

## Summit™ 2.0 + Vantage™ 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; Lymphocytic Neoplasm ICD10: R94.02	Type: CSF Collected: 01/01/2026 Received: 01/02/2026 Specimen ID: SumOnlyPos-PCNSL	Institution: Belay Diagnostics Referring Physician: Provider Test

### RESULT SUMMARY

## POSITIVE

Comments
<p><i>MYD88</i> and <i>CD79B</i> are characteristically altered in primary central nervous system lymphoma (PCNSL) and drive tumor biology via NF-κB activation (PMID: 40263702). <i>MYD88</i> L265P and <i>CD79B</i> oncogenic variants have been shown to predict response to R-MPV (rituximab, high-dose methotrexate, procarbazine, and vincristine) in PCNSL (PMID: 36478416). Clinical correlation is required.</p> <p><i>MGMT</i> promoter methylation is frequent in PCNSL, occurring in of 52% of cases, and may have therapeutic implications as a subset of elderly patients responded to temozolomide monotherapy (PMID: 16858686, 9546285, 15327516, 19494841, 19841864). Clinical correlation is required.</p> <p>NOTE: Summit™ 2.0 does NOT include evaluation of chromosomal arm-level and focal gains/losses. Aneuploidy analysis can be performed for this specimen with clinician authorized order of Ascent™. Please contact customer service (phone: 331-320-0155, email: customer.service@belaydiagnostics.com) to order the test; no additional sample is needed.</p>

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

SNV, MNV, Indel Variants				
Alteration	VAF	Actionability Summary		
		FDA/NCCN Therapies Associated	Prognostic/Diagnostic Guidelines	Clinical Trial Options
<i>CD79B</i> p.Y196S c.587A>C	32.2%	No	Yes	Yes
<i>CDKN1B</i> c.475+1G>A	40.3%	No	Yes	No
<i>MYD88</i> p.L265P c.794T>C	36.2%	No	Yes	Yes
<i>PIM1</i> p.E79K c.235G>A	10.0%	No	Yes	No

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

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Vantage™ MGMT Promoter Methylation				
Status	Guidelines	Actionability Summary		
		FDA/NCCN Therapies Associated	Prognostic/Diagnostic Guidelines	Clinical Trial Options
Methylated	NCCN	No	Yes	Yes

### VARIANTS OF UNKNOWN SIGNIFICANCE (Tier 3)

SNV/MNVs/Indels				
ADGRA2 C1196Y	FANCF P117T	IRF4 Q60*	NOTCH3 A38S	PIM1 N172S
ARID5B S73F	FANCI T163N	IRF4 E66fs	PIK3C2G H1274Y	PIM1 L184F
AURKB M298T	FOXO1 E178K	IRF4 E66K	PIM1 A22_T23delinsVS	PIM1 F201L
AURKB A52V	GATA6 V464M	IRF4 E66D	PIM1 T23S	PIM1 A300T
BCORL1 T1111M	H3C11 L127V	IRS1 Y800H	PIM1 A22V	PRDM1 P84_R85del
BCR L1010M	H3C12 L71fs	KLHL6 L90V	PIM1	RHOA G116R
CCND3 Q260*	H3C13 A112V	KLHL6 A70T	S75_E79delinsFDWVGK	RPS6KB2 P267L
CD79B C65Y	IL10 Q97fs	MAP3K4 c.4627-26_4630del	PIM1 S75F	SOCS1 A192T
CHD2 K1341R	IRF4 G13A	MCL1 G158A	PIM1 E89K	SOCS1 A17V
COP1 A7V	IRF4 S18R	MCL1 S155N	PIM1 E89_V90delinsKL	SOCS1 A16T
CUX1 S1043L	IRF4 G22E	MSH6 R1035Q	PIM1 V90L	SOCS1 V2_N5del
EP300 P1452R	IRF4 L24I	MYC T23I	PIM1 I104S	SOCS1 V2I
ERCC5 R964W	IRF4 L40fs	MYC P36S	PIM1 E135*	TGFBR2 S22N
ETV6 A6P	IRF4 S48N	MYC S107N	PIM1 L139fs	
			PIM1 L164F	

