

Clinical Background

Cancers have long been categorized and treated based on the anatomic site of origin of the cancer, e.g., lung, breast, colon, skin, etc. Increasingly, oncologists and pathologists are also focusing on the genomic alterations, in the genes that drive a cancer.

As we understand more about these underlying DNA alterations, cancer may be treated with targeted therapies that specifically attack those changes in a patient's tumor and that may be less toxic and more effective than traditional cytotoxic treatments.

Methods

FoundationOne is a comprehensive genomic profile that applies next-generation sequencing in a unique manner to identify all 4 types of genomic alterations across all genes known to be unambiguous drivers of solid tumors with high accuracy. The test simultaneously sequences the coding region of 315 cancer-related genes plus introns from 28 genes often rearranged or altered in cancer to a typical median depth of coverage of greater than 500X. Each covered read represents a unique DNA fragment to enable the highly sensitive and specific detection of genomic alterations that occur at low frequencies due to tumor heterogeneity, low tumor purity and small tissue samples. FoundationOne detects all classes of genomic alterations, including base substitutions, insertions and deletions (indels), copy number alterations (CNAs) and rearrangements using a small, routine FFPE sample (including core or fine needle biopsies).

Reporting

Test results are provided in an interpretive report, both in hard copy and via the FoundationOne Interactive Cancer Explorer $^{\text{TM}}$.

If a relevant alteration is found in any one of the genes on the current gene list, the report will identify the gene and alteration and will provide an interpretation that is specific to the patient's tumor.

The genes listed on the front page of the report are found to have one or more clinically relevant alterations. All other genes are not found to have any clinically relevant alterations. In some cases, pertinent negatives are displayed on the front of the report; these are genes that have no alterations but are particularly relevant for the specific tumor type (e.g., KRAS in colon cancer, EGFR in lung cancer). The complete list of genes that are tested appears in the "Current Gene List" table to the right, in the appendix of each FoundationOne report and at www.foundationone.com/genelist.

Variants of Unknown Significance (VUS)

Often an alteration is detected in one of the genes included on FoundationOne, but that specific alteration has not yet been adequately characterized in the scientific literature. We include these variants in the report so that they may be acted upon in the future should clinical evidence emerge.

Equivoca

Designation signifies when there is some, but not unambiguous, evidence of amplification or homozygous loss of a gene.

Subclonal

Designation signifies that the FoundationOne analytical methodology has identified the presence of the alteration in less than 10% of the estimated tumor DNA.

FoundationOne Includes Genes That Are Commonly Tested for in All Solid Tumors

FoundationOne is a comprehensive and fully informative genomic profile that can reveal all classes of actionable alterations, including those in cancer-driving genes that are rarely or never tested for in solid tumors. The FoundationOne report often reveals alterations that may lead to additional treatment options for physicians and their patients to consider.

* The analytic validation of FoundationOne, based on a prior version of the assay [236 genes, 19 select rearrangements] was published in Nature Biotechnology' and established the performance specifications required to deliver the high level of accuracy routinely obtained for all classes of genomic alteration by FoundationOne. This updated version of FoundationOne met these performance specifications by demonstrating high concordance with genomic profiles of ninety four clinical specimens previously profiled on the validated version of FoundationOne.

Technical Information	Base Substitutions ¹	Indels ¹	Copy Number Alterations ¹	Rearrangements					
Sensitivity	>99% MAF ≥5%	>97% MAF≥10%	>95% CN≥8or0 ≥30% tumor nuclei	≥90%² >99% for ALK fusion³ ≥20% tumor nuclei					
Specificity (PPV)	>99%	>99%	>99%	>99%					
Typical Median depth of coverage (each covered read is of a unique DNA fragment to enable detection of alterations at low frequency)	500 ¹								
Sample requirements	≥ 40 µm tissue, of which a minimum of 20% is of malignant origin, on 8 to 10 unstained slides or in an FFPE block. Needle biopsy is also acceptable.								
Turn-around time	14 day average*								

^{*}As measured from the date the Foundation Medicine laboratory receives a sample that meets requirements.

