

Technical Overview: Atlas Curated Screen*

A proactive risk screening tool that uses whole-genome sequencing (WGS) to detect a range of variant types underlying 40+ health conditions. This test produces a genomic dataset that MyOme can re-query as healthcare needs change.



Clinical Use

This test is intended for a wellness screening of germline heritable conditions in individuals from an asymptomatic population. MyOme annotates and interprets variants according to American College of Medical Genetics (ACMG) guidelines,¹ and reports pathogenic or likely pathogenic variants. Results may assist with risk assessment, support a clinical diagnosis, and inform a personalized management strategy in conjunction with standard clinical assessment.

Sample Types

- ✓ Blood (2 EDTA tubes)
- ✓ Buccal (2 swabs)

Turnaround Times

- Most results are delivered **5–6 weeks** from the day all samples are received.**
- Follow-up testing or re-requisitions are typically completed in under **1 week**.

**Turnaround times are provided as estimates and begin once sample(s) are processed at MyOme. Turnaround times may be extended in cases outside of MyOme's control, including delays related to confirmation testing or other unforeseen circumstances.

Methods

Genomic DNA obtained from submitted samples is sequenced using Illumina technology and reads are aligned to the human genome reference assembly GRCh38.p14. A high-coverage (mean 30X) PCR-free whole-genome library is constructed and sequenced with 2x150 bp paired-end reads. In-house pipeline analysis identifies single-nucleotide variants (SNVs), small insertions and deletions (indels), and copy number variants (CNVs). Variant interpretation is conducted by qualified scientists based on ACMG guidelines.

151 Genes Analyzed

PLUS (PR21037)

Gene Inclusion Criteria

Genes included in this test were chosen using MyOme's rigorous framework that prioritizes variants based on clinical validity, actionability, penetrance/prevalence and feasibility.

Gene List

ABCD1, ACTA2, ACTC1, ACTN2, ACVRL1, APC, APOB, ATM, ATP7B, BAG3, BAP1, BARD1, BMPR1A, BMPR2, BRCA1, BRCA2, BRIP1, BTBD, CACNA1C, CACNA1S, CALM1, CALM2, CALM3, CASQ2, CAV1, CDH1, CDK4, CDKN1B, CDKN2A, CHEK2, COL3A1, COL5A1, COL5A2, CRYAB, CSRP3, DES, DICER1, DMD, DSC2, DSG2, DSP, EGFR, EMD, ENG, EPCAM, F2, F5, F9, FBN1, FH, FHL1, FLCN, FLNC, G6PD, GAA, GCH1, GDF2, GLA, GREM1, HAMP, HFE, HJV, HMBS, HNF1A, HNF1B, HOXB13, JUP, KCNE1, KCNH2, KCNJ2, KCNQ1, KIT, LAMP2, LDLR, LDLRAP1, LMNA, LZTR1, MAX, MEFV, MEN1, MET, MIF, MLH1, MSH2, MSH3, MSH6, MUTYH, MYBPC3, MYH11, MYH7, MYL2, MYL3, MYLK, NF1, NF2, NTHL1, OTC, PALB2, PCSK9, PDGFRA, PKP2, PLN, PMS2, POLD1, POLE, POT1, PRKAG2, PRKG1, PROC, PROS1, PTEN, RAD51C, RAD51D, RB1, RBM20, RET, RPE65, RYR1, RYR2, SCN5A, SDHAF2, SDHB, SDHC, SDHD, SERPINA1, SERPINC1, SLC40A1, SMAD3, SMAD4, SMAD9, STK11, TFR2, TGFB2, TGFB3, TGFBRI, TGFBRI2, TMEM127, TMEM43, TNNC1, TNNT3, TNNT2, TP53, TPM1, TRDN, TSC1, TSC2, TTN, TTR, VCL, VHL, WT1

Condition–Gene Relationship Table

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Test Performance²

- 30x average genome-wide coverage
- >99.5% of exonic regions at ≥10x depth
- >99.5% ClinVar P/LP variants covered at ≥10x
- >99% sensitivity for SNVs and indels
- 98% sensitivity for benchmark CNVs >1 kb

Included in Report

- Analysis of SNVs, indels and CNVs (deletions and duplications)
- Orthogonal confirmation of P/LP variants (e.g., by Sanger sequencing)
- Actionable recommendations

*This test was previously offered as "Single–Gene Risk" under MyOme Proactive Health.

