Northwell Health Labs

Molecular Diagnostics Laboratory-CFAM
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OUTLINED AREAS MUST BE COMPLETED

PATIENT	PATIENT IDENTIFIER			
	NAME, LAST (Please Print)	FIRST	M.I.	
	BIRTHDATE	M/F	DATE/TIME COLLECTED	
	STREET	PHONE #		
	CITY	STATE	ZIP	
BILLING	INSURANCE CARRIER NAME	ADDRESS		
	INSURED NAME	INSURED ID#	PT. RELATIONSHIP TO INSURED: ☐ Self ☐ Spouse ☐ Dependent	
	GROUP # or NAME		☐ INSURANCE CHANGE	
	☐ MEDICARE #	☐ MEDICAID #	☐ SELF-PAY	

Ordering Facility ID:
Address:

Phone:

I attest that this patient has been informed about and has given consent for the test(s) I have ordered below under applicable law.

X _____
PHYSICIAN SIGNATURE

(Name, Fax or phone)

Responsible Pathologist:

Responsible Clinician:

Molecular Diagnostics Laboratory Requisition

SPECIMEN INFORMATION

Specimen Site:		Collection Date:	
Specimen Type:		Disease Type:	
Block ID#:		ICD-10:	

MSI and SINGLE GENE ASSAYS: PLEASE INDICATE THE TEST REQUESTED IN THE FIRST COLUMN.

Check Box	*Test*	*Gene/Assay*	*Targets covered by the qualitative assay*	*Specimen Requirements*
	KRAS Mutation Assay	*KRAS*	***KRAS*** mutations in codons 12, 13, 59, 61 and 146.	4x5 µm unstained FFPE slides (each with an area of 50-600 mm²) are required. If the tumor content is less than 10%, Please submit an additional H&E slide for macrodissection. Keep at room temperature (20-25°C).
	EGFR Mutation Assay	*EGFR*	Exon 18 (G719A/C/S), exon 20 (T790M, S768I), exon 21 (L858R, L861Q) mutations, exon 19 deletions and exon 20 insertions in the ***EGFR*** gene.	
	BRAF and ***NRAS*** Mutation Assay	*BRAF* and *NRAS*	Codons 12, 13, 59, 61, 117, and 146 of the ***NRAS*** gene and codon 600 of ***BRAF*** gene.	
	BRAF Mutation Assay	*BRAF*	***BRAF*** codon 600 (V600E/D and V600K/R/M mutations).	4x5 µm ustained FFPE slides (each with an area 50-600 mm²) are required. If the tumor content is less than 50%, please submit an additional H&E slide for macrodissection. Keep at room temperature (20-25°C).
	Microsatellite instability	MSI	PCR-based assay followed by capillary electrophoresis designed to detect microsatellite instability (MSI) in solid tumors.	10 unstained 5µm FFPE slides with dissectible tumor and adjacent normal tissue and 1 H&E-stained slide with circled tumor and normal areas for macrodissection. Tissue sections should have a tumor content ≥30% and range in volume from 0.1mm3 to 2.0mm3. Keep at room temperature (20-25°C).

NGS PANELS: PLEASE INDICATE TEST REQUESTED IN THE FIRST COLUMN

Check Box	*NGS Gene Panels*	*Description of the NGS Panel*	*Specimen Requirements*
	POINT Solid	This 161-gene NGS panel is designed to detect hotspots (SNVs, MNVs, indels) , CNV, and fusions in solid tumors. See gene list in Table 1.	15x5 µm unstained FFPE slides. Please submit an additional H&E slide for macrodissection. Keep at room temperature (20-25°C).
	POINT Heme	This NGS panel covers the major myeloid disorders and is designed to detect hotspots (SNVs, MNVs and indels) across 45 genes and gene fusions involving 34 gene. See gene list in Table 2.	2x5 ml of peripheral blood (PB) or bone marrow (BM) collected in lavender tubes (EDTA) are optimal. Volumes below 2 ml for PB, and 1 ml for BM, might be rejected.Keep at room temperature (20-25°C) or refrigerate at 4°C. Do not freeze.

