CARIS®
LIFE SCIENCES

Caris Molecular Profiling

Enabling the Delivery of Precision Medicine

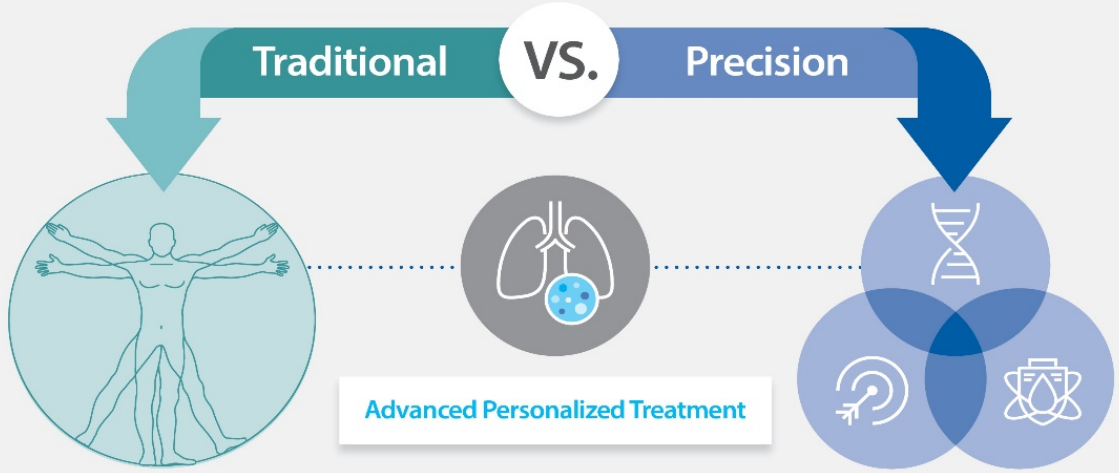
Ben Doron, PhD
Director, Molecular Science Liaisons

Meet your local MSL Team

- **Ben Doron, PhD** is the MSL director for the West Region and is located in Portland, OR.
- He received his PhD in Molecular Biology from Oregon Health and Sciences University in 2018. His dissertation work involved understanding how Acute Myeloid Leukemia reprograms the bone marrow into a pro-leukemic niche.
- He then did a post doc at the Fred Hutchinson Cancer Research Center where he studied epigenetic mechanisms of pathogenesis in Pancreatic Adenocarcinoma.

- **Omkara Veeranki, DVM, PhD** is the local MSL for the Seattle and Puget Sound Area.
- She received her PhD in Cancer Pathology and Prevention at Roswell Park Comprehensive Cancer Center. Her dissertation was focused on assessing Sulforaphane as a chemopreventive agent in Bladder Cancer and developing biomarkers for clinical trials.
- She then moved to Houston for a postdoc at MD Anderson Cancer Center. Here her research was focused on identifying the impact of tumor mutation burden on immune microenvironment of esophagogastric adenocarcinomas.

Traditional Medicine vs. Precision Medicine



Radiation
- High-energy particles damage or destroy cancer cells

Chemotherapy
- Chemicals attack cancer Surgery
- Operate on part of the body to diagnose or treat cancer

Genetics
- Gene sequencing
- Locate cancer causing genes

Immunotherapy
- Identify ways to customize treatment
- Find ways to tum immune system on
- Personalize treatment with immune-activating drugs

Targeted Therapies
- Drugs turn specific genes on or off

+ Traditional therapies

Caris Molecular Profiling

- ✓ **Unmatched Experience Across DNA, RNA and Proteins**
  - 3,933,000+ tests completed
  - 313,000+ clinical cases performed
  - Staff: bioinformaticians, oncologists, molecular geneticists, pathologists and PhD scientists
- ✓ **Immunotherapy Dx Expertise**
  - PD-L1
  - Microsatellite Instability (MSI)
  - Mismatch Repair (MMR)
  - Tumor Mutational Burden (TMB)
- ✓ **Rigorous Quality Standards**
  - CAP, CLIA, NYSDOH, ISO15189 accredited
  - 66,000 square-foot central laboratory
  - 38,000 square-foot R&D facility
- ✓ **Limited Tissue Testing Capabilities**
  - Tumor enrichment via microdissection
  - Multiple reflex options to alternative technologies/methods
- ✓ **Rapid Turnaround Time**
  - 10-14 calendar days (8 days in NSCLC)
  - 11 days is the most frequent turnaround time reported in 2021 YTD

Collaborations:

ASCO TAPUR
Targeted Agent and Profiling Utilization Registry Study

FDA

NATIONAL CANCER INSTITUTE
NCI-MATCH CLINICAL TRIAL

FRIENDS of CANCER RESEARCH

IBM

side-out FOUNDATION

cholangiocarcinoma FOUNDATION

GBM AGILE
Adaptive Global Innovative Learning Environment

PMC PERSONALIZED MEDICINE COALITION

Caris Molecular Intelligence® – MI Profile™

Standard of Care + Clinical Trial Biomarkers

Immunotherapy	Targeted Therapy	Chemotherapy/Hormonal Therapies	Clinical Trials

DNA

Whole Exome Sequencing
(Mutations, Indels & Copy Number Alterations)

- ~22,000 full gene coverage (whole exome coverage)
- 719 clinically-relevant genes at 1,000x
- Point mutations, indels, and copy number alterations
- ~250,000 exonic/intronic/intergenic SNPs – LOH, gene loss or amplification
- Genomic Signatures: TMB, MSI and LOH

RNA

Whole Transcriptome Sequencing
(Fusions & Variant Transcripts)

- ~22,000 full gene coverage (whole transcriptome coverage)
- 60 million read count
- Gene fusions and variant transcripts
- Novel translocation detection independent of intronic breakpoint
- Genomic Signatures: HLA Genotype

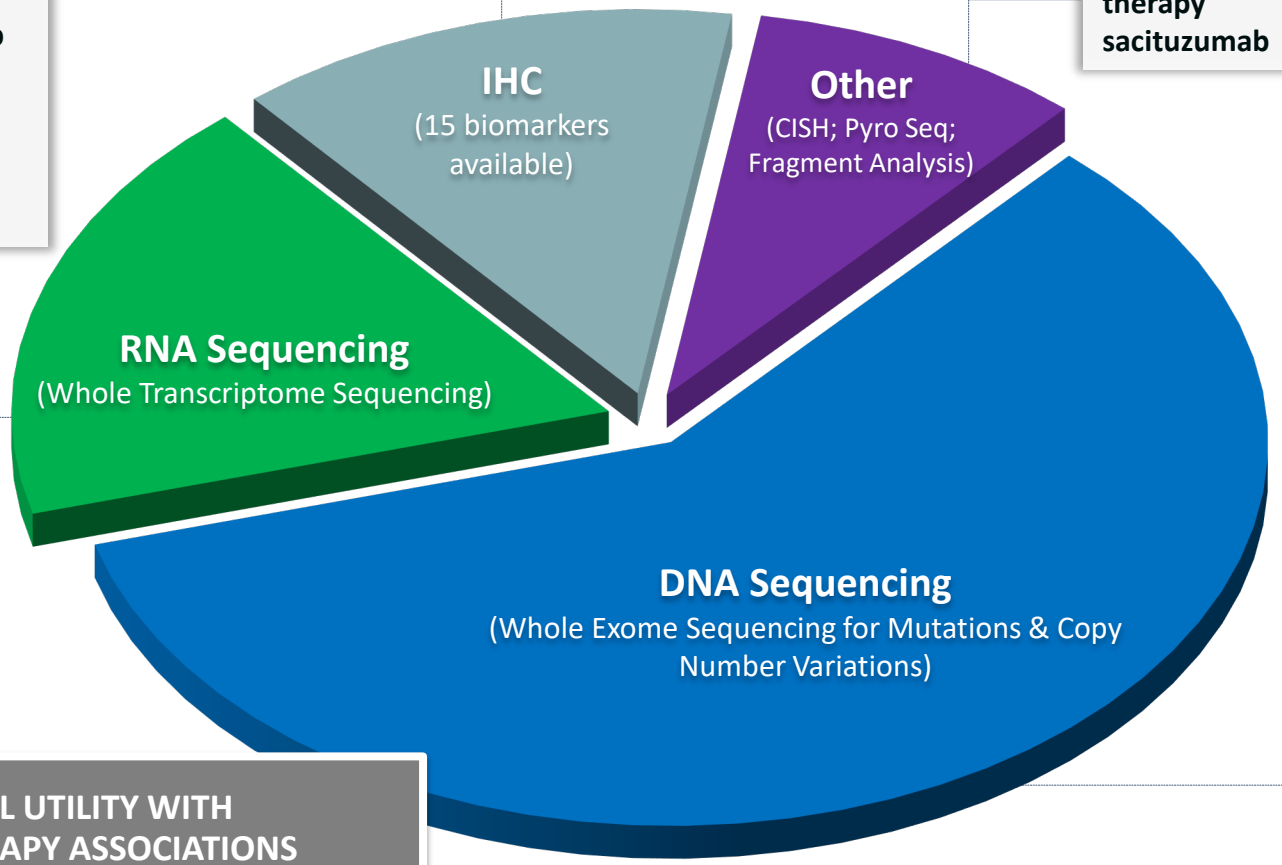
PROTEINS

Immunohistochemistry

- Up to 15 clinically relevant IHCs (optimized across 25 tumor types)
- Multiple FDA approved CDx PD-L1 tests for different disease types (per label)
- Controls on every IHC
- 4 µm cuts to preserve tissue

Companion Dxs & NCCN-Guidelines® Require a Multi-Technology Approach

alectinib
atezolizumab
bicalutamide
brigatinib
CDK4/6 inhibitors
ceritinib, crizotinib
endocrine therapy
entrectinib
enzalutamide
everolimus
HER2-targeted therapy
leuprolide, lorlatinib
nivolumab +/- ipilimumab
pembrolizumab
sacituzumab govitecan



HER2-targeted therapy
sacituzumab govitecan
temozolomide

alectinib, brigatinib
ceritinib, crizotinib
cabozantinib, capmatinib
entrectinib
larotrectinib, lorlatinib
pralsetinib, selpercatinib
vandetanib, pemigatinib
erdafitinib

afatinib
alpelisib
avapritinib
binimetinib
capmatinib
carboplatin
cetuximab
cisplatin
crizotinib
dabrafenib
cobimetinib
encorafenib
erlotinib
gefitinib
imatinib
ivosedinib
niraparib
imatinib
olaparib
osimertinib
oxaliplatin
panitumumab
pembrolizumab
regorafenib
rucaparib
sunitinib
T-DM1
temozolomide
trametinib
vemurafenib

MAXIMIZING CLINICAL UTILITY WITH 60+ FDA-APPROVED THERAPY ASSOCIATIONS

For illustrative purposes. For a complete list of therapies assessed, please view the profile menu.

