Table SI. List of all 10 patient sample contributors participating in the study.

| Patient sample contributors | Number of patients <br> included in the <br> study |
| :--- | :--- |
| The Bank of Clinical Samples, First Faculty of Medicine, Charles <br> University, Prague, Czech Republic | 235 |
| Institute of Medical Biochemistry and Laboratory Diagnostics, First <br> Faculty of Medicine, Charles University and General University Hospital <br> in Prague, Prague, Czech Republic | 51 |
| Department of Cancer Epidemiology and Genetics, Masaryk Memorial <br> Cancer Institute, Brno, Czech Republic | 29 |
| Department of Medical Genetics, AGEL Laboratories, AGEL Research <br> and Training Institute, Novy Jicin, Czech Republic | 15 |
| Centre for Medical Genetics and Reproductive Medicine, Gennet, Prague, <br> Czech Republic | 140 |
| Institute of Biology and Medical Genetics, First Faculty of Medicine and <br> General University Hospital in Prague, Prague, Czech Republic | 25 |
| Department of Medical Genetics, GHC Genetics, Prague, Czech Republic | 4 |
| Department of Medical Genetics, Faculty of Medicine in Pilsen, Charles <br> University, and University Hospital Pilsen, Pilsen, Czech Republic | 10 |
| Department of Medical Genetics, Pronatal, Prague, Czech Republic | 2 |
| Department of Medical Genetics, University Hospital Olomouc, Faculty of <br> Medicine and Dentistry, Palacky University Olomouc, Czech Republic | 16 |

Table SII. List of all 226 genes included in the CZECANCA panel with used transcript variants and full names.

| A, Established EC-predisposition genes ( $\mathrm{N}=19$ ) |  |  |
| :---: | :---: | :---: |
| Gene name | Transcript variant | Gene name (alternative denominations) |
| ATM | NM_000051.3 | Ataxia telangiectasia mutated |
| BARD1 | NM_000465.3 | BRCA1 associated RING domain 1 |
| BRCAI | NM_007294.3 | Breast cancer 1, early onset |
| BRCA2 | NM_000059.3 | Breast cancer 2, early onset |
| BRIP1 | NM_032043.2 | BRCA1 interacting protein Cterminal helicase 1 |
| CDH1 | NM_004360.4 | Cadherin 1, type 1, E-cadherin |
| EPCAM $^{\text {a }}$ | NM_002354.2 | Epithelial cell adhesion molecule |
| CHEK2 | NM_007194.3 | Checkpoint kinase 2 |
| MLH1 | NM_000249.3 | mutL homolog 1 , colon cancer, nonpolyposis type 2 |
| MSH2 | NM_000251.2 | mutS homolog 2, colon cancer, nonpolyposis type 1 |
| MSH6 | NM_000179.2 | mutS homolog 6 |
| NF1 | NM_000267.3 | Neurofibromin 1 |
| PALB2 | NM_024675.3 | Partner and localizer of BRCA2 |
| PMS2 | NM_000535.6 | PMS1 homolog 2 |
| PTEN | NM_000314.6 | Phosphatase and tensin homolog |
| RAD51C | NM_058216.2 | RAD51 homolog C |
| RAD51D | NM_002878.3 | RAD51 homolog D |
| STK11 | NM_000455.4 | Serine/threonine kinase 11 |
| TP53 | NM_000546.5 | Tumor protein p53 |
| B, Candidate genes ( $\mathrm{N}=207$ ) |  |  |
| Gene name | Transcript variant | Gene name (alternative denominations) |


| AIP | NM_003977.3 | Aryl hydrocarbon receptor interacting protein |
| :---: | :---: | :---: |
| ALK | NM_004304.4 | Anaplastic lymphoma kinase |
| APC | NM_000038.5 | Adenomatous polyposis coli |
| APEX1 | NM_001641.3 | APEX nuclease (multifunctional DNA repair enzyme) 1 |
| ATMIN | NM_015251.2 | ATM interactor |
| ATR | NM_001184.3 | Ataxia telangiectasia and Rad3 related |
| ATRIP | NM_130384.2 | ATR interacting protein |
| AURKA | NM_198433.2 | Aurora kinase A |
| AXIN1 | NM_003502.3 | Axin 1 |
| BABAM1 | NM_001033549.2 | BRISC and BRCA1 A complex member 1 |
| BAP1 | NM_004656.3 | BRCA1 associated <br> (ubiquitin carotein-1 <br> hydrolase)  |
| BLM | NM_000057.3 | Bloom syndrome, RecQ helicase-like |
| BMPR1A | NM_004329.2 | Bone morphogenetic protein receptor, type IA |
| BRAP | NM_006768.4 | BRCA1 associated protein |
| BRCC3 | NM_024332.3 | BRCA1/BRCA2-containing complex, subunit 3 |
| BRE | NM_004899.4 | Brain and reproductive organexpressed (TNFRSF1A modulator) |
| BUB1B | NM_001211.5 | Budding uninhibited by  <br> benzimidazoles 1 homolog beta |
| CASP8 | NM_001080125.1 | Caspase 8, apoptosis-related cysteine peptidase |
| CCND1 | NM_053056.2 | Cyclin D1 |
| CDC73 | NM_024529.4 | Cell division cycle 73, Paf1/RNA polymerase II complex component, homolog |


