

Summit™ 2.0 + Ascent™ Report

Patient Information	Provisional Diagnosis	Specimen	Physician Information
Name: John Smith DOB: 01/01/1990 Sex Assigned at Birth: Male MRN: 11xx22xx33	Diagnosis: Glioblastoma ICD10: C71.9	Type: CSF Collected: 01/01/2026 Received: 01/02/2026 Specimen ID: SumPos-AscNeg-GBM	Institution: Belay Diagnostics Referring Physician: Provider Test

RESULT SUMMARY

POSITIVE

Comments
<i>TERT</i> promoter variants are a characteristic finding in IDH-wildtype glioblastoma (GBM) (see Actionability Summary). <i>EGFR</i> and <i>PTEN</i> variants are also common in GBM; alterations of RTK genes, PI3K pathway genes, or <i>PTEN</i> are found in about 90% of cases and about 60% of tumors show evidence of activating <i>EGFR</i> alterations (PMID: 24120142, 18772890). Clinical correlation is required.

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>EGFR</i> p.G598V c.1793G>T	7.0%	No	Yes	Yes
<i>PTEN</i> p.L320S c.959T>C	0.6%	No	Yes	Yes
<i>TERT</i> c.-124C>T	0.7%	No	Yes	Yes

Copy Number Variants: None

Fusion Variants: None

Biomarkers				
Tumor Mutation Burden (TMB)			Microsatellite Instability (MSI)	
Not Detected	Low	High	Stable	High

Ascent™ Chromosome Arm Level Loss or Gain: None

VARIANTS OF UNKNOWN SIGNIFICANCE (Tier 3)

SNV/MNVs/Indels				
<i>ALK</i> K1491_G1494delinsRVHR <i>ANKRD26</i> c.3655-4_3658delinsCCAGGTTC <i>ARID1A</i> P411L <i>FGF19</i> P142Q	<i>FLT1</i> L757V <i>ICOSLG</i> V202M <i>INSR</i> G749S <i>MAP3K1</i> A156V	<i>MDC1</i> A1734T <i>MGA</i> E2172G <i>MYD88</i> A158fs <i>RAD50</i> R884H	<i>RAD51C</i> R214H <i>RECQL4</i> A413R <i>SDHA</i> E472K <i>SLX4</i> D876N	<i>TCF3</i> D474E

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Gene Level CNVs
None
Fusions
None
Ascent™ Aneuploidy Variants of Unknown Significance
None

ACTIONABILITY SUMMARY

FDA / NCCN Therapies for the Patient's Tumor Type (Tier 1A): None			
FDA / NCCN Therapies with Resistance / Decreased Response (Tier 1A): None			
Prognostic Implications per NCCN			
Biomarker	Prognostic Association	Diseases	Note
TERT c.-124 C>T	Unfavorable	Glioma	In the absence of an IDH mutation, TERT mutations in diffusely infiltrative gliomas are associated with reduced overall survival compared to gliomas lacking TERT mutations.
Diagnostic Implications per WHO			
Biomarker	Diseases	Note	
EGFR G598V	Central Nervous System Neoplasm	EGFR mutations and fusions have been observed in several central nervous system neoplasms. In glioblastoma, IDH-wildtype, about 60% of tumors show evidence of EGFR amplification, mutation, rearrangement, or altered splicing (PMID:24120142), with mutations/fusions often co-occurring with amplification. EGFR gene fusions are observed in 6-13% of cases, typically as part of complex rearrangements at chromosome band 7p11.2 (PMID: 24120142). Fusion partners are mostly neighboring genes of EGFR (e.g. SEPTIN14, PSPH, SEC61G, SDK1). EGFR mutations also define an EGFR-mutant sub-type of diffuse midline glioma, H3 K27-altered. Within EGFR-mutant DMG, most tumors harbor small in-frame insertions/duplications within exon 20, which encodes the intracellular tyrosine kinase domain, whereas others harbor missense mutations in exons encoding parts of the extracellular domain, most commonly p.A289T or p.A289V. EGFR mutations have also been observed in diffuse pediatric-type high-grade glioma, H3-wildtype and IDH-wildtype.	
PTEN L320S	Central Nervous System Neoplasm	Among central nervous system neoplasms, PTEN alterations are common in glioblastoma, IDH-wildtype, in which alterations of RTK genes, PI3K pathway genes, and PTEN are found in about 90% of cases (PMID: 24120142; PMID: 18772890), and PTEN in particular shows mutation/deletion in about 40% of glioblastomas (PMID: 24120142). Germline PTEN mutations are a desirable diagnostic criterion in the diagnosis of dysplastic cerebellar gangliocytoma, a pathognomonic feature of Cowden syndrome. Germline PTEN mutations occur in 25%-85% of cases of Cowden syndrome (PMID:9140396; PMID:9467011; PMID:12844284). Genetic alterations of PTEN have also been reported in cases of papillary tumors of the pineal region (PMID:25003235).	
TERT c.-124C>T	Central Nervous System Neoplasm	Among central nervous system neoplasms, TERT promoter mutation is an essential diagnostic criteria for glioblastoma, IDH-wildtype. In oligodendroglioma, IDH-mutant and 1p/19q-codeleted, TERT promoter mutation is desirable for the diagnosis. Additionally, TERT promoter mutation is also observed in diffuse midline glioma, H3 K27-altered (PMID: 28966033; PMID: 29763623), diffuse pediatric-type high-grade glioma, H3-wildtype and IDH-wildtype (~64% of cases) (PMID: 2840133), high-grade astrocytoma with piloid features (2 [3%] of 74, both C228T mutations) (PMID:29564591), medulloblastoma, SHH-activated and TP53-wildtype, and meningioma. In pleomorphic xanthoastrocytoma, TERT promoter mutation and less frequently TERT amplifications have been identified (PMID: 24154961; PMID: 30240866; PMID: 30051528; PMID: 32619305).	

