Blueprint Genetics

# Hereditary Melanoma and Skin Cancer Panel

**Test code: ON0501**

Is ideal for patients with a clinical suspicion of an inherited susceptibility to melanoma and skin cancer. This panel is designed to detect heritable germline mutations and should not be used for the detection of somatic mutations in tumor tissue.

Skin cancer is one of the most common types of cancer. Some inherited conditions increase the risk of skin cancer and subset of the disease has familial origins. For example, 8% of individuals with melanoma have first-degree relatives with the same disease. Inhritance pattern is autosomal dominant with exception of xeroderma pigmentosum that is inherited in an autosomal recessive manner. The Hereditary Melanoma and Skin Cancer Panel is suited for detecting heritable germline mutations and may not be used for the detection of somatic mutations in tumor tissue. This Panel is part of the Comprehensive Hereditary Cancer Panel.

## About Hereditary Melanoma and Skin Cancer

Cancers arising in the skin include basal-cell cancer, squamous cell cancer, and melanoma. Melanomas may rarely also occur in the mouth, intestines or eye. Ultraviolet radiation from exposure to sun light or tanning beds is the main cause for skin cancer. A subset of skin cancers is associated with various hereditary cancer syndromes. Familial atypical multiple mole melanoma syndrome is caused by mutations in the *CDKN2A* gene that may be present in up to 40% of the familial cases of melanoma. Mutations in the *CDK4* gene also cause familial melanoma predisposition. Gorlin syndrome is associated with pathogenic mutations in the *PTCH1* and *SUFU* genes and increases the risk of developing basal cell carcinomas. Other cancer susceptibility syndromes/genes that increase the risk of developing skin cancers, either as a primary or secondary disease, include *BAP1*-related tumor predisposition syndrome (*BAP1*), hereditary breast and ovarian cancer syndrome (*BRCA1* and *BRCA2*), xeroderma pigmentosum (several genes), *MITF*-related melanoma and renal cell carcinoma predisposition syndrome (*MITF*), Li-Fraumeni syndrome (*TP53*), Cowden syndrome (*PTEN*), and Werner syndrome (*WRN*).

## Availability

Results in 3-4 weeks

## Gene set description

Genes in the Hereditary Melanoma and Skin Cancer Panel and their clinical significance

| Gene | Associated phenotypes | Inheritance | ClinVar | HGMD |
|---|---|---|---|---|
| BAP1 | Tumor predisposition syndrome | AD | 74 | 113 |
| BRCA1* | Pancreatic cancer, Breast-ovarian cancer, familial | AD | 2997 | 2631 |
| BRCA2 | Fanconi anemia, Medulloblastoma, Glioma susceptibility, Pancreatic cancer, Wilms tumor, Breast-ovarian cancer, familial | AD/AR | 3369 | 2659 |
| CDK4 | Melanoma, cutaneous malignant | AD | 4 | 14 |
| CDKN2A | Melanoma, familial, Melanoma-pancreatic cancer syndrome | AD | 87 | 232 |
| DDB2 | Xeroderma pigmentosum | AR | 4 | 17 |
| ERCC2 | Xeroderma pigmentosum, Trichothiodystrophy, photosensitive, Cerebrooculofacioskeletal syndrome 2 | AR | 26 | 98 |
| ERCC3 | Xeroderma pigmentosum, Trichothiodystrophy, photosensitive | AR | 10 | 19 |
| ERCC4 | Fanconi anemia, Xeroderma pigmentosum, XFE progeroid syndrome | AR | 13 | 70 |

| | | | | |
|---|---|---|---|---|
| ERCC5 | Xeroderma pigmentosum, Xeroderma pigmentosum/Cockayne syndrome | AR | 21 | 54 |
| MITF | Tietz albinism-deafness syndrome, Waardenburg syndrome, Coloboma, osteopetrosis, microphthalmia, macrocephaly, albinism, and deafness (COMMAD) | AD/AR | 32 | 58 |
| POT1 | Glioma susceptibility 9, Melanoma, cutaneous malignant, susceptibility to 10 | AD | 2 | 34 |
| PTCH1 | Basal cell nevus syndrome | AD | 193 | 522 |
| PTEN* | Bannayan-Riley-Ruvalcaba syndrome, Lhermitte-Duclos syndrome, Cowden syndrome | AD | 435 | 638 |
| SUFU | Medulloblastoma, Basal cell nevus syndrome | AD | 22 | 44 |
| TP53 | Colorectal cancer, Li-Fraumeni syndrome, Ependymoma, intracranial, Choroid plexus papilloma, Breast cancer, familial, Adrenocortical carcinoma, Osteogenic sarcoma, Hepatoblastoma, Non-Hodgkin lymphoma | AD | 393 | 505 |
| WRN* | Werner syndrome | AR | 64 | 107 |
| XPA | Xeroderma pigmentosum | AR | 49 | 47 |
| XPC | Xeroderma pigmentosum | AR | 67 | 91 |

*Some regions of the gene are duplicated in the genome. Read more.

