RAD51 foci as a functional biomarker of homologous recombination repair and PARP inhibitor resistance in germline BRCA-mutated breast cancer


1Experimental Therapeutics Group; 2High Risk and Familial Cancer, Vall d’Hebron Institute of Oncology, Barcelona, Spain; 3Department of Medical Oncology, Hospital Vall d’Hebron, Universitat Autònoma de Barcelona, Barcelona, Spain; 4Growth Factors Laboratory, Vall d’Hebron Institute of Oncology, Barcelona, Spain; 5Cancer Research UK Cambridge Institute, Cambridge, Cambridge, UK; 6AstraZeneca, Gatehouse Park, Waltham, USA; 7DNA Damage Response Biology Area, Oncology iMed, AstraZeneca, Cancer Research UK Cambridge Institute, Cambridge, UK; 8Division of Molecular Pathology and Cancer Genomics, The Netherlands Cancer Institute, Amsterdam, The Netherlands; 9Cancer Genomics Group; 10Molecular Oncology Group, Vall d’Hebron Institute of Oncology, Barcelona, Spain; 11Department of Radiology, Breast Surgical Unit, Breast Cancer Center, Vall d’Hebron, Universitat Autònoma de Barcelona, Barcelona, Spain; 12Division of Molecular Pathology and Cancer Genomics, The Netherlands Cancer Institute, Amsterdam, The Netherlands; 13Gynecological Malignancies Group, Vall d’Hebron Institute of Oncology, Barcelona, Spain; 14Department of Oncology and Cancer Research UK Cambridge Institute, University of Cambridge, Cambridge, UK; 15Cambridge Breast Unit, NIHR Cambridge Biomedical Research Centre and Cambridge Experimental Medicine Centre at Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK; 16Cambridge Experimental Medicine Centre at Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK; 17Human Oncology and Pathogenesis Program (HOPP), 18Department of Medicine, Memorial Sloan Kettering Cancer Center, New York, USA; 19Breast Cancer and Melanoma Group, Vall d’Hebron Institute of Oncology, Barcelona, Spain; 20Ramón y Cajal University Hospital, Madrid; 21Vall d’Hebron Institute of Oncology, Barcelona; 22Department of Biochemistry and Molecular Biology, Building M, Campus UAB, Bellaterra (Cerdanyola del Vallès); 23Instituto Catalán de Recerca i Estudis Avançats (ICREA), Barcelona; 24CIBERONC, Barcelona; 25Clinical and Molecular Genetics Area, Hospital Vall d’Hebron, Universitat Autònoma de Barcelona, Barcelona, Spain; 26DNA Damage Response Biology Area, Oncology Innovative Medicine and Early Development Biotech Unit, AstraZeneca, Cambridge, UK.

*Correspondence to: Dr Violeta Serra, Experimental Therapeutics Group, Vall d’Hebron Institute of Oncology, Carrer Natzaret 115-117, 08035 Barcelona, Spain. Tel: +34-93-2543450; E-mail: v.serra@vhio.net
†Both authors contributed equally as senior authors.

Background: BRCA1 and BRCA2 (BRCA1/2)-deficient tumors display impaired homologous recombination repair (HRR) and enhanced sensitivity to DNA damaging agents or to poly(ADP-ribose) polymerase (PARP) inhibitors (PARPi). Their efficacy in germline BRCA1/2-mutated metastatic breast cancers has been recently confirmed in clinical trials. Numerous mechanisms of PARPi resistance have been described, whose clinical relevance in gBRCA-mutated breast cancer is unknown. This highlights the need to identify functional biomarkers to better predict PARPi sensitivity.

Patients and methods: We investigated the in vivo mechanisms of PARPi resistance in gBRCA1 patient-derived tumor xenografts (PDXs) exhibiting differential response to PARPi. Analysis included exome sequencing and immunostaining of DNA damage response proteins to functionally evaluate HRR. Findings were validated in a retrospective sample set from gBRCA1/2-cancer patients treated with PARPi.

Results: RAD51 nuclear foci, a surrogate marker of HRR functionality, were the only common feature in PDX and patient samples with primary or acquired PARPi resistance. Consistently, low RAD51 was associated with objective response to PARPi. Evaluation of the RAD51 biomarker in untreated tumors was feasible due to endogenous DNA damage. In PARPi-resistant gBRCA1 PDXs, genetic analysis found no in-frame secondary mutations, but BRCA1 hypomorphic proteins in 60% of the models. TP53BP1-loss in 20% and RAD51-amplification in one sample, none mutually exclusive. Conversely, one of three PARPi-resistant
gBRCA2 tumors displayed BRCA2 restoration by exome sequencing. In PDXs, PARPi resistance could be reverted upon combination of a PARPi with an ataxia-telangiectasia mutated (ATM) inhibitor.

