

**ABOUT THE TEST** FoundationOne®CDx is a next-generation sequencing (NGS) based assay that identifies genomic findings within hundreds of cancer-related genes.

<b>PATIENT</b>	<b>DISEASE</b> Peritoneum serous carcinoma	<b>PHYSICIAN</b>	<b>ORDERING PHYSICIAN</b> Yeh, Yi-Chen	<b>SPECIMEN</b>	<b>SPECIMEN SITE</b> Omentum
	<b>NAME</b> Chen, Shu-Fan		<b>MEDICAL FACILITY</b> Taipei Veterans General Hospital		<b>SPECIMEN ID</b> S111-66946 N (PF22066)
	<b>DATE OF BIRTH</b> 25 March 1950		<b>ADDITIONAL RECIPIENT</b> None		<b>SPECIMEN TYPE</b> Slide Deck
	<b>SEX</b> Female		<b>MEDICAL FACILITY ID</b> 205872		<b>DATE OF COLLECTION</b> 31 May 2022
	<b>MEDICAL RECORD #</b> 25764390		<b>PATHOLOGIST</b> Not Provided		<b>SPECIMEN RECEIVED</b> 13 June 2022

## Biomarker Findings

**Loss of Heterozygosity score** - 24.9%

**Homologous Recombination status** - HRD Positive

**Microsatellite status** - MS-Stable

**Tumor Mutational Burden** - 6 Muts/Mb

## Genomic Findings

For a complete list of the genes assayed, please refer to the Appendix.

**RNF43** deletion exons 3-7

**TP53** R273H

**C11orf30 (EMSY)** amplification - equivocal<sup>†</sup>

2 Disease relevant genes with no reportable alterations: **BRCA1, BRCA2**

<sup>†</sup> See About the Test in appendix for details.

## Report Highlights

- Targeted therapies with **NCCN categories of evidence** in this tumor type: Niraparib (p. 8), Olaparib (p. 9), Rucaparib (p. 10)
- Evidence-matched **clinical trial options** based on this patient's genomic findings: (p. 12)

### BIOMARKER FINDINGS

**Loss of Heterozygosity score** - 24.9%

10 Trials see p. 12

**Homologous Recombination status** - HRD Positive

**Microsatellite status** - MS-Stable

**Tumor Mutational Burden** - 6 Muts/Mb

### THERAPIES WITH CLINICAL RELEVANCE (IN PATIENT'S TUMOR TYPE)

Niraparib	2A
Olaparib	2A
Rucaparib	2A

### THERAPIES WITH CLINICAL RELEVANCE (IN OTHER TUMOR TYPE)

Talazoparib

HRD Positive defined as presence of deleterious BRCA1/2 alteration and/or LOH score  $\geq 16\%$  (Coleman et al., 2017; 28916367).

No therapies or clinical trials. see Biomarker Findings section

No therapies or clinical trials. see Biomarker Findings section

GENOMIC FINDINGS	THERAPIES WITH CLINICAL RELEVANCE (IN PATIENT'S TUMOR TYPE)	THERAPIES WITH CLINICAL RELEVANCE (IN OTHER TUMOR TYPE)
<b>RNF43</b> - deletion exons 3-7	none	none
3 Trials <a href="#">see p. 14</a>		
<b>TP53</b> - R273H	none	none
2 Trials <a href="#">see p. 15</a>		

☐ NCCN category

## GENOMIC FINDINGS WITH NO REPORTABLE THERAPEUTIC OR CLINICAL TRIAL OPTIONS

For more information regarding biological and clinical significance, including prognostic, diagnostic, germline, and potential chemosensitivity implications, see the Genomic Findings section.

**C11orf30 (EMSY)** - amplification - equivocal ..... p. [7](#)

**NOTE** Genomic alterations detected may be associated with activity of certain approved therapies; however, the agents listed in this report may have varied clinical evidence in the patient's tumor type. Therapies and the clinical trials listed in this report may not be complete and exhaustive. Neither the therapeutic agents nor the trials identified are ranked in order of potential or predicted efficacy for this patient, nor are they ranked in order of level of evidence for this patient's tumor type. This report should be regarded and used as a supplementary source of information and not as the single basis for the making of a therapy decision. All treatment decisions remain the full and final responsibility of the treating physician and physicians should refer to approved prescribing information for all therapies.

Therapies contained in this report may have been approved by the US FDA.

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## BIOMARKER FINDINGS

## BIOMARKER

## Loss of Heterozygosity score

**RESULT**  
24.9%

### POTENTIAL TREATMENT STRATEGIES

#### — Targeted Therapies —

On the basis of emerging clinical data in ovarian cancer, elevated genomic LOH may be associated with greater sensitivity to PARP inhibitors<sup>1-2</sup>. In platinum-sensitive, BRCA1/2 wild-type ovarian, peritoneal, or Fallopian tube carcinoma, rucaparib elicited significantly longer median PFS (7.2 vs. 5.0 months, HR=0.51) and improved ORR (33.3% vs. 9.6%, p=0.0003) for patients with LOH score  $\geq$  16%. In the maintenance setting in platinum-sensitive, BRCA1/2 wild-type patients, rucaparib was superior to placebo in both the LOH score  $\geq$  16% (median PFS, 9.7 vs. 5.4 months; HR=0.44) and LOH score < 16% (median PFS, 6.7 vs. 5.4 months; HR=0.58) cohorts<sup>1</sup>. Similar results have been reported for maintenance treatment with

niraparib in ovarian cancer<sup>3</sup> when using a different measure of HRD that includes genomic LOH<sup>4-5</sup>. Increased LOH has also been associated with improved sensitivity to platinum-containing chemotherapy regimens in patients with ovarian or breast cancer<sup>6-8</sup>.

### FREQUENCY & PROGNOSIS

In a study of more than 4,000 ovarian, Fallopian tube, or peritoneal cancer samples, genomic LOH score  $\geq$  16% was identified in 24.2% of BRCA1/2 wild-type cases, deleterious BRCA1/2 mutation was identified in an additional 17.2% of cases, and the remaining 58.7% of cases had LOH score < 16% and were BRCA1/2 wild-type<sup>9</sup>. Among the histological subtypes, LOH score  $\geq$  16% or BRCA1/2 mutation was reported in 42.4% of serous carcinomas, 37.6% of endometrioid carcinomas, 23.5% of carcinosarcomas, 20.6% of neuroendocrine carcinomas, 13.6% of clear cell carcinomas, and 8.1% of mucinous carcinomas; in BRCA1/2 wild-type samples, the median LOH score was significantly higher in serous as compared with non-serous cases<sup>9</sup>. In ovarian carcinoma, the median LOH score is significantly higher for BRCA1/2-mutated cases than BRCA1/2 wild-type cases (22.2% vs. 9.8%)<sup>9</sup>, and mutation or

methylation of BRCA1, BRCA2, or RAD51C has been reported to be enriched in cases with increased genomic LOH<sup>6,10</sup>. One study reported no association between LOH and either tumor stage or grade in ovarian serous carcinoma<sup>11</sup>. In patients with high-grade serous ovarian carcinoma, the frequency of LOH has been reported to increase significantly with age<sup>12</sup>.

### FINDING SUMMARY

The loss of heterozygosity (LOH) score is a profile of the percentage of the tumor genome that is under focal loss of one allele<sup>2</sup>; focal LOH events accumulate as genomic "scars" as a result of incorrect DNA double-strand break repair when the homologous recombination pathway is deficient (HRD)<sup>6,10,13-14</sup>. HRD and consequent genomic LOH occur as a result of genetic or epigenetic inactivation of one or more of the homologous recombination pathway proteins, including BRCA1, BRCA2, RAD51C, ATM, PALB2, and BRIP1<sup>13-16</sup>. This sample harbors a genomic LOH score that has been shown to be associated with sensitivity to the PARP inhibitor rucaparib in platinum-sensitive, BRCA1/2 wild-type ovarian, peritoneal, or Fallopian tube carcinoma in both the treatment<sup>2</sup> and maintenance<sup>1</sup> settings.

## BIOMARKER

## Microsatellite status

**RESULT**  
MS-Stable

### POTENTIAL TREATMENT STRATEGIES

#### — Targeted Therapies —

On the basis of clinical evidence, MSS tumors are significantly less likely than MSI-H tumors to respond to anti-PD-1 immune checkpoint inhibitors<sup>17-19</sup>, including approved therapies nivolumab and pembrolizumab<sup>20</sup>. In a retrospective analysis of 361 patients with solid tumors treated with pembrolizumab, 3% were

MSI-H and experienced a significantly higher ORR compared with non-MSI-H cases (70% vs. 12%, p=0.001)<sup>21</sup>.