CLINICAL TRIALS / INVESTIGATIONAL THERAPIES

EGFR G598V			
Therapy	Clinical Trial	Location/Sponsor	
BDTX-1535 + temozolomide	NCT07326566 (Phase 2) Study of Silevertinib With Temozolomide for the Treatment of Newly Diagnosed GBM With Unmethylated MGMT and EGFRvIII	Pittsburgh, Pennsylvania Black Diamond Therapeutics, Inc. blackdiamondtx@careboxhealth.com	 https://genomoncology.wetrials.com/v1/NCT07326566

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ERAS-801 + surgery	NCT07089641 (Phase 1) ERAS-801 for the Treatment of Resectable and Progressive or Recurrent IDH Wildtype Grade IV Glioblastoma or Astrocytoma With an EGFR Amplification or Mutation, ERAS801-SARG Trial	Los Angeles, California Jonsson Comprehensive Cancer Center QuanLi@mednet.ucla.edu	 https://genomoncology.wetria.com/v1/NCT07089641
KQB198	NCT06507306 (Phase 1) A Study to Investigate the Safety and Efficacy of KQB198 as Monotherapy and in Combination in Participants With Advanced Solid Malignancies	Denver, Colorado Kumquat Biosciences Inc. kumquatstudies@kumquatbio.com	 https://genomoncology.wetria.com/v1/NCT06507306
MK-0472; MK-0472 + pembrolizumab; MK-0472 + calderasib	NCT05853367 (Phase 1) Study of MK-0472 in Participants With Advanced /Metastatic Solid Tumors (MK-0472-001)	Chicago, Illinois Merck Sharp & Dohme LLC Trialsites@msd.com	 https://genomoncology.wetria.com/v1/NCT05853367
verteporfin	NCT04590664 (Phase 1/Phase 2) Verteporfin for the Treatment of Recurrent High Grade EGFR-Mutated Glioblastoma	Atlanta, Georgia Emory University william.l.read@emory.edu	 https://genomoncology.wetria.com/v1/NCT04590664