Caris Molecular Profiling – How it Works

Tissue Sample Sent to Caris

A tissue sample of a tumor is obtained through biopsy. A pathology laboratory packages and ships to Caris.

Biomarker Testing

Caris analyzes tumor tissue through a series of advanced pathology and panomic assays to identify biomarkers (DNA, RNA and Proteins).

Informatics Analysis

The Caris expert team interprets the data using more than 120,000 clinical papers to match a tumor's biomarkers to potential treatment options.

Tumor Profile Generated

Results are organized into a report that includes relevant findings and treatment options.

CARIS® MI PROFILE Tissue

Physician Reviews Report

The report is sent to ordering physician for review. Physician may suggest a treatment based on the report, availability of drugs, medical history and other clinical factors.

Patient and Specimen Information

Results with Therapy Associations

Contains drug associations ranked by level of evidence:

Level 1 = Biomarker noted in FDA indication

Level 2 = endorsed by clinical guidelines

Level 3A = evidence exists in patients tumor type

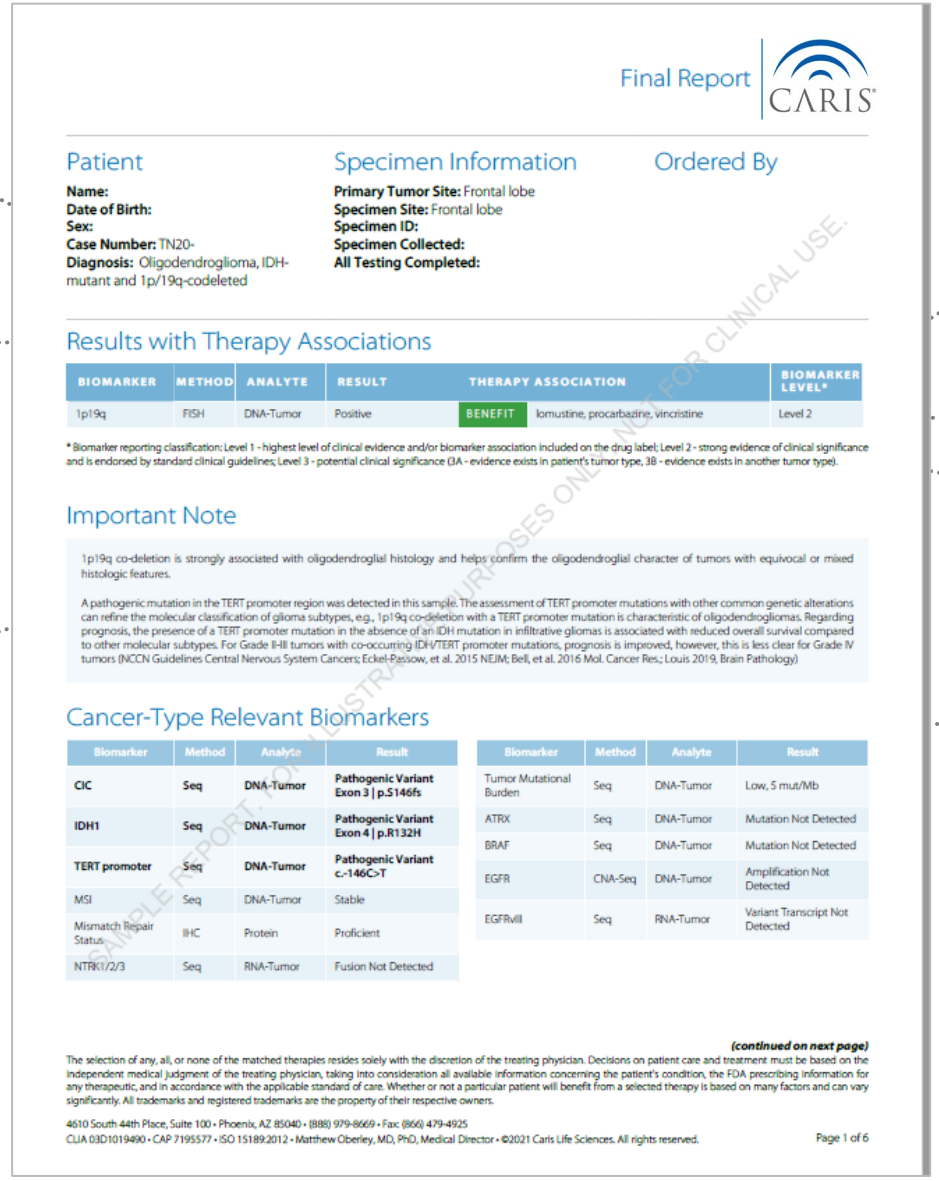
Level 3B = evidence exists in another tumor type

Important Note

contains significant information about drug/biomarker associations and comments from Caris pathologists and/or molecular geneticists, if applicable.

Constantly updating based on:

- FDA approvals
- Industry guidelines
- Literature
- **Physician** feedback



Final Report

CARIS

Patient

Name:
Date of Birth:
Sex:
Case Number: TN20-
Diagnosis: Oligodendroglioma, IDH-mutant and 1p/19q-codeleted

Specimen Information

Primary Tumor Site: Frontal lobe
Specimen Site: Frontal lobe
Specimen ID:
Specimen Collected:
All Testing Completed:

Ordered By

Results with Therapy Associations

BIOMARKER	METHOD	ANALYTE	RESULT	THERAPY ASSOCIATION		BIOMARKER LEVEL*
1p19q	FISH	DNA-Tumor	Positive	BENEFIT	lomustine, procarbazine, vincristine	Level 2

* Biomarker reporting classification: Level 1 - highest level of clinical evidence and/or biomarker association included on the drug label; Level 2 - strong evidence of clinical significance and is endorsed by standard clinical guidelines; Level 3 - potential clinical significance (3A - evidence exists in patient's tumor type, 3B - evidence exists in another tumor type).

Important Note

1p19q co-deletion is strongly associated with oligodendroglial histology and helps confirm the oligodendroglial character of tumors with equivocal or mixed histologic features.

A pathogenic mutation in the TERT promoter region was detected in this sample. The assessment of TERT promoter mutations with other common genetic alterations can refine the molecular classification of glioma subtypes, e.g., 1p19q co-deletion with a TERT promoter mutation is characteristic of oligodendrogliomas. Regarding prognosis, the presence of a TERT promoter mutation in the absence of an IDH mutation in infiltrative gliomas is associated with reduced overall survival compared to other molecular subtypes. For Grade II-III tumors with co-occurring IDH/TERT promoter mutations, prognosis is improved, however, this is less clear for Grade IV tumors (NCCN Guidelines Central Nervous System Cancers; Eckel-Passow, et al. 2015 NEJM; Bell, et al. 2016 Mol. Cancer Res.; Louis 2019, Brain Pathology)

Cancer-Type Relevant Biomarkers

Biomarker	Method	Analyte	Result
CIC	**Seq**	**DNA-Tumor**	**Pathogenic Variant Exon 3 | p.S146fs**
IDH1	**Seq**	**DNA-Tumor**	**Pathogenic Variant Exon 4 | p.R132H**
TERT promoter	**Seq**	**DNA-Tumor**	**Pathogenic Variant c.-146C>T**
MSI	Seq	DNA-Tumor	Stable
Mismatch Repair Status	IHC	Protein	Proficient
NTRK1/2/3	Seq	RNA-Tumor	Fusion Not Detected

Biomarker	Method	Analyte	Result
Tumor Mutational Burden	Seq	DNA-Tumor	Low, 5 mut/Mb
ATRX	Seq	DNA-Tumor	Mutation Not Detected
BRAF	Seq	DNA-Tumor	Mutation Not Detected
EGFR	CNA-Seq	DNA-Tumor	Amplification Not Detected
EGFRvIII	Seq	RNA-Tumor	Variant Transcript Not Detected

(continued on next page)

The selection of any, all, or none of the matched therapies resides solely with the discretion of the treating physician. Decisions on patient care and treatment must be based on the independent medical judgment of the treating physician, taking into consideration all available information concerning the patient's condition, the FDA prescribing information for any therapeutic, and in accordance with the applicable standard of care. Whether or not a particular patient will benefit from a selected therapy is based on many factors and can vary significantly. All trademarks and registered trademarks are the property of their respective owners.