Current Gene List⁴

FoundationOne identifies all classes of alterations in each of the genes listed below.

As a pan-cancer test, FoundationOne is designed to interrogate the entire coding sequence of 315 cancer-related genes plus introns from 28 genes often rearranged or altered in cancer. These genes are known to be somatically altered in solid cancers based on recent scientific and clinical literature.

ARID1A CCND2 DAXX FGF23 GSK3B KMT2A (MLL) NF1 POLD1 SETD2 TOP1 ARID1B CCND3 DDR2 FGF3 H3F3A (MLL3) NF2 POLE SF3B1 TOP2A ARID2 CCNE1 DICER1 FGF4 HGF (MLL3) NF2L2 PPP2R1A SLIT2 TP53 ASXL1 CD274 DNMT3A FGF6 HNF1A KRAS NFKBIA PRDM1 SMAD2 TSC1 ATM CD79A DOT1L FGFR1 HRAS LMO1 NKX2-1 PREX2 SMAD3 TSC2 ATR CD79B EGFR FGFR2 HSD3B1 LRP1B NOTCH1 PRKAR1A SMAD4 TSHR ATRX CDC73 EP300 FGFR3 HSP90AA1 LVN NOTCH2 PRKCI SMARCA4 U2AF1 AURKA CDH1 EPHA3 FGFR4 IDH1 LZTR1 NOTCH3 PRKCC SMARCB1 VEGFA AURKB CDK12 EPHA5 FH IDH2 MAGI2 NPM1 PRSS8 SMO VHL AXIN1 CDK4 EPHA7 FLCN IGF1R MAP2K1 NRAS PTCH1 SNCAIP WISP3 AXL CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK8 ERBB2 FLT3 IKBKE MAP2K4 NTRK1 PTPN11 SOX10 XPO1 BARD1 CDKN1A ERBB3 FLT4 IKZF1 MAP3K1 NTRK2 QKI SOX2 ZBTB2 BCL2L CDKN2B ERRF1 FRS2 INPP4B MDM4 PAK3 RAD50 SPEN ZNF703 BCL2L2 CDKN2B ERRF1 FRS2 INPP4B MDM4 PAK3 RAD51 SPOP BCL2L2 CDKN2B ERRF1 FRS2 INPP4B MDM4 PAK3 RAD51 SPOP BCCR CEBPA EZH2 GABRAB IRF4 MEF2B PARK2 RANBP2 SRC BCORL CEBPA EZH2 GABRAB IRF4 MEF2B PARK2 RANBP2 SRC BCM CHD4 FANCA GATA2 JAK1 MET PBRM1 RB1 STAT3 SELECT REARRANGEMENTS	CURRENT GENE LIST											
ACVR1B BRCA2 CIC FANCE GATAB JUN MPL POGFBB RICTOR SUFU AKT1 BRD4 CREBBP FANCF (GID4 (GID4 (GID4 (GID4) KATAB (MYST3) (MYST3	ABL1	BRAF	CHEK1	FANCC	GATA3	JAK2	MITF	PDCD1LG2	RBM10	STAT4		
