Title:

Secondary *BRCA1* mutations in *BRCA1*-mutated ovarian carcinomas with platinum resistance.

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Abstract

Although ovarian carcinomas with mutated *BRCA1* or *BRCA2* are sensitive to platinum compounds, such carcinomas eventually develop platinum resistance. Previously, we showed that acquired resistance to cisplatin in *BRCA2*-mutated tumors can be mediated by secondary intragenic mutations in *BRCA2* that restore the wild-type *BRCA2* reading frame. Here, we show that secondary mutations of *BRCA1* also occur in *BRCA1*-mutated ovarian cancer with platinum resistance. We evaluated 9 recurrent *BRCA1*-mutated ovarian cancers previously treated with platinum compounds, including five with acquired platinum resistance, one with primary platinum resistance, and three with platinum sensitivity. Four of the 6 recurrent platinum-resistant tumors had developed secondary genetic changes in *BRCA1* that restored the reading frame of the BRCA1 protein, while none of 3 platinum-sensitive recurrent tumors developed *BRCA1* sequence alterations. We immunohistochemically confirmed restored expression of BRCA1 protein in 2 cases with secondary mutations. Intriguingly, the case with primary platinum resistance showed back mutation of *BRCA1* in the primary tumor, and showed another secondary mutation in the recurrent tumor. Our results suggest that secondary mutations in *BRCA1* can mediate resistance to platinum in *BRCA1*-mutated ovarian tumors.

Introduction

DNA-crosslinking agents such as cisplatin, carboplatin, melphalan and cyclophosphamide are widely used anti-cancer drugs. Resistance to these agents is a major obstacle to effective cancer therapy. Patients with ovarian cancer usually respond well to initial chemotherapy with cisplatin and its derivative carboplatin, but over time the majority of patients become refractory to platinum-compounds. Ultimately, progression of chemoresistant disease is the major cause of death in women with ovarian carcinoma (1).

BRCA1 and *BRCA2* are tumor suppressor genes responsible for familial breast/ovarian cancer. *BRCA1* or *BRCA2* (*BRCA1/2*) mutation carriers have increased risks of developing breast and ovarian cancer (2). Ten to 15% of all epithelial ovarian cancers are associated with inherited mutations in *BRCA1/2* (3, 4). The vast majority of tumors from women with germline *BRCA1/2* mutations demonstrate loss of the wild-type *BRCA1/2* allele, and are considered to be BRCA1/2 deficient (5-7).

BRCA1/2-deficient cancer cells are hypersensitive to DNA-crosslinking agents including cisplatin (8-10). Consistently, patients developing *BRCA1/2*-mutated ovarian cancer have a better prognosis compared with non-carriers, if they receive platinum-based therapy (8, 11). However, even *BRCA1/2*-mutated ovarian cancers frequently develop platinum resistance.

Recently, we reported that acquired resistance to cisplatin in *BRCA2*-mutated tumors can be mediated by secondary mutations in *BRCA2* that restore the wild-type *BRCA2* reading frame (12). *BRCA2*-mutated cancer cells selected in the presence of cisplatin acquired secondary genetic changes on the mutated *BRCA2* allele, which

canceled the frameshift caused by the inherited mutation and restored expression of functional nearly-full length BRCA2 protein. Cells with secondary mutations were resistant to cisplatin (12). However, mechanisms of cisplatin-resistance in *BRCA1*-mutated ovarian cancer remain unclear. Because both BRCA1 and BRCA2 are involved in homologous recombination DNA repair (13, 14) and are required for cellular resistance to cisplatin (9, 10), we hypothesized that similar secondary mutations of the mutated *BRCA1* gene mediate acquired resistance to cisplatin in *BRCA1*-mutated ovarian cancer. Now we report that secondary mutations of *BRCA1* also occur in *BRCA1*-mutated ovarian cancer with platinum resistance.

