# Exploring the role of homologous recombination deficiency and BRCA1/2 mutations in endometrial cancer

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# Chapter 4

## Germline *BRCA*-associated endometrial carcinoma is a distinct clinicopathologic entity

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## Abstract

**Purpose**

Whether endometrial carcinoma (EC) should be considered part of the *gBRCA1/2*-associated hereditary breast and ovarian cancer (HBOC)-syndrome is topic of debate. We sought to assess whether ECs occurring in *gBRCA carriers are enriched for clinicopathologic and molecular characteristics, thereby supporting a causal relationship.*

**Experimental Design**

Thirty-eight *gBRCA* carriers that developed EC were selected from the nationwide cohort study on hereditary breast and ovarian cancer in the Netherlands (HEBON), and these were supplemented with four institutional cases. Tumor tissue was retrieved via PALGA (Dutch Pathology Registry). Nineteen morphologic features were scored and histotype was determined by three expert gynecologic pathologists, blinded for molecular analyses (UCM-OncoPlus Assay including 1213 genes). ECs with LOH of the *gBRCA*-wild-type allele (*gBRCA*/LOHpos) were defined "*gBRCA*-associated", those without LOH (*gBRCA*/LOHneg) were defined "sporadic".

**Results**

LOH could be assessed for 40 ECs (30 *gBRCA1,* 10 *gBRCA2*), of which 60% were *gBRCA/*LOHpos. *gBRCA/*LOHpos ECs were more frequently of nonendometrioid (58%, $P$=0.001) and grade 3 histology (79%, $P$<0.001). All but two were in the *TP53-mutated TCGA*-subgroup (91.7%, $P$<0.001). In contrast, *gBRCA/*LOHneg ECs were mainly grade 1 endometrioid EC (94%) and showed a more heterogeneous distribution of TCGA-molecular subgroups: *POLE-mutated* (6.3%), MSI-high (25%), NSMP (62.5%) and *TP53-mutated* (6.3%).

**Conclusions**

We provide novel evidence in favor of EC being part of the *gBRCA*-associated HBOC-syndrome. *gBRCA*-associated ECs are enriched for EC subtypes associated with unfavorable clinical outcome. These findings have profound therapeutic consequences as these patients may benefit from treatment strategies such as PARP-inhibitors. In addition, it should influence counseling and surveillance of *gBRCA* carriers.

## Translational relevance

We provide novel evidence in favor of endometrial carcinoma (EC) being part of the *gBRCA*-associated HBOC-syndrome. By stratifying ECs that occurred in *gBRCA*-mutation carriers by LOH of the *gBRCA* wild-type allele, we were able to identify ECs associated with the *gBRCA*-mutation (*gBRCA/*LOHpos) and those that occurred sporadically (*gBRCA/*LOHneg). *gBRCA*-associated ECs are distinctly different from sporadic ECs by histology (high grade) and by molecular subtype (*TP53* mutant), both of which are associated with worst clinical outcome. These findings support the concept that EC is part of HBOC-syndrome, which impacts genetic counseling and surveillance programs of *gBRCA* carriers. In addition, our work shows that LOH-status should be considered when assessing PARP-inhibitor sensitivity.



## Introduction

Inheritance of a pathogenic mutation in one allele of the breast cancer susceptibility genes, *BRCA1* or *BRCA2*, results in the hereditary breast and ovarian cancer (HBOC) syndrome, characterized by severely increased lifetime risk to develop breast cancer and tubo-ovarian cancer (OC).[1, 2] Other cancer types reported to be increased in patients with germline *BRCA2* mutations (*gBRCA*) are pancreatic and prostate cancer.[3, 4] Whether endometrial carcinoma (EC) should be considered part of *gBRCA*-associated HBOC-syndrome is still under debate due to conflicting data.[5-9] A number of studies have shown an increased risk to develop EC especially for *gBRCA1* carriers, with highest risks observed for an aggressive subtype of EC; the serous-like ECs.[5-7, 9-11] However, others did not observe this increased risk, or attributed it to previous tamoxifen treatment rather than to the *gBRCA* mutation.[8, 9, 11]

LOH of the wild-type *BRCA1* or *BRCA2* allele (g*BRCA*/LOHpos) is an important step in the carcinogenesis of *gBRCA*-associated tumors. This is supported by the observation that *gBRCA/*LOHpos breast cancers and OCs show significantly higher homologous recombination deficiency (HRD)-scores compared to their *gBRCA/*LOHneg counterparts.[12] The HRD-score is based on the presence and quantification of "genomic scars" associated with *BRCA*-deficiency, including the number of regions with LOH,[13] large-scale state transitions (LST),[14] and telomeric allelic imbalances (TAI).[15] Breast cancers and OCs arising in *gBRCA* carriers show variable LOH frequencies, with reported rates of 93% (*gBRCA1*) and 84% (*gBRCA2*) for OCs, and 90% (*gBRCA1*) and 54% (*gBRCA2*) for breast cancers.[12] This signifies the relevance of LOH as a marker of causality and implies that *gBRCA/*LOHneg cancers are in fact sporadic tumors that develop independently of the *gBRCA* mutation and are not HRD.

The finding of recurrent clinicopathologic and molecular features in *gBRCA*-associated breast cancers and OCs has supported the concept that these cancers are distinct entities belonging

to the *gBRCA*-associated HBOC-syndrome. These features can also help identify tumors more likely to harbor *BRCA1/2* mutations. For example, breast cancers arising in *gBRCA1* carriers prototypically are of high-grade and of the basal-like subtype with more frequent necrosis and lymphocytic infiltration.[16, 17] *BRCA1*-associated high-grade serous tubo-ovarian carcinoma (HGSOC) shows more frequent (partial) Solid, pseudoEndometrioid and/or Transitional morphology (SET-morphology), which is distinctly different from the prototypical papillary and infiltrative growth generally encountered in sporadic HGSOC. Other features more frequently observed in *BRCA1*-associated HGSOC are necrosis, a higher mitotic index and an increased number of tumor infiltrating lymphocytes.[18-20] On a molecular level, *gBRCA*-associated breast cancers and OCs share similar somatic copy-number profiles [somatic copy-number alteration (SCNA)-high] and frequent *TP53* mutations.[16-18, 20-22]

The Cancer Genome Atlas (TCGA) Research Network previously defined four distinct molecular subclasses with prognostic relevance in ECs.[22] The "serous-like/SCNA-high" molecular subclass has poorest clinical outcome and interestingly displays molecular similarities to both basal-like breast cancer and HGSOC, including a high number of SCNAs and frequent *TP53* mutations. Moreover, recent studies demonstrated that serous-like/SCNA-high ECs also frequently are HRD.[22-24] This raises the question whether ECs occurring in *gBRCA1/2* carriers might be enriched for certain features, but studies comprehensively evaluating this have not been performed to date.

We aimed to, for the first time, comprehensively describe the clinicopathologic and molecular features, stratified by LOH-status, of a large series of ECs that occurred in *gBRCA* carriers.

## Materials and methods

### Patient selection

Patients with a history of EC and a pathogenic *gBRCA1/2* mutation were identified from the "*He*reditary *B*reast and *O*varian cancer study, the *N*etherlands (HEBON-cohort study)".[25] The HEBON study is an ongoing nationwide study on families with HBOC for which all patients who undergo genetic testing for *BRCA1/2* and *CHEK2* mutations in one of the participating centers are eligible for inclusion [all eight university medical hospitals in the Netherlands and the Netherlands Cancer Institute (NKI)]. For participants, data on, among others, personal cancer history and therapeutic treatments are collected both retrospectively and prospectively through regular linkages with the Netherlands Cancer Registry (NCR). Data on prophylactic surgery are collected via the Dutch Pathology Registry (PALGA)[26]. All data is centrally collected and managed by trained data managers only. Women were eligible for inclusion when they had (i) a proven pathogenic germline *BRCA1/2* (*gBRCA1/2)* mutation (PLON class 4 or 5)[27], (ii) provided written informed consent for the HEBON-study, and (iii) had a history of epithelial EC

or developed an EC during follow-up, defined as a tumor with an International Classification of Diseases Oncology, Third Edition, First Revision (ICD-O-3.*1;* http://codes.iarc.fr/) topographical code of either C54 (Corpus Uteri) or C55 (Uterus, NOS).

In total, 3,726 *gBRCA* carriers provided informed consent between 1999 and 2014, of which the majority was provided in 2012 and 2013 (62.5%). Of these women, 41 (1.1%) developed an EC. We were able to retrieve 39 of 41 tumors from pathology laboratories across the Netherlands. One tumor was a sarcoma and was therefore excluded. Of these 38 HEBON-ECs, 21 ECs occurred preceding to study enrollment (mean 4.7 years, SD: 2.79) and 16 ECs occurred after study enrollment (mean 4.5 years, SD 3.52). For one case, the date of study enrollment was not available. The HEBON-ECs were supplemented with four ECs from known *gBRCA1/2* carriers previously diagnosed in the Leiden University Medical Center (LUMC).



For all ECs, haematoxylin and eosin (H&E)-stained slides, anonymized pathology reports, and at least one representative formalin-fixed, paraffin embedded (FFPE)-tumor block were collected through PALGA[26] from pathology laboratories across the Netherlands. If applicable, material from the (salpingo-)oophorectomy or OC specimen was also requested. The HEBON study is approved by the medical ethical committees of all participating centers, and all participants gave written informed consent to participate in the study. The HEBON study is performed in accordance with the Declaration of Helsinki. Our study was performed after the study protocol was approved by the HEBON steering committee (date; November 30, 2017) and by the Institutional Review Board of the Netherlands Cancer Institute; IRBd18086. All specimens were handled in compliance with the Code of Conduct for dealing responsibly with human tissue in the context of health research (2011) drawn up by the Federation of Dutch Medical Scientific Societies.

## Clinicopathologic characterization

All cases were independently reviewed by three expert gynecologic pathologist (V.T.H.B.M. Smit, T. Bosse, and B.E. Howitt). They were aware that the ECs occurred in *gBRCA* carriers, however they were blinded for LOH status. The World Health Organization (2014) criteria were used for histologic subtype diagnosis. Reviewers were not allowed to use immunostains to aid classification and diagnoses were solely based on H&E stains. Cases were classified ambiguous when overlapping features of both high-grade endometrioid and serous carcinomas were present in the tumor and when tumors failed to show prototypic features of a certain subtype. Discordant cases were discussed during a consensus meeting to assign final histological subtype. ECs with ambiguous morphology were considered non-endometrioid for statistical analyses. After final histologic subtype was assigned, histologic subgroups were made. For ambiguous cases, *TP53* mutation status was used to assign histologic subgroup. Cases were categorized as follows: “Endometrioid” for Endometrioid, mucinous and *TP53*-wildtype ambiguous carcinomas, “serous-like” for uterine serous carcinomas (USCs), uterine

carcinosarcomas (UCSs) and *TP53*-mutant ambiguous carcinomas, or "clear cell" for clear cell carcinomas. Review of adnexa, depth of myometrial invasion, cervical involvement, lymph node status and presence of lymphovascular space invasion was performed by one expert gynaecologic pathologist (T. Bosse) on which FIGO-2009 stage was based upon. When slides were not available, these data were retrieved from the original pathology reports.

Nineteen morphological characteristics were assessed by one expert gynecologic pathologist (B.E. Howitt) on all available tumor slides, blinded for LOH status. For additional details on this, see Supplementary Materials and Methods.

## IHC

Cases were stained for p53 (clone DO-7, 1:2,000, DAKO), Wilms tumor 1 (WT1, clone 6F-H1, 1:3,200, Invitrogen), estrogen receptor (ER, Clone EP1, 1:200, DAKO), progesterone receptor (PR, Clone Pgr636, 1:400, DAKO), and CD8 (Clone 4B11, 1:2,000, Novocastra). Procedures and scoring methods are described in the Supplementary Materials and Methods.

