Guidance Statement On BRCA1/2 Tumor Testing in Ovarian Cancer Patients


Published in:
Seminars in Oncology

Document Version:
Publisher's PDF, also known as Version of record

Queen's University Belfast - Research Portal:
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Guidance Statement On BRCA1/2 Tumor Testing in Ovarian Cancer Patients


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Keywords:
Ovarian cancer
BRCA1
BRCA2
Tumor testing

A B S T R A C T

The approval, in 2015, of the first poly (adenosine diphosphate-ribose) polymerase inhibitor (PARPi; olaparib, Lynparza) for platinum–sensitive relapsed high–grade ovarian cancer with either germline or somatic BRCA1/2 deleterious mutations is changing the way that BRCA1/2 testing services are offered to patients with ovarian cancer. Ovarian cancer patients are now being referred for BRCA1/2 genetic testing for treatment decisions, in addition to familial risk estimation, and irrespective of a family history of breast or ovarian cancer. Furthermore, testing of tumor samples to identify the estimated 3%–9% of patients with somatic BRCA1/2 mutations who, in addition to germline carriers, could benefit from PARPi therapy is also now being considered. This new testing paradigm poses some challenges, in particular the technical and analytical difficulties of analyzing chemically challenged DNA derived from formalin–fixed, paraffin–embedded specimens. The current manuscript reviews some of these challenges and technical recommendations to consider when undertaking BRCA1/2 testing in tumor tissue samples to detect both germline and somatic BRCA1/2 mutations. Also provided are considerations for incorporating genetic analysis of ovarian tumor samples into the patient pathway and ethical requirements.

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1. Introduction

1.1. BRCA1/2: Associated cancer risk and genetic testing

BRCA1 (OMIM#113705) and BRCA2 (OMIM# 600185) genes (chromosome 17q21 and 13q12, respectively) [1,2] are tumor suppressor genes encoding proteins primarily involved in DNA repair. Loss of function mutations in BRCA1/2 are associated with
increased risk of breast cancer and ovarian cancer (BC, OC) and to a lesser extent other cancers (eg, prostate cancer) [3,4]. Women carrying a pathogenic germline mutation in either BRCA1 or BRCA2 have a substantially increased lifetime risk of developing BC and OC: 40%–85% lifetime BC risk with BRCA1/2 mutations, with higher rates in BRCA1 mutation carriers [5,6]. Similarly, for OC the lifetime risk is estimated to be higher in women inheriting a BRCA1 mutation (25%–65%) compared with a BRCA2 mutation (15%–20%) [5,6]. The precise cancer risk in female BRCA1/2 germline mutation carriers and the factors that govern mutant allele penetrance depend on many factors, including personal and/or reproductive factors, mutation location, and as yet undefined genetic factors (‘modifier genes’) [7,8].

Pathogenic BRCA1/2 variants are distributed along the entire gene coding regions and overwhelmingly result in truncation and/or inactivation of the mutant protein. Genetic variants include nonsense, frameshift, splice-site, and some missense mutations, as well as large deletion duplications and rearrangements [9,10]. Since the cloning of BRCA1/2 genes, individuals with a strong family history of BC and/or OC have undergone oncogenetic counseling and BRCA1/2 genotyping to identify germline mutation carriers. In families where a pathogenic mutation is detected, the mutation serves as a relevant tool for assessing lifetime cancer risk. Asymptomatic, cancer–free female mutation carriers are offered surveillance for early BC detection and the possibility of risk–reducing surgery [11]. 

In 2015, the first poly (adenosine diphosphate-ribose) polymerase inhibitor (PARPi) olaparib, Lynparza) was licensed for the treatment of BRCA–mutated OC. In a Phase II clinical trial involving 265 patients with either platinum–sensitive recurrent ovarian, fallopian tube or primary peritoneal (high–grade) cancer, maintenance therapy with olaparib showed an improvement in median progression–free survival (PFS). This improvement was more pronounced in patients whose tumors had BRCA1/2 mutations; hazard ratio (HR) 0.18 compared with wild–type BRCA1/2 patients HR 0.54 [12]. More recently, results of the phase III trial (SOLO-2; N = 295) of olaparib tablets as maintenance therapy in patients with relapsed germline–mutated BRCA1/2 OC reported an HR of 0.25 for PFS of patients receiving olaparib versus placebo, and an HR of 0.50 for time to second progression or death for the olaparib versus placebo group [13]. In another Phase III trial of the PARPi niraparib (the European Network of Gynaecological Oncology Trial groups (ENGOT)-OV16/NOVA trial) involving 553 OC patients, an HR of 0.27 for PFS was observed for niraparib treatment compared with placebo in OC patients with germline BRCA1/2 mutations; HR 0.45 for PFS in wild–type BRCA1/2 mutation group and HR 0.38 for patients with germline wild–type BRCA1/2 patients with homologous recombination deoxyribonucleic acid (DNA) repair deficient (HRD) tumors [14].

Poly (adenosine diphosphate-ribose) polymerase (PARP) enzymes function in the repair of single–stranded DNA (ssDNA) breaks via the base–excision repair pathway [15,16]. Therefore, PARP inhibition results in an accumulation of ssDNA breaks; in normal cells these become converted to double–stranded DNA (dsDNA) breaks, which are repaired by the homologous recombination repair (HRR) pathway [15]. In cells lacking a functioning BRCA1/2 protein, repair by the HRR pathway is also inhibited; therefore, PARPi treatment of BRCA1– and BRCA2–associated cancers causes ‘synthetic lethality’ (when two non–lethal processes combine to cause cell death) specifically to cancer cells [15,17,18].

Olaparib is licensed in the European Union as maintenance therapy for adult patients with platinum–sensitive relapsed BRCA1– and BRCA2–mutated (germline and/or somatic deleterious mutations) high–grade serous (HGS) carcinoma of the ovary, fallopian tube, or peritoneum, who are in complete or partial response to platinum–based chemotherapy. Thus, OC patients are now also referred for BRCA1/2 genetic testing to determine their suitability for PARPi therapy, in the appropriate clinical context. This new indication for BRCA1/2 genetic testing has also introduced the concept of tumor testing of BRCA1/2 gene mutations, as this approach can potentially capture both germline and somatic BRCA1/2 pathogenic variants. As OC is the only indication for which PARPi have been licensed thus far, the remainder of this article will focus on BRCA1/2 tumor–based testing in OC.