Materials and Methods

Clinical specimens. Three DNA samples from recurrent *BRCA1*-mutated ovarian cancer patients were obtained from Cedars-Sinai Medical Center (Los Angeles, CA) through the Pacific Ovarian Cancer Research Consortium. Six DNA samples from *BRCA1*-mutated ovarian cancer patients with recurrent disease were obtained from the tissue bank of University of Washington (Seattle, WA) (Table 1). DNA from UW80, UW40, UWF27, and the recurrent tumor from UW91 were obtained after laser capture microdissection. The study was approved by Institutional Review Boards of Fred Hutchinson Cancer Research Center and University of Washington. Clinical data of UW40 patient and a cancer cell line derived from the same patient's recurrent tumor (UWB1.289) have been reported previously (15). Platinum sensitivity was defined as a complete response to treatment maintained without progression for at least six months after platinum therapy. Tumors that were resistant or refractory had progressive disease on platinum therapy, less than a complete response to platinum therapy or progression within 6 months of completing platinum therapy.

Sequencing of *BRCA1*. PCR products of genomic DNA were analyzed for sequence alterations with BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems; Foster City, CA) using ABI 3100 Genetic Analyzer (Applied Biosystems). All detected mutations were confirmed by sequencing of an independently amplified template. Information of all sequencing and PCR primers for *BRCA1* is available in Supplemental Table 1. All nucleotide numbers refer to the wild-type cDNA human sequence of *BRCA1* (U14680.1) as reported in the GenBank database.

Immunohistochemical studies. BRCA1 protein was detected in formalin fixed paraffin sections using the mouse monoclonal antibody MS110 (previously called Ab-1, Oncogene Research Products) as previously described (16). The MS110 antibody recognizes an amino terminal epitope at BRCA1 (amino acid residues 89-222) (16). Briefly, paraffin sections were deparaffinized, washed in PBS and treated with steam heat for 20 minutes using antigen target retrieval solution (DAKO). Endogenous peroxidase activity in paraffin sections was quenched by treatment with 3% H_2O_2 for 5 minutes. Sections were washed with PBS and non-specific binding was blocked by treatment for two hours in 2% bovine serum albumin in PBS. Primary antibody was applied (MS110 at 1:250 dilution) for 14-16 hours at 4°C. Secondary antibody and streptavidin biotin-peroxidase were from the Universal Large Volume LSAB+, Peroxidase kit (DAKO) and were each applied for 30 minutes at room temperature. DAB (3,3'diaminobenzidine)-nickel chromagen (Sigma) was used to visualize antibody complexes and sections were counterstained with hematoxylin. The MS110 antibody can result in non-staining of tissues under certain conditions and can be variable in its results. Therefore, we used non-tumor inflammatory and stromal cells as an internal positive control for BRCA1 protein staining for every section. Decreased protein was only scored if normal cells on the same section were positive. Primary and recurrent tumors were stained side by side under identical conditions. MS110 is the most reliable antibody for the immunohistochemical detection of BRCA1 (16). Because the MS110 antibody recognizes an amino terminal epitope in BRCA1, it cannot distinguish between wild-type BRCA1 protein and truncated non-functional protein resulting from frameshift mutations occurring distal to the antibody's epitope. Thus, MS110 is not suitable for distinguishing functional versus non-

functional BRCA1 protein in UW40, UW208, and UW317. Therefore, we evaluated immunohistochemistry in only those tumors with 185delAG mutations (proximal to the antibody's epitope) for which we had paired primary and recurrent paraffin embedded tumor samples.

Results and Discussion

We analyzed 9 clinical samples of recurrent *BRCA1*-mutated ovarian cancer previously treated with platinum (Table 1). Six of them were clinically platinum-resistant and 3 were platinum-sensitive. One case (UW40) showed primary resistance to platinum, while 5 cases were initially sensitive to platinum and acquired resistance during the disease course. Three of the 5 tumors with acquired platinum resistance (UW80, UW91 and UWF27) and the primarily resistant tumor (UW40) had secondary genetic changes in *BRCA1*, while none of the three cisplatin-sensitive recurrent tumors showed secondary genetic changes in *BRCA1*.

UW80 patient is a heterozygous carrier of a frameshift *BRCA1* mutation, 185delAG, which is common in the Ashkenazi Jewish population (17) (Fig. 1A). In the primary tumor specimen, only *BRCA1* sequence with 185delAG was detected, indicating that the tumor had lost the wild-type allele. Loss of heterozygosity (LOH) of an intragenic *BRCA1* single nucleotide polymorphism (SNP) was also confirmed. In the microdissected recurrent tumor from the same patient after development of resistance to platinum, LOH of the *BRCA1* SNP was confirmed, indicating that the recurrent tumor contained only the same single allele of *BRCA1* as present in the primary tumor and that contamination of non-tumor cells was negligible. In this recurrent sample, wild-type *BRCA1* sequence represented >80% of the sequences at the mutation site, suggesting that the recurrent tumor had acquired wild-type *BRCA1* by genetic reversion (back mutation to wild-type).