# The gene has suboptimal coverage (means <90% of the gene's target nucleotides are covered at >20x with mapping quality score (MQ>20) reads), and/or the gene has exons listed under Test limitations section that are not included in the panel as they are not sufficiently covered with high quality sequence reads.

The sensitivity to detect variants may be limited in genes marked with an asterisk (*) or number sign (#)

Gene refers to the HGNC approved gene symbol; Inheritance refers to inheritance patterns such as autosomal dominant (AD), autosomal recessive (AR), mitochondrial (mi), X-linked (XL), X-linked dominant (XLD) and X-linked recessive (XLR); ClinVar refers to the number of variants in the gene classified as pathogenic or likely pathogenic in this database (ClinVar); HGMD refers to the number of variants with possible disease association in the gene listed in Human Gene Mutation Database (HGMD). The list of associated, gene specific phenotypes are generated from CGD or Mitomap databases.

## Non-coding disease causing variants covered by the panel

| Gene | Genomic location HG19 | HGVS | RefSeq | RS-number |
|---|---|---|---|---|
| BAP1 | Chr3:52435659 | c.*644delG | NM_004656.3 | |
| BRCA1 | Chr17:41196352 | c.*1340_*1342delTGT | NM_007294.3 | rs1281551853 |
| BRCA1 | Chr17:41196424 | c.*1271T>C | NM_007294.3 | |
| BRCA1 | Chr17:41197167 | c.*528G>C | NM_007294.3 | rs1060504556 |
| BRCA1 | Chr17:41197588 | c.*103_*106delTGTC | NM_007294.3 | rs431825382 |
| BRCA1 | Chr17:41197637 | c.*58C>T | NM_007294.3 | rs137892861 |
| BRCA1 | Chr17:41197859 | c.5468-40T>A | NM_007294.3 | rs80358151 |
| BRCA1 | Chr17:41199745 | c.5407-25T>A | NM_007294.3 | rs758780152 |
| BRCA1 | Chr17:41201232 | c.5333-36_5333-22delTACTGCAGTGATTTT | NM_007294.3 | |
| BRCA1 | Chr17:41206122 | c.5277+2916_5277+2946delAAATTCTAGTGCTTTGGATTTTTTCCTCCATinsGG | NM_007294.3 | |
| BRCA1 | Chr17:41209164 | c.5194-12G>A | NM_007294.3 | rs80358079 |