AKT1 BRD4 CREBP FANCF GID4 (C170739) KAT6A (MYST3) MRE11A PDK1 RNF43 SYK AKT2 BRIP1 CRKL FANCG GLI1 KDM5A MSH2 PIK3C2B ROS1 TAF1 AKT3 BTG1 CRLP2 FANCL GNA11 KDM5C MSH6 PIK3CA RPTOR TBX3 ALK BTK CSF1R FAS GNA13 KDM6A MTOR PIK3CB RUNX1 TERC CMER1 (FAM123B) (EMSY) CTCF FAT1 GNAQ KDM MTOR PIK3CB RUNX1 TERC AMER1 C100130 (FAM123B) (EMSY) CTCF FAT1 GNAQ KDM MUTYH PIK3CG RUNX1T1 TERT AR CBFB CTNNB1 FGF10 GPR124 KEL (MYCL) PIK3R1 SDHA TET2 AR CBFB CTNNB1 FGF10 GPR124 KEL (MYCL) PIK3R2 SDHB TGFBR2 ARAF CBL CUL3 FGF14 GRIN2A KIT MYCN PLCG2 SDHC TNFAIP3 ARFRP1 CCND1 CYLD FGF19 GRM3 KLHL6 MYD88 PMS2 SDHD TNFRSF14 ARID1A CCND2 DAXX FGF23 GSK3B KMT2A MLL) NF1 POLD1 SETD2 TOP1 ARID1B CCND3 DDR2 FGF3 H3F3A (MXT2C (MLL)) NF2 POLE SF3B1 TOP2A ARID2 CCNE1 DICER1 FGF4 HGF (KLL) NF2L2 PPP2R1A SLIT2 TP53 ASXL1 CD274 DNNT3A FGF6 HNF1A KRAS NFKBIA PRDM1 SMAD2 TSC1 ATM CD79A DOT1L FGFR1 HRAS LMO1 NKX2-1 PREX2 SMAD3 TSC2 ATR CD79B EGFR FGFR2 HSD3B1 LRP1B NOTCH1 PRKARIA SMAD4 TSHR ATRX CDC73 EP300 FGFR3 HSP3DAA1 LYN NOTCH2 PRKCI SMARCA4 UJ2AF1 AURKA CDH1 PPHA3 FGFR4 IDH1 LZTR1 NOTCH3 PRKCI SMARCA4 UJ2AF1 AURKA CDH1 PPHA3 FGFR4 IDH1 LZTR1 NOTCH3 PRKCI SMARCA4 UJ2AF1 AXIN1 CDK4 EPHA7 FLCN IGF1R MAP2K1 NRAS PTCH1 SNCAIP WISP3 AXL CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 AXL CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK8 ERBS2 FLT3 IKBKE MAP2K4 NTRK1 PTFN11 SOCX10 WP1 BAP1 CDK8 ERBS3 FLT4 IKZF1 MAP3K1 NTRK2 OK1 SOX30 ZNF217 BGC12 CDKN1B ERBB4 FOXL2 IL/R MCL1 NTRK3 RAC1 SOX30 ZNF217 BGC12 CDKN1B ERBB4 FOXL2 II/R MCL1 NTRK3 RAC1 SOX30 ZNF217 BGC12 CDKN2A ERR FIFT FRS2 INPP4B MDM4 PAX3 RAD51 SPOP BGC12 CDKN2A ERR GATA11 IRS2 MED12 PARS2 RAF1 STAT3 SELECT REARRANGEMENTS ALK BRAF BB04 ETV4 FGFR1 KIT MYC NTRK2 RARA TMPSS2 BCL2 BRCA1 EGFR ETV5 FGFR2 MSH2 NOTCH2 PDGFRA RET	ABL2	BRCA1	CHEK2	FANCD2	GATA4	JAK3	MLH1	PDGFRA	RET	STK11		
AKT1 BR04 CREBBP FANCF (C17orl39) (MYST3) MRE11A PDM1 RNF43 SYK AKT2 BRIP1 CRIKL FANCG GLI1 KDM6A MSH2 PIK3C2B ROS1 TAF1 AKT3 BTG1 CRLF2 FANCL GNA11 KDM6C MSH6 PIK3CA RPTOR TBX3 ALK BTK CSF1R FAS GNA13 KDM6A MTOR PIK3CB RUNX1 TERC AMERI C110rl30 (EMSY) APC CARD11 CTNNA1 FBXW7 GNAS KEAP1 MYC PIK3R1 SDHA