Similarly, in 2 more *BRCA1.185delAG* cases (UW91 and UWF27), the primary tumor demonstrated only mutant sequence with loss of the wild-type allele. In the

recurrent tumors, we mainly detected wild-type *BRCA1* sequence, suggesting that these two platinum-resistant tumors acquired wild-type *BRCA1* by genetic reversion (back mutation to wild-type) (Fig. 1B). Both cases had confirmation of LOH at intragenic SNPs in the primary and recurrent tumors (Supplemental Fig. 1), indicating the presence of a single *BRCA1* allele that underwent a secondary genetic alteration.

BRCA1.185delAG encodes a severely truncated protein with 38 amino acids, and the back mutation should restore full length BRCA1 protein (Fig. 2A). Consistently, immunohistochemical study revealed that BRCA1 protein expression was absent in the primary tumors of UW80 and UW91, but strongly positive in their recurrent tumors (Fig. 2B and data not shown).

The mechanism for genetic reversion of 185delAG mutations in all three tumors is not clear. At the genomic level, the re-insertion of two missing nucleotides would seem less likely to occur than a secondary downstream deletion that corrects the frameshift and restores the open reading frame. Several possible explanations for this phenomenon are not mutually exclusive. First, we speculate that because 185delAG is in a critical portion of the BRCA1 gene close to the RING finger (Fig. 2A), a change of one single amino acid here is likely to have deleterious effect on protein function. Similarly, missense mutations in the RING finger such as C61G can be deleterious (18). Therefore restoration of BRCA1 function may require complete reversion of a mutant in this domain to wild-type. Another possibility is that the particular genomic sequence surrounding 185delAG somehow facilitates the genetic reversion. A third possibility is that other downstream mutations do occur in some tumors but are not detected with our relatively short PCR amplifications. We are unable to do long range PCR that might identify larger genomic

events because of the fragmented nature of our DNA. Thus, it is easier to identify genetic reversion in our samples than larger events that restore the open reading frame.

UW40 patient is a heterozygous carrier of a frameshift *BRCA1* mutation, 2594delC (Figs. 3A and 3B). The mutant allele encodes an 844 amino acid protein that lacks BRCT domains (Fig. 3C). The patient had a past history of breast cancer at the age of 42 and developed ovarian cancer at age 54. The primary ovarian carcinoma was clinically resistant to platinum. After 6 cycles of platinum and taxol, the patient was treated with taxol for 3 additional cycles with development of progression. She was re-treated with topotecan, then gemcitabine and adriamycin to obtain a partial remission. Recurrent tumor was then obtained at the time of surgery for a fistula.

LOH of three intragenic *BRCA1* SNPs (2201C/T, 2430T/C, and 2731C/T) that flank the mutation site was confirmed in both the primary and recurrent tumor (Figs. 3A and 3B, and data not shown), indicating that contamination by non-tumor cells was negligible and that both the primary and recurrent tumors had lost one *BRCA1* allele. Intriguingly, in the primary tumor, both wild-type *BRCA1* sequence and *BRCA1* sequence with 2594delC were detected (Figs. 3A and 3B). Careful laser microdissection of a separate second sample of this tumor revealed the same result. The presence of both wild-type *BRCA1* sequence and mutant sequence on one allele in the primary tumor suggests that genetic reversion (back mutation to wild-type) occurred on one copy of the mutant allele. We speculate that the presence of the genetically-reverted wild-type allele in the primary tumor contributed to the unusual initial platinum resistance of this tumor. The selective pressure for the genetically reverted tumor cells in the primary ovarian tumor is unknown, but may be related to the 11 months of cyclophoshamide, methotrexate and

fluorouracil that the patient previously received for breast cancer. Cyclophosphamide is a DNA cross-linking agent and could exert similar selection pressure for the correction of DNA repair defects as we have observed with exposure to platinum agents.

