

Accession Number: S26-1234567

Report Date: 16 Jul 2026

1 of 7

Molecular Pathology Report

Report Status: Final

CellSight™ DNA

CellSight™ DNA is a 517-gene next-generation sequencing assay that profiles DNA from intact circulating tumor cells (CTCs), reporting SNVs, indels, copy number variants, TMB, and MSI from a single blood draw.

Patient Demographics

Patient Information	Specimen Information	Client Information
Patient Name: John Doe	Accession Number: S26-1234567	Client Name: Sample Hospital
DOB: 1/1/1955	Sample Type: Peripheral Blood	Client ID: 1499
Biological Sex: M	Date Collected: 7/10/2026	Client Address: 1234 Sample Street Unit 12344 Sample City, FL 33928
Race: White	Date Received: 7/11/2026	Client Phone: 239-444-4444
Ethnicity: Hispanic or Latino	Date Reported: 7/15/2026	Provider Name: Justin White, MD, PhD
		Provider NPI: 123456789

Sample Cancer Type: Colon Cancer

5 Relevant Biomarkers

5 Therapies Available

16 Clinical Trials

Relevant Biomarkers

Tier	Genomic Alteration	Relevant Therapies (In this cancer type)	Relevant Therapies (In other cancer type)	Clinical Trials
IIC	<i>PIK3CA G118D</i> Allele Frequency: 54.68%	None*	inavolisib + palbociclib + hormone therapy ^{1/1}	4
IIC	<i>Microsatellite stable</i>	None*	None*	12
	<i>KRAS wild type</i>	cetuximab ¹ cetuximab + chemotherapy ¹ panitumumab ¹ panitumumab + chemotherapy ¹	-	-

* Public data sources included in relevant therapies: FDA¹, NCCN

* Public data sources included in prognostic and diagnostic significance: NCCN

Line of therapy: I: First-line therapy, II+: Other line of therapy

Tier Reference: Li et al. *Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists.* J Mol Diagn. 2017 Jan;19(1):4-23.

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Cancer Cell Diagnostics, Inc. | 555 Heritage Drive, Suite 114, Jupiter, FL 33458 | CLIA #10D2312417 | Medical Director: Frank Yang, MD, PhD

Electronically Signed By Kyle Dunn on 16 Jul 2026 07:40 PM

Disclaimer: The data presented here are from a curated knowledge base of publicly available information, but may not be exhaustive. The data version is 2026.07(005). The content of this report has not been evaluated or approved by the FDA, EMA or other regulatory agencies.

Relevant Biomarkers (continued)

Tier	Genomic Alteration	Relevant Therapies (In this cancer type)	Relevant Therapies (In other cancer type)	Clinical Trials
	NRAS wild type	panitumumab ¹ panitumumab + chemotherapy ¹	-	-

* Public data sources included in relevant therapies: FDA¹, NCCN
* Public data sources included in prognostic and diagnostic significance: NCCN
Line of therapy: I: First-line therapy, II+: Other line of therapy
Tier Reference: Li et al. Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists. J Mol Diagn. 2017 Jan;19(1):4-23.

 Alerts informed by public data sources:  Contraindicated,  Resistance,  Breakthrough,  Fast Track

BRAF wild type dabrafenib¹, encorafenib¹

Public data sources included in alerts: FDA¹, NCCN

Relevant Colon Cancer DNA Findings

Gene	Finding	Gene	Finding
BRAF	BRAF wild type	PIK3CA	PIK3CA G118D
ERBB2	No clinically significant variants detected	PIK3R1	No clinically significant variants detected
KRAS	KRAS wild type	POLD1	No clinically significant variants detected
NRAS	NRAS wild type	POLE	No clinically significant variants detected
NTRK1	No clinically significant variants detected	PTEN	No clinically significant variants detected
NTRK2	No clinically significant variants detected	RET	No clinically significant variants detected
NTRK3	No clinically significant variants detected		

Genomic Alteration	Finding
Tumor Mutational Burden	8.49 Mut/Mb measured (Low)

Prevalent cancer biomarkers without relevant evidence based on included data sources
Tumor Mutational Burden (Low)

