Comprehensive Molecular Profiling

WHERE MOLECULAR SCIENCE MEETS ARTIFICIAL INTELLIGENCE

Comprehensive Molecular Profiling for Cancer Care

Caris comprehensive tumor profiling assesses DNA, RNA, and Proteins with multiple technologies, revealing a more complete molecular blueprint to decode cancer and guide more precise and individualized treatment decisions.

DNA

Whole Exome Sequencing

- 23,000+ genes
- 1,500x for clinical genes
- SNVs, indels, CNA, Karyotyping*, Viruses*
- 250,000 evenly spaced genomic SNPs
- HLA Genotype*
- Genomic signatures

RNA

Whole Transcriptome Sequencing

- 23,000+ genes
- 17 million read count
- Fusions, variant transcripts and gene expression*
- Novel translocation detection independent of intronic breakpoint

Protein*

Immunohistochemistry

- 15+ clinically relevant IHCs (Optimized across ~25 Tumor Types)
- Multiple FDA approved CDx assays for different disease types (per label)
- Controls on every IHC slide
- 4 µm cuts to preserve tissue

Multiple options for tumor profiling, covering DNA, RNA, Proteins and Predictive Algorithms

	WES	WTS	IHC/Other	AI Signatures
MI Profile™ Comprehensive Testing MI Tumor Seek Hybrid™ + IHCs and Other Tests by Tumor Type.	✓	✓	✓	✓
MI Tumor Seek Hybrid™ Next-Generation Sequencing Only: Tissue-based WES and WTS analysis. Caris FOLFIRSTai™* reported for mCRC cases.	✓	✓	–	✓

*Not available in all locations.

Intuitive Reports to Guide Clinical Decisions

Clinicians need comprehensive results that are easy to comprehend. The Caris report helps guide decisions for a complex disease, with easy-to-interpret results and callouts for key biomarker-drug associations and clinical trials.

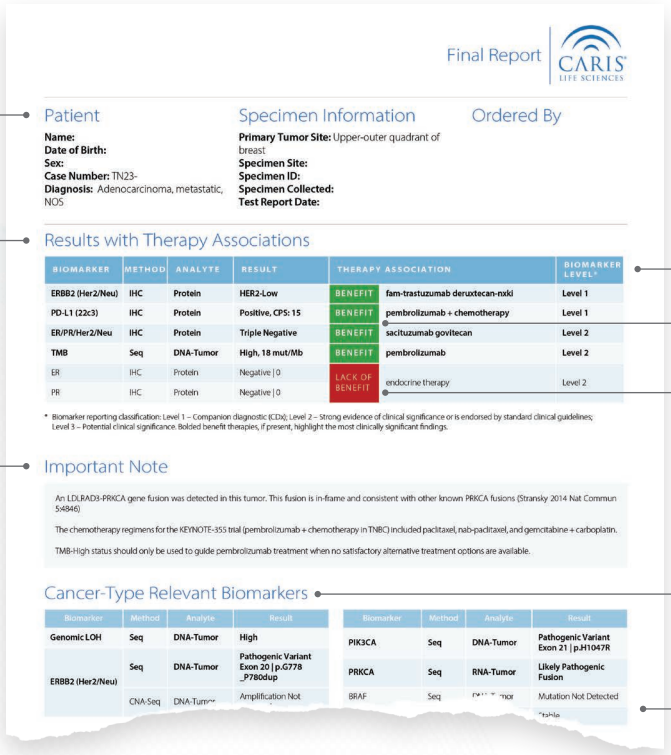
Patient and Specimen Information

Results with Therapy Associations*

Important Notes

Therapeutic associations are continuously updated based on:

- FDA approvals
- Industry guidelines
- Clinical literature



Final Report — CARIS LIFE SCIENCES

Patient
Name:
Date of Birth:
Sex:
Case Number: TN23-
Diagnosis: Adenocarcinoma, metastatic, NOS

Specimen Information
Primary Tumor Site: Upper-outer quadrant of breast
Specimen Site:
Specimen ID:
Specimen Collected:
Test Report Date:

Ordered By

Results with Therapy Associations

BIOMARKER	METHOD	ANALYTE	RESULT	THERAPY ASSOCIATION		BIOMARKER LEVEL*
ERBB2 (Her2/Neu)	IHC	Protein	HER2-Low	BENEFIT	fam-trastuzumab deruxtecan-nxki	Level 1
PD-L1 (22c3)	IHC	Protein	Positive, CPS: 15	BENEFIT	pembrolizumab + chemotherapy	Level 1
ER/PR/Her2/Neu	IHC	Protein	Triple Negative	BENEFIT	sacituzumab govitecan	Level 2
TMB	Seq	DNA-Tumor	High, 18 mut/Mb	BENEFIT	pembrolizumab	Level 2
ER	IHC	Protein	Negative | 0	LACK OF BENEFIT	endocrine therapy	Level 2
PR	IHC	Protein	Negative | 0			

* Biomarker reporting classification: Level 1 – Companion diagnostic (CDx); Level 2 – Strong evidence of clinical significance or is endorsed by standard clinical guidelines; Level 3 – Potential clinical significance. Bolded benefit therapies, if present, highlight the most clinically significant findings.

Important Note

An LDLRAD3-PRKCA gene fusion was detected in this tumor. This fusion is in-frame and consistent with other known PRKCA fusions (Stransky 2014 Nat Commun 5:4846)

The chemotherapy regimens for the KEYNOTE-355 trial (pembrolizumab + chemotherapy in TNBC) included paclitaxel, nab-paclitaxel, and gemcitabine + carboplatin.

TMB-High status should only be used to guide pembrolizumab treatment when no satisfactory alternative treatment options are available.

Cancer-Type Relevant Biomarkers

Biomarker	Method	Analyte	Result
Genomic LOH	Seq	DNA-Tumor	High
ERBB2 (Her2/Neu)	Seq	DNA-Tumor	Pathogenic Variant Exon 20 | p.G778_P780dup
	CNA-Seq	DNA-Tumor	Amplification Not

Biomarker	Method	Analyte	Result
PIK3CA	Seq	DNA-Tumor	Pathogenic Variant Exon 21 | p.H1047R
PRKCA	Seq	RNA-Tumor	Likely Pathogenic Fusion
BRAF	Seq	[illegible]-Tumor	Mutation Not Detected

Biomarker Levels

Therapies with potential Benefit are noted in **green**.

Therapies with potential Lack of Benefit are noted in **red**.

Cancer-Type Relevant Biomarkers

Clinical Trials

Caris Molecular AI

Caris Molecular Artificial Intelligence™ is the convergence of machine learning with WES and WTS to drive decision making. Caris Molecular AI™ analyzes historical clinical and outcomes data from the Caris clinico-genomic database to identify unique molecular signatures used to guide patient treatment.

Caris GPSai™
Genomic Prevalence Score

Caris Genomic Prevalence Score AI (GPSai)† is a predictive algorithm to help oncologists identify cancers of unknown primary (CUP) or cases with atypical clinical presentation or clinical ambiguity.

Caris FOLFIRSTai™
Chemotherapy Response Predictor for mCRC

Caris FOLFIRSTai† is the first clinically validated, AI-powered molecular predictor of chemotherapy efficacy and treatment sequence for mCRC patients.

†GPSai and FOLFIRSTai are not currently available in all locations.

Pioneering Molecular Intelligence for Cancer Care

Every cancer is unique, just as every patient is unique. Precision oncology provides doctors detailed molecular information to develop personalized treatment plans that are right for each individual patient. More than ever, oncologists need a trusted tumor profiling partner to provide reliable, high-quality molecular profiling to guide more precise and individualized treatment decisions.

Caris Life Sciences is leading the molecular revolution with the most comprehensive biomarker profiling available, including whole exome sequencing (WES – DNA), whole transcriptome sequencing (WTS – RNA), and immunohistochemistry (IHC – 15+ tumor-relevant). As a pioneer in precision oncology since the dawn of this exciting new industry, Caris is shaping the future of healthcare—and with Caris molecular profiling, we're setting a new standard for delivering accurate, actionable results that help improve patient outcomes and save lives.

Caris provides the most advanced and comprehensive tumor profiling enhanced by artificial intelligence, helping oncologists to:

- Navigate among therapies with potential benefit
- Identify therapies that may not have been considered
- Determine drugs with potential lack of benefit (avoiding unnecessary toxicities and costs)
- Match patients to clinical trials

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