

## Summit™ 2.0 + Ascent™ Report

Patient Information	Provisional Diagnosis	Specimen	Physician Information
Name: Jane Doe DOB: 01/01/1990 Sex Assigned at Birth: Female MRN: 11xx22xx33	Diagnosis: Central Nervous System Neoplasm ICD10: R94.02	Type: CSF Collected: 01/01/2026 Received: 01/02/2026 Specimen ID: Sum+AscNeg-CNS	Institution: Belay Diagnostics Referring Physician: Provider Test

### RESULT SUMMARY

## NEGATIVE

Comments
The absence of a clinically significant variant in this report does not necessarily indicate the absence of molecular variants in this specimen that could be present below the limit of detection of the test or are not included in the regions being evaluated. Clinical correlation is required.

### CLINICALLY SIGNIFICANT ALTERATION DETAILS (Tier 1 or 2 per AMP/ASCO/CAP)

SNV, MNV, Indel Variants: <i>None</i>
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Copy Number Variants: <i>None</i>
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Fusion Variants: <i>None</i>
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Biomarkers		
Tumor Mutation Burden (TMB)		Microsatellite Instability (MSI)
Not Detected	Low	High
		Stable
		High

Ascent™ Chromosome Arm Level Loss or Gain: <i>None</i>
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### VARIANTS OF UNKNOWN SIGNIFICANCE (Tier 3)

*None*

### ACTIONABILITY SUMMARY

*None*

### CLINICAL TRIALS / INVESTIGATIONAL THERAPIES

*None*

### TIER 1A THERAPY DETAILS

*None*

### TEST DETAILS

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PANEL CONTENT AND REPORTING TRANSCRIPTS				
ABL1 NM_005157.4 <sup>^</sup>	DNAJB1 NM_006145.1	H2BC5 NM_021063.3	MYC NM_002467.4 <sup>+</sup>	COP1 NM_022457.5