PTEN L320S			
Therapy	Clinical Trial	Location/Sponsor	
EIS-12656; EIS-12656 + olaparib; EIS-12656 + fam-trastuzumab deruxtecan	NCT06525298 (Phase 1/Phase 2) EIS-12656 as Single Agent and in Combination in Patients With Specified Solid Tumors	Houston, Texas Eisbach Bio GmbH adrian@eisbach.bio	 https://genomoncology.wetria.com/v1/NCT06525298
ISM3091; ISM3091 + olaparib	NCT05932862 (Phase 1) A Phase 1 Study of XL309 (ISM3091) Alone and in Combination in Participants With Advanced Solid Tumors	Jacksonville, Florida Exelixis druginfo@exelixis.com	 https://genomoncology.wetria.com/v1/NCT05932862
dostarlimab + niraparib	NCT05700721 (Phase 2) Phase II Trial of the PARP Inhibitor Niraparib and PD-1 Inhibitor Dostarlimab in Patients With Advanced Cancers With Active Progressing Brain Metastases (STARLET)	Houston, Texas M.D. Anderson Cancer Center tyap@mdanderson.org	 https://genomoncology.wetria.com/v1/NCT05700721
everolimus + ribociclib	NCT05843253 (Phase 2) Study of Ribociclib and Everolimus in HGG and DIPG or Ribociclib and Temozolomide in DHG, H3G34-mutant	Washington D.C., District of Columbia Nationwide Children's Hospital kelsey.troyer@nationwidechildrens.org	 https://genomoncology.wetria.com/v1/NCT05843253

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temsirolimus	NCT05773326 (Early Phase 1) Superselective Intra-arterial Cerebral Infusion of Temsirolimus in HGG	Phoenix, Arizona Nader Sanai research@ivybraintumorcenter.org	 https://genomoncology.wetria.com/v1/NCT05773326
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TERT c.-124C>T			
Therapy	Clinical Trial	Location/Sponsor	
bevacizumab + temozolomide + radiation therapy; temozolomide + radiation therapy	NCT05271240 (Phase 3) Repeated Superselective Intraarterial Cerebral Infusion (SIACI) of Bevacizumab With Temozolomide and Radiation Compared to Temozolomide and Radiation Alone in Newly Diagnosed GBM	New York, New York Northwell Health jboockvar@northwell.edu	 https://genomoncology.wetria.com/v1/NCT05271240
pembrolizumab + olaparib + temozolomide	NCT05463848 (Phase 2) Surgical Pembro +/- Olaparib w TMZ for rGBM	Boston, Massachusetts L. Nicolas Gonzalez Castro, MD, PhD lgonzalez-castro@partners.org	 https://genomoncology.wetria.com/v1/NCT05463848