| CDK4 | NM_000075.3 | Cyclin-dependent kinase 4 |
| :---: | :---: | :---: |
| CDKN1B | NM_004064.4 | Cyclin-dependent kinase inhibitor 1B (p27, Kip1) |
| CDKNIC | NM_000076.2 | Cyclin-dependent kinase inhibitor 1C (p57, Kip2) |
| CDKN2A | NM_000077.4 | Cyclin-dependent kinase inhibitor 2A |
| CEBPA | NM_004364.4 | CCAAT/enhancer binding protein (C/EBP), alpha |
| CEP57 | NM_014679.4 | Centrosomal protein 57 kDa |
| CLSPN | NM_022111.3 | Claspin |
| CSNK1D | NM_001893.4 | Casein kinase 1, delta |
| CSNKIE | NM_001894.4 | Casein kinase 1, epsilon |
| CWF19L2 | NM_152434.2 | CWF19-like 2, cell cycle control |
| CYLD | NM_015247.2 | Cylindromatosis (turban tumor syndrome) |
| DCLRE1C | NM_001033855.2 | DNA cross-link repair 1C |
| DDB2 | NM_000107.2 | Damage-specific DNA binding protein $2,48 \mathrm{kDa}$ |
| DHFR | NM_000791.3 | Dihydrofolate reductase |
| DICER1 | NM_030621.4 | Dicer 1, ribonuclease type III |
| DIS3L2 | NM_152383.4 | DIS3 like 3'-5' exoribonuclease 2 |
| DMBT1 | NM_007329.2 | Deleted in malignant brain tumors 1 |
| DMC1 | NM_007068.3 | DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination |
| DNAJC21 | NM_194283.3 | DnaJ (Hsp40) homolog, subfamily C, member 21 |
| DPYD | NM_000110.3 | Dihydropyrimidine dehydrogenase |
| EGFR | NM_005228.3 | Epidermal growth factor receptor |
| EMSY | NM_001300942.1 | EMSY transcriptional repressor, BRCA2 interacting |
| EPHX1 | NM_000120.3 | Epoxide hydrolase 1 |


| ERCC1 | NM_001983.3 | Excision repair cross-complementing rodent repair deficiency, complementation group 1 |
| :---: | :---: | :---: |
| ERCC2 | NM_000400.3 | Excision repair cross-complementing rodent repair deficiency, complementation group 2 |
| ERCC3 | NM_000122.1 | Excision repair cross-complementing rodent repair deficiency, complementation group 3 |
| ERCC4 | NM_005236.2 | Excision repair cross-complementing rodent repair deficiency, complementation group 4 |
| ERCC5 | NM_000123.3 | Excision repair cross-complementing rodent repair deficiency, complementation group 5 |
| ERCC6 | NM_000124.3 | Excision repair cross-complementing rodent repair deficiency, complementation group 6 |
| ESR1 | NM_000125.3 | Estrogen receptor 1 |
| ESR2 | NM_001437.2 | Estrogen receptor 2 (ER beta) |
| EXO1 | NM_006027.4 | Exonuclease 1 |
| EXT1 | NM_000127.2 | Exostosin 1 |
| EXT2 | NM_000401.3 | Exostosin 2 |
| EYA2 | NM_005244.4 | Eyes absent homolog 2 |
| EZH2 | NM_004456.4 | Enhancer of zeste homolog 2 |
| FAAP24 | NM_152266.4 | FA core complex associated protein 24 |
| FAM175A | NM_139076.2 | Family with sequence similarity 175 , member A |
| FAM175B | NM_032182.3 | Family with sequence similarity 175, member B |
| FAN1 | NM_014967.4 | FANCD2/FANCI-associated nuclease 1 |


| FANCA | NM_000135.2 | Fanconi anemia, complementation <br> group A |
| :--- | :--- | :--- |
| FANCB | NM_001018113.2 | Fanconi anemia, complementation <br> group B |
| FANCC | NM_000136.2 | Fanconi anemia, complementation <br> group C |
| FANCD2 | NM_033084.4 | Fanconi anemia, complementation <br> group D2 |
| FANCE | NM_021922.2 | Fanconi anemia, complementation <br> group E |
| FANCF | NM_022725.3 | Fanconi anemia, complementation <br> group F |
| FANCG | NM_004629.1 | Fanconi anemia, complementation <br> group G |
| FANCI | NM_001113378.1 | Fanconi anemia, complementation <br> group I |
| FANCL | NM_001114636.1 | Fanconi anemia, complementation <br> group L |
| HELQ | NM_133636.3 | Fanconi anemia, complementation |
| group M |  |  |


