SUPPLEMENTARY TABLE LEGENDS

Supplementary Table 1: Numbers of controls and EOC cases by genotyping array and country from population-based studies. The "cases" column (column E) is a total of the histotypes in columns F-K. LMP = low malignant potential, HGSOC = high-grade serous ovarian cancer, ENOC = endometrioid ovarian cancer, CCOC = clear cell ovarian cancer, MOC = mucinous ovarian cancer.

Supplementary Table 2: Numbers of unaffected *BRCA1*/*2* carriers and carriers diagnosed with EOC, by CIMBA study.

Supplementary Table 3: Previously identified genomic regions associated with EOC. Lookups are presented for the variant's association with its most strongly associated EOC histotype from the OCAC. Lookups are also presented from the present HGSOC meta-analysis of OCAC, UKBB and *BRCA1*/*2* carriers, and its component parts (associations from OCAC and UKBB combined, associations from *BRCA1* carriers, and associations from *BRCA2* carriers).
Chr = chromosome. Positions are on build 38. SNP = rsID of the most strongly associated variant with "best histotype". Alleles = reference/effect alleles. EAF = effect allele frequency. RR = relative risk (per effect allele). CI = confidence interval. P = P-value for association with HGSOC. P_{het} = P-value for heterogeneity between the general population OR (OCAC and UKBB meta-analysis, column U) and the PV carrier HRs (*BRCA1* PV carriers, column Z; *BRCA2* PV carriers, column AF).

SNPs and positions (columns E-F) highlighted in yellow are most strongly associated with HGSOC in OCAC that did not replicate ($P<5x10^{-8}$) in the OCAC+UKBB+CIMBA meta-analysis (columns N and S).

Histotypes: NMOC = non-mucinous, HGSOC = high-grade serous, LGSOC = low-grade serous, MOC = mucinous, CCOC = clear cell, EnOC = endometrioid.

* Previously identified through meta-analysis of OCAC and CIMBA. ** Previously identified through multi-cancer meta-analysis. *** When combining result with most recent results from CIMBA (unpublished).

Supplementary Table 4: Novel associations by major analysis units (OCAC, UKBB, *BRCA1* carriers and *BRCA2* carriers).

Positions are on build 38. EAF = effect allele frequency. OR = odds ratio per effect allele. HR = hazard ratio per effect allele. CI = confidence interval. P = P-value for association. UKBB did not contribute associations for rs1013698558 (chr6:53554782:A:T). * HRs were estimated but had large estimated standard errors resulting in wide CIs – these associations were used in the meta-analysis between OCAC, UKBB and CIMBA, but contributed little as the inverse variance weights were extremely small.

Supplementary Table 5: Further details for eight novel variants associated with HGSOC risk.

Positions are on build 38. Gene descriptions are taken from dbSNP[87].

Phenoscanner[102-104] and PheWeb[105] are lookups of relevant associations for these

variants/genes. GTEx[77] gene expression data is reported for human reproductive tissues with TPM (transcripts per million) > 5. eQTLGen[106,107] lookups for cis- and trans-eQTLs for variants and genes were performed.

Supplementary Table 6: List of credible causal variants (CCVs) at each novel region. Sentinel variants are highlighted in green. These data are presented graphically in Supplementary Figure 2.

Supplementary Table 7: List of variants contributing to the polygenic models (PGMs). Positions are on build 38. Weights are given for five PGMs and are per effect allele. Instances in which weights are not present (NA) means that that variant does not contribute to that PGM. The weights are taken from the OCAC, UKBB and CIMBA meta-analysis effect size estimates with the hyperparameters applied. Four of the eight variants found in the discovery GWAS were directly included in the 64,518 variant PGM (rs6979 chr16:67657765, rs143094271 chr17:7559785, rs78378222 chr17:7668434 and rs62107113 chr19:29797136, highlighted in green in the table).