TIER 1A THERAPY DETAILS

None

TEST DETAILS

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PANEL CONTENT AND REPORTING TRANSCRIPTS				
ABL1 NM_005157.4 [^] ABL2 NM_007314.3 ACVR1 NM_001105.4 ACVR1B NM_020328.3 AKT1 NM_001014432.1 ⁺ AKT2 NM_001626.4 ⁺ AKT3 NM_005465.4 ALK NM_004304.4 ^{^+} ANKRD11 NM_001256182.1 ANKRD26 NM_014915.2 APC NM_000038.5 ⁺ AR NM_000044.3 ⁺ ARAF NM_001654.4 ARFRP1 NM_003224.4 ARID1A NM_006015.4 ARID1B NM_020732.3 ARID2 NM_152641.2 ARID5B NM_032199.2 ASXL1 NM_015338.5 ASXL2 NM_018263.4 ATM NM_000051.3 ⁺ ATR NM_001184.3 ATRX NM_000489.3 ⁺ AURKA NM_198433.1 AURKB NM_004217.3	DNAJB1 NM_006145.1 DNMT1 NM_001130823.1 DNMT3A NM_022552.4 DNMT3B NM_006892.3 DOT1L NM_032482.2 E2F3 NM_001949.4 EED NM_003797.3 EGFL7 NM_016215.4 EGFR NM_005228.3 ^{^+} EIF1AX NM_001412.3 EIF4A2 NM_001967.3 EIF4E NM_001130679.1 EML4 NM_019063.3 EP300 NM_001429.3 EPCAM NM_002354.2 EPHA3 NM_005233.5 EPHA5 NM_004439.5 EPHA7 NM_004440.3 EPHB1 NM_004441.4 ERBB2 NM_004448.2 ⁺ ERBB3 NM_001982.3 ⁺ ERBB4 NM_005235.2 ⁺ ERCC1 NM_001983.3 ⁺ ERCC2 NM_000400.3 ⁺ ERCC3 NM_000122.1 ERCC4 NM_005236.2	H2BC5 NM_021063.3 H3C1 NM_003529.2 H3C2 NM_003537.3 H3C3 NM_003531.2 ⁺ H3C4 NM_003530.4 H3C6 NM_003532.2 H3C7 NM_021018.2 H3C8 NM_003534.2 H3C10 NM_003536.2 H3C11 NM_003533.2 H3C12 NM_003535.2 H3C15 NM_001005464.2 H3C14 NM_021059.2 H3C13 NM_001123375.2 H3-4 NM_003493.2 HLA-A NM_002116.7 HLA-B NM_005514.6 HLA-C NM_002117.5 HNF1A NM_000545.5 HNRNP NM_002140.3 HOXB13 NM_006361.5 HRAS NM_005343.2 ⁺ HSD3B1 NM_000862.2 HSP90A1 NM_001017963.2 ICOSLG NM_015259.4 ID3 NM_002167.4 IDH1 NM_005896.2 ⁺	MYC NM_002467.4 ⁺ MYCL NM_001033082.2 ⁺ MYCN NM_005378.4 ⁺ MYD88 NM_002468.4 ⁺ MYOD1 NM_002478.4 [^] NAB2 NM_005967.3 NBN NM_002485.4 NCOA3 NM_181659.2 NCOR1 NM_006311.3 NEGR1 NM_173808.2 NF1 NM_001042492.2 ⁺ NF2 NM_000268.3 ⁺ NFE2L2 NM_006164.4 ⁺ NFKB1A NM_020529.2 NKX2-1 NM_001079668.2 NKX3-1 NM_006167.3 NOTCH1 NM_017617.3 NOTCH2 NM_024408.3 NOTCH3 NM_000435.2 NOTCH4 NM_004557.3 NPM1 NM_002520.6 NRAS NM_002524.4 ⁺ NRG1 NM_013964.3 ⁺ NSD1 NM_022455.4	COP1 NM_022457.5 RHEB NM_005614.3 RHOA NM_001664.2 RICTOR NM_152756.3 ⁺ RIT1 NM_006912.5 RNF43 NM_017763.4 [^] ROS1 NM_002944.2 RPS6KA4 NM_003942.2 RPS6KB1 NM_003161.3 ⁺ RPS6KB2 NM_003952.2 RPTOR NM_020761.2 RUNX1 NM_001754.4 RUNX1T1 NM_175635.2 RYBP NM_012234.5 SDHA NM_004168.2 SDHAF2 NM_017841.2 SDHB NM_003000.2 SDHC NM_003001.3 SDHD NM_003002.3 SETBP1 NM_015559.2 SETD2 NM_014159.6 ⁺ SF3B1 NM_012433.2 SH2B3 NM_005475.2 SH2D1A NM_002351.4 SHQ1 NM_018130.2 SLIT2 NM_004787.1 SLX4 NM_032444.2

