**Supplemental Table S1:** Number of invasive EOC patients by study site

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Set** | **Study Site** | **Enroll-ment Years** | **Study Name** | **Follow-Up Method** | **Number (% by Set)** | **N Deaths (%)** | **Person-years** | **Median survival (days)** | **Median Follow-up (days)** |
| Set 1 | DOV | 2002-2005 | Diseases of the Ovary and their Evaluation | Standard US NCI SEER-registry follow up methods | 789 (18.4%) | 387 (49%) | 2755.37 | 1885 | 1398 |
| HAW | 1993-2008 | Hawaii Ovarian Cancer Case-Control Study | Standard US NCI SEER-registry follow up methods and review of the medical charts for additional treatment information | 56 (1.3%) | 24 (42.9%) | 242.01 | 2867 | 1896.5 |
| HOP | 2003-2009 | Novel Risk Factors and Potential Early Detection Markers for Ovarian Cancer | Medical records abstraction, the National Death Index, and/or Social Security Death Index | 357 (8.3%) | 206 (57.7%) | 1263.98 | 1553 | 1441 |
| LAX | 1989+ | Women's Cancer Program at the Samuel Oschin Comprehensive Cancer Institute | Annual chart abstraction and cancer registry updates | 248 (5.8%) | 162 (65.3%) | 1147.36 | 1642 | 1465 |
| MAC | 2000-2011 | Mayo Clinic Case-Only Ovarian Cancer Study | Patient contact and vital statistics | 130 (3.0%) | 61 (46.9%) | 477.23 | 2180 | 1123.5 |
| MAY | 2000-2011 | Mayo Clinic Ovarian Cancer Case-Control Study | Patient contact and vital statistics | 644 (15.0%) | 376 (58.4%) | 1970.93 | 1264 | 915.5 |
| MSK | 1997-2010 | Memorial Sloan-Kettering Cancer Center | Institutional databases and medical records | 131 (3.1%) | 42 (32.1%) | 267.68 | 1354 | 551 |
| NCO | 1999-2008 | North Carolina Ovarian Cancer Study | Social Security Death Index and North Carolina Central Cancer Registry every 18-24 months | 455 (10.6%) | 287 (63.1%) | 1997.38 | 1720 | 1535 |
| NEC | 1992-2003 | New England Case Control Study | Annual medical record abstraction and death record database updates | 615 (14.3%) | 306 (49.8%) | 3727.59 | 3233 | 3605 |
| NJO | 2002-2008 | New Jersey Ovarian Cancer Study | Linkage with the New Jersey State Cancer Registry | 100 (2.3%) | 24 (24%) | 191.93 | NA\* | 953.5 |
| ORE | 2007+ | Oregon Ovarian Cancer Registry | Cancer registry and electronic medical record reviews every 3 months | 72 (1.7%) | 16 (22.2%) | 221.03 | NA\* | 950 |
| POL | 2000-2003 | Polish Ovarian Cancer Case Control Study | Linkage with cancer registry | 127 (3.0%) | 79 (62.2%) | 422.27 | 1242 | 1242 |
| UCI | 1993-2005 | University California Irvine Ovarian Study | Linkage with cancer registry and death records databases | 160 (3.7%) | 77 (48.1%) | 704.94 | 2711 | 2636.5 |
| USC | 1992-2009 | Los Angeles County Case-Control Studies of Ovarian Cancer | Standard US NCI SEER-registry follow up methods | 409 (9.5%) | 210 (51.3%) | 1516.83 | 1661 | 1184 |
| Set 2 | AUS | 2002-2006 | Australian Ovarian Cancer Study/Australian Cancer Study | Medical records reviewed at 6-12 month intervals | 499 (28.6%) | 353 (70.7%) | 1966.88 | 1400 | 1502 |
| MAL | 1994-1999 | MALignant OVArian cancer | Danish Civil Registration System and Danish Register of Causes of Death | 208 (11.9%) | 164 (78.8%) | 881.97 | 1013 | 1038.5 |
| POC | 1998-2006 | Polish Ovarian Cancer Study | Institutional medical records, linkage to vital statistics database of the Polish Ministry of Administration and Internal Affairs | 39 (2.2%) | 26 (66.7%) | 147.05 | 1200 | 1350 |
| RMH | 1993-1995 | Royal Marsden Hospital Ovarian Cancer Study | Death certification through the NHS Information Centre for Health and Social Care (England and Wales) | 62 (3.6%) | 30 (48.4%) | 314.93 | 2438 | 1873 |
| SEA | 1998+ | Study of Epidemiology and Risk Factors in Cancer Heredity | Death certification through the NHS Information Centre for Health and Social Care (England and Wales) | 609 (34.9%) | 320 (52.5%) | 1893.34 | 1656 | 1777 |
| UKO | 2006-2010 | United Kingdom Ovarian Cancer Population Study | NHS Information Centre for Health and Social Care (England and Wales) and Central Services Agency (Northern Ireland) | 327 (18.8%) | 134 (41%) | 1146.81 | 1948 | 1609 |

