

Supplementary Table S2

| Gene symbol | Gene name | ASE size, type in EOC | In frame/ in coding region | Function | EOC or epithelial specific? | Conserved splice in mouse | Normal Ψ_{mean} n=25 | Cancer Ψ_{mean} n=21 | Primers Forward Reverse |
|----------------|--|-----------------------|-----------------------------------|---------------------------------|-----------------------------|---------------------------|----------------------------------|----------------------------------|---|
| AFF3 | AF4/FMR2 family, member 3 | +75 exon | Coding region in frame | Transcription factor | ES | | 0.5 | 10.4 | 5'CATGGACAGCTTCGACTTAGC3' 5'TACAGATAGACGAGGGCTGGTT3' |
| AGR3 (BCMP 11) | Anterior gradient homolog 3 | -136 exon | Removes ATG Downstream initiation | Breast cancer | n.d. | | 92.5 | 58.2 | 5'AAGAGCACTGGCCAAGTCAG3' 5'CCTCCAGGTGATGAATAACCA3' |
| APP | Amyloid beta (A4) precursor protein | -57 exon | Coding region in frame | Transmembrane /secreted | CS | Yes | 64.8 | 20.0 | 5'ACCACCACCACCACAGAGTC3' 5'GGGCATGTTTCATTCTCATCC3' |
| AXIN1 | Axin 1 | -108 exon | Coding region in frame | G protein signalling | ES | Yes | 39.3 | 22.8 | 5'CATGCAGTGGATCATTGAGG3' 5'ACCTTCTCTGCGATCTTGTC3' |
| BMP4 | Bone morphogenetic protein 4 | +209 alt 5' | 5'UTR | Bone growth factor | CS | | 28.3 | 43.4 | 5'CGAGAAGGCAGAGGAGGAG3' 5'CAAACCTTGCTGGAAAGGCTC3' |
| BTC | Betacellulin | -147 exon | Coding region in frame | EGF family of growth factors. | CS | | 67.4 | 50.7 | 5'ACCACCACACAATCAAAGCG3' 5'TTACGACGTTTCCGAAGAGG3' |
| C11orf17 | C11orf17 | +81 exon | Coding region in frame | PKA-interacting protein | ES | | 17.7 | 35.9 | 5'AGCCATGGACAACCTGTTTGG3' 5'CATGCTCTGATATTTGATAGCTGC3' |
| CADM1 (IGSF4) | Cell adhesion molecule 1 | +33 exon | Coding region in frame | Adhesion | CS | Yes | 1.8 | 22.8 | 5'CACCACCATCCTTACCATCATC3' 5'AGAATGATGAGCAAGCACAGC3' |
| CCNE1 | Cyclin E1 | +135 exon | Coding region in frame | S phase progression | ES | | 65.6 | 82.2 | 5'CACAGGGAGACCTTTTACTTGG3' 5'TCAAGGCAGTCAACATCCAG3' |
| CHEK2 | Checkpoint kinase 2 | +62 exon | Out of frame truncating | cell cycle checkpoint regulator | ES | | 74.2 | 86.6 | 5'CAGCTCTCAATGTTGAAACAGAA3' 5'TCTGGCTTTAAGTCACGGTGT3' |
| DNMT3B | DNA (cytosine-5-)-methyltransferase 3 beta | +189 (2exons) | Coding region in frame | De novo methylation | CS | | 1.4 | 47.8 | 5'CAAGAGGGACATCTCACGGT3' 5'AGTGCACAGGAAAGCCAAAG3' |
| FANCA | Fanconi anemia, complementation group A | -129 exon | Coding region in frame | Genome stability | ES | | 78.9 | 66.1 | 5'AACCTGAAGCTGATGCTCTTTTC3' 5'TATCCTCATTTCTGTGCGG3' |