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Biomarker Levels

indicates the strength of evidence as defined by the FDA tiered biomarker reporting classification. **Replaces the on/off NCCN compendium function**

Therapies with Potential Benefit

are noted in **green**.

Therapies with Potential Lack of Benefit

are noted in **red**.

Cancer Type Relevant Biomarkers

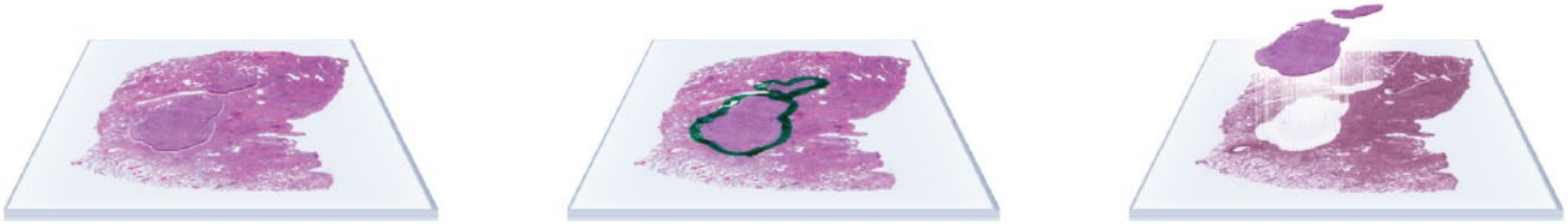
Pre-defined biomarkers whose results will show regardless of presence or absence of an alteration.

If biomarker result is in the high impact section, it will not repeat in this section

Microdissection – Enhancing Patient Care

Tumor enrichment of the specimen is performed by tissue microdissection:

- Slides are examined and areas containing tumor cells are circled. PATHOLOGY DIRECTED MICROTOMY
- A Pathology Assistant extracts the tumor tissue from the marked areas.
- Critically important for limited tissue cases and low density tumors



Tumor is 10% of Total Tissue → ***Enriched for Tumor Tissue***

Microdissection isolates specific tumor cells for testing and reduces non-cancer material diluting the tissue section.

The Importance of RNA Sequencing

Fusion genes are an emerging class of highly important targets for cancer diagnosis and treatment.

- **Clinical Setting:** High quality clinical care requires screening for RNA fusions, which are rare but with efficacy in the 70%+ range
- **Biopharma Setting:** Compelling need to find responsive patients for both clinical trials and commercial purposes

NTRK Gene Fusions Across Various Cancers

<5%	Colon cancer Melanoma Various sarcomas Cholangiocarcinoma Glioma Pancreatic cancer Appendiceal cancer Lung adenocarcinoma
5-75%	Thyroid cancer GIST
>75%	Secretory carcinoma of the salivary gland Secretory breast carcinoma

Other Gene Fusions: RET, FGFR, ALK, ROS1, RSPO3...

Mounting evidence of higher fusion detection through RNA-based analysis over DNA-based analysis.

Memorial Sloan Kettering Cancer Center

(Benayed, et. Al)

RNA-based analysis identifies more fusions than DNA-based analysis

-- Study based on MSK-IMPACT (DNA) and MSK-Fusion (RNA) (April 2019)

MI Transcriptome

Direct comparison between DNA and RNA shows RNA is the superior method for fusion analysis

-- Caris internal data based on 10x the size of the of Benayed, et. al study

NCCN National Comprehensive Cancer Network®

NCCN Guidelines (i) recommend RNA-based NGS for patients with no identifiable driver oncogenes to maximize detection of fusion events; and (ii) state that RNA-based NGS may be considered to assess for fusions as DNA-based NGS may not detect some NTRK1 and NTRK3 fusions

-- NCCN updated guidelines for NSCLC (May 2020)

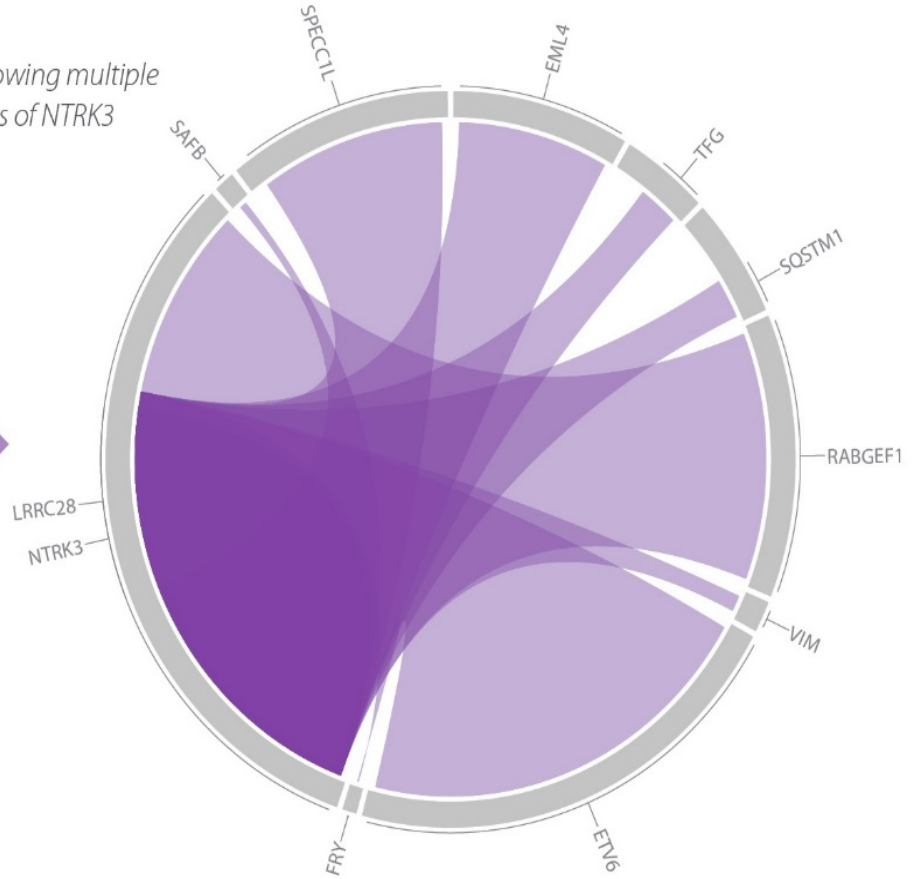
RNA Fusion Analysis Finds 50% More Actionable NTRK3 Partners than DNA

Distribution of NTRK fusions found in Caris database of cases run for RNA fusion testing

NTRK1	NTRK2	NTRK3
40%	22%	38%

ETV6	OTHER
50%	50%

Circos plot showing multiple fusion partners of NTRK3



* FoundationOneCDx (Source: https://www.accessdata.fda.gov/cdrh_docs/pdf17/P170019C.pdf

Complex State of PD-L1 Testing: Caris Uses the Right Assay for the Right Patient

PD-L1 antibody IO Therapy	SP142 (Ventana) atezoluzumab (Roche)	22c3 (Dako) pembrolizumab (Merck)	28-8 (Dako) nivolumab & ipilimumab (BMS)	22c3 cemiplimab (Regeneron)
Non-small cell lung cancer (NSCLC)	Companion TC ≥50% or IC ≥10%	Companion TPS ≥1	Companion Tumor cell ≥1%	TPS > 50%
Bladder Cancer	Companion IC ≥5%	Companion CPS ≥10		
Head and neck squamous cell carcinoma (HNSCC)	-	Companion CPS ≥1		
Gastric and Gastroesophageal Junction (GE/GEJ)	-	Companion CPS ≥1	-	
Ovarian		Consensus* CPS>=1		
Esophageal (SCC)	-	Companion CPS ≥10	-	
Cervical Cancer	-	Companion CPS ≥1	-	
Breast (association only in TNBC)	Companion IC ≥1%	Companion CPS ≥10	-	
Vulvar Cancer (SCC)	-	NCCN-recommended CPS ≥1	-	

Lab Developed Test (LDT) SP142 in the following tumor types with no drug association: melanoma, uveal melanoma, Merkel cell carcinoma, HCC, GBM/LGG, kidney, colorectal, uterine, GIST, pancreatic, prostate, salivary gland, soft tissue sarcomas
LDT SP142 with rules (pembro/nivo): CUP, thyroid, all other
** Recommendations based off Caris POA Tumor working groups*

Industry Leading Offerings With A Deep Pipeline

2019 Commercial Launches

MI Transcriptome™

Whole Transcriptome Sequencing

~22,000 full-gene RNA coverage

Received FDA breakthrough device designation (May 2019) as the only CDx to detect RNA gene fusions across all tumor types

First company to receive FDA BTD status for WTS

Launched in February 2019

2020 Commercial Launches & Pipeline

MI Exome™

Whole Exome Sequencing

~22,000 full-gene DNA coverage

Enhanced detection on 719 cancer relevant genes, MSI and TMB Includes LOH measurement

Cancer-associated pathogen assay – viruses, bacteria, fungi

Launched in April 2020

CARIS MAI™
MOLECULAR ARTIFICIAL INTELLIGENCE

Molecular Artificial Intelligence™

Machine learning from combined molecular and clinical data to create molecular signatures for:

Molecular diagnosis of the cancer

Predict patient response to treatment

Ongoing launches in 2020

Future Pipeline

CARISOME®

Liquid Profiling

Circulating Exome Assay

Comprehensive, blood-based molecular profiling approach for therapy selection

Early 2021.