Variant Details

DNA Sequence Variants							
Gene	Tier	Amino Acid Change	Locus	Coding	Allele Frequency	Oncomine Gene Class	Variant Effect
PIK3CA	IIC	p.(G118D)	chr3:178917478	c.353G>A	54.68%	Gain of Function	missense
CASQ2		p.(Y55H)	chr1:116311000	c.163T>C	55.51%		missense
GCFC2		p.(V254G)	chr2:75923398	c.761T>G	19.22%		missense
PBRM1		p.(L297I)	chr3:52678730	c.889C>A	3.70%		missense
BCL6		p.(Q552*)	chr3:187444573	c.1654C>T	2.95%		nonsense
PABPC4L		p.(M352I)	chr4:135121119	c.1056G>T	49.00%		missense

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Tier	Amino Acid Change	Locus	Coding	Allele Frequency	Oncomine Gene Class	Variant Effect
MSH3		p.(A57_A62del)	chr5:79950707	c.162_179del	47.70%		nonframeshift Deletion
MSH3		p.(A61_P63dup)	chr5:79950735	c.189_190insGCAGCGC CC	39.96%		nonframeshift Insertion
APC		p.(S2134C)	chr5:112177692	c.6401C>G	33.32%		missense
HLA-B		p.([T118=;L119W])	chr6:31324206	c.354_357delCCTCinsT TGG	100.00%		synonymous, missense
PARP4		p.(?)	chr13:25021149	c.3285_3285+5delinsA GT	100.00%		unknown

Copy Number Variations

Gene	Locus	Copy Number	CNV Ratio
PCBP1	chr2:70314852	0.29	0.44
FGFR3	chr4:1801456	0.02	0.35
FLT4	chr5:180030092	0.06	0.37
NBN	chr8:90947783	5.34	2.08
RUNX1T1	chr8:92982878	9.72	3.51
HRAS	chr11:532637	0	0.21
FLT3	chr13:28578185	0.29	0.44
AKT2	chr19:40739751	0.52	0.52
AXL	chr19:41725295	0.22	0.42
BCL2L12	chr19:50169053	0	0.3

Clinical Trials Summary

PIK3CA G118D

NCT ID	Title	Phase
NCT06993844	A Phase I/II, Open-label, First-in-human Study of the Safety, Tolerability, Pharmacokinetics, and Preliminary Efficacy of ETX-636, a Pan-mutant-selective PI3Kα Inhibitor, as Monotherapy and in Combination With Other Anticancer Therapies in Participants With Advanced Solid Tumors	I/II
NCT06736704	A Phase I/II, Open-Label Dose Escalation and Expansion Study of SNV4818 as Monotherapy or in Combination With Other Anticancer Agents in Participants With Advanced Solid Tumors	I/II

Clinical Trials Summary (continued)

PIK3CA G118D (continued)

NCT ID	Title	Phase
NCT05944237	A Cancer Research UK Phase I/IIa Trial of HTL0039732, Given Orally as Monotherapy and in Combination With Immunotherapy or Other Approved Therapies in Participants With Advanced Solid Tumours	I/II
NCT07109726	A Phase 1/2 Trial of TER-2013 in Patients With Solid Tumors Harboring AKT/PI3K/PTEN Pathway Alterations	I/II

