

## Patient

**Name:**  
**Date of Birth:**  
**Sex:** Female  
**Case Number:** TN22-  
**Diagnosis:** High-grade serous carcinoma

## Specimen Information

**Primary Tumor Site:** Endometrium  
**Specimen Site:** Cervix, NOS  
**Specimen ID:**  
**Specimen Collected:**  
**Test Report Date:**

## Ordered By

## Results with Therapy Associations

BIOMARKER	METHOD	ANALYTE	RESULT	THERAPY ASSOCIATION	BIOMARKER LEVEL*
Mismatch Repair Status	IHC	Protein	Proficient	<b>BENEFIT</b> pembrolizumab + lenvatinib	Level 2
MSI	Seq	DNA-Tumor	Stable		
ER	IHC	Protein	Positive   2+, 60%	<b>BENEFIT</b> endocrine therapy	Level 3
PR	IHC	Protein	Positive   1+, 10%		
ERBB2 (Her2/Neu)	CISH	DNA-Tumor	Not Amplified	<b>LACK OF BENEFIT</b> trastuzumab + chemotherapy	Level 2
	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

This report includes IHC and/or CISH results from FDA-approved and laboratory-developed tests performed on tissue preserved with an unknown fixative. Caris and the manufacturer of these tests have validated their use only with formalin-fixed, paraffin-embedded tissues. The use of these stains on tissues processed with other fixatives is not recommended. IHC/CISH results should be interpreted with caution given the potential for false negative results.

The FDA has granted regular approval of pembrolizumab in combination with lenvatinib, for the treatment of patients with advanced endometrial carcinoma that are not microsatellite instability high (MSI-H) or mismatch repair deficient (dMMR), who have disease progression following prior systemic therapy and are not candidates for curative surgery or radiation.

## Cancer-Type Relevant Biomarkers

Biomarker	Method	Analyte	Result
ARID1A	Seq	DNA-Tumor	Pathogenic Variant Exon 18   p.S1516fs
		DNA-Tumor	Pathogenic Variant Exon 20   p.R1721*
	CNA-Seq	DNA-Tumor	Deletion Not Detected

Biomarker	Method	Analyte	Result
PIK3CA	Seq	DNA-Tumor	Pathogenic Variant Exon 2   p.R108H
		DNA-Tumor	Pathogenic Variant Exon 10   p.E542K

**(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.

## Cancer-Type Relevant Biomarkers (continued)

Biomarker	Method	Analyte	Result	Biomarker	Method	Analyte	Result
PTEN	Seq	DNA-Tumor	Pathogenic Variant Exon 5   p.R130G	BRCA1	CNA-Seq	DNA-Tumor	Deletion Not Detected
		DNA-Tumor	Pathogenic Variant Exon 7   c.635-1G>T		Seq	DNA-Tumor	Mutation Not Detected
	IHC	Protein	Positive   1+, 100%	BRCA2	CNA-Seq	DNA-Tumor	Deletion Not Detected
	CNA-Seq	DNA-Tumor	Deletion Not Detected		Seq	DNA-Tumor	Mutation Not Detected
	NTRK1/2/3	Seq	RNA-Tumor	Fusion Not Detected	KRAS	Seq	DNA-Tumor
Tumor Mutational Burden	Seq	DNA-Tumor	Low, 9 mut/Mb	POLE	CNA-Seq	DNA-Tumor	Deletion Not Detected
					Seq	DNA-Tumor	Mutation Not Detected

## Genomic Signatures

Biomarker	Method	Analyte	Result
Microsatellite Instability (MSI)	Seq	DNA-Tumor	Stable
Tumor Mutational Burden (TMB)	Seq	DNA-Tumor	<p>Result: Low</p> <p>Low 10 High</p>
Genomic Loss of Heterozygosity (LOH)	Seq	DNA-Tumor	Low - 7% of tested genomic segments exhibited LOH (assay threshold is ≥ 16%)

## Genes Tested with Pathogenic or Likely Pathogenic Alterations

Gene	Method	Analyte	Variant Interpretation	Protein Alteration	Exon	DNA Alteration	Variant Frequency %
ARHGAP35	Seq	DNA-Tumor *	Pathogenic Variant	p.T55fs	1	c.162dupT	17
ARID1A	Seq	DNA-Tumor	Pathogenic Variant	p.S1516fs	18	c.4544dupG	32
	Seq	DNA-Tumor	Pathogenic Variant	p.R1721*	20	c.5161C>T	29
CREBBP	Seq	DNA-Tumor	Pathogenic Variant	p.P383fs	4	c.1148delC	42
FBXW7	Seq	DNA-Tumor	Likely Pathogenic Variant	p.S462F	9	c.1385C>T	31
	Seq	DNA-Tumor	Pathogenic Variant	p.P64fs	2	c.191delC	30
FGFR2	Seq	DNA-Tumor	Pathogenic Variant	p.S252W	7	c.755C>G	20

Additional results continued on the next page. >

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## Genes Tested with Pathogenic or Likely Pathogenic Alterations

Gene	Method	Analyte	Variant Interpretation	Protein Alteration	Exon	DNA Alteration	Variant Frequency %
PIK3CA	Seq	DNA-Tumor	Pathogenic Variant	p.R108H	2	c.323G>A	30
	Seq	DNA-Tumor	Pathogenic Variant	p.E542K	10	c.1624G>A	31
PTEN	Seq	DNA-Tumor	Pathogenic Variant	p.R130G	5	c.388C>G	34
	Seq	DNA-Tumor	Pathogenic Variant	c.635-1G>T	7	c.635-1G>T	18
TP53	Seq	DNA-Tumor	Pathogenic Variant	p.R306*	8	c.916C>T	37
	Seq	DNA-Tumor	Pathogenic Variant	p.R213Q	6	c.638G>A	19

Unclassified alterations for RNA sequencing can be found in the MI Portal.

Formal nucleotide nomenclature and gene reference sequences can be found in the Appendix of this report.

## Human Leukocyte Antigen (HLA) Genotype Results

The impact of HLA genotypes on drug response and prognosis is an active area of research. These results can help direct patients to clinical trials recruiting for specific genotypes. Please see [www.clinicaltrials.gov](http://www.clinicaltrials.gov) for more information.

Gene	Method	Analyte	Genotype
MHC CLASS I			
HLA-A	Seq	DNA-Tumor	A*02:01, A*30:01
HLA-B	Seq	DNA-Tumor	B*07:02, B*13:02
HLA-C	Seq	DNA-Tumor	C*06:02, C*07:02

HLA genotypes with only one allele are either homozygous or have loss-of-heterozygosity at that position.

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