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|--------------------|--|-----------------|--|---------------------------------|----|-----|------|------|--|--|--|--|--|
| FANCL | Fanconi anemia, complementation group L | +278 (4 exons) | Out of frame truncating Or alternate ATG used | Stem cell maintenance | ES | | | | | | | 5'CTGTGTTTTCTCCGGACTTCG3' 5'ATGGTACTGAAGCAGGTATCCG3' | |
| FGFR1 | Fibroblast growth factor receptor 1 | +267exon | Coding region in frame | Mitogenesis and differentiation | CS | Yes | 47.0 | 72.5 | | | | | |
| FGFR2 | Fibroblast growth factor receptor 2 | +267 exon | Coding region in frame | Mitogenesis and differentiation | ES | Yes | 6.3 | 17.5 | | | | 5'AGAACTGGGATGTGGAGCTG3' 5'TGTTTTCTTTCTCCTCTGAAGAGG3' | |
| FGFR4 | Fibroblast growth factor receptor 4 | +194 alt 3' | Longer form is truncated | Mitogenesis and differentiation | ES | | 20.8 | 37.4 | | | | 5'TGCAGATGGGATTAACGTCC3' 5'GTGTCATCCTCATCATCTCCG3' | |
| FN1-EDA | Fibronectin | -270 exon | Coding region in frame | Cell adhesion and migration | ES | Yes | 50.4 | 82.4 | | | | 5'GAAGCACATCGTCATCAACG3' 5'AAGTGGGAGACTTGGTTCTGCG3' | |
| FN1-EDB | | -273 exon | Coding region in frame | | ES | Yes | 11.8 | 4.8 | | | | | 5'AATCCAAGCGGAGAGAGTCA3' 5'AACATTGGGTGGTGTCCACT3' |
| FN1-IIICS intron | | -93 intron | Coding region in frame | | ES | Yes | 7.2 | 0.2 | | | | | 5'GGATGACAAGGAAAGTGTCCC3' 5'GAGGTGTGCTCTCATGTTGTTCC3' |
| FN1-IIICS upstream | | -75 alt 3' | Coding region in frame | | ES | Yes | 29.2 | 13.3 | | | | | 5'CCATAAGGCATAGGCCAAGA3' 5'TCAGTGCCTCCACTATGACG3' |
| GATA3 | GATA binding protein 3 | +143 exon | Out of frame | Transcription factor | ES | | 86.1 | 75.4 | | | | 5'AATAATCAGAAGAGCGAGCCC3' 5'ACTGGGTTGCTGACCAGAAG3' 5'CTTCGGATGCAAGTCCAGG3' | |
| GNB3 | Guanine nucleotide binding protein (G protein), beta polypeptide 3 | +241 intron | Removes ATG Downstream initiation | Hypertension | CS | Yes | 30.4 | 71.4 | | | | 5'AAGTCTCCAGTGAGTCATGC3' | |
| GPR137 (C11orf4) | G protein-coupled receptor 137 | - 376 (2 exons) | Out of frame truncating | Unknown | ES | | 6.2 | 23.9 | | | | 5'AGGTCCAGCCAGAGCCCAA3' 5'ACTCGTCCCACCACCTCTAG3' | |
| HMGA1 | High mobility group AT-hook 1 | +33 alt 5' | Coding region in frame | Transcription factor | ES | Yes | 96.3 | 48.1 | | | | 5'TGTTCAAGGCCAAGGTGAAG3' 5'TCAAAGAAGTAGGACCGAGAGG3' 5'CCCAGCCATCACTCTTCC3' | |
| | | | | | | | 55.1 | 63.3 | | | | 5'GAGATGCCCTCCTCTTCTC3' | |