Microsatellite stable

NCT ID	Title	Phase
NCT07058012	A Phase II Platform Study to Evaluate Treatment With Cemiplimab Monotherapy or Cemiplimab Plus Fianlimab and Other Novel Combinations in Patients With Colorectal Cancer With Minimal Residual Disease Following Definitive Surgery and Chemotherapy	II
NCT03526835	Phase 1/2 Dose Escalation and Cohort Expansion Study Evaluating MCLA-158 (Petosemtamab) as Single Agent or in Combination in Advanced Solid Tumors	I/II
NCT06997497	A Phase III, Randomized, Open-label, Multicenter Clinical Study to Evaluate the Safety and Efficacy of MK-1084, Cetuximab, and mFOLFOX6 Versus mFOLFOX6 With or Without Bevacizumab as First-line Treatment of Participants With KRAS G12C-mutant, Locally Advanced Unresectable or Metastatic Colorectal Cancer (KANDLELIT-012)	III
NCT06509126	Randomized Phase III Study of Intermittent or Continuous Panitumumab Plus FOLFIRI for First-line Treatment of Patients With Unresectable Left Sided RAS/B-RAF Wild-type Metastatic Colorectal Cancer (IMPROVE-2 Trial)	III
NCT05462613	Induction Regorafenib in Combination With Metronomic Cyclophosphamide, Capecitabine, and Low-dose Aspirin Followed by Chemotherapy in Second Line Metastatic Colorectal Cancer Carcinoma An Open-label Randomized Phase II-III Study	II/III
NCT04659382	A Prospective, Multicenter, Open-label, Phase II Study to Evaluate Efficacy and Safety of Selective Internal Radiation Therapy Plus Xelox, Bevacizumab and Atezolizumab (Immune Checkpoint Inhibitor) in Patients With Liver-dominant Metastatic Colorectal Cancer	II
NCT07503756	An Open-label, Multicenter Phase II Clinical Study to Evaluate the Safety, Tolerability, Pharmacokinetics, and Preliminary Efficacy of JS212 Combination Therapies in Patients With Metastatic Colorectal Cancer	II
NCT07604909	A Phase II, Prospective, Randomized Study of Serplulimab Plus Second-Line Chemotherapy and Targeted Therapy vs Second-Line Chemotherapy and Targeted Therapy Alone in Patients With Early Relapse of Colorectal Cancer After Adjuvant Chemotherapy	II
No NCT ID	A multicenter phase II clinical study to evaluate the efficacy and tolerability of HB0025 injection combined with different chemotherapy regimens in the first-line treatment of patients with unresectable metastatic colorectal cancer	II
NCT06943820	A Phase Ib/II Study of Anti-PD-1/LAG-3 Bispecific Antibody AK129 Combinations in Advanced Solid Tumors	I/II
NCT07147231	A Phase I and Randomized Phase II Trial of Pidnarulex (CX-5461) and Cemiplimab (REGN2810) in Refractory Microsatellite Stable Colorectal Cancer	I/II

Clinical Trials Summary (continued)

Microsatellite stable (continued)

NCT ID	Title	Phase
NCT06654037	A Phase I Study of 5-Fluorouracil in Combination With Abemaciclib in Metastatic, Refractory CRC	I

Genes Assayed

Genes Assayed for the Detection of DNA Sequence Variants

ABL1, ABL2, ACVR1, ACVR2A, AKT1, AKT2, AKT3, ALK, AMER1, APC, AR, ARAF, ARID1A, ARID1B, ARID2, ASXL1, ASXL2, ATM, ATP1A1, ATR, ATRX, AURKA, AURKC, AXIN1, AXIN2, AXL, B2M, BAP1, BCL2, BCL2L12, BCL6, BCOR, BCR, BLM, BMP5, BRAF, BRCA1, BRCA2, BRIP1, BTK, CACNA1D, CALR, CARD11, CASP8, CBL, CCND1, CCND2, CCND3, CCNE1, CD79B, CDC73, CDH1, CDK4, CDK6, CDKN2A, CDKN2C, CHD4, CHEK2, CIC, CREBBP, CSF1R, CTCF, CTNNB1, CUL1, CUL3, CYP2D6, CYSLTR2, DDR2, DDX3X, DGCR8, DICER1, DNMT3A, DPYD, DROSHA, E2F1, EGFR, EIF1AX, EP300, EPAS1, EPHA2, ERBB2, ERBB3, ERBB4, ERCC2, ERCC5, ERFFI1, ESR1, EZH2, FAM135B, FANCM, FBXW7, FGF7, FGFR1, FGFR2, FGFR3, FGFR4, FLT3, FLT4, FOXA1, FOXL2, FOXO1, FUBP1, GATA2, GATA3, GLI1, GNA11, GNA13, GNAQ, GNAS, GPS2, H2BC5, H3-3A, H3-3B, H3C2, HIF1A, HNF1A, HRAS, ID3, IDH1, IDH2, IKBKB, IL6ST, IL7R, IRF4, IRS4, JAK1, JAK2, JAK3, KDM6A, KDR, KEAP1, KIT, KLF4, KLF5, KMT2B, KMT2D, KNSTRN, KRAS, LARP4B, LATS1, MAGOH, MAP2K1, MAP2K2, MAP2K4, MAP2K7, MAP3K4, MAPK1, MAPK8, MAX, MDM4, MECOM, MED12, MEF2B, MEN1, MET, MGA, MITF, MLH3, MPL, MSH3, MSH6, MTOR, MYC, MYCN, MYD88, MYOD1, NBN, NCOR1, NF1, NF2, NFE2L2, NOTCH1, NOTCH2, NRAS, NSD2, NT5C2, NTRK1, NTRK2, NTRK3, NUP93, PARP1, PAX5, PBRM1, PCBP1, PDGFRA, PDGFRB, PHF6, PIK3C2B, PIK3CA, PIK3CB, PIK3CD, PIK3CG, PIK3R1, PIK3R2, PIM1, PLCG1, PMS2, POLE, PPM1D, PPP2R1A, PPP6C, PRKACA, PTCH1, PTEN, PTPN11, PTPRD, PXDNL, RAC1, RAD50, RAD51, RAF1, RARA, RB1, RET, RGS7, RHEB, RHOA, RICTOR, RIT1, RNF43, ROS1, RPL10, RPL5, RUNX1, RUNX1T1, SDHD, SETBP1, SETD2, SF3B1, SIX1, SIX2, SLC01B3, SLX4, SMAD2, SMAD4, SMARCA4, SMARCB1, SMC1A, SMO, SNCAIP, SOCS1, SOS1, SOX2, SPOP, SRC, SRSF2, STAG2, STAT3, STAT5B, STAT6, STK11, TAF1, TCF7L2, TERT, TET2, TGFB1, TGFB2, TNFAIP3, TOP1, TP53, TPMT, TRRAP, TSC2, TSHR, U2AF1, UGT1A1, USP8, VHL, WAS, WT1, XPO1, XRCC2, ZFH3, ZNF217, ZNF429