## Molecular analysis

### *DNA isolation*

Tumor DNA was isolated from FFPE-tissue blocks either by using three 0.6 mm tumor cores (*n*=16) or by using microdissected tissue from 5 to 10 tissue sections (10 µm; *n*=26). DNA isolation was performed fully automated using the Tissue Preparation System (Siemens Healthcare Diagnostics) as described previously.[28] The median tumor cell percentage of the isolated areas was 80% (range: 25%-90%).

### *Next-generation sequencing*

Following extraction, DNA was quantified using the Qubit fluorometric assay (Thermo Fisher Scientific) and further assessed for quantity and quality using a quantitative PCR assay (hgDNA Quantitation and QC kit, KAPA Biosystems). Library preparation and sequencing were performed as previously described for the UCM-OncoPlus Assay.[29] Briefly, approximately 100 ng DNA was fragmented using the Covaris S2 (Covaris). The fragmented DNA was amplified using the KAPA HTP Library Preparation Kit (Kapa Biosystems) along with a set of patient-specific indexes (Roche). The pooled library was captured using a custom SeqCap EZ capture panel (Roche) featuring a collection xGen LockdownProbes (IDT) for 1,213 genes. The pooled captured library was sequenced on the Illumina HiSeq 2500 system (Illumina) in rapid run mode (2 x 101 bp paired end sequencing). Somatic mutation and copy number calling was performed across all 1,213 genes using a custom in-house bioinformatics pipeline previously described.[29] The five-tier pathogenicity classification described by Plon and colleagues, 2008 was used to categorize variants.[27] Only class 4 (likely pathogenic) and 5 (pathogenic) mutations are reported in the manuscript.

***LOH of gBRCA1/2 mutations***

Known *gBRCA1/2* mutations were assessed for LOH of the wild-type allele by evaluating the following parameters: estimated tumor cell purity, *BRCA1/2* mutation variant allele frequency (VAF), local copy number status, and adjacent SNP-VAF, using a similar approach to what has been described by Khiabanian and colleagues, 2018.[30] For LOH analyses, we applied the following model, taking into account the chromosomal copy number at the *BRCA* locus; VAF=[(1-p)+cmut x p] / [2 x (1-p) + Y x p], with p being the tumor purity, cMut being the mutation's chromosomal copy number and Y being the ploidy of the tumor cells. LOH events occur when cMut = 1 and Y = 1 or cMut > 1 and Y > 1. Because all *BRCA1/2* mutations were germline mutations, the expected VAF in the absence of LOH was 1/2 (50%) for all cases. LOH of the *gBRCA1/2* wild-type allele was considered to be present if (i) cMut = 1 and Y = 1 or cMut > 1 and Y > 1 (ii) the observed *gBRCA1/2* mutation VAF was similar to the expected VAF according to the formula, (iii) adjacent observed SNP VAF (if present) supported the findings and (iv) sequencing quality was sufficient. Mutations that were considered to have an LOH event were classified as either copy-neutral (no evidence of local copy number change) or copy number loss. *gBRCA/*LOHpos ECs were defined as *gBRCA*-associated, *gBRCA/*LOHneg ECs as "sporadic".

***Copy-number calling***

For the copy-number calling we used a clinically validated bioinformatic tool that has previously been detailed and published.[29] Briefly, copy-number analysis involved evaluation of average exon interval depths recorded via the Genome Analysis Tool Kit DepthofCoverage module. A historical normalized baseline for each interval in the panel was generated using 24 nonmalignant clinical samples. Test sample data were subjected to a normalization algorithm to control for individual gene profile run-specific variability. To detect the potential copy-number regions, fold change and Z-scores were calculated for each interval, and thresholds were set at >200% (gain) or <66% (loss) with Z-score >3 or <-2, respectively. Genes with more than half the intervals showing copy-number changes in the same direction were then identified. Overall copy-number status was assessed manually by assessing the copy-number plots across the entire territory and determining how many large-scale (arm or subarm-level changes) copy-number alterations were present in each case. Cases considered to be "low" copy-number had 0 large-scale copy-number alterations, "borderline" had 1-2 large-scale copy number alterations, and those considered "high" had >2 large-scale copy-number changes.

***Microsatellite instability status***

For MSI testing, a metric similar to that proposed by Kautto and colleagues, 2017[31] was employed to quantify the stability of a homopolymer locus. For each locus, distribution over different homopolymer lengths (normalized to a fraction of total depth at the locus) was generated. Then, absolute value of the stepwise difference between that sample distribution and normal distribution was calculated as a distance score (*d*). The baseline distribution

was generated using average values across 23 non-malignant spleen samples. Thresholds for assignment of "stable" or "instable" status for a locus involved using training sets of MSI-stable and MSI-high samples, tested previously by PCR assay or IHC staining. Samples with unstable loci <9% were classified as microsatellite stable, 9 to 15% were classified as indeterminate, and >15% were classified as microsatellite instable (MSI).

***Tumor mutational burden***

Tumor mutational burden (TMB) was quantified as mutations/Mb using a 1,132 gene territory from the UCM-OncoPlus assay. Variants that met any of the following criteria were excluded from the calculation: <10% VAF, synonymous, variants present in either 1,000 Genomes or ExAC population databases. In addition, variants were rescued if there were >10 entries in COSMIC database with an ExAC frequency of <0.001.

## Molecular subgroups

The following surrogate markers were used to classify ECs in the four molecular subgroups defined by the TCGA;[22, 32, 33] *POLE* exonuclease domain mutations for the *POLE/*ultramutated group, MSI-high profile for MSI-high/hypermutated group, *TP53* mutations for SCNA-high/serous-like group, and the absence of surrogate markers for no surrogate marker profile (NSMP)/SCNA-low group.[22, 32, 33] When two molecular classifiers were present, subgroups were assigned in line with what has previously been published by the TCGA;[22] *POLE*&MSI-high or *POLE*&*TP53* as *POLE* and MSI-high&*TP53* as MSI-high.

## Statistical analysis

Associations between categorical variables were tested using a two-sided Fisher exact test or Chi-square statistics when more than two variables were compared. Associations between continuous variables were tested using the Mann-Whitney *U* test. Overall survival was calculated using the Kaplan-Meier Method with log-rank test, and was calculated from the date of EC diagnosis to the date of death while patients who were alive were censored at the date of last follow-up. For HEBON cases, the date of last linkage with the Dutch Municipal Personal Record Database was used as last date of follow-up (April 11, 2019 for all except for case 2; December 23, 2016). *P* values <0.05 were considered significant. Statistical analysis was performed using IBM SPSS version 23.0 (SPSS, Inc.) and GraphPad Prism (GraphPad Software Inc.).

# Results

In total, 42 ECs that occurred in *gBRCA1/2* carriers were analyzed (32 *gBRCA1,* 10 *gBRCA2*). Clinicopathologic characteristics of the complete cohort are described in Supplementary Table S1. The cohort comprised 26 endometrioid ECs (61.9%), of which 17 (40.5%) were

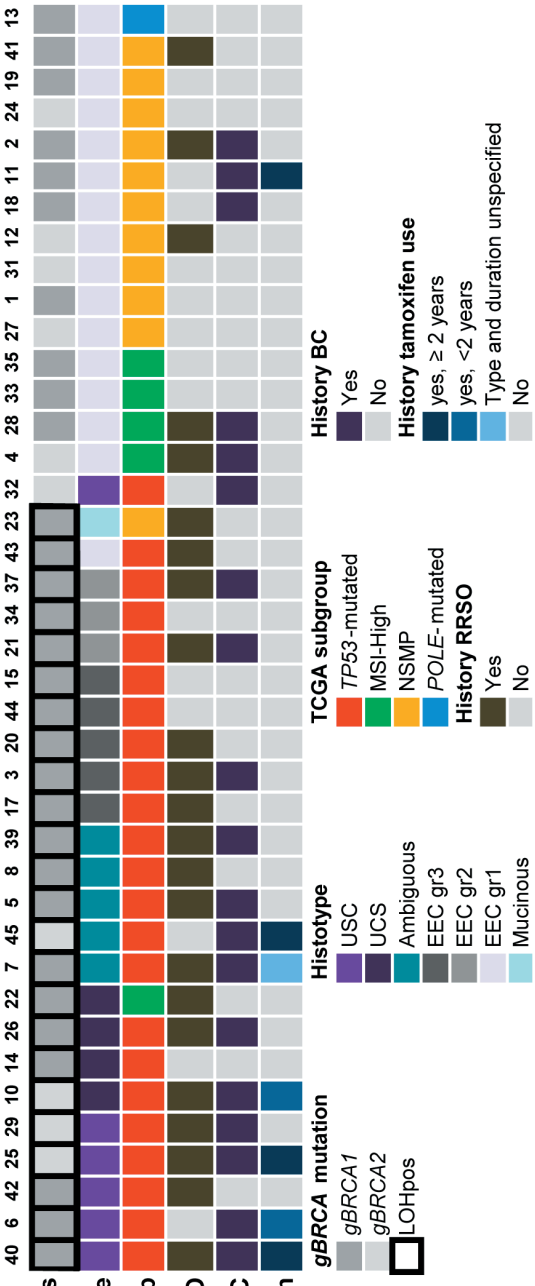


**Figure 1: Clinicopathologic and molecular characteristics stratified by LOH status.** Case 22 and case 4 were MSI-high and had a *TP53* mutation; they were classified in the MSI-high subgroup in accordance to what is described in the Supplementary Material and Methods. Abbreviations: EEC, endometrioid endometrial carcinoma grade; gr, grade; LOH, Loss of heterozygosity of the *gBRCA1/2* wild-type allele; UCS, Uterine Carcinosarcoma; USC, Uterine serous carcinoma.

**Table 1. Clinicopathologic characteristics stratified by LOH status**

| | **LOHpos (n=24)** | **LOHneg (n=16)** | ***P*** |
|---|---|---|---|
| Germline *BRCA1/2* mutation, *n* (%) | | | |
| g*BRCA1* | 20 (83.3) | 10 (62.5) | 0.159 |
| g*BRCA2* | 4 (16.7) | 6 (37.5) | |
| Age at Diagnosis, median (range), years | 60.5 (33-74) | 57 (44-67) | 0.267 |
| FIGO 2009, No. (%) | | | |
| I, II | 19 (79.2) | 14 (87.5) | 0.681 |
| III, IV | 5 (20.8) | 2 (12.5) | |
| Salpingo-oophorectomy, *n* (%)[a] | | | |
| History of RRSO | 18(75)[b] | 5 (31.3) | **0.009**[c] |
| RRSO at time of EC diagnoses | 0 (0) | 2 (12.5) | |
| At time of hysterectomy | 5 (20.8) | 8 (50) | |
| Therapeutic | 0 (0) | 1 (6.3) | |
| History of, *n* (%) | | | |
| OC | 0 (0) | 0 (0) | |
| BC | 13 (54.2) | 6 (37.5) | 0.349 |
| Tamoxifen use | 6[d](25) | 1 (6.3) | 0.21 |
| STIC or adnexal involvement, *n* (%) | 0 (0) | 0 (0) | |
| LVSI present, *n* (%) | 10 (41.7) | 0 (0) | **0.003** |
| *Not assessable* | *1 (2.4)* | *1 (6.3)* | |
| Histologic subtype, *n* (%) | | | |
| Endometrioid | 10 (41.7) | 15 (93.8) | **0.001**[e] |
| *Mucinous* | *1 (4.2)* | *0 (0)* | 1.00 |
| Non-endometrioid | 14 (58.3) | 1 (6.3) | |
| *Serous* | *5 (20.8)* | *1* (6.3) | 0.373 |
| *Carcinosarcoma, serous* | *2 (8.3)* | *0 (0)* | 0.136[g] |
| *Carcinosarcoma, ambiguous* | *2 (8.3)* | *0 (0)* | |
| *Ambiguous* | *5 (20.8)* | *0 (0)* | 0.071 |
| Histologic subgroups, *n* (%) | | | |
| Endometrioid | 10 (41.7) | 15 (93.8) | **0.001** |
| Serous-like | 14 (58.3) | 1 (6.3) | |
| Histologic grade, *n* (%) | | | |
| 1&2 | 5 (20.8) | 15 (93.8) | **<0.001** |
| 3 | 19 (79.2) | 1 (6.3) | |

NOTE: *P* values in boldface are considered significant ($P < 0.05$). Abbreviations: CN, Copy Number; LOH, Loss of heterozygosity of the *gBRCA1/2* wild-type allele; LVSI, Lymphovascular space invasion. [a]For one case (case 15), no history of salpingo-oophorectomy was reported and they were not removed during hysterectomy. [b]For one case, only an ovariectomy (without salpingectomy) was performed, this was not considered as RRSO. [c]*P* value was calculated over history of RRSO or not. [d]Includes one patient for which the specific hormone treatment was unknown. [e]P value was calculated over endometrioid and nonendometrioid ECs. [g]P value was calculated over carsinosarcoma versus other histotype (independent of epithelial component).

