

Copy Number Variation and Ovarian Cancer Risk—Letter

Georgia Chenevix-Trench



I am writing regarding the conclusion of this article by Reid and colleagues (1): “Since the initiation of this study, SNP array data from the Oncoarray (3) have become available and present opportunity for future CNV studies.” Most of the authors of this article are members of

QIMR Berghofer Medical Research Institute, Brisbane, Queensland, Australia.

Corresponding Author: Georgia Chenevix-Trench, QIMR Berghofer Medical Research Institute, 300 Herston Road, Brisbane, Queensland 400, Australia. Phone: 617-3362-0390; E-mail: georgiaT@qimr.edu.au

Cancer Epidemiol Biomarkers Prev 2020;29:1278

doi: 10.1158/1055-9965.EPI-19-0944

©2020 American Association for Cancer Research.

the Ovarian Cancer Association Consortium (OCAC) and know that the Oncoarray data (based on over 30,000 cases and 18,000 controls) have been available to OCAC members since 2014. Nonetheless, they did not apply to OCAC for these data until after July 2018, once they had submitted the article that you subsequently published (on approximately 3,500 cases and controls). In the era of large consortia, it is very unfortunate that *CEBP* still publishes small association studies that do not seek to replicate the findings in the much bigger sample sizes available.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Received September 3, 2019; revised February 2, 2020; accepted February 4, 2020; published first June 1, 2020.

Reference

1. Reid BM, Permuth JB, Chen YA, Fridley BL, Iversen ES, Chen Z, et al. Genome-wide analysis of common copy number variation and

epithelial ovarian cancer risk. *Cancer Epidemiol Biomarkers Prev* 2019; 28:1117–26.