TET2 AR CBFB CTNNB1 FGF10 GPR124 KEL MYCL (MYCL) PIK3R1 SDHA TET2 ARAFF CBL CUL3 FGF14 GRIN2A KIT MCVN PLCG2 SDHC TNFAIP3 ARFRP1 CCND1 CYLD FGF19 GRM3 KLHL6 MYD88 PMS2 SDHD TNFAIF3 ARID1A CCND2 DAXX FGF23 GSK3B KMT2A (MLL) NF1 POLD1 SETD2 TOP1 ARID1B CCND3 DDR2 FGF3 H3F3A (MLL) NF1 POLD1 SETD2 TOP1 ARID1C CCNC1 DICER1 FGF4 HGF (MUL) NFE2L PPP2R1A SLIT2 TPS3 ASXL1 CD274 DNMT3A FGF6 HNF1A KRAS NFKBIA PRDM1 SMAD2 TSC1 ATM CD79A DOT1L FGFR1 HRAS LMO1 NKX2-1 PREXZ SMAD3 TSC2 ATR CD79B EGFR FGFR2 HSD3B1 LRP1B NOTCH1 PRKAR1A SMAD4 TSHR AURKA CDH1 EPHA3 FGFR4 IDH1 LZTR1 NOTCH2 PRKCI SMARCA1 UZAF1 AURKA CDH1 EPHA3 FGFR4 IDH1 LZTR1 NOTCH3 PREXZ SMAD3 TSC2 BARD CDK12 EPHA5 FH IDH2 MAGIZ NPM1 PRSSS SMO VHL AXIN1 CDK4 EPHA5 FH IDH2 MAGIZ NPM1 PRSSS SMO VHL AXIN1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT4 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK6 EPHB1 FLT4 IGF2 MAP2K1 NTRK2 PARA STAG2 BCC2 CDKN1B ERBB4 FOXE2 IL7R MCL1 NTRK5 RABA STAG2 BCC2 CDKN1B ERBB4 FOXE2 FAFF1 IFF2 MED12 PARE2 RABF1 SP	ACVR1B	BRCA2	CIC	FANCE	GATA6	JUN	MPL	PDGFRB	RICTOR	SUFU		
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FAMILYBB (EMSY) CTCF	ALK	втк	CSF1R	FAS	GNA13	KDM6A	MTOR	PIK3CB	RUNX1	TERC		
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AURKB CDK12 EPHAS	ATRX	CDC73	EP300	FGFR3	HSP90AA1	LYN	NOTCH2	PRKCI	SMARCA4	U2AF1		
AXIN1 CDK4 EPHA7 FLCN IGF1R MAP2K1 NRAS PTCH1 SNCAIP WISP3 AXL CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK8 ERBB2 FLT3 IKBKE MAP2K4 NTRK1 PTPN11 SOX10 XPO1 BARD1 CDKN1A ERBB3 FLT4 IKZF1 MAP3K1 NTRK2 QKI SOX2 ZBTB2 BCL2 CDKN1B ERBB4 FOXL2 ILTR MCL1 NTRK3 RAC1 SOX9 ZNF217 BCL2L1 CDKN2A ERG FOXP1 INHBA MDM2 NUP93 RAD50 SPEN ZNF703 BCL2L2 CDKN2B ERRFI1 FRS2 INPP4B MDM4 PAK3 RAD51 SPON BCL6L CDKN2C ESR1 FUBP1 IRF2 MED12 PALB2 RAF1 SPTA1 BCOR CEBPA EZH2 GABRA6 IRF4 MEF2B PARK2 RANBP2 SRC BCORL1 CHD2 FAM46C GATA1 IRS2 MEN1 PAX5 RARA STAG2 BLM CHD4 FANCA GATA2 JAK1 MET PBRM1 RB1 STAT3 SELECT REARRANGEMENTS ALK BRAF BRD4 ETV4 FGFR1 KIT MYC NTRK2 RARA TMPRSS2 BCL2 BRCA1 EGFR ETV5 FGFR2 MSH2 NOTCH2 PDGFRA RET	AURKA	CDH1	EPHA3	FGFR4	IDH1	LZTR1	NОТСН3	PRKDC	SMARCB1	VEGFA		