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AXIN1 NM_003502.3	ERCC5 NM_000123.3	IDH2 NM_002168.2 ⁺	NTRK1 NM_002529.3 [^]	SMAD2 NM_005901.5
AXIN2 NM_004655.3	ERG NM_001136154.1	IGF1 NM_001111283.1	NTRK2 NM_006180.3 [^]	SMAD3 NM_005902.3
AXL NM_021913.4	ERRF1 NM_018948.3	IGF1R NM_000875.3	NTRK3 NM_001012338.2	SMAD4 NM_005359.5 ⁺
B2M NM_004048.2	ESR1 NM_001122742.1 ⁺	IGF2 NM_001127598.1	NUP93 NM_014669.4	SMARCA4 NM_001128849.1 ⁺
BAP1 NM_004656.3	ETS1 NM_001143820.1	IKBKE NM_014002.3	NUTM1 NM_175741.1 [^]	SMARCB1 NM_003073.3 ⁺
BARD1 NM_000465.2	ETV1 NM_004956.4 [^]	IKZF1 NM_006060.4	PAK1 NM_001128620.1	SMARCD1 NM_003076.4
BBC3 NM_001127240.2	ETV4 NM_001079675.2 [^]	IL10 NM_000572.2	PAK3 NM_002578.3	SMC1A NM_006306.3
BCL10 NM_003921.4	ETV5 NM_004454.2 [^]	IL7R NM_002185.3	PAK5 NM_020341.3	SMC3 NM_005445.3
BCL2 NM_000633.2	ETV6 NM_001987.4 [^]	INHBA NM_002191.3	PALB2 NM_024675.3	SMO NM_005631.4 ⁺
BCL2L1 NM_138578.1	EWSR1 NM_013986.3 [^]	INPP4A NM_001134224.1	PRKN NM_004562.2	SNCAP NM_005460.2
BCL2L2 NM_001199839.1	EZH2 NM_004456.4	INPP4B NM_003866.2	PARP1 NM_001618.3 [^]	SOCS1 NM_003745.1
BCL6 NM_001706.4	AMER1 NM_152424.3	INSR NM_000208.2	PAX3 NM_181457.3 [^]	SOX10 NM_006941.3
BCOR NM_001123385.1	ABRAXAS1 NM_139076.2	IRF2 NM_002199.3	PAX5 NM_016734.2	SOX17 NM_022454.3
BCORL1 NM_021946.4	TENT5C NM_017709.3	IRF4 NM_002460.3	PAX7 NM_001135254.1 [^]	SOX2 NM_003106.3
BCR NM_004327.3 [^]	FANCA NM_000135.2	IRS1 NM_005544.2	PAX8 NM_013953.3 [^]	SOX9 NM_000346.3
BIRC3 NM_001165.4	FANCC NM_000136.2	IRS2 NM_003749.2	PBRM1 NM_018313.4	SPEN NM_015001.2
BLM NM_000057.2	FANCD2 NM_033084.3	JAK1 NM_002227.2	PDCD1 NM_005018.2	SPOP NM_001007228.1
BMPR1A NM_004329.2	FANCE NM_021922.2	JAK2 NM_004972.3 ⁺	PDCD1LG2 NM_025239.3	SPTA1 NM_003126.2
BRAF NM_004333.4 ^{^+}	FANCF NM_022725.3	JAK3 NM_000215.3	PDGFRA NM_006206.4 ⁺	SRC NM_198291.2
BRCA1 NM_007294.3 ⁺	FANCG NM_004629.1	JUN NM_002228.3	PDGFRB NM_002609.3 ⁺	SRSF2 NM_003016.4
BRCA2 NM_000059.3 ⁺	FANCI NM_001113378.1	KAT6A NM_006766.3	PDK1 NM_001278549.1	STAG1 NM_005862.2
BRD4 NM_058243.2	FANCL NM_001114636.1	KDM5A NM_001042603.1	PDPK1 NM_002613.4	STAG2 NM_001042749.1
BRIP1 NM_032043.2	FAS NM_000043.4	KDM5C NM_004187.3	PGR NM_000926.4	STAT3 NM_139276.2
BTG1 NM_001731.2	FAT1 NM_005245.3	KDM6A NM_021140.2	PHF6 NM_032458.2	STAT4 NM_003151.3
BTX NM_000061.2	FBXW7 NM_033632.3 ⁺	KDR NM_002253.2	PHOX2B NM_003924.3	STAT5A NM_003152.3
EMSY NM_020193.3	FGF1 NM_001144934.1 ⁺	KEAP1 NM_012289.3	PIK3C2B NM_002646.3	STAT5B NM_012448.3
CALR NM_004343.3	FGF10 NM_004465.1 ⁺	KEL NM_000420.2	PIK3C2G NM_004570.4	STK11 NM_000455.4
CARD11 NM_032415.4	FGF14 NM_175929.2 ⁺	KIF5B NM_004521.2	PIK3C3 NM_002647.2	STK40 NM_032017.1
CASP8 NM_001228.4	FGF19 NM_005117.2 ⁺	KIT NM_000222.2 ⁺	PIK3CA NM_006218.2 ⁺	SUFU NM_016169.3 ⁺
CBFB NM_001755.2	FGF2 NM_002006.4 ⁺	KLF4 NM_004235.4	PIK3CB NM_006219.2 ⁺	SUZ12 NM_015355.2