Gene Level CNVs
None

Fusions
None

### ACTIONABILITY SUMMARY

FDA / NCCN Therapies for the Patient's Tumor Type (Tier 1A): <i>None</i>
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FDA / NCCN Therapies with Resistance / Decreased Response (Tier 1A): <i>None</i>
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Prognostic Implications per NCCN: <i>None</i>
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Diagnostic Implications per WHO		
Biomarker	Diseases	Note
CD79B Y196S	Lymphocytic Neoplasm	Among lymphocytic neoplasms, CD79B mutations are most closely associated with large B-cell lymphomas. In DLBCL-NOS, the activated B cell (ABC) subtype is enriched for BCR pathway mutations including CD79B (PMID: 25805586), and co-mutation of CD79B and MYD88 defines the MCD molecular subtype (PMID: 32289277). Additionally, CD79B hotspot mutations are genetic hallmarks of primary large B-cell lymphoma of immune-privileged sites (CNS, vitreoretinal, testis), are reported in ~2/3 of intravascular large B-cell lymphoma, and are also observed in primary cutaneous DLBCL, leg type, as well as in DLBCL/HGBCL with MYC and BCL6 rearrangements.
CDKN1B c.475+1G>A	Lymphocytic Neoplasm	Among lymphocytic neoplasms, CDKN1B mutations have been identified in hairy cell leukemia, T-cell lymphoblastic leukemia/lymphoma (PMID:28801450; PMID: 25283840; PMID:26941398; PMID:29989027; PMID:32185137; PMID:24140475; PMID:33467425; PMID:29034206; PMID:34661151).
MGMT Promoter	Central Nervous	Among central nervous system neoplasms, MGMT promoter methylation is detectable in the majority of oligodendrogliomas (PMID: 15455350). The MGMT gene encodes a DNA repair protein (PMID: 24071851) and is transcriptionally silenced by promoter methylation in approximately 40-50% of IDH-wildtype glioblastomas (PMID: 15455350).

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Methylation Positive	System Neoplasm	24120142; PMID: 10029064; PMID: 15758010; PMID: 22294349). MGMT promoter methylation in glioblastoma is a strong predictive marker of response to alkylating agents such as temozolomide and is associated with longer overall survival (PMID: 15758010; PMID: 22877848; PMID: 22578793; PMID: 19805672; PMID: 25655102; PMID: 24068788; PMID: 25035291; PMID: 24912512; PMID: 30782343), with more than 90% of long-term survivors harboring MGMT promoter methylation (PMID: 19269895). A higher frequency of methylation (>75%) is also associated with gliomas exhibiting the glioma CpG island methylator phenotype (G-CIMP), characteristic of IDH-mutant tumors (PMID: 22810491; PMID: 24120142; PMID: 23209033). Although H3 G34-mutant diffuse hemispheric gliomas display widespread DNA hypomethylation, MGMT is often methylated and may be associated with longer overall survival in the absence of oncogene amplifications (PMID: 23079654; PMID: 28966033; PMID: 30101054; PMID: 26482474). In high-grade astrocytoma with piloid features, a methylated MGMT promoter was reported in 46% of tumors, though no association with outcome was observed, and treatment data were unavailable (PMID: 29564591). In primary diffuse large B-cell lymphoma of the CNS, MGMT promoter methylation is observed in approximately 52% of cases and may have therapeutic implications, as a subset of elderly patients responded to temozolomide monotherapy (PMID: 16858686; PMID: 9546285; PMID: 15327516; PMID: 19494841; PMID: 19841864). In pituitary adenoma/pituitary neuroendocrine tumor (PitNET), MGMT protein expression appears inversely related to temozolomide response; however, promoter methylation status does not correlate with treatment outcomes (PMID: 29046323; PMID: 29330228; PMID: 20668043).
MYD88 L265P	Lymphocytic Neoplasm	MYD88 mutations are observed in many B-cell lymphocytic neoplasms. MYD88 mutation is a desirable diagnostic criterion for LPL/WM, and in 93-97% of cases the driver mutation is MYD88 p.L252P (formerly known as L265P) (PMID: 21179087), with 1-2% of cases having other MYD88 mutations. These mutations result in gain of function of MYD88 and constitutive activation of the NF- B pathway. MYD88 mutations are also detectable in as many as 80% of IgM MGUS cases, which are at higher risk of progression to WM. MYD88 mutation are observed in other small B-cell disorders, such as the non-CLL/SLL type of monoclonal B-cell lymphocytosis, the DMT molecular subtype of splenic MZL, splenic diffuse red pulp small B-cell lymphoma, and Mu heavy chain disease, but are rare or absent in Gamma heavy chain disease, primary cutaneous follicle centre lymphoma, nodal and extra-nodal MZL, and cold agglutinin disease. Among large B-cell lymphomas, MY88 mutations are associated with primary cutaneous DLBCL, leg type (70-75%), the ABC molecular subtype of DLBCL-NOS, intravascular LBCL (~50%), LBCL with IRF4 rearrangement, primary LBCL of immune-privileged sites, and fluid overload-associated LBCL, but tend to be absent in EBV+ DLBCL (PMID: 31123031).
PIM1 E79K	Lymphocytic Neoplasm	Among lymphocytic neoplasms, mutations in PIM1 have been observed. PIM1 mutations are frequent in primary cutaneous diffuse large B-cell Lymphoma, leg type (PCLBCL-LT), 70% of cases (PMID:28479318, PMID:31150604).