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|-----------------|--|-----------------|-------------------------|---|------|-----|------|------|---|
| HSCB (HSC20) | HscB iron-sulfur cluster co-chaperone homolog | -145 exon | Coding region in frame | Protein folding chaperone | CS | | 96.9 | 77.8 | 5'TCAGAGAAGCATTGACCCT3' 5'TTGTATCCACCCACCTCA3' |
| KITLG | KIT ligand | -84 exon | Coding region in frame | Tyrosine-kinase receptor ligand Cell migration | CS | Yes | | | |
| LGALS9 | Lectin, galactoside-binding, soluble, 9 (galectin 9) | +96 exon | Coding region in frame | Modulating cell-cell and cell-matrix interactions | CS | | 89.8 | 67.9 | 5'TGATGCCTTCAAGGACTTTGT3' 5'CTGCCCTTGTAAGACTTGGC3' |
| MCL1 | Myeloid cell leukemia sequence 1 (BCL2-related) | +248 exon | Out of frame | Apoptosis | ES | | 5.6 | 28.3 | 5'GTGATGGTGAACGGGATCCT3' 5'GTTGGCAGGCCACACGCC3' |
| NRG1 | Neuregulin 1 | -24 exon | Coding region in frame | Glycoprotein Ligand of ERBB family | CS | Yes | 61.0 | 88.5 | 5'CCAAGGACACAAAGCCAATG3' 5'TGGAAGAACTCCACAAACCC3' |
| NUP98 | Nucleoporin 98kDa | -222 exon | Coding region in frame | Signal-mediated nuclear transport | CS | | 74.8 | 33.4 | 5'GTTTACTGGTGTATCGCTGCC3' 5'TGGGCTGTGGAAGTATAGTGAC3' |
| PAXIP1 | PAX interacting (with transcription-activation domain) protein 1 | -71 alt 5' | Out of frame truncating | Genome stability, condensation of chromatin and mitotic progression | ES | | 87.7 | 69.2 | 5'TCGTATCTGGAGGGTTCTGG3' 5'TCAGATTCCATGTGTGCTCG3' |
| PLD1 | Phospholipase D1, phosphatidylcholine-specific | -114 exon | Coding region in frame | Regulation of mitosis | ES | | 28.2 | 13.2 | 5'GGCACACGTTTTCTCCACTCT3' 5'GATAACACCTTTCTCCTGCAC3' |
| POLI | Polymerase (DNA directed) iota | +106 intron | Out of frame truncating | DNA damage checkpoint | CS | | 47.4 | 8.4 | 5'ACGACGCAGATAGCATCAGC3' 5'TTGCAGTAGTCCTTTCCATGC3' |
| POLM | Polymerase (DNA directed), mu | + 270 (2 exons) | Coding region in frame | DNA repair | ES | | 35.5 | 63.2 | 5'AATGGCTCAAACCTAAGGACAAGAG3' 5'TCACGACCATAGTGCTTCTCAG3' |
| PSAP | Prosaposin | -9 exon | Coding region in | Secreted | n.d. | | 63.5 | 88.3 | 5'GAGTCGCCATCTACCTGGTC3' 5'TCCTCACACACTCCATGCTC3' |
| | | | | | | | 1.7 | 57.0 | 5'TGCTATCCAGATGATGATGCAC3' |