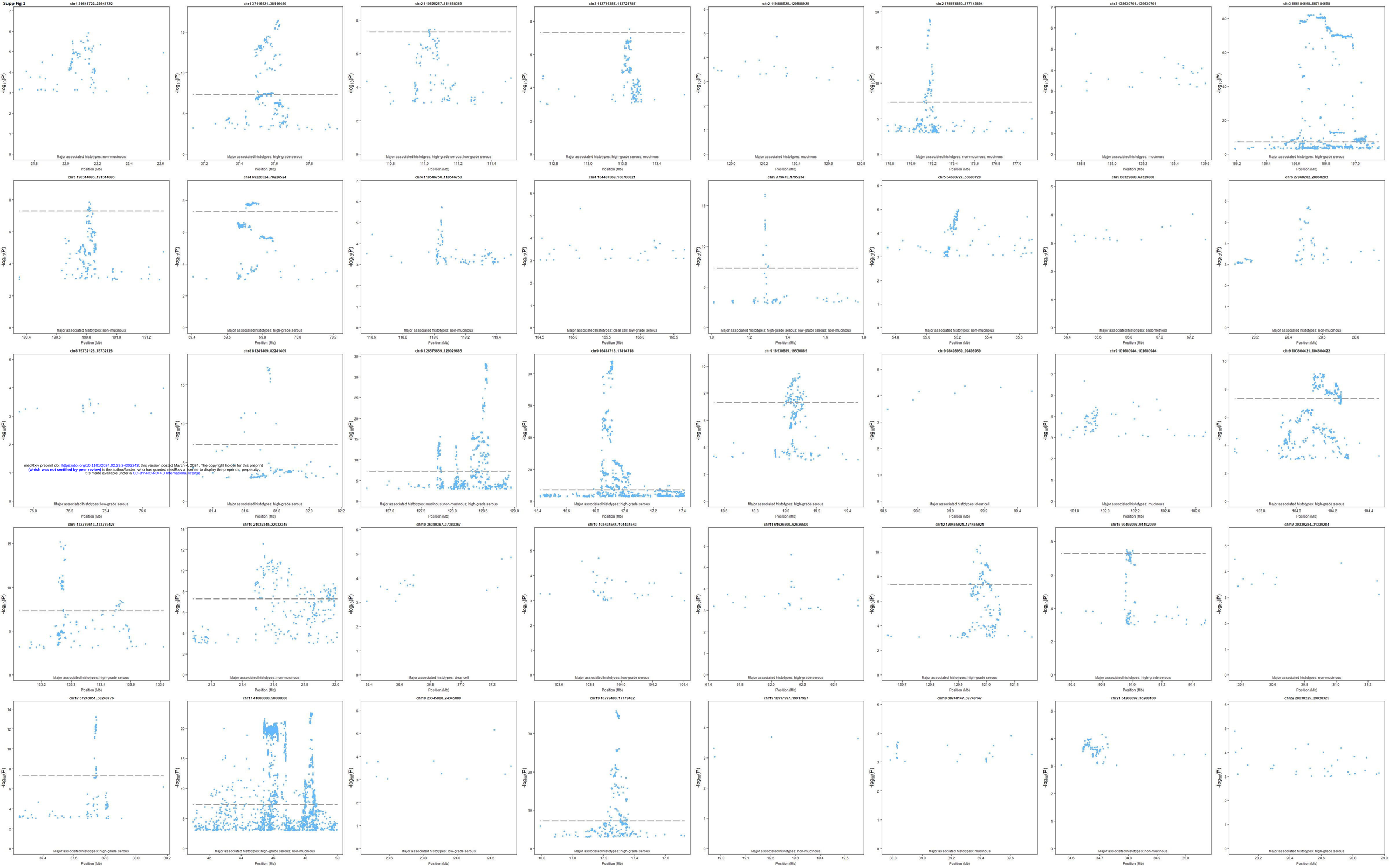
Supplementary Table 8: Risk reclassification based on different polygenic scores for *BRCA2* carriers. Lifetime risks were categorized as lower risk (lifetime risk below 10%) or higher risk (10% or greater). The PGM_{64518} and PGM_{400} were compared with the 36 SNP PGS currently used in the CanRisk prediction algorithm.