CARISOME®

Blood-Based Dx

Circulating Exome Assay

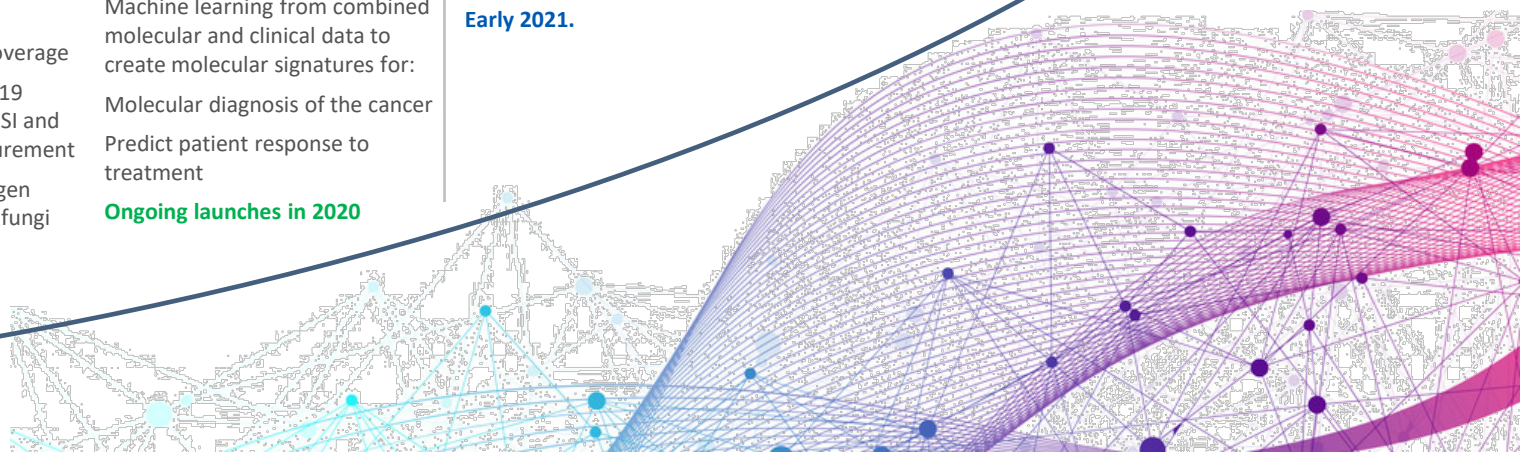
Comprehensive, blood-based molecular profiling approach for blood-based diagnostics

CARISOME®

MRD and Monitoring

Circulating Exome Assay

Comprehensive, blood-based molecular profiling approach for MRD and recurrence monitoring



CARIS®
LIFE SCIENCES

Caris MAI™ – Molecular Artificial Intelligence

Caris MAI™ Powered by DEAN (Caris Deliberation Analytics Engine)

A revolutionary platform to identify unique "molecular signatures" using **machine learning** and **multi-variate analysis** across our **clinical-genomic database.**

Molecular Testing + Matched Data + Proprietary Algorithms

NGS (DNA Alterations)
- Single Variants
- Insertions/Deletions
- Total Mutational Burden
- Microsatellite Instability

ISH (DNA Copies)
- Gene Copies
- Gene Translocations

RNA (Gene Expression)

IHC (Protein Expression)

ADAPT (Complexes)

+

Matched Clinical Outcomes Data

(~215,000+ patients and growing)

→

CARIS DEAN™ DELIBERATION ANALYTICS

(AI Cognitive Computing)

- Support Vector Machine
- Random Forest
- Linear Regression
- Logistic Regression
- Boosting
- Neural Networks
- Machine Learning

→

MI GPSai™

Genomic prevalence score for DNA/RNA classification. Intended for cancer of unknown primary (CUP), or cases with atypical clinical presentation or clinical ambiguity.

MI FOLFOXai™

Frontline therapy predictor for mCRC. Outcomes data from the MI FOLFOXai validation demonstrated a 71% difference in overall survival.

MI GPSai™– Machine Learning Applied to 55,780 Profiles

MI GPSai™

Genomic Prevalence Score analyzes a tumor's molecular signature and provides the prevalence of that signature in the Caris genomic (DNA) and transcriptomic (RNA) database across 21 cancer categories. Intended for Cancer of unknown primary (CUP) and atypical clinical presentation or cases with clinical ambiguity.

Brain	Gastroesophageal Carcinoma
Breast Carcinoma	Lung Carcinoma
Liver Hepatocellular Carcinoma	Colon Carcinoma
Urothelial Carcinoma	Pancreas Carcinoma
Prostate adenocarcinoma	Kidney Renal Cell Carcinoma
Melanoma	Cervical Carcinoma
Meningioma	Ovary Granulosa Cell Tumor
GIST	Ovary, Fallopian Tube Carcinoma
Thyroid Carcinoma	Endometrial Carcinoma
Squamous Cell Carcinoma	Uterus Sarcoma
Cholangiocarcinoma	

Overall performance metrics of assay on an independent test set of 15,473 cases

Sensitivity	Specificity	PPV	NPV	Accuracy	Call Rate
90.0%	98.0%	90.1%	98.6%	97.3%	97.5%

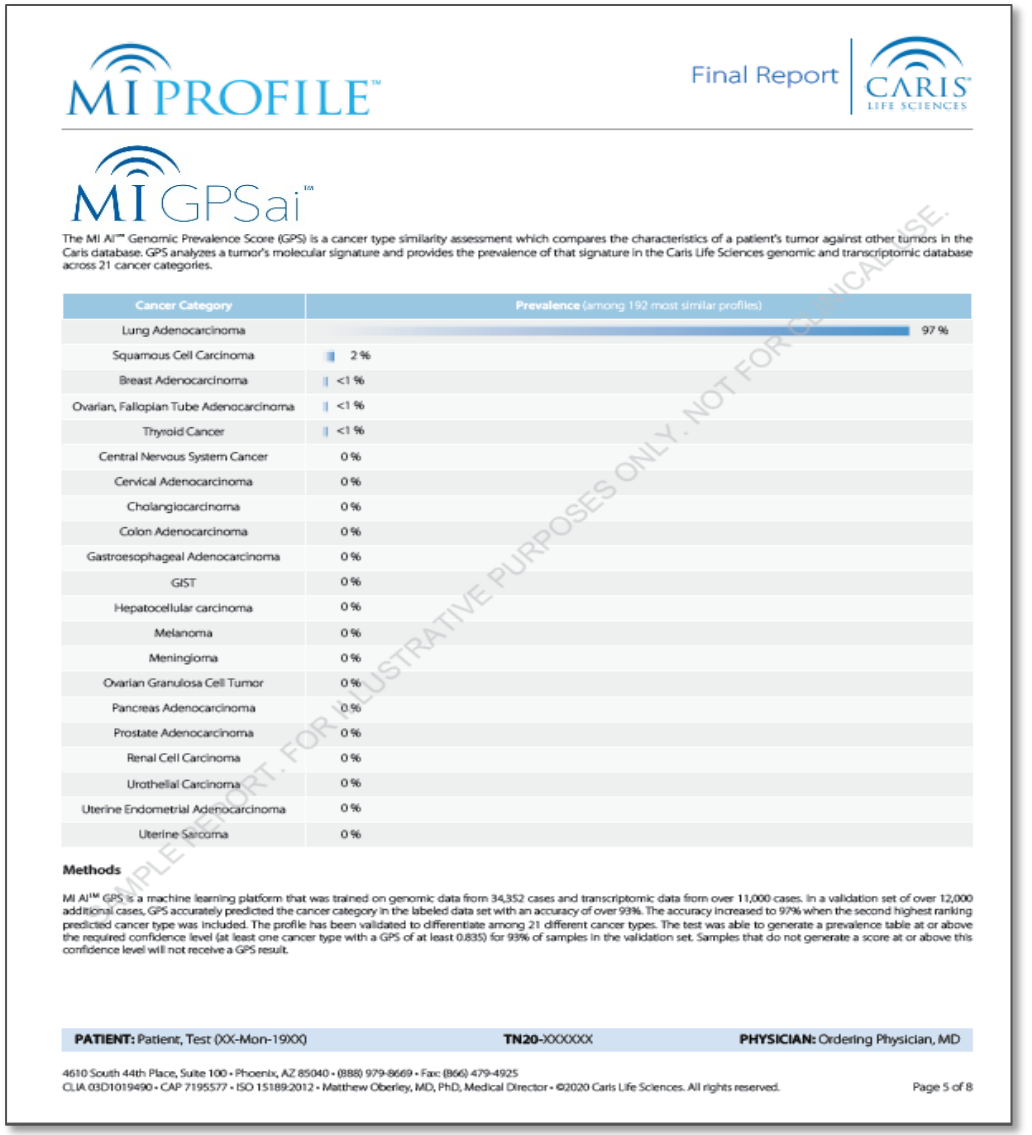
Robust on Biopsy Location and and Tumor Percentage

	Sensitivity	Specificity	PPV	NPV	Accuracy	Call Rate
Primary	91%	98%	91%	99%	98%	97%
Metastatic	89%	98%	89%	98%	97%	98%
20-50% Tumor	90%	98%	91%	98%	97%	97%
>50% Tumor	90%	98%	91%	98%	97%	97%

Abraham et al. J Clin Oncol 37, 2019 (suppl; abstr 3083)

MI GPSai™ Results

- Reports a prevalence score based off both genomic (DNA) and now transcriptomic (RNA) profiling data.
- Includes 21 cancer categories based off of histologic subtypes.
- Can be added to most solid tumor orders at the oncologist's discretion. Intent is for the test to only be requested for CUP and cases with atypical clinical presentation or clinical ambiguity.
- Must be requested by selecting the appropriate box on the requisition.