| | | | | |
|---|---|---|---|---|
| BRCA1 | Chr17:41215994 | c.5075-27delA | NM_007294.3 | |
| BRCA1 | Chr17:41251909 | c.442-22_442-13delTGTTCTTTAC | NM_007294.3 | rs879254224 |
| BRCA1 | Chr17:41256984 | c.213-11T>G | NM_007294.3 | rs80358061 |
| BRCA1 | Chr17:41256985 | c.213-12A>G | NM_007294.3 | rs80358163 |
| BRCA1 | Chr17:41256988 | c.213-15A>G | NM_007294.3 | |
| BRCA1 | Chr17:41276134 | c.-19-2A>G | NM_007294.3 | |
| BRCA2 | Chr13:32889805 | c.-40+1G>A | NM_000059.3 | |
| BRCA2 | Chr13:32890469 | c.-39-89delC | NM_000059.3 | |
| BRCA2 | Chr13:32890556 | c.-39-1_-39delGA | NM_000059.3 | rs758732038 |
| BRCA2 | Chr13:32890558 | c.-39-1G>A | NM_000059.3 | rs1060499566 |
| BRCA2 | Chr13:32900222 | c.426-12_426-8delGTTTT | NM_000059.3 | rs276174844 |
| BRCA2 | Chr13:32945079 | c.8488-14A>G | NM_000059.3 | |
| BRCA2 | Chr13:32953872 | c.8954-15T>G | NM_000059.3 | |
| BRCA2 | Chr13:32971007 | c.9502-28A>G | NM_000059.3 | rs397508059 |
| BRCA2 | Chr13:32971023 | c.9502-12T>G | NM_000059.3 | rs81002803 |
| CDKN2A | Chr9:21968346 | c.458-105A>G | NM_000077.4 | |
| CDKN2A | Chr9:21972311 | c.151-1104C>G | NM_000077.4 | |
| CDKN2A | Chr9:21973573 | c.150+1104C>A | NM_000077.4 | rs756102261 |
| CDKN2A | Chr9:21974401 | c.*73+2T>G | NM_058197.4 | |
| CDKN2A | Chr9:21974847 | c.-21C>T | NM_000077.4 | |
| CDKN2A | Chr9:21974875 | c.-49C>A | NM_000077.4 | rs1064797383 |
| CDKN2A | Chr9:21974882 | c.-56G>T | NM_000077.4 | |
| CDKN2A | Chr9:21974916 | c.-93_-91delAGG | NM_000077.4 | |
| ERCC5 | Chr13:103514354 | c.881-26T>G | NM_000123.3 | |
| PTCH1 | Chr9:98226337 | c.2561-2057A>G | NM_000264.3 | |
| PTEN | Chr10:89622883–89623482 | | | |
| PTEN | Chr10:89622988 | c.-1239A>G | NM_000314.6 | |
| PTEN | Chr10:89623049 | c.-1178C>T | NM_000314.6 | |
| PTEN | Chr10:89623056 | c.-1171C>T | NM_000314.6 | rs587779981 |
| PTEN | Chr10:89623116 | c.-1111A>G | NM_000314.6 | |
| PTEN | Chr10:89623226 | c.-1001T>C | NM_000314.4 | |
| PTEN | Chr10:89623296 | c.-931G>A | NM_000314.4 | rs587781959 |
| PTEN | Chr10:89623306 | c.-921G>T | NM_000314.4 | |
| PTEN | Chr10:89623331 | c.-896T>C | NM_000314.4 | |
| PTEN | Chr10:89623365 | c.-862G>T | NM_000314.4 | rs587776675 |
| PTEN | Chr10:89623373 | c.-854C>G | NM_000314.4 | |
| PTEN | Chr10:89623392 | c.-835C>T | NM_000314.4 | rs587779994 |
| PTEN | Chr10:89623428 | c.-799G>C | NM_000314.4 | rs587779992 |
| PTEN | Chr10:89623462 | c.-765G>A | NM_000314.4 | |

| | | | | |
|---|---|---|---|---|
| PTEN | Chr10:89690791 | c.210-8dupT | NM_000314.4 | |
| PTEN | Chr10:89692749 | c.254-21G>C | NM_000314.4 | |
| PTEN | Chr10:89725294 | c.*65T>A | NM_000314.4 | |
| PTEN | Chr10:89725304 | c.*75_*92delTAATGGCAATAGGACATTinsCTATGGCAATAGGACATTG | NM_000314.4 | |
| TP53 | Chr17:7571520 | | NM_000546.5 | |
| TP53 | Chr17:7577647 | c.673-39G>A | NM_000546.5 | |
| TP53 | Chr17:7579601 | c.97-11C>G | NM_000546.5 | |
| TP53 | Chr17:7590694 | c.-29+1G>T | NM_000546.5 | |
| WRN | Chr8:30966107 | c.2089-3024A>G | NM_000553.4 | rs281865157 |
| WRN | Chr8:30999982 | c.3234-160A>G | NM_000553.4 | |
| XPA | Chr9:100449555 | c.390-12A>G | NM_000380.3 | |
| XPC | Chr3:14187285 | c.*156G>A | NM_004628.4 | rs121965092 |
| XPC | Chr3:14209904 | c.413-24A>G | NM_004628.4 | rs794729657 |

## Test Strengths

Assesses for non-coding disease causing variants in one or more genes, including promoter variants in *PTEN*.

**The strengths of this test include:**

- CAP accredited laboratory
- CLIA-certified personnel performing clinical testing in a CLIA-certified laboratory
- Powerful sequencing technologies, advanced target enrichment methods and precision bioinformatics pipelines ensure superior analytical performance
- Careful construction of clinically effective and scientifically justified gene panels
- Some of the panels include the whole mitochondrial genome (please see the Panel Content section)
- Our Nucleus online portal providing transparent and easy access to quality and performance data at the patient level
- Our publicly available analytic validation demonstrating complete details of test performance
- ~2,000 non-coding disease causing variants in our clinical grade NGS assay for panels (please see 'Non-coding disease causing variants covered by this panel' in the Panel Content section)
- Our rigorous variant classification scheme
- Our systematic clinical interpretation workflow using proprietary software enabling accurate and traceable processing of NGS data
- Our comprehensive clinical statements

## Test Limitations

Genes with partial, or whole gene, segmental duplications in the human genome are marked with an asterisk (*) if they overlap with the UCSC pseudogene regions. The technology may have limited sensitivity to detect variants in genes marked with these symbols (please see the Panel content table above).