**\*less than 50% events occurred**

**Supplemental Table S2:** Results of Set 1 single variant analysis, for variants with P<5.0E-5. Analysis was adjusted for age, stage, grade, histology, site and PCs, and includes all variants genotyped in Set 1 (including variants non-overlapping with Set 2).

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **rsID** | **Chr** | **BP Position\*** | **Gene** | **HR** | **95% LB** | **95% UB** | **P-value** | **MAF** | **Content** | **Function** | **Included Set 2** |
| rs2484246 | 1 | 64909690 | *UBE2U,CACHD1*† | 1.23 | 1.12 | 1.35 | 2.04E-05 | 0.1100 | Custom†† |  | No |
| rs2484247 | 1 | 64910985 | *UBE2U,CACHD1*† | 1.23 | 1.12 | 1.35 | 2.43E-05 | 0.1101 | Custom†† |  | No |
| rs305531 | 1 | 64912566 | *UBE2U,CACHD1*† | 1.23 | 1.12 | 1.35 | 2.15E-05 | 0.1107 | Custom†† |  | No |
| rs188613 | 1 | 64913601 | *UBE2U,CACHD1*† | 1.24 | 1.13 | 1.36 | 1.70E-05 | 0.1102 | Custom†† |  | No |
| rs305534 | 1 | 64914357 | *UBE2U,CACHD1*† | 1.24 | 1.12 | 1.36 | 1.59E-05 | 0.1103 | Custom†† |  | No |
| rs305535 | 1 | 64914437 | *UBE2U,CACHD1*† | 1.23 | 1.12 | 1.35 | 2.78E-05 | 0.1097 | Custom†† |  | No |
| rs305538 | 1 | 64916457 | *UBE2U,CACHD1*† | 1.23 | 1.12 | 1.35 | 2.46E-05 | 0.1101 | Custom†† |  | No |
| rs305544 | 1 | 64918776 | *UBE2U,CACHD1*† | 1.23 | 1.12 | 1.35 | 2.72E-05 | 0.1100 | Custom†† |  | No |
| rs186256 | 1 | 64920558 | *UBE2U,CACHD1*† | 1.23 | 1.12 | 1.35 | 2.33E-05 | 0.1100 | Custom†† |  | No |
| rs305541 | 1 | 64921341 | *UBE2U,CACHD1*† | 1.23 | 1.12 | 1.35 | 2.27E-05 | 0.1104 | Custom†† |  | No |
| rs305551 | 1 | 64923227 | *UBE2U,CACHD1*† | 1.24 | 1.12 | 1.36 | 1.79E-05 | 0.1097 | Custom†† |  | No |
| rs305550 | 1 | 64923647 | *UBE2U,CACHD1*† | 1.23 | 1.12 | 1.35 | 2.66E-05 | 0.1090 | Custom†† |  | No |
| rs305545 | 1 | 64926761 | *UBE2U,CACHD1*† | 1.23 | 1.11 | 1.35 | 3.99E-05 | 0.1083 | Custom†† |  | No |
| --- | 2 | 168114435 | *XIRP2* | 13.49 | 5.54 | 32.87 | 4.55E-05 | 0.0006 | Standard | Non-synonymous | Yes |
| rs7642051 | 3 | 8301600 | *LMCD1-AS1* | 1.15 | 1.08 | 1.22 | 4.10E-06 | 0.4570 | Standard | IBD | No |
| rs11915398 | 3 | 119212417 | *POGLUT1* | 1.49 | 1.26 | 1.77 | 1.18E-05 | 0.0274 | Custom§ |  | No |
| rs16829878 | 3 | 119212998 | *POGLUT1* | 1.53 | 1.29 | 1.81 | 4.74E-06 | 0.0272 | Custom§ |  | No |
| rs57168946 | 3 | 119236104 | *TIMMDC1* | 1.48 | 1.25 | 1.75 | 2.34E-05 | 0.0267 | Standard | Non-synonymous | Yes |
| rs17170878 | 7 | 147886864 | *CNTNAP2,MIR548T* | 1.16 | 1.09 | 1.25 | 1.72E-05 | 0.2216 | Custom§§ |  | No |
| rs144809355 | 9 | 35704339 | *TLN1* | 7.88 | 3.72 | 16.70 | 4.79E-05 | 0.0008 | Standard | Non-synonymous | Yes |
| rs10770032 | 11 | 9432316 | *IPO7* | 1.14 | 1.07 | 1.21 | 3.58E-05 | 0.3392 | Standard | IBD | No |
| rs140703308 | 14 | 24975382 | *CMA1* | 0.13 | 0.03 | 0.54 | 3.59E-05 | 0.0014 | Standard | Non-synonymous | Yes |
| rs17740607 | 15 | 50555544 | *HDC* | 0.81 | 0.74 | 0.90 | 3.10E-05 | 0.1032 | Standard | Non-synonymous | Yes |
| rs139874813 | 15 | 80191338 | *ST20* | 4.07 | 2.39 | 6.93 | 2.34E-05 | 0.0016 | Standard | Non-synonymous | Yes |

