

Therapy Selection

TISSUE-FREE LIQUID BIOPSY FOR LATE-STAGE SOLID TUMORS

ABOUT THE ASSAY

Northstar Select® is an ultra-sensitive comprehensive genomic profiling (CGP) assay for therapy selection, intended for use in late-stage, solid tumor cancers. Maximize treatment opportunities with a non-invasive circulating tumor DNA (ctDNA) blood test that evaluates 102 guideline-recommended genes for SNVs/indels, fusions, and copy number alterations (CNAs), including amplifications and losses, and assesses MSI-H status.

PERFORMANCE CHARACTERISTICS^a

Alteration Type	Gene Coverage	LOD 95% ^b	Specificity	Reportable Range
SNVs / Indels	99 genes	0.15% VAF	>99.9999%	≥0.01%
CN: Amplifications	20 genes	2.11 copies ^c	>99.9999%	≥2.10 copies
CN: Losses	7 genes	1.80 copies	>99.9%	≤1.90 copies
Fusions	10 genes	0.30% TF	>99.9%	≥0.02%
Biomarker	MSI-H status ^d	0.07% TF	>99.9%	NA

a. Internal data on file, Aug 2026

b. LOD95: the lowest concentration of an analyte in a sample that can be consistently detected with ≥95% probability

c. 25% tumor fraction at 6 copies of amplification

d. Microsatellite instability-high, impacted by biological variability

SPECIMEN REQUIREMENTS & PROCESSING

Sample Collection



3* x 10 mL tubes

Stroke of DNA BCT blood tubes filled to the top (≥8 mL)

* minimum 2 tubes

Mobile phlebotomy available by request

Storage & Shipping



Room temperature

Do not freeze or refrigerate

Ordering



Provider portal

Online convenience:
portal.northstaronc.com

Turnaround Time



5-8 days or less

From sample receipt to results

Northstar Select is covered by Medicare.

Qualified beneficiaries have \$0 out-of-pocket costs.¹



BillionToOne is committed to making their tests accessible to all and have created the **Northstar Financial Assistance Program** to support and advocate for each patient depending on their individual needs.

SNVs / Indels 99 genes						CNAs: Amplifications 20 genes			Fusions 10 genes	
AKT1	CD274 (PD-L1)	FBXW7	KEAP1	NPM1	RB1	AR	EGFR	MET	ALK	
AKT2	CDH1	FGFR1	KIT	NRAS	RET	BRAF	ERBB2 (HER2)	MYC	BRAF	
ALK	CDK12	FGFR2	KRAS	NTRK1	RHOA	CCND1	ESR1	PDGFRA	FGFR2	
APC	CDK4	FGFR3	MAP2K1 (MEK1)	PALB2	RIT1	CCNE1	FGFR1	PIK3CA	FGFR3	
AR	CDK6	FGFR4	MAP2K2 (MEK2)	PDGFRA	ROS1	CD274 (PD-L1)	FGFR2	RAF1	NRG1	
ARAF	CDKN2A	GATA3	MET	PIK3CA	SF3B1	CDK4	KIT	RET	NTRK1	
ARID1A	CDKN2B	GNA11	MLH1	PIK3R1	SMAD4	CDK6	KRAS		NTRK2	
ATM	CHEK1	GNAQ	MPL	PMS2	SMO				NTRK3	
ATR	CHEK2	GNAS	MRE11	POLD1	STK11				RET	
BARD1	CTNNB1	H3-3A	MSH2	POLE	TERT				ROS1	
BRAF	DDR2	H3C2	MSH6	PTEN	TP53	CNAs: Losses 7 genes				
BRCA1	EGFR	H3C3	MTAP	PTPN11	TSC1	ATM	MTAP			
BRCA2	ERBB2 (HER2)	HRAS	MTOR	RAD51B	TSC2	BRCA1	PTEN			
BRIP1	ESR1	IDH1	MYC	RAD51C	VHL	BRCA2	RB1			
CCND1	EZH2	IDH2	NBN	RAD51D		CDKN2A				
CCND2	FANCA	JAK2	NF1	RAD54L						
CCNE1	FANCL	JAK3	NOTCH1	RAF1						
									Biomarker	
									MSI-H status	

BIOMARKERS by Most Common Solid Tumor Types as Recommended by Guidelines

Breast			Colorectal		Lung			All Solid Tumors		
AKT1	ESR1	PALB2	BRAF	NRAS	ALK	FGFR2	MET	BRAF	NTRK1	RET
BRCA1	FGFR1	PIK3CA	ERBB2 (HER2)	MSI-H	BRAF	FGFR3	NRG1	ERBB2 (HER2)	NTRK2	MSI-H
BRCA2	FGFR2	PTEN	KRAS		EGFR	FGFR4	RET		NTRK3	
ERBB2 (HER2)	FGFR3				ERBB2	KRAS	ROS1			
					FGFR1					

CNA Amplifications: Focal vs Aneuploidy

Northstar Select is the only CGP that differentiates between “driver” focal amplifications from broad aneuploidies that exhibit “passenger” copy number differences.

Normal

gene of interest 2 copies

Chromosome Arm Aneuploidy

3 copies

copy number = 2.1
tumor fraction = 10%

Focal Amplification

10 copies

copy number = 2.1
tumor fraction = 1.3%

VS

With ~90% of solid tumors found to harbor chromosome instability that can lead to aneuploidy², differentiation from focal amplification is critical as aneuploidies currently lack specific targeted therapies and are often associated with resistance.

1. Northstar Select has obtained Medicare for eligible beneficiaries with advanced solid tumors who meet the coverage criteria outlined in the local coverage determination.

2. Sheltzer, J.M., et al. Cancer Cell. 2017 Feb 13;31(2):240-255. doi: 10.1016/j.xccell.2016.12.004

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