### FREQUENCY & PROGNOSIS

MSI-high (MSI-H) has been reported in 1.6-19.7% of ovarian cancer samples<sup>22-23</sup>, including 3.8% (1/26) of ovarian endometrioid adenocarcinomas<sup>24</sup>, and 10.0% (3/30) of ovarian clear cell carcinomas (CCOCs)<sup>25</sup>. No association of MSI-H with stage or survival was found in patients with ovarian cancer<sup>22,26</sup>.

### FINDING SUMMARY

Microsatellite instability (MSI) is a condition of genetic hypermutability that generates excessive

amounts of short insertion/deletion mutations in the genome; it generally occurs at microsatellite DNA sequences and is caused by a deficiency in DNA mismatch repair (MMR) in the tumor<sup>27</sup>. Defective MMR and consequent MSI occur as a result of genetic or epigenetic inactivation of one of the MMR pathway proteins, primarily MLH1, MSH2, MSH6, or PMS2<sup>27-29</sup>. This sample is microsatellite-stable (MSS), equivalent to the clinical definition of an MSS tumor: one with mutations in none of the tested microsatellite markers<sup>30-32</sup>. MSS status indicates MMR proficiency and typically correlates with intact expression of all MMR family proteins<sup>27,29,31-32</sup>.

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## BIOMARKER FINDINGS

## BIOMARKER

# Tumor Mutational Burden

## RESULT

6 Muts/Mb

## POTENTIAL TREATMENT STRATEGIES

### — Targeted Therapies —

On the basis of clinical evidence in solid tumors, increased TMB may be associated with greater sensitivity to immunotherapeutic agents, including anti-PD-L1<sup>33-35</sup>, anti-PD-1 therapies<sup>33-36</sup>, and combination nivolumab and ipilimumab<sup>37-42</sup>. In multiple pan-tumor studies, increased tissue tumor mutational burden (TMB) was associated with sensitivity to immune checkpoint inhibitors<sup>33-36,43-47</sup>. In the KEYNOTE 158 trial of pembrolizumab monotherapy for patients with solid tumors, significant improvement in ORR was observed for patients with TMB  $\geq 10$  Muts/Mb (as measured by this assay) compared with those with TMB  $< 10$  Muts/Mb in a large cohort that included multiple tumor types<sup>43</sup>; similar findings were observed in the KEYNOTE 028 and 012 trials<sup>36</sup>. At the same TMB cutpoint, retrospective analysis of

patients with solid tumors treated with any checkpoint inhibitor identified that tissue TMB scores  $\geq 10$  Muts/Mb were associated with prolonged time to treatment failure compared with scores  $< 10$  muts/Mb (HR=0.68)<sup>47</sup>. For patients with solid tumors treated with nivolumab plus ipilimumab in the CheckMate 848 trial, improved responses were observed in patients with a tissue TMB  $\geq 10$  Muts/Mb independent of blood TMB at any cutpoint in matched samples<sup>48</sup>. However, support for higher TMB thresholds and efficacy was observed in the prospective Phase 2 MyPathway trial of atezolizumab for patients with pan-solid tumors, where improved ORR and DCR was seen in patients with TMB  $\geq 16$  Muts/Mb than those with TMB  $\geq 10$  and  $< 16$  Muts/Mb<sup>46</sup>. Similarly, analyses across several solid tumor types reported that patients with higher TMB (defined as  $\geq 16$ -20 Muts/Mb) achieved greater clinical benefit from PD-1 or PD-L1-targeting monotherapy compared with patients with higher TMB treated with chemotherapy<sup>49</sup> or those with lower TMB treated with PD-1 or PD-L1-targeting agents<sup>34</sup>.

## FREQUENCY & PROGNOSIS

Ovarian carcinomas, including peritoneal and Fallopian tube carcinomas, harbor a median TMB of 2.7-3.6 mutations per megabase (muts/Mb)

depending upon subtype, and up to 2.1% of cases have high TMB ( $> 20$  muts/Mb)<sup>50</sup>. In a study of high grade serous ovarian cancer, homologous recombination (HR)-deficient tumors, which comprised ~50% of all samples, harbored a higher neoantigen load compared to HR-proficient tumors; higher neoantigen load was associated with longer OS but not disease free survival<sup>51</sup>.

## FINDING SUMMARY

Tumor mutation burden (TMB, also known as mutation load) is a measure of the number of somatic protein-coding base substitution and insertion/deletion mutations occurring in a tumor specimen. TMB is affected by a variety of causes, including exposure to mutagens such as ultraviolet light in melanoma<sup>52-53</sup> and cigarette smoke in lung cancer<sup>54-55</sup>, treatment with temozolomide-based chemotherapy in glioma<sup>56-57</sup>, mutations in the proofreading domains of DNA polymerases encoded by the POLE and POLD1 genes<sup>58-62</sup>, and microsatellite instability (MSI)<sup>58,61-62</sup>. This sample harbors a TMB level associated with lower rates of clinical benefit from treatment with PD-1- or PD-L1-targeting immune checkpoint inhibitors compared with patients with tumors harboring higher TMB levels, based on several studies in multiple solid tumor types<sup>34-35,43</sup>.

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## GENOMIC FINDINGS

## GENE

# RNF43

## ALTERATION

deletion exons 3-7

## POTENTIAL TREATMENT STRATEGIES

### — Targeted Therapies —

Preclinical studies have reported that RNF43 is a negative regulator of WNT signaling, and RNF43 loss or inactivation leads to WNT activation and confers sensitivity to WNT pathway inhibitors, particularly Porcupine inhibitors, in multiple tumor types<sup>63-67</sup>. In a Phase 1 basket study for the Porcupine inhibitor RXCoo4, 1 of 2 patients with

tumors harboring an RNF43 mutation achieved SD<sup>68</sup>. Of the patients with WNT-ligand-dependent tumors, including those with RNF43 mutations, RSPO fusions, or those with biliary tract or thymus cancer, 71% (5/7) experienced SD<sup>68</sup>. Therefore, patients whose tumors harbor inactivating alterations in RNF43 may benefit from WNT pathway inhibitors, which are under investigation in clinical trials.

## FREQUENCY & PROGNOSIS

Mutations in RNF43 have been reported in 18-27% of endometrial cancers<sup>69-70</sup>, 3-5% of pancreatic cancers<sup>71</sup>, 21% of ovarian mucinous carcinomas<sup>72</sup>, 9% of liver fluke-associated cholangiocarcinomas<sup>73</sup>, and up to 18% of colorectal cancers<sup>61,70</sup>. RNF43 mutations are associated with

mismatch repair deficiency and microsatellite instability (MSI) in colorectal<sup>70</sup>, endometrial<sup>70</sup>, and gastric cancers<sup>74-75</sup>; one study reported RNF43 alterations in more than 50% of MSI gastric carcinomas<sup>74</sup>.

## FINDING SUMMARY

RNF43 encodes a ubiquitin ligase<sup>76</sup> that was discovered because it is overexpressed in colon cancer<sup>77</sup>. RNF43 and the homologous E3 ubiquitin ligase ZNRF3 are tumor suppressors that function as negative regulators of WNT signaling<sup>63-67</sup>. An additional tumor-suppressor-like role for RNF43 in colon cancer is hypothesized to occur via its interaction with the ubiquitin-protein ligase NEDL1, which is predicted to enhance the pro-apoptotic effects of p53<sup>78</sup>.

