

NGS targeted cancer gene analysis with unsurpassed sensitivity and specificity

CancerPRO™ Tissue targets specific cancer genes to identify tumor-specific sequence mutations, micro-satellite instability (MSI), amplifications and genomic rearrangements using proprietary, one-of-a-kind, bioinformatics software. As part of our PROGENEUS™ platform for molecular pathology research labs, CancerPRO Tissue analyzes the regions of a targeted panel of either 88 (CancerPRO T88) or 203 (CancerPRO T203) well-characterized cancer genes from tumors (frozen or FFPE) using proprietary methods that can accommodate low tumor purity samples.



CancerPRO Tissue Highlights

- Option to collect and use either tumor only or tumor/normal samples
- Targeted capture design approach to sequencing
- Identification of tumor-specific sequence alterations (single base and indels)
- Reports sequence mutations with a Mutant Allele Frequency (MAF) down to 2% for sequence mutations and indels
- Micro-satellite instability (MSI) analysis when matched normal is used
- Proprietary bioinformatics algorithms capable of identifying sequence mutations, MSI, amplifications, and genomic rearrangements
- Turnaround time in as little as one week

Specifications

Sample Requirements	≥50 micron thickness tissue sample; ≥20% or more of which is tumor; (unstained slides or in FFPE block)
Limit of Detection	2% MAF for sequence mutations and indels
Use of Normal Sample	Maximizes both sensitivity and specificity; option to run without matched normal is available
Target Depth of Coverage (recommended)	>1,500x
DNA Amount	50 ng (minimum)
Turnaround Time	1 week

Comparison of CancerPRO Tissue to Other Options*

Panel Characteristics	CancerPRO Tissue -203 OR -88	TruSeq® Amplicon	Ion Ampliseq™	Foundation One™
Genes Analyzed for Mutations	195 or 76	48	50	315
Point Mutation Analysis	Entire gene coding sequence	Hotspot only	Hotspot only	Entire gene coding sequence
Genes Analyzed for Copy Number Variation	69 or 14	None	None	315
Genes Analyzed for Rearrangements	24 or 14	None	None	28
Microsatellite Instability Analysis	Yes	No	No	No
Assay Sensitivity	>99%	Not reported	98%	>99%
Assay Limit of Detection	2% MAF	Not reported	5%	5%
Assay Specificity (PPV); 5% MAF	>99%	Not reported	Not reported	>99%
Assay Specificity (PPV); 2-4% MAF	>90%	Not reported	Not reported	Not available
Average Distinct Coverage	500x	Not reported	Not reported	500x
Use Matched Normal DNA as Option to Maximize Accuracy†	Yes	No	No	No
Equipment Required	HiSeq® 2500 or MiSeq®	HiSeq® 2500 or MiSeq®	Ion PGM™ System	Service only

*Other company product specifications taken from product specification sheets as of 7/24/15; all products are for research use only.

†Jones et. al., Sci Transl Med 7, 283ra53 (2015)

Genes Evaluated in CancerPRO T88

Sequence analyses for 76 well-characterized cancer genes

ABL1	BRIPI	ERBB4	FANCL	GNAQ	KDR	MTOR	PDGFRA	RET	TP53
AKT1	CDH1	EZH2	FBXW7	GNAS	KIT	NF1	PDGFRB	ROS1	TSC1
ALK	CDKN2A	FANCA	FGFR1	HNF1A	KRAS	NF2	PIK3CA	SMAD4	TSC2
APC	CSF1R	FANCC	FGFR2	HRAS	MET	NOTCH1	PMS2	SMARCB1	VHL
ATM	CTNNB1	FANCD2	FGFR3	IDH1	MLH1	NPM1	PTCH1	SMO	
BRAF	DDR2	FANCE	FLT3	IDH2	MPL	NRAS	PTEN	SRC	
BRCA1	EGFR	FANCF	FOXL2	JAK2	MSH2	NTRK1	PTPN11	STK11	
BRCA2	ERBB2	FANCG	GNA11	JAK3	MSH6	PALB2	RB1	TERT	