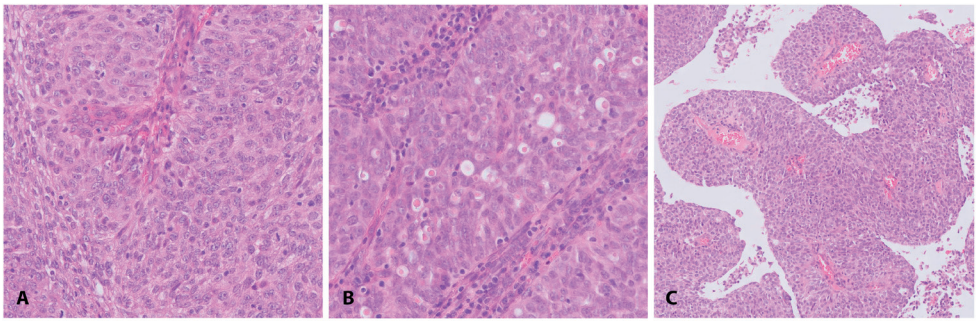




**Figure 2: Growth pattern associated with LOH.** Hematoxylin and Eosin (H&E) slide of a *gBRCA/*LOHpos endometrial carcinoma classified as ambiguous showing Solid (**A**), pseudoEndometrioid (**B**) and Transitional (**C;** SET)-features.

grade 1, three (7.1%) were grade 2, five (11.9%) were grade 3 and one (2.4%) was a mucinous carcinoma. Sixteen ECs were classified as non-endometrioid (38.1%), of which seven (16.7%) were USC, four (9.5%) were UCS and five (11.9%) were classified as high-grade ambiguous.

Molecular analysis was conducted to stratify for LOH of the *gBRCA1/2* wild-type allele, which succeeded for all but two cases (*n*=40, 95.2%), which were excluded from final analyses (one USC and one EEC grade 1, Supplementary Table S2). The known *gBRCA1/2* mutation was confirmed in all 40 cases included in final analyses. Overall, 60% (24/40) of ECs were *gBRCA/*LOHpos. When stratified for *gBRCA1* and *gBRCA2* mutations, 66.7% (*n*=20/30*)* and 40% (*n*=4/10) showed LOH, respectively (*P*=0.159; Fig. 1; Supplementary Table S2). Plotting the position of the *gBRCA* mutations across the coding DNA sequence for *BRCA1* and *BRCA2* did not show enrichment of mutations in a specific region of the gene [www.cbioportal.org/visualize;[34, 35] Supplementary Fig. S1].

## Clinicopathologic, morphologic, and molecular characteristics of g*BRCA* ECs stratified by LOH status

Clinicopathologic characteristics stratified by LOH status are summarized in Table 1 and Fig. 1. Compared with *gBRCA/*LOHneg ECs, *gBRCA/*LOHpos ECs were significantly more often FIGO grade 3 (6.3% vs. 79.2%, *P*<0.001) with non-endometrioid and serous-like histology (both 6.3% vs. 58.3%, *P*=0.001) and more often presented with lymphovascular space invasion (41.7% vs. 0%, *P*=0.003). The 5-year overall survival rate of *gBRCA/*LOHpos ECs was lower (81.3%) compared with *gBRCA/*LOHneg ECs (93.3%, *P*=0.084; Supplementary Fig. S2).

In total, morphologic characteristics were informative for 39 cases (one case was excluded because of neoadjuvant therapy). A higher frequency of “SET features” in *gBRCA/*LOHpos ECs was observed compared with *gBRCA/*LOHneg ECs (52.2% vs. 0%, *P*<0.001; Fig. 2). Other histologic features that were significantly more often observed in *gBRCA/*LOHpos ECs were:

**Table 2. Morphologic characteristics stratified by LOH status**

| | LOHpos (n=23) | LOHneg (n=16) | *P* |
|---|---|---|---|
| Tumor slides assessed/case, median (range) | 7 (1-21) | 4.5 (1-18) | 0.074 |
| Invasion type, *n* (%) | | | |
| Destructive | 17 (73.9) | 4 (25) | **0.004**[a] |
| Pushing/broad front | 2 (8.7) | 3 (18.8) | |
| MELF-type | 0 (0) | 1 (6.3) | |
| Adenomyosis-like | 0 (0) | 3 (18.8) | |
| No invasion | 2 (8.7) | 3 (18.8) | |
| Not analyzable | 2 (8.7) | 2 (12.5) | |
| Desmoplastic stromal reaction, *n* (%)[b] | 16 (69.6) | 5 (31.3) | **0.042** |
| Predominant growth pattern, *n* (%) | | | |
| Glandular | 7 (30.4) | 16 (100) | **0.001** |
| "SET-like" | 8 (34.8) | 0 (0) | |
| Papillary | 4 (17.4) | 0 (0) | |
| Solid | 3 (13) | 0 (0) | |
| Mucinous | 1 (4.3) | 0 (0) | |
| SET-features (any percentage), *n* (%) | | | |
| Solid | 15 (65.2) | 0 (0) | **<0.001** |
| Cribriform/pseudoEndometrioid | 9 (39.1) | 0 (0) | **0.005** |
| Transitional cell carcinoma-like | 5 (21.7) | 0 (0) | 0.066 |
| SET-features present ≥25%, *n* (%) | 12 (52.2) | 0 (0) | **<0.001** |
| Comedo necrosis, *n* (%) | 10 (43.5) | 2 (12.5) | 0.076 |
| Geographic necrosis, *n* (%)[c] | 6 (26.1) | 0 (0) | **0.03** |
| Squamous differentiation, *n* (%) | 4 (17.4) | 6 (37.5) | 0.264 |
| Papillary growth, *n* (%) | 15 (65.2) | 13 (81.3) | 0.471 |

*Continue*

destructive type of invasion, desmoplastic stromal reaction, non-glandular dominant growth pattern, geographic necrosis, trabecular growth pattern, slit-like spaces, high nuclear grade, tumor giant cells and a higher median mitotic index (Table 2; Supplementary Fig. S3). We did not find a significant difference for intraepithelial TILs or peritumoral lymphocytes assessed on H&E, nor for CD8-positive T-cells (Supplementary Fig. S4). *gBRCA/*LOHpos ECs were more often estrogen receptor negative (45.5% vs. 6.8%, *P*=0.012) and progesterone receptor negative (79.2% vs. 12.5%, *P*<0.001) compared with *gBRCA/*LOHneg ECs.

All ECs were classified into one of the four molecular subgroups previously defined by the TCGA (Fig. 1). All but two *gBRCA/*LOHpos ECs were classified in the *TP53*-mutated subgroup, compared with only one of the *gBRCA/*LOHneg ECs (91.7% vs. 6.3%, *P*<0.001*)*. In line with

*Continued*

| | **LOHpos (n=23)** | **LOHneg (n=16)** | ***P*** |
|---|---|---|---|
| Trabecular growth, *n* (%)[d] | 8 (34.8) | 0 (0) | **0.006** |
| Jagged lumina, *n* (%) | 8 (34.8) | 1 (6.3) | 0.056 |
| Slit-like spaces, *n* (%)[c] | 10 (43.5) | 2 (12.5) | **0.04** |
| Hobnailing, *n* (%)[c] | 1 (4.3) | 1 (6.3) | 1 |
| Nuclear atypia, *n* (%) | | | |
| grade 1/2 | 4 (17.4) | 15 (93.8) | **<0.001** |
| grade 3 | 19 (82.6) | 1 (6.3) | |
| Tumor giant cells, *n* (%) | 11 (47.8) | 1 (6.3) | **0.012** |
| Mitotic index/10 HPF, median (range) | 48 (1-197) | 12 (1-28) | **<0.001** |
| Intra-epithelial TILs, *n* (%) | 9 (39.1) | 6 (37.5) | 1 |
| Peritumoral lymphocytes, *n* (%)[c] | 16 (69.6) | 9 (56.3) | 0.323 |
| <10% ER, *n* (%) | 11 (45.8) | 1 (6.3) | **0.012** |
| <10% PR, *n* (%) | 19 (79.2) | 2 (12.5) | **<0.001** |
| WT-1, *n* (%) | | | |
| Negative; ≤1% | 17 (70.8) | 16 (100) | **0.029**[e] |
| Heterogeneous; 2-75% | 3 (12.5) | 0 (0) | |
| Diffuse positive >75% | 4 (16.7) | 0 (0) | |

NOTE: *P* values in boldface are considerd significant ($P < 0.05$)
Abbreviations: HPF, High power field (0,2 $mm^2$); LOH, Loss of heterozygosity of the g*BRCA1/2* wild-type allele; MELF, microcystic, elongated and fragmented; SET, **S**olid, psuedo**E**ndometrioid, **T**ransitional; TILs, Tumor infiltrating lymphocytes.
[a]*P* value was calculated over Destructive type of invasion versus other. [b]Not applicable for nine cases which were left out from statistical analysis [five times absence of invasion, four times invasion not analyzable (curettage)], [c]Not evaluable for one case, which was left out from statistical analysis, [d]Not evaluable for two cases, which were left out from statistical analysis. [e]*P* value was calculated over negative nuclear WT-1 expression or positive nuclear WT-1 expression (encompassing both heterogeneous and diffuse positive staining).

this, *gBRCA/*LOHpos ECs more often had a CN-high profile compared to *gBRCA/*LOHneg ECs (95.5% vs.0%, *P*<0.001; Fig. 3). Compared with *gBRCA/*LOHneg ECs, *gBRCA/*LOHpos ECs had significantly more mutations in *TP53* (95.8% vs. 12.5%, *P*<0.001), and fewer mutations in *PTEN* (16.7% vs. 93.8%, *P*<0.001)*, PIK3CA* (16.7% vs. 56.3%, *P*=0.015)*, PIK3R1* (4.2% vs. 43.8%, *P*=0.004)*, ARID1A* (4.2% vs. 43.8%, *P*=0.004) and *CTNNB1* (0% vs. 37.5%, *P*=0.002; Fig. 3). In total, *gBRCA/*LOHpos ECs harbored significantly fewer class 4 or 5 mutations (other than the *gBRCA* mutation) compared with *gBRCA/*LOHneg ECs, no statistically significant difference was observed for TMB (Supplementary Fig. S5A and S5B).

