



OncoTrack Ultima

NGS based genomic profiling of solid tumors from blood (SNVs & InDels)

High precision multibiomarker

CAP accredited & extensively validated assay

Depth of Sequencing ≥20,000X (pre UMI)



Salient Features

- Tumor agnostic assay covering 117 Pan cancer genes as recommended by guidelines (FDA, NCCN, ASCO, ESMO etc.)
- Comprehensive coverage of complete coding regions of all the genes and intron/exon boundaries for SNVs & InDels detection
- Highly sensitive and can accurately detect low frequency mutations upto 0.2% Variant Allele
 Frequency (VAF) at high confidence
- Analysis and reporting as per AMP/ASCO/CAP guidelines
- Detects Primary driver mutation and Secondary resistance markers
- Enables Minimal Residual Disease (MRD) detection

Peripheral Blood in Streck Tube (10ml X 2)

Can be Complementary, Alternative, Reflex and Serial to Tissue Biopsy NGS Test

Use in Clinical Practice Indicated for Average depth of sequencing Advanced solid tumors ≥20,000X (pre UMI) Before first-line therapy or at progression ≥2000X (post UMI) Sample type Overall concordance with tissue testing

98% (PMID: 29379323)

Limit of Detection (LOD)

Alteration Type	Analytical Sensitivity#	Limit of Detection (LOD)	Analytical Specificity##		
		30ng		#Analytical Sensitivity defined as the Detection Rate for variants present at	
SNVs*	≥95%	>0.2 AF%	100%	or above the limit of detection (LoD).	
INDELS*	≥95%	>0.2 AF%	100%	##Analytical Specificity defined as 1 minus the	
* Tested on cfDNA reference stand	per-sample false positive rate				

Assay Specifications

Well - validated	100% Scored in	i	High throughput Illumina's	1	Global standards for
as per CAP	CAP proficiency		sophisticated NGS		the best laboratory
guidelines	evaluation program		sequencing platforms		practices followed

Test Details

Sample Type

Peripheral Blood in Streck Tube (10ml X 2) Test code: MGM455

Shipping Condition

Ship same or next day at room temperature. Do not freeze or refrigerate

TAT

14 Working days from sample receipt at the laboratory to result

Gene List (SNVs & InDels - 117 Genes)									
ABL1	BAP1	CDX2	EZH2	GNAQ	KIT	MYC	PDGFRA	RAD54L	SMO
ABL2	BARD1	CHEK1	FANCL	GNAS	KRAS	MYCN	PIK3CA	RAF1	SPOP
AKT1	BRAF	CHEK2	FBXW7	HNF1A	MAP2K1	MYD88	PMS2	RB1	SRC
ALK	BRCA1	CSF1R	FGFR1	HRAS	MAP2K2	NF1	POLD1	RET	STK11
APC	BRCA2	CTNNB1	FGFR2	IDH1	MAPK1	NF2	POLE	RHEB	TERT
AR	BRIP1	DDR2	FGFR3	IDH2	MET	NOTCH1	PPP2R2A	RHOA	TP53
ARAF	C11orf65	EGFR	FGFR4	JAK1	MLH1	NPM1	PTCH1	RIT1	TSC1
ARID1A	CCND1	ERBB2	FLT3	JAK2	MPL	NRAS	PTEN	ROS1	TSC2
ARID1B	CDH1	ERBB3	FOXA1	JAK3	MSH2	NTRK1	PTPN11	SETD2	VHL
ATM	CDK12	ERBB4	FOXL2	KDM5C	MSH6	NTRK3	RAD51B	SF3B1	
ATR	CDK4	ERCC2	GATA3	KDM6A	MTOR	PALB2	RAD51C	SMAD4	
ATRX	CDKN2A	ESR1	GNA11	KEAP1	MUTYH	PBRM1	RAD51D	SMARCB1	
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All HRR genes are covered including BRCA1 and BRCA2

Case Studies

Biopsy material is degraded/damaged/insufficient and difficulty in obtaining biopsy material Test performed - OncoTrack Ultima



60-year-old Female | Adenocarcinoma lung | Tissue Biopsy was not feasible.

Gene	CDS variant	Amino acid change/	Overall Depth/Mutant Allele	FDA Approved drugs
	details	Exon No.	Percentage	against variant
ERBB2	c.2313_2324dup(ENS T00000269571.10)	p.Tyr772_Ala775d up/Exon20	3248X/1.4%	Trasuzumab Deruxtecan

The OncoTrack Ultima test successfully identified actionable mutation for which FDA drug is available. This helped the patient in getting the right treatment.

Determine actionable mutations

Test performed - Oncotrack Ultima



36-year-old Female | Stage IV Triple-Negative Breast Cancer

No molecular study was done earlier | Clinically relevant mutations was detected in BRCA1 and TP53 gene

Gene	CDS variant details	Amino acid change/ Exon No.	Overall Depth/Mutant Allele Percentage	Impact on Protein Function	Function of the gene in cancer	Pathway in which the gene functions
BRCA1	c.5251C>T (ENST000003576 54.9)	p.Arg1751Ter / Exon 19	4182X / 46.8%	Loss of Function	Tumor Suppressor	HRR Pathway
TP53	c.861_870del (ENST000002693 05.9)	p.Asn288ArgfsTer 54 / Exon 8	4808X / 6.1%	Loss of Function	Tumor Suppressor	P53 Pathway

BRCA1 mutation is loss of functional mutation detected at 46.8% VAF and germline confirmation is under process. If it is confirmed to be germline variation PARP inhibitors are indicated for targeted treatment.