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ABL2 NM_007314.3	DNMT1 NM_001130823.1	H3C1 NM_003529.2	MYCL NM_001033082.2 <sup>+</sup>	RHEB NM_005614.3
ACVR1 NM_001105.4	DNMT3A NM_022552.4	H3C2 NM_003537.3	MYCN NM_005378.4 <sup>+</sup>	RHOA NM_001664.2
ACVR1B NM_020328.3	DNMT3B NM_006892.3	H3C3 NM_003531.2 <sup>+</sup>	MYD88 NM_002468.4 <sup>+</sup>	RICTOR NM_152756.3 <sup>+</sup>
AKT1 NM_001014432.1 <sup>+</sup>	DOT1L NM_032482.2	H3C4 NM_003530.4	MYOD1 NM_002478.4 <sup>+</sup>	RIT1 NM_006912.5
AKT2 NM_001626.4 <sup>+</sup>	E2F3 NM_001949.4	H3C6 NM_003532.2	NAB2 NM_005967.3 <sup>^</sup>	RNF43 NM_017763.4 <sup>^</sup>
AKT3 NM_005465.4	EED NM_003797.3	H3C7 NM_021018.2	NBN NM_002485.4	ROS1 NM_002944.2 <sup>^</sup>
ALK NM_004304.4 <sup>^+</sup>	EGFL7 NM_016215.4	H3C8 NM_003534.2	NCOA3 NM_181659.2	RPS6KA4 NM_003942.2
ANKRD11 NM_001256182.1	EGFR NM_005228.3 <sup>^+</sup>	H3C10 NM_003536.2	NCOR1 NM_006311.3	RPS6KB1 NM_003161.3 <sup>+</sup>
ANKRD26 NM_014915.2	EIF1AX NM_001412.3	H3C11 NM_003533.2	NEGR1 NM_173808.2	RPS6KB2 NM_003952.2
APC NM_000038.5 <sup>+</sup>	EIF4A2 NM_001967.3	H3C12 NM_003535.2	NF1 NM_001042492.2 <sup>+</sup>	RPTOR NM_020761.2
AR NM_000044.3 <sup>+</sup>	EIF4E NM_001130679.1	H3C15 NM_001005464.2	NF2 NM_000268.3 <sup>+</sup>	RUNX1 NM_001754.4
ARAF NM_001654.4	EML4 NM_019063.3	H3C14 NM_021059.2	NFE2L2 NM_006164.4 <sup>+</sup>	RUNX1T1 NM_175635.2
ARFRP1 NM_003224.4	EP300 NM_001429.3	H3C13 NM_001123375.2	NFKBIA NM_020529.2	RYBP NM_012234.5
ARID1A NM_006015.4	EPCAM NM_002354.2	H3-4 NM_003493.3 <sup>+</sup>	NKX2-1 NM_001079668.2	SDHA NM_004168.2
ARID1B NM_020732.3	EPHA3 NM_005233.5	HLA-A NM_002116.7	NKX3-1 NM_006167.3	SDHAF2 NM_017841.2
ARID2 NM_152641.2	EPHA5 NM_004439.5	HLA-B NM_005514.6	NOTCH1 NM_017617.3	SDHB NM_003000.2
ARID5B NM_032199.2	EPHA7 NM_004440.3	HLA-C NM_002117.5	NOTCH2 NM_024408.3	SDHC NM_003001.3
ASXL1 NM_015338.5	EPHB1 NM_004441.4	HNF1A NM_000545.5	NOTCH3 NM_000435.2	SDHD NM_003002.3
ASXL2 NM_018263.4	ERBB2 NM_004448.2 <sup>+</sup>	HNRNPKN NM_002140.3	NOTCH4 NM_004557.3	SETBP1 NM_015559.2
ATM NM_000051.3 <sup>+</sup>	ERBB3 NM_001982.3 <sup>+</sup>	HOXB13 NM_006361.5	NPM1 NM_002520.6	SETD2 NM_014159.6 <sup>+</sup>