1.2. Ovarian cancer treatment and impact of BRCA1/2 mutations on treatment outcomes

Platinum and paclitaxel combination chemotherapy has been the first–line standard of care for OC [19], with carboplatin recently replacing cisplatin because it is equally effective and bettertolerated. Since 2011, bevacizumab has been approved in Europe in combination with first–line standard of care treatment of patients with advanced epithelial ovarian, fallopian tube, or primary peritoneal cancer. Nonetheless, advanced OC patient prognosis remains poor, with a median PFS and 5–year overall survival (OS) of 14–19 months and 30%–35%, respectively, (ICON 7 and GOG 140), and ultimately most patients will relapse [20–22].

Ovarian cancer comprises different histological subtypes, of which high–grade serous (HGSOC) is the most common, representing ~70% of advanced cases [23–25]. In women unselected for family history, germline BRCA1/2 mutations have been found in 4%–14% of all OCs, 5%–18% of serous OCs, and ~22% of HGS cases [26–32].

Patients with germline BRCA1/2–mutated OC tend to respond well to platinum–based chemotherapy and have a longer median OS than sporadic OC patients [33–39]. The main histological subtype associated with BRCA1/2 mutations and response to platinum is HGS carcinoma. Other OC histological types have been found to harbor deleterious mutations in other HRR genes [40]; 31% of OCs have a deleterious germline (24%) or somatic (9%) mutation in 1 of 13 HRR genes (mutations also associated with primary platinum sensitivity and improved OS).

1.3. Somatic BRCA1/2 mutations in ovarian cancer

In the Phase II trial of olaparib in patients with platinum–sensitive serous OC, 136 out of 265 patients had a BRCA1/2 mutation; 20 (15%) were somatically acquired [41]. In another study, BRCA1/2 mutations were identified in 44 out of 235 (19%) unselected OC tumors; 39% of which were somatic [27]. No additional somatic mutations were detected in tumors from patients with germline mutations, suggesting that loss of heterozygosity (LOH) is responsible in most cases for the bi–allelic inactivation in neoplastic cells. Another study, by The Cancer Genome Atlas (TCGA) consortium, of HGSOC patients found BRCA1/2 mutations in 64 out of 316 (20%) patients: 9% and 8% were germline BRCA1 and BRCA2 mutations, respectively, and 3% were somatic mutations [42].

Whole exome sequencing analysis of the combined germline–somatic landscape in OC in a series of 429 TCGA OCs found germline truncation variants and large deletions across Fanconi pathway genes in 20% of cases [43]. In this analysis, somatic mutations in BRCA1 and BRCA2 with potential functional consequences were detected in 4.9% and 2.6% of OCs, respectively.

An analysis of a large set of OC patients for germline (n = 899), somatic (n = 279) and epigenetic alterations (n = 482) in the BRCA1, BRCA2 and RAD51C genes revealed deleterious germline BRCA1 mutations in 32 (3.6%), BRCA2 in 28 (3.1%), and RAD51C in
26 (2.9%) patients [44]. Deleterious somatic mutations in BRCA1/2 were observed in 3.6% of tumors.

Whether a deleterious mutation has been inherited or acquired somatically, it is thought to be essential that the remaining BRCA1/2 allele in 17q21 or 13q12, respectively, should be lost in the pre-malignant cells for malignant transformation to occur. In OC tumor samples with deleterious mutations in BRCA1/2, LOH of the functional allele was detectable in virtually all cases with BRCA1 mutations [45–47] and in ~70% of cases with BRCA2 mutations. These LOH events increase the allelic frequency of the mutation in tumor samples.

1.4. Rationale for BRCA1/2 tumor testing

When using tumor tissue DNA to detect BRCA1/2 variants, both germline and somatic BRCA1/2 mutations are identified. This could be advantageous (time saving and cost saving), as potentially only one test needs to be performed to identify all patients with deleterious BRCA1/2 variants that may benefit from PARPi treatment. An estimated 10%–20% of OC patients are likely to harbor either a germline or somatic BRCA1/2 mutation; this approach could facilitate a focused germline testing effort and overall reduction in genetic testing.

2. Considerations and Recommendations for Ovarian Cancer Tumor BRCA1/2 Genetic Testing

Key recommendations for conducting BRCA1/2 genetic testing on OC tumor tissue samples are summarized in Table 1.

2.1. Recommendations for BRCA1/2 tumor testing sample types

Ovarian cancers are characterized by a complex and changing genetic profile [48]; consequently, BRCA1/2 tumor testing results can potentially vary depending on disease stage and sample site. There is also the possibility that a pathogenic germline or somatic BRCA1/2 mutation can revert to a functional gene during disease progression, due to development of acquired resistance via somatic revertant mutations [49–54].

In a small study, secondary BRCA1/2 mutations were identified in 7 out of 10 platinum–resistant OCs and 0 out of 5 platinum–sensitive tumors, leading to the hypothesis that BRCA1/2 revertant mutations could be associated with treatment resistance [55]. In another study, a second BRCA1/2 mutation was found in 13 out of 46 (28.3%) recurrent OCs (12 of 13 were platinum resistant), compared with 2 out of 64 (3.1%) primary tumors (one platinum resistant, other unknown platinum response) [50]. A larger study of 92 primary refractory, resistant, sensitive OCs and matched acquired resistant disease used whole-genome sequencing of tumor and germline DNA samples, and found several molecular events associated with acquired resistance, including multiple independent somatic BRCA1/2 revertant mutations [51].

The limited information available on somatic BRCA1/2 mutations and response to PARPi from clinical trials relates to analysis of primary ovarian tumors [12,41]. In light of this limited information, it is suggested that BRCA1/2 tumor testing be performed on primary tumors, as this is the most likely sample type available. However, it should be noted that the analysis of metastatic tissue at the time of progression may provide a more accurate indication of tumors likely to respond to PARPi treatment, due to the evidence supporting the association of revertant mutations and treatment resistance. Surgeons responsible for OC patients need to be made aware of the potential need for tissue testing further down the line and thus the need for adequate collection of tumor samples prior to surgery (ie, multiple biopsy specimens with a high tumor content).

