

FINAL REPORT

PATIENT	SPECIMEN INFORMATION	ORDERED BY
Name: Patient, Test Date of Birth: XX-Mon-19XX Sex: Female Case Number: TN16-XXXXXX Diagnosis: Carcinosarcoma, NOS	Primary Tumor Site: Ovary Specimen Site: Pelvis, NOS Specimen ID: ABC-1234-XY Specimen Collected: XX-Mon-2016 Testing Completed: XX-Mon-2016	Ordering Physician, MD The Cancer Center 123 Main Street Springfield, XY 12345 (123) 456-7890

Bold Therapies = On NCCN Compendium® Therapies

THERAPIES WITH POTENTIAL BENEFIT (PAGE 4)			
carboplatin, cisplatin, oxaliplatin	ERCC1, BRCA2 [★]	gemcitabine	RRM1 [★]
docetaxel, nab-paclitaxel, paclitaxel	TUBB3 [★]	olaparib	BRCA2 [★]
doxorubicin, liposomal-doxorubicin	TOP2A	Mitomycin-C	BRCA2 [★]
		epirubicin	TOP2A

★ Indicates Clinical Trial Opportunity • 224 Chemotherapy Trials • 55 Targeted Therapy Trials (See Clinical Trials Connector™ on page 7 for details.)

THERAPIES WITH POTENTIAL LACK OF BENEFIT (PAGE 5)			
anastrozole, exemestane, letrozole, leuprolide, megestrol acetate, tamoxifen	PR, ER	ado-trastuzumab emtansine (T-DM1), pertuzumab, trastuzumab	Her2/Neu
capecitabine, pemetrexed	TS	dabrafenib, vemurafenib	BRAF
irinotecan, topotecan	TOPO1	fluorouracil	TS
		fulvestrant, goserelin, toremifene	PR, ER

THERAPIES WITH INDETERMINATE BENEFIT (PAGE 6)		
everolimus, temsirolimus	imatinib	

Therapies associated with potential benefit or lack of benefit, as indicated above, are based on biomarker results provided in this report and are based on published medical evidence. This evidence may have been obtained from studies performed in the cancer type present in the tested patient's sample or derived from another tumor type. 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 in addition to this report concerning the patient's condition in accordance with the applicable standard of care.

SUMMARY OF RESULTS (SEE APPENDIX FOR FULL DETAILS)

Biomarker	Method	Result	Biomarker	Method	Result
ABL1	NGS	Mutation Not Detected	IDH1	NGS	Mutation Not Detected
AKT1	NGS	Mutation Not Detected	JAK2	NGS	Mutation Not Detected
ALK	NGS	Mutation Not Detected	JAK3	NGS	Mutation Not Detected
APC	NGS	Mutation Not Detected	KDR (VEGFR2)	NGS	Mutation Not Detected
ATM	NGS	Mutation Not Detected	KRAS	NGS	Mutation Not Detected
BRAF	NGS	Mutation Not Detected	MPL	NGS	Mutation Not Detected
BRCA1	NGS	Mutation Not Detected	NOTCH1	NGS	Mutation Not Detected
BRCA2	NGS	Mutated, Pathogenic Exon 11 E1953X	NPM1	NGS	Mutation Not Detected
c-KIT	NGS	Mutation Not Detected	NRAS	NGS	Mutation Not Detected
CDH1	NGS	Mutation Not Detected	PD-L1	IHC	Negative 0, 100%
cMET	NGS	Mutation Not Detected	PDGFRA	NGS	Mutation Not Detected
CSF1R	NGS	Mutation Not Detected	PIK3CA	NGS	Mutation Not Detected
CTNNB1	NGS	Mutation Not Detected	PR	IHC	Negative 0, 100%
EGFR	IHC (H-Score)	Positive 200	PTEN	IHC	Positive 2+, 80%
ER	IHC	Negative 1+, 1%	PTEN	NGS	Mutation Not Detected
ERBB4	NGS	Mutation Not Detected	PTPN11	NGS	Mutation Not Detected
ERCC1	IHC	Negative 2+, 10%	RB1	NGS	Mutation Not Detected
FBXW7	NGS	Mutation Not Detected	RET	NGS	Mutation Not Detected
FGFR1	NGS	Mutation Not Detected	RRM1	IHC	Negative 2+, 30%
FGFR2	NGS	Mutation Not Detected	SMAD4	NGS	Mutation Not Detected
FLT3	NGS	Mutation Not Detected	SMARCB1	NGS	Mutation Not Detected
GNA11	NGS	Mutation Not Detected	SMO	NGS	Mutation Not Detected
GNAQ	NGS	Mutation Not Detected	STK11	NGS	Mutation Not Detected
GNAS	NGS	Mutation Not Detected	TOP2A	IHC	Positive 1+, 10%
Her2/Neu	CISH	Not Amplified	TOPO1	IHC	Negative 0, 100%
Her2/Neu (ERBB2)	IHC	Negative 1+, 20%	TP53	NGS	Mutated, Pathogenic Exon 5 H178fs
Her2/Neu (ERBB2)	NGS	Mutation Not Detected	TS	IHC	Positive 1+, 20%
HRAS	NGS	Mutation Not Detected	TUBB3	IHC	Negative 2+, 2%
			VHL	NGS	Mutation Not Detected

IHC: Immunohistochemistry

CISH: Chromogenic *in situ* hybridization **NGS:** Next-Generation Sequencing

The Next-Generation Sequencing results above include only the genes most commonly associated with cancer. See summary below and for full Next-Generation Sequencing results, see Appendix page 1.

See the Appendix section for a detailed overview of the biomarker test results for each technology.

Biomarker Results continued on the next page. >

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

NOTES OF SIGNIFICANCE

SEE APPENDIX FOR FULL DETAILS

Mutation analysis of BRCA1 and BRCA2 identified a E1953X (Mutated, Pathogenic) mutation in BRCA2.