ATR NM_001184.3	ERBB4 NM_005235.2 <sup>+</sup>	HRAS NM_005343.2 <sup>+</sup>	NRAS NM_002524.4 <sup>+</sup>	SFBF1 NM_012433.2
ATRX NM_000489.3 <sup>+</sup>	ERCC1 NM_001983.3 <sup>+</sup>	HSD3B1 NM_000862.2	NRG1 NM_013964.3 <sup>+</sup>	SH2B3 NM_005475.2
AURKA NM_198433.1	ERCC2 NM_000400.3 <sup>+</sup>	HSP90AA1 NM_001017963.2	NSD1 NM_022455.4 <sup>^</sup>	SH2D1A NM_002351.4
AURKB NM_004217.3	ERCC3 NM_000122.1	ICOSLG NM_015259.4	NTRK1 NM_002529.3 <sup>^</sup>	SHQ1 NM_018130.2
AXIN1 NM_003502.3	ERCC4 NM_005236.2	ID3 NM_002167.4	NTRK2 NM_006180.3 <sup>^</sup>	SLIT2 NM_004787.1
AXIN2 NM_004655.3	ERCC5 NM_000123.3	IDH1 NM_005896.2 <sup>+</sup>	NTRK3 NM_001012338.2	SLX4 NM_032444.2
AXL NM_021913.4	ERG NM_001136154.1	IDH2 NM_002168.2 <sup>+</sup>	NUP93 NM_014669.4 <sup>^</sup>	SMAD2 NM_005901.5
B2M NM_004048.2	ERRFI1 NM_018948.3	IGF1 NM_001111283.1	NUTM1 NM_175741.1 <sup>^</sup>	SMAD3 NM_005902.3
BAP1 NM_004656.3	ESR1 NM_001122742.1 <sup>+</sup>	IGF1R NM_000875.3	PAK1 NM_001128620.1	SMAD4 NM_005359.5 <sup>+</sup>
BARD1 NM_000465.2	ETS1 NM_001143820.1	IGF2 NM_001127598.1	PAK3 NM_002578.3	SMARCA4 NM_001128849.1 <sup>+</sup>
BBC3 NM_001127240.2	ETV1 NM_004956.4 <sup>^</sup>	IKBKE NM_014002.3	PAK5 NM_020341.3	SMARCB1 NM_003073.3 <sup>+</sup>
BCL10 NM_003921.1	ETV4 NM_001079675.2 <sup>^</sup>	IKZF1 NM_006060.4	PAK6 NM_024675.3	SMARCD1 NM_003076.4
BCL2 NM_000633.2	ETV5 NM_004454.2 <sup>^</sup>	IL10 NM_000572.2	PALB2 NM_024675.3	SMC1A NM_006306.3
BCL2L1 NM_138578.1	ETV6 NM_001987.4 <sup>^</sup>	IL7R NM_002185.3	PARP1 NM_001618.3 <sup>^</sup>	SMC3 NM_005445.3
BCL2L1L NM_001204108.1	EWSR1 NM_013986.3	INHA NM_002191.3	PAX3 NM_181457.3 <sup>^</sup>	SMO NM_005631.4 <sup>+</sup>
BCL2L2 NM_001199839.1	EZH2 NM_004456.4	INHBA NM_002192.2	PAX5 NM_016734.2	SNCAIP NM_005460.2
BCL6 NM_001706.4	AMER1 NM_152424.3	INPP4A NM_001134224.1	PAX7 NM_001135254.1 <sup>^</sup>	SOC31 NM_003745.1
BCOR NM_001123385.1	ABRAXAS1 NM_139076.2	INPP4B NM_003866.2	PAX8 NM_013953.3 <sup>^</sup>	SOX10 NM_006941.3
BCORL1 NM_021946.4 <sup>^</sup>	TENT5C NM_017709.3	INSR NM_000208.2	PBRM1 NM_018313.4	SOX17 NM_022454.3
BCR NM_004327.3 <sup>^</sup>	FANCA NM_000135.2	IRF2 NM_002199.3	PDCD1 NM_005018.2	SOX2 NM_003106.3
BIRC3 NM_001165.4	FANCC NM_000136.2	IRF4 NM_002460.3	PDCD1LG2 NM_025239.3 <sup>^</sup>	SOX9 NM_000346.3