## *gBRCA/*LOHpos ECs are not misclassified ovarian cancers

To ensure that the ECs did not represent misclassified OCs, salpingo-oophorectomy specimens were rereviewed to detect (pre)malignant lesions. Of the 40 cases included in our final cohort, 39 (97.5%) cases underwent salpingo-oophorectomy either prior to or at the time of hysterectomy. Women who developed *gBRCA/*LOHpos ECs more often previously underwent a risk-reducing salpingo-oophorectomy (RRSO) compared with women with *gBRCA/*LOHneg ECs (75% vs. 31.3%, *P*=0.009), and the time-interval between the RRSO and EC diagnosis was significantly longer; 73.2 months (range: 35.7-187) versus 12.2 months (range, 4.9-82.9, *P*=0.037). Because this is a historical cohort, sectioning and extensively examining the fimbriated end (SEE-FIM) was not routinely performed. In total, 36 of 39 (92%) adnexal specimens were available for rereview, of which the fimbriae could be (partially) examined for 16 of 22 (72.7%) of *gBRCA/*LOHpos ECs and seven of 14 (50%) of *gBRCA/*LOHneg ECs. None of the ECs showed adnexal involvement and none of the RRSO-specimens showed a serous tubal intraepithelial carcinoma (STIC). In two cases, tubal lesions were detected at the time of hysterectomy; one *TP53* signature (case 6, USC) and one serous tubal intraepithelial lesion (STIL, case 35, EEC grade 1). In addition, according the pathology report of case 31 (EEC grade 1, adnexa not available for review), the tubal lining showed focal epithelial “atypia and p53 positivity”, which could indicate the presence of a p53 signature, STIL, or STIC. Case 31 presented with a simultaneous EEC and endometrioid ovarian cancer, which were considered to be synchronous primary tumors and not to be secondary adnexal involvement of the EC.

A minority of cases displayed WT-1 positivity (*n*=7, 17.5%), of which three (7.5%) displayed heterogenous staining; two USCs, one UCS, and four (10%) displayed diffuse staining; one USC, one UCS, and two ambiguous cases (Table 2). Six out of seven women with a WT-1 positive EC had a history of RRSO, none of which showed a (pre)malignant lesion upon rereview. For all but one (case 5), slides available for rereview included sections through the fimbriae. For case 5 (EC diagnosis 2015), the fimbriae could not be examined because of scarring of the fimbriae as a result of a previous bilateral oophorectomy (1995) performed prior to the salpingectomy (2005), as the complete tubes were submitted for histology review. For the one WT-1 positive EC that did not have a history of RRSO (case 6), both adnexa were removed during therapeutic hysterectomy and a p53 signature was detected in one fallopian tube. When excluding all ECs that displayed WT-1 staining, non-endometroid and serous-like histology remained significantly more common in *gBRCA/*LOHpos ECs compared to *gBRCA/*LOHneg ECs (both *n*=7/17, 41.2% vs. *n*=1/16, 6.3%, *P*=0.039).

## *gBRCA*/LOHpos ECs are not exclusively the result of previous tamoxifen treatment

In total, 19 women had a history of breast cancer, which was not significantly different for women with *gBRCA/*LOHpos ECs compared with *gBRCA/*LOHneg ECs (54.2% vs. 37.5%, *P*=0.349). Although women with *gBRCA/*LOHpos ECs more frequently had a history of

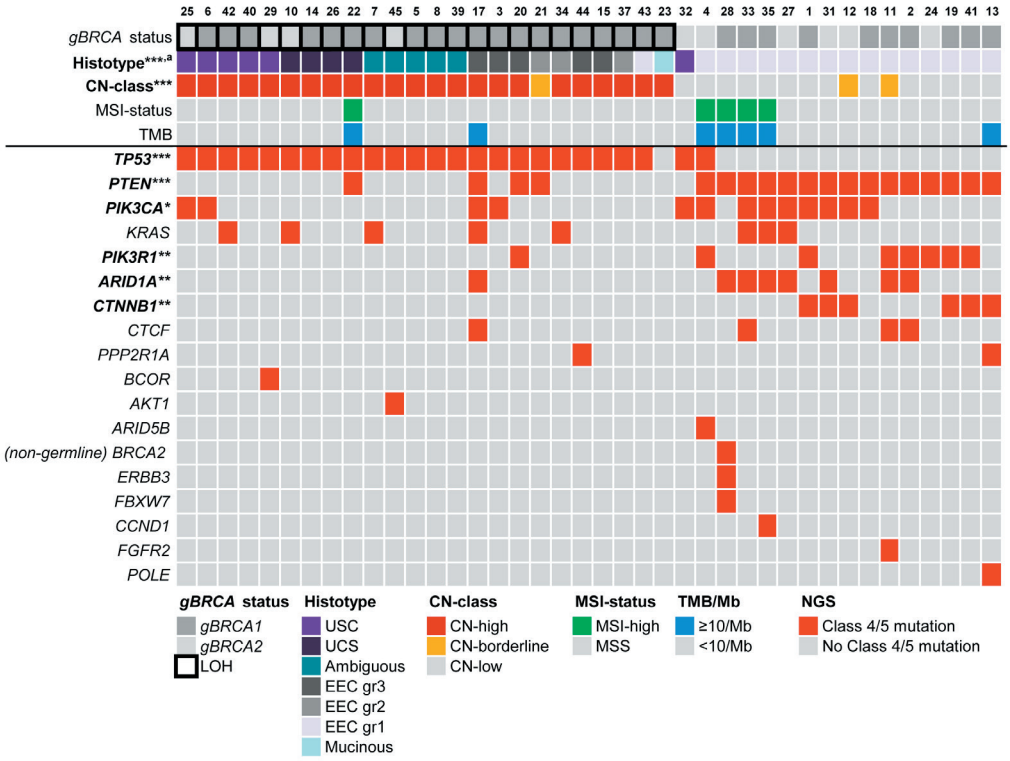


**Figure 3: Molecular characteristics of *gBRCA1/2* ECs grouped by LOH status**. Case 29 contains a *TP53* mutation NM_000546.5:c.375+5G>T that was considered as likely pathogenic given the predicted effect on splicing in combination with abnormal p53 expression ("null-pattern") in IHC. Bolded cases were considered significant; **P*<0.05, ***P*<0.01, ****P*<0.001. [a]*P* value was calculated over endometrioid and nonendometrioid EC. Abbreviations: CN, Copy number; EEC, endometrioid endometrial carcinoma; gr, grade; LOH, Loss of heterozygosity of the g*BRCA1/2* wild-type allele; UCS, Uterine Carcinosarcoma; USC, Uterine serous carcinoma; MSI-high, Microsatellite instability high; MSS, Microsatellite stable; TMB/Mb, Tumor Mutational Burden / Megabase;

tamoxifen use (including one case for which the type of hormone treatment was not specified), this difference was not significant (*n*=6, 25% vs. *n*=1, 6.3%, *P*=0.210; Table 1;Fig. 1). When excluding all tamoxifen treated individuals, non-endometroid and serous-like histology remained significantly more common in *gBRCA/*LOHpos ECs than in *gBRCA/*LOHneg ECs (both *n*=8/18, 44.4% vs. *n*=1/15, 6.7%, *P*=0.021). Across the entire cohort (both *gBRCA/*LOHpos and *gBRCA/*LOHneg), a history of tamoxifen use was significantly associated with serous-like histology (*n*=6/15, 40% vs. *n*=1/25, 4.0%, *P*=0.007). When only including women who received tamoxifen for 2 or more years (excluding the patient for which hormone treatment duration was unknown), this association was not observed anymore (*n*=3/14, 21.4% vs. *n*=1/25, 4%, *P*=0.123).

## Discussion

This is the first study to describe *gBRCA*-associated EC as a distinct entity enriched for high-grade, non-endometrioid tumors with frequent *TP53* mutations and recurring morphologic features. LOH of the wild-type *gBRCA* allele was present in 60% of ECs diagnosed in *gBRCA* carriers**,** and therefore these should be regarded as "*gBRCA*-associated ECs". Importantly, the remaining 40% did not show LOH and therefore are "sporadic ECs" despite the presence of a *gBRCA* mutation. *gBRCA*-associated ECs were histologically high-grade in 79%, which is much more frequent than the 21 to 28% of ECs that would be expected based on population frequencies.[36, 37] We have shown that these tumors are not misclassified OCs, nor exclusively the result of previous tamoxifen treatment. In summary, our findings strongly support that EC is part of the *gBRCA*-associated HBOC syndrome.

There are no strict criteria to which a tumortype should adhere to be considered part of a hereditary cancer syndrome. It is generally accepted, however, that tumors part of a cancer syndrome should occur more frequently and develop at a younger age compared with what would be expected in the general population. A distinct phenotype of tumors in a cancer syndrome is considered to be in support of a causal relationship. Although previous studies show contradictory results about excess risk of EC (all histotypes) for *gBRCA*-carriers,[6-11, 38] most recent studies did find increased risks to develop serous-like ECs, with reported standardized incidence ratios (SIR) ranging from 14.29 to 32.2.[6, 7, 10] These SIRs are comparable to the reported relative risk increase for prostate cancer (up to 20-fold) and pancreatic cancer (up to 10 fold) for *gBRCA2* carriers.[1] The *gBRCA*-associated ECs in our study were diagnosed at a median age of 60.5 years (range 33-74 years). Because these tumors were enriched for EC histotypes that generally occur at an older age (e.g. USC, UCS, EEC grade 3),[36, 37] our data are suggestive that *gBRCA*-associated ECs indeed occur at a younger age compared with their sporadic counterparts, although no definitive conclusions can be drawn without a proper control group. The combination of the excess risk reported in literature and the phenotype of *gBRCA*-associated EC described here strongly support adding (*TP53*-mutated/serous-like) EC to the HBOC syndrome.

Our observation that *gBRCA*-associated (*gBRCA/*LOHpos) EC and sporadic (*gBRCA/*LOHneg) EC show marked histologic and molecular differences supports previous findings that tumors arising in *gBRCA* carriers are not necessarily causally related to the *gBRCA1/*2 mutation.[12] ECs arising in g*BRCA* carriers showed LOH relatively infrequently (67.7% of *gBRCA1* and 40% *gBRCA2*) compared with OCs and breast cancers in *gBRCA1* carriers (93% and 90%) and OCs in *gBRCA2* carriers (84%), but with similar rates to what has been found for breast cancers in *gBRCA2* carriers (54%).[12] This is an important finding, as it emphasizes that tumors that develop in *gBRCA* carriers are not HRD per default, and thereby may not respond to treatments targeting this DNA repair defect. This concept impacts the interpretation of

clinical trials assessing efficacy of PARP inhibitors in tumors with *BRCA1/2* mutations that show LOH relatively infrequently, and suggests that LOH should be included in stratification algorithms for studies assessing therapy efficacy in tumors from *gBRCA*-carriers.[39-42] In fact, LOH status may explain the less pronounced efficacy of olaparib (PARP-inhibitor) for *gBRCA2* carriers with HER2-negative metastatic BC compared to g*BRCA1* carriers as observed in the OlympiAD-trial.[42]

Our observation should increase awareness of the association between *gBRCA* and high-grade EC and may have clinical implications in selecting patients with EC and their families for *gBRCA* testing. Previous studies testing *gBRCA* mutations in unselected EC cohorts resulted in relatively low incidences (0.5% and 0.6%), with only minor increase (1.1% and 3%) when limited to USC and UCS.[43, 44] The morphologic clues described in our study, however, may serve to enrich for *gBRCA* carriers and therefore facilitate cost-effective *gBRCA* testing in patients with EC and their families, a concept that merits further study. Currently, one might consider *gBRCA* testing in patients with high-grade EC with a previous history of breast cancer or a positive family history for *gBRCA*-associated malignancies. Although our study was not aimed to determine the excess risk in women with *gBRCA1/2* mutations to develop EC compared with the general population, our study supports to at least inform *gBRCA* carriers about the association with EC, as the ECs arising in this background are of an unfavorable subtype.

