Breast Cancer Polygenic Risk Score Test
AnteBC

AnteBC is a genetic test that assesses a woman's risk of developing breast cancer using polygenic risk score (PRS) technology. It is a clinical tool that estimates the breast cancer risk level of an individual for precise and efficient prevention and screening. Its aim is to reduce breast cancer morbidity and mortality. AnteBC test is recommended for women between the ages of 30 and 75.

AnteBC is a clinical test registered as a CE-marked medical device (in vitro diagnostics, IVD) in the EUDAMED database (UDI-DI: 04745010362019), in the Estonian Medical Devices Database (EMDDB code: 14726), and the UK MHRA Registry (GMDN code: 59918).

The test results provide information about the individual's polygenic risk level for breast cancer. This includes a breast cancer-specific PRS value, the absolute risk for breast cancer in the next 10 years, and the relative risk in comparison to other women in the same age group and population on average.

Depending on the application, the test report may include individual clinical recommendations to reduce the risk of developing breast cancer such as:

- What age the individual should start breast cancer screening and how
- Whether the individual should take additional measures to prevent breast cancer
- What possible changes and symptoms regarding her breasts should the individual focus on.

Aim of the AnteBC Test

The purpose of the AnteBC test is to reduce the risk of premature mortality from breast cancer. It provides more precise recommendations for breast cancer screening and additional preventive measures. Breast cancer risk stratification increases the precision and efficiency of methods in breast cancer prevention. The AnteBC test incorporates PRS technology into screening programs, enabling targeted recommendations for more efficient primary and secondary prevention.

AnteBC Test Methodology

For the PRS calculation, AnteBC uses the patient’s DNA data from genotyping and summarizes the impact of 2803 breast cancer-related single nucleotide polymorphisms (SNPs).

To develop the AnteBC test, different PRSs and their risk differentiation estimations were validated using anonymous data from the Estonian Biobank and UK Biobank. Based on large-scale genetic data, various risk prediction models published in the international scientific literature were compared. The prediction accuracy of the best-performing model was evaluated on independent data and developed further for the test (1, 2). The PRS underlying AnteBC is adapted and independently validated for practical use based on the report by Mavaddat et al. (3).
The test is based on genome-wide association studies of patients and study participants of primarily European ancestry. However, the test is adapted to other ethnicities based on the analyses of risk performance in the ethnically diverse UK Biobank data.

AnteBC has been developed by the health-tech company Antegenes and is performed by Antegenes’ medical lab.

AnteBC Test Limitations

- AnteBC cannot be used to diagnose breast cancer.
- High risk does not necessarily mean that the patient will develop breast cancer during her lifetime.
- Moderate or lower risk does not necessarily mean that the patient will never develop breast cancer during her lifetime.
- AnteBC test results are individual and patient specific. The AnteBC test does not assess the risk for the patient's family members or relatives. The inheritance pattern of PRS is complex and each person has to be tested separately.
- AnteBC does not analyse rare monogenic pathogenic variants in genes that significantly increase the risk of breast cancer, such as *ATM, BARD1, BRCA1, BRCA2, CDH1, CHEK2, NF1, PALB2, RAD51C, RAD51D, TP53*, and others. If a woman's biological relative has a monogenic pathogenic variant in these genes, or if a woman has several breast or ovarian cancer cases in her family, Antegenes recommends additional counselling and testing for such monogenic variants.
- AnteBC test is based on the most recent scientific data, which may be supplemented and/or changed in the future if additional information becomes available. The field of genetics is constantly evolving, which may lead to changes in risk assessments over time, changes in test selection, and clinical recommendations.
- Different polygenic risk scores predicting risks of the same trait may give different estimates of the individual's risks due to differences in the genetic variants included in these models and their weights.
- The results of this test should be applied in combination with other relevant clinical data. In addition to genetic predisposition, other risk factors influence the risk of developing breast cancer.

Getting started with AnteBC Test

To perform the test, a DNA sample must be taken using a buccal swab or saliva kit. This is an easy and safe procedure. The buccal swab or saliva collection kit is convenient to use independently at home or at a medical facility. Detailed instructions are included in each kit.
The sample is sent to the Antegenes laboratory via organized delivery.

Based on patient data, individual test reports are generated. Reports are available only for an individual or for her doctor if a test is ordered by a healthcare professional.
Genetic data is managed, stored, and protected safely within Antegenes' server according to GDPR and healthcare data regulations.
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AnteBC test can also be used in healthcare facilities only as CE-marked software as medical device if genotyping or sequencing is performed by an on-site laboratory.

References

1. Padrik P, Puustusmaa M, Tõnisson N, Kolk B, Saar R, Padrik A, et al. Implementation of Risk-Stratified Breast Cancer Prevention With a Polygenic Risk Score Test in Clinical Practice. Breast Cancer (Auckl). 2023;17:11782234231205700.
2. Tasa T, Puustusmaa M, Tõnisson N, Kolk B, Padrik P. Precision Breast Cancer Screening with a Polygenic Risk Score. medRxiv. 2020:2020.08.17.20176263.
3. Mavaddat N, Michailidou K, Dennis J, Lush M, Fachal L, Lee A, et al. Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. Am J Hum Genet. 2019;104(1):21-34.