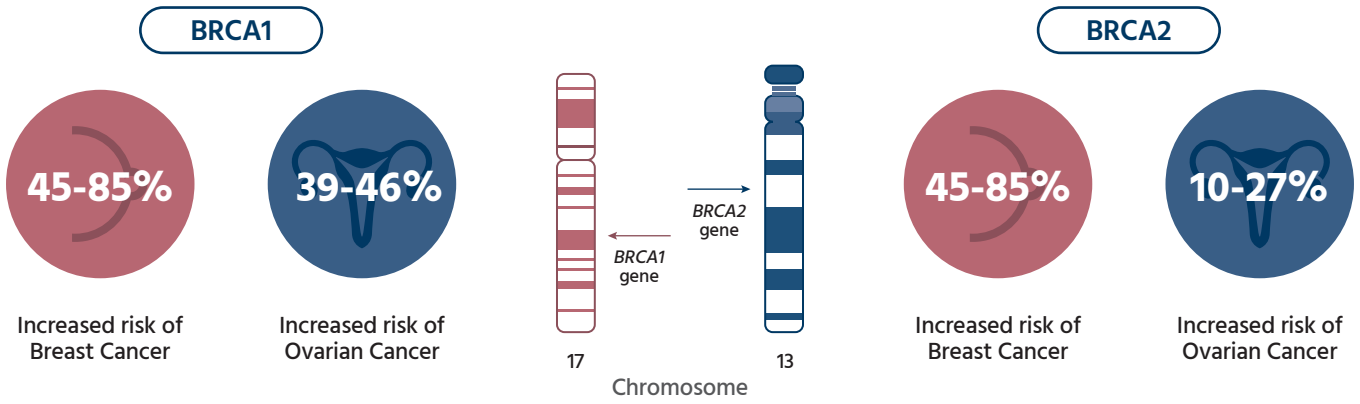
Know Your Risk, Empower Yourself with Women's Cancer Panel Test

Women's Cancer Panel

What are the BRCA genes? [1]



BRCA1 and BRCA2 are the two most common genes associated with hereditary breast and ovarian cancers.
Certain variants in these genes can increase the risk of a person developing not only breast and ovarian cancers but also **prostate, pancreatic, fallopian tube, peritoneal cancers and melanoma.**

Mutation in BRCA1/2 is more common than what you may think. The frequency of BRCA1/2 mutation found in both men and women is about 1 in 300 to 1 in 800.

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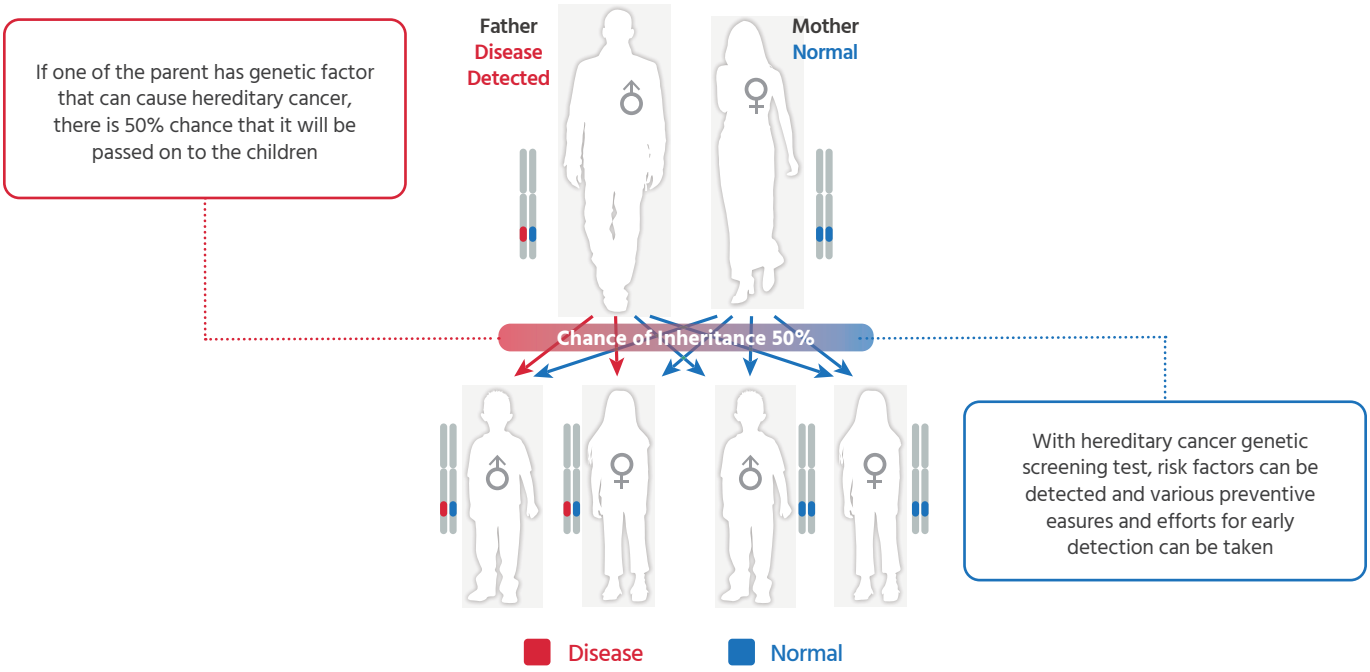