CBL NM_005188.3	FGF23 NM_020638.2 ⁺	KLHL6 NM_130446.2	PIK3CD NM_005026.3	SYK NM_003177.5
CCND1 NM_053056.2 ⁺	FGF3 NM_005247.2 ⁺	KMT2B NM_014727.1	PIK3CG NM_002649.2	TBX3 NM_016569.3
CCND2 NM_001759.3	FGF4 NM_002007.2 ⁺	KMT2C NM_170606.2	PIK3R1 NM_181523.2	ELOC NM_005648.3
CCND3 NM_001760.3 ⁺	FGF5 NM_004464.3 ⁺	KMT2D NM_003482.3	PIK3R2 NM_005027.3	TCF3 NM_003200.3
CCNE1 NM_001238.2 ⁺	FGF6 NM_020996.1 ⁺	KRAS NM_004985.3 ⁺	PIK3R3 NM_003629.3	TCF7L2 NM_030756.4
CD274 NM_014143.3	FGF7 NM_002009.3 ⁺	LAMP1 NM_005561.3 ⁺	PIM1 NM_002648.3	TERC
CD276 NM_001024736.1	FGF8 NM_033163.3 ⁺	LATS1 NM_004690.3	PLCG2 NM_002661.3	TERT NM_198253.2 ⁺
CD74 NM_001025159.2 [^]	FGF9 NM_002010.2 ⁺	LATS2 NM_014572.2	PLK2 NM_006622.3	TET1 NM_030625.2
CD79A NM_001783.3	FGFR1 NM_023110.2 ⁺	LMO1 NM_002315.2	PMAIP1 NM_021127.2	TET2 NM_001127208.2
CD79B NM_000626.2 ⁺	FGFR2 NM_000141.4 ^{^+}	LRP1B NM_018557.2	PMS1 NM_000534.4	TFE3 NM_006521.4 [^]
CDC73 NM_024529.4	FGFR3 NM_000142.4 ^{^+}	LYN NM_002350.3	PMS2 NM_000535.5	TFRC NM_003234.2 ⁺
CDH1 NM_004360.3 ⁺	FGFR4 NM_213647.1 ⁺	LZTR1 NM_006767.3	PNRC1 NM_006813.2	TGFBF1 NM_004612.2
CDK12 NM_016507.2	FH NM_000143.3	MAGI2 NM_012301.3	POLD1 NM_001256849.1	TGFBF2 NM_001024847.2
CDK4 NM_000075.3 ⁺	FLCN NM_144997.5	MALT1 NM_006785.3	POLE NM_006231.2	TMEM127 NM_017849.3
CDK6 NM_001259.6 ⁺	FLI1 NM_002017.4	MAP2K1 NM_002755.3	PPARG NM_138712.3 [^]	TMPPRSS2 NM_001135099.1 [^]
CDK8 NM_001260.1	FLT1 NM_002019.4	MAP2K2 NM_030662.3	PPM1D NM_003620.3	TNFAIP3 NM_006290.3
CDKN1A NM_000389.4	FLT3 NM_004119.2	MAP2K4 NM_003010.3	PPP2R1A NM_014225.5	TNFRSF14 NM_003820.2
CDKN1B NM_004064.3	FLT4 NM_182925.4	MAP3K1 NM_005921.1	PPP2R2A NM_001177591.1	TOP1 NM_003286.2
CDKN2A NM_000077.4 ⁺	FOXA1 NM_004496.3	MAP3K13 NM_004721.4	PPP6C NM_001123355.1	TOP2A NM_001067.3
CDKN2B NM_004936.3 ⁺	FOXO1 NM_002015.3	MAP3K4 NM_005922.2	PRDM1 NM_001198.3	TP53 NM_000546.5 ⁺
CDKN2C NM_001262.2	FOXO2 NM_023067.3	MAPK1 NM_002745.4	PREX2 NM_024870.2	TP63 NM_003722.4
CEBPA NM_004364.3	FOXO3 NM_032682.5	MAPK3 NM_002746.2	PRKAR1A NM_212472.2	TRAF2 NM_021138.3
CENPA NM_001809.3	FRS2 NM_001278351.1	MAX NM_002382.4	PRKDC NM_006904.6	TRAF7 NM_032271.2 ⁺
CHD2 NM_001271.3	FUBP1 NM_003902.3 ⁺	MCL1 NM_021960.4	PRSS8 NM_002773.3	TSC1 NM_000368.4
CHD4 NM_001273.2	FYN NM_002037.5	MDC1 NM_014641.2	PTCH1 NM_000264.3 ⁺	TSC2 NM_000548.3
CHEK1 NM_001114122.2 ⁺	GABRA6 NM_000811.2	MDM2 NM_002392.5 ⁺	PTEN NM_000314.4 ⁺	TSHR NM_000369.2
CHEK2 NM_007194.3 ⁺	GATA1 NM_002049.3	MDM4 NM_002393.4 ⁺	PTPN11 NM_002834.3	U2AF1 NM_006758.2
CIC NM_015125.3 ⁺	GATA2 NM_032638.4	MED12 NM_005120.2	PTPRD NM_002839.3	VEGFA NM_001025366.2
CREBBP NM_004380.2		MEF2B NM_001145785.1	PTPRS NM_002850.3	VHL NM_000551.3 ⁺
		MEN1 NM_130799.2	PTPRT NM_133170.3	VTGN1 NM_024626.3
		MET NM_000245.2 ⁺	QKI NM_006775.2	CCN6 NM_003880.3
		MGA NM_001164273.1		WT1 NM_024426.4