BLM NM_000057.2	FANCD2 NM_033084.3	IRS1 NM_005544.2	PDGFRA NM_006206.4 <sup>+</sup>	SPEN NM_015001.2
BMPR1A NM_004329.2	FANCE NM_021922.2	IRS2 NM_003749.2	PDGFRB NM_002609.3 <sup>+</sup>	SPOP NM_001007228.1
BRAF NM_004333.4 <sup>^+</sup>	FANCF NM_022725.3	JAK1 NM_002227.2	PDK1 NM_001278549.1	SPTA1 NM_003126.2
BRCA1 NM_007294.3 <sup>+</sup>	FANCG NM_004629.1	JAK2 NM_004972.3 <sup>+</sup>	PDPK1 NM_002613.4	SRC NM_198291.2
BRCA2 NM_000059.3 <sup>+</sup>	FANCI NM_001113378.1	JAK3 NM_000215.3	PGR NM_000926.4	SRSF2 NM_003016.4
BRD4 NM_058243.2	FANCL NM_001114636.1	JUN NM_002228.3	PHF6 NM_032458.2	STAG1 NM_005862.2
BRIP1 NM_032043.2	FAS NM_000043.4	KAT6A NM_006766.3	PHOX2B NM_003924.3	STAG2 NM_001042749.1
BTG1 NM_001731.2	FAT1 NM_005245.3	KDM5A NM_001042603.1	PIK3C2B NM_002646.3	STAG3 NM_139276.2
BTK NM_000061.2	FBXW7 NM_033632.3 <sup>+</sup>	KDM5C NM_004187.3	PIK3C2G NM_004570.4	STAT3 NM_139276.2
EMSY NM_020193.3	FGF1 NM_001144934.1 <sup>+</sup>	KDM6A NM_021140.2	PIK3C3 NM_002647.2	STAT4 NM_003151.3
CALR NM_004343.3	FGF10 NM_004465.1 <sup>+</sup>	KDR NM_002253.2	PIK3CA NM_006218.2 <sup>+</sup>	STAT5A NM_003152.3
CARD11 NM_032415.4	FGF14 NM_175929.2 <sup>+</sup>	KEAP1 NM_012289.3	PIK3CB NM_006219.2 <sup>+</sup>	STAT5B NM_012448.3
CASP8 NM_001228.4	FGF19 NM_005117.2 <sup>+</sup>	KEL NM_000420.2	PIK3CD NM_005026.3	STK11 NM_000455.4
CBFB NM_001755.2	FGF2 NM_002006.4 <sup>+</sup>	KIF5B NM_004521.2	PIK3CG NM_002649.2	STK40 NM_032017.1
CBL NM_005188.3	FGF23 NM_020638.2 <sup>+</sup>	KIT NM_000222.2 <sup>+</sup>	PIK3R1 NM_181523.2	SUFU NM_016169.3 <sup>+</sup>
CCND1 NM_053056.2 <sup>+</sup>	FGF3 NM_005247.2 <sup>+</sup>	KLHL6 NM_130446.2	PIK3R2 NM_005027.3	SUZ12 NM_015355.2
CCND2 NM_001759.3	FGF4 NM_002007.2 <sup>+</sup>	KMT2B NM_014727.1	PIK3R3 NM_003629.3	SYK NM_003177.5
CCND3 NM_001760.3 <sup>+</sup>	FGF5 NM_004464.3 <sup>+</sup>	KMT2C NM_170606.2	PIM1 NM_002648.3	TBX3 NM_016569.3
CCNE1 NM_001238.2 <sup>+</sup>		KMT2D NM_003482.3	PLCG2 NM_002661.3	ELOC NM_005648.3
CD274 NM_014143.3		KRAS NM_004985.3 <sup>+</sup>		TCF3 NM_003200.3
CD276 NM_001024736.1		LAMP1 NM_005561.3 <sup>+</sup>		TCF7L2 NM_030756.4
		LATS1 NM_004690.3		TERC
				TERT NM_198253.2 <sup>+</sup>