An alternative explanation for the existence of genetic reversion and other secondary mutations on a mutant allele in this primary tumor is that these events are more common than we appreciate but usually occur in only a small number of primary tumor cells before exposure to chemotherapy. Then, chemotherapy provides the selection pressure for expansion of these sub-clones in recurrent tumors. Perhaps some reports of retention of the wild-type *BRCA1/2* allele in breast cancers (19) actually represent genetic reversion. Only careful haplotyping distinguishes tumors with retention of the wild-type allele from those with genetic reversion.

The genetically-reverted wild-type allele was then lost at some point during the disease course. In the recurrent tumor, we could no longer detect wild-type sequence, but we found a second site small deletion (2606_2628del23) in addition to the inherited mutation (2594delC). The second mutation corrects the frameshift caused by the inherited mutation and the allele *BRCA1.2594delC;2606_2628del23* encodes a BRCA1 protein with intact C-terminal region, which may be functional (Fig. 3C). The actual genomic DNA sequence of *BRCA1* in the UW40 recurrent tumor is a mixture of 2594delC;2606_2628del23 and 2594delC without a secondary mutation (Fig. 3A). The mixture of sequences on one allele in both the primary and recurrent tumor may have occurred by secondary genetic alterations (reversion to wild-type in the primary tumor and 23 bp deletion in the recurrent tumor) occurring on just one of the duplicated mutant alleles (Fig. 3B), similar to the situation occurring in Capan-1 clones with secondary

mutations of *BRCA2* observed in the *in vitro* experiment in the previous report (12). Alternatively, the two sequences could represent tumor heterogeneity, with only a subset of tumor cells acquiring a secondary mutation on the mutant allele. We favor the explanation of tumor heterogeneity in this case, given that a cell line developed from this recurrent tumor contains only mutant sequence without secondary genetic changes (15).

Taken together, secondary mutations that restore the reading frame of mutated *BRCA1* alleles were frequently observed in ovarian tumors with resistance to platinum. These results suggest that secondary mutations of *BRCA1* can be a mechanism of acquired resistance to cisplatin in *BRCA1*-mutated ovarian cancer. In addition, the observation of the back mutation of *BRCA1* in cisplatin-resistant primary tumor of UW40 patient suggests that secondary mutations of *BRCA1* can be a mechanism of primary resistance to cisplatin.

Our studies in this paper and in the previous paper (12) emphasize that *BRCA1* and *BRCA2* are not only cancer susceptibility genes, but are also critical determinants of clinical sensitivity and resistance to chemotherapy. These studies support the general concept that defective DNA repair leads to chemosensitivity, while restoration of functional DNA repair contributes to acquired chemoresistance in tumor cells *in vitro* and *in vivo*.

Testing for secondary mutations in platinum-treated *BRCA1*-mutated cancers may be clinically important, because tumors with secondary mutations are likely to be resistant to platinum and could demonstrate cross-resistance to other agents that exploit BRCA1 defects such as poly(ADP-ribose) polymerase 1 inhibitors. A larger clinical

study is warranted to further determine the prevalence and clinical significance of secondary mutations of *BRCA1* in *BRCA1*-mutated cancer.

Our finding could have implications for sporadic ovarian carcinoma. Although somatic mutation of *BRCA1/2* is rare in sporadic ovarian carcinoma, BRCA1 is reported to be down-regulated in a subset of sporadic ovarian carcinomas by promoter methylation and other unknown mechanisms (20). *BRCA2* mRNA expression is reported to be undetectable by reverse transcription PCR in 13% of ovarian carcinoma (20). Therefore, it is tempting to hypothesize that down-regulation of BRCA1/2 causes initial sensitivity to cisplatin, and restoration of functional BRCA1/2 expression by demethylation of the *BRCA1* promoter or other mechanisms leads to acquired resistance. Testing this hypothesis will be important to elucidate the more general roles of BRCA1/2 in platinum-sensitivity and resistance.

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Table 1. Secondary genetic changes of *BRCA1* in *BRCA1*-mutated ovarian cancer treated with platinum.