**Conclusion:** Detection of RAD51 foci in gBRCA tumors correlates with PARPi resistance regardless of the underlying mechanism restoring HRR function. This is a promising biomarker to be used in the clinic to better select patients for PARPi therapy. Our study also supports the clinical development of PARPi combinations such as those with ATM inhibitors.

**Key words:** germline BRCA, PARP inhibitor resistance, homologous recombination, RAD51, TP53BP1, ATM

### Methods

#### Study design

A collection of patient-derived tumor xenograft (PDX) models was generated by implanting tumor samples from patients with a germline BRCA1/2 mutation and breast or ovarian cancer. Their sensitivity to PARPi was evaluated, and the functionality of the HRR pathway was analyzed and compared between the PARPi-sensitive versus the PARPi-resistant PDX samples to find a functional test correlating with response. An exploratory analysis in a set of 20 tumor samples including patients treated with PARPi at our institution was employed to confirm the findings and the potential clinical interest of the functional test. A new therapeutic PARPi combination was tested *in vivo* in PARPi-resistant PDX models.

See further methods in supplementary material, available at *Annals of Oncology* online.

#### Results

**gBRCA PDX panel**

Fresh tumor samples prospectively collected for implantation into nude mice yielded a total of 12 PDX models (11 gBRCA1 and 1 gBRCA2) ([supplementary Table S1](https://academic.oup.com/annonc/article-abstract/29/5/1203/4955904), available at *Annals of Oncology* online). Five models were derived from patients with metastatic disease who had been treated with PARPi, three of which prior to olaparib treatment and two at progression after a sustained partial response (PR) ([supplementary Table S1](https://academic.oup.com/annonc/article-abstract/29/5/1203/4955904), available at *Annals of Oncology* online). Persistence of the gBRCA mutations was confirmed in all models but PDX274, and they were associated with loss of heterozygosity, i.e. loss of the wild type allele ([supplementary Figure S1](https://academic.oup.com/annonc/article-abstract/29/5/1203/4955904), available at *Annals of Oncology* online).

Olaparib treatment in the gBRCA PDX collection distinguished a subset of PARPi-resistant tumors (Figure 1A) (assessed by modified Response Evaluation In Solid Tumors (mRECIST)), see [supplementary methods](https://academic.oup.com/annonc/article-abstract/29/5/1203/4955904), available at *Annals of Oncology* online.

**HRR function** [26]. In order to improve patient selection for PARPi monotherapy among gBRCA mutation carriers, especially in the metastatic setting, there is a clear need for a functional biomarker of HRR status to be used in the clinic. Previous work by others showed that induction of nuclear foci of the HRR protein RAD51 after neoadjuvant chemotherapy is a measure of HRR functionality in BC biopsies and predicts treatment response [27]. Here, we sought to investigate RAD51 foci as an indicator of functional HRR and its correlation with PARPi resistance in the gBRCA setting. We further explored potential treatment strategies for PARPi-resistant BC.

---

*Original article* Annals of Oncology

---

**Introduction**

BRCA1 and BRCA2 encode essential proteins for DNA homologous recombination repair (HRR) [1]. Loss of function of either gene impairs this high-fidelity DNA repair pathway and results in genetic instability and an increased risk of breast or ovarian cancer in germline BRCA1/2 (gBRCA) mutation carriers [2, 3]. Defective HRR increases sensitivity of gBRCA-mutated tumors to DNA damaging agents including anthracyclines, platinum salts, or to novel agents that block parallel DNA repair pathways, including poly(ADP-ribose) polymerase inhibitors (PARPi) [4–6]. PARP inhibition blocks the repair of DNA single-strand breaks and results in stalling of replication fork progression by trapping PARP on the DNA break [7]. Both contribute to the accumulation of DNA double-strand breaks (DSBs) that HRR-deficient cells cannot repair efficiently.