| HOXB13 | NM_006361.5 | Homeobox B13 |
| :---: | :---: | :---: |
| HRAS | NM_005343.3 | v-Ha-ras Harvey rat sarcoma viral oncogene homolog |
| HUS1 | NM_004507.3 | HUS1 checkpoint homolog |
| CHEK1 | NM_001114122.2 | Checkpoint kinase 1 |
| KAT5 | NM_182710.2 | K(lysine) acetyltransferase 5 |
| KCNJ5 | NM_000890.3 | Potassium inwardly-rectifying channel, subfamily J, member 5 |
| KIT | NM_000222.2 | V-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog |
| LIG1 | NM_000234.2 | Ligase I, DNA, ATP-dependent |
| LIG3 | NM_013975.3 | Ligase III, DNA, ATP-dependent |
| LIG4 | NM_002312.3 | Ligase IV, DNA, ATP-dependent |
| LMO1 | NM_002315.2 | LIM domain only 1 |
| LRIG1 | NM_015541.2 | Leucine-rich repeats and immunoglobulin-like domains 1 |
| MAX | NM_002382.4 | MYC associated factor X |
| MCPH1 | NM_024596.4 | Microcephalin 1 |
| MDC1 | NM_014641.2 | Mediator of $\quad$ DNA-damage checkpoint 1 |
| MDM2 | NM_002392.5 | Mdm2, p53 E3 ubiquitin protein ligase homolog |
| MDM4 | NM_002393.4 | Mdm4 p53 binding protein homolog |
| MEN1 | NM_000244.3 | Multiple endocrine neoplasia I |
| MET | NM_001127500.2 | Met proto-oncogene $\quad$ (hepatocyte growth factor receptor) |
| MGMT | NM_002412.4 | O-6-methylguanine-DNA methyltransferase |
| MLH3 | NM_001040108.1 | mutL homolog 3 |
| MMP8 | NM_002424.2 | Matrix metallopeptidase 8 <br> (neutrophil collagenase)  |
| MPL | NM_005373.2 | Myeloproliferative leukemia virus oncogene |


| MRE11 | NM_005591.3 | MRE11 meiotic recombination 11 <br> homolog A |
| :--- | :--- | :--- |
| MSH3 | NM_002439.4 | mutS homolog 3 |
| MSH5 | NM_002441.4 | mutS homolog 5 |
| MSR1 | NM_138715.2 | Macrophage scavenger receptor 1 |
| MUS81 | NM_025128.4 | MUS81 endonuclease homolog |
| MUTYH | NM_001128425.1 | mutY homolog |
| NAT1 | NM_000662.7 | acetyltransferase) |
| NBN | NM_002485.4 | Nibrin |
| NCAM1 | NM_001242607.1 | Neural cell adhesion molecule 1 |
| NELFB | NM_015456.4 | Nofactor of BRCA1 |
| NF2 | NM_000268.3 | Nuclear factor <br> polypeptide gene enhancer in B-cells |
| NFKBIZ | NM_031419.3 | Poly |
| inhibitor, zeta |  |  |


| POLE | NM_006231.3 | Polymerase (DNA directed), epsilon, catalytic subunit |
| :---: | :---: | :---: |
| PPM1D | NM_003620.3 | Protein phosphatase, $\mathrm{Mg} 2+/ \mathrm{Mn} 2+$ dependent, 1D |
| PREX2 | NM_024870.3 | Phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2 |
| PRF1 | NM_001083116.1 | Perforin 1 (pore forming protein) |
| PRKAR1A | NM_212471.2 | Protein kinase, cAMP-dependent, regulatory, type I, alpha |
| PRKDC | NM_006904.6 | Protein kinase, DNA-activated, catalytic polypeptide |
| PTCH1 | NM_000264.3 | Patched 1 |
| PTTG2 | NM_006607.2 | Pituitary tumor-transforming 2 |
| RAD1 | NM_002853.3 | RAD1 homolog |
| RAD17 | NM_133338.2 | RAD17 homolog |
| RAD18 | NM_020165.3 | RAD18 homolog |
| RAD23B | NM_002874.4 | RAD23 homolog B |
| RAD50 | NM_005732.3 | RAD50 homolog |
| RAD51 | NM_133487.3 | RAD51 homolog |
| RAD51AP1 | NM_001130862.1 | RAD51 associated protein 1 |
| RAD51B | NM_133509.3 | RAD51 homolog B |
| RAD52 | NM_134424.3 | RAD52 homolog |
| RAD54B | NM_012415.3 | RAD54 homolog B |
| RAD54L | NM_003579.3 | RAD54-like |
| RAD9A | NM_004584.2 | RAD9 homolog A |
| RB1 | NM_000321.2 | Retinoblastoma 1 |
| RBBP8 | NM_002894.2 | Retinoblastoma binding protein 8 |
| RECQL | NM_002907.3 | RecQ protein-like (DNA helicase Q1-like) |
| RECQLA | NM_004260.3 | RecQ protein-like 4 |
| RECQL5 | NM_004259.6 | RecQ protein-like 5 |
| RET | NM_020975.4 | Ret proto-oncogene |


