EPHA7*
- *EPHB1*
- *ERBB2*
- *ERBB3*
- *ERBB4*
- *ERG*
- *ESR1*
- *ETS1*
- *ETV6*
- *EXOSC6*
- *EZH2*
- *FAF1*
- *FAM46C*
- *FANCA*
- *FANCC*
- *FANCD2*
- *FANCE*
- *FANCF*
- *FANCG*
- *FANCL*
- *FAS* (TNFRSF6)
- *FBXO11*
- *FBXO31*
- *FBXW7*
- *FGF10*
- *FGF14*
- *FGF19*
- *FGF23*
- *FGF3*
- *FGF4*
- *FGF6*
- *FGFR1*
- *FGFR2*
- *FGFR3*
- *FGFR4*
- *FHIT*
- *FLCN*
- *FLT1*
- *FLT3*
- *FLT4*
- *FLYWCH1*
- *FOXL2*
- *FOXO1*
- *FOXO3*
- *FOXP1*
- *FRS2*
- *GADD45B*
- *GATA1*
- *GATA2*
- *GATA3*
- *GID4* (C17orf39)
- *GNA11*
- *GNA12*
- *GNA13*
- *GNAQ*
- *GNAS*
- *GPR124*
- *GRIN2A*
- *GSK3B*
- *GTSE1*
- *HDAC1*
- *HDAC4*
- *HDAC7*
- *HGF*
- *HIST1H1C*
- *HIST1H1D*
- *HIST1H1E*
- *HIST1H2AC*
- *HIST1H2AG*
- *HIST1H2AL*
- *HIST1H2AM*
- *HIST1H2BC*
- *HIST1H2BJ*
- *HIST1H2BK*
- *HIST1H2BO*
- *HIST1H3B*
- *HNF1A*
- *HRAS*
- *HSP90AA1*
- *ICK*
- *ID3*
- *IDH1*
- *IDH2*
- *IGF1R*
- *IKBKE*
- *IKZF1*
- *IKZF2*
- *IKZF3*
- *IL7R*
- *INHBA*
- *INPP4B*
- *INPP5D* (SHIP)
- *IRF1*
- *IRF4*
- *IRF8*
- *IRS2*
- *JAK1*
- *JAK2*
- *JAK3*
- *JARID2*
- *JUN*
- *KAT6A* (MYST3)
- *KDM2B*
- *KDM4C*
- *KDM5A*
- *KDM5C*
- *KDM6A*
- *KDR*
- *KEAP1*
- *KIT*
- *KLHL6*
- *KMT2A* (MLL)
- *KMT2C* (MLL3)
- *KMT2D* (MLL2)
- *KRAS*
- *LEF1*
- *LRP1B*
- *LRRK2*
- *MAF*
- *MAFB*
- *MAGED1*
- *MALT1*
- *MAP2K1* (MEK1)
- *MAP2K2* (MEK2)
- *MAP2K4*
- *MAP3K1*
- *MAP3K14*
- *MAP3K6*
- *MAP3K7*
- *MAPK1*
- *MCL1*
- *MDM2*
- *MDM4*
- *MED12*
- *MEF2B*
- *MEF2C*
- *MEN1*
- *MET*
- *MIB1*
- *MITF*
- *MKI67*
- *MLH1*
- *MPL*
- *MRE11A*
- *MSH2*
- *MSH3*
- *MSH6*
- *MTOR*
- *MUTYH*