Patient	Inherited mutation	Specimen	Clinical platinum sensitivity	Secondary genetic change
		Paired specimens		
CS1	185delAG	pre-platinum	sensitive	
		post-platinum	sensitive	No
CS4	185delAG	pre-platinum	sensitive	
		post-platinum	sensitive	No
UW91	185delAG	pre-platinum	sensitive	
		post-platinum	resistant	Yes (back mutation)
CS14	185delAG	pre-platinum	sensitive	
		post-platinum	resistant	No
UW40	2594delC	pre-platinum	resistant	Yes (back mutation)
		post-platinum	resistant	Yes (2606_2628del23)
UW80	185delAG	pre-platinum	sensitive	
		post-platinum	resistant	Yes (back mutation)
UWF27	185delAG	pre-platinum	sensitive	
		post-platinum	resistant	Yes (back mutation)
		Non-paired post-treatment specimens		
UW208	3867G>T (E1250X)	post-platinum	sensitive	No
UW317	3171insTGAGA	post-platinum	resistant	No

Figure legends

Figure 1. Genetic reversion of *BRCA1* mutation in 3 recurrent *BRCA1*-mutated ovarian cancer cases.

A, DNA sequences of *BRCA1* in peripheral blood lymphocytes and the primary and recurrent tumors from a patient (UW80) with *BRCA1*-mutated ovarian cancer. In the lymphocytes, a heterozygous single nucleotide polymorphism (SNP) of the *BRCA1* locus (4956A/G) was detected, in addition to a heterozygous mutation (185delAG). In the primary tumor, a hemizygous mutation (185delAG) was detected and loss of heterozygosity (LOH) of the SNP was confirmed. In the microdissected recurrent tumor, LOH of the SNP was confirmed, but wild-type sequence was 80-90% of the sequences identified at the site of 185delAG. Importantly, the SNP in the recurrent tumor (4956G) is identical to that in the primary tumor (4956G). This indicates that the recurrent tumor had acquired wild-type *BRCA1* by genetic reversion (back mutation to wild-type). Residual wild-type sequence could represent heterogeneity in the tumor. A speculative model of *BRCA1* alleles in samples from this patient is also depicted.

B, DNA sequences of *BRCA1* in peripheral blood lymphocytes, the primary and recurrent tumors from 2 patients (UW91 and UWF27) with *BRCA1*-mutated ovarian cancer. In the lymphocytes, a heterozygous mutation (185delAG) was detected. In the primary tumors, a hemizygous mutation (185delAG) was detected. In the microdissected recurrent tumor specimens, wild-type sequence was detected, suggesting that the recurrent tumors had acquired wild-type *BRCA1* by back mutation. Analyses of intragenic SNPs of these cases are shown in Supplemental Figure 1.

Figure 2. BRCA1 protein expression is restored in recurrent ovarian tumors with genetic reversion of *BRCA1* mutation.

A, Schematic presentation of BRCA1 proteins encoded by 185delAG and wild-type *BRCA1*. Functional domains of BRCA1 protein (RING finger, nuclear localization signals (NLS) and BRCT domains) are depicted. The region that the BRCA1 antibody (MS110) for immunohistochemical staining recognizes (aa 89-222) (16) is also depicted. *B*, Immunohistochemical staining of BRCA1 in a primary tumor with *BRCA1.185delAG* mutation and a recurrent tumor with genetic reversion of the BRCA1 mutation (UW91 patient). The primary tumors are negative for BRCA1 immunostaining, while the recurrent tumors are positive for nuclear BRCA1 immunostaining. Scale bar = 10μm.

Figure 3. Genetic reversion of *BRCA1* mutation in a primary ovarian tumor with platinum resistance and another secondary *BRCA1* mutation in a recurrent tumor of the same patient.

A, DNA sequences of *BRCA1* in peripheral blood lymphocytes and the primary and recurrent tumors from a patient (UW40) with *BRCA1*-mutated ovarian cancer. In the lymphocytes, heterozygous SNPs of the *BRCA1* locus (2201C/T, 2430T/C) were detected, in addition to a heterozygous mutation (2549delC). In the primary tumor, LOH of the SNPs was confirmed, but the primary tumor specimen shows heterozygous sequence of wild-type *BRCA1* and a *BRCA1* mutation (2594delC). In the recurrent tumor specimen, LOH of the SNPs was confirmed and mixed sequences of 2594delC and 2594delC;2606_2628del23 were detected.