In this study, it was relevant to ascertain that all included carcinomas were of endometrioid and not of tubo-ovarian origin. To exclude misclassification of secondary involvement of the endometrium by HGSOC as EC, we rereviewed all available salpingo-oophorectomy slides with emphasis on putative precursor lesions in the distal fallopian tube. None of the serous-like ECs showed adnexal involvement, supporting the endometrium as primary origin. In addition, we stained all ECs for WT-1, a marker that assists in distinguishing between USC and HGSOC, with reported nuclear positivity rates ranging from 0 to 44% for USCs and 95 to 100% for serous OCs.[45-48] Although cutoff values for WT-1 positivity are unclear, “diffuse WT-1” is generally accepted to be uncommon in EC. WT-1 positivity was observed in seven of 40 ECs (17.5%), of which four (10%) showed diffuse WT-1 positivity. There was no macro- and microscopic indication for a tubo-ovarian carcinoma in the WT-1 positive ECs; nevertheless we cannot completely rule out the theoretical possibility of a “drop-metastasis” from the fallopian tube. The large time interval between the RRSO and EC diagnosis (median 5.7 years, range, 4.0-9.4 years) that was previously performed in six out of seven cases, in combination with the absence of any tubal involvement upon rereview favors primary endometrial origin. For the remainder WT-1-positive EC (case 6), both adnexa were removed during therapeutic hysterectomy, in which a p53 signature was detected unrelated to the EC. We therefore conclude that all cancers in this study, including those that showed WT-1 positivity, are most likely of primary endometrial origin.

Another relevant aspect is a history tamoxifen treatment, as 2 or more years of tamoxifen treatment has been associated with a two- to sevenfold increased risk to develop ECs.[49-52] ECs of tamoxifen-treated individuals are enriched for less favorable histologic subtypes compared to nontreated individuals, especially carcinosarcomas and sarcomas (10.6%-13.8% vs. 2.9%-8.7% respectively), and for ECs with abnormal p53 expression.[49, 53, 54] Tamoxifen is thought to have a stimulatory effect on the endometrium and uterine body while having an anti-estrogenic effect in breast tissue.[49, 55] This stimulatory effect on the endometrium is unlikely the responsible mechanism for the observed association with serous-like ECs as these ECs are mostly hormone independent.[49] A more plausible, alternative hypothesis for this association may be the DNA damaging effect of tamoxifen. It has been suggested that tamoxifen induces the generation of reactive oxygen species (ROS).[56] ROS can cause DNA damage resulting in replicative stress and DNA double-stranded break formation.[1, 57] Previous literature showing the association between tamoxifen use and EC risk did not take *gBRCA* status into account. In our study cohort of *gBRCA* carriers, we found an enrichment for serous-like histology in women previously treated with tamoxifen. We recently showed that BRCA1/2 mediated HR is commonly abrogated in *TP53*-mutated serous-like ECs.[24] Cells that are HRD are more prone to DNA damage due to the error-prone repair of the DNA double-strand breaks caused by ROS and estrogen metabolites.[58] Thereby, we hypothesize that tamoxifen might facilitate (but not initiate) early carcinogenesis of serous-like precursors in *gBRCA1/2* carriers, as these women are already more prone to develop these tumors. This hypothesis should be further studied, as it may alter the balance between advantages and disadvantages of tamoxifen treatment in *gBRCA* carriers.

This study has some limitations. First, we did not include a matched control group of ECs from non-*gBRCA1/2* carriers. Therefore, we are unable to assign sensitivity and specificity of the morphologic features described. Second, we have defined *gBRCA*-associated EC based on LOH status alone and did not interrogate the presence of *BRCA*-related genomic scars to support our definition of *gBRCA*-associated EC. Third, the study design, in which women were included only after providing informed consent and in which ECs were collected both retrospectively (period before providing informed consent) and prospectively (period after providing informed consent), may have led our study cohort to be enriched for ECs with more favorable histotype and survival.

In conclusion, we provide novel evidence that EC is part of the *gBRCA*-related tumor spectrum, with enrichment for EC subtypes associated with unfavorable clinical outcome and distinct histopathologic and molecular features. We also show that tumors with and without LOH of the *gBRCA1/2* wild-type allele are clearly different, thereby providing evidence that establishing LOH status is critical when assessing treatment efficacy of drugs targeting HRD in *BRCA1/2*-mutated tumors.

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## Disclosure of potential conflicts of interest

No potential conflicts of interest were disclosed.

## References


1. Roy R, Chun J, Powell SN. BRCA1 and BRCA2: different roles in a common pathway of genome protection. Nat Rev Cancer. 2012;12(1):68-78.
2. Chen S, Parmigiani G. Meta-analysis of BRCA1 and BRCA2 penetrance. J Clin Oncol 2007;25(11):1329-33.
3. van Asperen CJ, Brohet RM, Meijers-Heijboer EJ, Hoogerbrugge N, Verhoef S, Vasen HF, et al. Cancer risks in BRCA2 families: estimates for sites other than breast and ovary. J Med Genet 2005;42(9):711-9.
4. Moran A, O'Hara C, Khan S, Shack L, Woodward E, Maher ER, et al. Risk of cancer other than breast or ovarian in individuals with BRCA1 and BRCA2 mutations. Fam Cancer 2012;11(2):235-42.
5. de Jonge MM, Mooyaart AL, Vreeswijk MP, de Kroon CD, van Wezel T, van Asperen CJ, et al. Linking uterine serous carcinoma to BRCA1/2-associated cancer syndrome: A meta-analysis and case report. Eur J Cancer 2017;72:215-25.
6. Shu CA, Pike MC, Jotwani AR, Friebel TM, Soslow RA, Levine DA, et al. Uterine Cancer After Risk-Reducing Salpingo-oophorectomy Without Hysterectomy in Women With BRCA Mutations. JAMA oncol 2016; 2(11):1434-1440.
7. Saule C, Mouret-Fourme E, Briaux A, Becette V, Rouzier R, Houdayer C, et al. Risk of Serous Endometrial Carcinoma in Women With Pathogenic BRCA1/2 Variant After Risk-Reducing Salpingo-Oophorectomy. J Natl Cancer Inst 2018; 110(2).
8. Reitsma W, Mourits MJ, de Bock GH, Hollema H. Endometrium is not the primary site of origin of pelvic high-grade serous carcinoma in BRCA1 or BRCA2 mutation carriers. Mod Pathol 2013;26(4):572-8.
9. Beiner ME, Finch A, Rosen B, Lubinski J, Moller P, Ghadirian P, et al. The risk of endometrial cancer in women with BRCA1 and BRCA2 mutations. A prospective study. Gynecol Oncol 2007;104(1).
10. Laitman Y, Michaelson-Cohen R, Levi E, Chen-Shtoyerman R, Reish O, Josefsberg Ben-Yehoshua S, et al. Uterine cancer in Jewish Israeli BRCA1/BRCA2 mutation carriers. Cancer 2019; 125(5):698-703
11. Segev Y, Iqbal J, Lubinski J, Gronwald J, Lynch HT, Moller P, et al. The incidence of endometrial cancer in women with BRCA1 and BRCA2 mutations: an international prospective cohort study. Gynecol Oncol 2013;130(1):127-131
12. Maxwell KN, Wubbenhorst B, Wenz BM, De Sloover D, Pluta J, Emery L, et al. BRCA locus-specific loss of heterozygosity in germline BRCA1 and BRCA2 carriers. Nat Commun 2017;8(1):319.
13. Abkevich V, Timms KM, Hennessy BT, Potter J, Carey MS, Meyer LA, et al. Patterns of genomic loss of heterozygosity predict homologous recombination repair defects in epithelial ovarian cancer. Br J Cancer 2012;107(10):1776-1782.
14. Popova T, Manie E, Rieunier G, Caux-Moncoutier V, Tirapo C, Dubois T, et al. Ploidy and large-scale genomic instability consistently identify basal-like breast carcinomas with BRCA1/2 inactivation. Cancer Res 2012;72(21):5454-5462.
15. Birkbak NJ, Wang ZC, Kim JY, Eklund AC, Li Q, Tian R, et al. Telomeric allelic imbalance indicates defective DNA repair and sensitivity to DNA-damaging agents. Cancer discov 2012;2(4):366-375.

16. Wittersheim M, Buttner R, Markiefka B. Genotype/Phenotype correlations in patients with hereditary breast cancer. Breast care (Basel) 2015;10(1):22-26.
17. Comprehensive molecular portraits of human breast tumours. Nature 2012;490(7418):61-70.
18. Soslow RA, Han G, Park KJ, Garg K, Olvera N, Spriggs DR, et al. Morphologic patterns associated with BRCA1 and BRCA2 genotype in ovarian carcinoma. Mod Pathol 2012;25(4):625-636.
19. Howitt BE, Hanamornroongruang S, Lin DI, Conner JE, Schulte S, Horowitz N, et al. Evidence for a dualistic model of high-grade serous carcinoma: BRCA mutation status, histology, and tubal intraepithelial carcinoma. Am J Surg Pathol 2015;39(3):287-293.
20. Ritterhouse LL, Nowak JA, Strickland KC, Garcia EP, Jia Y, Lindeman NI, et al. Morphologic correlates of molecular alterations in extrauterine Mullerian carcinomas. Mod Pathol 2016;29(8):893-903.
21. TCGA. Integrated genomic analyses of ovarian carcinoma. Nature 2011;474(7353):609-15.
22. Kandoth C, Schultz N, Cherniack AD, Akbani R, Liu Y, Shen H, et al. Integrated genomic characterization of endometrial carcinoma. Nature 2013;497(7447):67-73.
23. Konstantinopoulos PA, Ceccaldi R, Shapiro GI, D'Andrea AD. Homologous Recombination Deficiency: Exploiting the Fundamental Vulnerability of Ovarian Cancer. Cancer Discov 2015;5(11):1137-1154.
24. de Jonge MM, Auguste A, van Wijk LM, Schouten PC, Meijers M, Ter Haar N, et al. Frequent homologous recombination deficiency in high-grade endometrial carcinomas. Clin Cancer Res 2019; 25(3):1087-1097.
25. Pijpe A, Manders P, Brohet RM, Collee JM, Verhoef S, Vasen HF, et al. Physical activity and the risk of breast cancer in BRCA1/2 mutation carriers. Breast Cancer Res Treat 2010;120(1):235-244.
26. Casparie M, Tiebosch AT, Burger G, Blauwgeers H, van de Pol A, van Krieken JH, et al. Pathology databanking and biobanking in The Netherlands, a central role for PALGA, the nationwide histopathology and cytopathology data network and archive. Cell Oncol 2007;29(1):19-24.
27. Plon SE, Eccles DM, Easton D, Foulkes WD, Genuardi M, Greenblatt MS, et al. Sequence variant classification and reporting: recommendations for improving the interpretation of cancer susceptibility genetic test results. Hum mutat 2008;29(11):1282-91.
28. van Eijk R, Stevens L, Morreau H, van Wezel T. Assessment of a fully automated high-throughput DNA extraction method from formalin-fixed, paraffin-embedded tissue for KRAS, and BRAF somatic mutation analysis. Exp Mol Pathol 2013;94(1):121-5.
29. Kadri S, Long BC, Mujacic I, Zhen CJ, Wurst MN, Sharma S, et al. Clinical Validation of a Next-Generation Sequencing Genomic Oncology Panel via Cross-Platform Benchmarking against Established Amplicon Sequencing Assays. J Mol Diagn 2017;19(1):43-56.
30. Khiabanian H, Hirshfield KM, Goldfinger M, Bird S, Stein M, Aisner J, et al. Inference of Germline Mutational Status and Evaluation of Loss of Heterozygosity in High-Depth, Tumor-Only Sequencing Data. JCO Precis Oncol 2018; Epub 2018 Jan 19.
31. Kautto EA, Bonneville R, Miya J, Yu L, Krook MA, Reeser JW, et al. Performance evaluation for rapid detection of pan-cancer microsatellite instability with MANTIS. Oncotarget 2017;8(5):7452-63.
32. Talhouk A, McConechy MK, Leung S, Li-Chang HH, Kwon JS, Melnyk N, et al. A clinically applicable molecular-based classification for endometrial cancers. Br J Cancer 2015;113(2):299-310.