Formalin–fixed, paraffin–embedded (FFPE) specimens may be used for BRCA1/2 mutation analysis; this is likely to be the most widely available sample type. Fresh–frozen specimens provide better quality DNA; however, they are not routinely available from most referring centers. Other tissue treatments (eg, alcohol–based, acidic or heavy metal fixatives, or decalcifying solutions) and necrotic samples should be avoided, as they lead to increased DNA degradation. The College of American Pathologists guidelines for Human epidermal growth factor receptor 2 testing in BC can be followed for the fixation of tissue samples [56]. The fixation time should be 8–48 hours, depending on specimen or tissue block size; prolonged cold ischemia time or a fixation duration <6 hours or >32 hours increases the likelihood of DNA being of suboptimal quality and unsuitable for BRCA1/2 testing. Table 2 outlines parameters to consider to ensure a good quality FFPE samples for DNA analysis.

Formalin–fixed, paraffin–embedded sections for DNA extraction should be derived from a single representative block per case and contain ≥30–50 μm depth (eg, 5 x 10 μm or 10 x 5 μm) tissue sections. Appropriately trained pathologists should confirm diagnosis, determine the adequacy of specimens for BRCA1/2 genetic testing by assessing neoplastic cell content in the specimen, and mark the relevant areas of the tissue to guide macro-dissection as required. Each laboratory should establish the minimum proportion and number of neoplastic cells needed for mutation detection during validation of the methodology. A set of dilutional standards from cells with known BRCA1/2 pathogenic variants could be used to assess the lower limit of detection.

2.2. Recommendations for DNA extraction from tumor samples

DNA for BRCA1/2 testing should be extracted from the tumor tissue sample using a validated protocol that ensures sufficient quality and quantity of DNA for the particular methodology, which may widely differ. Tumor samples must have a sufficiently high percentage of neoplastic cells for DNA analysis. Generally, a sample for BRCA1/2 tumor testing is recommended to contain a percentage of neoplastic cells that is at least three times the method’s limit of detection (eg, methodology with 5% limit of detection requires the area of tumor sample selected for DNA extraction to contain ≥15% neoplastic cells). This should allow for overestimation of neoplastic cell content, particularly in samples with large areas of inflammation and, to a lesser degree, account for tumor heterogeneity.

The quantity of DNA analyzed can vastly influence result accuracy (eg, analysis of 1 ng of DNA corresponding to the DNA content from ~15,000 cells can lead to stochastic variation in the sample, increasing the risk of false negative results when the mutation–carrying alleles are not sufficiently represented in the sample or are negatively selected during the process), or false positive results (when artefactual sequences are predominantly amplified during the process). Conversely, 100 ng of DNA corresponds to the DNA content from ~15,000 cells, allowing for a statistically representative sample of tumor DNA. Thus, increasing the quantity and proportion of analyzed tumor DNA improves the likelihood and accuracy of detecting somatic mutations. Although FFPE samples with low tumor content may still allow for the detection of germline mutations (present in all cells) it is always recommended that specimens with sufficient tumor content be analyzed to reliably detect acquired (ie, somatic) mutations.

DNA extraction protocols specific for FFPE tissue are recommended, as they tend to account for the shorter average fragment size compared with high molecular weight (HMW) DNA extraction methods. Fluorometric quantification of DNA should be
undertaken using intercalating dyes to specifically assess dsDNA quantity, and spectrophotometric quantification should be abandoned. The quantity of dsDNA required ranges from 10–200 ng depending on the library preparation procedure used [57]. It is essential to perform a DNA quality control upfront, to test quality and amplifiability of the DNA. Laboratories can consider using validated library preparation kits with the in vitro diagnostic device CE–marked certification for specific use of testing in FFPE samples, if available. Use of standard DNA samples (commercially available or in–house validated) as positive and negative controls

Table 1

<table>
<thead>
<tr>
<th>Recommendation Category</th>
<th>Key recommendations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sample types appropriate for BRCA1/2 tumor testing</td>
<td>Use tissue samples from either primary HGS carcinomas or related metastases; FFPE specimens or fresh-frozen specimens if available. Follow The College of American Pathologists guidelines for breast cancer for fixation of tissue samples (Hammond 2010); fixation time 8–48 hours, depending on size of specimen. FFPE sections (in total) should be ≥50 µm in depth derived from a single representative block per case, using macrodissection to enrich the neoplastic content when needed. Diagnostic H&amp;E stained slides, reviewed by appropriately trained pathologists with molecular pathology experience, should be used for tumor assessment. Sample should contain a percentage of tumor cells that is at least three times the limit of detection of the method being used (eg, if a method has a 5% limit of detection, the area of tumor sample selected for DNA extraction should contain at least 15% tumor cells).</td>
</tr>
<tr>
<td>DNA extraction from tumor samples</td>
<td>Use a DNA extraction protocol specific for FFPE tissues, deparaffinisation process and recommended starting material should be adhered to. Fluorometric quantification of DNA should be undertaken using intercalating dyes (ie, PicoGreen® or Qubit®) as these can more specifically assess the amount of dsDNA in the sample than spectrophotometric methods. The quantity of dsDNA ranges from 10–200 ng depending on the procedure used for library preparation.</td>
</tr>
<tr>
<td>Methodologies for tumor testing</td>
<td>Laboratories should use BRCA1/2 test methods that are able to detect mutations in specimens with at least 50% cancer cell content, although laboratories are strongly encouraged to use (or have available an external reference laboratory) more sensitive tests that are able to reliably detect mutations in specimens with ≥10% variant allele frequency, corresponding to 10–20% neoplastic cell content. NGS, not Sanger sequencing, should be used for analysis. Amplicons must be shorter when using DNA derived from FFPE material compared with blood samples, and ideally &lt; 150 bp. An average sequencing coverage of 500–2000 reads, considering sequencing coverage uniformity, is recommended to avoid false negative assessment and enable detection of somatic mutations when using amplicon-based NGS; however, this is dependent on the assay limits of detection, level of sensitivity desired, and the sample content of neoplastic cells.</td>
</tr>
<tr>
<td>Avoiding false positive and false negative results</td>
<td>Use duplicate analysis or repeat analysis from the same starting genomic DNA to eliminate artefacts and use sufficient input DNA. Any method used should have been validated using FFPE tumor samples. Any pipeline established and validated on germline BRCA1/2 mutations needs to be validated for tumor mutations. Collated information is available via a public website that enables the user to search for available information on individual BRCA1/2 genetic variants and their current classification of benign or pathogenic at <a href="http://brcaexchange.org/">http://brcaexchange.org/</a>; ClinVar for FFPE–specific recommendations. Written information as well as a discussion on the implications for the patient and their families of the test result, which may either be performed personally or via a host of telemedicine technologies, is highly recommended for patients referred for testing. Informed consent from patients must be obtained in writing before undertaking germline testing. Individual countries vary in their recommendations and legal requirements, and all local criteria must be adhered to.</td>
</tr>
<tr>
<td>Informed consent and ethical considerations</td>
<td>Timing of testing</td>
</tr>
</tbody>
</table>

