CASE STUDY

18-year-old male with a clinical diagnosis of polyposis (benign)

The patient was diagnosed with a benign form of polyposis without any indication of family history.

PreSENTIA Colorectal Polyposis Syndrome was then performed to identify potential germline mutations linked with polyposis. The test identified:

- A gross genomic **deletion** of the entire coding sequence and promoter 1A of the **APC** gene
- This deletion is associated with **familial adenomatous polyposis (FAP)**

PreSENTIA led to:

- Accurate identification of the inherited genetic alterations associated with increased cancer risk
- Clinical management plan tailored to the patient
- Medical management recommendations, including:
  - Annual colonoscopy
  - Endoscopic evaluation
  - Chemoprevention (in selected patients)
  - Duodenal surveillance
  - Ultrasound for thyroid cancer

Clinical utility

PreSENTIA accurately identified the genetic affection that is associated with FAP, an autosomal dominant disorder. If not identified early or treated, FAP increases the risk of developing colorectal cancer in the future. PreSENTIA enabled an early treatment plan that will benefit the patient.

ABOUT MEDICOVER GENETICS

Medicover Genetics is a leading healthcare company specialising in genetic medicine, with more than 25 years of experience in genetics diagnostics. Medicover Genetics offers genetic testing services and genetic counselling, proprietary CE-IVD marked solutions and a versatile Technology Transfer Platform which enables partners to perform high fidelity genetic tests in-house. With services in over 30 countries across Europe, Asia, and Africa, the company empowers laboratories, healthcare professionals and patients to place genetics at the core of medical decisions. Committed to enhancing health and well-being, Medicover Genetics provides meaningful, actionable diagnostic solutions, improving disease prognosis, clinical management, and therapy selection for genetic disorders. The CAP-accredited, CLIA-, GMP- and ISO9001, 15189, and 13485 certified laboratories ensure the highest quality standards. www.medicover-genetics.com

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MKT-ONC-PS-GEN-DR-EN-V02

PreSENTIA®
hereditary cancer

Genes and genetic alterations

MEDICOVER GENETICS

WHAT IS PreSENTIA?

PreSENTIA is a genetic test for hereditary cancer. It identifies hereditary genetic alterations which are implicated in hereditary cancer syndromes and increase the risk of developing cancer in the future.

CLINICAL UTILITY

PreSENTIA is designed to identify the genetic alterations which can predispose to cancer development in the future

- Better classification of the genetic variants
- Identify individuals and family members who are at high risk of developing cancer
- Take early prophylactic measures to minimize the risk of developing cancer
- Identify the best clinical management

LIST OF HEREDITARY CANCER SYNDROMES TESTED

Hereditary cancer susceptible genes can be associated with hereditary cancer syndromes which increase the risk of developing cancer in the future. The table below indicates the syndromes tested in PreSENTIA.

PreSENTIA HEREDITARY CANCER SYNDROMES TESTED	
Ataxia-telangiectasia syndrome	Li-Fraumeni syndrome
BAP1 mutation associated disease	Li-Fraumeni syndrome 2
Constitutional mismatch repair syndrome	Lynch syndrome
DICER 1 syndrome	Multiple endocrine neoplasia type 1
Familial adenomatous polyposis / Attenuated familial adenomatous polyposis	Multiple endocrine neoplasia type 2
Fanconi anemia syndrome	MUTYH-associated polyposis syndrome
Hereditary breast & ovarian cancer syndrome	Peutz-Jeghers syndrome
Hereditary diffuse gastric syndrome	Polymerase proofreading associated syndrome
Hereditary mixed polyposis syndrome	PTEN hamartoma syndrome
Hereditary melanoma-pancreatic cancer syndrome	Retinoblastoma
Hereditary paraganglioma – pheochromocytoma syndrome	Von-Hippel Lindau syndrome
Juvenile polyposis syndrome	Xeroderma pigmentosum syndrome

FEATURES AND SPECIFICATIONS

Target capture enrichment technology

Genetic alterations: SNVs, INDELs, CNAs

Sample type: Buccal swab

TAT: 2-3 weeks

LIST OF GENES AND GENETIC ALTERATIONS TESTED

PreSENTIA examines a spectrum of genetic alterations such as single nucleotide variants (**SNVs**), insertions and deletions (**INDELs**), and copy number alterations (**CNAs**) via next generation sequencing (NGS). PreSENTIA targets **full coding exons***. The following table indicates the type of genetic alterations covered by PreSENTIA in the different panels.

