**Online-Only Supplemental Material**

**Study population and methods**

The study population was based on the following cohorts: the ‘Washington Country, MD Study ‘Give us a clue to cancer and heart disease’ (CLUE) II, European Prospective Investigation into Cancer and Nutrition (EPIC), the Finnish Maternity Cohort (FMC), the Nurses’ Health Study (NHS), NHS II, the Harvard Women’s Health Study (WHS) and the New York University Women’s Health Study (NYUWHS) (Table S1). In all cohorts, cases were individually matched to two (CLUE II, EPIC, NYUWHS, WHS) or up to three controls (FMC, NHS, NHS II) on age, date (or follow-up time in EPIC), menopausal status at blood collection and day or phase of menstrual cycle in premenopausal women (with exception of the FMC, which was restricted to currently pregnant women).

*Selection of case patients and control participants*

EOC cases in the participating cohorts are ascertained by (1) self-report with subsequent medical record confirmation (2) and/or linkage to cancer registries that in each study generally is estimated to be >95% complete. Analyses were limited to women diagnosed with invasive ovarian carcinomas and with data on histologic subtype.

*Data on tumor characteristics*

The OC3 database contained complete information on histomorphology: 50% of tumors were of serous histology (n=667), 15% mucinous (n=193), 12% endometrioid (n=166), 5% clear cell (n=61) and 18% other (malignant epithelial neoplasms, carcinoma, malignant mixed Müllerian or malignant Brenner tumors; n=244). Information on tumor stage was 82% complete and cases with local disease were classified as low stage (23%), whereas cases with regional or metastatic disease were classified as high stage (77%). Data on grade were provided by CLUE II, EPIC, NHS, NHS II, WHS and NYUWHS, and were available for 36% of cases. Well differentiated tumors were classified as low grade (12%); moderately and poorly/undifferentiated tumors as high grade (88%). In the absence of data on molecular genetics and immunohistochemistry, information on histology and grade can be used to classify tumors as put forward by Kurman and colleagues [[1](#_ENREF_1)].

*Assessment of reproductive factors and lifestyle characteristics*

Data on reproductive and lifestyle characteristics at blood collection were collected from participating cohorts. Available data from each cohort were sent to the coordinating center at the Brigham and Women’s Hospital for centralized harmonization. Information was requested for (1) general data (e.g., ID, matched Case-Set ID, matching variables, sample types and laboratory batches), (2) lifestyle related data (e.g., BMI, smoking status) and (3) reproductive and hormone-related data (e.g., parity, menopausal status at blood collection, phase of menstrual cycle in premenopausal women, OC or postmenopausal hormone therapy (HT) use).

To account for potential interference of exogenous hormones with circulating concentrations [[2](#_ENREF_2)], women using OC or HT at the time of blood collection were either: (1) excluded a priori (e.g., EPIC, NHS II premenopausal) or (2) cases and controls were matched on HT use at blood donation (e.g., CLUE II, NHS, NHS II postmenopausal or WHS). It was presumed that FMC participants (pregnant at blood collection) were not using exogenous hormones at the time of blood donation.

*Laboratory methods*

All participating studies used a nested case-control design, with assays arranged so that case-control sets were measured in the same batch and technicians performing the assays were blinded to case-control status and quality control samples. Hormone concentrations were measured in serum in EPIC (except Sweden), FMC and the NYUWHS; heparin plasma specimens were used in CLUEII and the NHS and NHS II; and EDTA plasma was used for Harvard WHS and Swedish participants from the EPIC cohort. The assays used, along with intra- and interbatch coefficients, are presented in Table S2. Free testosterone was calculated for CLUE II, EPIC, FMC and NYUWHS, based on measured concentrations of testosterone and SHBG, with albumin assumed to be a constant 40g/L, according to the mass law of action [[3](#_ENREF_3)].

*Statistical analyses*

Outliers were identified and removed using the ESD approach [[4](#_ENREF_4)]. As biomarker data deviated from the normal distribution, we applied the log2 transformation to limit heteroscedasticity. To account for differences in study-specific mean concentrations and a slightly different case-control ratio between studies (1:2 vs. 1:3), data were standardized based on the cohort-specific mean concentrations in controls (Table S3).

Statistical analyses were conducted using a two-stage approach (I) using random effect meta- analyses and (II) an aggregated data approach based on individual participant data. First, the log2 relative risks were calculated from conditional logistic regression models within each cohort and pooled using DerSimonian and Laird random effects models (random effects pooling, [[5](#_ENREF_5)]). Heterogeneity between cohort-specific effect estimates was tested by DerSimonian and Lairds Q statistic [[5](#_ENREF_5)] and conducted for all analyses (invasive EOC, by histologic subtype, stage, grade, type I / type II model, menopausal status at blood donation, age at diagnosis and exclusion of women diagnosed within 2 years after blood donation). NHS, NHS II and WHS data were combined for meta-analysis, as these studies were evaluated together in a previous publication [[6](#_ENREF_6)], and specimens were analyzed in the same laboratory. Based on the relatively small case numbers in some cohorts (e.g., CLUE II: cases n=46) meta-analyses were performed in the crude model (accounting for matching factors), and limited to cohorts contributing more than 5 cases for any given subgroup analyses.

Second, in the aggregated approach, individual participant data from all cohorts were pooled and a combined effect estimate was calculated from a conditional logistic regression model [[7](#_ENREF_7)]. The original matched sets were retained for all statistical analyses.

Data analysis was conducted using the Unix SAS system to access data remotely on the external servers at the study coordinating center at Brigham and Women’s Hospital (SAS Statistical Software, version 9.3 (SAS Institute, Cary NC, USA)). P-values<0.05 were considered as statistically significant; all statistical tests and corresponding p-values were two-sided. Forest plots were prepared using the R software (package ‘rmeta’, function ‘forestplot’) version 2.15.2 (R Core Team 2014).

**References**

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