Abbreviations: dsDNA, double–stranded deoxyribonucleic acid; H&E, haematoxylin and eosin; HGS, high–grade serous; FFPE, formalin fixed paraffin embedded; NGS, next–generation sequencing; OC, ovarian cancer

Table 2

<table>
<thead>
<tr>
<th>Parameter considerations</th>
<th>Recommendations</th>
</tr>
</thead>
<tbody>
<tr>
<td>10% buffered formalin</td>
<td>Fixation method</td>
</tr>
<tr>
<td>8–48 hours, depending on size of specimen</td>
<td>Fixation time</td>
</tr>
<tr>
<td>Replace knife blades before each new FFPE tissue block is cut</td>
<td>Prevention of cross-contamination</td>
</tr>
<tr>
<td>Use disposable plasticware to transfer sections to glass slides</td>
<td>Use of DNA taps or bleach on microtome blades</td>
</tr>
<tr>
<td>Should be avoided, as are likely to degrade DNA and inhibit PCR</td>
<td>Percentage of neoplastic cells</td>
</tr>
<tr>
<td>3 × the limit of detection of the method</td>
<td>Selection of tumor area</td>
</tr>
<tr>
<td>Avoid areas of inflammation or immune infiltrate, areas of necrosis, and selecting many different small regions</td>
<td>Thickness of section</td>
</tr>
<tr>
<td>Careful dissection under a magnifier glass is recommended. Pre-wet the scalpel or pipette tip to avoid flakes of tissue coming off the slides</td>
<td>Macro-dissection</td>
</tr>
<tr>
<td>Any method including a purification step suitable for small DNA fragments can be used</td>
<td>DNA extraction</td>
</tr>
<tr>
<td>Not advised – reduces DNA yield and quality. If decalcification is needed (ie, bone biopsies), EDTA must be used instead of acidic decalcification</td>
<td>Use of decalcification</td>
</tr>
</tbody>
</table>

Abbreviations: DNA, deoxyribonucleic acid; EDTA, ethylenediaminetetraacetic acid; FFPE, formalin fixed paraffin embedded; PCR, polymerase chain reaction
are recommended to assess potential variation in analytical performance over time. Alternatively, clinical samples with known BRCA1/2 genetic status can be periodically included as controls. Continuous evaluation of the employed procedure in the context of an accreditation program (such as ISO15189 or equivalent), as well as participation in certified external quality assessment (EQA) programs specific for tumor BRCA1/2 testing from FFPE (ie, EMQN, QuIP or UKNEQAS) is highly recommended.

2.3. Advantages and pitfalls of different methodologies for BRCA1/2 tumor testing

BRCA1/2 are both large genes, and mutations can occur anywhere along the coding region in most populations lacking founder mutations [58]. Thus, it can be more challenging to detect BRCA1/2 mutations than mutations in oncogenes with known mutation ‘hot spots’ (eg, KRAS). Additionally, a significant proportion of BRCA1 variants consists of large intragenic deletions or rearrangements (≥8% of known BRCA1 mutations; > 33% in some northern European countries), which are generally more difficult to detect in DNA derived from FFPE than in HMW germline DNA. The proportion of BRCA2 large rearrangement is very low (< 2%) [59] and the proportion of these events that are acquired somatically in OC tumors is still unknown. Moreover, the mutations with an impact on splicing should be carefully checked using algorithms (eg, MaxEntScan). Some variants may seem to have no functional impact but in fact effect exon splicing (ie, exon 23 in BRCA1 [60]) and these events should be carefully analyzed [61,62]. Currently, there is little information in the literature to inform the medical community regarding the decision to test for BRCA1/2 mutations in OC tumor tissue samples first and then blood, or vice versa. The quality and yield of DNA extracted from FFPE tumors is poorer than DNA extracted from blood and fresh tissue, and tends to be variable [63,64]. FFPE tissue poses specific diagnostic challenges, and fragment sizes of DNA extracted from FFPE tumor tissue is lower, requiring specific adjustment of diagnostic procedures, including expert handling of tissue specimen for DNA extraction, amplicon composition, and diagnostic evaluation. Laboratories should use BRCA1/2 test methods that are able to detect mutations in specimens with at least ≥10% variant allele frequency, corresponding to a minimum content of 10%–20% neoplastic cells.

Next–generation sequencing (NGS) is highly recommended as the sequencing method of choice for BRCA1/2 tumor testing, due to the quantity of DNA available from tumor samples and the size of BRCA1/2 coding regions and amplicon composition (160–220 amplicons per test and ideally < 250 bp). Sanger sequencing should be abandoned in tumor testing, as it is not sensitive enough for tumor tissue sample analysis, especially in samples with < 50% tumor cells, and it also requires a large amount of DNA for the screening of these two large genes. Established methods used for detecting germline BRCA1/2 mutations from blood samples may not be suitable for tumor tissue testing; it is therefore imperative that any method used must be validated for use on FFPE samples. Amplicon–based NGS approaches for analysis of FFPE material are now commercially available, although each laboratory should internally validate the specific complete pipeline.

The accuracy of tumor BRCA1/2 testing is influenced by multiple variables, including the specimen’s percentage of neoplastic cells and the sensitivity, specificity, and lower limit of detection, as previously discussed. It is important to note that when using amplicon–based sequencing strategies, the number of unique template molecules analyzed is easily overestimated, especially if the amount or quality of input DNA is suboptimal; therefore, extreme care needs to be taken in the analysis of such samples.