Next-Generation Sequencing:

Genes tested: 45 | Genes with actionable mutations: 2 | Genes with unclassified mutations: 0 | Genes with no mutations detected: 43

Note: The Caris Molecular Intelligence NGS test is not intended to identify or diagnose a hereditary condition. Mutations detected in this assay may be somatic or germline in origin and are used primarily for theranostic purposes. Appropriate genetic counseling and testing may be considered.

Immunohistochemistry:

Inflammatory PD-L1 cells expression is seen in approximately 5% of the tumor volume.

Chromogenic in situ Hybridization:

Her2/Neu by CISH also reviewed by another Pathologist who agrees with the above entered results.

✓ THERAPIES WITH **POTENTIAL BENEFIT**

Therapies	Test	Method	Result	Value [†]	Clinical Association				
					Potential Benefit	Decreased Potential Benefit	Lack of Potential Benefit	Highest Level of Evidence*	Reference
Mitomycin-C	BRCA1	NGS	Mutation Not Detected					II-3 / Good	1 [#] , 2, 3
	BRCA2	NGS	Mutated, Pathogenic	E1953X	✓			II-3 / Good	1 [#] , 2, 3
carboplatin, cisplatin, oxaliplatin	ATM	NGS	Mutation Not Detected					II-2 / Good	32, 33 [#] , 34
	BRCA1	NGS	Mutation Not Detected					II-2 / Good	29 [#] , 30 [#] , 31
	BRCA2	NGS	Mutated, Pathogenic	E1953X	✓			II-2 / Good	29 [#] , 30 [#] , 31
	ERCC1	IHC	Negative	2+ 10%	✓			II-3 / Good	27 [#] , 28 [#]
docetaxel, nab-paclitaxel, paclitaxel	TUBB3	IHC	Negative	2+ 2%	✓			II-3 / Good	39 [#] , 40 [#] , 41
doxorubicin, epirubicin, liposomal-doxorubicin	TOP2A	IHC	Positive	1+ 10%	✓			I / Good	42, 43
gemcitabine	RRM1	IHC	Negative	2+ 30%	✓			I / Good	47
olaparib	BRCA1	NGS	Mutation Not Detected					I / Good	56 [#] , 57 [#] , 58 [#] , 59
	BRCA2	NGS	Mutated, Pathogenic	E1953X	✓			I / Good	56 [#] , 57 [#] , 58 [#] , 59

* The level of evidence for all references is assigned according to the Literature Level of Evidence Framework consistent with the US Preventive Services Task Force described further in the Appendix of this report. The data level of each biomarker-drug interaction is the highest level of evidence based on the body of evidence, overall clinical utility, competing biomarker interactions and tumor type from which the evidence was gathered.

Evidence reference includes data from the same lineage as the tested specimen.

†Refer to Appendix for detailed Result and Value information for each biomarker, including appropriate cutoffs, unit of measure, etc.

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

X THERAPIES WITH POTENTIAL LACK OF BENEFIT

Therapies	Test	Method	Result	Value [†]	Clinical Association				Reference
					Potential Benefit	Decreased Potential Benefit	Lack of Potential Benefit	Highest Level of Evidence*	
ado-trastuzumab emtansine (T-DM1), pertuzumab, trastuzumab	Her2/Neu	CISH	Not Amplified	1.39			✓	I / Good	4 [#] , 5, 6, 7, 9, 10, 11, 12
	Her2/Neu	IHC	Negative	1+ 20%			✓	I / Good	4 [#] , 5, 6, 7, 8 [#] , 9, 10, 11
anastrozole, exemestane, fulvestrant, goserelin, letrozole, leuprolide, megestrol acetate, tamoxifen, toremifene	ER	IHC	Negative	1+ 1%			✓	I / Good	13, 16, 17, 18, 19, 20, 21, 22, 23
	PR	IHC	Negative	0+ 100%			✓	I / Good	13, 14, 15, 16, 17, 18, 19, 20, 21
capecitabine, fluorouracil, pemetrexed	TS	IHC	Positive	1+ 20%			✓	II-1 / Good	24, 25, 26
dabrafenib, vemurafenib	BRAF	NGS	Mutation Not Detected				✓	I / Good	35, 36, 37, 38
irinotecan, topotecan	TOPO1	IHC	Negative	0+ 100%			✓	II-1 / Good	53, 54 [#] , 55 [#]

* The level of evidence for all references is assigned according to the Literature Level of Evidence Framework consistent with the US Preventive Services Task Force described further in the Appendix of this report. The data level of each biomarker-drug interaction is the highest level of evidence based on the body of evidence, overall clinical utility, competing biomarker interactions and tumor type from which the evidence was gathered.

Evidence reference includes data from the same lineage as the tested specimen.

†Refer to Appendix for detailed Result and Value information for each biomarker, including appropriate cutoffs, unit of measure, etc.

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

? THERAPIES WITH INDETERMINATE BENEFIT
(Biomarker results do not impact potential benefit or lack of potential benefit)

Therapies	Test	Method	Result	Value [†]	Clinical Association				
					Potential Benefit	Decreased Potential Benefit	Lack of Potential Benefit	Highest Level of Evidence*	Reference
everolimus, temsirolimus	PIK3CA	NGS	Mutation Not Detected			✓		II-2 / Good	44 [#] , 45 [#] , 46 [#]
imatinib	c-KIT	NGS	Mutation Not Detected				✓	II-2 / Good	51, 52
	PDGFRA	NGS	Mutation Not Detected				✓	II-3 / Good	48, 49, 50

* The level of evidence for all references is assigned according to the Literature Level of Evidence Framework consistent with the US Preventive Services Task Force described further in the Appendix of this report. The data level of each biomarker-drug interaction is the highest level of evidence based on the body of evidence, overall clinical utility, competing biomarker interactions and tumor type from which the evidence was gathered.

Evidence reference includes data from the same lineage as the tested specimen.

†Refer to Appendix for detailed Result and Value information for each biomarker, including appropriate cutoffs, unit of measure, etc.