1. American College of Medical Genetics and Genomics. ACMG SF v3.2 list for reporting of secondary findings. *Genet Med.* 2023;25(8):100866. doi:10.1016/j.jim.2023.100866. 2. MyOme Inc. Data on file.

Condition–Gene Relationship Table

PLUS (PR21037)

Cancer		Cardiovascular Conditions	
CONDITION	GENE	CONDITION	GENE
BAP1-related tumor predisposition syndrome	<i>BAP1</i>	Arrhythmogenic right ventricular cardiomyopathy	<i>DES, DSC2, DSG2, DSP, JUP, PKP2, PLN, TMEM43</i>
Birt-Hogg-Dube syndrome	<i>FLCN</i>	Brugada syndrome	<i>SCN5A</i>
CDH1-related diffuse gastric and lobular breast cancer syndrome	<i>CDH1</i>	CACNA1C-related disorders	<i>CACNA1C</i>
DICER1-related tumor predisposition	<i>DICER1</i>	Catecholaminergic polymorphic ventricular tachycardia	<i>CALM1, CALM2, CALM3, CASQ2, RYR2, TRDN</i>
Familial adenomatous polyposis	<i>APC, MSH3</i>	Danon disease	<i>LAMP2</i>
Familial ovarian cancer	<i>BRIP1, PALB2, RAD51C, RAD51D</i>	Dilated cardiomyopathy	<i>ACTC1, BAG3, DES, FLNC, LMNA, MYH7, RBM20, SCN5A, TNNC1, TNNI3, TNNT2, TPM1, TTN, VCL</i>
Gastrointestinal stromal tumor	<i>KIT, PDGFRA</i>	Ehlers-Danlos syndrome, vascular type	<i>COL3A1</i>
Hereditary breast cancer	<i>ATM, BARD1, CHEK2, PALB2</i>	Emery-Dreifuss muscular dystrophy	<i>EMD, FHL1, LMNA</i>
Hereditary breast and ovarian cancer	<i>BRCA1, BRCA2</i>	Fabry disease	<i>GLA</i>
Hereditary leiomyomatosis and renal cell cancer	<i>FH</i>	Familial hypercholesterolemia	<i>APOB, LDLR, LDLRAP1, PCSK9</i>
Hereditary mixed polyposis syndrome (HMPS)	<i>GREM1</i>	Familial thoracic aortic aneurysm and dissection	<i>ACTA2, MYH11, MYLK, PRKG1, SMAD3, TGFB2, TGFB3</i>
Hereditary nonpolyposis colon cancer	<i>ATM</i>	Hereditary transthyretin-related amyloidosis	<i>TTR</i>
Hereditary paraganglioma-pheochromocytoma syndrome	<i>MAX, SDHAF2, SDHB, SDHC, SDHD, TMEM127</i>	Hypertrophic cardiomyopathy	<i>ACTC1, CSRP3, MYBPC3, MYH7, MYL2, MYL3, PRKAG2, TNNC1, TNNI3, TNNT2, TPM1</i>
Juvenile polyposis syndrome	<i>BMPRIA</i>	Intrinsic cardiomyopathy	<i>ACTN2, PLN</i>
Juvenile polyposis with hereditary hemorrhagic telangiectasia	<i>SMAD4</i>	Loeys-Dietz syndrome	<i>SMAD3, TGFB2, TGFB3, TGFBFR1, TGFBFR2</i>
Li-Fraumeni syndrome	<i>TP53</i>	Long QT syndrome	<i>CALM1, CALM2, CALM3, KCNH2, KCNQ1, SCN5A, TRDN</i>
Lynch syndrome	<i>EPCAM, MLH1, MSH2, MSH6, PMS2</i>	Long QT syndrome, acquired	<i>KCNE1</i>
Melanoma	<i>CDK4, MITF</i>	Marfan syndrome	<i>FBN1</i>