AXL CDK6 EPHB1 FLT1 IGF2 MAP2K2 NSD1 PTEN SOCS1 WT1 BAP1 CDK8 ERBB2 FLT3 IKBKE MAP2K4 NTRK1 PTPN11 SOX10 XPO1 BARD1 CDKN1A ERBB3 FLT4 IKZF1 MAP3K1 NTRK2 QKI SOX2 ZBTB2 BCL2 CDKN1B ERBB4 FOXL2 IL7R MCL1 NTRK3 RAC1 SOX9 ZNE717 BCL2L1 CDKN2A ERG FOXP1 INHBA MDM2 NUP93 RAD50 SPEN ZNF703 BCL2L2 CDKN2A ERRFI1 FRS2 INPP4B MDM4 PAK3 RAD50 SPEN ZNF703 BCL6 CDKN2C ESR1 FUBP1 IRF2 MED12 PALB2 RAF1 SPT01 BCOR CEBPA EZH2 GABRA6 IRF4 MEF2B PARK2 RANBP2 SRC BCM CHD4 FANGA GATA1 IRS2	AURKB	CDK12	EPHA5	FH	IDH2	MAG12	NPM1	PRSS8	SMO	VHL		
BAP1 CDK8 ERBB2 FLT3 IKBKE MAP2K4 NTRK1 PTPN11 SOX10 XPO1 BARD1 CDKN1A ERBB3 FLT4 IKZF1 MAP3K1 NTRK2 QKI SOX2 ZBTB2 BCL2 CDKN1B ERBB4 FOXL2 IL7R MCL1 NTRK3 RAC1 SOX9 ZNF217 BCL2L1 CDKN2A ERG FOXP1 INHBA MDM2 NUP93 RAD50 SPEN ZNF703 BCL6L2 CDKN2B ERRFI1 FRS2 INP4B MDM4 PAK3 RAD51 SPEN ZNF703 BCOR CEBPA EZH2 GABRAB IRF2 MED12 PALB2 RAF1 SPEN BCORL1 CHD2 FAM46C GATA1 IRS2 MEN1 PAX5 RARA STAG2 BLM CHD4 FANCA GATA2 JAK1 MET PBRM1 RB1 STAT3 SELECT REARRANGEMENTS ALK BRAF BRD4	AXIN1	CDK4	EPHA7	FLCN	IGF1R	MAP2K1	NRAS	PTCH1	SNCAIP	WISP3		
BARD1 CDKN1A EBBB3 FLT4 IKZF1 MAP3K1 NTRK2 QKI SOX2 ZBBB2 BCL2 CDKN1B ERBB4 FOXL2 IL7R MCL1 NTRK3 RAC1 SOX9 ZNF217 BCL2L1 CDKN2A ERG FOXP1 INHBA MDM2 NUP93 RAD50 SPEN ZNF703 BCL2L2 CDKN2B ERRFI1 FRS2 INPP4B MDM4 PAK3 RAD51 SPOP BCL6 CDKN2C ESR1 FUBP1 IRF2 MED12 PALB2 RAF1 SPTA1 BCOR CEBPA EZH2 GABRA6 IRF4 MEF2B PARK2 RANBP2 SRC BCORL1 CHD2 FAM46C GATA1 IRS2 MEN1 PAX5 RARA STAG2 BLM CHD4 FANCA GATA2 JAK1 MET PBRM1 RB1 STAT3 SELECT REARRANGEMENTS ALK BRAF BRD4 ETV4 FGFR1	AXL	CDK6	EPHB1	FLT1	IGF2	MAP2K2	NSD1	PTEN	SOCS1	WT1		