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

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

CLINICAL TRIALS CONNECTOR™

For a complete list of open, enrolling clinical trials visit MI Portal to access the [Clinical Trials Connector](#). This personalized, real-time web-based service provides additional clinical trial information and enhanced searching capabilities, including, but not limited to:

- Location: filter by geographic area
- Biomarker(s): identify specific biomarkers associated with open clinical trials to choose from
- Drug(s): search for specific therapies
- Trial Sponsor: locate trials based on the organization supporting the trial(s)

Visit www.CarisMolecularIntelligence.com to view all matched trials.

CHEMOTHERAPY CLINICAL TRIALS (224)

Drug Class	Biomarker	Method	Investigational Agent(s)
DNA minor groove binding agents (8)	BRCA2	NGS	PM01183 (lurbinectedin), trabectedin
Nucleoside analog (37)	RRM1	IHC	gemcitabine
Platinum compounds (92)	BRCA2	NGS	carboplatin, cisplatin, oxaliplatin
Taxanes (87)	TUBB3	IHC	cabazitaxel, docetaxel, paclitaxel

TARGETED THERAPY CLINICAL TRIALS (55)

Drug Class	Biomarker	Method	Investigational Agent(s)
Cell cycle inhibitors (6)	TP53	NGS	LY2606368, MK-1775
EGFR monoclonal antibody (8)	EGFR	IHC	cetuximab
p53 activators (1)	TP53	NGS	PRIMA
p53-targeted biological agents (2)	TP53	NGS	modified vaccinia virus ankara vaccine expressing p53
PARP inhibitors (38)	BRCA2	NGS	BMN-673, olaparib, rucaparib, veliparib

() = represents the total number of clinical trials identified by the Clinical Trials Connector for the provided drug class or table.

REFERENCES

SOURCE	LEVEL OF EVIDENCE*
1. Moiseyenko, V.M, E.N. Imyantiov, et al. (2014). "Evidence for clinical efficacy of Mitomycin C in heavily pretreated ovarian cancer patients carrying germ-line BRCA1 mutation." <i>Med Oncol</i> 31:199. View Citation Online	II-3 / Good
2. Vyas, O., M.W. Saif, et al. (2015). "Clinical outcomes in pancreatic adenocarcinoma associated with BRCA-2 mutation." <i>Anti-Cancer Drugs</i> 26:224-226. View Citation Online	III / Good
3. Chalasani, P., T. Dragovich, et al. (2008). "Response to a Third-Line Mitomycin C (MMC)-Based Chemotherapy in a Patient with Metastatic Pancreatic Adenocarcinoma Carrying Germline BRCA2 Mutation." <i>JOP</i> 9(3): 305-308. View Citation Online	III / Good
4. McAlpine, J.N., D.M. Miller, et al. (2009). "HER2 overexpression and amplification is present in a subset of ovarian mucinous carcinomas and can be targeted with trastuzumab therapy." <i>BMC Cancer</i> . 9:433. doi: 10.1186/1471-2407/9/433. View Citation Online	II-3 / Fair
5. Baselga, J., S.M. Swain, et al. (2012). "Pertuzumab plus trastumab plus docetaxel for metastatic breast cancer". <i>N. Engl. J. Med.</i> 36:109-119. View Citation Online	I / Good
6. Yin, W., J. Lu, et al. (2011). "Trastuzumab in adjuvant treatment HER2-positive early breast cancer patients: A meta-analysis of published randomized controlled trials." <i>PLoS ONE</i> 6(6): e21030. doi:10.1371/journal.pone.0021030. View Citation Online	I / Good
7. Cortes, J., J. Baselga, et al. (2012). "Pertuzumab monotherapy after trastuzumab-based treatment and subsequent reintroduction of trastuzumab: activity and tolerability in patients with advanced human epidermal growth factor receptor-2-positive breast cancer." <i>J. Clin. Oncol.</i> 30. DOI: 10.1200/JCO.2011.37.4207. View Citation Online	II-1 / Good
8. Bookman, M.A., I.R. Horowitz, et al. (2003). "Evaluation of Monoclonal Humanized Anti-HER2 Antibody, Trastuzumab, in Patients With Recurrent or Refractory Ovarian or Primary Peritoneal Carcinoma With Overexpression of HER2: A Phase II Trial of the Gynecologic Oncology Group." <i>J. Clin. Oncol.</i> 21:283-290. View Citation Online	II-2 / Fair
9. Hurvitz, S.A., E.A. Perez, et al. (2013) "Phase II randomized study of trastuzumab emtansine versus trastuzumab plus docetaxel in patients with human epidermal growth factor receptor 2-positive metastatic breast cancer." <i>J Clin Oncol.</i> 31(9):1157-63 View Citation Online	I / Good
10. Slamon, D., M. Buys, et al. (2011). "Adjuvant trastuzumab in HER2-positive breast cancer." <i>N. Engl. J. Med.</i> 365:1273-83. View Citation Online	I / Good
11. Verma, S., K. Blackwell, et al. (2012) "Trastuzumab Emtansine for HER2-Positive Advanced Breast Cancer" <i>N Engl J Med.</i> 367(19):1783-91. View Citation Online	I / Good
12. Bartlett, J.M.S., K. Miller, et al. (2011). "A UK NEQAS ISH multicenter ring study using the Ventana HER2 dual-color ISH assay." <i>Am. J. Clin. Pathol.</i> 135:157-162. View Citation Online	II-3 / Good
13. Bartlett, J.M.S., D. Rea, et al. (2011). "Estrogen receptor and progesterone receptor as predictive biomarkers of response to endocrine therapy: a prospectively powered pathology study in the Tamoxifen and Exemestane Adjuvant Multinational trial." <i>J Clin Oncol</i> 29 (12):1531-1538. View Citation Online	I / Good
14. Stendahl, M., L. Ryden, et al. (2006). "High progesterone receptor expression correlates to the effect of adjuvant tamoxifen in premenopausal breast cancer patients." <i>Clin Cancer Res</i> 12(15): 4614-8. View Citation Online	I / Good
15. Yamashita, H., Y. Yando, et al. (2006). "Immunohistochemical evaluation of hormone receptor status for predicting response to endocrine therapy in metastatic breast cancer." <i>Breast Cancer</i> 13(1): 74-83. View Citation Online	II-3 / Good
16. Stuart, N.S.A., H. Earl, et al. (1996). "A randomized phase III cross-over study of tamoxifen versus megestrol acetate in advanced and recurrent breast cancer." <i>European Journal of Cancer</i> . 32(11):1888-1892. View Citation Online	II-2 / Fair
17. Coombes, R.C., J.M. Bliss, et al. (2007). "Survival and safety of exemestane versus tamoxifen after 2-3 years' tamoxifen treatment (Intergroup Exemestane Study): a randomized controlled trial." <i>The Lancet</i> 369:559-570. View Citation Online	I / Good

* See Appendix page 6 for Level of Evidence description.