| RFC1 | NM_002913.4 | Replication factor C (activator 1) 1, $145 \mathrm{kDa}$ |
| :---: | :---: | :---: |
| RFC2 | NM_181471.2 | Replication factor C (activator 1) 2, 40 kDa |
| RFC4 | NM_181573.2 | Replication factor C (activator 1) 4, $37 \mathrm{kDa}$ |
| RHBDF2 | NM_024599.5 | Rhomboid 5 homolog 2 |
| RNF146 | NM_001242844.1 | Ring finger protein 146 |
| RNF168 | NM_152617.3 | Ring finger protein 168, E3 ubiquitin protein ligase |
| RNF8 | NM_003958.3 | Ring finger protein 8, E3 ubiquitin protein ligase |
| RPAI | NM_002945.3 | Replication protein A1, 70kDa |
| RUNX1 | NM_001754.4 | Runt-related transcription factor 1 |
| SBDS | NM_016038.2 | SBDS ribosome maturation factor |
| SDHA | NM_004168.3 | Succinate dehydrogenase complex flavoprotein subunit A |
| SDHAF2 | NM_017841.2 | Succinate dehydrogenase complex assembly factor 2 |
| SDHB | NM_003000.2 | Succinate dehydrogenase complex, subunit B, iron sulfur (Ip) |
| SDHC | NM_003001.3 | Succinate dehydrogenase complex subunit C |
| SDHD | NM_003002.3 | Succinate dehydrogenase complex subunit D |
| SETBP1 | NM_002894.2 | SET binding protein 1 |
| SETX | NM_015046.5 | Senataxin |
| SHPRH | NM_001042683.2 | SNF2 histone linker PHD RING helicase, E3 ubiquitin protein ligase |
| SLX4 | NM_032444.2 | SLX4 structure-specific endonuclease subunit homolog |
| SMAD4 | NM_005359.5 | SMAD family member 4 |


| SMARCA4 | NM_001128849.1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 |
| :---: | :---: | :---: |
| SMARCB1 | NM_003073.4 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily $b$, member 1 |
| SMARCEI | NM_003079.4 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1 |
| SUFU | NM_016169.3 | Suppressor of fused homolog |
| TCL1A | NM_021966.2 | T-cell leukemia/lymphoma 1A |
| TELO2 | NM_016111.3 | TEL2, telomere maintenance 2, homolog |
| TERF2 | NM_005652.4 | Telomeric repeat binding factor 2 |
| TERT | NM_198253.2 | Telomerase reverse transcriptase |
| TLR2 | NM_003264.4 | Toll-like receptor 2 |
| TLR4 | NM_138554.4 | Toll-like receptor 4 |
| TMEM127 | NM_017849.3 | Transmembrane protein 127 |
| TOPBP1 | NM_007027.3 | Topoisomerase (DNA) II binding protein 1 |
| TP53BP1 | NM_133487.3 | Tumor protein p53 binding protein 1 |
| TSC1 | NM_000368.4 | Tuberous sclerosis 1 |
| TSC2 | NM_000548.4 | Tuberous sclerosis 2 |
| TSHR | NM_000369.2 | Thyroid stimulating hormone receptor |
| UBE2A | NM_003336.3 | Ubiquitin-conjugating enzyme E2A |
| UBE2B | NM_003337.3 | Ubiquitin-conjugating enzyme E2B |
| UBE2I | NM_003345 | Ubiquitin-conjugating enzyme E2I |
| UBE2V2 | NM_003350.2 | Ubiquitin-conjugating enzyme E2 variant 2 |
| UBE4B | NM_001105562.2 | Ubiquitination factor E4B |
| UIMC1 | NM_001199297.2 | Ubiquitin interaction motif <br> containing 1   |


| VHL | NM_000551.3 | Von Hippel-Lindau tumor suppressor, E3 ubiquitin protein ligase |
| :---: | :---: | :---: |
| WRN | NM_000553.4 | Werner syndrome, RecQ helicaselike |
| WT1 | NM_024426.4 | Wilms tumor 1 |
| XPA | NM_000380.3 | Xeroderma pigmentosum, complementation group A |
| XPC | NM_004628.4 | Xeroderma pigmentosum, complementation group C |
| XRCC1 | NM_006297.2 | X-ray repair complementing defective repair in Chinese hamster cells 1 |
| XRCC2 | NM_005431.1 | X-ray repair complementing defective repair in Chinese hamster cells 2 |
| XRCC3 | NM_005432.3 | X-ray repair complementing defective repair in Chinese hamster cells 3 |
| XRCC4 | NM_022406.3 | X-ray repair complementing defective repair in Chinese hamster cells 4 |
| XRCC5 | NM_021141.3 | X-ray repair complementing defective repair in Chinese hamster cells 5 |
| XRCC6 | NM_001469.4 | X-ray repair complementing defective repair in Chinese hamster cells 6 |
| ZNF350 | NM_021632.3 | Zinc finger protein 350 |
| ZNF365 | NM_014951.2 | Zinc finger protein 365 |

${ }^{\text {a }}$ Only deletions causing inactivation of MSH2 were considered. EC, endometrial cancer; N , number.