MI PROFILE™ Final Report | CARIS LIFE SCIENCES

MI GPSai™

The MI AI™ Genomic Prevalence Score (GPS) is a cancer type similarity assessment which compares the characteristics of a patient's tumor against other tumors in the Caris database. GPS analyzes a tumor's molecular signature and provides the prevalence of that signature in the Caris Life Sciences genomic and transcriptomic database across 21 cancer categories.

Cancer Category	Prevalence (among 192 most similar profiles)
Lung Adenocarcinoma	97 %
Squamous Cell Carcinoma	2 %
Breast Adenocarcinoma	<1 %
Ovarian, Fallopian Tube Adenocarcinoma	<1 %
Thyroid Cancer	<1 %
Central Nervous System Cancer	0 %
Cervical Adenocarcinoma	0 %
Cholangiocarcinoma	0 %
Colon Adenocarcinoma	0 %
Gastroesophageal Adenocarcinoma	0 %
GIST	0 %
Hepatocellular carcinoma	0 %
Melanoma	0 %
Meningioma	0 %
Ovarian Granulosa Cell Tumor	0 %
Pancreas Adenocarcinoma	0 %
Prostate Adenocarcinoma	0 %
Renal Cell Carcinoma	0 %
Urothelial Carcinoma	0 %
Uterine Endometrial Adenocarcinoma	0 %
Uterine Sarcoma	0 %

SAMPLE REPORT. FOR ILLUSTRATIVE PURPOSES ONLY. NOT FOR CLINICAL USE.

Methods

MI AI™ GPS is a machine learning platform that was trained on genomic data from 34,352 cases and transcriptomic data from over 11,000 cases. In a validation set of over 12,000 additional cases, GPS accurately predicted the cancer category in the labeled data set with an accuracy of over 93%. The accuracy increased to 97% when the second highest ranking predicted cancer type was included. The profile has been validated to differentiate among 21 different cancer types. The test was able to generate a prevalence table at or above the required confidence level (at least one cancer type with a GPS of at least 0.835) for 93% of samples in the validation set. Samples that do not generate a score at or above this confidence level will not receive a GPS result.

PATIENT: Patient, Test (XX-Mon-19XX) **TN20-**XXXXXX **PHYSICIAN:** Ordering Physician, MD

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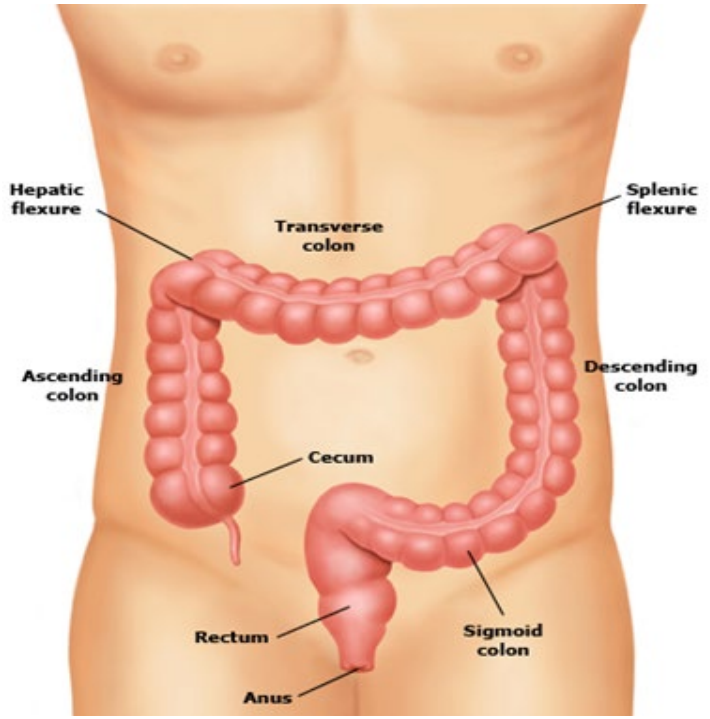
MI FOLFIRSTai™ Intended Use Statement

MI FOLFOXai™

MI FOLFIRSTai™ is the first clinically validated, AI-powered molecular predictor of chemotherapy efficacy for mCRC patients. MI FOLFIRSTai is intended to gauge a mCRC patient's likelihood of benefit from first-line FOLFOX (plus bevacizumab) treatment followed by FOLFIRI, versus FOLFIRI followed by FOLFOX (plus bevacizumab) treatment.

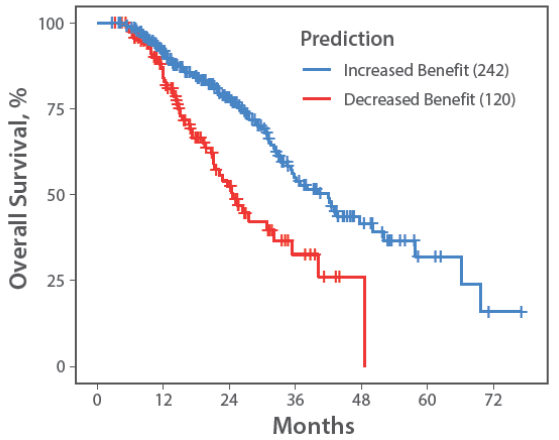


MI FOLFIRSTai™: 1st Clinically Validated AI-Driven Frontline Chemotherapy Predictor

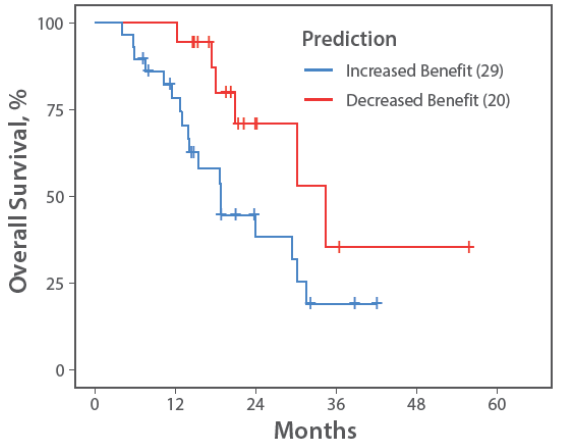
Median Overall Survival	MI FOLFIRSTai™ Indicates:	
	FOLFOX+BV 1st → FOLFIRI+BV 2nd (FOLFOX/BV RWE cohort)	**FOLFIRI+BV 1st → FOLFOX+BV 2nd** (FOLFIRI/BV RWE cohort)
OS When Patient Received: FOLFOX+BV 1st → FOLFIRI+BV 2nd	**42.0 months**	18.7 months
OS When Patient Received: FOLFIRI+BV 1st → FOLFOX+BV 2nd	24.5 months	**34.4 months**

1. Abraham JP, Magee D, Cremolini C, Antoniotti C, Halbert DD, Xiu J, Stafford P, Berry DA, Oberley MJ, Shields AF, Marshall JL, Salem ME, Falcone A, Grothey A, Hall MJ, Venook AP, Lenz HJ, Helmstetter A, Korn WM, Spetzler DB. Clinical validation of a machine-learning derived signature predictive of outcomes from first-line oxaliplatin-based chemotherapy in advanced colorectal cancer. Clin Cancer Res. 2020 Dec 8:clincanres.3286.2020. doi: 10.1158/1078-0432.CCR-20-3286. Epub ahead of print. PMID: 33293373