Table 1. POINT Solid Gene Panel

Hotspot genes (87)				Full-length genes (48)			Copy number genes (43)		Gene fusions (inter- and intragenetic)		
AKT1	ESR1	KIT	PDGFRB	ARID1A	FBXW7	PTEN	AKT1	FGFR4	AKT2	FGFR2	NUTM1
AKT2	EZH2	KNSTRN	PIK3CB	ATM	MLH1	RAD50	AKT2	FLT3	ALK	FGFR3	PDGFRA
AKT3	FGFR1	KRAS	PIK3CA	ATR	MRE11	RAD51	AKT3	IGF1R	AR	FGR	PDGFRB
ALK	FGFR2	MAGOH	PPP2R1A	ATRX	MSH6	RAD51B	ALK	KIT	AXL	FLT3	PIK3CA
AR	FGFR3	MAP2K1	PTPN11	BAP1	MSH2	RAD51C	AXL	KRAS	BRCA1	JAK2	PRKACA
ARAF	FGFR4	MAP2K2	RAC1	BRCA1	NBN	RAD51D	AR	MDM2	BRCA2	KRAS	PRKACB
AXL	FLT3	MAP2K4	RAF1	BRCA2	NF1	RNF43	BRAF	MDM4	BRAF	MDM4	PTEN
BRAF	FOXL2	MAPK1	RET	CDK12	NF2	RB1	CCND1	MET	CDKN2A	MET	PPARG
BTK	GATA2	MAX	RHEB	CDKN1B	NOTCH1	SETD2	CCND2	MYC	EGFR	MYB	RAD51B
CBL	GNA11	MDM4	RHOA	CDKN2A	NOTCH2	SLX4	CCND3	MYCL	ERBB2	MYBL1	RAF1
CCND1	GNAQ	MED12	ROS1	CDKN2B	NOTCH3	SMARCA4	CCNE1	MYCN	ERBB4	NF1	RB1
CDK4	GNAS	MET	SF3B1	CHEK1	PALB2	SMARCB1	CDK2	NTRK1	ERG	NOTCH1	RELA
CDK6	H3F3A	MTOR	SMAD4	CREBBP	PIK3R1	STK11	CDK4	NTRK2	ESR1	NOTCH4	RET
CHEK2	HIST1H3B	MYC	SMO	FANCA	PMS2	TP53	CDK6	NTRK3	ETV1	NRG1	ROS1
CSF1R	HNF1A	MYCN	SPOP	FANCD2	POLE	TSC1	EGFR	PDGFRA	ETV4	NTRK1	RSPO2
CTNNB1	HRAS	MYD88	SRC	FANCI	PTCH1	TSC2	ERBB2	PDGFRB	ETV5	NTRK2	RSPO3
DDR2	IDH1	NFE2L2	STAT3				ESR1	PIK3CB	FGFR1	NTRK3	TERT
EGFR	IDH2	NRAS	TERT				FGF19	PIK3CA			
ERBB2	JAK1	NTRK1	TOP1				FGF3	PPARG			
ERBB3	JAK2	NTRK2	U2AF1				FGFR1	RICTOR			
ERBB4	JAK3	NTRK3	XPO1				FGFR2	TERT			
ERCC2	KDR	PDGFRA					FGFR3				

Table 2. POINT Heme Gene Panel

Hotspot Genes (23)		Full genes (17)		Fusion driver genes (34)			Expression genes (5)	Expression control genes (5)
ABL1	KRAS	ASXL1	PRPF8	ABL1	JAK2	NUP98	BAALC	EIF2B1
BRAF	MPL	BCOR	RB1	ABL2	KAT6A (MOZ)	NUP214	MECOM	FBXW2
CBL	MYD88	CALR	RUNX1	BCL2	KAT6B	PAX5	MYC	PSMB2
CSF3R	NPM1	CEBPA	SH2B3	BRAF	KMT2A	PDGFRA	SMC1A	PUM1
DNMT3A	NRAS	ETV6	STAG2	CCND1	MECOM	PDGFRB	WT1	TRIM27
FLT3	PTPN11	EZH2	TET2	CREBBP	MET	RARA		
GATA2	SETBP1	IKZF1	TP53	EGFR	MLLT10	RUNX1		
HRAS	SF3B1	NF1	ZRSR2	ETV6	MRTFA (MKL1)	TCF3		
IDH1	SRSF2	PHF6		FGFR1	MYBL1	TFE3		
IDH2	U2AF1			FGFR2	MYH11	ZNF384		
JAK2	WT1			FUS	NTRK2			
KIT				HMGA2	NTRK3			