Table SIII. List of all carriers of pathogenic variant in EC-predisposition genes, including their clinical information.

| Gene groups | Gene | Variant | Age at EC diagnosi s, years | Histology | Fulfille <br> d LS criteria | Fulfille <br> d <br> HBOC <br> criteria | ClinVar ID |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| LS | MLHI | c.350C>T, p.(Thr117Met) | 46 | Endometrioid | Yes | Yes | 17094 |
| LS | MLH1 | c. $677 \mathrm{G}>\mathrm{A}, \mathrm{p} .(\operatorname{Arg} 226 \mathrm{Gln})$ | 60 | Endometrioid | Yes | No | 90318 |
| LS | MLHI | c. $790+1 \mathrm{G}>\mathrm{A}, \mathrm{p} .(?)$ | 58 | Endometrioid | No | No | 90356 |
| LS | MLH1 | c.1489dup, p.(Arg497ProfsTer6) | 55 | Endometrioid | Yes | No | 89753 |
| LS | MLHI | Deletion of exons 1-13 | 50 | Endometrioid | Yes | No | a |
| LS | MSH2 | c.1500dup, p.(Arg501GlnfsTer12) | 46 | Endometrioid | Yes | Yes | 90683 |
| LS | MSH2 | c.1720del, p.(Gln574ArgfsTer16) | 45 | Unknown | Yes | No | 90761 |
| LS | MSH2 | c.2459-2_2472del, p.(Gly820fs) | 51 | Unknown | Yes | Yes | 2430176 |
| LS | MSH2 | Deletion of exons 1-8 | 29 | Endometrioid | Yes | No | a |
| LS | MSH2 | Deletion of exons 1-16 | 32 | Endometrioid | Yes | No | a |
| LS | MSH2 | Deletion of exons 3 | 42 | Endometrioid | Yes | No | a |
| LS | MSH2 | Deletion of exons 5-6 | 54 | Unknown | Yes | No | a |
| LS | MSH6 | c.643del, p.(Val215Ter) | 67 | Endometrioid | No | No | 479909 |
| LS | MSH6 | c.741dup, p.(Arg248ThrfsTer8) | 55 | Unknown | Yes | No | 410494 |
| LS | MSH6 | c.885dup, p.(Val296SerfsTer16) | 73 | Endometrioid | Yes | No | 641585 |


| LS | MSH6 | c.964_967del, p.(Ala322ProfsTer15) | 62 | Endometrioid/clear cell | No | No | 2430174 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| LS | MSH6 | c. $1444 \mathrm{C}>\mathrm{T}, \mathrm{p} .(\operatorname{Arg} 482 \mathrm{Ter})$ | 65 | Endometrioid | No | No | 89194 |
| LS | MSH6 | c.1754T>C, p.(Leu585Pro) | 53 | Endometrioid/serou S | No | No | 89220 |
| LS | MSH6 | c.1754T>C, p.(Leu585Pro) | 43 | Endometrioid | Yes | No | 89220 |
| LS | MSH6 | c.2348_2349del, p.(Cys783Ter) | 45 | Endometrioid/clear cell | Yes | No | 89274 |
| LS | MSH6 | c.2677_2678del, p.(Leu893AlafsTer6) | 42 | Endometrioid | Yes | No | 821660 |
| LS | MSH6 | c.2759del, p.(Lys920ArgfsTer25) | 51 | Unknown | Yes | No | 428433 |
| LS | MSH6 | c.3261del, p.(Phe1088SerfsTer2) | 62 | Endometrioid | Yes | No | 89363 |
| LS | MSH6 | c.3261dup, p.(Phe1088LeufsTer5) | 49 | Endometrioid | Yes | Yes | 89364 |
| LS | MSH6 | c.3995T>G, p.(Leu1332Ter) | 60 | Endometrioid | Yes | No | 2430173 |
| $\begin{aligned} & \text { LS/HBO } \\ & \mathrm{C} \end{aligned}$ | $\begin{aligned} & \text { MLH1/BRC } \\ & A 1 \end{aligned}$ | c.1483dup, p.(His495ProfsTer29)/c.5266dup, <br> p.(Gln1756ProfsTer74)  | 48 | Endometrioid | Yes | Yes | $2430175 / 176$ <br> 77 |
| $\begin{aligned} & \text { LS/HBO } \\ & \mathrm{C} \end{aligned}$ | MSH2/ATM | c.1676del, p.(Leu559Ter)/c.8147T>C p.(Val2716Ala) | 53 | Unknown | Yes | No | $\begin{aligned} & 90743 / 14270 \\ & 0 \end{aligned}$ |
| HBOC | ATM | c.601C>T, p.(Gln201Ter) | 78 | Endometrioid | No | No | 265611 |
| HBOC | ATM | c. $2921+1 \mathrm{G}>\mathrm{A}, \mathrm{p} .(?)$ | 55 | Endometrioid | No | No | 141182 |
| HBOC | ATM | c.3250C>T, p.(Gln1084Ter) | 63 | papillary serous | Yes | Yes | 665551 |
| HBOC | ATM | Deletion of exons 35-44 | 70 | Unknown | No | No | a |