**This test does not detect the following:**

- Complex inversions
- Gene conversions
- Balanced translocations
- Some of the panels include the whole mitochondrial genome but not all (please see the Panel Content section)

- Repeat expansion disorders unless specifically mentioned
- Non-coding variants deeper than ±20 base pairs from exon-intron boundary unless otherwise indicated (please see above Panel Content / non-coding variants covered by the panel).

**This test may not reliably detect the following:**

- Low level mosaicism in nuclear genes (variant with a minor allele fraction of 14.6% is detected with 90% probability)
- Stretches of mononucleotide repeats
- Low level heteroplasmy in mtDNA (>90% are detected at 5% level)
- Indels larger than 50bp
- Single exon deletions or duplications
- Variants within pseudogene regions/duplicated segments
- Some disease causing variants present in mtDNA are not detectable from blood, thus post-mitotic tissue such as skeletal muscle may be required for establishing molecular diagnosis.

The sensitivity of this test may be reduced if DNA is extracted by a laboratory other than Blueprint Genetics.

For additional information, please refer to the Test performance section and see our Analytic Validation.

## Test performance

Our panels are sectioned from our high-quality, clinical grade NGS assay. Please see our sequencing and detection performance table for details regarding our ability to detect different types of alterations (Table).

Assays have been validated for various sample types including EDTA-blood, isolated DNA (excluding from formalin fixed paraffin embedded tissue), saliva and dry blood spots (filter cards). These sample types were selected in order to maximize the likelihood for high-quality DNA yield. The diagnostic yield varies depending on the assay used, referring healthcare professional, hospital and country. Plus analysis increases the likelihood of finding a genetic diagnosis for your patient, as large deletions and duplications cannot be detected using sequence analysis alone. Blueprint Genetics' Plus Analysis is a combination of both sequencing and deletion/duplication (copy number variant (CNV)) analysis.

## Performance of Blueprint Genetics high-quality, clinical grade NGS sequencing assay for panels.

| | Sensitivity % (TP/(TP+FN) | Specificity % |
|---|---|---|
| Single nucleotide variants | 99.89% (99,153/99,266) | >99.9999% |
| Insertions, deletions and indels by sequence analysis | | |
| 1-10 bps | 99.2% (7,745/7,806) | >99.9999% |
| 11-50 bps | 99.13% (2,524/2,546) | >99.9999% |
| Copy number variants (exon level dels/dups) | | |
| 1 exon level deletion (heterozygous) | 100% (20/20) | NA |
| 1 exon level deletion (homozygous) | 100% (5/5) | NA |
| 1 exon level deletion (het or homo) | 100% (25/25) | NA |
| 2-7 exon level deletion (het or homo) | 100% (44/44) | NA |
| 1-9 exon level duplication (het or homo) | 75% (6/8) | NA |

| | | |
|---|---|---|
| Simulated CNV detection | | |
| 5 exons level deletion/duplication | 98.7% | 100.00% |
| | | |
| Size range (0.1-47 Mb) | 100% (25/25) | |
| | | |
| The performance presented above reached by Blueprint Genetics high-quality, clinical grade NGS sequencing assay with the following coverage metrics | | |
| | | |
| Mean sequencing depth | 143X | |
| Nucleotides with >20x sequencing coverage (%) | 99.86% | |

