Cancer Risk

genetic test that establishes the risk of hereditary cancer





CancerRisk

What is CancerRisk?

CancerRisk is a genetic test that provides information on the risk of developing different types of hereditary cancer.

What does the test include?

CancerRisk utilizes Whole Exome Sequencing to analyze 40 genes related to hereditary cancer. The test detects single nucleotide variants, small insertions/deletions and copy number variants (large deletions/duplications) in specific genes, related to the most frequent hereditary cancers.

Why prescribe CancerRisk?

Extended genetic panels can detect close to 50% more patients with cancer risk. This allows establishing preventive and/or monitoring measures to reduce the risk or allow early diagnosis.

Pancancer panels detect up to 50% more patients at risk compared to panels targeting a single type of cancer.(1)

The detection of variants in genes related to cancer development is key to implement preventive measures.

Who is it intended for?

CancerRisk is specially indicated for:

- Patients with cancer diagnosis.
- Individuals who have first grade family members with cancer before the age of 50.
- Individuals with a family history of cancer, suggesting a hereditary component.
- Individuals who want to know their hereditary cancer risk.

Counseling service for the specialist

If needed, Veritas provides expert genetic counseling to the physician for patient results interpretation.

Which sample type is needed?

Saliva or blood sample in a specific kit provided by Veritas.

CancerRisk advantages

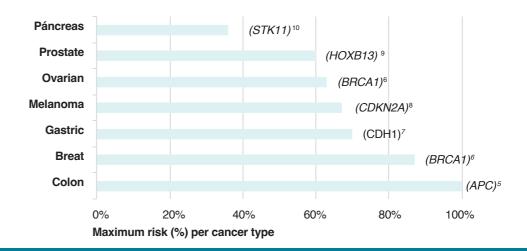
CancerRisk can detect a higher number of at risk hereditary cancer patients. The test has a higher sensitivity and a negative predictive value in comparison with other more targeted panels.

- About 50% of individuals with BRCA1 or BRCA2 mutations, do not have breast or ovarian cancer family history.²
- At least 25% of patients with a mutation in mismatch repair genes (MLH1, MSH2, MSH6, PMS2 and EPCAM) do not meet clinical criteria for Lynch syndrome genetic testing.3
- Only about 25% of breast and ovarian hereditary cancer cases are due to mutations in BRCA1 and BRCA2 genes⁴. CancerRisk includes genes with scientific evidence related to breast and ovarian hereditary cancer.

Possible outcomes

Pathogenic variants, likely pathogenic variants and Variants of Uncertain Significance (VUS), classified according to the American College of Medical Genetics and Genomics (ACMG) (PMID: 25741868) are included in the report.

Lifetime cancer risk in individuals with mutations in specific genes



Genes and cancer types included in CancerRisk



^{1.} Rosenthal ET, et al. Cancer genetics. 2017; 218;58-68. 2. King MC, et al. JAMA. 2014;312(11):1091-2. 3. Hissong E, et al. Modern Pathology, 2018;31(11):1756.

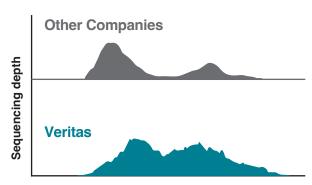
Nielsen FC et al. Nature Reviews. 2016;16:599-612 Jasperson KW, et.al GeneReviews@[Internet], 2017 6. Petrucelli N. et al. GeneReviews®[Internet]. 2016.

Kaurah P & Huntsman DG, GeneReviews@[Internet], 2018 8. Cremin et al. Hereditary Cancer in Clinical Practice. 2018;16:7. 9. MacInnis RJ, et al. PLoS One. 2013;8(2):e54727.

^{10.} Van Lier MG, et al. Am J Gastroenterol. 2010 Jun;105(6):1258-64. * Genes with copy number variants analysis

Whole exome technical information

- Whole exome sequencing (WES) with 100x average coverage, sequencing more than 99% of the genes of interest at ≥20x.
- Veritas whole exome sequencing has an optimized design that improves the coverage for a more homogeneous sequencing of the exome.
- Veritas has a team of expert curators who perform the interpretation based on the most up-to-date scientific knowledge, with a specialized software developed for a detailed variant classification.



Example of the different coverage of a specific region in the exome with Veritas WES versus other companies.

References

- Zook JM. et al. Extensive sequencing of seven human genomes to characterize benchmark reference materials. Sci Data 2016;3:160025 doi: 10.1038/sdata.2016.25. PMID: 27271295.
- Mandelker D et al. Navigating highly homologous genes in a molecular diagnostic setting: a resource for clinical next-generation sequencing. Genet Med 2016;18:1282-1289. PMID: 27228465.
- Landrum MJ et al. ClinVar: public archive of interpretations of clinically relevant variants. Nuc Acids Res. 2016;44(1):D862–D868. doi: 10.1093/nar/qkv1222. PMID: 26582918.
- Richards S et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genet Med 2015;17:405-424. PMID: 25741868.
- Stenson PD et al. The Human Gene Mutation Database: towards a comprehensive repository of inherited mutation data for medical research, genetic diagnosis and next-generation sequencing studies. Hum Genet 2017;136:665-677. PMID: 28349240.

About Veritas

Veritas Genetics, a *LetsGetChecked* company, is one of the world leaders in advanced genetic sequencing and clinical interpretation of the exome and whole genome, driving the transition to personalized and preventive medicine.

Using state-of-the-art technologies and the highest safety standards, Veritas Genetics helps individuals, healthcare professionals and institutions worldwide to understand and anticipate genetic risks, enabling more informed and proactive health decisions.

With a focus on innovation and accessibility, Veritas Genetics transforms the way we understand and care for health at every stage of life.



info@veritasint.com | veritasint.com