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## GENOMIC FINDINGS

## GENE

## TP53

## ALTERATION

R273H

## TRANSCRIPT ID

NM\_000546

## CODING SEQUENCE EFFECT

818G&gt;A

## VARIANT ALLELE FREQUENCY (% VAF)

73.0%

## POTENTIAL TREATMENT STRATEGIES

## — Targeted Therapies —

There are no approved therapies to address TP53 mutation or loss. However, tumors with TP53 loss of function alterations may be sensitive to the WEE1 inhibitor adavosertib<sup>79-82</sup>, or p53 gene therapy and immunotherapeutics such as SGT-53<sup>83-87</sup> and ALT-801<sup>88</sup>. In a Phase 1 study, adavosertib in combination with gemcitabine, cisplatin, or carboplatin elicited PRs in 9.7% and SDs in 53% of patients with solid tumors; the response rate was 21% (4/19) for patients with TP53 mutations versus 12% (4/33) for patients who were TP53 wildtype<sup>89</sup>. A Phase 2 trial of adavosertib in combination with chemotherapy (gemcitabine, carboplatin, paclitaxel, or doxorubicin) reported a 32% (30/94, 3 CR) ORR and a 73% (69/94) DCR for patients with platinum-refractory TP53-mutated ovarian, Fallopian tube, or peritoneal cancer<sup>90</sup>. A smaller Phase 2 trial of adavosertib in combination with carboplatin achieved a 43% (9/21, 1 CR) ORR and a 76% (16/21) DCR for patients with platinum-refractory TP53-mutated ovarian cancer<sup>91</sup>. The combination of adavosertib with paclitaxel and carboplatin for patients with TP53-mutated ovarian cancer also significantly increased PFS compared with paclitaxel and carboplatin alone<sup>92</sup>. In the Phase 2 VIKTORY trial, patients with TP53-mutated metastatic and/or recurrent gastric cancer experienced a 24% (6/25) ORR with adavosertib combined with paclitaxel<sup>93</sup>. A Phase 1 trial of neoadjuvant adavosertib in combination with cisplatin and docetaxel for head and neck squamous cell carcinoma (HNSCC) elicited a 71% (5/7) response rate for patients with TP53 alterations<sup>94</sup>. The Phase 2 FOCUS4-C trial for patients with TP53- and RAS-mutated colorectal

cancer reported improvement in PFS (3.61 vs. 1.87 months, HR=0.35, p=0.0022), but not OS (14.0 vs 12.8 months, p=0.93), following adavosertib treatment compared with active monitoring<sup>95</sup>. In a Phase 1b clinical trial of SGT-53 in combination with docetaxel for patients with solid tumors, 75% (9/12) of evaluable patients experienced clinical benefit, including 2 confirmed and 1 unconfirmed PRs and 2 instances of SD with significant tumor shrinkage<sup>87</sup>. Missense mutations leading to TP53 inactivation may also be sensitive to therapies that reactivate mutated p53 such as APR-246<sup>96-98</sup>. In a Phase 1b trial for patients with p53-positive high-grade serous ovarian cancer, APR-246 combined with carboplatin and pegylated liposomal doxorubicin achieved a 52% (11/21) response rate and 100% DCR<sup>99</sup>. ATR inhibitor treatment of chronic lymphocytic leukemia (CLL) cells with biallelic inactivation of TP53 suppressed cell viability, promoted DNA damage, and attenuated xenograft growth in preclinical studies<sup>100-101</sup>; however, ATR inhibitors as monotherapy had little effect on these parameters in solid tumor models in other preclinical studies<sup>102-103</sup>. Therefore, it is unclear whether TP53 inactivation predicts sensitivity to ATR inhibition.

## FREQUENCY &amp; PROGNOSIS

TP53 alterations have been reported in 29-80% of ovarian tumors, with a higher incidence in high-grade pelvic (primary ovarian, tubal, or peritoneal) serous carcinoma, with incidence of 91-97%<sup>15,104-110</sup>. TP53 alterations have also been reported in serous tubal intraepithelial carcinomas (STICs) of the Fallopian tube, which are suggested to be precursor lesions of tubo-ovarian high grade serous carcinomas<sup>111-114</sup>. Aberrant p53 expression has been associated with higher ovarian serous carcinoma grade (89-90% of high-grade vs. 6.6-9% of low-grade vs. 0% of benign)<sup>115-117</sup>. In one study, p53 expression was not prognostic in regard to outcome in patients with peritoneum serous carcinoma<sup>118</sup>. TP53 mutations have been reported to be more frequent in advanced stage (63%, 55/87) and higher grade (65%, 42/64) than earlier stage (31%, 14/45) and lower grade (41%, 7/17) ovarian carcinomas<sup>109</sup>. Meta-analysis has suggested that TP53 expression was associated with poorer survival in ovarian epithelial cancers, although the effect was modest and considerable variability was observed between studies<sup>119</sup>.

## FINDING SUMMARY

Functional loss of the tumor suppressor p53, which is encoded by the TP53 gene, is common in aggressive advanced cancers<sup>120</sup>. Alterations such as seen here may disrupt TP53 function or expression<sup>121-125</sup>.

## POTENTIAL GERMLINE IMPLICATIONS

One or more of the TP53 variants observed here has been described in the ClinVar database as a likely pathogenic or pathogenic germline mutation (by an expert panel or multiple submitters) associated with Li-Fraumeni syndrome (ClinVar, Mar 2022)<sup>126</sup>. Follow-up germline testing would be needed to distinguish whether the finding in this patient is somatic or germline. Germline mutations in TP53 are associated with the very rare autosomal dominant disorder Li-Fraumeni syndrome and the early onset of many cancers<sup>127-129</sup>, including sarcomas<sup>130-131</sup>. Estimates for the prevalence of germline TP53 mutations in the general population range from 1:5,000<sup>132</sup> to 1:20,000<sup>131</sup>. For pathogenic TP53 mutations identified during tumor sequencing, the rate of germline mutations was 1% in the overall population and 6% in tumors arising before age 30<sup>133</sup>. In the appropriate clinical context, germline testing of TP53 is recommended.

## POTENTIAL CLONAL HEMATOPOIESIS IMPLICATIONS

Variants seen in this gene have been reported to occur in clonal hematopoiesis (CH), an age-related process in which hematopoietic stem cells acquire somatic mutations that allow for clonal expansion<sup>134-139</sup>. CH in this gene has been associated with increased mortality, risk of coronary heart disease, risk of ischemic stroke, and risk of secondary hematologic malignancy<sup>134-135</sup>. Clinical management of patients with CH in this gene may include monitoring for hematologic changes and reduction of controllable risk factors for cardiovascular disease<sup>140</sup>. Comprehensive genomic profiling of solid tumors detects nontumor alterations that are due to CH<sup>138,141-142</sup>. Patient-matched peripheral blood mononuclear cell sequencing is required to conclusively determine if this alteration is present in tumor or is secondary to CH.

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## GENOMIC FINDINGS

## GENE

## C11orf30 (EMSY)

## ALTERATION

amplification - equivocal

### POTENTIAL TREATMENT STRATEGIES

#### — Targeted Therapies —

EMSY overexpression in breast cancer cell lines has been reported to mimic the effects of inactivating BRCA2 mutations<sup>143</sup>. Unlike BRCA2 inactivation, which predicts sensitivity to DNA repair-associated inhibitors such as the PARP inhibitor olaparib<sup>144-145</sup>, EMSY amplification in breast cancer lines was not associated with

enhanced sensitivity to this drug in one preclinical study<sup>146</sup>. There are no therapies that target EMSY alterations.

### FREQUENCY & PROGNOSIS

In the TCGA datasets, EMSY amplification has been most frequently observed in ovarian carcinoma (8%)<sup>15</sup>, breast invasive carcinoma (6%)<sup>147</sup>, esophageal carcinoma (5%) (cBioPortal, 2022), and head and neck squamous cell carcinoma (3.5%)<sup>148-150</sup>. EMSY overexpression has been primarily reported in breast and high grade ovarian cancers, where it is implicated in BRCA2 inactivation and correlates with poor prognosis or advanced disease<sup>146,151-157</sup>. The consequences of EMSY alterations in other solid tumors or hematologic malignancies have not been studied

in detail in the scientific literature (PubMed, 2022).

### FINDING SUMMARY

EMSY, also known as C11orf30, encodes a BRCA2-interacting protein with roles in transcriptional regulation<sup>157-158</sup>. Preclinical studies have suggested that EMSY binds to and suppresses the function of BRCA2, and EMSY overexpression may therefore mimic BRCA2 inactivation<sup>143,157</sup>. Amplification of the EMSY gene correlates with increased mRNA expression<sup>146,159</sup>, although conflicting data have been reported<sup>160</sup>. The functional consequences of other EMSY alterations have not been extensively studied (PubMed, 2022).

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THERAPIES WITH CLINICAL BENEFIT

IN PATIENT'S TUMOR TYPE

## Niraparib

Assay findings association

**Loss of Heterozygosity  
score**  
24.9%

### AREAS OF THERAPEUTIC USE

The PARP inhibitor niraparib is FDA approved to treat patients with epithelial ovarian, fallopian tube, or primary peritoneal cancer, with or without homologous recombination deficiency (HRD)-positive status. Please see the drug label for full prescribing information.