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CD74 NM_001025159.2 <sup>^</sup>	FGF6 NM_020996.1 <sup>+</sup>	LATS2 NM_014572.2	PLK2 NM_006622.3	TET1 NM_030625.2
CD79A NM_001783.3	FGF7 NM_002009.3 <sup>+</sup>	LMO1 NM_002315.2	PMAIP1 NM_021127.2	TET2 NM_001127208.2
CD79B NM_000626.2 <sup>+</sup>	FGF8 NM_033163.3 <sup>+</sup>	LRP1B NM_018557.2	PMS1 NM_000534.4	TFE3 NM_006521.4 <sup>^</sup>
CDC73 NM_024529.4	FGF9 NM_002010.2 <sup>+</sup>	LYN NM_002350.3	PMS2 NM_000535.5	TFRC NM_003234.2 <sup>+</sup>
CDH1 NM_004360.3 <sup>+</sup>	FGFR1 NM_023110.2 <sup>+</sup>	LZTR1 NM_006767.3	PNRC1 NM_006813.2	TGFBR1 NM_004612.2
CDK12 NM_016507.2	FGFR2 NM_000141.4 <sup>^+</sup>	MAGI2 NM_012301.3	POLD1 NM_001256849.1	TGFBR2 NM_001024847.2
CDK4 NM_000075.3 <sup>+</sup>	FGFR3 NM_000142.4 <sup>^+</sup>	MALT1 NM_006785.3	POLE NM_006231.2	TMEM127 NM_017849.3
CDK6 NM_001259.6 <sup>+</sup>	FGFR4 NM_213647.1 <sup>+</sup>	MAP2K1 NM_002755.3	PPARG NM_138712.3 <sup>^</sup>	TMPRSS2 NM_001135099.1 <sup>^</sup>
CDK8 NM_001260.1	FH NM_000143.3	MAP2K2 NM_030662.3	PPM1D NM_003620.3	TNFAIP3 NM_006290.3
CDKN1A NM_000389.4	FLCN NM_144997.5	MAP2K4 NM_003010.3	PPP2R1A NM_014225.5	TNFRSF14 NM_003820.2
CDKN1B NM_004064.3	FLI1 NM_002017.4	MAP3K1 NM_005921.1	PPP2R2A NM_001177591.1	TOP1 NM_003286.2
CDKN2A NM_000077.4 <sup>+</sup>	FLT1 NM_002019.4	MAP3K13 NM_004721.4	PPP6C NM_001123355.1	TOP2A NM_001067.3
CDKN2B NM_004936.3 <sup>+</sup>	FLT3 NM_004119.2	MAP3K14 NM_003954.3	PRDM1 NM_001198.3	TP53 NM_000546.5 <sup>+</sup>
CDKN2C NM_001262.2	FLT4 NM_182925.4	MAP3K4 NM_005922.2	PREX2 NM_024870.2	TP63 NM_003722.4
CEBPA NM_004364.3	FOXA1 NM_004496.3	MAPK1 NM_002745.4	PRKAR1A NM_212472.2	TRAF2 NM_021138.3
CENPA NM_001809.3	FOXL2 NM_023067.3	MAPK3 NM_002746.2	PRKCI NM_002740.5	TRAF7 NM_032271.2 <sup>+</sup>
CHD2 NM_001271.3	FOXO1 NM_002015.3	MAX NM_002382.4	PRKDC NM_006904.6	TSC1 NM_000368.4
CHD4 NM_001273.2	FOXO1 NM_002015.3	MCL1 NM_021960.4	PRSS8 NM_002773.3	TSC2 NM_000548.3
CHEK1 NM_001114122.2 <sup>+</sup>	FRS2 NM_001278351.1	MDC1 NM_014641.2	PTCH1 NM_000264.3 <sup>+</sup>	TSC3 NM_000369.2
CHEK2 NM_007194.3 <sup>+</sup>	FUBP1 NM_003902.3 <sup>+</sup>	MDM2 NM_002392.5 <sup>+</sup>	PTEN NM_000314.4 <sup>+</sup>	U2AF1 NM_006758.2