Genes Assayed for the Detection of Copy Number Variations

ABCB1, ABL1, ABL2, ABRAXAS1, ACVR1B, ACVR2A, ADAMTS12, ADAMTS2, AKT1, AKT2, AKT3, ALK, AMER1, APC, AR, ARAF, ARHGAP35, ARID1A, ARID1B, ARID2, ARID5B, ASXL1, ASXL2, ATM, ATR, ATRX, AURKA, AURKC, AXIN1, AXIN2, AXL, B2M, BAP1, BARD1, BCL2, BCL2L12, BCL6, BCOR, BLM, BMPR2, BRAF, BRCA1, BRCA2, BRIP1, CARD11, CASP8, CBFB, CBL, CCND1, CCND2, CCND3, CCNE1, CD274, CD276, CDC73, CDH1, CDH10, CDK12, CDK4, CDK6, CDKN1A, CDKN1B, CDKN2A, CDKN2B, CDKN2C, CHD4, CHEK1, CHEK2, CIC, CREBBP, CSMD3, CTCF, CTLA4, CTNND2, CUL3, CUL4A, CUL4B, CYLD, CYP2C9, DAXX, DDR1, DDR2, DDX3X, DICER1, DNMT3A, DOCK3, DPYD, DSC1, DSC3, EGFR, EIF1AX, ELF3, EMSY, ENO1, EP300, EPCAM, EPHA2, ERAP1, ERAP2, ERBB2, ERBB3, ERBB4, ERCC2, ERCC4, ERFFI1, ESR1, ETV6, EZH2, FAM135B, FANCA, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FAT1, FBXW7, FGF19, FGF23, FGF3, FGF4, FGF9, FGFR1, FGFR2, FGFR3, FGFR4, FLT3, FLT4, FOXA1, FUBP1, FYN, GATA2, GATA3, GLI3, GNA13, GNAS, GPS2, H3-3A, H3-3B, HDAC2, HDAC9, HLA-A, HLA-B, HNF1A, IDH2, IGF1R, IKBKB, IL7R, INPP4B, JAK1, JAK2, JAK3, KDM5C, KDM6A, KDR, KEAP1, KIT, KLF5, KMT2A, KMT2B, KMT2C, KMT2D, KRAS, LARP4B, LATS1, LATS2, MAGOH, MAP2K1, MAP2K4, MAP2K7, MAP3K1, MAP3K4, MAPK1, MAPK8, MAX, MCL1, MDM2, MDM4, MECOM, MEF2B, MEN1, MET, MGA, MITF, MLH1, MLH3, MPL, MRE11, MSH2, MSH3, MSH6, MTAP, MTOR, MUTYH, MYC, MYCL, MYCN, MYD88, NBN, NCOR1, NF1, NF2, NFE2L2, NOTCH1, NOTCH2, NOTCH3, NOTCH4, NRAS, NTRK1, NTRK3, PALB2, PARP1, PARP2, PARP3, PARP4, PBRM1, PCBP1, PDCD1, PDCD1LG2, PDGFRA, PDGFRB, PDIA3, PGD, PHF6, PIK3C2B, PIK3CA, PIK3CB, PIK3R1, PIK3R2, PIM1, PLCG1, PMS1, PMS2, POLD1, POLE, POT1, PPM1D, PPP2R1A, PPP2R2A, PPP6C, PRDM1, PRDM9, PRKACA, PRKAR1A, PTCH1, PTEN, PTPN11, PTPRT, PXDNL, RAC1, RAD50, RAD51, RAD51B, RAD51C, RAD51D, RAD52, RAD54L, RAF1, RARA, RASA1, RASA2, RB1, RBM10, RECQL4, RET, RHEB, RICTOR, RIT1, RNASEH2A, RNASEH2B, RNF43, ROS1, RPA1, RPS6KB1, RPTOR, RUNX1, SDHA, SDHB, SDHD, SETBP1, SETD2, SF3B1, SLC01B3, SLX4, SMAD2, SMAD4, SMARCA4, SMARCB1, SMC1A, SMO, SOX9, SPEN, SPOP, SRC, STAG2, STAT3, STAT6, STK11, SUFU, TAP1, TAP2, TBX3, TCF7L2, TERT, TET2, TGFB2, TNFAIP3, TNFRSF14, TOP1, TP53, TP63, TPMT, TPP2, TSC1, TSC2, U2AF1, USP8, USP9X, VHL, WT1, XPO1, XRCC2, XRCC3, YAP1, YES1, ZFH3, ZMYM3, ZNF217, ZNF429, ZRSR2