B, A speculative model of *BRCA1* alleles in samples from this patient. The lymphocytes have both the wild-type and mutant (2549delC) alleles. The primary tumor has lost the wild-type *BRCA1* allele with SNPs 2201T and 2430C, but has retained the allele with the inherited mutation (2549delC) and SNPs 2201C and 2430T. This mutant allele has been presumably duplicated, and the one of the mutated allele is reverted to wild-type by genetic reversion (back mutation to wild-type). In the recurrent tumor, the allele with wild-type *BRCA1* sequence is lost, and the allele with the inherited mutation (2549delC) was again duplicated. One of them obtained a different second mutation (2606_2628del23), which cancels the frameshift caused by the inherited mutation (2549delC). This model explains why we see mixed sequences of *BRCA1* in the primary and recurrent tumors.

C, Schematic presentation of BRCA1 proteins encoded by 2594delC and 2594delC;2606_2628del23.

Table 1. Secondary genetic changes of *BRCA1* in *BRCA1*-mutated ovarian cancer treated with platinum.

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UW91	185delAG	pre-platinum	sensitive	
		post-platinum	resistant	Yes (back mutation)
CS14	185delAG	pre-platinum	sensitive	
		post-platinum	resistant	No
UW40	2594delC	pre-platinum	resistant	Yes (back mutation)
		post-platinum	resistant	Yes (2606_2628del23)
UW80	185delAG	pre-platinum	sensitive	
		post-platinum	resistant	Yes (back mutation)
UWF27	185delAG	pre-platinum	sensitive	
		post-platinum	resistant	Yes (back mutation)
		Non-paired post-treatment specimens		
UW208	3867G>T (E1250X)	post-platinum	sensitive	No
UW317	3171insTGAGA	post-platinum	resistant	No

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A

UW80

SNP (rs1799966)

mutation (185delAG)

BRCA1

lymphocyte

4956

A T C T G C C C A G A G T C C A G C T G C
G

185

A A A A T C T T A G A G T G T C C C A T C : wild-type
A G T G T C C C A T C T G : 185delAG

wild-type O

X 185delAG

SNP 4956A A

G SNP 4956G

heterozygous

platinum-sensitive primary tumor

4956

A T C T G C C C A G G G T C C A G C T G C

185

A A A A T C T T A G T G T C C C A T C : 185delAG

X 185delAG

G SNP 4956G

LOH

platinum-resistant recurrent tumor

4956

A T C T G C C C A G G G T C C A G C T G C

185

A A A A T C T T A G A G T G T C C C A T C : revertant
a g t g t c c c a t c t g : 185delAG

O revertant

G SNP 4956G

LOH

B

UW91

lymphocyte

185

A A A A T C T T A G A G T G T C C C A T C : wild-type
A G T G T C C C A T C T G : 185delAG

platinum-sensitive primary tumor

185

A A A A T C T T A G T G T C C C A T C T G : 185delAG

platinum-resistant recurrent tumor

185

A A A A T C T T A G A G T G T C C C A T C : revertant
a g t g t c c c a t c t g : 185delAG

UWF27

lymphocyte

185

A A A A T C T T A G A G T G T C C C A T C : wild-type
A G T G T C C C A T C T G : 185delAG

platinum-sensitive primary tumor

185

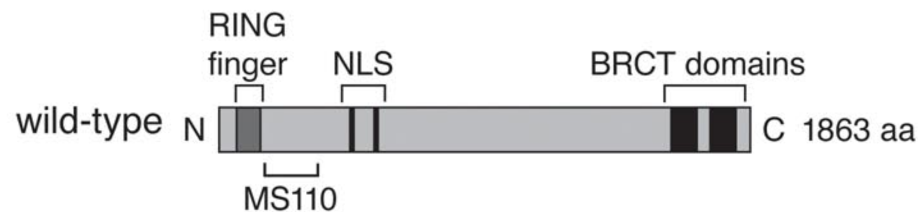
A A A A T C T T A G T G T C C C A T C T G : 185delAG