### CLINICAL TRIALS / INVESTIGATIONAL THERAPIES

CD79B Y196S + MYD88 L265P			
Therapy	Clinical Trial	Location/Sponsor	WeTrials
zanubrutinib + R-CHOP regimen	<a href="#">NCT06846463</a> (Phase 2) Zanubrutinib in Patients With DLBCL and MYD88 or NOTCH1 Mutation or CD5+	Richmond, Virginia Virginia Commonwealth University masseyepd@vcu.edu	 <a href="https://genomoncology.wetrials.com/v1/NCT06846463">https://genomoncology.wetrials.com/v1/NCT06846463</a>

MGMT Promoter Methylation Positive			
Therapy	Clinical Trial	Location/Sponsor	WeTrials
tuvusertib + temozolomide	<a href="#">NCT05691491</a> (Phase 1/Phase 2) Testing the Combination of the Anti-Cancer Drugs Temozolomide and M1774 to Evaluate Their Safety and Effectiveness	Irvine, California National Cancer Institute (NCI)	 <a href="https://genomoncology.wetrials.com/v1/NCT05691491">https://genomoncology.wetrials.com/v1/NCT05691491</a>

TMB-Low			
Therapy	Clinical Trial	Location/Sponsor	WeTrials
VSV-hiFNbeta-NIS	<a href="#">NCT03017820</a> (Phase 1) A Vaccine (VSV-hiFN -NIS) With or Without Cyclophosphamide and Combinations of Ipilimumab, Nivolumab, and Cemiplimab in Treating Relapsed or Refractory Multiple Myeloma, Acute Myeloid Leukemia or Lymphoma	Scottsdale, Arizona Mayo Clinic mayocliniccancerstudies@mayo.edu	 <a href="https://genomoncology.wetrials.com/v1/NCT03017820">https://genomoncology.wetrials.com/v1/NCT03017820</a>