PARPi are well-tolerated agents and elicit anticancer efficacy in metastatic gBRCA tumors. Their use has been approved for advanced ovarian cancer [olaparib (Lynparza®), rucaparib (Rubraca®) and niraparib (Zejula®)] and for gBRCA breast cancer (BC) [8–10]. Final results from other phase III clinical trials are awaited, both in the early and advanced BC setting (NCT01905592, NCT01945775, NCT02032823).

Primary resistance to PARPi in a subset of gBRCA patients limits the potential of gBRCA status as the only biomarker of response to that of an enrichment strategy [11]. In addition, acquired resistance in monotherapy responders is a challenge. Previous studies using in vitro models, transgenic mice and human tumor samples have delineated two types of resistance mechanisms to PARPi in gBRCA cells: (i) independent of HRR (cellular extrusion of the PARPi, PARP1 loss, FANCD2 overexpression, SLFN11 inactivation or CHD4 loss) and (ii) dependent on HRR recovery, either by BRCA-independent mechanisms (loss of 53BP1, REV7/MAD2L2, PAXIP1/PTIP, Artemis) or by BRCA-dependent mechanisms [12–22]. The latter include secondary BRCA1/2 mutations that restore the reading frame and the expression of partially functional hypomorphic BRCA1 proteins (BRCA1-11q alternative splice isoform, the RING-less BRCA1 generated by downstream translation initiation, or HSP90-mediated stabilization of BRCA1 C-terminal mutants). Most work in gBRCA clinical samples has focused on ovarian cancer and has established that HRR recovery through secondary BRCA1/2 mutations may act as a resistance mechanism to platinum salts and PARPi. Conversely, little is known about *in vivo* PARPi resistance mechanisms in gBRCA BC [22].

Patterns of DNA aberrations in the tumors (genomic scars) resulting from HRR deficiency may aid in distinguishing HRR-deficient from HRR-proficient tumors [23–25]. However, genomic scars in gBRCA tumors may persist after restoration of
**Figure 1.** Homologous recombination repair markers and PARPi response. (A) Antitumor activity of olaparib in gBRCA patient-derived tumor xenografts (PDXs). Best response to olaparib is plotted as the percentage of tumor volume change after at least 21 days of treatment. +20%, −30% and −95% are marked by dashed lines to indicate the range of CR (complete response), PR (partial response), SD (stable disease) and PD (progressive disease). Mut, mutation; B1, mutation in \( BRCA1 \); B2, mutation in \( BRCA2 \); Metastatic, PDX derived from a metastatic lesion (otherwise, derived from a primary tumor); TNBC, triple negative BC; ER+ , estrogen receptor positive BC; OvCa, ovarian cancer. (B) Immunofluorescence staining of \( BRCA1 \), 53BP1 and RAD51 across the PARPi-sensitive and PARPi-resistant gBRCA PDX models. Detection of
BRCA1/2 sequencing, BRCA1 expression and nuclear foci formation in gBRCA PDX samples

No frameshift-correction or genetic reversion of the inherited mutation—the so-called secondary BRCA1 mutations—occurred in the gBRCA1 PARPi-resistant PDXs. BRCA1 mRNA expression was variable across models and absent in PDX280, a model with a mutation—the so-called secondary BRCA mutations—occurred (supplementary Figure S2, available at Annals of Oncology online), totaling 13 gBRCA1/2 models. Among the four PDX derived from gBRCA primary tumors, 50% showed CR. The sensitivity to PARPi-treatment in the PDXs from metastatic patients previously treated with olaparib mirrored the patients’ clinical response to olaparib (supplementary Table S1 and Figure S3, available at Annals of Oncology online).

Analysis of 53BP1 loss and exome sequencing in gBRCA PDX samples

The assessment of 53BP1 nuclear foci by IF in olaparib-treated PDX samples identified 53BP1 loss in two PARPi-resistant models: PDX230OR and STG316 (Figure 1B). Exome sequencing unveiled somatic mutations in TP53BP1 in both models (supplementary Table S1, available at Annals of Oncology online). The PD model PDX280 harbors a non-previously reported missense mutation in the PARPi resistance gene SLEN11 p.H661D. The SD model PDX124 displays a focal RAD51 amplification and high protein expression (supplementary Figure S8A and B, available at Annals of Oncology online). Mutations in other known PARPi resistance genes (PARPI, REV7/MAD2L2, PAXIP1/PTIP, Artemis, CHD4) were not identified.