| HBOC | BARD1 | c. $1690 \mathrm{C}>\mathrm{T}, \mathrm{p} .(\mathrm{Gln} 564 \mathrm{Ter})$ | 28 | Endometrioid | Yes | Yes | 127720 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| HBOC | BRCAI | c.68_69del, p.(Glu23ValfsTer17) | N.A. | Endometrioid | Yes | No | 17662 |
| HBOC | BRCAI | c. $1687 \mathrm{C}>\mathrm{T}, \mathrm{p} .(\mathrm{Gln} 563 \mathrm{Ter})$ | 80 | EIN | No | No | 37426 |
| HBOC | BRCAI | c.2411_2412del, p.(Gln804LeufsTer5) | 53 | EIN | Yes | Yes | 37466 |
| HBOC | BRCAI | c.5095C>T, p. (Arg1699Trp) | 69 | Endometrioid | Yes | Yes | 55396 |
| HBOC | BRCAI | c.5510G>A, p.(Trp1837Ter) | N.A. | Unknown | Yes | No | 55608 |
| HBOC | BRCAl | c.5266dup, p.(Gln1756ProfsTer74) | 61 | Unknown | Yes | Yes | 17677 |
| HBOC | BRCAI | c.5266dup, p.(Gln1756ProfsTer74) | 68 | Leiomyosarcoma | No | Yes | 17677 |
| HBOC | BRCAI | c.5266dup, p.(Gln1756ProfsTer74) | N.A. | Unknown | Yes | Yes | 17677 |
| HBOC | BRCAI | c.5266dup, p.(Gln1756ProfsTer74) | 41 | Papillary serous | Yes | Yes | 17677 |
| HBOC | BRCAI | Deletion of exons 1-17 | 57 | Endometrioid | No | Yes | a |
| HBOC | BRCA2 | c.658_659del, p.(Val220IlefsTer4) | N.A. | Unknown | No | No | 9342 |
| HBOC | BRCA2 | c.2808_2811del, p.(Ala938ProfsTer21) | 41 | Unknown | Yes | No | 9322 |
| HBOC | BRCA2 | c.5213_5216del, p.(Thr1738IlefsTer2) | 50 | Endometrioid | No | No | 37951 |
| HBOC | BRCA2 | c.5946del, p.(Ser1982ArgfsTer22) | 55 | Endometrioid | No | No | 9325 |
| HBOC | BRCA2 | c.6275_6276del, p.(Leu2092ProfsTer7) | 57 | Endometrioid | No | Yes | 9318 |
| HBOC | BRCA2 | c.6591_6592del, p.(Glu2198AsnfsTer4) | 62 | Unknown | No | No | 9319 |
| HBOC | BRCA2 | c.7878G>C, p.(Trp2626Cys) | 63 | Leiomyosarcoma | No | No | 38125 |
| HBOC | BRIP1 | c.2038_2039dup, p.(Leu680PhefsTer9) | 71 | Leiomyosarcoma | No | No | 128166 |
| HBOC | CHEK2 | c.444+1G>A, p.(Gln149IlefsTer6) | 62 | Endometrioid | No | No | 128075 |
| HBOC | CHEK2 | c. $444+1 \mathrm{G}>\mathrm{A}, \mathrm{p} . \mathrm{Gln} 149$ IlefsTer6 | 37 | Unknown | Yes | Yes | 128075 |


| HBOC | CHEK2 | c.846+4_846+7del, p.Asp265_His282del | 64 | Endometrioid | No | No |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| HBOC | CHEK2 | c.846+4_846+7del, p.Asp265_His282del | 65 | Unknown | Yes | No |
| HBOC | CHEK2 | c.846+4_846+7del, p.Asp265_His282del | 44 | Endometrioid | Yes | No |
| HBOC | CHEK2 | c.894T>G, p.(Tyr298Ter) | 61 | Unknown | Yes | No |
| HBOC | PALB2 | c.761C>G, p.(Ser254Ter) | 232048 |  |  |  |
| HBOC | PTEN | c.170T>G, p.(Leu57Trp) | 53 | Leiomyosarcoma | Yes | No |
| HBOC | RAD51C | c.502A>T, p.(Arg168Ter) | 57 | Unknown | Yes | No |
| HBOC | RAD51C | c.1026+5_1026+7del | 62 | Endometrioid | Yes | Yes |

${ }^{\text {a }}$ Copy number variations were not submitted to ClinVar because the exact nucleotide coordinates of the breakpoints required for the ClinVar submission were not determined. EC, endometrial cancer; EIN, endometrial intraepithelial neoplasia; HBOC, hereditary breast and ovarian cancer; LS, Lynch syndrome; N.A., not available.