Acronyms: BP=base pair, HR=hazard ratio, LB=lower bound, UB=upper bound, MAF=minor allele frequency, IBD=identity by descent

\*Based on Genome Assembly GRCh37/hg19

†Region is intergenic, between *UBE2U* and *CACHD1*; other variants located within the annotated gene region.

†† Selected based on suggested regional association with serous ovarian cancer survival time in meta-analysis of existing data.

§ Selected as a tagging variant to nearby candidate gene *TIMMDC1*encodingtranslocase of inner mitochondrial membrane domain containing 1.

§§ Selected based on suggested association with risk of serous ovarian cancer in meta-analysis of existing data.

**Supplemental Table S3:** Results of Set 1 gene-level analysis with P<1.0E-4 based on the burden test. Analysis was adjusted for age, stage, grade, histology, site and PCs. CMAF=combined (sum) minor allele frequency across all variants in the gene.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Chr** | **Gene** | **N variants** | **CMAF** | **Burden P** | **SKAT P** |
| 1 | *SUCO* | 33 | 8.2612 | 7.81E-05 | 4.48E-03 |
| 3 | *POGLUT1* | 6 | 0.8495 | 7.10E-06 | 8.33E-06 |
| 14 | *ATG2B* | 34 | 1.7512 | 5.16E-05 | 3.23E-02 |
| 15 | *ST20* | 2 | 0.4358 | 2.32E-05 | 2.32E-05 |
| 17 | *DLG4* | 6 | 0.3719 | 8.70E-05 | 1.15E-03 |