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

REFERENCES

SOURCE	LEVEL OF EVIDENCE*
18. Thurlimann, B., A. Goldhirsch, et al. (1997). "Formestane versus Megestrol Acetate in Postmenopausal Breast Cancer Patients After Failure of Tamoxifen: A Phase III Prospective Randomised Cross Over Trial of Second-line Hormonal Treatment (SAKK 20/90). E J Cancer 33 (7): 1017-1024. View Citation Online	II-2 / Fair
19. Lewis, J.D., M.J. Edwards, et al. (2010). "Excellent outcomes with adjuvant toremifene or tamoxifen in early stage breast cancer." Cancer 116:2307-15. View Citation Online	I / Good
20. Dowsett, M., C. Allred, et al. (2008). "Relationship between quantitative estrogen and progesterone receptor expression and human epidermal growth factor receptor 2 (HER-2) status with recurrence in the Arimidex, Tamoxifen, Alone or in Combination trial." J Clin Oncol 26(7): 1059-65. View Citation Online	II-2 / Fair
21. Cuzick J, LHRH-agonists in Early Breast Cancer Overview group. (2007). "Use of luteinising-hormone-releasing hormone agonists as adjuvant treatment in premenopausal patients with hormone-receptor-positive breast cancer: a meta-analysis of individual patient data from randomised adjuvant trials." The Lancet 369: 1711-1723. View Citation Online	I / Good
22. Anderson, H., M. Dowsett, et al. (2011). "Relationship between estrogen receptor, progesterone receptor, HER-2 and Ki67 expression and efficacy of aromatase inhibitors in advanced breast cancer. Annals of Oncology. 22:1770-1776. View Citation Online	II-3 / Good
23. Viale, G., M. M. Regan, et al. (2008). "Chemoendocrine compared with endocrine adjuvant therapies for node-negative breast cancer: predictive value of centrally reviewed expression of estrogen and progesterone receptors--International Breast Cancer Study Group." J Clin Oncol 26(9): 1404-10. View Citation Online	II-3 / Good
24. Chen, C.-Y., P.-C. Yang, et al. (2011). "Thymidylate synthase and dihydrofolate reductase expression in non-small cell lung carcinoma: The association with treatment efficacy of pemetrexed." Lung Cancer 74(1): 132-138. View Citation Online	II-1 / Good
25. Yu, Z., Q. Yang, et al. (2005). "Thymidylate synthase predicts for clinical outcome in invasive breast cancer." Histology and Histopathology. 20:871-878. View Citation Online	II-3 / Good
26. Lee, S.J., Y.H. Im, et al. (2010). "Thymidylate synthase and thymidine phosphorylase as predictive markers of capecitabine monotherapy in patients with anthracycline- and taxane-pretreated metastatic breast cancer." Cancer Chemother. Pharmacol. DOI 10.1007/s00280-010-1545-0. View Citation Online	II-3 / Good
27. Scheil-Bertram, S., A. Fisseler-Eckhoff, et al. (2010). "Excision repair cross-complementation group 1 protein overexpression as a predictor of poor survival for high-grade serous ovarian adenocarcinoma." Gynecologic Oncology. 119, 325-331. View Citation Online	II-3 / Good
28. Steffensen, K.D., A. Jakobsen, et al. (2009). "The Relationship of Platinum Resistance and ERCC1 Protein Expression in Epithelial Ovarian Cancer." Int. J. Gynecol. Cancer 19: 820-825. View Citation Online	II-3 / Good
29. Tan, D.S.P., M.E. Gore, et al. (2008). "BRCAness" syndrome in ovarian cancer: a case-control study describing the clinical features and outcome of patients with epithelial ovarian cancer associated with BRCA1 and BRCA2 mutations." J Clin Oncol. 26(34):5530-6. View Citation Online	II-2 / Good
30. Hennessy, B.T., G.B. Mills, et al. (2010). "Somatic mutations in BRCA1 and BRCA2 could expand the number of patients that benefit from poly (ADP ribose) polymerase inhibitors in ovarian cancer" J Clin Oncol. 28(22):3570-6. View Citation Online	II-3 / Good
31. Lowery, M.A., E.M. O'Reilly, et al. (2011). "An emerging entity: pancreatic adenocarcinoma associated with a known BRCA mutation: clinical descriptors, treatment implications, and future directions." Oncologist. 16(10):1397-402. View Citation Online	II-3 / Fair
32. Bambury, R.M., J.E. Rosenberg, et al. (2015). "Association of somatic mutations in DNA damage repair (DDR) genes with efficacy of platinum-based chemotherapy in advanced urothelial carcinoma". J Clin Oncol. 33, (suppl; abstr 4532).	III / Good
33. Pennington, K.P., E.M. Swisher, et al. (2014). "Germline and somatic mutations in homologous recombination genes predict platinum response and survival in ovarian, fallopian tube, and peritoneal carcinomas". Clin Cancer Res. 20(3):764-775.	II-3 / Good
34. Plimack, E.R., E.A. Ross, et al. (2015). "Defects in DNA repair genes predict response to neoadjuvant cisplatin-based chemotherapy in muscle-invasive bladder cancer". Eur Urol. 68:959-967.	II-2 / Good

* See Appendix page 6 for Level of Evidence description.