### GENE ASSOCIATION

On the basis of emerging clinical data in ovarian cancer, elevated genomic LOH may be associated with greater sensitivity to PARP inhibitors<sup>1-2,161</sup>. In platinum-sensitive, BRCA1/2 wild-type ovarian, peritoneal, or Fallopian tube carcinoma, the PARP inhibitor rucaparib elicited significantly longer median PFS and improved ORR for patients with LOH score  $\geq 16\%$ <sup>2,161</sup>.

### SUPPORTING DATA

For patients with platinum-sensitive, recurrent ovarian cancer (OC), the Phase 3 ENGOT-OV16/NOVA study showed that niraparib maintenance therapy significantly increased median PFS (mPFS) relative to placebo, regardless of germline BRCA (gBRCA) mutation (21.0 vs. 5.5 months, HR=0.27 for patients with gBRCA mutations; 9.3 vs. 3.9 months, HR=0.45 for patients without gBRCA mutations) or homologous recombination deficiency (HDR) status (12.9 vs. 3.8 months, HR=0.38)<sup>3,162</sup>. Similarly, the Phase 3 PRIMA trial for patients with newly diagnosed advanced OC reported an extended mPFS from

niraparib maintenance therapy after response to first-line platinum chemotherapy compared with placebo (13.8 vs. 8.2 months, HR=0.62); subgroup analysis showed that patients with HRD-positive OC experienced the longest mPFS, which was irrespective of BRCA mutational status (21.9 vs. 10.4 months, HR=0.43)<sup>163</sup>. The Phase 2 QUADRA study evaluating niraparib monotherapy as late-line treatment for patients with relapsed high-grade serous epithelial ovarian cancer (HGSOC) reported a median OS (mOS) of 12.2 months for all HGSOC patients, with highest mOS seen for those with BRCA1/2-mutated and HRD-positive tumors (26.0 and 19.0 months, respectively)<sup>164</sup>. A Phase 2 trial for patients with platinum-sensitive HGSOC and endometrioid recurrent ovarian cancer reported significantly improved mPFS from the addition of bevacizumab to niraparib compared with niraparib alone (11.9 vs. 5.5 months, HR=0.35)<sup>165</sup>. In a Phase 1/2 study of niraparib in combination with pembrolizumab for patients with recurrent platinum-resistant OC, patients experienced an ORR of 19% (11/59) and mPFS of 3.4 months; no significant differences in ORR were noted among analyzed subgroups: 14% (3/21) versus 19% (6/32) for patients with HRD-positive versus HRD-negative tumors, 18% (2/11) versus 19% (9/47) for patients with BRCA-mutated versus BRCA-wildtype tumors, and 21% (7/33) versus 10% (2/21) for patients with PD-L1-positive versus PD-L1-negative tumors<sup>166</sup>.

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ORDERED TEST # ORD-1388894-01

**THERAPIES WITH CLINICAL BENEFIT**
**IN PATIENT'S TUMOR TYPE**

# Olaparib

*Assay findings association*
**Loss of Heterozygosity  
score**  
 24.9%

## AREAS OF THERAPEUTIC USE

The PARP inhibitor olaparib is FDA approved to treat patients with epithelial ovarian, Fallopian tube, or primary peritoneal cancer, patients with deleterious or suspected deleterious gBRCA-mutated pancreatic adenocarcinoma or HER2-negative breast cancer, and patients with prostate cancer and mutations in homologous recombination repair genes. Olaparib is also approved in combination with bevacizumab to treat patients with ovarian, Fallopian tube, or primary peritoneal cancer with deleterious or suspected deleterious somatic or gBRCA mutation and/or genomic instability. Please see the drug label for full prescribing information.

## GENE ASSOCIATION

On the basis of emerging clinical data in ovarian cancer, elevated genomic LOH may be associated with greater sensitivity to PARP inhibitors<sup>1-2,161</sup>. In platinum-sensitive, BRCA1/2 wild-type ovarian, peritoneal, or Fallopian tube carcinoma, the PARP inhibitor rucaparib elicited significantly longer median PFS and improved ORR for patients with LOH score  $\geq 16\%$ <sup>2,161</sup>.

## SUPPORTING DATA

Olaparib has been studied primarily to treat patients with ovarian cancer harboring BRCA1/2 mutations. Numerous Phase 2 studies have demonstrated significant clinical activity for patients with BRCA-mutated ovarian cancer, with response rates often significantly higher for patients with BRCA mutations than for those without<sup>167-168</sup>, and for patients with platinum-sensitive (vs. platinum-resistant) cancer<sup>168-171</sup>. As maintenance therapy for patients with newly diagnosed or platinum-sensitive relapsed ovarian cancer, olaparib monotherapy demonstrated significantly improved median PFS (mPFS) and OS compared with placebo in the Phase 3 SOLO-1 study<sup>172</sup> and multiple later-phase studies<sup>173-177</sup>. At the 5-year follow-up of SOLO-1, olaparib continued to improve mPFS compared with placebo for patients with ovarian cancer<sup>178</sup>. In the first study of PARPi rechallenge

for patients with ovarian cancer, the Phase 3 OReO/ENGOT Ov-38 study of maintenance olaparib compared with placebo reported statistically improved mPFS for both patients with BRCA-mutated (4.3 vs. 2.8 months, HR=0.57) and BRCA-unmutated (5.3 vs. 2.8 months, HR=0.43) cancer; in an exploratory analysis of the BRCA-unmutated cohort, improved mPFS was reported regardless of homologous recombination deficiency status<sup>179</sup>. Olaparib has also been evaluated in combination with other therapies. A statistically superior median PFS from treatment with olaparib in combination with the VEGF inhibitor bevacizumab compared with bevacizumab monotherapy was reported in the Phase 3 PAOLA-1 study for patients with newly diagnosed advanced ovarian cancer in the intent-to-treat population (PFS: 22.1 vs. 16.6 months), the BRCA1/2-mutated population (PFS: 37.2 vs. 21.7 months), and the BRCA1/2-wildtype population harboring homologous recombination deficiency (HRD)-positive status (PFS: 28.1 vs. 16.6 months)<sup>180</sup>. For patients with platinum-sensitive recurrent ovarian cancer who previously progressed on chemotherapy, statistically increased median PFS was reported in a Phase 2 study of olaparib in combination with chemotherapy (PFS: 12.2 months) compared with chemotherapy alone (PFS: 9.6 months)<sup>181</sup>, as well as from treatment with the VEGFR inhibitor cediranib compared with olaparib monotherapy in a Phase 1/2 trial<sup>182</sup>. The Phase 2 CAPRI study for PARP inhibitor-resistant patients with HRD, platinum-sensitive, high-grade ovarian cancer treated with combination therapy of olaparib and the ATR inhibitor ceralasertib reported an ORR of 46% (n=13, 6 PRs) and a PFS of 7.5 months<sup>183</sup>. For patients with PARP-resistant ovarian cancer, the combination of olaparib and the WEE1-inhibitor adavosertib elicited improved clinical benefit (ORR: 29%; DCR: 89%) compared to adavosertib alone (ORR: 23%; DCR: 63%); however, in the BRCA-mutated cohort, no significant difference in clinical benefit was observed between the combination (ORR: 19%) and monotherapy (ORR: 20%) treatments<sup>184</sup>.

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ORDERED TEST # ORD-1388894-01

THERAPIES WITH CLINICAL BENEFIT

IN PATIENT'S TUMOR TYPE

## Rucaparib

*Assay findings association*

**Loss of Heterozygosity  
score**  
24.9%

### AREAS OF THERAPEUTIC USE

The PARP inhibitor rucaparib is FDA approved to treat patients with metastatic castration-resistant prostate cancer (mCRPC) or epithelial ovarian, Fallopian tube, or primary peritoneal cancer and deleterious somatic or germline BRCA mutations. Rucaparib is also approved as a maintenance treatment of patients with recurrent epithelial ovarian, Fallopian tube, or primary peritoneal cancer. Please see the drug label for full prescribing information.

### GENE ASSOCIATION

On the basis of emerging clinical data in ovarian cancer, elevated genomic LOH may be associated with greater sensitivity to PARP inhibitors<sup>1-2,161</sup>. In platinum-sensitive, BRCA1/2 wild-type ovarian, peritoneal, or Fallopian tube carcinoma, the PARP inhibitor rucaparib elicited significantly longer median PFS and improved ORR for patients with LOH score  $\geq 16\%$ <sup>2,161</sup>.