33. Stelloo E, Bosse T, Nout RA, MacKay HJ, Church DN, Nijman HW, et al. Refining prognosis and identifying targetable pathways for high-risk endometrial cancer; a TransPORTEC initiative. Mod Pathol 2015;28(6):836-844.
34. Gao J, Aksoy BA, Dogrusoz U, Dresdner G, Gross B, Sumer SO, et al. Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal. Sci Signal 2013;6(269):pl1.
35. Cerami E, Gao J, Dogrusoz U, Gross BE, Sumer SO, Aksoy BA, et al. The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. Cancer Discov 2012;2(5):401-404.
36. Hamilton CA, Cheung MK, Osann K, Chen L, Teng NN, Longacre TA, et al. Uterine papillary serous and clear cell carcinomas predict for poorer survival compared to grade 3 endometrioid corpus cancers. Br J of Cancer 2006;94(5):642-646.
37. McGunigal M, Liu J, Kalir T, Chadha M, Gupta V. Survival Differences Among Uterine Papillary Serous, Clear Cell and Grade 3 Endometrioid Adenocarcinoma Endometrial Cancers: A National Cancer Database Analysis. Int J Gynecol Cancer 2017;27(1):85-92.
38. Lee YC, Milne RL, Lheureux S, Friedlander M, McLachlan SA, Martin KL, et al. Risk of uterine cancer for BRCA1 and BRCA2 mutation carriers. Eur J Cancer 2017;84:114-20.
39. Mirza MR, Monk BJ, Herrstedt J, Oza AM, Mahner S, Redondo A, et al. Niraparib Maintenance Therapy in Platinum-Sensitive, Recurrent Ovarian Cancer. N Engl J Med 2016;375(22):2154-2164.
40. Moore K, Colombo N, Scambia G, Kim BG, Oaknin A, Friedlander M, et al. Maintenance Olaparib in Patients with Newly Diagnosed Advanced Ovarian Cancer. N Engl J Med 2018;379(26):2495-2505.
41. Ledermann J, Harter P, Gourley C, Friedlander M, Vergote I, Rustin G, et al. Olaparib maintenance therapy in patients with platinum-sensitive relapsed serous ovarian cancer: a preplanned retrospective analysis of outcomes by BRCA status in a randomised phase 2 trial. Lancet Oncol 2014;15(8):852-861.
42. Robson M, Im SA, Senkus E, Xu B, Domchek SM, Masuda N, et al. Olaparib for Metastatic Breast Cancer in Patients with a Germline BRCA Mutation. N Engl J Med 2017;377(6):523-533.
43. Long B, Lilyquist J, Weaver A, Hu C, Gnanaolivu R, Lee KY, et al. Cancer susceptibility gene mutations in type I and II endometrial cancer. Gynecol Oncol 2019;152(1):20-25.
44. Ring KL, Bruegl AS, Allen BA, Elkin EP, Singh N, Hartman AR, et al. Germline multi-gene hereditary cancer panel testing in an unselected endometrial cancer cohort. Modern pathol 2016; 29(11):1381-1389.
45. Goldstein NS, Uzieblo A. WT1 immunoreactivity in uterine papillary serous carcinomas is different from ovarian serous carcinomas. Am J Surg Pathol 2002;117(4):541-545.
46. Hashi A, Yuminamochi T, Murata S, Iwamoto H, Honda T, Hoshi K. Wilms tumor gene immunoreactivity in primary serous carcinomas of the fallopian tube, ovary, endometrium, and peritoneum. Int J Gynecol Pathol 2003;22(4):374-377.
47. Al-Hussaini M, Stockman A, Foster H, McCluggage WG. WT-1 assists in distinguishing ovarian from uterine serous carcinoma and in distinguishing between serous and endometrioid ovarian carcinoma. Histopathology 2004;44(2):109-115.

48. Hedley C, Sriraksa R, Showeil R, Van Noorden S, El-Bahrawy M. The frequency and significance of WT-1 expression in serous endometrial carcinoma. Human Pathol 2014;45(9):1879-1884.
49. Bergman L, Beelen ML, Gallee MP, Hollema H, Benraadt J, van Leeuwen FE. Risk and prognosis of endometrial cancer after tamoxifen for breast cancer. Comprehensive Cancer Centres' ALERT Group. Assessment of Liver and Endometrial cancer Risk following Tamoxifen. Lancet 2000;356(9233):881-887.
50. Early Breast Cancer Trialists' Collaborative Group. Tamoxifen for early breast cancer: an overview of the randomised trials. Early Breast Cancer Trialists' Collaborative Group. Lancet 1998;351(9114):1451-1467.
51. Rutqvist LE, Johansson H, Signomklao T, Johansson U, Fornander T, Wilking N. Adjuvant tamoxifen therapy for early stage breast cancer and second primary malignancies. Stockholm Breast Cancer Study Group. J Natl Cancer Inst 1995;87(9):645-651.
52. Swerdlow AJ, Jones ME. Tamoxifen treatment for breast cancer and risk of endometrial cancer: a case-control study. J Natl Cancer Inst 2005;97(5):375-384.
53. Jones ME, van Leeuwen FE, Hoogendoorn WE, Mourits MJ, Hollema H, van Boven H, et al. Endometrial cancer survival after breast cancer in relation to tamoxifen treatment: pooled results from three countries. Breast Cancer Res 2012;14(3):R91.
54. Hoogendoorn WE, Hollema H, van Boven HH, Bergman E, de Leeuw-Mantel G, Platteel I, et al. Prognosis of uterine corpus cancer after tamoxifen treatment for breast cancer. Breast cancer res treat 2008;112(1):99-108.
55. Kedar RP, Bourne TH, Powles TJ, Collins WP, Ashley SE, Cosgrove DO, et al. Effects of tamoxifen on uterus and ovaries of postmenopausal women in a randomised breast cancer prevention trial. Lancet 1994;343(8909):1318-1321.
56. Lee YH, Kang BS, Bae YS. Premature senescence in human breast cancer and colon cancer cells by tamoxifen-mediated reactive oxygen species generation. Life Sci 2014;97(2):116-122.
57. Karanjawala ZE, Murphy N, Hinton DR, Hsieh CL, Lieber MR. Oxygen metabolism causes chromosome breaks and is associated with the neuronal apoptosis observed in DNA double-strand break repair mutants. Curr Biol 2002;12(5):397-402.
58. Gorski JJ, Kennedy RD, Hosey AM, Harkin DP. The complex relationship between BRCA1 and ERalpha in hereditary breast cancer. Clin Cancer Res 2009;15(5):1514-1518.

# Supplementary material and methods

## H&E slides, pathology reports and FFPE-tumor blocks

Eligible patients from the HEBON-study were linked to PALGA by a HEBON-datamanager. Hysterectomy specimens (with/without curetting) were retrieved from throughout the Netherlands, including the ovarian cancer (OC) and (salpingo-)oophorectomy specimens when applicable. The original pathology reports (pseudonomizyed), haematoxylin and eosin (H&E) slides and a representative formalin fixed paraffin embedded (FFPE)-tumor block were requested via PALGA from pathology laboratories across the Netherlands.

## Cancer history and other variables

Data on the following variables were retrieved from the central HEBON-database; *gBRCA1/2* mutation, date of birth, date of death, date of diagnosis of EC, history of breast cancer (BC), history of OC and if applicable, the date of diagnosis, date of risk reducing salpingo-oophorectomy (RRSO). Additionally, we retrieved data on whether a patient retrieved hormone-treatment for BC. As the type of hormone treatment was not specified, we collected more specific information on this from pathology reports and regular questionnaires performed by the HEBON-study (not available for all patients). All data was pseudonymised.

## Morphological characterization

Cases were only included for morphological characterization if they did not receive neoadjuvant chemotherapy, as this might affect morphological characteristics. Morphological characteristics were assessed either on the curettage sample (*n*=4) or on the hysterectomy specimen with/without curettage (*n*=35) Slides were first examined at scanning magnification (x40) to determine the dominant pattern of invasion which was categorized as either no invasion (endometrial involvement only), pushing/broad front, destructive, “microcystic, elongated and fragmented”-type of invasion (MELF) or adenomyosis-like.[1] The presence or absence of readily identifiable desmoplastic stromal reaction surrounding the infiltrative glands, squamous differentiation, papillary growth, trabecular growth, jagged lumina, hobnailing, slit-like spaces, tumor giants cells,[2] comedo-necrosis, geographic necrosis,[3] intra-epithelial tumor infiltrating lymphocytes (TILs) and peritumoral lymphocytes were evaluated. The total percentage of **S**olid, cribriform/pseudo**E**ndometrioid and **T**ransitional growth pattern (SET-features) was estimated over all available tumor slides, applying the same criteria as described by Soslow et al.[3] If SET-features were present in >25% of the tumor, it was considered as SET-features being present. Additionally, the predominant growth pattern (glandular, papillary, solid, SET-like or mucinous) was assessed. Nuclear atypia was scored on higher magnification (200x) and was graded as low/grade 1, intermediate/grade 2 or marked/grade 3. Mitotic index was determined per 10 high power files (x400) in enriched areas found upon scanning magnification.

## Procedures IHC

One representative formalin-fixed paraffin-embedded (FFPE) tissue block was selected for immunohistochemistry and stains were manually performed on 4 µm whole slides.

Slides were first deparaffinized and rehydrated via graded ethanol series. After blocking the endogenic peroxidase activity (0.3% Methanol/$H_2O_2$), antigen retrieval was achieved using a microwave oven procedure either in 10 mmol/L Tris-EDTA buffer, pH9.0 (P53, ER, PR, WT-1, CD8) for 10 minutes. Tissue sections were incubated overnight with primary antibodies against P53, ER, PR, WT1 and CD8 at room temperature, followed by incubation with a secondary antibody (Poly-HRP-GAM/R/R; DPV0110HRP; ImmunoLogic) for 30 minutes. DAB+ (K3468, DAKO) was used as chromogen and sections were counterstained with haematoxylin.



## Scoring methods

Slides were evaluated by two independent observers and discrepancies were discussed during a consensus meeting.

p53 was categorized as “wild-type” when only focal, weak and heterogeneous staining was present. p53 was considered “abnormal” when either diffuse and strong nuclear staining was observed in >90% of the tumor cell nuclei (“mutant pattern”) or when nuclear staining was completely absent in the presence of “wild-type” staining of stromal cell nuclei/infiltrate as an internal control (“null pattern”).[4]

ER and PR were considered positive when >10% of the tumor cell nuclei showed positive expression. WT-1 was considered positive when nuclear expression was present and samples were divided in the following categories; negative (≤1% nuclear staining), heterogeneous (2-75% nuclear staining) and diffusely positive (>75% nuclear staining).

Besides the assessment of readily identifiable intra-epithelial TILs and peritumoral lymphocytes on H&E slides, we also manually quantified intraepithelial and intrastromal CD8-positive T-lymphocytes, using CD8 immunostained slides. After digitalization, two high power fields (HPF; 0,2 $mm^2$) were selected in areas enriched for T-lymphocytes in the CD8 immunostain, detected upon scanning magnifications (x20). One HPF was selected in the center of the tumor and one HPF was selected in the invasive margin of the tumor when present. Estimated tumor percentage was at least 70% if possible.

## References

1. Quick CM, May T, Horowitz NS, Nucci MR. Low-grade, low-stage endometrioid endometrial adenocarcinoma: a clinicopathologic analysis of 324 cases focusing on frequency and pattern of myoinvasion. Int J Gynecol Pathol 2012;31(4):337-43.
2. Van Gool IC, Ubachs JEH, Stelloo E, de Kroon CD, Goeman JJ, Smit V, et al. Blinded histopathological characterisation of POLE exonuclease domain-mutant endometrial cancers: sheep in wolf's clothing. Histopathology 2018;72(2):248-58.
3. Soslow RA, Han G, Park KJ, Garg K, Olvera N, Spriggs DR, et al. Morphologic patterns associated with BRCA1 and BRCA2 genotype in ovarian carcinoma. Mod Pathol 2012;25(4):625-36.
4. McCluggage WG, Soslow RA, Gilks CB. Patterns of p53 immunoreactivity in endometrial carcinomas: 'all or nothing' staining is of importance. Histopathology 2011;59(4):786-8.

