CENTOGENE
THE RARE DISEASE COMPANY

NGS Panels for Hereditary Cancers

Genetic Testing for an Improved Prognosis

PRODUCT SHEET

NGS Panels for Hereditary Cancers

Genetic testing for hereditary cancers can provide life-changing results in affected patients and their relatives, accompanied by potential actionable steps for genetic-related cancers. With many different applications of genetic testing to detect and care for cancer, we can guide you in selecting the right options to enhance the treatment of your patients suffering from hereditary cancers. Having identified genetic variants associated with oncological diseases in more than 200 different genes, we can provide a comprehensive range to foster cancer diagnosis, prognosis, treatment selection, and monitoring.

CENTOGENE's NGS panels for hereditary cancers include all relevant clinical genes, as well as genes necessary for differential diagnosis of syndromes with overlapping phenotype – therefore allowing the diagnosis of a disease that otherwise would be missed. This approach maximizes the clinical utility, de-risks panel choice, increases cost-effectiveness, and ultimately simplifies the diagnostic process.

The CENTOGENE Advantage

- Coverage of **all relevant disease-causing genes** and non-coding and coding pathogenic variants
- The most **up-to-date panel gene content** including the latest medical and in-house findings
- **World-class expertise** and life-long commitment to our patients
- **High-quality analysis for precise clinical interpretation** using advanced bioinformatics and artificial intelligence-powered tools
- **First-class medical reports** powered by CentoMD® database, containing > 12.7 million unique variants and multiomics data from over 120 countries

PANEL	GENES INCLUDED
BRCA 1/2[1]	*BRCA1, BRCA2*
CentoBreast®	*ABRAXAS1, ATM, BARD1, BRCA1, BRCA2, BRIP1, CDH1, CHEK2, DICER1, EPCAM, FANCC, MEN1, MLH1, MRE11, MSH2, MSH6, MUTYH, NBN, PALB2, PMS1, PMS2, PTEN, RAD50, RAD51C, RAD51D, RECQL, SMARCA4, STK11, TP53, XRCC2*
CentoColon	*APC, ATM, AXIN2, BLM, BMPR1A, BRCA1, BRCA2, CDH1, CDKN2A, CHEK2, EPCAM, FLCN, GALNT12, MLH1, MLH3, MSH2, MSH3, MSH6, MUTYH, NBN, NTHL1, PALB2, PMS2, POLD1, POLE, PRSS1, PTEN, RNF43, SMAD4, STK11, TGFBR2, TP53, VHL*
CentoCancer®	*ABRAXAS1, APC, ATM, AXIN2, BAP1, BARD1, BLM, BMPR1A, BRCA1, BRCA2, BRIP1, CDH1, CDK4, CDKN2A, CHEK2, DICER1, DIS3L2, EPCAM, FANCC, FH, FLCN, GALNT12, HNF1B, HOXB13, KIT, MC1R, MEN1, MET, MITF, MLH1, MLH3, MRE11, MSH2, MSH3, MSH6, MUTYH, NBN, NF1, NTHL1, PALB2, PMS1, PMS2, POLD1, POLE, POT1, PRSS1, PTCH1, PTEN, RAD50, RAD51C, RAD51D, RECQL, RET, RNF43, SDHA, SDHAF2, SDHB, SDHC, SDHD, SMAD4, SMARCA4, STK11, TGFBR2, TP53, TSC1, TSC2, VHL, WT1, XRCC2, XRCC3*
CentoCancer® Comprehensive	*ABRAXAS1, ACVRL1, AKT1, APC, ATM, AXIN2, BAP1, BARD1, BLM, BMPR1A, BRCA1, BRCA2, BRIP1, BUB1B, CASR, CDC73, CDH1, CDK4, CDKN1B, CDKN1C, CDKN2A, CEBPA, CHEK2, CTNNA1, DDX41, DICER1, DIS3L2, EGFR, EPCAM, ETV6, EXT1, EXT2, FANCC, FH, FLCN, GALNT12, GATA2, GPC3, GREM1, HNF1A, HNF1B, HOXB13, HRAS, KIF1B, KIT, MAX, MC1R, MEN1, MET, MITF, MLH1, MLH3, MRE11, MSH2, MSH3, MSH6, MUTYH, NBN, NF1, NF2, NTHL1, PALB2, PDGFRA, PHOX2B, PIK3CA, PMS1, PMS2, POLD1, POLE, POT1, PRKAR1A, PRSS1, PTCH1, PTCH2, PTEN, RAD50, RAD51C, RAD51D, RB1, RECQL, REST, RET, RNF43, RPS20, RUNX1, SAMD9L, SDHA, SDHAF2, SDHB, SDHC, SDHD, SMAD4, SMARCA2, SMARCA4, SMARCB1, SMARCE1, STK11, SUFU, TERT, TGFBR2, TMEM127, TP53, TRIP13, TSC1, TSC2, VHL, WRN, WT1, XRCC2, XRCC3*

Key Features and Performance

COVERAGE

- ≥ 99.5 % targeted regions covered at ≥ 20 x
- Mean depth coverage ≥ 150 x
- For each gene, all SNVs described in HGMD and CentoMD® are covered, including relevant deep intronic and regulatory variants

GENES

For a complete overview of included genes, please visit:
www.centogene.com/ngspanels-medical-reporting

SPECIFICITY

≥ 99.9 % guaranteed for all reported variants. Variants with low quality and / or unclear zygosity are confirmed by orthogonal methods (Sanger, MLPA, qPCR).

CNV SENSITIVITY

NGS-based copy number variations (CNV) are detected with a sensitivity of above 90 % for all homozygous deletions and heterozygous deletions / duplications spanning at least three consecutive exons. Heterozygous CNVs spanning less than three exons cannot reliably be detected, are therefore excluded from routine analysis, and will only be inspected and reported upon medical or technical indication.

REPORTING

Pathogenic and likely pathogenic variants are reported following American College of Medical Genetics and Genomics (ACMG) classification guidelines. Variants of uncertain significance (VUS) are not reported.

TAT

15 business days

SNVs: single nucleotide variants; InDels: small insertions / deletions; CNVs: copy number variations; MLPA: Multiplex ligation-dependent probe amplification; qPCR: quantitative polymerase chain reaction.

[1] Different versions of this panel exist. For details please visit: www.centogene.com/diagnostics/ngspanels/oncology

Going The Extra Mile

All our high quality NGS panels detect single nucleotide variants (SNV), small insertions/deletions (InDels), and NGS-based deletion/duplication (CNV) analysis in one single assay - ultimately providing the most complete NGS panels for the maximum diagnostic yield.

DELETION/DUPLICATION	High resolution NGS-based CNV analysis to detect larger deletions and duplications is included in all our panels at no extra cost. Deletion/duplications constitute 5 – 10% of disease-causing variants. By including CNV analysis in our panels, the potential of providing the most accurate diagnosis increases.
IMPROVED INTERPRETATION	Our proprietary database CentoMD® enables access to more than 31 million unique variants for best medical interpretation.
VARIANT RECLASSIFICATION PROGRAM	All our panels are automatically entered into our variant reclassification program. This program supports the identification of new genetic evidence, and physicians will be notified free of charge for life