BCL2 CDKN1B ERBB4 FOXL2 IL7R MCL1 NTRK3 RAC1 SOX9 ZNF217 BCL2L1 CDKN2A ERG FOXP1 INHBA MDM2 NUP93 RAD50 SPEN ZNF703 BCL2L2 CDKN2B ERRFI1 FRS2 INPP4B MDM4 PAK3 RAD51 SPOP BCL6 CDKN2C ESR1 FUBP1 IRF2 MED12 PALB2 RAF1 SPTA1 BCOR CEBPA EZH2 GABRA6 IRF4 MEF2B PARK2 RANBP2 SRC BCORL1 CHD2 FAM46C GATA1 IRS2 MEN1 PAX5 RARA STAG2 BL CHD4 FANCA GATA2 JAK1 MET PBRM1 RB1 STAT3 SELECT REARRANGEMENTS ALK BRAF BRD4 ETV4 FGFR1 KIT MYC NTRK2 RARA TMPRSS2 BCL2 BRCA1 EGFR ETV5 FGFR2	BAP1	CDK8	ERBB2	FLT3	IKBKE	MAP2K4	NTRK1	PTPN11	SOX10	XPO1		
BCL2L1 CDKN2A ERG FOXP1 INHBA MDM2 NUP93 RAD50 SPEN ZNF703 BCL2L2 CDKN2B ERRFI1 FRS2 INPP4B MDM4 PAK3 RAD51 SPOP BCL6 CDKN2C ESR1 FUBP1 IRF2 MED12 PALB2 RAF1 SPTA1 BCOR CEBPA EZH2 GABRA6 IRF4 MEF2B PARK2 RANBP2 SRC BCORL1 CHD2 FAM46C GATA1 IRS2 MEN1 PAX5 RARA STAG2 BLM CHD4 FANCA GATA2 JAK1 MET PBRM1 RB1 STAT3 SELECT REARRANGEMENTS ALK BRAF BRD4 ETV4 FGFR1 KIT MYC NTRK2 RARA TMPRSS2 BCL2 BRCA1 EGFR ETV5 FGFR2 MSH2 NOTCH2 PDGFRA RET	BARD1	CDKN1A	ERBB3	FLT4	IKZF1	MAP3K1	NTRK2	QKI	SOX2	ZBTB2		
BCL2L2 CDKN2B ERRFI1 FRS2 INPP4B MDM4 PAK3 RAD51 SPOP BCL6 CDKN2C ESR1 FUBP1 IRF2 MED12 PALB2 RAF1 SPTA1 BCOR CEBPA EZH2 GABRA6 IRF4 MEF2B PARK2 RANBP2 SRC BCORL1 CHD2 FAM46C GATA1 IRS2 MEN1 PAX5 RARA STAG2 BLM CHD4 FANCA GATA2 JAK1 MET PBRM1 RB1 STAT3 SELECT REARRANGEMENTS ALK BRAF BRD4 ETV4 FGFR1 KIT MYC NTRK2 RARA TMPRSS2 BCL2 BRCA1 EGFR ETV5 FGFR2 MSH2 NOTCH2 PDGFRA RET	BCL2	CDKN1B	ERBB4	FOXL2	IL7R	MCL1	NTRK3	RAC1	SOX9	ZNF217		
BCL6 CDKN2C ESR1 FUBP1 IRF2 MED12 PALB2 RAF1 SPTA1 BCOR CEBPA EZH2 GABRA6 IRF4 MEF2B PARK2 RANBP2 SRC BCORL1 CHD2 FAM46C GATA1 IRS2 MEN1 PAX5 RARA STAG2 BLM CHD4 FANCA GATA2 JAK1 MET PBRM1 RB1 STAT3 SELECT REARRANGEMENTS ALK BRAF BRD4 ETV4 FGFR1 KIT MYC NTRK2 RARA TMPRSS2 BCL2 BRCA1 EGFR ETV5 FGFR2 MSH2 NOTCH2 PDGFRA RET	BCL2L1	CDKN2A	ERG	FOXP1	INHBA	MDM2	NUP93	RAD50	SPEN	ZNF703		
BCOR CEBPA EZH2 GABRA6 IRF4 MEF2B PARK2 RANBP2 SRC BCORL1 CHD2 FAM46C GATA1 IRS2 MEN1 PAX5 RARA STAG2 BLM CHD4 FANCA GATA2 JAK1 MET PBRM1 RB1 STAT3 SELECT REARRANGEMENTS ALK BRAF BRD4 ETV4 FGFR1 KIT MYC NTRK2 RARA TMPRSS2 BCL2 BRCA1 EGFR ETV5 FGFR2 MSH2 NOTCH2 PDGFRA RET	BCL2L2	CDKN2B	ERRFI1	FRS2	INPP4B	MDM4	PAK3	RAD51	SPOP			