### TIER 1A THERAPY DETAILS

None

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## 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
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	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
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_003493.2	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>	HNRNP11 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	HRAS NM_005343.2 <sup>+</sup>	NRAS NM_002524.4 <sup>+</sup>	SF3B1 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	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	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_003921.4	ETV4 NM_001079675.2 <sup>^</sup>	IKZF1 NM_006060.4	PAK7 NM_001135254.1	SMARCD1 NM_003076.4
BCL2 NM_006633.2	ETV5 NM_004454.2	IL10 NM_000572.2	PARP1 NM_001618.3	SMC1A NM_006306.3
BCL2L1 NM_138578.1	ETV6 NM_001987.4 <sup>^</sup>	IL7R NM_002185.3	PAX3 NM_181457.3 <sup>^</sup>	SMC3 NM_005445.3
BCL2L11 NM_001204108.1	EWSR1 NM_013986.3	INH1 NM_002191.3	PAX5 NM_016734.2	SMO NM_005631.4 <sup>+</sup>
BCL2L2 NM_001199839.1	EZH2 NM_004456.4	INHBA NM_002192.2	PAX7 NM_001135254.1	SNCAIP NM_005460.2
BCL6 NM_001706.4	AMER1 NM_152424.3	INPP4A NM_001134224.1	PBRM1 NM_018313.4	SOCS1 NM_003745.1
BCOR NM_001123385.1	ABRAXAS1 NM_139076.2	INPP4B NM_003866.2	PDCD1 NM_005018.2	SOX10 NM_006941.3
BCORL1 NM_021946.4	TENT5C NM_017709.3	INSR NM_000208.2	PDCD1LG2 NM_025239.3	SOX17 NM_022454.3
BCR NM_004327.3 <sup>^</sup>	FANCA NM_000135.2	IRF2 NM_002199.3	PDGFRA NM_006206.4 <sup>+</sup>	SOX2 NM_003106.3
BIRC3 NM_001165.4	FANCC NM_000136.2	IRF4 NM_002460.3	PDGFRB NM_002609.3 <sup>+</sup>	SOX9 NM_000346.3
BLM NM_000057.2	FANCD2 NM_033084.3	IRS1 NM_005544.2	PDK1 NM_001278549.1	SPEN NM_015001.2
BMPR1A NM_004329.2	FANCD2 NM_033084.3	IRS2 NM_003749.2	PDPK1 NM_002613.4	SPOP NM_001007228.1
BRAF NM_004333.4 <sup>^+</sup>	FANCE NM_021922.2	JAK1 NM_002227.2	PGR NM_000926.4	SPTA1 NM_003126.2
BRCA1 NM_007294.3 <sup>+</sup>	FANCF NM_022725.3	JAK2 NM_004972.3 <sup>+</sup>	PHF6 NM_032458.2	SRC NM_198291.2
BRCA2 NM_000059.3 <sup>+</sup>	FANCG NM_004629.1	JAK3 NM_000215.3	PHOX2B NM_003924.3	SRSF2 NM_003016.4
BRD4 NM_058243.2	FANCI NM_001113378.1	JUN NM_002228.3	PIK3C2B NM_002646.3	STAG1 NM_005862.2
BRIP1 NM_032043.2	FANCL NM_001114636.1	KAT6A NM_006766.3	PIK3C2G NM_004570.4	STAG2 NM_001042749.1
BTG1 NM_001731.2	FAS NM_000043.4	KDM5A NM_001042603.1	PIK3C3 NM_002647.2	STAT3 NM_139276.2
BTK NM_000061.2	FAT1 NM_005245.3	KDM5C NM_004187.3	PIK3CA NM_006218.2 <sup>+</sup>	STAT4 NM_003151.3
EMSY NM_020193.3	FBXW7 NM_033632.3 <sup>+</sup>	KDM6A NM_021140.2		STAT5A NM_003152.3
CALR NM_004343.3	FGF1 NM_001144934.1 <sup>+</sup>	KDR NM_002253.2		STAT5B NM_012448.3
CARD11 NM_032415.4	FGF10 NM_004465.1 <sup>+</sup>	KEAP1 NM_012289.3		STK11 NM_000455.4
CASP8 NM_001228.4	FGF14 NM_175929.2 <sup>+</sup>	KEL NM_000420.2		STK40 NM_032017.1
		KIF5B NM_004521.2		SUFU NM_016169.3 <sup>+</sup>
		KIT NM_000222.2 <sup>+</sup>		