### SUPPORTING DATA

In the Phase 3 ARIEL3 study of rucaparib maintenance treatment for patients with platinum-sensitive, high-grade serous or endometrioid ovarian, primary peritoneal, or fallopian tube carcinoma, median PFS (mPFS) was significantly improved with rucaparib compared with placebo for patients irrespective of homologous-recombination deficient (HRD) or BRCA status, with benefit observed for both the high-loss of heterozygosity (LOH) subgroup (13.6 vs. 5.4 months, HR=0.32) and the overall population (10.8 vs. 5.4 months, HR=0.36), with CR rates of 12% (HRD) and 7% (overall); PFS benefit was also observed for the BRCA wildtype and low-LOH group (HR=0.58)<sup>1</sup>. In the Phase 2 ARIEL2 trial for patients with recurrent, platinum-sensitive ovarian, peritoneal, or fallopian tube carcinoma, mPFS on rucaparib was 5.7 months for patients with high LOH and 5.2 months for patients with low LOH<sup>2</sup>.

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THERAPIES WITH CLINICAL BENEFIT

IN OTHER TUMOR TYPE

## Talazoparib

*Assay findings association*

**Loss of Heterozygosity  
score**  
24.9%

### AREAS OF THERAPEUTIC USE

The PARP inhibitor talazoparib is FDA approved to treat HER2-negative locally advanced or metastatic breast cancer with deleterious or suspected deleterious germline BRCA mutations. Please see the drug label for full prescribing information.

### GENE ASSOCIATION

On the basis of emerging clinical data in ovarian cancer, elevated genomic LOH may be associated with greater sensitivity to PARP inhibitors<sup>1-2,161</sup>. In platinum-sensitive, BRCA1/2 wild-type ovarian, peritoneal, or Fallopian tube

carcinoma, the PARP inhibitor rucaparib elicited significantly longer median PFS and improved ORR for patients with LOH score  $\geq 16\%$ <sup>2,161</sup>.

### SUPPORTING DATA

An ORR of 42% (5/12) was reported for patients with BRCA1/2-mutated ovarian cancer treated with talazoparib in a Phase 1 study<sup>185</sup>. In a Phase 2 study of talazoparib in advanced solid tumors, 1 patient with BRIP1-mutated ovarian carcinoma with wildtype BRCA status experienced a prolonged SD<sup>186</sup>.

**NOTE** Genomic alterations detected may be associated with activity of certain FDA approved drugs, however, the agents listed in this report may have varied evidence in the patient's tumor type.

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ORDERED TEST # ORD-1388894-01

**CLINICAL TRIALS**

**NOTE** Clinical trials are ordered by gene and prioritized by: age range inclusion criteria for pediatric patients, proximity to ordering medical facility, later trial phase, and verification of trial information within the last two months. While every effort is made to ensure the accuracy of the information contained below, the information available in the public domain is continually updated and

should be investigated by the physician or research staff. This is not a comprehensive list of all available clinical trials. Foundation Medicine displays a subset of trial options and ranks them in this order of descending priority: Qualification for pediatric trial → Geographical proximity → Later trial phase. Clinical trials listed here may have additional enrollment criteria that may require

medical screening to determine final eligibility. For additional information about listed clinical trials or to conduct a search for additional trials, please see [clinicaltrials.gov](https://clinicaltrials.gov). Or visit <https://www.foundationmedicine.com/genomic-testing#support-services>.

**BIOMARKER**

## Loss of Heterozygosity score

**RESULT**

24.9%

**RATIONALE**

On the basis of emerging clinical data in ovarian cancer, elevated genomic LOH may be associated

with greater sensitivity to PARP inhibitors.

**NCT04729387**
**PHASE 3**

Alpelisib Plus Olaparib in Platinum-resistant/Refractory, High-grade Serous Ovarian Cancer, With no Germline BRCA Mutation Detected

**TARGETS**  
 PARP, PI3K-alpha

**LOCATIONS:** Taipei (Taiwan), Taichung (Taiwan), Shanghai (China), Wuhan (China), Jinan (China), Seoul (Korea, Republic of), Tianjin (China), Beijing (China), Kota Kinabalu (Malaysia), Kuching (Malaysia)

**NCT04884360**
**PHASE 3**

D9319C00001- 1L OC Mono Global RCT

**TARGETS**  
 PARP

**LOCATIONS:** Rui'an (China), Wenzhou (China), Hangzhou (China), Shanghai (China), Nanjing (China), Hefei (China), Urumqi (China), Beijing (China), Changchun (China), Guangzhou (China)

**NCT03737643**
**PHASE 3**

Durvalumab Treatment in Combination With Chemotherapy and Bevacizumab, Followed by Maintenance Durvalumab, Bevacizumab and Olaparib Treatment in Advanced Ovarian Cancer Patients.

**TARGETS**  
 VEGFA, PD-L1, PARP

**LOCATIONS:** Shanghai (China), Hefei (China), Wuhan (China), Bengbu (China), Nanning (China), Dalian (China), Chongqing (China), Xi'an (China), Hangzhou (China), Beijing (China)

**NCT04517357**
**PHASE 2**

A Phase 2 Trial of Fluzoparib Combined With Apatinib Versus Fluzoparib Monotherapy in Treatment With Relapsed Ovarian Cancer Patients

**TARGETS**  
 RET, VEGFR2, PARP

**LOCATIONS:** Hangzhou (China)

**NCT03983226**
**PHASE 2**

Surgery and Niraparib in Secondary Recurrent Ovarian Cancer (SOC-3 Trial)

**TARGETS**  
 PARP

**LOCATIONS:** Shanghai (China)

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ORDERED TEST # ORD-1388894-01

CLINICAL TRIALS

**NCT03742895**

PHASE 2

Efficacy and Safety of Olaparib (MK-7339) in Participants With Previously Treated, Homologous Recombination Repair Mutation (HRRm) or Homologous Recombination Deficiency (HRD) Positive Advanced Cancer (MK-7339-002 / LYNK-002)

**TARGETS**  
PARP

**LOCATIONS:** Seongnam-si (Korea, Republic of), Seoul (Korea, Republic of), Nedlands (Australia), Port Macquarie (Australia), Darlinghurst (Australia), Adana (Turkey), Ankara (Turkey), Jerusalem (Israel), Konya (Turkey), Ramat Gan (Israel)

**NCT02264678**

PHASE 1/2

Ascending Doses of AZD6738 in Combination With Chemotherapy and/or Novel Anti Cancer Agents

**TARGETS**  
ATR, PARP, PD-L1

**LOCATIONS:** Seongnam-si (Korea, Republic of), Seoul (Korea, Republic of), Goyang-si (Korea, Republic of), Cambridge (United Kingdom), Withington (United Kingdom), Manchester (United Kingdom), Coventry (United Kingdom), Sutton (United Kingdom), Oxford (United Kingdom), Villejuif (France)

**NCT04644068**

PHASE 1/2

Study of AZD5305 as Monotherapy and in Combination With Anti-cancer Agents in Patients With Advanced Solid Malignancies

**TARGETS**  
ERBB2, TROP2, PARP

**LOCATIONS:** Seoul (Korea, Republic of), Chuo-ku (Japan), Koto-ku (Japan), Melbourne (Australia), Warszawa (Poland), Gdynia (Poland), Grzegnica (Poland), Budapest (Hungary), Brno (Czechia), Padova (Italy)

**NCT04284852**

PHASE 2

Niraparib Maintenance in Patients With Advanced Ovarian Cancer at Neoadjuvant Setting

**TARGETS**  
PARP

**LOCATIONS:** Hong Kong (Hong Kong)

**NCT04556071**

PHASE 2

Efficacy and Safety of Niraparib Combined With Bevacizumab in Platinum Refractory/Resistant Recurrent Ovarian Cancer

**TARGETS**  
VEGFA, PARP

**LOCATIONS:** Nanjing (China)

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ORDERED TEST # ORD-1388894-01

**GENE**
**RNF43**
**RATIONALE**

Based on preclinical evidence, tumors with loss or inactivation of RNF43 may be sensitive to inhibitors of the WNT signaling pathway.