Nuclear foci formation of the HRR protein RAD51

The observed recruitment of hypomorphic BRCA1 isoforms to DNA damage sites and/or 53BP1 loss in PARPi-resistant PDXs may help restore their ability to accomplish HRR. As a functional surrogate of HRR, we sought to detect RAD51 nuclear foci in geminin-positive cells and nuclear co-localization with BRCA1. RAD51 nuclear foci were detected in 11 PDXs in olaparib-treated samples, including all models expressing hypomorphic BRCA1 isoforms and/or lacking 53BP1 (Figure 1B). RAD51 foci co-localized with BRCA1 foci in all PDX models expressing hypomorphic BRCA1 isoforms (supplementary Figure S9, available at Annals of Oncology online). The three PARPi-resistant models that lacked hypomorphic BRCA1 isoform expression or 53BP1 loss (PDX127, PDX252 and PDX280) exhibited RAD51 foci suggesting that recovery of HRR occurs via BRCA1-independent mechanisms in these models (Figure 1B). Olaparib-treated samples from PARPi-resistant PDXs showed higher percentage of RAD51-positive cells versus those from PARPi-sensitive models (36 ± 2% in PARPi-resistant versus 5 ± 3% in PARPi-sensitive, P = 0.0017) (Figure 1C). Analysis of γH2AX foci ruled out PARPi pharmacodynamic differences as the reason for this differential response.
Figure S12, available at Annals of Oncology online. The unexpected evidence of endogenous DNA damage and repair markers in untreated samples (supplementary Figure S5 and S10, available at Annals of Oncology online) prompted us to also score RAD51 foci in untreated tumors (Figure 1C). Importantly, untreated samples of PARPi-resistant tumors showed a significantly higher baseline percentage of RAD51-positive cells compared with PARPi-sensitive tumors (24 ± 2% versus 3 ± 2%, P = 0.0025). Thus, HRR functionality was frequent and associated with PARPi resistance in this gBRCA PDX panel.

RAD51/geminin score and response to PARPi in patients’ samples

We confirmed the feasibility of detecting RAD51 and γH2AX foci in FFPE tumor samples from patients, by firstly staining for RAD51 and geminin in 20 patients’ tumor samples including some matched with the gBRCA PDX models (n = 7) (supplementary Figure S11A–C, available at Annals of Oncology online). These results prompted us to further assess the potential clinical utility of the RAD51/geminin score as a functional biomarker of PARPi treatment in patients treated with PARPi at our institution (n = 10 tumors), including two paired pre-/post-PARPi samples. This cohort included eight patients with germline mutations in BRCA1/2 (BRCA1, n = 5; BRCA2, n = 3; diagnosis of BC, n = 6; ovarian cancer, n = 2). The samples had been collected prior to (n = 7) or at progression to treatment with a PARPi (n = 3). We stained and scored for RAD51 (Figure 1D and E). Importantly, PARPi-resistant tumor samples showed an inverse relationship between the RAD51 score and clinical efficacy of the PARPi. Exome sequencing identified a BRCA2-secondary mutation in one tumor with acquired resistance and RAD51 foci (supplementary Figure S12, available at Annals of Oncology online).

Platinum salts in olaparib-resistant tumors

HRR recovery/retention that limits PARPi efficacy may not imply resistance to platinum-based treatments in gBRCA cancers. A previous study in gBRCA ovarian cancer showed a 40% response rate to platinum chemotherapy in the setting of resistance to olaparib [28]. We next assessed the efficacy of cisplatin in the two HRR proficient, RAD51-positive ovarian cancer PDX models (PDX196 and PDX280) (Figure 2A). Response to cisplatin was confirmed in both PDX models and in the clinic for Pt280 (data not available for Pt196 due to carboplatin hypersensitivity). Next, we assessed the activity of platinum-based chemotherapy in advanced/metastatic BC in the context of PARPi resistance. We previously reported that PDX127 showed resistance to PARPi but response to platinum, in agreement with the clinical response of the patient [29]. Similarly, the PARPi-resistant models, RAD51-positive model PDX252 exhibited significant tumor regression when treated with cisplatin (Figure 2A). In the PARPi-resistant PDX236 and PDX274, cisplatin-only slowed tumor growth as compared with vehicle, while its combination with olaparib achieved PR and SD, respectively (Figure 2B). These results highlight that platinum-based therapies can be active in PARPi-resistant metastatic BC and suggests that RAD51 foci formation does not predict resistance to platinum in this setting.