- *MYC*
- *MYCL* (MYCL1)
- *MYCN*
- *MYD88*
- *MYO18A*
- *NCOR2*
- *NCSTN*
- *NF1*
- *NF2*
- *NFE2L2*
- *NFKBIA*
- *NKX2-1*
- *NOD1*
- *NOTCH1*
- *NOTCH2*
- *NPM1*
- *NRAS*
- *NSD1*
- *NT5C2*
- *NTRK1*
- *NTRK2*
- *NTRK3*
- *NUP93*
- *NUP98*
- *P2RY8*
- *PAG1*
- *PAK3*
- *PALB2*
- *PASK*
- *PAX5*
- *PBRM1*
- *PC*
- *PCBP1*
- *PCLO*
- *PDCD1* (PD-1)
- *PDCD11*
- *PDCD1LG2* (PD-L2)
- *PDGFRA*
- *PDGFRB*
- *PDK1*
- *PHF6*
- *PIK3CA*
- *PIK3CG*
- *PIK3R1*
- *PIK3R2*
- *PIM1*
- *PLCG2*
- *POT1*
- *PPP2R1A*
- *PRDM1*
- *PRKAR1A*
- *PRKDC*
- *PRSS8*
- *PTCH1*
- *PTEN*
- *PTPN11*
- *PTPN2*
- *PTPN6* (SHP-1)
- *PTPRO*
- *RAD21*
- *RAD50*
- *RAD51*
- *RAF1*
- *RARA*
- *RASGEF1A*
- *RB1*
- *RELN*
- *RET*
- *RHOA*
- *RICTOR*
- *RNF43*
- *ROS1*
- *RPTOR*
- *RUNX1*
- *S1PR2*
- *SDHA*
- *SDHB*
- *SDHC*
- *SDHD*
- *SERP2*
- *SETBP1*
- *SETD2*
- *SF3B1*
- *SGK1*
- *SMAD2*
- *SMAD4*
- *SMARCA1*
- *SMARCA4*
- *SMARCB1*
- *SMC1A*
- *SMC3*
- *SMO*
- *SOCS1*
- *SOCS2*
- *SOCS3*
- *SOX10*
- *SOX2*
- *SPEN*
- *SPOP*
- *SRC*
- *SRSF2*
- *STAG2*
- *STAT3*
- *STAT4*
- *STAT5A*
- *STAT5B*
- *STAT6*
- *STK11*
- *SUFU*
- *SUZ12*
- *TAF1*
- *TBL1XR1*
- *TCF3* (E2A)
- *TCL1A* (TCL1)
- *TET2*
- *TGFBR2*
- *TLL2*
- *TMEM30A*
- *TMSB4XP8* (TMSL3)
- *TNFAIP3*
- *TNFRSF11A*
- *TNFRSF14*
- *TNFRSF17*
- *TOP1*
- *TP53*
- *TP63*
- *TRAF2*
- *TRAF3*
- *TRAF5*
- *TSC1*
- *TSC2*
- *TSHR*
- *TUSC3*
- *TYK2*
- *U2AF1*
- *U2AF2*
- *VHL*
- *WDR90*
- *WHSC1* (MMSET or NSD2)
- *WISP3*
- *WT1*
- *XBP1*
- *XPO1*
- *YY1AP1*
- *ZMYM3*
- *ZNF217*
- *ZNF24* (ZSCAN3)
- *ZNF703*
- *ZRSR2*