**ALTERATION**

deletion exons 3-7

**NCT02521844**
**PHASE 1**

A Study to Evaluate the Safety and Tolerability of ETC-1922159 in Advanced Solid Tumours

**TARGETS**  
PORCN

**LOCATIONS:** Singapore (Singapore), Colorado, Texas, North Carolina

**NCT01351103**
**PHASE 1**

A Study of LGK974 in Patients With Malignancies Dependent on Wnt Ligands

**TARGETS**  
PORCN, PD-1

**LOCATIONS:** Utrecht (Netherlands), Rotterdam (Netherlands), Barcelona (Spain), Hospitalet de Llobregat (Spain), Valencia (Spain), Madrid (Spain), California, New York, Maryland, Texas

**NCT03447470**
**PHASE 1**

Study to Evaluate the Safety and Tolerability of RXC004 in Advanced Malignancies

**TARGETS**  
PORCN

**LOCATIONS:** Newcastle (United Kingdom), Manchester (United Kingdom), London (United Kingdom), Sutton (United Kingdom), Oxford (United Kingdom)

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CLINICAL TRIALS

## GENE

**TP53**

## RATIONALE

TP53 loss of function alterations may predict sensitivity to WEE1 inhibitors. TP53 missense

mutations may predict sensitivity to therapies that reactivate mutant p53.

## ALTERATION

R273H

**NCT04516447**

## PHASE 1

A Study of ZN-c3 in Patients With Platinum-Resistant Ovarian Cancer

**TARGETS**  
WEE1

**LOCATIONS:** Seoul (Korea, Republic of), Nedlands (Australia), Sunshine Coast (Australia), South Brisbane (Australia), Melbourne (Australia), Panagyurishte (Bulgaria), Belgrade (Serbia), Tuzla (Bosnia and Herzegovina), Sarajevo (Bosnia and Herzegovina), Banja Luka (Bosnia and Herzegovina)

**NCT03968653**

## PHASE 1

Study of Oral Debio 0123 in Combination With Carboplatin in Participants With Advanced Solid Tumors

**TARGETS**  
WEE1

**LOCATIONS:** Groningen (Netherlands), Nijmegen (Netherlands), Leiden (Netherlands), Barcelona (Spain)

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**APPENDIX**
**Variants of Unknown Significance**

**NOTE** One or more variants of unknown significance (VUS) were detected in this patient's tumor. These variants may not have been adequately characterized in the scientific literature at the time this report was issued, and/or the genomic context of these alterations makes their significance unclear. We choose to include them here in the event that they become clinically meaningful in the future.

**ARAF**  
F107del

**ARID1A**  
G1375A

**AXL**  
L299fs\*40

**BARD1**  
R99\_D102del

**CIC**  
rearrangement

**DAXX**  
E457del

**EED**  
amplification

**ERBB2**  
R1230P

**GSK3B**  
Q206H

**IRS2**  
P813S

**MTOR**  
V649M

**NTRK1**  
R220W

**POLE**  
D89A

**SNCAIP**  
rearrangement

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**APPENDIX**

Genes Assayed in FoundationOne®CDx

FoundationOne CDx is designed to include genes known to be somatically altered in human solid tumors that are validated targets for therapy, either approved or in clinical trials, and/or that are unambiguous drivers of oncogenesis based on current knowledge. The current assay interrogates 324 genes as well as introns of 36 genes involved in rearrangements. The assay will be updated periodically to reflect new knowledge about cancer biology.

**DNA GENE LIST: ENTIRE CODING SEQUENCE FOR THE DETECTION OF BASE SUBSTITUTIONS, INSERTION/DELETIONS, AND COPY NUMBER ALTERATIONS**

ABL1	ACVR1B	AKT1	AKT2	AKT3	ALK	ALOX12B	AMER1 (FAM123B or WTX)	
APC	AR	ARAF	ARFRP1	ARID1A	ASXL1	ATM	ATR	ATRX
AURKA	AURKB	AXIN1	AXL	BAP1	BARD1	BCL2	BCL2L1	BCL2L2
BCL6	BCOR	BCORL1	BRAF	BRCA1	BRCA2	BRD4	BRIP1	BTG1
BTG2	BTK	CALR	CARD11	CASP8	CBFB	CBL	CCND1	CCND2
CCND3	CCNE1	CD22	CD274 (PD-L1)	CD70	CD79A	CD79B	CDC73	CDH1
CDK12	CDK4	CDK6	CDK8	CDKN1A	CDKN1B	CDKN2A	CDKN2B	CDKN2C
CEBPA	CHEK1	CHEK2	CIC	CREBBP	CRKL	CSF1R	CSF3R	CTCF
CTNNA1	CTNNB1	CUL3	CUL4A	CXCR4	CYP17A1	DAXX	DDR1	DDR2
DIS3	DNMT3A	DOT1L	EED	EGFR	EMSY (C11orf30)	EP300	EPHA3	EPHB1
EPHB4	ERBB2	ERBB3	ERBB4	ERCC4	ERG	ERRF1	ESR1	EZH2
FANCA	FANCC	FANCG	FANCL	FAS	FBXW7	FGF10	FGF12	FGF14
FGF19	FGF23	FGF3	FGF4	FGF6	FGFR1	FGFR2	FGFR3	FGFR4
FH	FLCN	FLT1	FLT3	FOXL2	FUBP1	GABRA6	GATA3	GATA4
GATA6	GID4 (C17orf39)	GNA11	GNA13	GNAQ	GNAS	GRM3	GSK3B	H3-3A (H3F3A)
HDAC1	HGF	HNF1A	HRAS	HSD3B1	ID3	IDH1	IDH2	IGF1R
IKBKE	IKZF1	INPP4B	IRF2	IRF4	IRS2	JAK1	JAK2	JAK3
JUN	KDMSA	KDMSB	KDM6A	KDR	KEAP1	KEL	KIT	KLHL6
KMT2A (MLL)	KMT2D (MLL2)	KRAS	LTK	LYN	MAF	MAP2K1 (MEK1)	MAP2K2 (MEK2)	MAP2K4
MAP3K1	MAP3K13	MAPK1	MCL1	MDM2	MDM4	MED12	MEF2B	MEN1
MERTK	MET	MITF	MKNK1	MLH1	MPL	MRE11 (MRE11A)	MSH2	MSH3
MSH6	MST1R	MTAP	MTOR	MUTYH	MYC	MYCL (MYCL1)	MYCN	MYD88
NBN	NF1	NF2	NFE2L2	NFKB1A	NKX2-1	NOTCH1	NOTCH2	NOTCH3
NPM1	NRAS	NSD2 (WHSC1 or MMSET)	NSD3 (WHSC1L1)	NTSC2	NTRK1	NTRK1	NTRK2	NTRK3
P2RY8	PALB2	PARP1	PARP2	PARP3	PAX5	PBRM1	PDCD1 (PD-1)	PDCD1LG2 (PD-L2)
PDGFRA	PDGFRB	PDK1	PIK3C2B	PIK3C2G	PIK3CA	PIK3CB	PIK3R1	PIM1
PMS2	POLD1	POLE	PPARG	PPP2R1A	PPP2R2A	PRDM1	PRKAR1A	PRKCI
PRKN (PARK2)	PTCH1	PTEN	PTPN11	PTPRO	QKI	RAC1	RAD21	RAD51
RAD51B	RAD51C	RAD51D	RAD52	RAD54L	RAF1	RARA	RB1	RBM10
REL	RET	RICTOR	RNF43	ROS1	RPTOR	SDHA	SDHB	SDHC
SDHD	SETD2	SF3B1	SGK1	SMAD2	SMAD4	SMARCA4	SMARCB1	SMO
SNCAIP	SOC1	SOX2	SOX9	SPEN	SPOP	SRC	STAG2	STAT3
STK11	SUFU	SYK	TBX3	TEK	TENTSC (FAM46C)	TET2	TGFBR2	TIPARP
TNFAIP3	TNFRSF14	TP53	TSC1	TSC2	TYRO3	U2AF1	VEGFA	VHL
WT1	XPO1	XRCC2	ZNF217	ZNF703				

**DNA GENE LIST: FOR THE DETECTION OF SELECT REARRANGEMENTS**

ALK	BCL2	BCR	BRAF	BRCA1	BRCA2	CD74	EGFR	ETV1
ETV4	ETV5	ETV6	EWSR1	EZR	FGFR1	FGFR2	FGFR3	KIT
KMT2A (MLL)	MSH2	MYB	MYC	NOTCH2	NTRK1	NTRK2	NUTM1	PDGFRA
RAF1	RARA	RET	ROS1	RSPO2	SDC4	SLC34A2	TERC*	TERT**
TPRSS2								

\*TERC is an NCRNA

\*\*Promoter region of TERT is interrogated

**ADDITIONAL ASSAYS: FOR THE DETECTION OF SELECT CANCER BIOMARKERS**

Homologous Recombination status  
Loss of Heterozygosity (LOH) score  
Microsatellite (MS) status  
Tumor Mutational Burden (TMB)

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**APPENDIX**
**About FoundationOne®CDx**

FoundationOne CDx fulfills the requirements of the European Directive 98/79 EC for in vitro diagnostic medical devices and is registered as a CE-IVD product by Foundation Medicine's EU Authorized Representative, Qarad b.v.b.a, Cipalstraat 3, 2440 Geel, Belgium.