Ataxia-telangiectasia mutated blockade plus PARP inhibition in olaparib-resistant tumors

We further explored the potential of DDR inhibitors to enhance PARPi antitumor activity. The ataxia-telangiectasia mutated (ATM) kinase is activated in response to DNA DSBs, signals to cell cycle checkpoints and DNA repair pathways, and is reciprocally synthetic lethal with PARP [30]. As previously suggested, we hypothesized that ATM inhibition is a treatment option for PARPi-resistant BRCA1-deficient tumors that restore HRR through loss of TP53BP1 or REV7/MAD2L2 by enabling ATM-dependent end resection [17, 18]. We tested this hypothesis in three ATM-expressing PDXs (supplementary Figure S13A, available at Annals of Oncology online): STG316, a model that lacks TP53BP1, and in PDX127 and PDX280, which are devoid of hypomorphic BRCA1 isoforms, and presumably achieve PARPi resistance by a ‘loss of 53BP1’-like mechanism. In fact, PDX127 harbors a missense mutation in PRCC p.P55T, within the interaction domain with REV7/MAD2L2 (supplementary Figure S13B, available at Annals of Oncology online). The best antitumor activity of the olaparib combination with the ATM inhibitor AZD0156 was achieved in PDX127 (SD) (Figure 2C). We investigated whether ATM inhibition resulted in restoration of HRR deficiency by impairing RAD51 foci formation [17, 18] (supplementary Figure S13C, available at Annals of Oncology online). Unexpectedly, RAD51 foci formation was marginally reduced in combination-treated tumors, arguing that ATM inhibition may exert a broader effect in signaling the olaparib-induced DDR beyond its effects on HRR (supplementary Figure S13C, available at Annals of Oncology online). Quantification of DNA damage by γH2AX staining (pan-nuclear, Figure 2D and foci formation, supplementary Figure S13D, available at Annals of Oncology online) showed a significant increase of pan-γH2AX-positive cells upon ATM plus PARPi as compared with olaparib monotherapy in combination-responders PDX127 and STG316. These results suggest an induction of replication stress in these combination-sensitive models. These results are of interest since an international phase I clinical trial testing the tolerability of olaparib in combination with AZD0156 in solid tumors is currently ongoing (NCT 02588105).

Discussion

There is a need to refine the determinants of PARPi efficacy beyond gBRCA mutations, especially in the metastatic setting. Our analysis of RAD51 foci in a total of 20 BC patient samples, 10 gBRCA1 and 10 gBRCA2, provides new evidence in favor of restoration of HRR functionality as a frequent mechanism of PARPi resistance, and demonstrates the potential of functional biomarkers to discriminate tumors that will fail PARPi monotherapy. The RAD51 foci assay may capture the dynamic changes in DNA repair that occur throughout tumor evolution and may, therefore, more effectively identify the HRR-deficient BRCA1/2-mutated tumors. Unexpectedly, while previous studies reported low levels of baseline DNA damage as a potential limitation to evaluate HRR [27, 31], we were able to detect it and score for RAD51 in untreated samples, which correlated with PARPi response. This highlights that an IF assay for RAD51 staining is feasible in FFPE samples and suggests that testing for RAD51 may...
be directly transferrable to the clinical setting when a larger study confirms our findings.

Restoration of HRR can be achieved by secondary BRCA mutations and may be captured by sequencing techniques [32, 33]. We identified a BRCA2 secondary mutation in one BC patient with acquired resistance to olaparib, whereas we did not detect in-frame secondary mutations in any gBRCA1 PDX model. Our data suggest that hypomorphic BRCA1 isoforms contribute to HRR restoration in gBRCA1 BC [20, 21]. Importantly, high RAD51 score predicted poor response to PARPi monotherapy independently of the underlying mechanism of HRR restoration. Further research is needed to establish the RAD51 score cut-off that differentiates responders from nonresponders to PARPi monotherapy and to evaluate the potential impact of RAD51-independent resistance mechanisms that involve replication fork stabilization [14, 16, 34, 35]. A high RAD51 foci score may encourage the use of combination therapies with PARPi, such as those that inhibit HRR [29, 36], or that enhance DNA damage [9, 37, 38]. Here, we propose that a subset of PARPi-resistant gBRCA tumors benefit from combined PARP plus ATM blockade [17, 30, 39].