The methods used to detect larger deletions or duplications may not directly translate from germline analysis of HMW DNA to FFPE–derived DNA analysis, due to smaller DNA fragment size, DNA chemical modification, chromosomal copy number changes (ie, aneuploidy), and the frequent instability of tumor samples [65]. Furthermore, the frequency of somatically acquired deletions and rearrangements in tumor tissue is unknown; larger cohort studies are required. Bioinformatic approaches using NGS data analysis of copy number variation from capture–enrichment strategies are recommended for identification of large deletions and duplications, if previously validated. Multiplex ligation–dependent probe amplification is a commonly used method for detecting large genomic rearrangements in germline DNA. However, it may not be appropriate for use without adaptation in tumor tissue analysis, as the control reference regions are not suitable to use in the calculations due to aneuploidy present in the tumor cells. Using normalization with intragenic probes allows for detection of intragenic exon deletions and duplication [47]. Such methods need to be extensively validated in the laboratory if all types of variants need to be detected in the tumor sample. Point mutations and small indels are best identified using amplicon and capture–based NGS [66], the advantages and disadvantages of which are outlined in Table 3. An average sequencing coverage of 500x–2000x reads, considering sequencing coverage uniformity is recommended to avoid false

Table 3
Advantages and disadvantages of amplicon versus capture–based sequencing methods for analysis of tumor tissue samples.

<table>
<thead>
<tr>
<th>Methods</th>
<th>Advantages</th>
<th>Disadvantages</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Amplicon–based NGS</strong></td>
<td>Little sample input (DNA from small biopsies)</td>
<td>Fixation artefacts/PCR duplicates</td>
</tr>
<tr>
<td></td>
<td>Defined target regions</td>
<td>Very difficult to detect large deletions/rearrangements</td>
</tr>
<tr>
<td></td>
<td>Improved inter–center comparability</td>
<td>Lower coverage uniformity</td>
</tr>
<tr>
<td></td>
<td>Higher on target reads</td>
<td>Mutations at amplicon ends might be problematic</td>
</tr>
<tr>
<td></td>
<td>Faster sample preparation</td>
<td>Impossible to calculate experimental limit of detection of the assay as unique coverage is generally unknown</td>
</tr>
<tr>
<td></td>
<td>Simpler workflow and easier bioinformatics</td>
<td>Vulnerable to false positive results and sensitivity as to required amount of tumor DNA</td>
</tr>
<tr>
<td></td>
<td>Lower complexity in library preparation</td>
<td>More sample input required (× 10)</td>
</tr>
<tr>
<td></td>
<td><strong>Capture–based NGS</strong></td>
<td>Longer and more laborious methods</td>
</tr>
<tr>
<td></td>
<td>Potential to detect large deletions/ rearrangements (depending on the captured area)</td>
<td>Increased turnaround times</td>
</tr>
<tr>
<td></td>
<td>Fixation artefacts and/or PCR duplicates are reduced</td>
<td>More data output (more detected genomic aberrations and/or interpretation might be more difficult)</td>
</tr>
<tr>
<td></td>
<td>Higher coverage uniformity</td>
<td>Complexity of library preparation</td>
</tr>
<tr>
<td></td>
<td>Possibility to determine amount of unique reads and thus to assess experimental limit of detection</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Performed better with respect to sequencing complexity and uniformity</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Less likely than amplicon–based NGS to generate false positive SNVs</td>
<td></td>
</tr>
</tbody>
</table>

Abbreviations: DNA, deoxyribonucleic acid; NGS, next–generation sequencing; PCR, polymerase chain reaction; SNV, single nucleotide variants.
negative assessment and enable detection of somatic mutations when using amplicon–based NGS; however, this is dependent on the level of sensitivity desired and the sample content of neoplastic cells. It should also be noted that the number of reads does not necessarily correlate with sensitivity, as many reads may be derived from a single template molecule (ie, polymerase chain reaction [PCR] duplicates). Using a method with single molecule tags overcomes this problem [47]. Moreover, it also depends on the amount of samples loaded onto the sequencer, the type of reagents or chips used for sequencing, and the type of instrument.

Any assay used clinically should be validated in terms of specificity, sensitivity, limit of detection, repeatability (intra–batch variation), and interim precision (inter–batch variation). Laboratory–developed tests need to be fully validated, and commercially available tests also require verification at least (if they are used according to manufacturer's instructions). Assay validation and verification must be performed on typical sample types; in the case of tumor BRCA1/2 testing, typical samples are OC FFPE, including biopsies and resection specimens. Ideally, a range of typical DNA yields should be evaluated to determine optimal conditions, and to determine any potential assay performance issues if suboptimal conditions are used (eg, low DNA input where artefacts are often more apparent) [67]. In Germany, the Institute of Pathology and Germany's National Accreditation Body (Dakks) can provide validation, and Dakks guidelines according to ISO 17020 are available for assay validations. In most other countries, ISO15189 accreditation is necessary.

An EQA testing exercise, involving a number of central European countries, has demonstrated broad, high–quality diagnostic availability of NGS–based BRCA1/2 mutation testing on FFPE tumor tissue in > 20 centers, providing broad community–based availability of the test [68]. This trial has also shown the diagnostic usefulness of the commonly available NGS platforms and the feasibility of NGS–based testing within time spans required in oncological patient care.

2.4. Avoiding false positive and false negative results

Due to the quality of the DNA extracted from FFPE tissue, artefactual errors caused by the fixation process can result in false positive results. Duplicate analysis or repeat analysis from the same starting DNA can help eliminate artefacts, as they are not generally reproducible due to their stochastic nature [67]. Artefacts can also be reduced if the method being used can discriminate between sense and antisense strands, and/or involve molecular barcodes, which have the additional benefit of being able to assess the number of template molecules analyzed [69–72]. These artefactual errors are a particular issue for amplicon–based sequencing, when DNA concentration is low [67,71], as the rate of PCR duplicates increases with decreased DNA input amounts. This is relevant for FFPE tumor biopsy samples, as the number of PCR duplicates is expected to be higher due to limited specimen material that restricts DNA input amounts and poor sample quality that limits the amount of DNA that can be amplified. However, provided DNA input for the assays is sufficient, many artefacts can be screened out by filtering out variants with an allele frequency < 5%–10%, depending on neoplastic cell content. Mutations should pass quality checks and filter settings, and repetitive variants or artefacts in many samples on the same sequencing run should be excluded.