**ABOUT FOUNDATIONONE CDx**

FoundationOne CDx was developed and its performance characteristics determined by Foundation Medicine, Inc. (Foundation Medicine). FoundationOne CDx may be used for clinical purposes and should not be regarded as purely investigational or for research only. Foundation Medicine's clinical reference laboratories are qualified to perform high-complexity clinical testing.

Please refer to technical information for performance specification details:  
[www.rochefoundationmedicine.com/f1cdxtech](http://www.rochefoundationmedicine.com/f1cdxtech).

**INTENDED USE**

FoundationOne®CDx (F1CDx) is a next generation sequencing based in vitro diagnostic device for detection of substitutions, insertion and deletion alterations (indels), and copy number alterations (CNAs) in 324 genes and select gene rearrangements, as well as genomic signatures including microsatellite instability (MSI), tumor mutational burden (TMB), and for selected forms of ovarian cancer, loss of heterozygosity (LOH) score, using DNA isolated from formalin-fixed, paraffin-embedded (FFPE) tumor tissue specimens. The test is intended as a companion diagnostic to identify patients who may benefit from treatment with therapies in accordance with approved therapeutic product labeling. Additionally, F1CDx is intended to provide tumor mutation profiling to be used by qualified health care professionals in accordance with professional guidelines in oncology for patients with solid malignant neoplasms.

**TEST PRINCIPLES**

FoundationOne CDx will be performed exclusively as a laboratory service using DNA extracted from formalin-fixed, paraffin-embedded (FFPE) tumor samples. The proposed assay will employ a single DNA extraction method from routine FFPE biopsy or surgical resection specimens, 50-1000 ng of which will undergo whole-genome shotgun library construction and hybridization-based capture of all coding exons from 309 cancer-related genes, one promoter region, one non-coding (ncRNA), and select intronic regions from 34 commonly rearranged genes, 21 of which also include the coding exons. The assay therefore includes detection of alterations in a total of 324 genes.

Using an Illumina® HiSeq platform, hybrid capture-selected libraries will be sequenced to high uniform depth (targeting >500X median coverage with >99% of exons at coverage >100X). Sequence data will be processed using a customized analysis pipeline designed to accurately detect all classes of genomic alterations, including base substitutions, indels, focal copy number amplifications, homozygous gene deletions, and selected genomic rearrangements (e.g., gene fusions). Additionally, genomic signatures including loss of heterozygosity (LOH), microsatellite instability (MSI) and tumor mutational burden (TMB) will be reported.

**THE REPORT**

Incorporates analyses of peer-reviewed studies and other publicly available information identified by Foundation Medicine; these analyses and information may include associations between a molecular alteration (or lack of alteration) and one or more drugs with potential clinical benefit (or potential lack of clinical benefit), including drug candidates that are being studied in clinical research. The F1CDx report may be used as an aid to inform molecular eligibility for clinical trials. Note: A finding of biomarker alteration does not necessarily indicate pharmacologic effectiveness (or lack thereof) of any drug or treatment regimen; a finding of no biomarker alteration does not necessarily indicate lack of pharmacologic effectiveness (or effectiveness) of any drug or treatment regimen.

**Diagnostic Significance**

FoundationOne CDx identifies alterations to select cancer-associated genes or portions of genes (biomarkers). In some cases, the Report also highlights selected negative test results regarding biomarkers of clinical significance.

**Qualified Alteration Calls (Equivocal and Subclonal)**

An alteration denoted as "amplification - equivocal" implies that the FoundationOne CDx assay data provide some, but not unambiguous, evidence that the copy number of a gene exceeds the threshold for identifying copy number amplification. The threshold used in FoundationOne CDx for identifying a copy number amplification is four (4) for ERBB2 and six (6) for all other genes. Conversely, an alteration denoted as "loss - equivocal" implies that the FoundationOne CDx assay data provide some, but not unambiguous, evidence for homozygous deletion of the gene in question. An alteration denoted as "subclonal" is one that the FoundationOne CDx analytical methodology has identified as being present in <10% of the assayed tumor DNA.

**Ranking of Therapies and Clinical Trials**

*Ranking of Therapies in Summary Table*  
 Therapies are ranked based on the following criteria: Therapies with clinical benefit (ranked alphabetically within each evidence category), followed by therapies associated with resistance (when applicable).

**Ranking of Clinical Trials**

Pediatric trial qualification → Geographical proximity → Later trial phase.

**NATIONAL COMPREHENSIVE CANCER NETWORK® (NCCN®) CATEGORIZATION**

Biomarker and genomic findings detected may be associated with certain entries within the NCCN Drugs & Biologics Compendium® (NCCN Compendium®) ([www.nccn.org](http://www.nccn.org)). The NCCN Categories of Evidence and Consensus indicated reflect the highest possible category for a given therapy in association with each biomarker or genomic finding. Please note, however, that the accuracy and applicability of these NCCN categories within a report may be impacted by the patient's clinical history, additional biomarker information, age, and/or co-occurring alterations. For additional information on the NCCN categories, please refer to the NCCN Compendium®. Referenced with permission from the NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines®). © National Comprehensive Cancer Network, Inc. 2022. All rights reserved. To view the most recent and complete version of the guidelines, go online to [NCCN.org](http://NCCN.org). NCCN makes no warranties of any kind whatsoever regarding their content, use or application and disclaims any responsibility for their application or use in any way.

**Limitations**

1. In the fractional-based MSI algorithm, a tumor specimen will be categorized as MSI-H, MSS, or MS-Equivocal according to the fraction of microsatellite loci determined to be altered or unstable (i.e., the fraction unstable loci score). In the F1CDx assay, MSI is evaluated based on a genome-wide analysis across >2000 microsatellite loci. For a given microsatellite locus, non-somatic alleles are discarded, and the microsatellite is categorized as unstable if remaining alleles differ from the reference genome. The final fraction unstable loci score is calculated as the number of unstable microsatellite loci divided by the number of evaluable microsatellite loci. The MSI-H and MSS cut-off thresholds were determined by analytical concordance to a PCR comparator assay using a pan-tumor FFPE tissue sample set. Patients with results categorized as "MS-

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## APPENDIX

## About FoundationOne®CDx

- Stable" with median exon coverage <300X, "MS-Equivocal," or "Cannot Be Determined" should receive confirmatory testing using a validated orthogonal (alternative) method.
- TMB by F1CDx is determined by counting all synonymous and non-synonymous variants present at 5% allele frequency or greater (after filtering) and the total number is reported as mutations per megabase (mut/Mb) unit. Observed TMB is dependent on characteristics of the specific tumor focus tested for a patient (e.g., primary vs. metastatic, tumor content) and the testing platform used for the detection; therefore, observed TMB results may vary between different specimens for the same patient and between detection methodologies employed on the same sample. The TMB calculation may differ from TMB calculations used by other assays depending on variables such as the amount of genome interrogated, percentage of tumor, assay limit of detection (LoD), filtering of alterations included in the score, and the read depth and other bioinformatic test specifications. Refer to the SSED for a detailed description of these variables in FMI's TMB calculation [https://www.accessdata.fda.gov/cdrh\\_docs/pdf17/P170019B.pdf](https://www.accessdata.fda.gov/cdrh_docs/pdf17/P170019B.pdf). The clinical validity of TMB defined by this panel has been established for TMB as a qualitative output for a cut-off of 10 mutations per megabase but has not been established for TMB as a quantitative score.
  - Homologous Recombination status may be reported for epithelial ovarian, peritoneal, or Fallopian tube carcinomas (Coleman et al., 2017; 28916367). Samples with deleterious *BRCA1/2* alteration and/or Loss of Heterozygosity (LOH) score  $\geq 16\%$  will be reported as "HRD Positive" and samples with absence of these findings will be reported as "HRD Not Detected," agnostic of potential secondary *BRCA1/2* reversion alterations. Certain potentially deleterious missense or small in-frame deletions in *BRCA1/2* may not be classified as deleterious and, in the absence of an elevated LOH profile, samples with such mutations may be classified as "HRD Not Detected." A result of "HRD Not Detected" does not rule out the presence of a *BRCA1/2* alteration or an elevated LOH profile outside the assay performance characteristic limitations.
  - The LOH score is determined by analyzing SNPs spaced at 1Mb intervals across the genome on the FoundationOne CDx test and extrapolating an LOH profile, excluding arm- and chromosome-wide LOH segments. Detection of LOH has been verified only for ovarian cancer patients, and the LOH score result may be reported for epithelial ovarian,