PANEL	SNVs/INDELs, CNAs
Pan-Cancer *62 genes*	AKT1, ATM, BARD1, BRAF, BRCA1, BRCA2, BRIP1, CHEK2, CTNNB1, DICER1, EGFR, ERBB2, ERBB3, ESR1, FBXW7, FOXA1, FOXL2, GATA3, KIT, KRAS, MAP3K1, MLH1, MRE11A, MSH2, MSH6 MTOR, NBN, NRAS, PALB2, PIK3CA, PIK3CB, PMS2, POLE, PTEN, RAD51C, RAD51D, RAF1, RET, RUNX1, SMAD4, TP53
Breast & Gynecological *26 genes*	ATM, BARD1, BRCA1, BRCA2, BRIP1, CDH1, CHEK2, DICER1, EPCAM†, MLH1, MRE11, MSH2, MSH6, MUTYH, NBN, PALB2, PMS2, POLD1, POLE, PTEN, RAD50, RAD51C, RAD51D, SMARCA4, STK11, TP53
Breast/Gynecological Guidelines-Based *19 genes*	ATM, BARD1, BRCA1, BRCA2, BRIP1, CDH1, CHEK2, EPCAM†, MLH1, MSH2, MSH6, NBN, PALB2, PMS2, PTEN, RAD51C, RAD51D, TP53, STK11
Breast High Risk *7 genes*	BRCA1, BRCA2, CDH1, PALB2, PTEN, STK11, TP53
BRCA1 / BRCA2 *2 genes*	BRCA1, BRCA2
Colorectal *17 genes*	APC, BMPR1A, CDH1, CHEK2, EPCAM†, GREM1†, MLH1, MSH2, MSH6, MUTYH, PMS2, POLD1, POLE, PTEN, SMAD4, STK11, TP53
Colorectal High-Risk *10 genes*	APC, BMPR1A, EPCAM†, MLH1, MSH2, MSH6, MUTYH, PMS2, SMAD4, STK11
Colorectal Non-Polyposis *5 genes*	EPCAM†, MLH1, MSH2, MSH6, PMS2
Colorectal Polyposis Syndrome *7 genes*	APC, BMPR1A, MUTYH, POLD1, POLE, SMAD4, STK11
Myelodysplastic Syndrome Leukemia *24 genes*	ATM, BRCA1, BRCA2, BRIP1, EPCAM†, ERCC4, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, MLH1, MSH2, MSH6, PALB2, PMS2, RAD51C, SLX4, TP53
Gastric *14 genes*	APC, BMPR1A, CDH1, EPCAM†, MLH1, MSH2, MSH6, PMS2, SDHB, SDHC, SDHD, SMAD4, STK11, TP53
Prostate *15 genes*	ATM, BRCA1, BRCA2, CHEK2, EPCAM†, HOXB13‡, MLH1, MSH2, MSH6, NBN, PALB2, PMS2, PTEN, RAD51D, TP53
Pancreatic *17 genes*	APC, ATM, BRCA1, BRCA2, BMPR1A, CDK4, CDKN2A, ($CDKN2A^{p16(INK4A)}$, $CDKN2A^{p14(ARF)}$), EPCAM†, MEN1, MLH1, MSH2, MSH6, PALB2, PMS2, SMAD4, STK11, TP53
Renal *13 genes*	BAP1, EPCAM†, MLH1, MSH2, MSH6, PMS2, PTEN, SDHAF2, SDHB, SDHC, SDHD, TP53, VHL
Skin (XP-Associated) *9 genes*	DDB2, ERCC1, ERCC2, ERCC3, ERCC4, ERCC5, POLH, XPA, XPC
Familial Melanoma *7 genes*	BAP1, BRCA2, CDK4, CDKN2A ($CDKN2A^{p16(INK4A)}$, $CDKN2A^{p14(ARF)}$), PTEN, RB1, TP53
Paraganglioma/ Pheochromocytoma *6 gene*	RET, SDHAF2, SDHB, SDHC, SDHD, VHL
Parathyroid *1 gene*	MEN1
Thyroid *1 gene*	RET

†SNVs/INDELs are not covered ‡ CNAs are not covered

Exceptions on regions containing repeats, sequences of high homology (pseudogenes and segmental duplications) or high GC-content