mCRC RWE FOLFOX+BV–FOLFIRI+BV



mCRC RWE FOLFIRI+BV–FOLFOX+BV

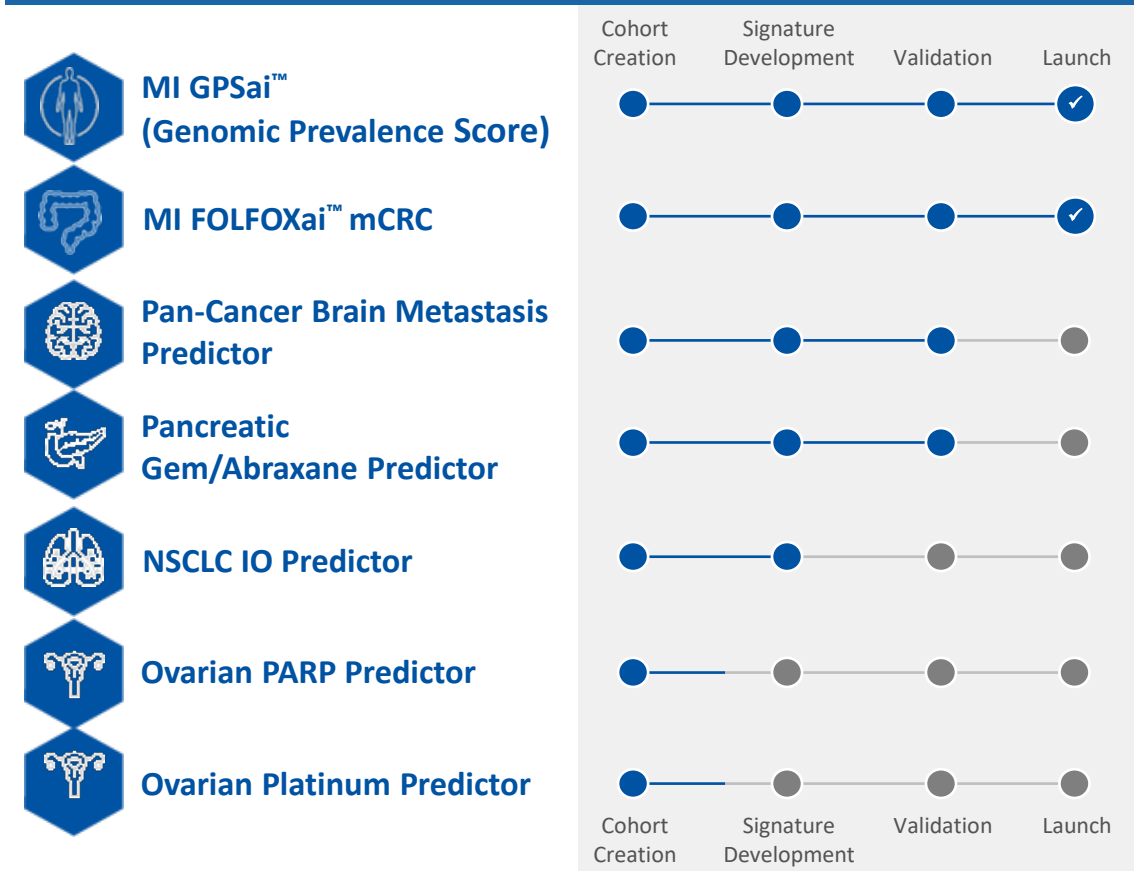


Leading Through Artificial Intelligence

The Largest Oncology Focused Clinico-Genomic Database

- 313,000+ Molecular Profiles
- 244,000+ Patients with longitudinal clinical outcome data
- 1,000,000+ data points per patient

Caris MAI™ Launches and Pipeline



Molecular Science Liaisons (MSL) – Local Scientific Support

PhDs, PharmDs or MDs with advanced oncology experience:

- Tumor Biology
- Molecular Diagnostic Techniques/Technologies
- Biomarker/Therapy Implications
- NCCN Guidelines for Biomarker Testing
- Clinical Trials

MSLs provide a wide range of support:

- **Educational:** supporting training and continuing molecular education of fellows, oncologists and others on the healthcare team
- **Technical:** explaining the capabilities of Caris NGS-based clinical offering
- **Clinical:** providing evidence to support the clinical utility of molecular profiling, including case consults, Molecular Tumor Board support, etc.
- **Research**: assessing research feasibility utilizing Caris' real world data, supporting the development of research proposals, and supporting the integration of Caris testing into investigator initiated trials

Caris has 40+ MSLs across the country providing local scientific and medical support.

MultiOmic Report

Cancer Type Relevant Genes

Certain genes were selected by their importance in Soft Tissue Tumors (ref per cancer). Each gene's expression is listed for the patient, along with that gene's percentile in Caris' cohort of Soft Tissue Tumors patients. Genes with expression between the 20th and 80th percentile are conservatively expressed within the variability of natural expression in cancer cells. Genes with expression above the 80th or below the 20th percentile may be considered an unusual outlier.

Gene	Transcript Per Million	Percentile in Cancer Type
NTRK3	486.337000	99.5%
CD274	3.895940	38.0%
NTRK1	0.277485	18.5%
TERT	0.029209	14.5%
NTRK2	0.279247	11.0%

Tumor Immmune Cell Content

Cell type	Percentage in Sample	Percentile in Cancer Type
"B cell"	9.4%	88.0%
"Macrophage M1"	0.0%	0.0%
"Macrophage M2"	6.3%	61.5%
"Monocyte"	0.1%	0.0%
"Neutrophil"	0.0%	0.0%
"NK cell"	3.1%	51.0%
"T cell CD4+ (non-regulatory)"	0.0%	0.0%
"T cell CD8+"	0.1%	62.0%
"T cell regulatory (Tregs)"	0.7%	33.0%
"Myeloid dendritic cell"	4.8%	82.0%
"uncharacterized cell"	75.6%	80.5%

Human Leukocyte Antigen

The genotype representing MHC Class I (HLA-A, B, C) or Class II (DPA1, DPB1, DQA1, DQB1, DRB1) are listed per patient, along with the expression and percentile for each gene. HLA molecules present neoantigens.

Gene	HLA Type by WTS	HLA Type by WES
HLA-A	A*24:02:01,A*02:01:01	A*02:01:126,A*24:419
HLA-B	B*39:01:01,B*35:01:01	B*39:136,B*58:01:17
HLA-C	C*07:02:01,C*04:01:01	C*04:01:88,C*07:02:01
HLA-DPA1	DPA1*01:03:01	DPA1*01:03:01
HLA-DPB1	DPB1*04:01:01,DPB1*04:02:01	DPB1*677:01,DPB1*701:01
HLA-DQA1	DQA1*04:01:01	DQA1*04:01:01
HLA-DQB1	QNS	DQB1*04:02:01,DQB1*03:96
HLA-DRB1	DRB1*08:02:01	DRB1*08:02:01,DRB1*16:04:01

Homologous Recombination Deficiency

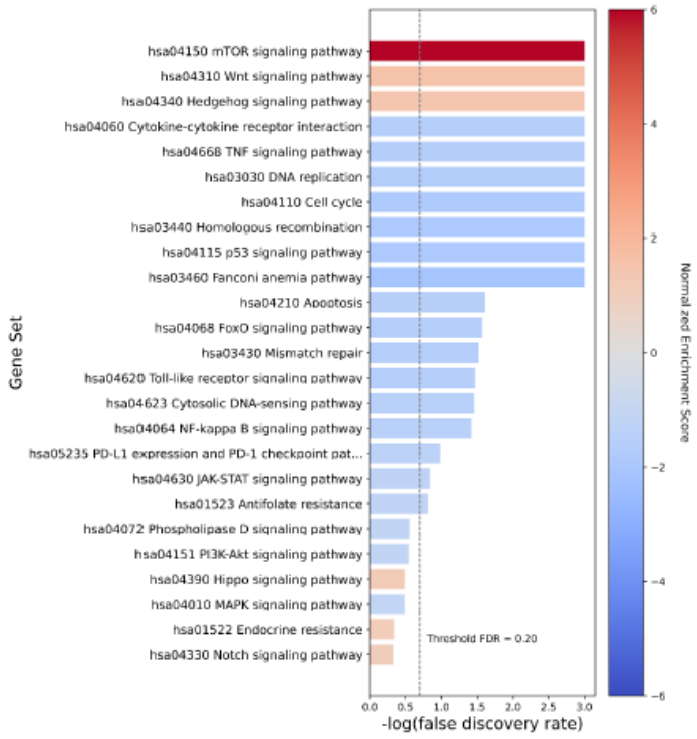
Marker	Score	Percentile in Cancer Type
LOH	28	96.0%
TAI	31	97.0%
LST	15	76.0%
HRD	74	96.0%

Loss of Heterozygosity in Cancer Type Relevant Genes

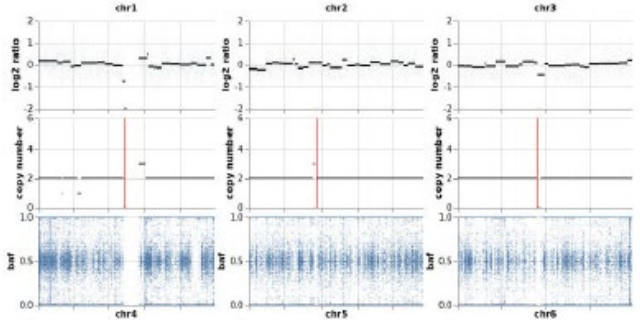
Copy number variation (CNV) include net gain or loss from parts of a chromosome. We measure gene-level copy variation. Results can range from complete deletion of both wild-type alleles of a gene (0:0) to gain at both alleles (i.e. 2:3). Some CNV changes can impact mRNA expression, however not all genes exhibit a linear relationship between gene dosage and transcript changes. The table below illustrates the different combinations that can appear.

Gene	Total_Copy	Copy_A	Copy_B	LoHcall
EPHA2	3.0	3.0	0.0	Copy Gain LoH
BRCA1	1.0	1.0	0.0	Copy Loss LoH
ERBB2	1.0	1.0	0.0	Copy Loss LoH
TP53	1.0	1.0	0.0	Copy Loss LoH
AKT1	1.0	1.0	0.0	Copy Loss LoH
RB1	1.0	1.0	0.0	Copy Loss LoH
BRCA2	1.0	1.0	0.0	Copy Loss LoH
GATA3	1.0	1.0	0.0	Copy Loss LoH