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|--------|--|-------------|---|---|----|-----|------|------|--|
| PTK2 | Protein tyrosine kinase 2 | +9 exon | frame Coding region in frame | glycoprotein precursor Focal adhesion tyrosine kinase | CS | Yes | 5.7 | 22.1 | 5'AAACATCAGACTTTGCTGGGAC3' 5'TGACAGCTACAACGAGGGTG3' 5'GATGACAGCTTTCACCAGGC3' |
| PTPN13 | Protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) | +57 exon | Coding region in frame | Signalling, apoptosis | ES | | 13.0 | 32.9 | 5'GACTCCTCATCCATTGAAGACC3' 5'CCAAGCCATACTTTGCATCTTT3' |
| RAD52 | RAD52 homolog (S. cerevisiae) | +151 exon | Inclusion causes reading frame truncation | DNA double-strand break repair and homologous recombination | ES | | 21.7 | 4.9 | 5'GCCTCAAGTCCAAGGCTTTAT3' 5'TCGGCAGCTGTTGTATCTTG3' |
| SHMT1 | Serine hydroxymethyltransferase 1 | +117 exon | Coding region in frame | Purine synthesis | ES | | 57.6 | 73.4 | 5'GAACACTGCCATGTGGTGAC3' 5'CATAGCTTGCTTCAGTGCCA3' |
| SLIT2 | Slit homolog 2 (Drosophila) | -12 exon | Coding region in frame | Migration and metastasis | CS | Yes | 67.9 | 47.1 | 5'GGCAAGTTTCAACCATATGCC3' 5'GGAGCCATAAATGACTGGTGAC3' |
| SRP19 | Signal recognition particle 19kDa | +112 exon | Out of frame truncating | Protein transport to ER | CS | | 23.6 | 43.5 | 5'TCCTACAGCTACAGAGATTCAAGATG3' 5'TCTCTCAGTCGAGCAAGTTCC3' |
| STIM1 | Stromal interaction molecule 1 | -93 exon | Coding region in frame | Transmembrane protein | ES | | 35.7 | 2.1 | 5'ATCGAGATCCTCTGTGGCTTC3' 5'GAACACTGCTCTGCAGGCTAG3' |
| SYK | Spleen tyrosine kinase | -69 exon | Coding region in frame | Lamellipodia formation | ES | Yes | 95.4 | 69.1 | 5'CACAACCTCCAGGTTCCCAT3' 5'CCCAGTTCCTTGTCTTCCAGC3' |
| SYNE2 | Synaptic nuclear envelope protein 2 | -69 exon | Coding region in frame | Nuclear anchorage to cytoskeleton | CS | Yes | 64.5 | 7.0 | 5'CTCACGAAGAGGACGAGGAG3' 5'TTGCTTGTAGTGATGCTCGG3' |
| TOPBP1 | Topoisomerase (DNA) II binding protein 1 | +15 alt 3' | Coding region in frame | Genomic stability | ES | | 58.0 | 71.6 | 5'TGCCCAATTCTTCAACTCCT3' 5'TGTAGGCTCCAGTTTGTCTGTT3' |
| TSSC4 | Tumor suppressing subtransferable | -192 intron | Coding region in frame | Tumor suppressor | CS | | 97.6 | 85.6 | 5'TTGGCTGTCCAATCACACTC3' 5'ATGCCTTCAGATGGAATGG3' |

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|-----------------------------------|----------------------------------|-----------|----------------------------|---|----|------|------|---|--|
| TUBA4 A (TUBA1) UTRN | candidate 4 Tubulin, alpha 1a | +223 exon | Out of frame truncating | Cytoskeleton | ES | | | | |
| | | | | | | 74.2 | 94.1 | 5'GACTCAACGTGAGACGCACC3' 5'CTCTTTCCCAGTGATGAGCTG3' | |
| | Utrophin | -39 exon | Coding region in frame | Dystrophin, neuromuscul ar junction | CS | | | 5'CAAACACCCTCGACTTGGTT3' 5'TGGCAATACTGCTGGATGAG3' | |
| | | | | | | 93.6 | 73.7 | | |

Supplementary Table 2. Properties of ovarian cancer-specific alternative splicing (AS) variants. Epithelial ovarian cancer (EOC) associated splice events are presented in alphabetical order. First columns show gene symbol and gene name. Column 3 shows the ASE type and direction of the shift between normal and cancer tissue. Positive numbers indicate a shift to the larger isoform in cancer, negative numbers indicate a shift toward the shorter isoform in cancer. Column 4 describes the location and effect of the splicing event with respect to the reading frame. Column 5 gives an indication of the protein's function. Column 6 indicates whether the EOC-associated splicing pattern is likely cancer-specific (CS) or epithelium-specific (ES). Unavailable data are indicated as not determined (n. d.). Column 7 indicates conservation of the splice event between man and mouse. Columns 8 and 9 indicate the mean Ψ values in normal (n=25) and cancer tissue (n=21) respectively. The final column indicates the PCR primers used to detect the AS event.