

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 opportunities for treatment by evaluating 84 guideline-recommended genes for SNV / indels (82), copy number alterations (CNA); amplifications (19) and losses (5), fusions (9) and MSI-H status, all with a non-invasive, circulating tumor DNA (ctDNA) blood test.

PERFORMANCE CHARACTERISTICS^a

Variant Type	LOD at 95% Confidence ^b	Specificity	Reportable Range
SNVs	0.15% VAF	>99.9999%	≥0.01%
Indels			
CNA ^c	2.11 copies (amplification) 1.80 copies (loss)	>99.9%	≥2.10 copies (amplification) ≤1.90 copies (loss)
Fusion	0.30% tumor fraction	>99.9%	≥0.02%
MSI-H ^d	0.07% tumor fraction	>99.9%	n/a

a. Internal data on file, Aug 2025

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

c. 2.5% 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
Streck ctDNA 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



**7-10 days
or less**

From sample
receipt to results

**Northstar Select is
covered by Medicare.**

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



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.

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

SNVs / Indels82 genes						CNAs: Amplifications19 genes			Fusions9 genes
AKT1	CCNE1	EZH2	JAK2	NOTCH1	RB1	AR	ERBB2	MYC	ALK
AKT2	CD274 (PD-L1)	FANCA	JAK3	NPM1	RET	BRAF	ESR1	PDGFRA	BRAF
ALK	CDH1	FBXW7	KIT	NRAS	RHOA	CCNE1	FGFR1	PIK3CA	FGFR2
APC	CDK12	FGFR1	KRAS	NTRK1	RIT1	CD274 (PD-L1)	FGFR2	RAF1	FGFR3
AR	CDK4	FGFR2	MAP2K1 (MEK1)	PALB2	ROS1	CDK4	KIT	RET	NTRK1
ARAF	CDK6	FGFR3	MAP2K2 (MEK2)	PDGFRA	SF3B1	CDK6	KRAS		NTRK2
ARID1A	CDKN2A	FGFR4	MET	PIK3CA	SMAD4	EGFR	MET		NTRK3
ATM	CDKN2B	GATA3	MLH1	PMS2	SMO				RET
BRAF	CHEK2	GNA11	MPL	PTEN	STK11				ROS1
BRCA1	CTNNB1	GNAQ	MSH2	PTPN11	TERT				
BRCA2	DDR2	GNAS	MSH6	RAD51C	TP53				
BRIP1	EGFR	HRAS	MTOR	RAD51D	TSC1				
CCND1	ERBB2 (HER2)	IDH1	MYC	RAF1	VHL				
CCND2	ESR1	IDH2	NF1						
						CNAs: Losses5 genes			
						ATM	CDKN2A		
						BRCA1	PTEN		
						BRCA2			
									Biomarker
									MSI-H

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

copy number = 2.1
tumor fraction = 1.3%

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