Prevalence of deleterious mutations (DMs) and variants of unknown significance (VUS).

The majority of the non-BRCA1/2 DMs were consistent with the family cancer history and would result in a clinical management change for patients and/or family members.

The prevalence of VUS vary by gene and by ethnicity, and nearly 50% of individuals tested for the 29-gene panel had ≥1 VUS as the only finding.

Central collection of data on multi-gene tested patients should be undertaken to accelerate the development of effective management guidelines and to improve outcomes for all-risk individuals.

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