2.5. Bioinformatics considerations

The bioinformatic process, used to analyze and interpret BRCA1/2 mutational analysis results, is a critical part of the whole testing process and requires as much consideration, validation, and accreditation (eg, ISO15189 or CLIA) as the laboratory methods selected to perform the BRCA1/2 mutation analysis. Individual samples in a pooled reaction must be identified and de–multiplexed according to the indices used in the library preparation and the raw data aligned to the reference sequence. Any variations between the reference sequence and the test samples need to be identified by appropriate variant–calling algorithms, correctly annotated using human genome variant society (HGVS) nomenclature, and classified through interrogation of internal and external databases (list provided in Appendix A). Bioinformatics pipelines are therefore a complex mix of different tools tailored to fit the laboratories in their BRCA1/2 testing process. A pipeline established and validated on germline BRCA1/2 testing may not be suitable or may require modification for tumor–tissue–based BRCA1/2 testing or for testing in a different laboratory with a different methodology, mainly due to the length of amplicons obtained through library design.

Pipelines are typically composed of a combination of commercial software, open–source third–party software and bespoke elements. The amount of validation previously conducted on each of these components is likely to vary; however, commercially available solutions should have undergone some level of verification and so may require less in–house testing. Commercial solutions may be particularly useful for testing laboratories with little or no bioinformatics support. Information security management is important where sensitive information is shared, such as in database queries or variant annotation processes, and local and international legislation relating to this issue must be adhered to. The ISO 27001 is an internationally recognized best practice framework for an information security management system, which is important for bioinformatics platforms that share information among users or manage information from clinical scenarios.

Mutation detection threshold levels that are suitable for detecting germline mutations will need to be modified to detect potentially low–variant frequencies of somatic mutations. There is no set recommendation to where this level should be, as this depends on the performance criteria for the test, including any pre–analytical steps such as DNA yield, test DNA input, and neoplastic cell content.

The bioinformatics processes should be validated on all BRCA1/2 mutation types. If laboratories do not have access to a sufficient spectrum of data, there is an increasing repository of NGS data in the public domain. This data could be a useful tool to ensure that all variants are being identified, characterized and classified using a laboratory’s own pipeline. There are a number of international initiatives for the sharing of genetic data: ENIGMA is a consortium of investigators focused on determining all unclassified variants and variants of unknown significance (VUS) in BRCA1 and BRCA2. The BRCA Challenge is a joint initiative of the Global Alliance for Genomic and Global Health and the Human Variome Project, involving several hundred institutes and academic organizations around the world, which aims to pool global available data on BRCA1/2 genetic variants to further the understanding of BRCA1/2 genetic variation.

2.6. Reporting tumor BRCA1/2 results

Recommendations for information to include when reporting BRCA1/2 testing results are listed in Table 4.

The minimum dataset required in a clinical report for tumor BRCA1/2 testing should include:

- Suitability of the tumor sample, including neoplastic content estimation, cellularity, and whether these are acceptable for the specific testing method
Table 4
Recommendations for information to be included when reporting tumor BRCA1/2 results.

<table>
<thead>
<tr>
<th>Information to include</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Histology and grade of the tumor</td>
<td>If available and not previously performed</td>
</tr>
<tr>
<td>Percentage of neoplastic content in the analyzed sample and if macrodissection has been performed</td>
<td>Defined as the percentage of neoplastic cells out of the total nucleated cells in the area used for DNA extraction (e.g., NGS or Sanger sequencing)</td>
</tr>
<tr>
<td>Procedure used</td>
<td>Prevalent mutations vs the recommended whole coding regions including flanking intron sequences</td>
</tr>
<tr>
<td>Coverage of the analysis</td>
<td>Commercial or on demand or multipanel gene (e.g., panels including more than BRCA1/BRCA2 genes)</td>
</tr>
<tr>
<td>Panel used</td>
<td>Any regions for which there was insufficient sequencing read coverage (e.g., 33 reads, dependent on assay limits of detection) should be declared to avoid false negative assessment (e.g., 'large rearrangements/deletions cannot be detected using this methodology')</td>
</tr>
<tr>
<td>Minimum coverage and guaranteed analytical sensitivity with the employed methodology</td>
<td>Models include: MiSeq, NextSeq 500, PGM, IonProton</td>
</tr>
<tr>
<td>If the analysis includes all types of alterations or just single point mutations or small indel alterations</td>
<td>Freeware or commercial; indicate if they have been validated or not for this type of analysis. If the tools are web based, include the https address</td>
</tr>
<tr>
<td>Sequencer</td>
<td>UMD and ClinVar-DB, etc.</td>
</tr>
<tr>
<td>Bioinformatic tools employed</td>
<td>It is important to correlate with neoplastic tumor content and potential LOH, which is present in the vast majority of cases</td>
</tr>
<tr>
<td>Requested databases for grading of detected mutation</td>
<td>Mutation class 4 or 5 – pathogen = possibility of therapy with PARPi; mutation class 1–3 or wild type = no therapeutic consequence and should not be reported (see text for VUS)</td>
</tr>
<tr>
<td>Variant allele frequency</td>
<td>Germline analysis should be always considered if not already performed</td>
</tr>
<tr>
<td>Explanation of therapeutic consequence of mutations according to the classification of the variants</td>
<td>ISO15189, CAP, CLIA or equivalent</td>
</tr>
<tr>
<td>A recommendation of germline analysis and genetic counseling in cases of pathogenic mutations</td>
<td>For example: EMQN, QuIP, UK NEQAS</td>
</tr>
<tr>
<td>Accreditation of the laboratory</td>
<td>Participation in EQA</td>
</tr>
<tr>
<td>ISO15189, CAP, CLIA or equivalent</td>
<td>Participation in EQA For example: EMQN, QuIP, UK NEQAS</td>
</tr>
</tbody>
</table>

Abbreviations: CAP, College of American Pathologists; CLIA, Clinical Laboratory Improvement Amendments; DNA, deoxyribonucleic acid; EMQN, the European Molecular Genetics Quality Network; EQA, external quality assessment schemes; LOH, loss of heterozygosity; NGS, next generation sequencing; PARPi, poly (adenosine diphosphate-ribose) polymerase inhibitor; PGM, personal genome machine; QuIP, Arbeitsgruppe für Qualitätssicherung in der Molekularpathologie der Österreichischen Gesellschaft für Pathologie; UK NEQAS, United Kingdom National External Quality Assessment Service; UMD, Universal Mutation Database; VUS, variants of unknown significance

- Targets analyzed (i.e, BRCA1 and/or BRCA2)
- The regions covered for each gene (e.g., coding region only or intronic and exonic regions)
- Overall results: either pathogenic or deleterious variants present or absent
- Mutation details (when present): cDNA and amino acid change according to HGVS nomenclature
- Reference sequence, including version used for annotation and HGVS nomenclature
- Summary and interpretation: including pathogenic or likely pathogenic classification of the identified variants. Non–pathogenic variants should not be reported, although the laboratory may keep a record of these. Variants of unknown significance should be reported separately and clearly indicate the lack of sufficient clinical or biological evidence. Information regarding the potential therapeutic implications should be included when possible.

