Technical Specifications

FOUNDATIONONE®HEME

FoundationOne®Heme is a comprehensive† genomic profiling assay for haematologic malignancies and sarcomas.

Methods[1]

FoundationOne Heme:

- Uses hybrid-capture next-generation sequencing.
- Identifies the four classes of genomic alterations (base substitutions, insertions and deletions, copy number alterations, rearrangements, and reports microsatellite instability and tumour mutational burden).
- Sequences DNA of the entire coding region of 406 genes and selected introns of 31 genes involved in rearrangements.
- Sequences RNA of 265 genes commonly rearranged in cancer to better identify known and novel gene fusions.
- Sequences to a median depth of ~500X unique coverage for DNA and RNA to an average of ~6.9 million unique pairs.
- All specimen are reviewed by a haematopathologist or pathologist to ensure specimen viability and tumour content.

PERFORMANCE SPECIFICATIONS		
Sensitivity	Base Substitutions at ≥5% Minor Allele Frequency	> 99%
	Insertions/Deletions (1–40 base pairs) at ≥10% Minor Allele Frequency	98%
	Focal Copy Number Alterations (homozygous deletions or amplifications ≥8 copies)	> 95%
	Known Gene Fusions	> 95%
Specificity (PPV)	Positive Predictive Value (PPV) for Base Substitutions, Insertions/Deletions and Focal Copy Number Alterations	> 99%
	Positive Predictive Value (PPV) for Known Gene Fusions	> 95%
Reproducibility	Concordance between replicates inter-batch	97%
	Concordance between replicates intra-batch	97%
Immunotherapy Biomarkers	TMB[a] and MSI[b]	
Specimen Type	Peripheral whole blood, bone marrow aspirate, FFPE block or slides, or extracted nucleic acid (see Specimen Instructions for more details)	
Turnaround Time	3 Weeks[c]	

[a] Chalmers ZR, et. al. "Analysis of 100,000 human cancer genomes reveals the landscape of tumor mutational burden". Genome Med. 2017;9(1):34.
[b] Hall MJ, et al. Multigene Panels to Evaluate Hereditary Cancer Risk: Reckless or Relevant? J Clin Oncol. 2016 Dec;34(34):418–4187."
[c] Based on typical turnaround time from receipt of sample

Reporting

- Test results are provided in an interpretive report, curated by biomedical informatics scientists, and approved by board-certified and licensed pathologists and haematopathologists.
- Genomic findings are listed with clinically relevant targeted therapies, immunotherapies, and clinical trials (if applicable).
- Reported alterations may indicate response or lack of response to validated targets for therapy (approved or in clinical trials), or may be drivers of oncogenesis based on reported scientific knowledge.
- Reports include tumor mutational burden (TMB) status and microsatellite instability (MSI) status.

Current Gene List‡

Entire coding sequence (base substitutions, indels, copy number alterations)

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

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

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*			

† Comprehensive Genomic Profiling with FoundationOne Heme involves:
- Next generation sequencing of the DNA of 406 cancer-related genes known to be clinically relevant to solid tumours
- Uniform coverage across the entire coding sequence of each gene plus select introns from 31 genes frequently rearranged in cancer
- Next generation sequencing of the RNA of 265 cancer-related genes known to be clinically relevant to solid tumours
- Use of hybrid-capture technology to identify base substitutions, insertions/deletions, copy number alterations and rearrangements

‡ Current as of November 2019. Please visit www.foundationmedicine.com for the most up-to-date gene list.

Reference

1. He, J. et al. (2016) Integrated genomic DNA/RNA profiling of hematologic malignancies in the clinical setting. Blood. 127(24):3004–14.

If you require this information in an accessible format, please contact Roche at 1-800-561-1759.

FoundationOne®Heme is a next-generation sequencing service performed by Foundation Medicine, Inc. at laboratories in the USA. Hoffmann-La Roche Limited markets the service in Canada under an exclusive license from Foundation Medicine, Inc. The service was developed and its performance characteristics determined by Foundation Medicine. As an in-house laboratory-developed test, the service has not been submitted to Health Canada for evaluation and is not subject to Health Canada approval. Reports generated from the service are prepared by Foundation Medicine, without Hoffmann-La Roche Limited's involvement, and may include scientific information about experimental medicinal products or uses that are not approved or available in Canada.

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