

Personalis®

ACE CancerPlus Test

Increasingly, oncologists and pathologists are utilizing information on genomic alterations in solid tumors, such as lung, colon, breast, skin, and prostate cancers, to help guide and optimize therapeutic options for patients. The Personalis ACE CancerPlus Test provides clinicians a comprehensive and accurate next generation sequencing based testing solution for solid tumors.

Clinical Reports for Today, Data for the Future

Personalis ACE CancerPlus Test is a comprehensive genomic testing solution that provides physicians a clinical report on the genetic alterations found in cancer genes of medical importance. We use our leading ACE cancer platform to provide high accuracy, clinical grade next generation sequencing and analysis to identify base substitutions, insertions/deletions, copy number alterations and gene fusions.

Test results are provided to clinicians in hard copy and PDF format. The ACE CancerPlus Test report describes clinically important genomic alterations and potentially relevant therapies and clinical trials.

For patients who are consented under research protocol, Personalis can, at the same time, provide genomic alterations and expression data for over 1400 cancer genes and over 200 miRNA genes (listed on second page).

What Makes Our Test Unique

The Personalis ACE CancerPlus Test goes beyond typical cancer genomics tests in a few key areas:

- Proprietary methods for improving sequencing coverage in traditionally difficult to sequence regions typically missed or excluded from other cancer panel tests.
- Analysis of DNA and RNA from the same sample to enable robust identification of gene fusions over a broad number of genes.
- The over 1400 genes and 200 miRNA genes assayed by our test enables focused clinical reporting on 181 genes, while providing broad DNA and RNA data for research protocols vital for targeted therapy, immuno-oncology, and neoantigen research.

ACE CancerPlus Performance Specifications

Requisition Required	Yes	
Specimen Types	FFPE, Fresh Frozen, ≥20% tumor content	
Regions Analyzed	Coding regions of 181 genes	
Type of Sequencing	DNA and RNA using Illumina NGS	
Typical Median Depth	>500x	
Turnaround Time	~3 weeks	
Specifications		
Sensitivity	Base Substitutions	(AF* ≥ 5%) >99%
	Indels	(AF ≥ 10%) >99%
	Copy Number Alterations	96% for tumor content ≥30%
	Gene Fusions	>95%
Specificity (PPV**)	Base Substitutions	(AF ≥ 5%) 99%
	Indels	(AF ≥ 10%) >99%

*AF = Allele Fraction

**PPV = Positive Predictive Value



Cancer Genes of Clinical Importance Analyzed for Base Substitutions, Indels, and Gene Fusions

ABL1	CEBPA	HIF1A	MYC	RET
AKT1	CHEK1	HRAS	MYCN	RHEB
AKT2	CREBBP	IDH1	MYD88	RHOA
AKT3	CRLF2	IDH2	MYH11	RIT1
ALK	CRTC1	IGF1R	NF1	ROS1
APC	CSF1R	IL6R	NF2	RPN1
AR	CTNNB1	JAK1	NFE2L2	RUNX1
ARAF	DDR2	JAK2	NFKBIA	RUNX1T1
ARID1A	DEK	JAK3	NKX2-1	SF3B1
ASXL1	DNMT3A	KDR	NOTCH1	SMAD2
ATM	EGFR	KIF5B	NOTCH2	SMAD4
ATR	EPHB4	KIT	NPM1	SMARCA4
AURKA	ERBB2	KMT2A	NRAS	SMO
AURKB	ERBB3	KRAS	NTRK1	SRC
AURKC	ERBB4	LYN	NTRK2	SRSF2
BAP1	ERG	MAP2K1	NTRK3	STAG2
BCL2	ERRF1	MAP2K2	NUP214	STK11
BCOR	ESR1	MAP2K4	PDCD1	SYK
BCR	ETV1	MAP3K1	PDGFRA	TERT
BRAF	ETV4	MAPK1	PDGFRB	TET2
BRC A1	ETV5	MAPK3	PGR	TGFB R1
BRC A2	ETV6	MCL1	PIK3CA	TMPRSS2
BTK	EWSR1	MDM2	PIK3CB	TNFSF13B
CBFB	EZH2	MDM4	PIK3CD	TP53
CCND1	FBXW7	MECOM	PIK3CG	TSC1
CCND2	FGFR1	MED12	PIK3R1	TSC2
CCND3	FGFR2	MEN1	PML	U2AF1
CCNE1	FGFR3	MET	PRKCB	VEGFA
CDH1	FGFR4	MITF	PTCH1	VEGFB
CDK1	FLCN	MKL1	PTEN	VHL
CDK2	FLT1	MLH1	PTPN11	WT1
CDK4	FLT3	MLL T10	RAB35	XPO1
CDK6	FLT4	MLL T3	RAD21	ZRSR2
CDKN1A	FOXO1	MPL	RAF1	
CDKN1B	GNA11	MSH2	RARA	
CDKN2A	GNAQ	MSH6	RB1	
CDKN2B	GNAS	MTOR	RBM15	

41 Cancer Genes Analyzed for Copy Number Alterations

ABL1	CDK4	FGFR3	MET	PDGFRA
AKT2	CDKN2A	FGFR4	MITF	PIK3CA
AKT3	CDKN2B	JAK2	MLL T3	PTEN
ALK	EGFR	KIT	MSH2	RAD21
AURKA	ERBB2	KRAS	MYC	RB1
BCR	ERBB3	MAPK1	NKX2-1	RET
CCNE1	FGFR1	MCL1	NTRK1	ROS1
CDK1	FGFR2	MDM2	NUP214	SMAD4
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