KEGG Cancer-Type Relevant Pathways



Electronic Karyotype



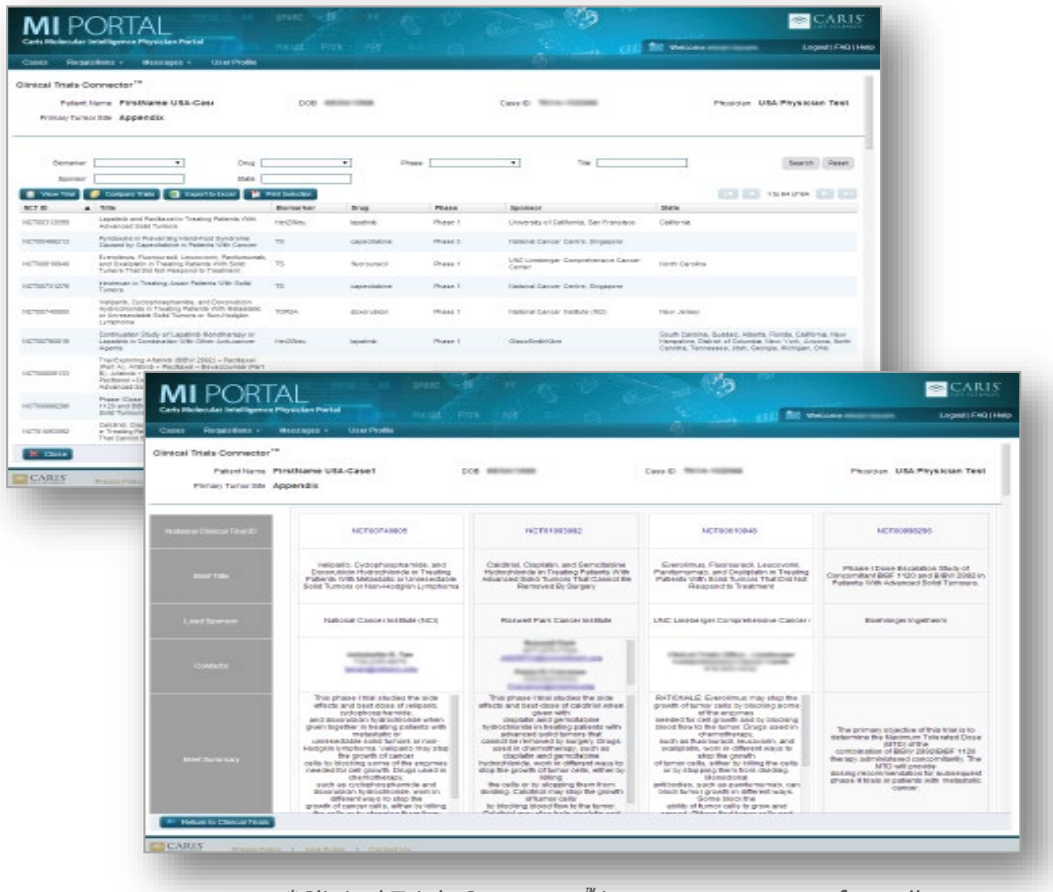
Clinical Trials Connector™

Molecularly Targeted Clinical Trials Matching Service

- Examines thousands of open and enrolling clinical trials
- Synced with ClinicalTrials.gov and other sources

- Matches clinical trials based on:
  - Gender
  - Age (date-of-birth)
  - Tumor type
  - Biomarker profile

- Includes interactive and customizable trial search filters by:
  - Biomarker
  - Therapeutic regimen
  - Phase of study
  - Study location(s)
  - Study sponsor



**Clinical Trials Connector™ is not a guarantee of enrollment.*

Private Payor Relationships

62 contracts, including Medicare, representing over 236M Covered Lives

National Payors In-Network

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Exclusive to Caris

aetna

Other Selected Managed Care Relationships

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BlueCross BlueShield of Illinois

Kansas City

CareFirst Maryland

Healthy Blue

HIGHMARK Pennsylvania

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Medicare
Medicare Advantage Plans

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Scott&White HEALTH PLAN
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Scripps

Teachers Health Trust
For Teachers By Teachers

TRICARE

TRPN
THREE RIVERS PROVIDER NETWORK

Wellmark Iowa

9.11 WTC Health Program

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Caris Support: Patient Responsibility & Assistance Programs

- Limited patient exposure across all payors, including Medicare:
  - 90% of patients do not receive a bill (no out of pocket expense)
  - Of the 10% that receive a bill, the average is $350.00

- Patient Billing Practices
  - File claims regardless of network status
  - Insurance verification
  - Submit appeals as needed
  - Typically limited to the patient's in-network deductible, co-payments and co-insurance

- Tumor Profiling Assistance
  - Patient Navigator support
  - Patient educational materials
  - Financial assistance program
  - Compassionate Care program
  - Payment plans

MI Portal - Online Resource for Physicians

- Order services via eRequisitions
  - Ensuring the most current req is available
- View interactive reports; links to:
  - ClinicalTrials.gov
  - PubMed.com
  - CarisMolecularIntelligence.com
- Download results
- Track patient reports & ETAs
- HIPAA-compliant