**Performance of Blueprint Genetics Mitochondrial Sequencing Assay.**

| | | Specificity |
|---|---|---|
| ANALYTIC VALIDATION (NA samples; n=4) | | |
| Single nucleotide variants | | |
| Heteroplasmic (45-100%) | 100.0% (50/50) | 100.0% |
| Heteroplasmic (35-45%) | 100.0% (87/87) | 100.0% |
| Heteroplasmic (25-35%) | 100.0% (73/73) | 100.0% |
| Heteroplasmic (15-25%) | 100.0% (77/77) | 100.0% |
| Heteroplasmic (10-15%) | 100.0% (74/74) | 100.0% |
| Heteroplasmic (5-10%) | 100.0% (3/3) | 100.0% |
| Heteroplasmic (<5%) | 50.0% (2/4) | 100.0% |
| CLINICAL VALIDATION (n=76 samples) | | |
| All types | | |
| Single nucleotide variants n=2084 SNVs | | |
| Heteroplasmic (45-100%) | 100.0% (1940/1940) | 100.0% |
| Heteroplasmic (35-45%) | 100.0% (4/4) | 100.0% |
| Heteroplasmic (25-35%) | 100.0% (3/3) | 100.0% |
| Heteroplasmic (15-25%) | 100.0% (3/3) | 100.0% |
| Heteroplasmic (10-15%) | 100.0% (9/9) | 100.0% |
| Heteroplasmic (5-10%) | 92.9%(12/13) | 99.98% |
| Heteroplasmic (<5%) | 88.7% (47/53) | 99.93% |

| | | |
|---|---|---|
| Insertions and deletions by sequence analysis n=42 indels | | |
| Heteroplasmic (45-100%) 1-10bp | 100.0% (32/32) | 100.0% |
| Heteroplasmic (5-45%) 1-10bp | 100.0% (3/3) | 100.0% |
| Heteroplasmic (<5%) 1-10bp | 100.0% (5/5) | >0.9999 |
| SIMULATION DATA /(mitomap mutations) | | |
| Insertions, and deletions 1-24 bps by sequence analysis; n=17 | | |
| Homoplasmic (100%) 1-24bp | 100.0% (17/17) | 99.98% |
| Heteroplasmic (50%) | 100.0% (17/17) | 99.99% |
| Heteroplasmic (25%) | 100.0% (17/17) | 100.0% |
| Heteroplasmic (20%) | 100.0% (17/17) | 100.0% |
| Heteroplasmic (15%) | 100.0% (17/17) | 100.0% |
| Heteroplasmic (10%) | 94.1% (16/17) | 100.0% |
| Heteroplasmic (5%) | 94.1% (16/17) | 100.0% |
| Copy number variants (separate artifical mutations; n=1500) | | |
| Homoplasmic (100%) 500 bp, 1kb, 5 kb | 100.0% | 100.0% |
| Heteroplasmic (50%) 500 bp, 1kb, 5 kb | 100.0% | 100.0% |
| Heteroplasmic (30%) 500 bp, 1kb, 5 kb | 100.0% | 100.0% |
| Heteroplasmic (20%) 500 bp, 1kb, 5 kb | 99.7% | 100.0% |
| Heteroplasmic (10%) 500 bp, 1kb, 5 kb | 99.0% | 100.0% |
| The performance presented above reached by following coverage metrics at assay level (n=66) | | |
| | Mean of medians | Median of medians |
| Mean sequencing depth MQ0 (clinical) | 18224X | 17366X |
| Nucleotides with >1000x MQ0 sequencing coverage (%) (clinical) | 100% | |
| rho zero cell line (=no mtDNA), mean sequencing depth | 12X | |

## Bioinformatics

The target region for each gene includes coding exons and ±20 base pairs from the exon-intron boundary. In addition, the panel includes non-coding and regulatory variants if listed above (Non-coding variants covered by the panel). Some regions of the gene(s) may be removed from the panel if specifically mentioned in the 'Test limitations" section above. The sequencing data generated in our laboratory is analyzed with our proprietary data analysis and annotation pipeline, integrating state-of-the art algorithms and industry-standard software solutions. Incorporation of rigorous quality control steps throughout the workflow of the pipeline ensures the consistency, validity and accuracy of results. Our pipeline is streamlined to maximize sensitivity without sacrificing specificity. We have incorporated a number of reference population databases and mutation databases including, but not limited, to 1000 Genomes Project, gnomAD, ClinVar and HGMD into our clinical interpretation

software to make the process effective and efficient. For missense variants, *in silico* variant prediction tools such as SIFT, PolyPhen, MutationTaster are used to assist with variant classification. Through our online ordering and statement reporting system, Nucleus, ordering providers have access to the details of the analysis, including patient specific sequencing metrics, a gene level coverage plot and a list of regions with <20X sequencing depth if applicable. This reflects our mission to build fully transparent diagnostics where ordering providers can easily visualize the crucial details of the analysis process.

## Clinical interpretation

We provide customers with the most comprehensive clinical report available on the market. Clinical interpretation requires a fundamental understanding of clinical genetics and genetic principles. At Blueprint Genetics, our PhD molecular geneticists, medical geneticists and clinical consultants prepare the clinical statement together by evaluating the identified variants in the context of the phenotypic information provided in the requisition form. Our goal is to provide clinically meaningful statements that are understandable for all medical professionals regardless of whether they have formal training in genetics.