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

REFERENCES

SOURCE	LEVEL OF EVIDENCE*
35. Flaherty, K.T., P.B. Chapman, et al. (2010). "Inhibition of Mutated, Activated BRAF in Metastatic Melanoma." N Engl J Med 363:809-819. View Citation Online	II-2 / Good
36. Hauschild, A., P.B. Chapman, et al. (2012). "Dabrafenib in BRAF-mutated metastatic melanoma: a multicentre, open-label, phase 3 randomised controlled trial." Lancet 358-365. View Citation Online	I / Good
37. Chapman, P.B., G.A. McArthur, et al. (2011). "Improved survival with vemurafenib in melanoma with BRAF V600E mutation." N. Engl. J. Med. This article (10.1056/NEJMoa1103782) was published on June 5, 2011, at nejm.org. View Citation Online	I / Good
38. Falchook, G.S., R. F. Kefford, et al. (2012). "Dabrafenib in patients with melanoma, untreated brain metastases, and other solid tumours: a phase I dose-escalation trial." Lancet 379:1893-901. View Citation Online	II-2 / Good
39. Ferrandina, G., C. Ferlini, et al. (2006). "Class III b-tubulin overexpression is a marker of poor clinical outcome in advanced ovarian cancer patients." Clin. Can. Res. 12(9): 2774-2779. View Citation Online	II-3 / Good
40. Gao, S., J. Gao, et al. (2012). "Clinical implications of REST and TUBB3 in ovarian cancer and its relationship to paclitaxel resistance." Tumor Biol 33:1759-1765. View Citation Online	II-3 / Good
41. Seve, P., C. Dumontet, et al. (2005). "Class III β -tubulin expression in tumor cells predicts response and outcome in patients with non-small cell lung cancer receiving paclitaxel." Mol Cancer Ther 4(12): 2001-2007. View Citation Online	II-3 / Good
42. O'Malley, F.P., K.I. Pritchard, et al. (2011). "Topoisomerase II alpha protein and responsiveness of breast cancer to adjuvant chemotherapy with CEF compared to CMF in the NCIC CTG randomized MA.5 adjuvant trial." Breast Can Res Treat. 128, 401-409. View Citation Online	I / Good
43. Rodrigo, R.S., C. Axel le, et al. (2011). "Topoisomerase II-alpha protein expression and histological response following doxorubicin-based induction chemotherapy predict survival of locally advanced soft tissues sarcomas." Eur J of Can. 47, 1319-1327. View Citation Online	II-3 / Good
44. Moroney, J.W., R. Kurzrock, et al. (2011). "A phase I trial of liposomal doxorubicin, bevacizumab, and temsirolimus in patients with advanced gynecologic and breast malignancies." Clin. Cancer Res. 17:6840-6846. View Citation Online	II-3 / Fair
45. Janku, F., R. Kurzrock, et al. (2012). "PIK3CA Mutation H1047R Is Associated with Response to PI3K/AKT/mTOR Signaling Pathway Inhibitors in Early-Phase Clinical Trials", Cancer Res; 73(1); 276-84. View Citation Online	II-2 / Good
46. Janku, F., R. Kurzrock, et al. (2012). "PI3K/Akt/mTOR inhibitors in patients with breast and gynecologic malignancies harboring PIK3CA mutations." Journal of Clinical Oncology. DOI: 10.1200/JCO.2011.36.1196. View Citation Online	II-3 / Good
47. Gong, W., J. Dong, et al. (2012). "RRM1 expression and clinical outcome of gemcitabine-containing chemotherapy for advanced non-small-cell lung cancer: A meta-analysis." Lung Cancer. 75:374-380. View Citation Online	I / Good
48. Cassier, P.A., P. Hohenberger, et al. (2012). "Outcome of Patients with Platelet-Derived Growth Factor Receptor Alpha-Mutated Gastrointestinal Stromal Tumors in the Tyrosine Kinase Inhibitor Era." Clin Cancer Res 18:4458-4464. View Citation Online	II-3 / Good
49. Debiec-Rychter, M., I. Judson, et al. (2006). "KIT mutations and dose selection for imatinib in patients with advanced gastrointestinal stromal tumours." Eur J Cancer 42:1093-1103. View Citation Online	II-3 / Good
50. Heinrich, M.C., J.A. Fletcher, et al. (2008). "Correlation of kinase genotype and clinical outcome in North American Intergroup phase III trial of imatinib mesylate for treatment of advanced gastrointestinal stromal tumor: CALGB 150105 study by Cancer and Leukemia Group B and Southwest Oncology Group." J Clin Oncol 26(33):5360-5367. View Citation Online	II-3 / Good
51. Guo, J., S. Qin, et al. (2011). "Phase II, open-label, single-arm trial of imatinib mesylate in patients with metastatic melanoma harboring c-Kit mutation or amplification." J. Clin. Oncol. 29:2904-2909. View Citation Online	II-2 / Good
52. Carvajal, R.D., G.K. Schwartz, et al. (2011). "KIT as a therapeutic target in metastatic melanoma." JAMA. 305(22):2327-2334. View Citation Online	II-2 / Good

* See Appendix page 6 for Level of Evidence description.