This test is a NGS-based test that analyses the genetic variants that cause hereditary breast cancer and ovarian cancer. It is estimated approximately 5-10% of all hereditary breast cancer and hereditary ovarian cancer are caused by inherent cancerous factors.
Both men and women can inherit the BRCA genes change and pass it on to their children.

1 ACOG (The American College of Obstetricians and Gynecologists) : https://www.acog.org/womens-health/faqs/brca1-and-brca2-mutations

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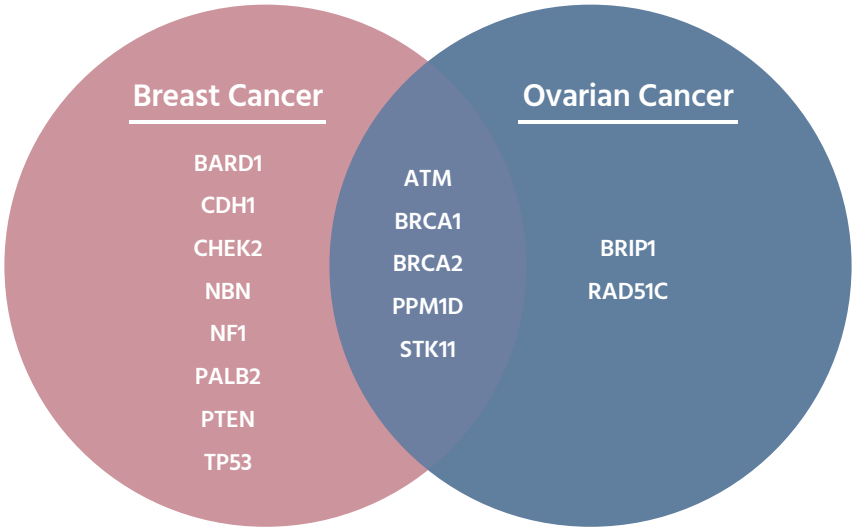

This test provides comprehensive analysis of the genetic variants that cause hereditary cancer with **13 relevant genes related to Breast Cancer** and 7 **relevant genes related to Ovarian Cancer.**

Service features

Test	Women's Cancer Panel	**Code**	ON001
Specimen	EDTA WB 3 ml	**TAT**	12 days
Method	NGS (Next Generation Sequencing)	**Sample Storage**	Room temperature (Refrigerated is recommended.)
Test description	This test analyses 15 genes related to Breast and Ovarian Cancer. Anyone with personal or family history of Breast Cancer, Ovarian Cancer, or Pancreatic Cancer is recommended to take this test for the diagnosis of the probability of incidence of hereditary Breast & Ovarian Cancer.		
Caution & Limitation	• This test is performed by NGS technique. The genes included in the test include the entire exon, but in some areas sequencing may not be sufficiently covered. • In addition, if a highly homologous sequence exists, the sequencing of the base may not be accurate, and exonic deletion/duplication, regulatory or deep intronic region, repeat expansion, imprinting defect etc. may be difficult to detect. • Genetic variation is divided into five categories, pathogenic variant (PV), likely pathogenic variant (LPV), variant of unknown significance (VUS), likely benign variant (LBV), and benign variant (BV), according to 2015 ACMG/AMP (Genet Med 2015;17:405-24). • Likely benign variant (LBV) and Benign variant (BV) are not reported. However, the interpretation of the variation could be changed as additional evidence builds up after the results are reported.		

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