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CBFB NM_001755.2	FGF19 NM_005117.2 <sup>+</sup>	KLF4 NM_004235.4	PIK3CB NM_006219.2 <sup>+</sup>	SUZ12 NM_015355.2
CBL NM_005188.3	FGF2 NM_002006.4 <sup>+</sup>	KLHL6 NM_130446.2	PIK3CD NM_005026.3	SYK NM_003177.5
CCND1 NM_053056.2 <sup>+</sup>	FGF23 NM_020638.2 <sup>+</sup>	KMT2B NM_014727.1	PIK3CG NM_002649.2	TBX3 NM_016569.3
CCND2 NM_001759.3	FGF3 NM_005247.2 <sup>+</sup>	KMT2C NM_170606.2	PIK3R1 NM_181523.2	ELOC NM_005648.3
CCND3 NM_001760.3 <sup>+</sup>	FGF4 NM_002007.2 <sup>+</sup>	KMT2D NM_003482.3	PIK3R2 NM_005027.3	TCF3 NM_003200.3
CCNE1 NM_001238.2 <sup>+</sup>	FGF5 NM_004464.3 <sup>+</sup>	KRAS NM_004985.3 <sup>+</sup>	PIK3R3 NM_003629.3	TCF7L2 NM_030756.4
CD274 NM_014143.3	FGF6 NM_020996.1 <sup>+</sup>	LAMP1 NM_005561.3 <sup>+</sup>	PIM1 NM_002648.3	TERC
CD276 NM_001024736.1	FGF7 NM_002009.3 <sup>+</sup>	LATS1 NM_004690.3	PLCG2 NM_002661.3	TERT NM_198253.2 <sup>+</sup>
CD74 NM_001025159.2 <sup>^</sup>	FGF8 NM_033163.3 <sup>+</sup>	LATS2 NM_014572.2	PLK2 NM_006622.3	TET1 NM_030625.2
CD79A NM_001783.3	FGF9 NM_002010.2 <sup>+</sup>	LMO1 NM_002315.2	PMAIP1 NM_021127.2	TET2 NM_001127208.2
CD79B NM_000626.2 <sup>+</sup>	FGFR1 NM_023110.2 <sup>+</sup>	LRP1B NM_018557.2	PMS1 NM_000534.4	TFE3 NM_006521.4 <sup>^</sup>
CDC73 NM_024529.4	FGFR2 NM_000141.4 <sup>^+</sup>	LYN NM_002350.3	PMS2 NM_000535.5	TFRC NM_003234.2 <sup>+</sup>
CDH1 NM_004360.3 <sup>+</sup>	FGFR3 NM_000142.4 <sup>^+</sup>	LZTR1 NM_006767.3	PNRC1 NM_006813.2	TGFB1 NM_004612.2
CDK12 NM_016507.2	FGFR4 NM_213647.1 <sup>+</sup>	MAGI2 NM_012301.3	POLD1 NM_001256849.1	TGFB2 NM_001024847.2
CDK4 NM_000075.3 <sup>+</sup>	FH NM_000143.3	MALT1 NM_006785.3	POLE NM_006231.2	TMEM127 NM_017849.3
CDK6 NM_001259.6 <sup>+</sup>	FLCN NM_144997.5	MAP2K1 NM_002755.3	PPARG NM_138712.3 <sup>^</sup>	TMPPRSS2 NM_001135099.1 <sup>^</sup>
CDK8 NM_001260.1	FLI1 NM_002017.4	MAP2K2 NM_030662.3	PPM1D NM_003620.3	TNFAIP3 NM_006290.3
CDKN1A NM_000389.4	FLT1 NM_002019.4	MAP2K4 NM_003010.3	PPP2R1A NM_014225.5	TNFRSF14 NM_003820.2
CDKN1B NM_004064.3	FLT3 NM_004119.2	MAP3K1 NM_005921.1	PPP2R2A NM_001177591.1	TOP1 NM_003286.2
CDKN2A NM_000077.4 <sup>+</sup>	FLT4 NM_182925.4	MAP3K13 NM_004721.4	PPP6C NM_001123355.1	TOP2A NM_001067.3
CDKN2B NM_004936.3 <sup>+</sup>	FOXA1 NM_004496.3	MAP3K14 NM_003954.3	PRDM1 NM_001198.3	TP53 NM_000546.5 <sup>+</sup>
CDKN2C NM_001262.2	FOXL2 NM_023067.3	MAP3K4 NM_005922.2	PREX2 NM_024870.2	TP63 NM_003722.4
CEBPA NM_004364.3	FOXO1 NM_002015.3	MAPK1 NM_002745.4	PRKAR1A NM_212472.2	TRAF2 NM_021138.3
GENPA NM_001809.3	FOXO2 NM_023067.3	MAPK3 NM_002746.2	PRKCI NM_002740.5	TRAF7 NM_032271.2 <sup>+</sup>
CHD2 NM_001271.3	FOXO3 NM_002015.3	MAX NM_002382.4	PRKDC NM_006904.6	TSC1 NM_000368.4
CHD4 NM_001273.2	FRS2 NM_001278351.1	MCL1 NM_021960.4	PRSS8 NM_002773.3	TSC2 NM_000548.3
CHEK1 NM_001114122.2 <sup>+</sup>	FUBP1 NM_003902.3 <sup>+</sup>	MDC1 NM_014641.2	PTCH1 NM_000264.3 <sup>+</sup>	TSHR NM_000369.2
CHEK2 NM_007194.3 <sup>+</sup>	FYN NM_002037.5	MDM2 NM_002392.5 <sup>+</sup>	PTEN NM_000314.4 <sup>+</sup>	U2AF1 NM_006758.2
CIC NM_015125.3 <sup>+</sup>	GABRA6 NM_000811.2	MDM4 NM_002393.4 <sup>+</sup>	PTPN11 NM_002834.3	VEGFA NM_001025366.2
CREBBP NM_004380.2	GATA1 NM_002049.3	MED12 NM_005120.2	PTPRD NM_002839.3	VHL NM_000551.3 <sup>+</sup>