2.7. Should genetic testing be limited to BRCA1/2 testing?

Currently, genetic testing in OC should be limited to BRCA1/2 for clinical– and therapeutic–driven decisions, as indications to date are restricted to these genes. However, additional genes involved in the HRR pathway are being evaluated in a number of clinical trials (NCT02422498, NCT02489058, and NCT01434316) and are likely to become part of the standard testing methodology in the future [73]. A recent study has shown increased efficacy of PARPi in OC with HRD without a germline BRCA1/2 mutation [14].

3. Integrating BRCA1 and BRCA2 Tumor Testing In The Patient’s Pathway

Commissioning strategies in different countries relating to both BRCA1/2 tumor and germline testing are diverse. In October 2014, the Society of Gynecological Cancer recommended that all women diagnosed with ovarian, fallopian tube, or peritoneal carcinoma, regardless of age or family history, should receive genetic counseling and be offered BRCA1/2 genetic testing [74]. Many individual country guidelines now also recommend offering BRCA1/2 genetic testing to OC patients irrespective of a family history of BC or OC, an approach that may in fact be cost-effective for universal healthcare systems [75] (Appendix B) [11,76–84]. Although the prevalence of BRCA1/2 pathogenic variants is highly associated with a familial history, with a > 75% probability of a mutation in women with a strong BC or OC familial history [85], the availability of PARPi and lack of accurate family history for many patients make it appropriate to refer all OC patients for genetic testing.

3.1. Germline v tumor BRCA1/2 testing from the clinical perspective

It is necessary to determine the BRCA1/2 status of an OC patient in order to be able to determine eligibility for PARPi therapy, and testing the tumor samples can in principle detect both somatic and germline variants. The limitations of tumor testing must, however, be considered. It is difficult to distinguish between germline and somatic mutations by analyzing tumor tissue in isolation and it is therefore inappropriate to draw any conclusions concerning familial risk based on this analysis alone. Any patient found to have a deleterious BRCA1/2 mutation in a tumor specimen should be offered genetic counseling to undergo germline analysis to assess the existence of the mutation in germline DNA, a finding affecting familial risk. On the other hand, genetic analysis in blood samples can only identify germline mutations, missing approximately 3%–5% of patients who have an acquired BRCA1/2 pathogenic variant [12,41] and who could also benefit from PARPi therapy. The advantages and disadvantages of BRCA1/2 tumor testing versus blood germline testing are outlined in Table 5.

3.2. When in the patient journey should BRCA1/2 testing be carried out?

Tumor testing for BRCA1/2 status should be undertaken in order for the result to be available at a clinically relevant time frame,
factoring in the local testing turnaround times, the potential need for genetic counseling, and other relevant considerations (Figure 1). Referral timing for OC patients’ genetic testing is not specified in many guidelines, but where it is, it is either recommended at diagnosis (Italy [76,82]) or as soon as possible during the first treatment cycle (Austria [83]; Belgium [77]). Given the experience thus far in germline BRCA1/2 testing in OC and microsatellite instability testing of colorectal cancer patients for Lynch syndrome, most patients are willing to undergo testing early on in their management pathway.

Obtaining a tumor tissue sample for BRCA1/2 genetic testing earlier on in the patient pathway may be advantageous. When testing is for treatment decisions, it is desirable to have the test within a maximum of 30–40 day of requesting. For countries considering BRCA1/2 testing to be initially tumor–based rather than germline–based, a proportion of OC patients may never undergo BRCA1/2 testing if testing is limited to the time when PARPi may be used (eg, patients that do not fulfill the approved indication or have unsuitable tissue specimens or are deceased prior to tumor testing). And for those OC patients in this latter group who may harbor a germline mutation, a lack of BRCA1/2 genotyping may have grave implications for family members.

All of the above considerations should of course be reviewed if and when PARPi treatment could be considered for first-line treatment.

### 3.3. Informed consent and ethical considerations

Tumor testing for somatic mutations to better define therapeutic options is a well–accepted concept and practice in the management of other malignancies (eg, EGFR and ALK testing in lung cancer or KRAS and NRAS in colorectal cancer). However, these mutations and genetic variants are clearly somatic by nature and do not have any ethical ramifications. BRCA1/2 tumor tissue genotyping poses different challenges given that an identified tumor BRCA1/2 mutation may represent a germline BRCA1/2 mutation in the majority of cases. Therefore, it is important that patients are adequately counseled prior to testing regarding both the personal clinical implications of the test results and the possible impact of BRCA1/2 genotyping on asymptomatic family members. Informed patient consent and/or institutional review board approval is, at least to some degree, required prior to performing any genetic analysis.

