CONCLUSIONS

- Among nearly 100,000 women tested clinically for hereditary breast cancer risk, multiple-gene panel testing identified a wide spectrum of PVs in genes associated with breast cancer risk, approximately half of which were in genes other than BRCA1 or BRCA2.
- Eight genes were associated with a 2- to 6-fold increase in breast cancer risk and showed significant associations for CDH1 (Table 2).
- Relative risk estimates for breast cancer for these genes ranged from approximately 2-fold (ATM) to 6-fold (BRCA1).

OUTLOOK

- These results inform the estimation of BC risk for mutation carriers of diverse high-risk genes.

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REFERENCES


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Additional analysis with analogous models to predict lobular breast cancer risk in (40.6%).

- Among women with a personal diagnosis of breast cancer, 10%, 20%, 30%, and 40% of any one pathogenic variant were in BRCA1 or BRCA2.

- Eight genes were associated with a 2- to 6-fold increase in breast cancer risk.

- These results inform the estimation of BC risk for mutation carriers of diverse high-risk genes.