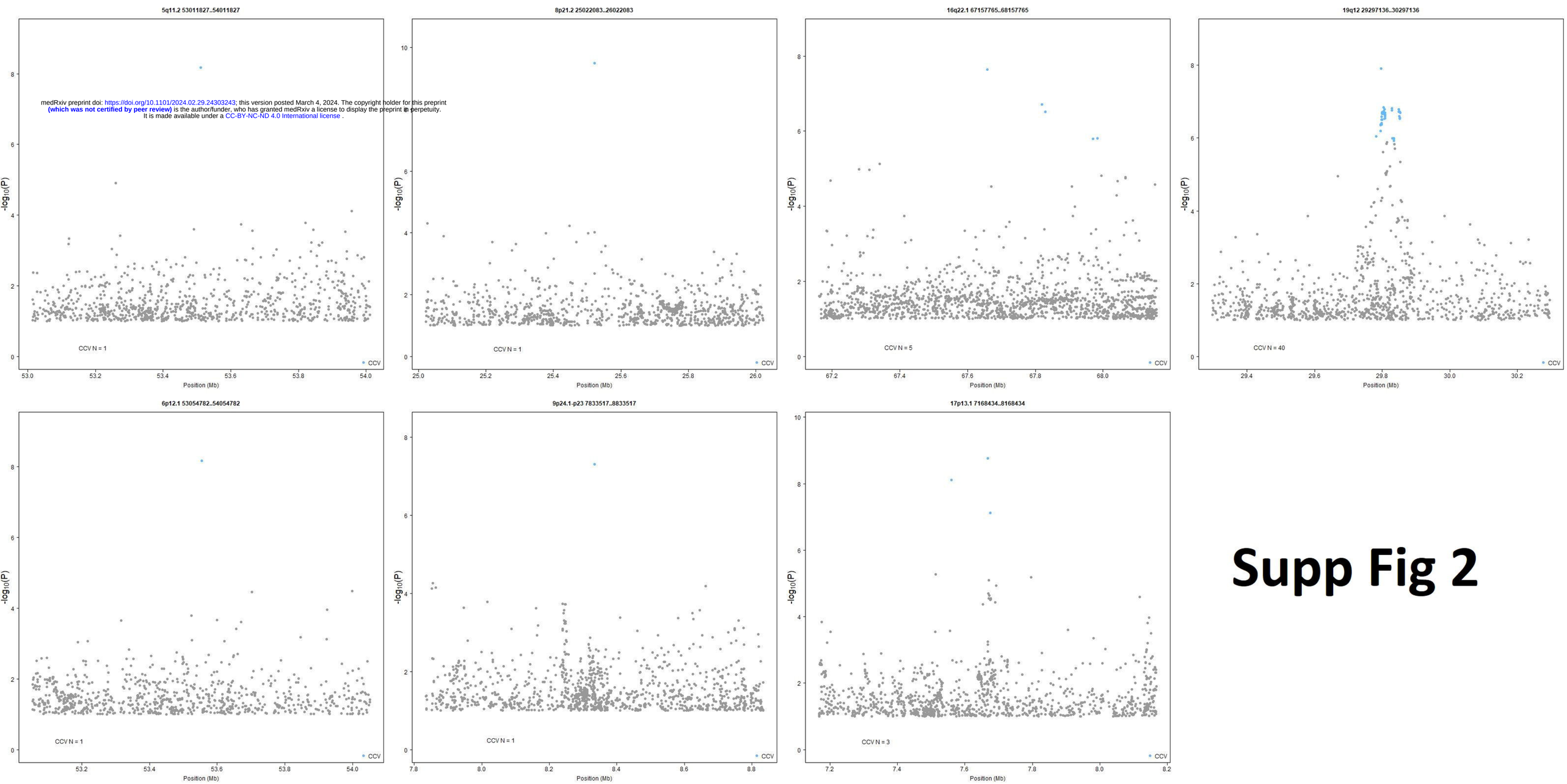
SUPPLEMENTARY FIGURE LEGENDS

Supplementary Figure 1: Regional association plots for 40 genomic regions previously associated with any EOC histotype. Regions are described in Supplementary Table 3.

Supplementary Figure 2: Regional association plots for seven novel genomic regions associated with HGSOC. Credible causal variants (CCVs) are highlighted in blue. Lists of CCVs are presented in Supplementary Table 6.

Supp Fig 1





Supp Fig 2