Variant classification is the corner stone of clinical interpretation and resulting patient management decisions. Our classifications follow the Blueprint Genetics Variant Classification Schemes based on the ACMG guideline 2015. Minor modifications were made to increase reproducibility of the variant classification and improve the clinical validity of the report. Our experience with tens of thousands of clinical cases analyzed at our laboratory allowed us to further develop the industry standard.

The final step in the analysis is orthogonal confirmation. Sequence variants classified as pathogenic, likely pathogenic and variants of uncertain significance (VUS) are confirmed using bi-directional Sanger sequencing when they do not meet our stringent NGS quality metrics for a true positive call.  Reported heterozygous and homo/hemizygous copy number variations with a size <10 and <3 target exons are confirmed by orthogonal methods such as qPCR if the specific CNV has been seen and confirmed less than three times at Blueprint Genetics.

Our clinical statement includes tables for sequencing and copy number variants that include basic variant information (genomic coordinates, HGVS nomenclature, zygosity, allele frequencies, in silico predictions, OMIM phenotypes and classification of the variant). In addition, the statement includes detailed descriptions of the variant, gene and phenotype(s) including the role of the specific gene in human disease, the mutation profile, information about the gene's variation in population cohorts and detailed information about related phenotypes. We also provide links to the references, abstracts and variant databases used to help ordering providers further evaluate the reported findings if desired. The conclusion summarizes all of the existing information and provides our rationale for the classification of the variant.

Identification of pathogenic or likely pathogenic variants in dominant disorders or their combinations in different alleles in recessive disorders are considered molecular confirmation of the clinical diagnosis. In these cases, family member testing can be used for risk stratification. We do not recommend using variants of uncertain significance (VUS) for family member risk stratification or patient management. Genetic counseling is recommended.

Our interpretation team analyzes millions of variants from thousands of individuals with rare diseases. Our internal database and our understanding of variants and related phenotypes increases with every case analyzed. Our laboratory is therefore well-positioned to re-classify previously reported variants as new information becomes available. If a variant previously reported by Blueprint Genetics is re-classified, our laboratory will issue a follow-up statement to the original ordering health care provider at no additional cost.

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## ICD codes

Commonly used ICD-10 codes when ordering the Hereditary Melanoma and Skin Cancer Panel

| ICD-10 | Disease |
|---|---|
| Q87.89 | Gorlin syndrome |
| C50 C56 | Hereditary breast and ovarian cancer syndrome |

| | |
|---|---|
| E34.8 | Werner syndrome |
| Q85.8 | Cowden syndrome |
| D48.9 | Li-Fraumeni syndrome 1 |
| C43.9 | Familial atypical multiple mole melanoma syndrome |
| C43.9 | Melanoma |
| Z12.83 | Skin cancer |
| Q87.89 | Basal cell nevus syndrome |
| C43.9 | Familial melanoma |
| C69.2 | Retinoblastoma |
| Q82.1 | Xeroderma pigmentosum complementation |

## Accepted sample types

- EDTA blood, min. 1 ml
- Purified DNA, min. 3µg*
- Saliva (Oragene DNA OG-500 kit)

Label the sample tube with your patient's name, date of birth and the date of sample collection.

Note that we do not accept DNA samples isolated from formalin-fixed paraffin-embedded (FFPE) tissue.

## Resources

- American Melanoma Foundation
- Bright Pink
- Cancer.Net - Cowden Syndrome
- Cancer.net - Gorlin Syndrome
- Fighting Hereditary Breast and Ovarian Cancer
- Forgotten Diseases Research Foundation
- GeneReviews - *BAP1* Tumor Predisposition Syndrome
- GeneReviews - Gorlin Syndrome
- GeneReviews - Li-Fraumeni Syndrome
- GeneReviews - Nevoid Basal Cell Carcinoma Syndrome
- GeneReviews - Retinoblastoma
- GeneReviews - Werner Syndrome
- GeneReviews - Xeroderma Pigmentosum
- HBOC Society
- International Registry of Werner Syndrome
- Li-Fraumeni Syndrome Association
- NORD - Atypical Mole Syndrome
- NORD - Gorlin Syndrome
- NORD - Melanoma, Malignant
- NORD - Retinoblastoma
- NORD - Werner Syndrome
- NORD - Xeroderma Pigmentosum
- Skin Cancer Foundation
- The Eye Cancer Foundation