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

REFERENCES

SOURCE	LEVEL OF EVIDENCE*
53. Braun, M.S., M.T. Seymour, et. al. (2008). "Predictive biomarkers of chemotherapy efficacy in colorectal cancer: results from the UK MRC FOCUS trial." J. Clin. Oncol. 26:2690-2698. View Citation Online	II-1 / Good
54. Naniwa, J., N. Terakawa, et. al. (2007). "Genetic diagnosis for chemosensitivity with drug-resistance genes in epithelial ovarian cancer." Int. J. Gynecol. 17:76-82. View Citation Online	II-3 / Fair
55. Litzow, M.R., S.H Kaufmann, et. al. (2010). "Phase I trial of autologous hematopoietic SCT with escalating doses of topotecan combined with CY and carboplatin in patients with relapsed or persistent ovarian or primary peritoneal carcinoma." Bone Marrow Transplantation. 45:490-497. View Citation Online	II-3 / Good
56. Oza, A.M., M. Friedlander, et.al. (2015). "Olaparib combined with chemotherapy for recurrent platinum-sensitive ovarian cancer: a randomised phase 2 trial." Lancet Oncol. 16:87-97 View Citation Online	I / Good
57. Ledermann, J., U. Matulonis, et.al. (2014). "Olaparib maintenance therapy in patients with platinum-sensitive relapsed serous ovarian cancer: a preplanned retrospective analysis of outcomes by BRCA status in a randomised phase 2 trial." Lancet Oncol. 15(8):852-61. View Citation Online	I / Good
58. Kaufman, B., S.M. Domcheck, et al. (2015). "Olaparib monotherapy in patients with advanced cancer and a germline BRCA1/2 mutation". J Clin Oncol. 33(3): 244-250. View Citation Online	II-1 / Good
59. Mateo, J., J.S. de Bono, et al. (2015). "DNA-repair defects and olaparib in metastatic prostate cancer". N Engl J Med. 373(18): 1697-1708. View Citation Online	II-1 / Good
60. Wells, S.A., M.J. Schlumberger, et al. (2012). "Vandetanib in Patients with Locally Advanced or Metastatic Medullary Thyroid Cancer: A Randomized, Double-Blind Phase III Trial." J Clin Oncol 30: 134-141. View Citation Online	I / Good

* See Appendix page 6 for Level of Evidence description.

PATIENT: Patient, Test (XX-Mon-19XX)

TTN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

SPECIMEN INFORMATION

Specimen ID: ABC-123-XY

Specimen Collected: XX-Mon-2016

Specimen Received: XX-Mon-2016

Testing Initiated: XX-Mon-2016

Gross description: 1 (A) Paraffin Block, site: Pelvis, NOS - Client ID (ABC-123-XY).

Clinical History: Per the submitted documents, the patient is a XX year-old female with adenocarcinoma in ovary. Per the physician's office this tumor is of pelvis origin.

Pathologic Diagnosis: Pelvic mass, resection: Carcinosarcoma with heterologous elements.

Interpretation (Caris Life Sciences Microscopic Diagnosis):

Interpretation (Caris Life Sciences Microscopic Diagnosis)

Please Note:

Electronic Signature

By my electronic signature, I as the attending pathologist affirm that I have personally reviewed and examined microscopically the prepared slide(s) and that the above diagnosis has been made or confirmed by me.

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

Disclaimer

All of the individual assays that are available through Caris Molecular Intelligence™ were developed and validated by Caris MPI, Inc. d/b/a Caris Life Sciences® and their test performance characteristics were determined and validated by Caris Life Sciences pursuant to the Clinical Laboratory Improvements Amendments and accompanying regulations ("CLIA"). Some of the assays that are part of Caris Molecular Intelligence have been approved by the U.S. Food and Drug Administration (FDA). For any remaining assays, Caris MPI, Inc. is certified under CLIA to perform high complexity testing, including all of the assays that comprise the Caris Molecular Intelligence.

The CLIA certification number of Caris MPI, Inc. laboratory performing testing in connection with Caris Molecular Intelligence can be found at the bottom of each page. This report includes information about therapies that appear to be associated with clinical benefit based on NCCN Compendium® guidelines, relevance of tumor lineage, level of published evidence and strength of biomarker results. This report, neither ranks biomarkers listed nor therapies associated with such biomarkers, in order of potential or predicted efficacy, and such therapies may or may not be suitable for administration to a particular patient. A determination of biomarker results do not necessarily indicate pharmacologic effectiveness or lack thereof. This report does not guarantee or suggest that any particular agent will be effective with the treatment of any particular condition. Caris Life Sciences expressly disclaims and makes no representation or warranty whatsoever relating, directly or indirectly, to review of identified scientific literature, the conclusions drawn from such review or any of the information set forth in this report that is derived from such review, including information and conclusions relating to therapies that are included or omitted from this report.

Decisions regarding care and treatment should not be based on a single test such as this test or the information contained in this report. The decision to select any, all or none of the listed therapies resides solely within 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 applicable information concerning the patient's condition, including but not limited to, patient and family history, physical examinations, information from other diagnostic tests, and patient preferences, in accordance with the applicable standard of care.

The information presented in the Clinical Trials Connector™ section of this report (if applicable) is compiled from sources believed to be reliable and current. We have used our best efforts to make this information as accurate as possible. However, the accuracy and completeness of this information cannot be guaranteed. The contents are to be used for clinical trial guidance and may not include all relevant trials. Current enrollment status for these trials is unknown. The clinical trials information present in the biomarker description was compiled from www.clinicaltrials.gov. The contents are to be used only as a guide, and health care providers should employ their judgment in interpreting this information for a particular patient. Specific eligibility criteria for each clinical trial should be reviewed as additional inclusion criteria may apply. Caris Life Sciences makes no promises or guarantees that a healthcare provider, insurer or other third party private or government payor, will provide reimbursement for any of the tests performed.

The next-generation sequencing assay performed by Caris Life Sciences examines nucleic acids obtained from tumor tissue only and does not examine normal tissue such as tumor adjacent tissue or whole or peripheral blood. As such, the origin of any mutation detected may be a somatic mutation (not inherited) or a germline mutation (inherited) and will not be distinguishable by this assay. It is recommended that results be considered within the patient's clinical and health history. If a germline inheritance pattern is suspected then counseling by a board certified genetic counselor is recommended.

A laboratory technician harvested targeted tissues for extraction from the marked areas using a dissection microscope. The areas marked and extracted were microscopically reexamined on post-scraped slides and adequacy of scraping was verified by a board certified Pathologist.

