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RESEARCH SUMMARY

BreastNext can Identify More Patients with Hereditary Breast Cancer to Guide Medical Management

NOVEMBER 2018

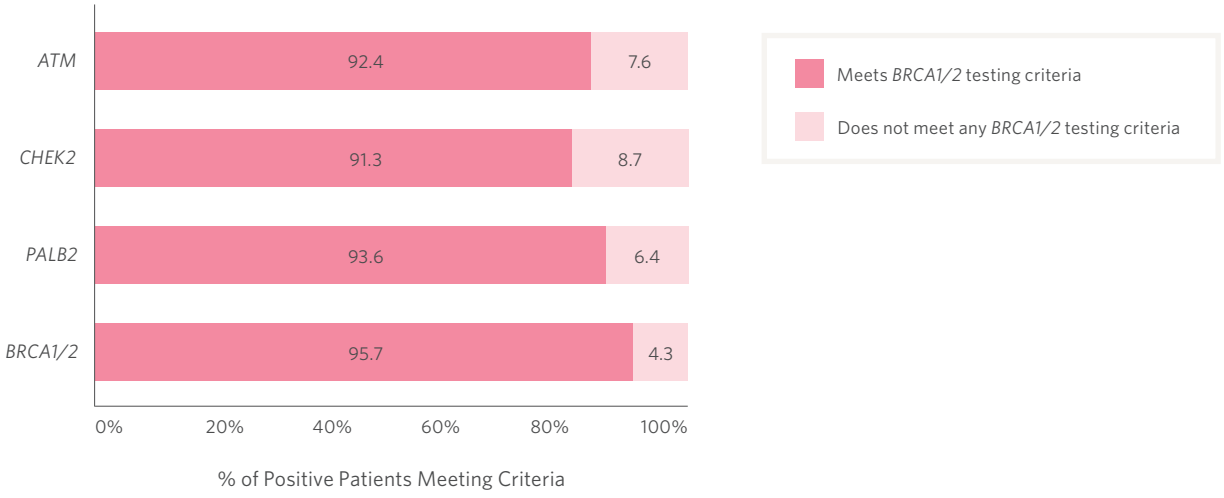
BreastNext, a 17-gene hereditary breast cancer panel, increases identification of clinically actionable results in patients with breast cancer.

Studies support inclusion of moderate risk breast cancer genes when testing patients at-risk for hereditary breast cancer

KEY STUDY FINDINGS[1,2]

- A large-scale exome sequencing study of >11,000 breast and ovarian cancer patients confirmed *ATM*, *CHEK2*, and *PALB2* as moderate risk breast cancer genes.[1]
- Based on a study of >89,000 breast cancer patients undergoing multigene panel testing, National Comprehensive Cancer Network (NCCN®) (v2.2017) *BRCA1/2* testing criteria can help to identify patients with *ATM*, *CHEK2*, or *PALB2* mutations.[2,5]

Overall Clinical Sensitivity of NCCN® (v.2.2017) *BRCA1/2* Testing Criteria by Gene



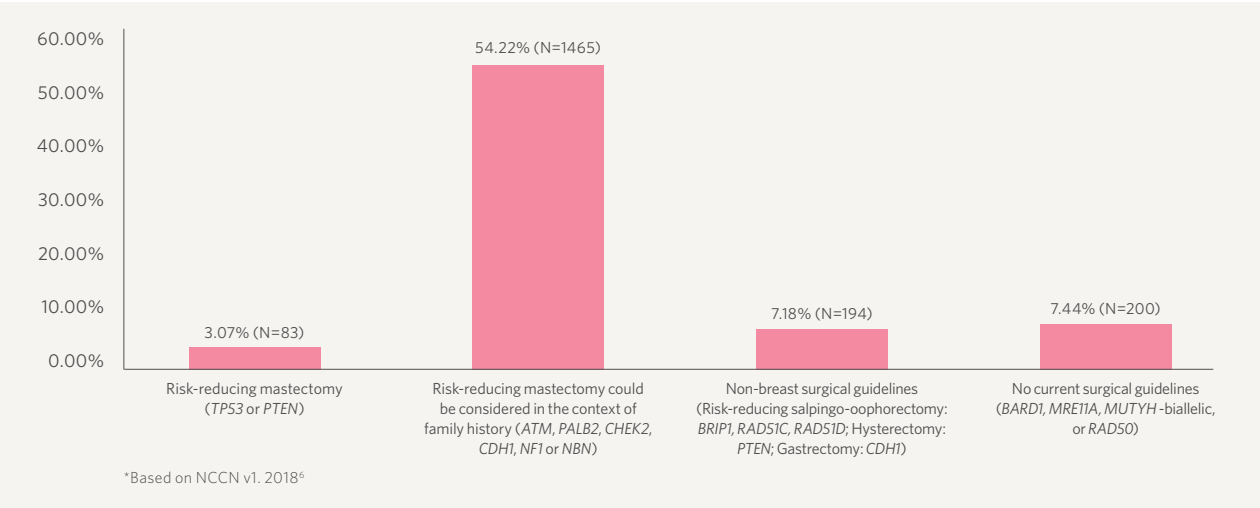
Studies show that multigene panels (MGP) identify more patients with hereditary cancer allowing for personalized medical management.

KEY STUDY FINDINGS[3,4]

- Retrospective review of >86,000 breast cancer patients indicated that compared to a 5-gene breast cancer panel, the positive rate increased by 25% with BRCAplus (8 genes) and by 44% with BreastNext (17 genes). This suggests that larger MGP increase the identification of patients with hereditary breast cancer.[3]

- Expanding testing beyond *BRCA1/2* identifies more patients who may benefit from risk reducing surgical options for breast and other cancers.[4]

Surgically Actionable Findings (beyond *BRCA1/2*)*



*Based on NCCN v1. 2018[6]

POINTS FOR YOUR PRACTICE

- Larger multigene panels, like BreastNext, can help you identify more patients with hereditary breast cancer.
- Several genes, including *ATM, CHEK2*, and *PALB2* have been established as genes associated with a moderately increased risk for breast cancer.
- Maximizing identification of patients with hereditary breast cancer is important for early detection and prevention.

REFERENCES

1. Lu *et al.* Association of breast and ovarian cancers with predisposition genes identified by large-scale sequencing. JAMA Oncol (2018).
2. Horton C *et al. BRCA1/2* testing criteria offer high clinical sensitivity for *ATM, PALB2* and *CHEK2* carriers in a multigene panel cohort. Poster Presentation. ACMG 2018.
3. Horton C *et al.* Germline mutation likelihood in breast cancer patients: Navigating the nuances of multi-gene panel testing. Poster Presentation. MBCC 2018.
4. Palaniappan S *et al.* Multi-gene panel testing increases yield of surgically-actionable results among breast cancer patients. Poster Presentation. ASBrS 2018.
5. National Comprehensive Cancer Network®. NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines®). Genetic/Familial High-Risk Assessment: Breast and Ovarian. Version 2.2017. Available from nccn.org.
6. National Comprehensive Cancer Network®. NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines®). Genetic/Familial High-Risk Assessment: Breast and Ovarian. Version 1.2018. Available from nccn.org.