The legal framework in different countries for the performance of genetic testing is heterogeneous. Germline genetic testing is protected or restricted by law and pre–test genetic counseling is mandatory in many countries. Counseling for germline BRCA1/2 testing is traditionally performed by genetic counselors or medical geneticists who specialize in oncogenetics. Due to increased demand on services, some European centers have adopted an oncogenetic pathway for germline BRCA1/2 testing, in which

<table>
<thead>
<tr>
<th>Tumor BRCA testing</th>
<th>Blood BRCA testing</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Advantages</strong></td>
<td><strong>Disadvantages</strong></td>
</tr>
<tr>
<td>Can detect both somatic and germline mutations</td>
<td>Validated methods are available and professionals are experienced in testing and interpreting variants</td>
</tr>
<tr>
<td>Identifies a greater number of patients who may benefit from PARPi therapy</td>
<td>Patient protocols, pathways and procedures are well established</td>
</tr>
<tr>
<td>Potentially requires less extensive genetic counseling at the outset, and less involvement for the wider family</td>
<td>Evidence is strong for the association between BRCA germline mutations and response to PARPi therapy</td>
</tr>
<tr>
<td>Reverted BRCA1/2 mutations can identify patients resistant to treatment</td>
<td>Sample is easily obtained and contains high–quality DNA</td>
</tr>
<tr>
<td>Types of mutations not yet widely available</td>
<td>Analysis feasible in 100% of cases</td>
</tr>
<tr>
<td>Only preliminary data are available on the response to PARPi associated with somatic mutations</td>
<td>Does not identify patients with somatic mutations who could benefit from PARPi therapy</td>
</tr>
<tr>
<td>Sample with sufficiently high percentage of tumor cells/quality of DNA may be hard to obtain, leading to the need for repeat testing and/or biopsy</td>
<td>Genetic profile of the tumor may change with disease progression and chemotherapy</td>
</tr>
<tr>
<td>Analysis not always possible for technical reasons. Investment in new NGS technology may be required as most traditional methods are unsuitable due to limited DNA</td>
<td>Requires additional expertise in pathology to determine sample adequacy</td>
</tr>
</tbody>
</table>

Abbreviations: NGS, next–generation sequencing; PARPi, poly(adenosine diphosphate–ribose) polymerase inhibitor

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**Table 5**

Advantages and disadvantages of BRCA1/2 tumor testing versus blood germline testing.

![Figure 1](image.png)

**Figure 1.** Timeline of factors to consider when determining the time to request BRCA tumor testing.
counseling and consent for genetic testing takes place in the oncology unit, with support from the genetic department, provided by gynecologists or oncologists with training in Germany and Austria [83] and oncologists with specialist training in the UK [86]. Advanced Nurse Practitioners and Clinical Nurse Specialists are another integral part of the oncology team, who, with the support of the genetics and/or oncology team, are now also involved in patient consenting for testing of somatic or germline BRCA1/2 mutations [87]. For tumor BRCA1/2 testing, counseling and obtaining consent in the context of oncology clinics is likely to be a more practical option than referring all patients for presurgical genetic counseling at the relevant genetics institute. Because of this ever increasing need, it is likely that new models of counseling will be adopted in the near future [88]. Appropriate pre–test counseling is required prior to testing even if analysis is only initially being performed on a tumor tissue sample, because germline testing should be offered to the patient and family members in the event that a mutation is detected. When a hereditary OC is identified, the patient’s relatives have possibilities for prevention and should be informed about undergoing genetic testing and treatment options, particularly prophylactic surgery. This type of genetic counseling is also required to be non-directive in several countries (eg, Austria, Germany, Netherlands).

4. Conclusion

With the recent approval of olaparib for platinum–sensitive OC with BRCA1/2 deleterious mutations, a review in BRCA1/2 testing strategy is warranted in most countries. The current paper reviewed the different national and local strategies for BRCA1/2 testing, in particular how germline testing may now be offered to all women with OC based on a > 10% prevalence of BRCA1/2 mutations in this unselected population, raising to > 15% in patients with HGSOC. Based on the European license for olaparib, genetic testing of tumor samples is needed to capture all possible patients that may benefit from PARPi treatment. This new testing paradigm poses some challenges, in particular the technical and analytical difficulties of analyzing chemically challenged DNA derived from FFPE specimens.

The question of whether germline or tumor testing needs to be performed in sequence or in combination will likely be answered differently in different countries, as such strategy is impacted by local or national regulatory elements as well as existing clinical pathways. In any case, identification of deleterious BRCA1/2 mutations in tumor tissue requires subsequent germline testing to assess the inheritability of such variation after appropriate genetic counseling. Moreover, cascade testing of relatives of patients with a germline mutation should be available. Similarly, OC patients without deleterious germline BRCA1/2 mutations will require tumor testing to identify the additional 3%–9% of patients that could benefit from PARPi. Tumor BRCA1/2 testing is currently available in most European countries by different methodologies, although all of them make use of the current NGS technology available. It is important to note that stringent validation of both the NGS methodology and the bioinformatics pipelines for analysis of NGS data derived from FFPE–extracted DNA is required, as this poses different challenges to germline testing, including the influence of neoplastic cell content in the variant allele frequency and the potential artefacts derived from chemical modification of the DNA during the processing of the specimen.

Regardless of the testing algorithm and methodology chosen, it is paramount that any change in practice is linked to the patient’s pathway to ensure that all patients have access to the tests required for their care. This means both germline and tumor testing need to be taken into consideration when designing a new testing strategy, as there is a risk of patients missing important information if one of the tests is not performed as and when appropriate. Such pathways would likely be affected by the requirements for informed consent prior to germline and/or tumor testing, and national and international policies and guidelines will be required to establish best practice for OC patients in the context of PARPi therapies. Furthermore, new scientific evidence regarding the potential benefit of PARPi for OC patients without BRCA1/2 mutations, but with deleterious variants in other HRR genes, is becoming available, and clinical trials assessing the value of other biomarkers are being performed. It is therefore likely that a completely new and comprehensive testing strategy will be required in the next few years for the clinical management of OC patients, in line with the advances of precision medicine in other oncology areas.

Conflicts of interest

DGC has received honoraria and research funds from AstraZeneca.

MJLL has received honoraria and research funds from AstraZeneca and is a member of the onconetwork consortium of Life Technologies.

GE was, at the time of the study, an employee of AstraZeneca, plc.

CS, RS, RB have received honoraria from AstraZeneca.

EF has no conflict of interest to declare.

IRC has received honoraria for lecturing and advisory board attendance from Pharmamar, Roche and AstraZeneca.

JAI has no conflict of interest to declare.

SB has received honoraria for advisory board attendance from AstraZeneca and Clovis Oncology.

CJvA has received research funds from AstraZeneca.

VE has acted as consultant scientist for Thermo Scientific/IonTorrent.

PS has received honorarium for advisory board attendance from AstraZeneca.

Acknowledgements

Editorial and writing support for development of this manuscript was provided by Dr Debra Sates, employed by integrated medhealth communication (imc), London, UK, supported by AstraZeneca.

Funding source

Funding for the development of this manuscript was provided by AstraZeneca.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1053/j.seminoncol.2017.08.004.

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