Electronic Signature



PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

MUTATIONAL ANALYSIS BY **NEXT-GENERATION SEQUENCING (NGS)**

GENES TESTED WITH ALTERATIONS

Gene	Alteration	Frequency (%)	Exon	Result
TP53	H178fs	90	5	Mutated, Pathogenic

Interpretation: A pathogenic frameshift mutation was detected in TP53

TP53, or p53, plays a central role in modulating response to cellular stress through transcriptional regulation of genes involved in cell-cycle arrest, DNA repair, apoptosis, and senescence. Inactivation of the p53 pathway is essential for the formation of the majority of human tumors. Mutation in p53 (TP53) remains one of the most commonly described genetic events in human neoplasia, estimated to occur in 30-50% of all cancers. Generally, presence of a disruptive p53 mutation is associated with a poor prognosis in all types of cancers, and diminished sensitivity to radiation and chemotherapy. Germline p53 mutations are associated with the Li-Fraumeni syndrome (LFS) which may lead to early-onset of several forms of cancer currently known to occur in the syndrome, including sarcomas of the bone and soft tissues, carcinomas of the breast and adrenal cortex (hereditary adrenocortical carcinoma), brain tumors and acute leukemias.

GENES TESTED WITH NO MUTATIONS DETECTED

ABL1	CDH1	FBXW7	HRAS	NOTCH1	RB1
AKT1	cMET	FGFR1	IDH1	NPM1	RET
ALK	CSF1R	FGFR2	JAK2	NRAS	SMAD4
APC	CTNNB1	FLT3	JAK3	PDGFRA	SMARCB1
ATM	EGFR	GNA11	KDR	PIK3CA	SMO
BRAF	ERBB2	GNAQ	KRAS	PTEN	STK11
c-KIT	ERBB4	GNAS	MPL	PTPN11	VHL

For Next-Generation Sequencing, a total of 45 genes were analyzed. The results above include genes most commonly associated with cancer and any additional mutations identified. No alterations were identified in 43 genes. For a complete list of genes tested, visit www.CarisMolecularIntelligence.com/profilemenu.

Electronic Signature

NGS Methods

Direct sequence analysis was performed on genomic DNA isolated from a formalin-fixed paraffin-embedded tumor sample using the Illumina MiSeq platform. Specific regions of the genome were amplified using the Illumina TruSeq Amplicon Cancer Hotspot panel. This panel only sequences selected regions of 44 genes and the amino acids sequenced by this assay can be found at www.carislifesciences.com. All variants reported by this are detected with >99% confidence based on the frequency of the mutation present and the amplicon coverage. This test is not designed to distinguish between germ line inheritance of a variant or acquired somatic mutation. This test has a sensitivity to detect as low as approximately 10% population of cells containing a mutation a sequenced amplicon. This test has not been cleared or approved by the United States Food and Drug Administration (FDA) as such approval is not necessary. All performance characteristics were determined by Caris Life Sciences. Insertions or deletions larger than 27 bp will not be detected by this assay. Benign and non-coding variants are not included in this report but are available upon request.

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

MUTATIONAL ANALYSIS BY **NEXT-GENERATION SEQUENCING (NGS)**

GENES TESTED WITH ALTERATIONS

Gene	Alteration	Frequency (%)	Exon	Result
BRCA2	E1953X	95	11	Mutated, Pathogenic

Interpretation: A pathogenic nonsense mutation was detected in BRCA2. This mutation (also known as c.5857G>T; 6085G>T) has been reported as a frequent germline mutation, causal for hereditary breast and ovarian cancer (Serova-Sinilnikova 1997 Am J Hum Genet 60:1236).

GENES TESTED WITH NO MUTATIONS DETECTED

BRCA1

Electronic Signature

BRCA1 Sequencing Methods

Direct sequence analysis was performed on genomic DNA isolated from a formalin-fixed paraffin-embedded tumor sample using the Illumina MiSeq platform. Specific regions of BRCA1 were amplified using primers flanking coding regions of this gene. All variants reported by this are detected with >99% confidence based on the frequency of the mutation present and the amplicon coverage. This test is not designed to distinguish between germ line inheritance of a variant or acquired somatic mutation. This test has a sensitivity to detect as low as approximately 20% population of cells containing a mutation a sequenced amplicon. This test has not been cleared or approved by the United States Food and Drug Administration (FDA) as such approval is not necessary. All performance characteristics were determined by Caris Life Sciences. Insertions or deletions larger than 27 bp will not be detected by this assay. Benign and non-coding variants are not included in this report but are available upon request.

BRCA2 Sequencing Methods

Direct sequence analysis was performed on genomic DNA isolated from a formalin-fixed paraffin-embedded tumor sample using the Illumina MiSeq platform. Specific regions of BRCA2 were amplified using primers flanking coding regions of this gene. All variants reported by this are detected with >99% confidence based on the frequency of the mutation present and the amplicon coverage. This test is not designed to distinguish between germ line inheritance of a variant or acquired somatic mutation. This test has a sensitivity to detect as low as approximately 20% population of cells containing a mutation a sequenced amplicon. This test has not been cleared or approved by the United States Food and Drug Administration (FDA) as such approval is not necessary. All performance characteristics were determined by Caris Life Sciences. Insertions or deletions larger than 27 bp will not be detected by this assay. Benign and non-coding variants are not included in this report but are available upon request.