To enroll, visit

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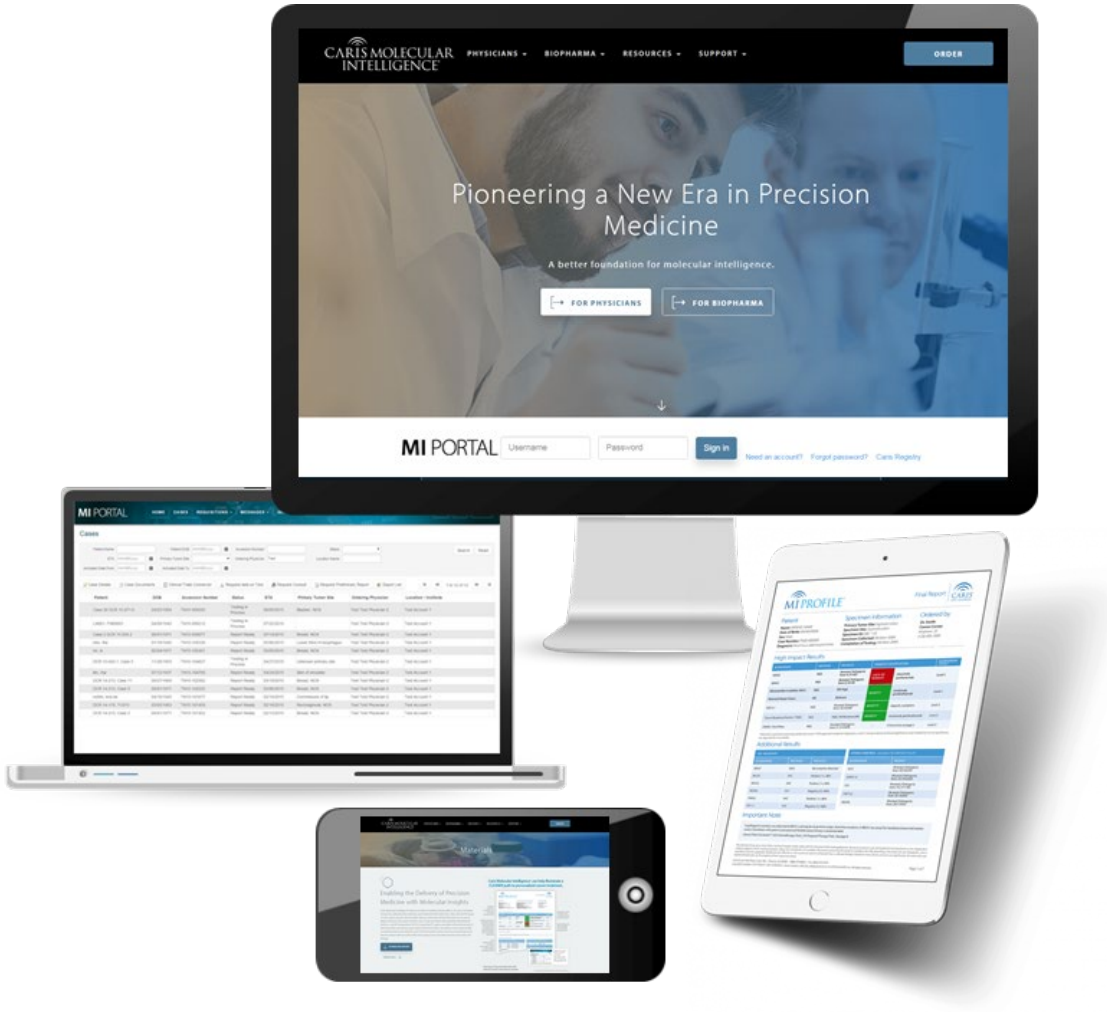
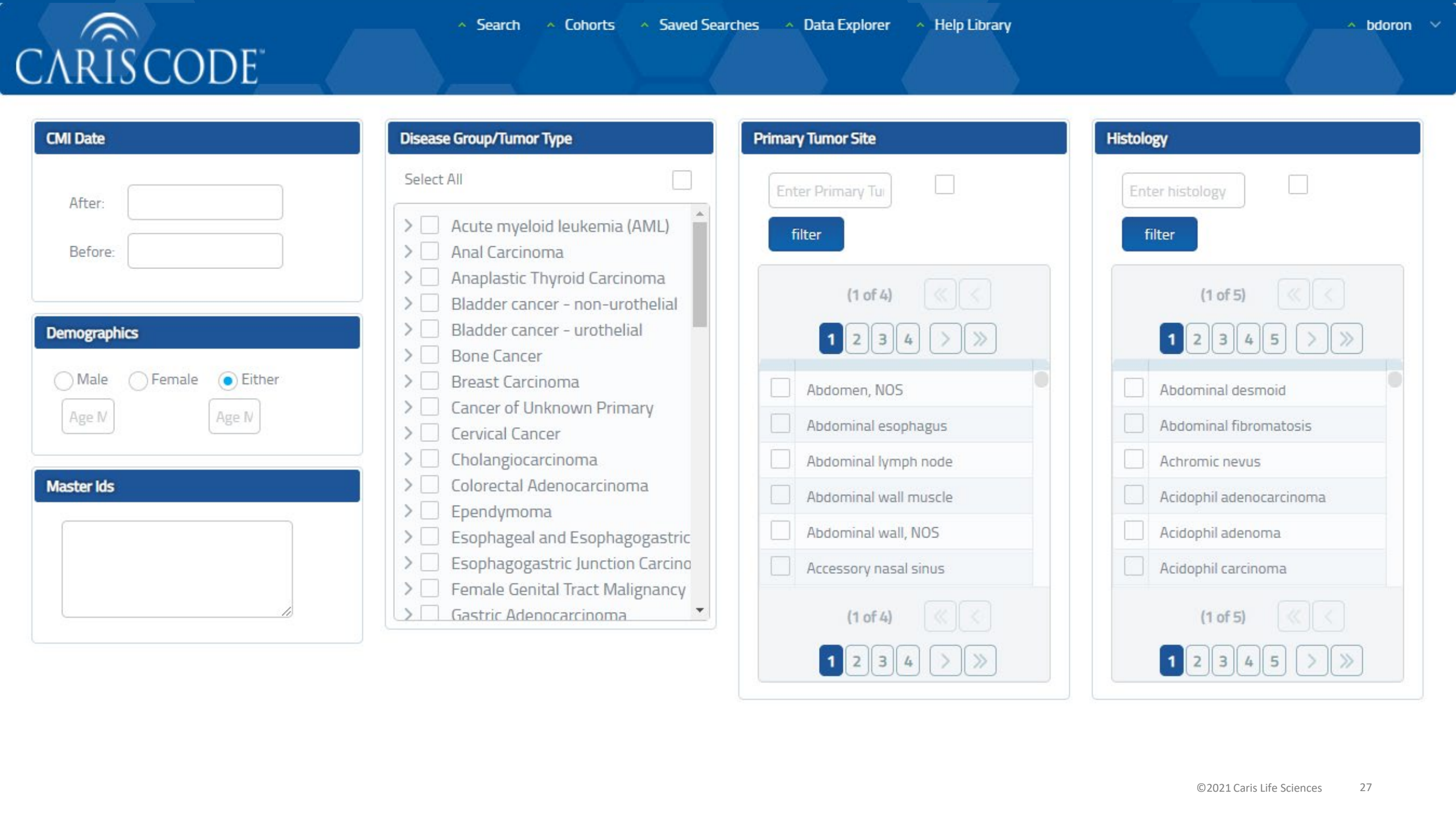
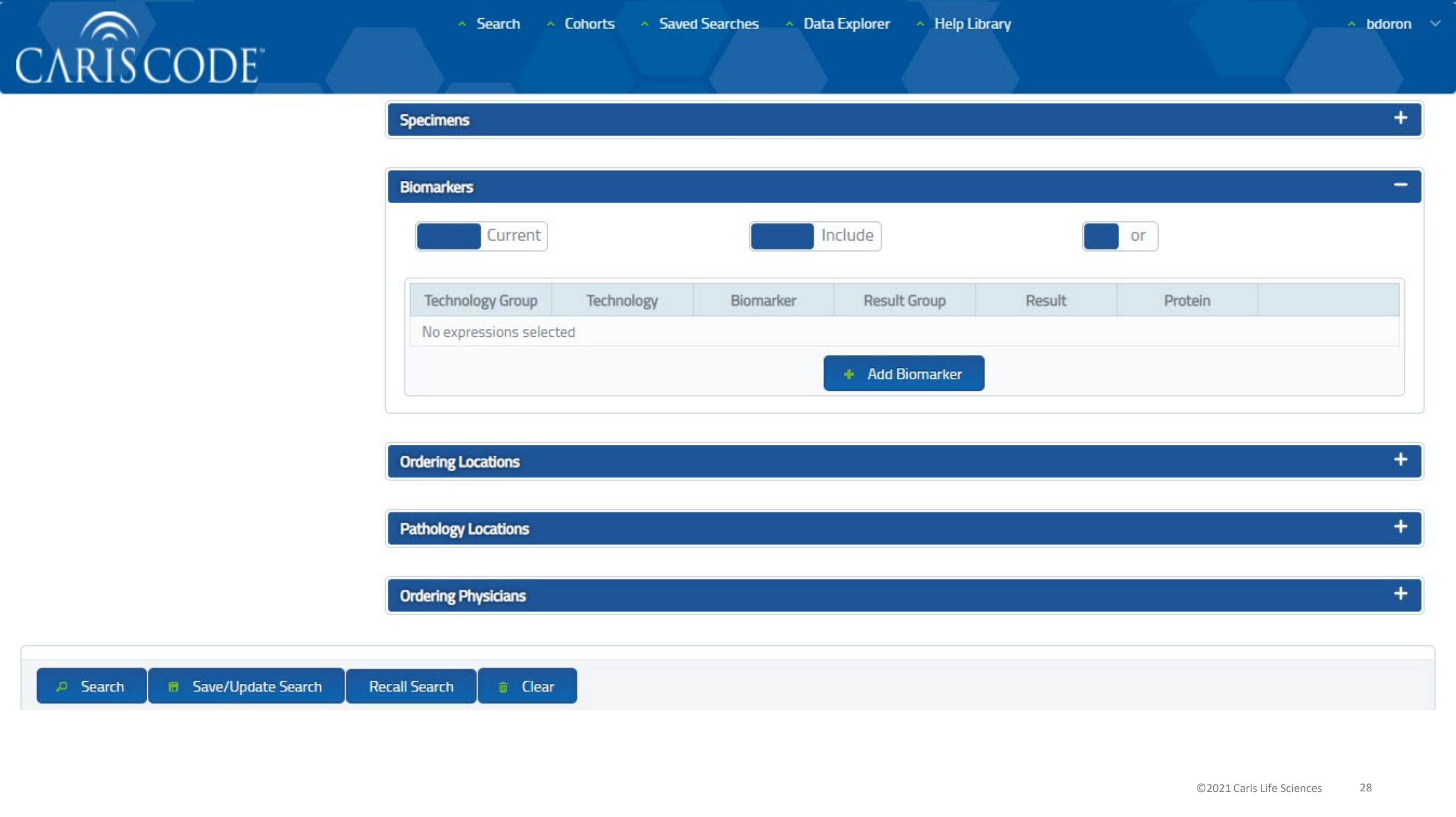
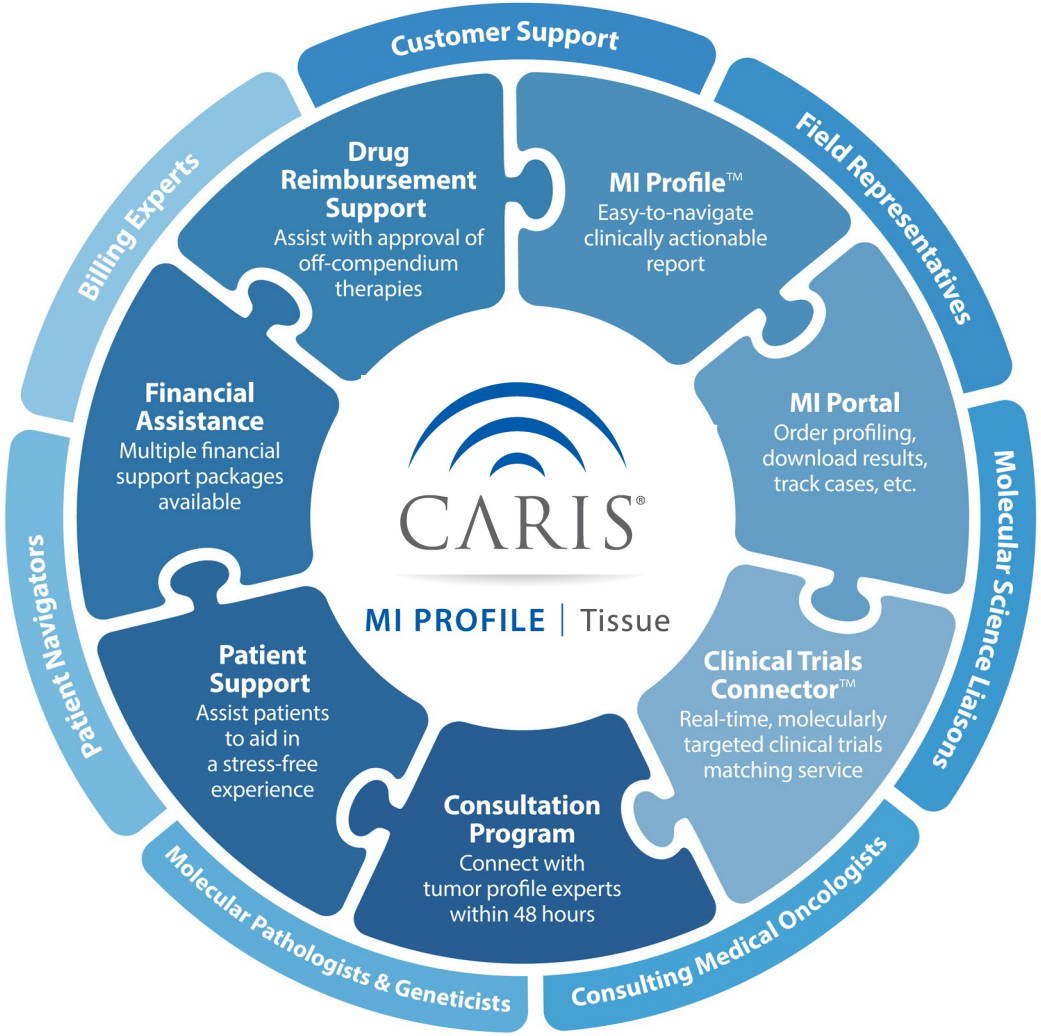






Integrated Commercial Team



- Fully integrated support from ordering to results interpretation:
  - MI Portal
  - Clinical Trials Connector
  - Consultation Program
  - Patient Support
  - Financial Assistance
  - Drug Reimbursement Support
- Supporting multiple audiences:
  - Physicians and staff
  - Patients and caregivers
  - Payors

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