Melanoma-pancreatic cancer syndrome	<i>CDKN2A</i>	Myofibrillar myopathy	<i>BAG3, CRYAB, DES, FLNC</i>
Multiple endocrine neoplasia	<i>CDKN1B, MEN1, RET</i>	Progressive muscular dystrophy	<i>DMD</i>
MUTYH-associated polyposis	<i>MUTYH</i>	Short QT syndrome	<i>KCNH2, KCNJ2, KCNQ1</i>
Neurofibromatosis type 1	<i>NF1</i>	Other	
Neurofibromatosis type 2	<i>NF2</i>	CONDITION	GENE
Non-small cell lung carcinoma	<i>EGFR</i>	Acute intermittent porphyria	<i>HMBS</i>
NTHL1-deficiency tumor predisposition syndrome	<i>NTHL1</i>	Adrenoleukodystrophy	<i>ABCD1</i>
Papillary renal cell carcinoma	<i>MET</i>	Alpha-1 antitrypsin deficiency	<i>SERPINA1</i>
Peutz-Jeghers syndrome	<i>STK11</i>	Biotinidase deficiency	<i>BTBD</i>
Polyposis and colorectal cancer	<i>POLD1, POLE</i>	Ehlers-Danlos syndrome, classic type	<i>COL5A1, COL5A2</i>
POT1 tumor predisposition	<i>POT1</i>	Familial Mediterranean fever	<i>MEFV</i>
Prostate cancer	<i>HOXB13</i>	G6PD deficiency	<i>G6PD</i>
PTEN hamartoma tumor syndrome	<i>PTEN</i>	GTP cyclohydrolase I deficiency	<i>GCH1</i>
Retinoblastoma	<i>RB1</i>	Hemophilia B	<i>F9</i>
Schwannomatosis	<i>LZTR1</i>	Hereditary antithrombin deficiency	<i>SERPINC1</i>
Tuberous sclerosis complex	<i>TSC1, TSC2</i>	Hereditary hemochromatosis	<i>HAMP, HFE, HJV, SLC40A1, TFR2</i>
Von Hippel-Lindau syndrome	<i>VHL</i>	Hereditary hemorrhagic telangiectasia	<i>ACVRL1, ENG, GDF2, SMAD4</i>
WT1-related Wilms tumor	<i>WT1</i>	Hereditary thrombophilia, protein C deficiency	<i>PROC</i>
		Hereditary thrombophilia, protein S deficiency	<i>PROS1</i>
		Malignant hyperthermia	<i>CACNA1S, RYR1</i>
		Monogenic diabetes	<i>HNF1A, HNF1B</i>
		Ornithine transcarbamylase deficiency	<i>OTC</i>
		Pompe disease	<i>GAA</i>
		Pulmonary arterial hypertension	<i>BMPR2, CAV1, GDF2, SMAD9</i>
		RPE65-related retinopathy	<i>RPE65</i>
		Thrombophilia	<i>F2, F5</i>
		Wilson disease	<i>ATP7B</i>

These tests were developed, and their performance characteristics were determined, by MyOme, Inc., a clinical laboratory certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA) and College of American Pathologist (CAP) accredited to perform high complexity clinical laboratory testing. These tests have not been cleared or approved by the U.S. Food and Drug Administration (FDA). Test results should always be interpreted by a clinician in the context of clinical and familial data with the availability of genetic counseling when appropriate. MyOme is not responsible for the content or accuracy of third-party websites.