platinum-resistant recurrent tumor

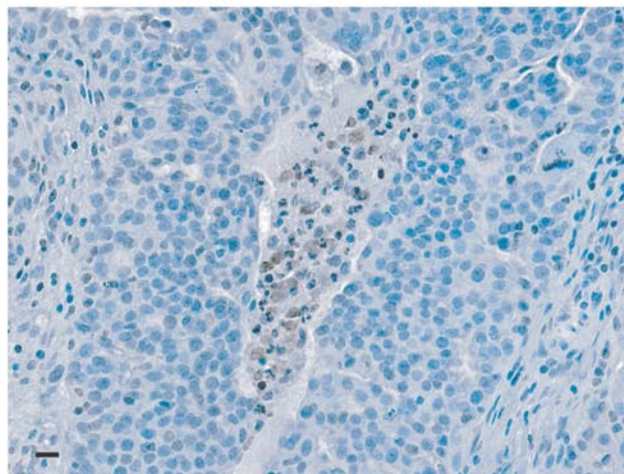
185

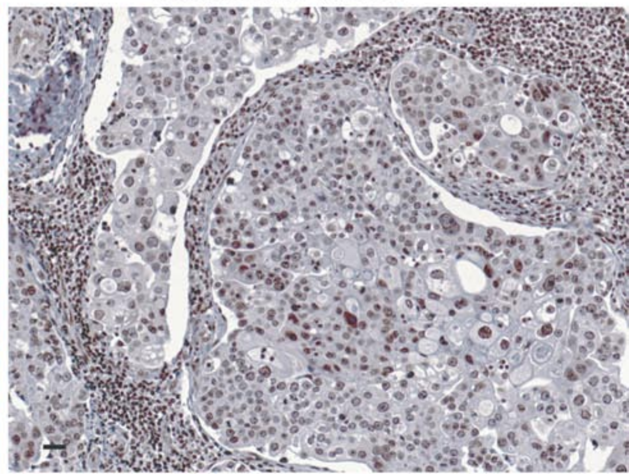
A A A A T C T T A G A G T G T C C C A T C : revertant

A



B





anti-BRCA1

A

UW40

SNP (rs1799949) SNP (rs16940)

lymphocyte

2201 2430 2593 2606

TGACAG T/C GATACT ATTTCA C/T TGGTAC AGAAATGA C ACAGAAGGCTTTAAGTATCCATTGGGACATGAAGTTAAC : wild-type
ACAGAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACC : 2594delC

1bp deletion C

primary ovarian tumor

2201 2430 2593 2606

TGACAGCGATACT ATTTCATTGGTAC AGAAATGACACAGAAGGCTTTAAGTATCCATTGGGACATGAAGTTAAC : revertant
ACAGAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACC : 2594delC

1bp insertion C 1bp deletion C

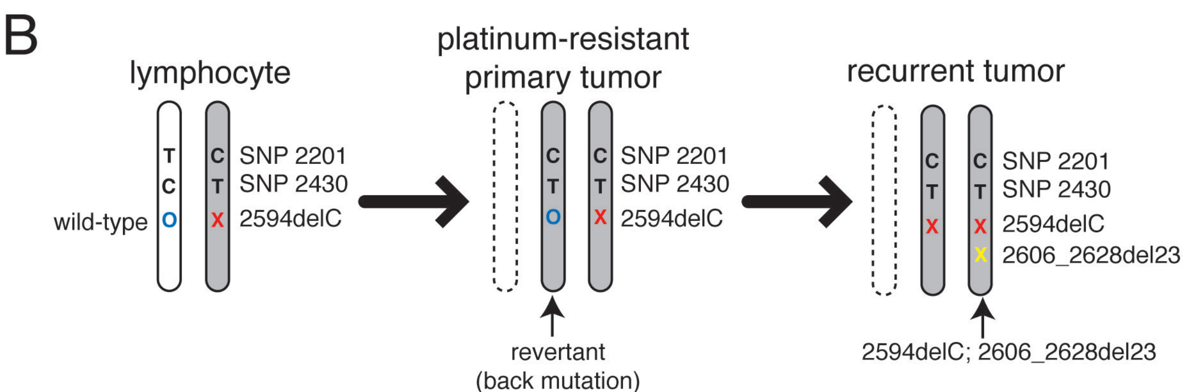
recurrent ovarian tumor

2201 2430 2593 2606

TGACAGCGATACT ATTTCATTGGTAC AGAAATGAACAGAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACC : 2594delC
TTAACCACAGTCGGGAAACAAGCATAGAA : 2594delC; 2606_2628del23

1bp deletion C 23bp deletion

B



C