Genes Assayed (continued)

Genes Assayed for the Detection of Fusions

AKT1, AKT2, AKT3, ALK, AR, BRAF, BRCA1, CDKN2A, EGFR, ERBB2, ERBB4, ERG, ESR1, ETV1, ETV4, ETV5, FGFR1, FGFR2, FGFR3, MAP3K8, MET, MTAP, MYB, MYBL1, NOTCH1, NOTCH2, NOTCH3, NRG1, NTRK1, NTRK2, NTRK3, NUTM1, PIK3CA, PIK3CB, PPARG, PRKACA, PRKACB, RAF1, RARA, RELA, RET, ROS1, RSP02, RSP03, STAT6, TERT, TFE3, TFEB, YAP1

Genes Assayed with Full Exon Coverage

ABRAXAS1, ACVR1B, ACVR2A, ADAMTS12, ADAMTS2, AMER1, APC, ARHGAP35, ARID1A, ARID1B, ARID2, ARID5B, ASXL1, ASXL2, ATM, ATR, ATRX, AXIN1, AXIN2, B2M, BAP1, BARD1, BCOR, BLM, BMPR2, BRCA1, BRCA2, BRIP1, CALR, CASP8, CBFB, CD274, CD276, CDC73, CDH1, CDH10, CDK12, CDKN1A, CDKN1B, CDKN2A, CDKN2B, CDKN2C, CHEK1, CHEK2, CIC, CIITA, CREBBP, CSMD3, CTCF, CTLA4, CUL3, CUL4A, CUL4B, CYLD, CYP2C9, CYP2D6, DAXX, DDX3X, DICER1, DNMT3A, DOCK3, DPYD, DSC1, DSC3, ELF3, ENO1, EP300, EPCAM, EPHA2, ERAP1, ERAP2, ERCC2, ERCC4, ERCC5, ERFF1, ETV6, FANCA, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FAS, FAT1, FBXW7, FUBP1, GATA3, GNA13, GPS2, HDAC2, HDAC9, HLA-A, HLA-B, HNF1A, ID3, INPP4B, JAK1, JAK2, JAK3, KDM5C, KDM6A, KEAP1, KLHL13, KMT2A, KMT2B, KMT2C, KMT2D, LARP4B, LATS1, LATS2, MAP2K4, MAP2K7, MAP3K1, MAP3K4, MAPK8, MEN1, MGA, MLH1, MLH3, MRE11, MSH2, MSH3, MSH6, MTAP, MTUS2, MUTYH, NBN, NCOR1, NF1, NF2, NOTCH1, NOTCH2, NOTCH3, NOTCH4, PALB2, PARP1, PARP2, PARP3, PARP4, PBRM1, PDCD1, PDCD1LG2, PDIA3, PGD, PHF6, PIK3R1, PMS1, PMS2, POLD1, POLE, POT1, PPM1D, PPP2R2A, PRDM1, PRDM9, PRKAR1A, PSMB10, PSMB8, PSMB9, PTCH1, PTEN, PTPRT, RAD50, RAD51, RAD51B, RAD51C, RAD51D, RAD52, RAD54L, RASA1, RASA2, RB1, RBM10, RECQL4, RNASEH2A, RNASEH2B, RNASEH2C, RNF43, RPA1, RPL22, RPL5, RUNX1, RUNX1T1, SDHA, SDHB, SDHC, SDHD, SETD2, SLX4, SMAD2, SMAD4, SMARCA4, SMARCB1, SOCS1, SOX9, SPEN, STAG2, STAT1, STK11, SUFU, TAP1, TAP2, TBX3, TCF7L2, TET2, TGFB2, TMEM132D, TNFAIP3, TNFRSF14, TP53, TP63, TPP2, TSC1, TSC2, UGT1A1, USP9X, VHL, WT1, XRCC2, XRCC3, ZBTB20, ZFH3, ZMYM3, ZRSR2

