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Full name:	Hereditary predisposition to cancer (47 genes) - IPG
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Version number:	V6
Laboratory:	Centre de Génétique-Institut de Pathologie et de Génétique (IPG)
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Related Diseases

- APC-related attenuated familial adenomatous polyposis
- Adrenocortical carcinoma
- Adult hepatocellular carcinoma
- Ataxia-telangiectasia
- Ataxia-telangiectasia-like disorder
- BAP1-related tumor predisposition syndrome
- Constitutional mismatch repair deficiency syndrome
- Desmoid tumor
- Familial adenomatous polyposis
- Familial adenomatous polyposis due to 5q22.2 microdeletion
- Familial atypical multiple mole melanoma syndrome
- Familial melanoma
- Familial pancreatic carcinoma
- Familial prostate cancer
- Fanconi anemia
- Gardner syndrome
- Generalized juvenile polyposis/juvenile polyposis coli
- Hereditary breast and/or ovarian cancer syndrome
- Hereditary breast cancer
- Hereditary diffuse gastric cancer
- Hereditary mixed polyposis syndrome

- Hereditary site-specific ovarian cancer syndrome
- Inherited cancer-predisposing syndrome due to biallelic BRCA2 mutations
- Juvenile polyposis of infancy
- Li-Fraumeni syndrome
- Lynch syndrome
- MSH3-related attenuated familial adenomatous polyposis
- MUTYH-related attenuated familial adenomatous polyposis
- Melanoma and neural system tumor syndrome
- Muir-Torre syndrome
- NTHL1-related attenuated familial adenomatous polyposis
- Nephroblastoma
- Nijmegen breakage syndrome
- Nijmegen breakage syndrome-like disorder
- Osteosarcoma
- Peutz-Jeghers syndrome
- Polymerase proofreading-related adenomatous polyposis
- Turcot syndrome with polyposis
- Uveal melanoma
- Von Hippel-Lindau disease

Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
APC	100.00	1	NM_000038.6
ATM	100.00	1	NM_000051.3
AXIN2	100.00	1	NM_004655.4
BAP1	100.00	1	NM_004656.4
BARD1	100.00	1	NM_000465.4
BMPR1A	100.00	1	NM_004329.3
BRCA1	100.00	1	NM_007294.4

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
BRCA2	100.00	1	NM_000059.3
BRIP1	100.00	1	NM_032043.3
CDH1	100.00	1	NM_004360.5
CDK4	100.00	1	NM_000075.4
CDKN1B	100.00	1	NM_004064.4
CDKN2A	100.00	1	NM_001195132.1
CHEK2	100.00	1	NM_007194.4
DICER1	100.00	1	NM_030621.4
EPCAM	100.00	1	NM_002354.3
GATA2	100.00	1	NM_032638.5
GREM1	100.00	1	NM_013372.7
HOXB13	100.00	1	NM_006361.6
MEN1	100.00	1	NM_001370259.2
MLH1	100.00	1	NM_000249.4
MSH2	100.00	1	NM_000251.3
MSH3	100.00	1	NM_002439.5
MSH6	100.00	1	NM_000179.3
MUTYH	100.00	1	NM_001128425.2
NBN	100.00	1	NM_002485.5
NF1	100.00	1	NM_001042492.3

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
NTHL1	100.00	1	NM_002528.7
PALB2	100.00	1	NM_024675.4
PIK3CA	100.00	1	NM_006218.4
PMS2	100.00	1	NM_000535.7
POLD1	100.00	1	NM_002691.4
POLE	100.00	1	NM_006231.4
POT1	100.00	1	NM_015450.3
PTCH1	100.00	1	NM_000264.5
PTEN	100.00	1	NM_000314.8
RAD50	100.00	1	NM_005732.4
RAD51C	100.00	1	NM_058216.3
RAD51D	100.00	1	NM_002878.3
RB1	100.00	1	NM_000321.2
RET	100.00	1	NM_020975.6
RPS20	100.00	1	NM_001146227.2
SCG5	100.00	1	NM_001144757.2
SMAD4	100.00	1	NM_005359.6
STK11	100.00	1	NM_000455.5
TP53	100.00	1	NM_000546.5
WWP1	100.00	1	NM_007013.4