CIC NM_015125.3 <sup>+</sup>	FYN NM_002037.5	MDM4 NM_002393.4 <sup>+</sup>	PTPN11 NM_002834.3	VEGFA NM_001025366.2
CREBBP NM_004380.2	GABRA6 NM_000811.2	MED12 NM_005120.2	PTPRD NM_002839.3	VHL NM_000551.3 <sup>+</sup>
CRKL NM_005207.3	GATA1 NM_002049.3	MEF2B NM_001145785.1	PTPRS NM_002850.3	VTCN1 NM_024626.3
CRLF2 NM_022148.2	GATA2 NM_032638.4	MEN1 NM_130799.2	PTPRT NM_133170.3	CCN6 NM_003880.3
CSF1R NM_005211.3	GATA3 NM_001002295.1 <sup>+</sup>	MET NM_000245.2 <sup>+</sup>	QKI NM_006775.2	WT1 NM_024426.4
CSF3R NM_156039.3	GATA4 NM_002052.3	MGA NM_001164273.1	RAB35 NM_006861.6	XIAP NM_001167.3
CSNK1A1 NM_001025105.2	GATA6 NM_005257.4	MITF NM_000248.3	RAC1 NM_018890.3	XPO1 NM_003400.3
CTCF NM_006565.3	GEN1 NM_182625.3	MLH1 NM_000249.3	RAD21 NM_006265.2	XRCC2 NM_005431.1
CTLA4 NM_005214.4	GID4 NM_024052.4	KMT2A NM_001197104.1	RAD50 NM_005732.3	YAP1 NM_001130145.2
CTNNA1 NM_001903.2	GLI1 NM_005269.2	MLL2 NM_004529.2	RAD51 NM_002875.4	YES1 NM_005433.3
CTNNA1 NM_001903.2	GNA11 NM_002067.2	MPL NM_005373.2	RAD51B NM_133509.3	ZBTB2 NM_020861.1
CTNNA1 NM_001903.2	GNA13 NM_006572.4	MRE11 NM_005591.3	RAD51C NM_058216.2	ZBTB7A NM_015898.2
CUL3 NM_003590.4	GNAQ NM_002072.3	MSH2 NM_000251.2	RAD51D NM_002878.3	ZFH3 NM_006885.3
CUX1 NM_181552.3	GNAS NM_000516.4 <sup>+</sup>	MSH3 NM_002439.4	RAD52 NM_134424.2	ZNF217 NM_006526.2
CXCR4 NM_003467.2	ADGRA2 NM_032777.9	MSH6 NM_000179.2	RAD54L NM_001142548.1	ZNF703 NM_025069.1
CYLD NM_015247.2	GPS2 NM_004489.4	MST1 NM_020998.3	RAF1 NM_002880.3 <sup>+</sup>	ZRSR2 NM_005089.3
DAXX NM_001141970.1	GREM1 NM_013372.6	MST1R NM_002447.2	RANBP2 NM_006267.4	MTAP NM_002451.3 <sup>^+</sup>
DCUN1D1 NM_020640.2	GRIN2A NM_000833.3	MTOR NM_004958.3	RARA NM_000964.3	
DDR2 NM_001014796.1	GRM3 NM_000840.2	MUTYH NM_001128425.1	RASA1 NM_002890.2	
DDX41 NM_016222.2	GSK3B NM_002093.3	MYB NM_001130173.1	RB1 NM_000321.2 <sup>+</sup>	
DHX15 NM_001358.2	H3-3A NM_002107.4 <sup>+</sup>		RBM10 NM_005676.4	
DICER1 NM_177438.2	H3-3B NM_005324.3		RECQL4 NM_004260.3	
DIS3 NM_014953.3	H3-5 NM_001013699.2		REL NM_002908.2	
	HGF NM_000601.4		RET NM_020975.4 <sup>^+</sup>	
	H1-2 NM_005319.3			