Table SIV. Frequencies of germline PV in 207 candidate genes.

| Germline PV | Indication for germline genetic testing |  |  |  | All EC-predisposition gene-negative patients, n (\%) ( $\mathrm{N}=467$ ) | EC-predisposition gene-negative PMC, $n$$\text { (\%) ( } \mathrm{N}=1616 \text { ) }$ | All patients with EC vs. PMC |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | $\begin{aligned} & \text { LS, n (\%) } \\ & (\mathrm{N}=126) \end{aligned}$ | $\mathrm{HBOC}, \mathrm{n}$(\%)$(\mathrm{N}=13)$ | LS + <br> HBOC, n <br> $(\%)(\mathrm{N}=67)$  | Nonindicated, n (\%) ( $\mathrm{N}=261$ ) |  |  |  |  |
|  |  |  |  |  |  |  | OR (95\% CI) | $\begin{aligned} & \hline \text { P- } \\ & \text { value } \end{aligned}$ |
| ATRIP ${ }^{\text {a }}$ | 0 | 0 | $1^{\text {a }}$ (1.5) | 1 (0.4) | $2^{\text {a }}$ (0.4) | 3 (0.2) | 2.3 (0.4-13.9) | 0.3 |
| CASP8 | 0 | 0 | 1 (1.5) | 0 | 1 (0.2) | 1 (0.1) | 3.2 (0.2-50.5) | 0.4 |
| CWF19L2 | 0 | 0 | 0 | 0 | 0 | 2 (0.1) | N.A. |  |
| DMBT1 $^{\text {b,c }}$ | 0 | $1^{\text {b }}$ (7.7) | $1^{\mathrm{c}}$ (1.5) | 1 (0.4) | $3^{\text {b,c }}$ (0.6) | 1 (0.1) | 9.5 (1-91.5) | 0.1 |
| EMSY | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 0 | N.A. |  |
| EPHX1 | 1 (0.8) | 0 | 0 | 0 | 1 (0.2) | 2 (0.1) | 1.6 (0.1-17.4) | 0.7 |
| ERCC3 ${ }^{\text {d,e }}$ | 0 | 0 | $1^{\text {d }}$ (1.5) | $1^{\mathrm{e}}(0.4)$ | $2^{\text {d,e }}$ (0.4) | 7 (0.4) | 1 (0.2-4.7) | >0.9 |
| ERCC4 ${ }^{\text {f }}$ | 0 | 0 | $1^{\mathrm{f}}(1.5)$ | 0 | $1^{\mathrm{f}}(0.2)$ | 2 (0.1) | 1.6 (0.1-17.4) | 0.7 |
| ERCC5 | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 0 | N.A. |  |
| ERCC6 ${ }^{\text {e }}$ | 0 | 0 | 1 (1.5) | $2^{\mathrm{e}}$ (0.8) | $3^{\mathrm{e}}(0.6)$ | 0 | N.A. |  |
| EXO1 | 2 (1.6) | 0 | 1 (1.5) | 0 | 3 (0.6) | 2 (0.1) | 4.8 (0.8-28.5) | 0.1 |
| FAN1 | 1 (0.8) | 0 | 0 | 1 (0.4) | 2 (0.4) | 3 (0.2) | 2.3 (0.4-13.9) | 0.3 |
| FANCA | 2 (1.6) | 0 | 0 | 2 (0.8) | 4 (0.9) | 10 (0.6) | 1.3 (0.4-4) | 0.7 |
| FANCD2 | 1 (0.8) | 0 | 0 | 0 | 1 (0.2) | 0 | N.A. |  |
| FANCE | 1 (0.8) | 0 | 0 | 0 | 1 (0.2) | 1 (0.1) | 3.2 (0.2-50.5) | 0.4 |
| FANCG | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 1 (0.1) | 3.2 (0.2-50.5) | 0.4 |