Figure 2. Cisplatin or ATM inhibition overcomes PARPi resistance. (A) Relative tumor volume (RTV) of vehicle, cisplatin or olaparib in PDX196, PDX280 and PDX252. Cisplatin was administrated 6 mg/kg weekly unless RTV < 0.5. Olaparib was administrated daily at 50 mg/kg (5 doses/week). Number of tumors per arm is indicated. (B) RTV of vehicle, cisplatin, olaparib or its thereof combination in PDX236 and PDX274. Cisplatin and olaparib were administrated as in panel A. (C) RTV of vehicle, olaparib, AZD0156 or the combination of treatments in PDX127, STG316 and PDX280. Olaparib was administrated daily at 50 mg/kg (5 doses/week) and AZD0156 was administrated three times per week at 2 or 2.5 mg/kg. (D) Quantification of pan-nuclear γH2AX-positive cells in PDX127, STG316 and PDX280 treated with vehicle, olaparib, AZD0156 or the combination of drugs at the end point of experiments shown in panel C. All figures show mean and SEM. Statistical P-values are shown when relevant: *P < 0.05; **P < 0.01; ***P < 0.001; ****P < 0.0001 (two-way ANOVA).
Our study unveils coexistence of various mechanisms of PARPi resistance in each individual tumor, such as hypomorphic BRCA1 isoforms together with RAD51 amplification or 53BP1 [40] loss. In conclusion, this emphasizes the need of comprehensive functional tests for measuring HRR activity such as the RAD51 assay to better select patients who will benefit most from PARPi monotherapy and those who may benefit from a combination therapy.

Acknowledgements

The authors thank Dr Geoffrey Shapiro, Dr Peter Bouwman, Dr Neil Johnson, the Molecular Pathology Group at VHI and the Breast Cancer and Melanoma Group at VHI for helpful discussions. The Breast Surgical Unit from Vall d’Hebron Hospital, as well as Cristina Bernadó, Pilar Antón, Maite Calvo, Patricia Cozar and Ambar Ahmed have provided technical support. The authors acknowledge the Cellnex Foundation for providing research facilities and equipment.

Funding

Spanish Instituto de Salud Carlos III (ISCIII) funding, an initiative of the Spanish Ministry of Economy and Innovation partially supported by European Regional Development FEDER Funds (FIS PI17/01080 to VS, PI12-02606 to JBal, PI15-00355 to OD, PI13/01711 to SG-E); European Research Area-NET, Trancan-2 (AC15/00063), Asociación Española contra el Cáncer (AECC) (LABAE16020PORTT) and the Agencia de Gestión d’Ajuts Universitaris i de Recerca (AGAUR) (2014 SGR 1331 and 2017 SGR 540) to VS; Conquer Cancer Foundation of ASCO Young Investigator Award to CC; NIH Grant P30CA008748, the Breast Cancer Research Foundation and the Geoffrey Beene Cancer Research Center to JB. Any opinions, findings and conclusions expressed in this material are those of the author(s) and do not necessarily reflect those of the American Society of Clinical Oncology or the Conquer Cancer Foundation. We acknowledge ‘Tumor Biomarkers Collaboration’ supported by the Banco Bilbao Vizcaya Argentaria (BBVA) Foundation, GHD, the FERO Foundation and the Orozco Foundation for supporting this study (to VS and JB). CC is recipient of a Sociedad Española de Oncología Médica (SEOM)—BUCKLER0’ grant and an AECC grant (AIOC15152806CRUZ). MC-B (LABAE16020PORTT) and SB are recipient of AECC grants. AL-G is recipient of a grant from the Generalitat de Catalunya, Health Department (PERIS, SLT002/16/00477). MC-B (LABAE16020PORTT) and SB are recipient of AECC grants. AL-G is recipient of a grant from the Generalitat de Catalunya, Health Department (PERIS, SLT002/16/00477). VS and SGE are supported by the Miguel Servet Program (ISCIII, CP14/00228 and CP10/00617, respectively). The xenograft program in the Caldas laboratory is supported by Cancer Research UK, and also received funding from an EU H2020 Network of Excellence (EuroCAN).

Disclosure

VS declares a noncommercial research agreement with AstraZeneca. JBal is an advisory board member for Clovis, Tesaro and Medivation, and has received speaker bureau honoraria from AstraZeneca. BD, ZL, UP, EC, GJ, WH, CB and MJO are employees of AstraZeneca. All remaining authors have declared no conflicts of interest.

References