Copy number analyses for 13 well-characterized cancer genes

ALK	ERBB2	FGFR1	FGFR3	MET	MYCN	RET			
EGFR	ERBB3	FGFR2	KIT	MYC	PDGFRA				

Rearrangement analyses for 14 well-characterized cancer genes

ALK	BCR	ETV1	ETV6	MLL	PDGFRB	ROS1			
BCL2	EGFR	ETV4	EWSR1	PDGFRA	RARA	TPRSS2			

Microsatellite instability analyses for 5 markers

BAT-25	BAT-26	MONO-27	NR-21	NR-24					
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Genes Evaluated in CancerPRO T203

Rearrangement analyses for selected regions of 24 well-characterized cancer genes

ALK	BCR	DNAJB1	ETV1	ETV5	EWSR1	MLL	NTRK1	PDGFRB	RAF1	RET	TACC3
BCL2	BRAF	EGFR	ETV4	ETV6	FGFR3	MYC	PDGFRA	PRKACA	RARA	ROS1	TPRSS2

Sequence and copy number analyses (*) for the coding regions of 195 well-characterized cancer genes

ABL1*	BLM	CDKN2A	ERBB2*	FANCC	FOXL2*	JAK2*	MSH6	NRAS*	PTCH1	SMAD2	TSHR*
ACVR1	BMPRIA	CDKN2B	ERBB3*	FANCD2	GATA1	JAK3*	MTOR	NTRK1	PTEN	SMAD3	VHL
AKT1*	BRAF*	CDKN2C	ERBB4*	FANCE	GATA2*	KDR*	MUTYH	PALB2	PTPN11*	SMAD4	WAS
AKT2*	BRCA1	CEBPA	ERCC1	FANCF	GNA11*	KIT*	MYC*	PAX5*	RAD51C	SMARCB1	WRN
ALK*	BRCA2	CHEK2	ERCC2	FANCG	GNAQ*	KRAS*	MYCL1*	PBRM1	RAF1	SMO*	WT1
APC	BRIPI	CIC	ERCC3	FANCI	GNAS*	MAML1*	MYCN*	PDGFRA*	RB1	SRC	XPA
AR*	BTK	CREBBP	ERCC4	FANCL	GPC3	MAP2K1*	MYD88*	PHOX2B	RECQL4	STAG2	XPC
ARID1A	BUB1B	CSF1R*	ERCC5	FANCM	H3F3A*	MAP2K4	NBN	PIK3CA*	RET*	STK11	XRCC1
ARID1B	CALR	CTNNB1*	ESR1	FBXW7	H3F3B	MDM2*	NCOA3*	PIK3R1	RNF43	SUFU	
ASXL1	CBL*	CYLD	ETV1	FGFR1	HNF1A	MDM4*	NF1	PMS1	ROS1	TERT	
ATM	CCND1*	DAXX	ETV5	FGFR2*	HRAS*	MED12*	NF2	PMS2	RUNX1*	TET2	
ATRX	CCNE1*	DDB2	EWSR1	FGFR3*	IDH1*	MEN1	NKX2-1*	POLD1	SBDS	TGFBR2	
AURKA	CDC73	DDR2	EXT1	FGFR4*	IDH2*	MET*	NOTCH1*	POLE	SDHAF2	TNFAIP3	
AXIN2	CDH1	DICER1	EXT2	FH	IGF1R*	MLH1	NOTCH2*	POLH	SDHB	TOP1	
BAP1	CDK4*	DNMT3A*	EZH2*	FLCN	IGF2R*	MLL*	NOTCH3*	POT1	SDHC	TP53	
BCL2*	CDK6*	EGFR*	FANCA	FLT3*	IKZF1	MPL*	NOTCH4*	PRKAR1A	SDHD	TSC1	
BCR	CDKN1B	EP300	FANCB	FLT4	JAK1*	MSH2	NPM1	PRSS1	SF3B1*	TSC2	

Microsatellite instability analyses for 5 markers

BAT-25	BAT-26	MONO-27	NR-21	NR-24					
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