BCORL1 CHD2 FAM46C GATA1 IRS2 MEN1 PAX5 RARA STAG2 BLM CHD4 FANCA GATA2 JAK1 MET PBRM1 RB1 STAT3 SELECT REARRANGEMENTS ALK BRAF BRD4 ETV4 FGFR1 KIT MYC NTRK2 RARA TMPRSS2 BCL2 BRCA1 EGFR ETV5 FGFR2 MSH2 NOTCH2 PDGFRA RET	BCL6	CDKN2C	ESR1	FUBP1	IRF2	MED12	PALB2	RAF1	SPTA1			
BLM CHD4 FANCA GATA2 JAK1 MET PBRM1 RB1 STAT3 SELECT REARRANGEMENTS ALK BRAF BRD4 ETV4 FGFR1 KIT MYC NTRK2 RARA TMPRSS2 BCL2 BRCA1 EGFR ETV5 FGFR2 MSH2 NOTCH2 PDGFRA RET	BCOR	CEBPA	EZH2	GABRA6	IRF4	MEF2B	PARK2	RANBP2	SRC			
SELECT REARRANGEMENTS ALK BRAF BRD4 ETV4 FGFR1 KIT MYC NTRK2 RARA TMPRSS2 BCL2 BRCA1 EGFR ETV5 FGFR2 MSH2 NOTCH2 PDGFRA RET	BCORL1	CHD2	FAM46C	GATA1	IRS2	MEN1	PAX5	RARA	STAG2			
ALK BRAF BRD4 ETV4 FGFR1 KIT MYC NTRK2 RARA TMPRSS2 BCL2 BRCA1 EGFR ETV5 FGFR2 MSH2 NOTCH2 PDGFRA RET	BLM	CHD4	FANCA	GATA2	JAK1	MET	PBRM1	RB1	STAT3			
BCL2 BRCA1 EGFR ETV5 FGFR2 MSH2 NOTCH2 PDGFRA RET	SELECT REARRANGEMENTS											
	ALK	BRAF	BRD4	ETV4	FGFR1	КІТ	MYC	NTRK2	RARA	TMPRSS2		
BCR BRCA2 ETV1 ETV6 FGFR3 MYB NTRK1 RAF1 ROS1	BCL2	BRCA1	EGFR	ETV5	FGFR2	MSH2	NOTCH2	PDGFRA	RET			
	BCR	BRCA2	ETV1	ETV6	FGFR3	MYB	NTRK1	RAF1	ROS1			

¹ G. Frampton, et al., "Development and validation of a clinical cancer genomic profiling test based on massively parallel DNA sequencing". Nat Biotechnol. 2013 Oct 20.



² Based on analysis of coverage and re-arrangement structure in the COSMIC database for solid tumor fusion genes where alteration prevalence could be established, complemented by detection of exemplar rearrangements in cell line titration experiments.

³ Based on ALK re-arrangement concordance analysis vs. a standard clinical FISH assay.

Current as of August 4th, 2014. Please visit www.foundationmedicine.com/genelist for the most current gene list.

⁵ Please contact client.services@foundationmedicine.com to set up an Interactive Cancer Explorer account