CRKL NM_005207.3	GATA2 NM_032638.4	MEF2B NM_001145785.1	PTPRS NM_002850.3	VTCN1 NM_024626.3
CRLF2 NM_022148.2	GATA3 NM_001002295.1 <sup>+</sup>	MEN1 NM_130799.2	PTPRT NM_133170.3	CCN6 NM_003880.3
CSF1R NM_005211.3	GATA4 NM_002052.3	MET NM_000245.2 <sup>+</sup>	QKI NM_006775.2	WT1 NM_024426.4
CSF3R NM_156039.3	GATA6 NM_005257.4	MGA NM_001164273.1	RAB35 NM_006861.6	XIAP NM_001167.3
CSNK1A1 NM_001025105.2	GEN1 NM_182625.3	MITF NM_000248.3	RAC1 NM_018890.3	XPO1 NM_003400.3
CTCF NM_006565.3	GID4 NM_024052.4	MLH1 NM_000249.3	RAD21 NM_006265.2	XRCC2 NM_005431.1
CTLA4 NM_005214.4	GLI1 NM_005269.2	KMT2A NM_001197104.1	RAD50 NM_005732.3	YAP1 NM_001130145.2
CTNNA1 NM_001903.2	GNA11 NM_002067.2	MLL73 NM_004529.2	RAD51 NM_002875.4	YES1 NM_005433.3
CTNNA1 NM_001903.2	GNA13 NM_006572.4	MPL NM_005373.2	RAD51B NM_133509.3	ZBTB2 NM_020861.1
CUL3 NM_003590.4	GNAQ NM_002072.3	MRE11 NM_005591.3	RAD51C NM_058216.2	ZBTB7A NM_015898.2
CUX1 NM_181552.3	GNAS NM_000516.4 <sup>+</sup>	MSH2 NM_000251.2	RAD51D NM_002878.3	ZFH3X NM_006885.3
CXCR4 NM_003467.2	ADGRA2 NM_032777.9	MSH3 NM_002439.4	RAD52 NM_134424.2	ZNF217 NM_006526.2
CYLD NM_015247.2	GPS2 NM_004489.4	MSH6 NM_000179.2	RAD54L NM_001142548.1	ZNF703 NM_025069.1
DAXX NM_001141970.1	GREM1 NM_013372.6	MST1 NM_020998.3	RAF1 NM_002880.3 <sup>+</sup>	ZRSR2 NM_005089.3
DCUN1D1 NM_020640.2	GRIN2A NM_000833.3	MST1R NM_002447.2	RANBP2 NM_006267.4	MTAP NM_002451.3 <sup>^+</sup>
DDR2 NM_001014796.1	GRM3 NM_000840.2	MTOR NM_004958.3	RARA NM_000964.3	
DDX41 NM_016222.2	GSK3B NM_002093.3	MUTYH NM_001128425.1	RASA1 NM_002890.2	
DHX15 NM_001358.2	H3-3A NM_002107.4 <sup>+</sup>	MYB NM_001130173.1	RB1 NM_000321.2 <sup>+</sup>	
DICER1 NM_177438.2	H3-3B NM_005324.3		RBM10 NM_005676.4	
DIS3 NM_014953.3	H3-5 NM_001013699.2		RECQL4 NM_004260.3	
	HGF NM_000601.4		REL NM_002908.2	
	H1-2 NM_005319.3		RET NM_020975.4 <sup>^+</sup>	

<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

## 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

## Summit™ 2.0 + Vantage™ Report

number variants (CNVs), and other biomarkers such as tumor mutation burden (TMB) and microsatellite instability (MSI). Methodology involves 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). Variants are called against the human genome build reference hg19 using Summit™ Omics pipeline version 1.3.0, developed at Belay Diagnostics.

The Vantage™ MGMT Promoter Methylation Assay utilizes a quantitative PCR (qPCR) followed by high-resolution melt analysis (HRM) using the EpiMelt MGMT kit (MethylDetect) after enzymatic conversion (NEBNext Enzymatic Methyl-seq, New England Biolabs) on a portion of the library generated in the Summit™ workflow. Methylated and unmethylated melting temperature peaks are evaluated using the LightCycler® 480 Software v. 1.5.1 (Roche LifeScience). Qualitative results are reported as "Negative - Unmethylated", "Positive - Methylated", or "Indeterminate Results were equivocal". Specimens with results above the validated 25% methylated control are interpreted as "Positive". Specimens with results between unmethylated and methylated control are interpreted as "Indeterminate".

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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