| FANCI | 1 (0.8) | 0 | 0 | 0 | 1 (0.2) | 7 (0.4) | 0.5 (0.1-3.7) | 0.7 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| FANCL ${ }^{\text {g }}$ | 0 | 0 | $1^{\mathrm{g}}$ (1.5) | 0 | $1^{\mathrm{g}}(0.2)$ | 0 | N.A. |  |
| FANCM | 1 (0.8) | 0 | 0 | 1 (0.4) | 2 (0.4) | 3 (0.2) | 2.3 (0.4-13.9) | 0.3 |
| KCNJ5 | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 1 (0.1) | 3.2 (0.2-50.5) | 0.4 |
| LIG3 | 0 | 0 | 1 (1.5) | 1 (0.4) | 2 (0.4) | 4 (0.2) | 1.6 (0.3-8.6) | 0.6 |
| LRIG1 | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 0 | N.A. |  |
| MCPH1 | 0 | 0 | 0 | 2 (0.8) | 2 (0.4) | 7 (0.4) | 1 (0.2-4.7) | >0.9 |
| MEN1 | 1 (0.8) | 0 | 0 | 0 | 1 (0.2) | 0 | N.A. |  |
| MLH3 | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 1 (0.1) | 3.2 (0.2-50.5) | 0.4 |
| MRE11A | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 0 | N.A. |  |
| MUTYH ${ }^{\text {d }}$ | 0 | 0 | $2^{\text {d }}$ (3) | 3 (1.1) | $5^{\text {d }}$ (1.1) | 18 (1.1) | 0.9 (0.3-2.4) | 0.8 |
| NBN ${ }^{\text {h }}$ | $2^{\text {h }}$ (1.6) | 0 | 0 | 0 | $2^{\mathrm{h}}$ (0.4) | 7 (0.4) | 1.0 (0.2-4.7) | >0.9 |
| PIK3CG | 0 | 0 | 0 | 0 | 0 | 0 | N.A. |  |
| POLD1 ${ }^{\text {g }}$ | 0 | 0 | $1^{\mathrm{g}}(1.5)$ | 0 | $1^{\mathrm{g}}(0.2)$ | 0 | N.A. |  |
| POLE | 0 | 0 | 1 (1.5) | 1 (0.4) | 2 (0.4) | 1 (0.1) | 6.3 (0.6-69.8) | 0.1 |
| PREX2 | 0 | 0 | 0 | 0 | 0 | 1 (0.1) | N.A. |  |
| PRF1 ${ }^{\text {a }}$ | 0 | 0 | $1^{\mathrm{a}}(1.5)$ | 0 | $1^{\mathrm{a}}(0.2)$ | 1 (0.1) | 3.2 (0.2-50.5) | 0.4 |
| RAD1 | 0 | 0 | 1 (1.5) | 0 | 1 (0.2) | 0 | N.A. |  |
| RAD17 ${ }^{\text {b,c }}$ | 0 | $1^{\text {b }}$ (7.7) | $1^{\mathrm{c}}$ (1.5) | 0 | $2^{\text {b,c }}$ (0.4) | 2 (0.1) | 3.2 (0.4-22.5) | 0.2 |
| RAD50 | 0 | 0 | 0 | 0 | 0 | 8 (0.5) | N.A. |  |
| RAD51B | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 0 | N.A. |  |


| RAD54L ${ }^{\text {f }}$ | 0 | 0 | $1{ }^{\text {f }}(1.5)$ | 0 | $1^{\mathrm{f}}(0.2)$ | 1 (0.1) | 3.2 (0.2-50.5) | 0.4 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| RBBP8 | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 0 | N.A. |  |
| RCF4 ${ }^{\text {h }}$ | $1^{\text {h }}(0.8)$ | 0 | 0 | 0 | $1^{\text {h }}(0.2)$ | 2 (0.1) | 1.6 (0.1-17.4) | 0.7 |
| RECQL | 0 | 1 (7.7) | 0 | 0 | 1 (0.2) | 1 (0.1) | 3.2 (0.2-50.5) | 0.4 |
| RECQL4 | 0 | 0 | 1 (1.5) | 0 | 1 (0.2) | 8 (0.5) | 1.1 (0.2-5.2) | >0.9 |
| RECQL5 | 0 | 0 | 0 | 0 | 0 | 6 (0.4) | N.A. |  |
| RNF168 | 1 (0.8) | 0 | 0 | 0 | 1 (0.2) | 1 (0.1) | 3.2 (0.2-50.5) | 0.4 |
| SBDS | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 21 (1.3) | 0.3 (0.1-1.3) | 0.1 |
| SETX | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 1 (0.1) | 3.2 (0.2-50.5) | 0.4 |
| SLX4 | 0 | 0 | 0 | 1 (0.4) | 1 (0.2) | 1 (0.1) | 3.2 (0.2-50.5) | 0.4 |
| XRCC4 | 0 | 0 | 1 (1.5) | 1 (0.4) | 2 (0.4) | 1 (0.1) | 6.3 (0.6-69.8) | 0.1 |
| All PV | 15 | 3 | 19 | 29 | 66 | 139 |  |  |
| All carriers | $14^{\mathrm{h}}$ (11.1) | $2^{\text {b }}$ (15.4) | $\begin{aligned} & 14^{\mathrm{a}, \mathrm{c}, \mathrm{~d}, \mathrm{f}, \mathrm{~g}} \\ & (20.9) \end{aligned}$ | $28^{\text {e }}$ (10.7) | $58^{\text {a-h }}$ (12.4) | 139 (8.6) |  |  |

Pathogenic variants in two candidate cancer susceptibility genes: ${ }^{a}$ ATRIP/PRF1, ${ }^{\text {b }}$ DMBT1/RAD17, ${ }^{\text {c DMBT1/RAD17, }}{ }^{d} E R C C 3 / M U T Y H$, ${ }^{\mathrm{e}}$ ERCC3/ERCC6, ${ }^{\mathrm{f}}$ ERCC4/RAD54L, ${ }^{\mathrm{g}}$ FANCL/POLD1, ${ }^{\text {h }}$ NBN/RCF4. Frequencies of germline PV found in a subgroup of patients fulfilling criteria for germline genetic testing for $\mathrm{LS}, \mathrm{HBOC}, \mathrm{LS}$ and HBOC , individuals not fulfilling any criteria (non-indicated), an aggregated group of all patients with EC, and a group of PMC. CI, confidence interval; EC, endometrial cancer; HBOC, hereditary breast and ovarian cancer; LS, Lynch syndrome; N , number; N.A., not available; OR, odds ratio; PMC, population-matched controls; PV, pathogenic variant.