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CRKL NM_005207.3	GATA3 NM_001002295.1 ⁺	MITF NM_000248.3	RAB35 NM_006861.6	XIAP NM_001167.3
CRLF2 NM_022148.2	GATA4 NM_002052.3	MLH1 NM_000249.3	RAC1 NM_018890.3	XPO1 NM_003400.3
CSF1R NM_005211.3	GATA6 NM_005257.4	KMT2A NM_001197104.1	RAD21 NM_006265.2	XRCC2 NM_005431.1
CSF3R NM_156039.3	GEN1 NM_182625.3	MLL73 NM_004529.2	RAD50 NM_005732.3	YAP1 NM_001130145.2
CSNK1A1 NM_001025105.2	GID4 NM_024052.4	MPL NM_005373.2	RAD51 NM_002875.4	YES1 NM_005433.3
CTCF NM_006565.3	GLI1 NM_005269.2	MRE11 NM_005591.3	RAD51B NM_133509.3	ZBTB2 NM_020861.1
CTLA4 NM_005214.4	GNA11 NM_002067.2	MSH2 NM_000251.2	RAD51C NM_058216.2	ZBTB7A NM_015898.2
CTNNA1 NM_001903.2	GNA13 NM_006572.4	MSH3 NM_002439.4	RAD51D NM_002878.3	ZFHX3 NM_006885.3
CTNNB1 NM_001904.3 ⁺	GNAQ NM_002072.3	MSH6 NM_000179.2	RAD52 NM_134424.2	ZNF217 NM_006526.2
CUL3 NM_003590.4	GNAS NM_000516.4 ⁺	MST1 NM_020998.3	RAD54L NM_001142548.1	ZNF703 NM_025069.1
CUX1 NM_181552.3	ADGRA2 NM_032777.9	MST1R NM_002447.2	RAF1 NM_002880.3 ⁺	ZRSR2 NM_005089.3
CXCR4 NM_003467.2	GPS2 NM_004489.4	MTOR NM_004958.3	RANBP2 NM_006267.4	MTAP NM_002451.3 ⁺
CYLD NM_015247.2	GREM1 NM_013372.6	MUTYH NM_001128425.1	RARA NM_000964.3	
DAXX NM_001141970.1	GRIN2A NM_000833.3	MYB NM_001130173.1	RASA1 NM_002890.2	
DCUN1D1 NM_020640.2	GRM3 NM_000840.2		RB1 NM_000321.2 ⁺	
DDR2 NM_001014796.1	GSK3B NM_002093.3		RBM10 NM_005676.4	
DDX41 NM_016222.2	H3-3A NM_002107.4 ⁺		RECQL4 NM_004260.3	
DHX15 NM_001358.2	H3-3B NM_005324.3		REL NM_002908.2	
DICER1 NM_177438.2	H3-5 NM_001013699.2		RET NM_020975.4 ^{^+}	
DIS3 NM_014953.3	HGF NM_000601.4			
	H1-2 NM_005319.3			

⁺Summit™ also reports fusion events for this gene

⁺Summit™ also reports copy number alterations for this gene

*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 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 ≥ 2 -fold change for amplifications and ≤ 0.5 -fold change for deletions, and for fusions was determined to be ≥ 2 supporting reads. Reporting thresholds for TMB and MSI are: < 10 Mut/Mb (TMB low), ≥ 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 $> 0.1 \times$ 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 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

Summit™ 2.0 + Ascent™ Report

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)

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WHO: World Health Organization Classification of Tumours online (tumourclassification.iarc.who.int)

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