peritoneal, or Fallopian tube carcinomas. The LOH score will be reported as "Cannot Be Determined" if the sample is not of sufficient quality to confidently determine LOH. Performance of the LOH classification has not been established for samples below 35% tumor content. There may be potential interference of ethanol with LOH detection. The interfering effects of xylene, hemoglobin, and triglycerides on the LOH score have not been demonstrated.

- Alterations reported may include somatic (not inherited) or germline (inherited) alterations; however, the test does not distinguish between germline and somatic alterations. The test does not provide information about susceptibility.
- Biopsy may pose a risk to the patient when archival tissue is not available for use with the assay. The patient's physician should determine whether the patient is a candidate for biopsy.
- Reflex testing to an alternative FDA approved companion diagnostic should be performed for patients who have an *ERBB2* amplification result detected with copy number equal to 4 (baseline ploidy of tumor +2) for confirmatory testing. While this result is considered negative by FoundationOne®CDx (F1CDx), in a clinical concordance study with an FDA approved FISH test, 70% (7 out of 10 samples) were positive, and 30% (3 out of 10 samples) were negative by the FISH test with an average ratio of 2.3. The frequency of *ERBB2* copy number 4 in breast cancer is estimated to be approximately 2%. Multiple references listed in <https://www.mycancergenome.org/content/disease/breast-cancer/ERBB2/238/> report the frequency of *HER2* overexpression as 20% in breast cancer. Based on the F1CDx *HER2* CDx concordance study, approximately 10% of *HER2* amplified samples had copy number 4. Thus, total frequency is conservatively estimated to be approximately 2%.

### REPORT HIGHLIGHTS

The Report Highlights includes select genomic and therapeutic information with potential impact on patient care and treatment that is specific to the genomics and tumor type of the sample analyzed. This section may highlight information including targeted therapies with potential sensitivity or resistance; evidence-matched clinical trials; and variants with potential diagnostic, prognostic, nontargeted treatment, germline, or clonal hematopoiesis implications. Information included in the Report Highlights is expected to evolve with advances in scientific and clinical research. Findings included in the Report Highlights should be considered in the context of all other information in this report and other relevant

patient information. Decisions on patient care and treatment are the responsibility of the treating physician.

### VARIANT ALLELE FREQUENCY

Variant Allele Frequency (VAF) represents the fraction of sequencing reads in which the variant is observed. This attribute is not taken into account for therapy inclusion, clinical trial matching, or interpretive content. Caution is recommended in interpreting VAF to indicate the potential germline or somatic origin of an alteration, recognizing that tumor fraction and tumor ploidy of samples may vary.

#### Precision of VAF for base substitutions and indels

BASE SUBSTITUTIONS	%CV*
Repeatability	5.11 - 10.40
Reproducibility	5.95 - 12.31
INDELS	%CV*
Repeatability	6.29 - 10.00
Reproducibility	7.33 - 11.71

\*Interquartile Range = 1<sup>st</sup> Quartile to 3<sup>rd</sup> Quartile

### VARIANTS TO CONSIDER FOR FOLLOW-UP GERMLINE TESTING

The variants indicated for consideration of follow-up germline testing are 1) limited to reportable short variants with a protein effect listed in the ClinVar genomic database (Landrum et al., 2018; 29165669) as Pathogenic, Pathogenic/Likely Pathogenic, or Likely Pathogenic (by an expert panel or multiple submitters), 2) associated with hereditary cancer-predisposing disorder(s), 3) detected at an allele frequency of >10%, and 4) in select genes reported by the ESMO Precision Medicine Working Group (Mandelker et al., 2019; 31050713) to have a greater than 10% probability of germline origin if identified during tumor sequencing. The selected genes are *ATM*, *BAP1*, *BRCA1*, *BRCA2*, *BRIP1*, *CHEK2*, *FH*, *FLCN*, *MLH1*, *MSH2*, *MSH6*, *MUTYH*, *PALB2*, *PMS2*, *POLE*, *RAD51C*, *RAD51D*, *RET*, *SDHA*, *SDHB*, *SDHC*, *SDHD*, *TSC2*, and *VHL*, and are not inclusive of all cancer susceptibility genes. The content in this report should not substitute for genetic counseling or follow-up germline testing, which is needed to distinguish whether a finding in this patient's tumor sequencing is germline or somatic. Interpretation should be based on clinical context.

### VARIANTS THAT MAY REPRESENT

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APPENDIX

About FoundationOne®CDx

## CLONAL HEMATOPOIESIS

Variants that may represent clonal hematopoiesis (CH) are limited to select reportable short variants in defined genes identified in solid tumors only. Variant selection was determined based on gene tumor-suppressor or oncogene status, known role in solid tumors versus hematological malignancies, and literature prevalence. The defined genes are *ASXL1*, *CBL*, *DNMT3A*, *IDH2*, *JAK2*, *KMT2D (MLL2)*, *MPL*, *MYD88*, *SF3B1*, *TET2*, and *U2AF1* and are not inclusive of all CH genes. The content in this report should not substitute for dedicated hematological workup. Comprehensive genomic profiling of solid tumors detects nontumor alterations that are due to CH. Patient-matched peripheral blood mononuclear cell sequencing is required to conclusively determine if this alteration is present in tumor or is secondary to CH. Interpretation should be based on clinical context.

## LEVEL OF EVIDENCE NOT PROVIDED

Drugs with potential clinical benefit (or potential lack of clinical benefit) are not evaluated for source or level of published evidence.

## NO GUARANTEE OF CLINICAL BENEFIT

This Report makes no promises or guarantees that a particular drug will be effective in the treatment of disease in any patient. This Report also makes no promises or guarantees that a drug with potential lack of clinical benefit will in fact provide no clinical benefit.

## NO GUARANTEE OF REIMBURSEMENT

Foundation Medicine makes no promises or guarantees that a healthcare provider, insurer or other third party payor, whether private or governmental, will reimburse a patient for the cost of FoundationOne CDx.

## TREATMENT DECISIONS ARE RESPONSIBILITY OF PHYSICIAN

Drugs referenced in this Report may not be suitable for a particular patient. The selection of any, all or none of the drugs associated with potential clinical benefit (or potential lack of clinical benefit) resides entirely within the discretion of the treating physician. Indeed, the information in this Report must be considered in conjunction with all other relevant information regarding a particular patient, before the patient's treating physician recommends a course of treatment. 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, such as patient and family history, physical examinations, information from other diagnostic tests, and patient preferences, in accordance with the standard of care in a given community. A treating physician's decisions should not be based on a single test, such as this Test, or the information contained in this Report. Certain sample or variant characteristics may result in reduced sensitivity. FoundationOne CDx is performed using DNA derived from tumor, and as such germline events may not be reported.

## SELECT ABBREVIATIONS

ABBREVIATION	DEFINITION
CR	Complete response
DCR	Disease control rate
DNMT	DNA methyltransferase
HR	Hazard ratio
ITD	Internal tandem duplication
MMR	Mismatch repair
mut/Mb	Mutations per megabase
NOS	Not otherwise specified
ORR	Objective response rate
OS	Overall survival
PD	Progressive disease
PFS	Progression-free survival
PR	Partial response
SD	Stable disease
TKI	Tyrosine kinase inhibitor

## REFERENCE SEQUENCE INFORMATION

Sequence data is mapped to the human genome, Genome Reference Consortium Human Build 37 (GRCh37), also known as hg19.

MR Suite Version 6.3.0

The median exon coverage for this sample is 899x

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**APPENDIX**
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**APPENDIX**
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