Methods, Limitations & Disclaimers

Methods and Limitations:

Blood is collected in preservative-containing tubes. CTCs are isolated and enriched via proprietary CCDx methods. **DNA** is extracted and amplified using a validated protocol. RNA is not analyzed. Nucleic acids are analyzed targeting 517 cancer-related genes. Detected alterations include SNVs, indels, splice-site changes, and CNAs. Analysis is aligned to GRCh37 (hg19). The assay does not detect genomic alterations outside targeted regions, including large structural variants, MSI, TMB, or promoter methylation. CNV ratio of 2 or greater is reported. Copy number loss is not evaluated. The assay does not differentiate between somatic, germline, or CHIP-related alterations. The test is not validated for hereditary cancer risk, germline mutations, or CHIP-associated alterations. For DNA, LOD95 is 5%, sensitivity exceeds 99%, and positive predictive value exceeds 97% for SNVs. CCDx Reporter only assigns tiers IA and IIC by default.

Disclaimer

Negative findings do not exclude malignancy or the presence of clinically significant genomic alterations. Additional tissue-based or other diagnostic testing may be warranted based on the patient's clinical presentation and the treating physician's judgment. The CCDx Reporter utilizes a modified AMP/ASCO/CAP somatic variant classification system. Only variants meeting established reporting criteria are included in this report. Variants not detected do not exclude the presence of genomic alterations in tissue or other biological specimens. Tumor Mutational Burden (TMB) results should be interpreted within the context of the tumor type, assay performance, and the patient's overall clinical findings. Unless otherwise indicated, reported variants were detected by next-generation sequencing (NGS) and have not been confirmed by an independent orthogonal method. This laboratory-developed test (LDT) was developed, and its performance characteristics were established and validated by Cancer Cell Diagnostics, Inc. (CCDx) under the Clinical Laboratory Improvement Amendments (CLIA) for high-complexity testing. This test has not been cleared or approved by the U.S. Food and Drug Administration (FDA). This report is intended to assist healthcare providers and should not be used as the sole basis for diagnosis or treatment. Detection of a genomic alteration does not establish the presence or absence of cancer, predict therapeutic response, or guarantee clinical benefit. Likewise, the absence of a reported alteration does not predict lack of response to therapy. Therapeutic associations and clinical trial information are provided for informational purposes only and may include investigational or off-label uses. All patient management decisions should be based on the treating physician's independent medical judgment and consideration

of the patient's complete clinical, pathologic, radiologic, laboratory, and family history, together with current standards of medical practice. Knowledgebase interpretations are derived from curated scientific literature and publicly available databases and are subject to periodic review and updates. Although every effort is made to maintain current and accurate information, the knowledgebase may not be comprehensive as new evidence continues to emerge.

Report Signed By

Name	Role	Date
Kyle Dunn	Medical Director	16 Jul 2026 07:40 PM