# Supplementary tables and figures

**Supplementary Table S1. Clinicopathologic characteristics of the complete cohort**

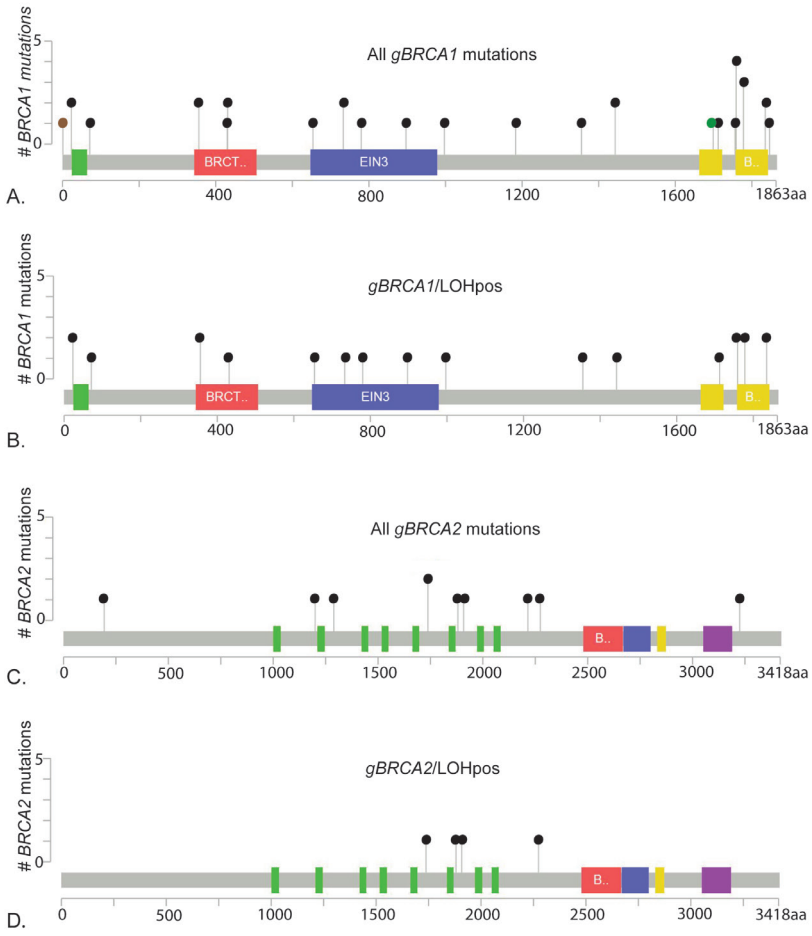
| | **Cases (n=42)** |
|---|---|
| **Germline *BRCA1/2* mutation, No. (%)** | |
| *gBRCA1* | 32 (76.2) |
| *gBRCA2* | 10 (23.8) |
| **Age at diagnoses, median range, years** | 58.5 (33-74) |
| **Histologic subtype, No. (%)** | |
| Endometrioid | 26 (61.9) |
| *Mucinous* | *1 (2.4)* |
| Non-endometrioid | 16 (38.1) |
| *Serous* | *7 (16.7)* |
| *Carcinosarcoma, serous* | *2 (4.8)* |
| *Carcinosarcoma, ambiguous* | *2 (4.8)* |
| *Ambiguous* | *5 (11.9)* |
| **FIGO 2009, No. (%)** | |
| I/II[a] | 35 (83.3) |
| III/IV | 7 (16.7) |
| **LVSI, No. (%)** | 10 (23.8) |
| *Not assessable* | *2 (4.8)* |
| **Salpingo-oophorectomy, No. (%)** | |
| History of RRSO | 23 (54.8) |
| During hysterectomy | 14 (33.3) |
| RRSO at time of EC diagnoses | 2 (4.8) |
| Therapeutic | 2 (4.8) |
| In situ | 1 (2.4) |
| **Ovarian/tubal involvement EC, No. (%)** | 0 (0)[a] |
| **Precursor lesions fallopian tube, No. (%)** | 3 (7.1) |
| "Atypia"[b] | 1 (2.4) |
| P53 signature | 1 (2.4) |
| STIL | 1 (2.4) |
| STIC | 0 (0) |
| **History of ovarian Cancer, No. (%)** | 1 (2.4)[a] |
| **History of Breast Cancer, No. (%)** | 20 (47.6) |
| **Neoadjuvant treatment, No. (%)** | 1 (2.4) |

[a]One case (case 31) presented with a bilateral endometrioid OC, shortly after which a endometrioid EC was diagnosed in a subsequent curettage. The tumors were considered as two primary tumors (EC FIGO 2009 stage I). The OC was not considered as a history of OC nor as adnexal involvement of the EC. [b]The fallopion tube showing "atypia" was not available for revision. Bolded P values are considered significant (P<0.05). Abbreviations: EC, Endometrial Carcinoma; STIC, Serous Tubal Intraepithelial Carcinoma; STIL, Serous Tubal Intraepithelial Lesion

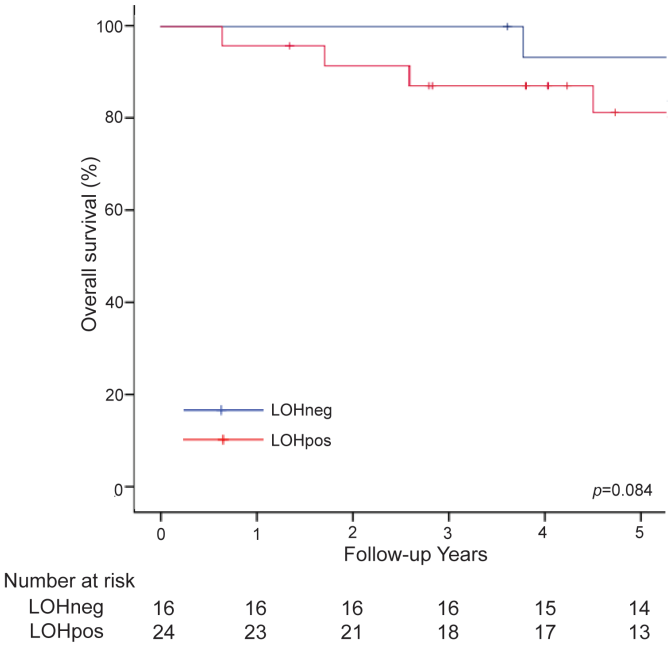
**Supplementary Table S2. Germline *BRCA1/2* mutations and variant allele frequencies detected in the FFPE-isolated tumor DNA**

| Case ID | Tumor (%) | Germline mutation | c.DNA change[a] | Amino Acid change[b] | VAF (%) | LOH | LOH type |
|---|---|---|---|---|---|---|---|
| 44 | 80 | *BRCA1* | c.66dup | p.(Glu23Argfs*18) | 72 | yes | copy loss |
| 15 | 90 | *BRCA1* | c.68_69del | p.(Glu23Valfs*17) | 87 | yes | copy neutral |
| 43 | 40 | *BRCA1* | c.213-12A>G | p.? | 74 | yes | copy neutral |
| 23 | 80 | *BRCA1* | c.1066C>T | p.(Gln356*) | 86 | yes | copy neutral |
| 8 | 90 | *BRCA1* | c.1066C>T | p.(Gln356*) | 73 | yes | copy loss |
| 35 | 70 | *BRCA1* | c.1287dup | p.(Asp430Argfs*6) | 49 | no | none |
| 20 | 80 | *BRCA1* | c.1292dup | p.(Leu431Phefs*5) | 77 | yes | copy loss |
| 19 | 70 | *BRCA1* | c.1292dup | p.(Leu431Phefs*5) | 47 | no | none |
| 22 | 90 | *BRCA1* | c.1961del | p.(Lys654Serfs*47) | 82 | yes | copy neutral |
| 21 | 70 | *BRCA1* | c.2197_2201del | p.(Glu733Thrfs*5) | 62 | yes | copy neutral |
| 11 | 80 | *BRCA1* | c.2197_2201del | p.(Glu733Thrfs*5) | 47 | no | none |
| 34[c] | 80 | *BRCA1* | c.2338C>T | p.(Gln780*) | 75 | yes | copy neutral |
| 6 | 90 | *BRCA1* | c.2685_2686del | p.(Pro897Lysfs*5) | 89 | yes | copy loss |
| 26 | 90 | *BRCA1* | c.2989_2990dup | p.(Asn997Lysfs*4) | 85 | yes | copy neutral |
| 1 | 80 | *BRCA1* | c.3549_3550delinsT | p.(Lys1183Asnfs*27) | 40 | no | none |
| 14 | 80 | *BRCA1* | c.4065_4068del | p.(Asn1355Lysfs*10) | 86 | yes | copy neutral |
| 2 | 60 | *BRCA1* | c.4327C>T | p.(Arg1443*) | 44 | no | none |
| 42 | 90 | *BRCA1* | c.4327C>T | p. (Arg1443Ter) | 98 | yes | copy neutral |
| 13 | 80 | *BRCA1* | c.5095C>T | p.(Arg1699Trp) | 44 | no | none |
| 37 | 30 | *BRCA1* | c.5136G>A | p.(Trp1712*) | 59 | yes | copy neutral |
| 17 | 70 | *BRCA1* | c.5277+1G>A | p.? | 71 | yes | copy neutral |
| 28 | 80 | *BRCA1* | c.5277+1G>A | p.? | 48 | no | none |
| 5 | 80 | *BRCA1* | c.5277+1G>A | p.? | 84 | yes | copy neutral |
| 33 | 80 | *BRCA1* | c.5277+1G>A | p.? | 26 | no | none |
| 40 | 80 | *BRCA1* | c.5503_5564del | p.(Arg1835Thrfs*24) | 77 | yes | copy loss |
| 7 | 90 | *BRCA1* | c.5503_5564del | p.(Arg1835Thrfs*24) | 89 | yes | copy neutral |
| 18 | 50 | *BRCA1* | c.5536C>T | p.(Gln1846*) | 48 | no | none |
| 39 | 80 | *BRCA1* | c.5333-36_5406+400del | p.? | n/a | yes | two copy loss |
| 41 | 80 | *BRCA1* | c.5333-36_5406+400del | p.? | n/a | no | none |
| 3 | 90 | *BRCA1* | c.5333-36_5406+400del | p.? | n/a | yes | two copy loss |
| 4 | 80 | *BRCA2* | c.582G>A | p.(Trp194*) | 50 | no | none |
| 32 | 30 | *BRCA2* | c.3599_3600del | p.(Cys1200*) | 46 | no | none |
| 27 | 70 | *BRCA2* | c.3865_3868del | p.(Lys1289Alafs*3) | 47 | no | none |
| 12 | 85 | *BRCA2* | c.5213_5216del | p.(Thr1738Ilefs*2) | 39 | no | none |
| 10 | 90 | *BRCA2* | c.5213_5216del | p.(Thr1738Ilefs*2) | 85 | yes | copy neutral |
| 45 | 90 | *BRCA2* | c.5637_5640delGAAT | p.Lys1881Glnfs*27 | 88 | yes | copy loss |
| 29 | 70 | *BRCA2* | c.5722_5723del | p.(Leu1908Argfs*2) | 62 | yes | copy loss |
| 31 | 80 | *BRCA2* | c.6644_6647del | p.(Tyr2215Serfs*13) | 46 | no | none |
| 25 | 60 | *BRCA2* | c.6816_6817del | p.(Gly2274Argfs*18) | 63 | yes | copy loss |
| 24 | 70 | *BRCA2* | c.9672dup | p.(Tyr3225Ilefs*30) | 46 | no | none |
| 38[d] | 80 | *BRCA1* | c.(?_-232)_(80+1_81-1)del | p.? | n/a | n/a | n/a |
| 16[e] | 25 | *BRCA1* | c.5266dup | p.(Gln1756Profs*74) | n/a | n/a | n/a |