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

PROTEIN EXPRESSION BY **IMMUNOHISTOCHEMISTRY (IHC)**

Biomarker	Patient Tumor			Thresholds*
	Staining Intensity (0, 1+, 2+, 3+)	Percent of cells	Result	Conditions for a Positive Result:
ER	1 +	1	Negative	Intensity of $\geq 3+$ with $\geq 50\%$ or $\geq 2+$ with $\geq 75\%$ of cells stained
ERCC1	2 +	10	Negative	Intensity of $\geq 3+$ with $\geq 10\%$ or $\geq 2+$ with $\geq 50\%$ of cells stained
Her2/Neu	1 +	20	Negative	Intensity $\geq 3+$ and $> 10\%$ of cells stained
PD-L1	0	100	Negative	Intensity $\geq 2+$ and $\geq 5\%$ of cells stained
PR	0	100	Negative	Intensity $\geq 1+$ and $\geq 10\%$ of cells stained
PTEN	2 +	80	Positive	Intensity $\geq 1+$ and $> 50\%$ of cells stained
RRM1	2 +	30	Negative	Intensity $\geq 2+$ and $\geq 50\%$ of cells stained
TOP2A	1 +	10	Positive	Intensity $\geq 1+$ and $\geq 10\%$ of cells stained
TOPO1	0	100	Negative	Intensity $\geq 2+$ and $\geq 30\%$ of cells stained
TS	1 +	20	Positive	Intensity $\geq 1+$ and $\geq 10\%$ of cells stained
TUBB3	2 +	2	Negative	Intensity $\geq 2+$ and $\geq 30\%$ of cells stained

Electronic Signature

IHC Methods

These tests were developed and their performance characteristics determined by Caris MPI, Inc. d/b/a Caris Life Sciences®

* Caris Life Sciences has defined threshold levels of reactivity of IHC to establish cutoff points based on published evidence. Polymer detection systems are used for each IHC.

* HER2 results and interpretation follow the ASCO/CAP scoring criteria. See reference section for more information.

* Please note that PD-L1 staining is read from the membrane staining of cancer cells.

Clones used: ER(SP1), PR(1E2), TOPO1(1D6), TOP2A(3F6), TUBB3(Polyclonal), Her2/Neu(4B5), ERCC1(8F1), PD-L1(SP142), PTEN(6H2.1), RRM1(Polyclonal), TS(TS106/4H4B1).

Additional IHC results continued on the next page. >

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

PROTEIN EXPRESSION BY **IMMUNOHISTOCHEMISTRY (IHC)**

Biomarker	H-Score	Result	Threshold (Condition for a Positive Result)
EGFR	200	Positive	H-Score \geq 200

Electronic Signature

IHC Methods

These tests were developed and their performance characteristics determined by Caris MPI, Inc. d/b/a Caris Life Sciences®

* Caris Life Sciences has defined threshold levels of reactivity of IHC to establish cutoff points based on published evidence. Polymer detection systems are used for each IHC.

Clones used: EGFR(2-18C9).

Comments on IHC Analysis

Inflammatory PD-L1 cells expression is seen in approximately 5% of the tumor volume.

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

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

AMPLIFICATION BY **CHROMOGENIC IN SITU HYBRIDIZATION (CISH)**

Gene / ISCN	Cells Counted	Result	Total/Avg Gene Copy Number	Total/Avg Control Copy Number	Cells with ≥4 Copies	Cells with ≥15 Copies	Ratio Calculation	Ratio
Her2/Neu nuc ish (D17Z1x1-2,HER2x1-2)[/30]	20	Not Amplified	2.85	2.05	N/A	N/A	Her2/neu/ Chromosome 17	1.39
<i>Reference Range:</i> Her2/Neu:CEP 17 signal ratio of ≥ 2.0 ; and non-amplification as < 2.0 per Ventana INFORM HER2 CISH Package insert.								

Electronic Signature

Comments on CISH Analysis

Her2/Neu by CISH also reviewed by another Pathologist who agrees with the above entered results.

CISH Methods

HER2 CISH test was carried out using the INFORM DUAL HER2 ISH Assay (Ventana Medical Systems, Inc.), which has been cleared by the US Food and Drug Administration (FDA) for enumerating the ratio of HER2/Chr 17 in Breast Cancer samples. The HER2 CISH testing for cancer lineages other than breast has been developed and their performance characteristics determined by Caris MPI, Inc. (d/b/a Caris Life Sciences), and have not been cleared or approved by the FDA.

cMET CISH was carried out using a probe specific for cMET and a probe for the pericentromeric region of chromosome 7 (Ventana). The cMET CISH testing for cancer lineages has been developed and its performance characteristics determined by Caris MPI, Inc. (d/b/a Caris Life Sciences), and has not been cleared or approved by the FDA.

TOP2A CISH was carried out using a probe specific for TOP2 and a probe for the pericentromeric region of chromosome 17 (Ventana). The TOP2A CISH testing for cancer lineages has been developed and its performance characteristics determined by Caris MPI, Inc. (d/b/a Caris Life Sciences), and has not been cleared or approved by the FDA.

The FDA has determined that such clearance or approval is not currently necessary. These tests should not be regarded as investigational or research as they are used for clinical purpose and determined to be medically necessary by the ordering physician, who is not employed by Caris MPI, Inc. or its affiliates. This laboratory is certified under Clinical Laboratory Improvement Amendment of 1988 (CLIA-88) and is qualified to perform high complexity testing. CLIA 03D1019490

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD

LITERATURE LEVEL OF EVIDENCE ASSESSMENT FRAMEWORK*

STUDY DESIGN	
Hierarchy of Design	Criteria
I	Evidence obtained from at least one properly designed randomized controlled trial .
II-1	Evidence obtained from well-designed controlled trials without randomization .
II-2	Evidence obtained from well-designed cohort or case-control analytic studies, preferably from more than one center or research group.
II-3	Evidence obtained from multiple time series with or without the intervention. Dramatic results in uncontrolled trials might also be regarded as this type of evidence.
III	Evidence obtained from multiple time series with or without the intervention. Dramatic results in uncontrolled trials might also be regarded as this type of evidence.

STUDY VALIDITY	
Grade	Criteria
Good	The study is judged to be valid and relevant as regards results, statistical analysis, and conclusions and shows no significant flaws.
Fair	The study is judged to be valid and relevant as regards results, statistical analysis, and conclusions, but contains at least one significant but not fatal flaw.
Poor	The study is judged to have a fatal flaw such that the conclusions are not valid for the purposes of this test.

* Adapted from Harris, T., D. Atkins, et al. (2001). "Current Methods of the U.S. Preventive Services Task Force." Am J Prev Med 20(3S)

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

PATIENT: Patient, Test (XX-Mon-19XX)

TN16-XXXXXX

PHYSICIAN: Ordering Physician, MD