

Belay Summit™

Tumor-derived DNA in CSF

BELAY
DIAGNOSTICS

Summit detects gene level variants and chromosome arm level alterations from tumor-derived DNA (tDNA) in CSF to help inform the diagnosis and management of primary and secondary CNS malignancies.

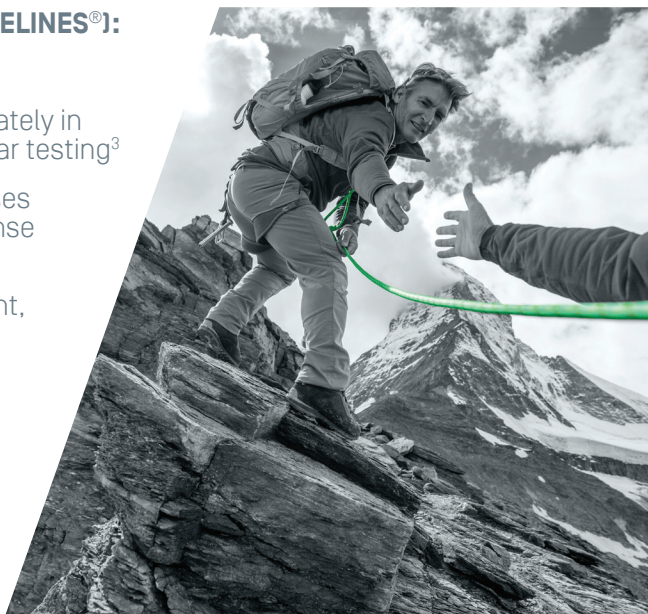
Next-generation
sequencing of
tDNA in CSF

WHY CHOOSE BELAY SUMMIT?

- 1 Molecular characterization can markedly enhance diagnostic accuracy, tumor classification, predictive prognosis, and treatment selection¹
- 2 CNS metastasis can have different molecular profiles than the primary tumors with distinct targetable mutations, due to clonal evolution during neoplasm migration²
- 3 Genomic abnormalities associated with CNS cancers can be detected prior to performing resections or biopsies that impose clinical risk

PER NCCN CLINICAL PRACTICE GUIDELINES IN ONCOLOGY (NCCN GUIDELINES®):

- 1 NGS is the preferred method for pathologic workup of CNS tumors³
- 2 Histologically similar CNS neoplasms can be differentiated more accurately in terms of prognosis and in response to different therapies with molecular testing³
- 3 Assessment of circulating tumor DNA or circulating tumor cells increases sensitivity of tumor cell detection and assessment of treatment response specifically in leptomeningeal disease³
- 4 CSF analysis should include flow cytometry, CSF cytology, and cell count, and may consider gene rearrangements, and CSF-tDNA in primary CNS lymphoma³
- 5 When available, CSF-tDNA testing can be considered with CSF cytology to increase sensitivity of tumor cell detection and assessment of residual disease after surgery in adult medulloblastoma. Additionally, molecular profiling to identify clinically relevant subtypes is recommended to encourage opportunities for clinical trial.³



Summit Clinical Sensitivity [n=124]⁴

Samples are tissue biopsy matched or have definitive diagnosis

Sensitivity **90%**

Specificity **95%**

Sensitivity

| | | |
|-----------------------------|--|------------|
| Metastatic Cancer (n=19) | Lung [7], Breast [5], Lymphatic (DLBCL) [4], Colon [1], Skin [1], Cancer of Unknown Primary [1] | 94% |
| Glioma (n=13) | Diffuse Midline Glioma [7], High Grade Glioma [6] | 92% |
| Glioblastoma (n=18) | GBM Astrocytoma Grade 4 [18] | 90% |
| Medulloblastoma (n=7) | Medulloblastoma [7] | 86% |
| Astrocytoma (n=6) | Astrocytoma Grade 3 [6] | 83% |
| Other (n=6) | Malignant Brain Neoplasm [2], Pineoblastoma [1], Rhabdosarcoma [1], High Grade Pineal Parenchymal Tumor [1], Mass in Pineal region [1] | 83% |

Traditional CNS tumor detection options have limitations

CSF CYTOLOGY

- Low sensitivity
- Excludes genomic data

CNS IMAGING

- Lacks specificity in differentiating cancer from inflammatory or non-neoplastic conditions
- Lacks personalized molecular data

BRAIN BIOPSY

- Highly invasive, risk of hemorrhage, neurological injury, stroke, death
- Nondiagnostic in 10-17% of cases^{5,6}
- Significant inter and intra-tumoral heterogeneity
- Biopsy infeasible: brain stem, spinal cord, optic pathway, diffuse midline gliomas, comorbidities



Summit also detects chromosome alterations associated with CNS tumors

| CHROMOSOME ARM LEVEL LOSS AND GAIN | | | | | | | | | |
|------------------------------------|----------------------------------|----------------------------------|----------------------------------|------------------------------------|--------------------------------------|--------------------------------------|--------------------------------------|--------------------------------------|----------------------------|
| chr1p chr1q chr2p chr2q | chr3p chr3q chr4p chr4q | chr5p chr5q chr6p chr6q | chr7p chr7q chr8p chr8q | chr9p chr9q chr10p chr10q | chr11p chr11q chr12p chr12q | chr13q chr14q chr15q chr16p | chr16q chr17p chr17q chr18p | chr18q chr19p chr19q chr20p | chr20q chr21q chr22q |