<sup>^</sup>Summit™ also reports fusion events for this gene  
<sup>+</sup>Summit™ also reports copy number alterations for this gene  
<sup>\*</sup>Summit™ only reports copy number alterations for this gene

Aneuploidy (chromosome arm level loss and gain)									
chr1p	chr3p	chr5p	chr7p	chr9p	chr11p	chr13q	chr16q	chr18q	chr20q
chr1q	chr3q	chr5q	chr7q	chr9q	chr11q	chr14q	chr17p	chr19p	chr21q
chr2p	chr4p	chr6p	chr8p	chr10p	chr12p	chr15q	chr17q	chr19q	chr22q
chr2q	chr4q	chr6q	chr8q	chr10q	chr12q	chr16p	chr18p	chr20p	

## Methods and Limitations

The Summit™ 2.0 comprehensive genomic profiling (CGP) next-generation sequencing (NGS) test investigates tumor derived nucleic acid extracted from cerebrospinal fluid (CSF) for clinically relevant single/multi nucleotide variants (SNVs, MNVs), insertions and deletions (indels), gene level copy number variants (CNVs), and other biomarkers such as tumor mutation burden (TMB) and microsatellite instability (MSI). Methodology involves

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evaluation of 520 genes for SNVs, MNVs, Indels, 62 genes for CNVs, 28 genes for fusions, as well as TMB and MSI (PMID: 41595175). The LOD (limit of detection) for SNVs, MNVs and Indels was determined to be 0.3% variant allelic frequency (VAF), for CNVs was determined to be  $\geq 2$ -fold change for amplifications and  $\leq 0.5$ -fold change for deletions, and for fusions was determined to be  $\geq 2$  supporting reads. Reporting thresholds for TMB and MSI are:  $< 10$  Mut/Mb (TMB low),  $\geq 10$  Mut/Mb (TMB high), and when total unstable sites are  $< 30\%$  (MSS) and  $\geq 30\%$  (MSI-High). Ascent™ evaluates chromosomal arm level loss/gain (aneuploidy), and focal alterations (gene level amplification/deletion) using  $> 0.1x$  low pass whole genome sequencing (LP-WGS) (PMID: 37014860). The LOD (limit of detection) for aneuploidy was determined to be  $\log_2(r)$  of abs (0.09), and for focal alteration was determined to be seq.mean cutoff of 0.1 for amplification and -0.2 for deletions. Variants are called against the human genome build reference hg19 using Summit™Omics pipeline version 1.3.0, developed at Belay Diagnostics.

Tertiary analysis is performed using the precision oncology workbench (GenomOncology) based on the joint AMP/ASCO/CAP consensus guidelines for interpretation of sequence variants in cancer (PMID: 27993330). Please reach out to [contact@belaydiagnostics.com](mailto:contact@belaydiagnostics.com) for additional information or queries.

### Disclaimers

This test was developed, and its performance characteristics determined by Belay Diagnostics Laboratory (CLIA# 14D2302605), which is certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA) as qualified to perform high complexity testing. This test has not been cleared or approved by the U.S. Food and Drug Administration (FDA). This test may be used for clinical purposes. However, the results of this test do not establish a diagnosis and should not be used alone for diagnosis or patient care decisions or otherwise replace the judgment of a treating physician and must always be interpreted in the context of all relevant clinical and pathological data.

This test is performed only to evaluate for somatic (i.e., tumor-specific) variants within the genes listed and cannot distinguish between germline and somatic alterations with absolute certainty. This test therefore does not report on incidental findings as defined by the American College for Medical Genetics and Genomics (ACMG) (PMID: 37347242). If a germline variant is suspected, follow-up germline testing using non-neoplastic (normal) tissue should be performed by a laboratory permitted to perform germline genetic testing along with genetic counseling. It is possible for a genomic variant to be present yet go undetected by our assay either due to the heterogeneous nature of the specimen or the limits of detection of our assay. Therefore, to the extent a particular genomic variant is not reported, Belay Diagnostics LLC does not guarantee that the variant does not exist in the specimen provided. Likely benign, and benign variants are not reported. For any reported variant of uncertain significance (VUS), if the classification changes, there is no obligation to send out a new report updating this information.

The information presented in the clinical trials and therapeutic sections of this report is compiled from public sources which are continuously updated. While we strive to ensure this information is accurate and complete, we cannot guarantee the accuracy or completeness of this information. This public sourced information is not ranked in order of potential or predicted efficacy and may not be complete. Specific eligibility criteria should be reviewed as applicable. This information may include associations between a genomic variant (or lack of a variant) and one or more therapeutic agents with potential clinical benefit (or lack of clinical benefit), including agents that are being studied in clinical research. The finding of a genomic variant does not necessarily indicate or demonstrate pharmacologic effectiveness (or lack thereof) of any agent or treatment regimen found in public source information. Similarly, the finding of "no clinically significant variant" does not necessarily indicate or demonstrate lack of pharmacologic effectiveness (or lack of effectiveness) of any agent or treatment regimen found in public source information. Belay Diagnostics expressly disclaims, and makes no representation of or warranty of, the accuracy or completeness with respect to the publicly available information included herein or reviewed or collected during creation of this report.

### ACTIONABILITY REFERENCES

**FDA:** U.S. Food & Drug Administration ([fda.gov](http://fda.gov))

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**WHO:** World Health Organization Classification of Tumours online ([tumourclassification.iarc.who.int](http://tumourclassification.iarc.who.int))

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