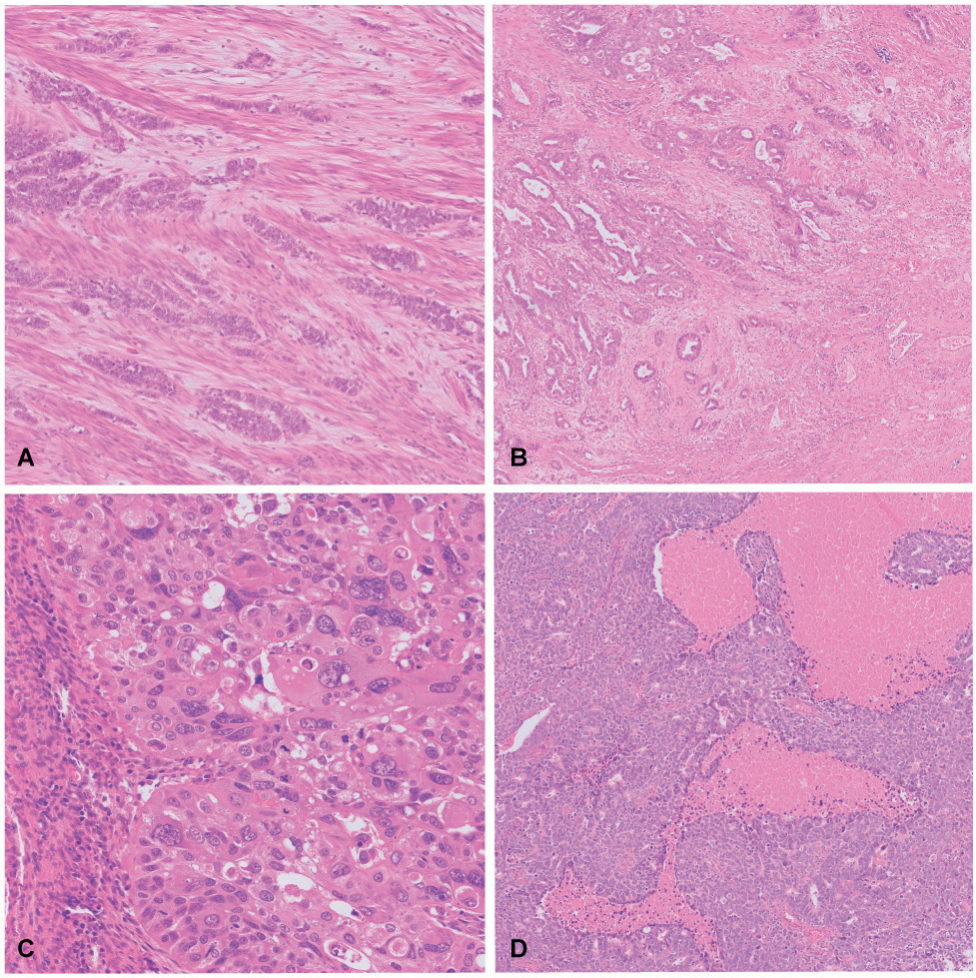
58.3% of the observed LOH (n=14) was copy neutral and 41.7% of LOH (n=10) was associated with copy loss. No somatic loss of function mutations were detected as "second hit". [a]Reference sequences used for mutation annotation; NM_007294.3 for *BRCA1*, NM_000059.3 for *BRCA2*. [b]Reference sequence used for protein annotation; NP_009225.1 for *BRCA1*, NP_000059.3 for *BRCA2*. [c]The patient was a known g*BRCA1* mutation carrier, however, the exact inherited mutation was not specified in the database. [d]The inherited *gBRCA1* exon1/2 deletion could not be confirmed in the tumor DNA and can likely be explained by the limited sensitivity of NGS to detect large exon deletions. Since LOH status could not be assessed, the case was left out from final analyses. [e]Molecular analyses failed due to poor DNA quality. Abbreviations: LOH, Loss of heterozygosity of the *gBRCA1/2* wild-type allele; VAF, Variant allele frequency



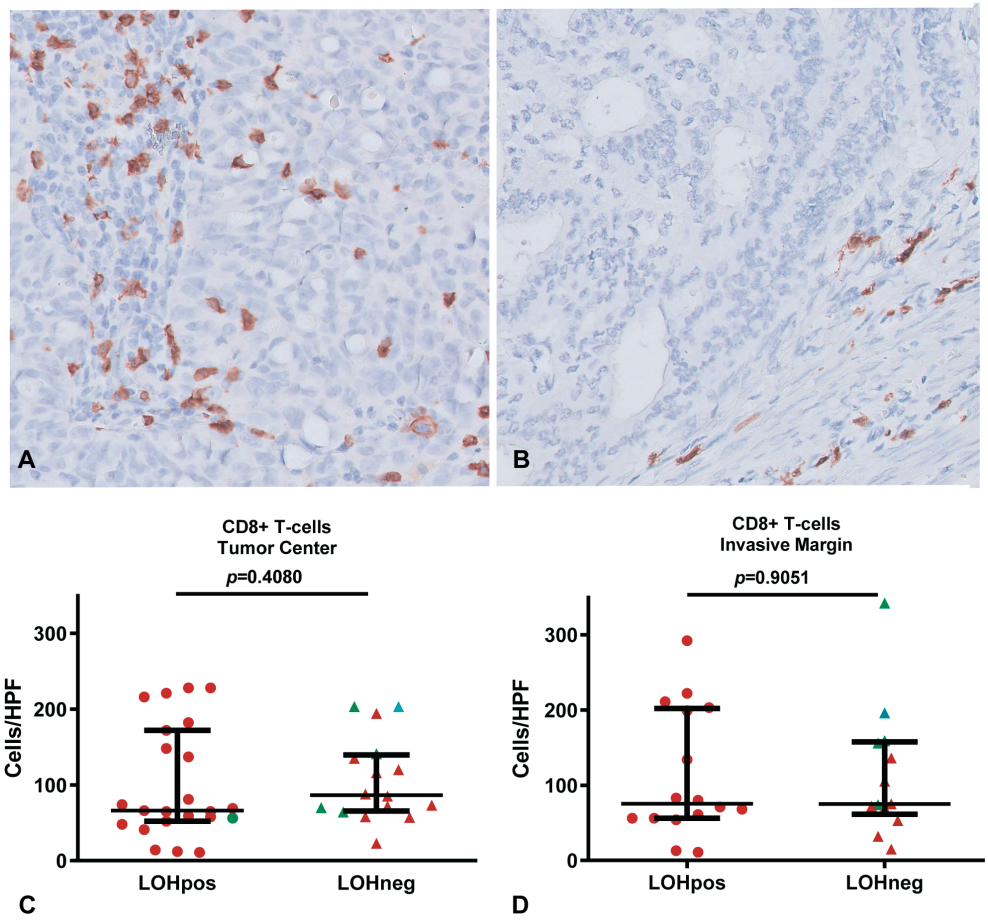

**Supplementary Fig. S1: Position and frequency of *gBRCA1/2* mutations across the coding DNA sequence.** Distribution and frequency of *gBRCA1* mutations in the study cohort **(A)** and for *gBRCA1/* LOHpos cases only **(B)**. Distribution and frequency of *gBRCA2* mutations in the study cohort **(C)** and for *gBRCA2/*LOHpos cases only **(D)**. Black dot, Truncating variant; Green dot, Missense variant; Brown dot, no protein.



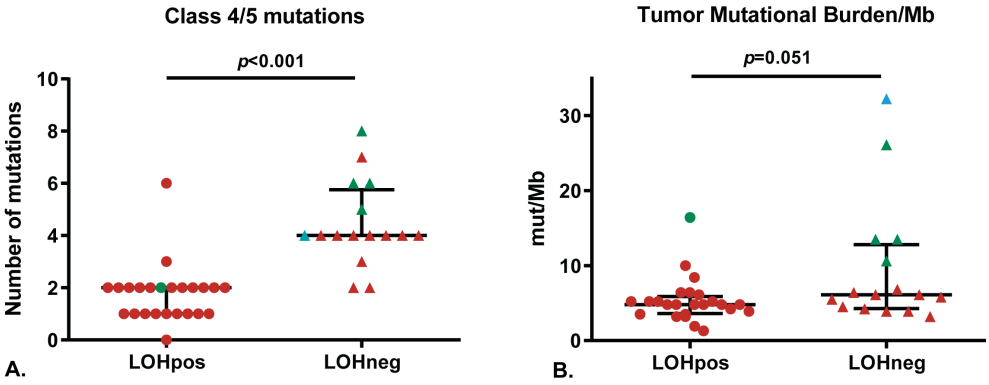

**Supplementary Fig. S2: Overall survival of women with *gBRCA*/LOHpos ECs (*n*=24) and *gBRCA*/LOHneg ECs (*n*=16).** The cross indicates a censoring event. Of the *gBRCA*/LOHpos ECs, five (20.8%) were diagnosed preceding to the date of enrolment (mean 4.8 years, SD: 4.3) and 19 (79.2%) were diagnosed after the date of enrolment or on the date of enrolment (LUMC cases) (mean 3.7 years, SD: 3.7). Of the g*BRCA*/LOHneg ECs, 14 (87.5%) were diagnosed preceding to the date of enrolment (mean 4.8 years, SD: 2.4) and one (6.3%) was diagnosed after the date of enrolment (mean 2.6 years). For one (6.3%) case, the date of enrolment was missing. Abbreviations: EC, endometrial carcinoma; LOH, loss of heterozygosity of the *gBRCA1/2* wild-type allele.




**Supplementary Fig. S3: Examples of morphological characteristics associated with g*BRCA*/LOHpos ECs. A:** Trabecular growth and desmoplastic stromal reaction, **B**: Destructive type of invasion, **C:** Tumor giant cells and high nuclear grade, **D**: Geographic necrosis.




**Supplementary Fig. S4: CD8-positive T-cell infiltrate stratified by loss of heterozygosity status.** Example of CD8-IHC in the center of the tumor (**A**) and at the invasive margin (**B**). The total number of CD8+ T-cells per High Power Field (0,2 $mm^2$) per case (both intra-epithelial and stromal) compared between *gBRCA*/LOHpos ECs and *gBRCA*/LOHneg ECs are shown for the center of the tumor (*n*=39) (**C**) and at the invasive margin (*n*=29) (**D**). Whiskers represent the interquartile range and the median values are indicated by the horizontal line. Blue dots/triangles indicate *POLE*-mutated ECs, green dots/triangles indicate MSI-high ECs. No significant difference was observed for the number of CD8+ T-cells between *gBRCA*/LOHpos and *gBRCA*/LOHneg ECs, neither was a difference observed when comparing only intra-epithelial CD8+ T-cells or only intrastromal CD8+ T-cells. When excluding the MSI-high (*n*=5) and *POLE*-mutated tumors (*n*=1) from analyses, neither a significant difference in CD8+ T-cell infiltration was detected. Abbreviations: IHC, Immunohistochemistry; LOH, Loss of Heterozygosity of the *gBRCA* wild-type allele.




**Supplementary Fig. S5: Class 4/5 mutations and tumor mutational burden stratified by loss of heterozygosity status. A**. *gBRCA/*LOHpos ECs harbored significantly fewer class 4/5 mutations (other than the *gBRCA* mutation) compared to *gBRCA/*LOHneg ECs (median 2, range: 0-6 versus 4, range: 2-8, $p<0.001$). The difference remained significant when excluding all *POLE*-mutated ECs and MSI-high ECs. **B.** No statistically significant difference was observed for Tumor Mutational Burden (TMB) when comparing *gBRCA*/LOHpos ECs with *gBRCA/*LOHneg ECs (median 4.8 mut/MB: range 1.3-16.4, versus 6.1 mut/Mb; range: 3.2-32.2, $p=051$). The TMB remained non-significant when excluding all *POLE*-mutated ECs and MSI-high ECs ($p=0.4943$). The whiskers represent the interquartile range and the median values are indicated by the horizontal line. Blue dots/triangles indicate *POLE*-mutated ECs. Green dots/triangles indicate MSI-high ECs. Abbreviations: LOH, Loss of heterozygosity of the *gBRCA* wild-type allele; Mb, Megabase.