Hotspots/regions covered by Summit [SNVs, MNVs, Indels]

| <i>AKT1</i> | <i>APC</i> | <i>BRAF</i> | <i>CD79B</i> | <i>CDH1</i> | <i>CDKN2A</i> | <i>CTNNB1</i> | <i>EGFR</i> |
|---|---|--|---------------------------------|--|--|-------------------------|--|
| E17K/* L52R/H | exon 6 exon 7 exon 9 exon 12 exon 16 | V600E/M/K | X185sp Y197H/C/D/F/N/S | Q23* R63* | exons 2-3 | codons 23-71 K335I/T | G719A/C/S codons 745-759 T790M/T L861Q L858R |
| <i>ERBB2</i> | <i>ERBB3</i> | <i>ERCC2</i> | <i>FBXW7</i> | <i>FGFR2</i> | <i>FGFR3</i> | <i>FUS</i> | <i>GATA3</i> |
| S310F/Y R678Q/W I767M D769Y/H codons 772-780 V842I T862A L869R | V140M/L N126K/I | exon 8 exon 23 | R367P/* R505C/G R658*/Q | S252W P253R/L | R248C S249C | exon 6 | M293K/R |
| <i>GNAS</i> | <i>H3F3A</i> [†] | <i>HRAS</i> | <i>IDH1</i> | <i>IDH2</i> | <i>KRAS</i> | <i>MYD88</i> | <i>NFE2L2</i> |
| R201H/C | K28M/R G35R/V/W | G12D/S/C G13R/V/D A59T/G Q61R/K/L | R132H/C/G | R140Q/W/L R172K/G/S | G12D/V/C/R/A/S G13D/C A59T/G Q61H/R/L/ K K117N | L265P | codons 21-42 codons 73-87 |
| <i>NRAS</i> | <i>PIK3CA</i> | <i>PTEN</i> | <i>RAF1</i> | <i>SMAD4</i> | <i>TERT</i> | <i>TP53</i> | <i>VHL</i> |
| G12D/C/S/A/V G13R/D/S/ C A59T/G Q61R/K/L/ H | N345K C420R E542K E545K Q546K/R/P H1047R/L | exon 1 exon 5 exon 7 | S257L/W S259F/P P261L/S/T | codons 351-353 codons 355-356 codons 357-377 | Promoter [-124 bp,-146 bp upstream of translation start site; C228T, C250T] | exon 2 exons 4-11 | exons 1-3 |

*Nonsense variant † Also referred to as *H3-3A*; variants in this gene shown on this table are based on latest nomenclature. Legacy variants are *K27M* and *G34R*.
SNV = single nucleotide variant MNV = multi nucleotide variant Indel = insertions and deletions sp = splice variant

| COPY NUMBER VARIANTS (CNVs) | | | |
|-----------------------------|--------------------------|----------------------------|----------------------------|
| <i>ERBB2</i> [HER2] | <i>EGFR</i> [‡] | <i>CDKN2A</i> [‡] | <i>CDKN2B</i> [‡] |

[‡] In development

Assay specifications

| | |
|------------------------------------|---|
| Sample Requirements | ≥ 6 mL of CSF. A sample <6 mL of CSF will be processed and results reported provided the sample meets established reporting thresholds |
| Transport Container | Standard CSF collection tube used at point of collection |
| Shipping and Transport Temperature | Sample should be collected and placed in shipping box: <ol style="list-style-type: none"> 1. Ship at room temperature within 24 hours of collection and send priority overnight OR 2. Collect and store refrigerated at 4°C for up to 3 days post collection and ship at room temperature priority overnight OR 3. Store frozen at -80°C (no time limit) within 2-4 hours of collection and ship on dry ice priority overnight |
| Methodology | Next-generation sequencing |
| Orders & Results | Include test requisition in shipping kit or fax form to 800-501-9246. Test results available via fax, encrypted email, or Belay portal. |
| Turnaround Time | Average 7-10 days from receipt of specimen |

References: **1.** Park SH, Won J, Kim SI, Lee Y, Park CK, Kim SK, Choi SH. Molecular Testing of Brain Tumor. J Pathol Transl Med. 2017 May;51(3):205-223. doi: 10.4132/jptm.2017.03.08. Epub 2017 May 12. PMID: 28535583; PMCID: PMC5445205. **2.** Shen E, Van Swearingen AED, Price MJ, Bulsara K, Verhaak RGW, Baëta C, Painter BD, Reitman ZJ, Salama AKS, Clarke JM, Anders CK, Fecci PE, Goodwin CR, Walsh KM. A Need for More Molecular Profiling in Brain Metastases. Front Oncol. 2022 Jan 25;11:785064. doi: 10.3389/fonc.2021.785064. PMID: 35145903; PMCID: PMC8821807. **3.** Referenced with permission from the NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines®) for Central Nervous System Cancers V.1.2025. © National Comprehensive Cancer Network, Inc. 2025. All rights reserved. Accessed June 23, 2025. To view the most recent and complete version of the guideline, go online to NCCN.org. **4.** DOI: 10.1016/j.jmoldx.2025.03.010 **5.** Bander, E.D., Jones, S.H., Pisapia, D. et al. Tubular brain tumor biopsy improves diagnostic yield for subcortical lesions. J Neurooncol 141, 121–129 (2019). <https://doi.org/10.1007/s11060-018-03014-w> **6.** Malone H, Yang J, Hershman DL, Wright JD, Bruce JN, Neugut AI. Complications Following Stereotactic Needle Biopsy of Intracranial Tumors. World Neurosurg. 2015;84(4):1084-1089. doi:10.1016/j.wneu.2015.05.025

This test was developed, and its performance characteristics determined by Belay Diagnostics, which is certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA) as qualified to perform high complexity clinical testing. It has not been cleared or approved by the U.S. Food and Drug Administration (FDA). This test may be used for clinical purposes.

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