Comprehensive Solid Tumor Panel

TEST NAME: COMPREHENSIVE SOLID TUMOR PANEL

TEST CODE: STP198

CPT CODE: 81455

CLINICAL USE:
Alterations in oncogenes and tumor suppressor genes can cause dysregulation of signaling pathways and cellular processes controlling proliferation, migration, metabolism, and apoptosis. Identification of these genetic alterations in the tumors is essential in the diagnosis, prognosis, and treatment of cancers.

The genes and regions covered in our panel are listed below.

ABL1	CBLB	CLSTN1	FUBP1	MAP2K2	PIK3CA	SHH	ZRSR2
ABL2	CCND1	CREBBP	GATA1	MCL1	PIK3CB	SMAD4	
AKT1	CCND2	CRLF2	GATA2	MEF2B	PIK3CG	SMARCB1	
AKT2	CCND3	CSF1R	GATA3	MET	PIK3R1	SMC1A	
AKT3	CCNE1	CSF3R	GNA11	MPL	PIK3R2	SMC3	
ALK	CD79B	CTNNB1	GNA13	MTOR	PIK3R5	SMO	
APC	CDH1	CUX1	GNAQ	MYBL2	PLCG2	SOCS1	
AR	CDK12	DDR2	GNAS	MYD88	PRDM1	SOD2	
ARAF	CDK4	DNAJB1	HNF1A	NF1	PRKACA	SRC	
ARID1A	CDK6	DNMT3A	HNRNPK	NF2	PRMT5	SRSF2	
ARNTL	CDKN1A	EGFR	HRAS	NFE2L2	PTCH1	STAG2	
ASXL1	CDKN1B	EP300	ID3	NOTCH1	PTEN	STAT3	
ATM	CDKN2A	EPHA2	IDH1	NOTCH2	PTPN11	STK11	
ATR	CDKN2B	ERBB2	IDH2	NOTCH3	PTPRD	SUFU	
ATRX	CDKN2C	ERBB4	IKZF1	NPM1	PTPRT	SUZ12	
AURKA	CEBPA	ESR1	IL7R	NRAS	RAC1	TCF3	

BAP1	chr10:43606914-43607546	ETV1	JAK1	NSD1	RAD21	TERT	
BARD1	chr10:43607673-43608300	ETV6	JAK2	NT5C2	RAF1	TET1	
BCL2	chr10:43608412-43609003	EWSR1	JAK3	NTRK1	RB1	TET2	
BCL6	chr10:43609124-43609927	EZH2	KDM6A	NTRK2	RELB	TMC6	
BCOR	chr10:43610185-43612031	FAM5C	KDR	NTRK3	RET	TNFAIP3	
BCORL1	chr2:29446395-29448326	FBXW7	KEAP1	PAWR	RHEB	TNFRSF14	
BIRC3	chr4:55140793-55141007	FGFR1	KIF17	PAX5	RHOA	TP53	
BRAF	chr6:117641194-117642421	FGFR2	KIT	PBRM1	RIT1	TSC1	
BRCA1	chr6:117642558-117645494	FGFR3	KLHL6	PDGFRA	ROS1	TSC2	
BRCA2	chr6:117645579-117647386	FLT3	KMT2A	PDGFRB	RPS6KB1	U2AF1	
BTK	chr6:117647578-117650491	FLT4	KMT2C	PHF6	RUNX1	VHL	
CALR	chr6:117650610-117658334	FOXL2	KMT2D	PIAS2	SETBP1	WHSC1	
CARD11	chr8:38275892-38277050	FOXO1	KRAS	PIK3C2A	SF3B1	WNT1	
CBL	CIC	FOXP1	MAP2K1	PIK3C2B	SH2B3	WT1	

METHODOLOGY: DNA is extracted and hybridized with custom-designed probes to enrich the targeted regions of 198 genes and 13 regions associated with cancer. Samples are then sequenced on the Illumina HiSeq 2500 (Illumina, Inc, CA). A custom bioinformatics pipeline aligns the data to human reference genome GRCh37 to call variants. The limit of detection (related in part to depth of coverage, neoplastic cell percentage, and allelic frequency for the mutation) was determined to be 5% allele frequency, at which our assay has sensitivity of 98% and 94%, respectively, to detect single nucleotide variants (SNVs) and insertions/deletions (indels). Mutant allele

populations below this detection limit will not be reliably detected by this method. Pseudogenes, highly homologous regions, and repeat regions may interfere with the detection of variants in this assay. This assay targets genes involved in cancer. Some of the genes targeted may also cause inherited genetic disorders; variants in these genes will not be reported unless they are determined to contribute to the diagnosis, prognosis, or treatment of cancer in the specimen analyzed.

COMPONENTS:

REFERENCE RANGE: NA

SPECIMEN REQUIREMENTS:

- Tissue sections and cell block preparations of FNAs and fluids
- 10-15 unstained FFPE slides, at 5-10 micron thickness (with 1 H&E slide indicating the location of the tumor).

SPECIAL HANDLING: NA

TEST PERFORMANCE SCHEDULE: Weekly

TURN AROUND TIME: 2-3 Weeks

STAT AVAILABILITY: NA