Genes With Select Intronic (Non-Coding) Coverage[2]

- *ALK*
- *BCL2*
- *BCL6*
- *BCR*
- *BRAF*
- *CCND1*
- *CRLF2*
- *EGFR*
- *EPOR*
- *ETV1*
- *ETV4*
- *ETV5*
- *ETV6*
- *EWSR1*
- *FGFR2*
- *IGH*
- *IGK*
- *IGL*
- *JAK1*
- *JAK2*
- *KMT2A* (MLL)
- *MYC*
- *NTRK1*
- *PDGFRA*
- *PDGFRB*
- *RAF1*
- *RARA*
- *RET*
- *ROS1*
- *TMPRSS2*
- *TRG*

Genes with RNA sequencing coverage

Please note, some VUS* rearrangements between targeted genes and unknown fusion partners may not be reported.

ABI1
ABL1
ABL2
ACSL6
AFF1
AFF4
ALK
ARHGAP26 (GRAF)
ARHGEF12
ARID1A
ARNT
ASXL1
ATF1
ATG5
ATIC
BCL10
BCL11A
BCL11B
BCL2
BCL3
BCL6
BCL7A
BCL9
BCOR
BCR
BIRC3
BRAF
BTG1
CAMTA1
CARS
CBFA2T3
CBFB
CBL
CCND1
CCND2
CCND3
CD274 (PD-L1)
CDK6
CDX2
CHIC2
CHN1
CIC
CIITA
CLP1
CLTC
CLTCL1
CNTRL (CEP110)
COL1A1
CREB3L1
CREB3L2
CREBBP
CRLF2
CSF1
CTNNB1
DDIT3
DDX10
DDX6
DEK
DUSP22
EGFR
EIF4A2
ELF4
ELL
ELN
EML4
EP300
EPOR
EPS15
ERBB2
ERG
ETS1
ETV1
ETV4
ETV5
ETV6
EWSR1
FCGR2B
FCRL4
FEV
FGFR1
FGFR1OP
FGFR2
FGFR3
FLI1
FNBP1
FOXO1
FOXO3
FOXO4
FOXP1
FSTL3
FUS
GAS7
GLI1
GMPS
GPHN
HERPUD1
HEY1
HIP1
HIST1H4I
HLF
HMGA1
HMGA2
HOXA11
HOXA13
HOXA3
HOXA9
HOXC11
HOXC13
HOXD11
HOXD13
HSP90AA1
HSP90AB1
IGH
IGK
IGL
IKZF1
IL21R
IL3
IRF4
ITK
JAK1
JAK2
JAK3
JAZF1
KAT6A (MYST3)
KDSR
KIF5B
KMT2A (MLL)
LASP1
LCP1
LMO1
LMO2
LPP
LYL1
MAF
MAFB
MALT1
MDS2
MECOM
MKL1
MLF1
MLLT1 (ENL)
MLLT10 (AF10)
MLLT3
MLLT4 (AF6)
MLLT6
MN1
MNX1
MSI2
MSN
MUC1
MYB
MYC
MYH11
MYH9
NACA
NBEAP1 (BCL8)
NCOA2
NDRG1
NF1
NF2
NFKB2
NIN
NOTCH1
NPM1
NR4A3
NSD1
NTRK1
NTRK2
NTRK3
NUMA1
NUP214
NUP98
NUTM2A
OMD
P2RY8
PAFAH1B2
PAX3
PAX5
PAX7
PBX1
PCM1
PCSK7
PDCD1LG2 (PD-L2)
PDE4DIP
PDGFB
PDGFRA
PDGFRB
PER1
PHF1
PICALM
PIM1
PLAG1
PML
POU2AF1
PPP1CB
PRDM1
PRDM16
PRRX1
PSIP1
PTCH1
PTK7
RABEP1
RAF1
RALGDS
RAP1GDS1
RARA
RBM15
RET
RHOH
RNF213
ROS1
RPL22
RPN1
RUNX1
RUNX1T1 (ETO)
RUNX2
SEC31A
SEPT5
SEPT6
SEPT9
SET
SH3GL1
SLC1A2
SNX29 (RUNDC2A)
SRSF3
SS18
SSX1
SSX2
SSX4
STAT6
STL
SYK
TAF15
TAL1
TAL2
TBL1XR1
TCF3 (E2A)
TCL1A (TCL1)
TEC
TET1
TFE3
TFG
TFPT
TFRC
TLX1
TLX3
TMPRSS2
TNFRSF11A
TOP1
TP63
TPM3
TPM4
TRIM24
TRIP11
TTL
TYK2
USP6
WHSC1 (MMSET or NSD2)
WHSC1L1
YPEL5
ZBTB16
ZMYM2
ZNF384
ZNF521

*VUS: Variants of Unknown Significance

FoundationOne Heme is a laboratory developed test that was developed and its performance characteristics determined by Foundation Medicine. FoundationOne Heme has not been cleared or approved by the U.S. Food and Drug Administration. For more information on FoundationOne Heme, please see its Technical Specifications at foundationmedicine.com/heme.

References:

1. Current as of July 2021. Please visit foundationmedicine.com/heme for the most up to date gene list.
2. Select Introns only. Detailed list available upon request.

FOUNDATION MEDICINE®

www.foundationmedicine.com | Tel 888.988.3639 | Fax 617.418.2290 | US-FH-2100006 V1.0 | RAL-0080
Roche Products (NZ) Ltd. 98 Carlton Gore Road, Newmarket, Auckland 1023. PO Box 109113, Newmarket, Auckland 1149. Tel: 0800 880 177 |
APAC.foundation@roche.com | www.foundationmedicine.co.nz | M-NZ-00000265v3/OCT2022