myome | atlas™ SELECT
CURATED SCREEN™

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 PCR-free whole-genome library is constructed and a sub-aliquot is taken through PCR amplification and exome selection. The blended genome-exome libraries are sequenced to generate 2x150 bp paired-end reads, resulting in low-coverage whole-genome and higher coverage exome data. In-house pipeline analysis identifies single-nucleotide variants (SNVs) and small insertions and deletions (indels). Variant interpretation is conducted by qualified scientists based on ACMG guidelines.

84 Genes Analyzed

SELECT (PR22020)

Gene Inclusion Criteria

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

Gene List

ACTA2, ACTC1, ACVRL1, APC, APOB, ATM, ATP7B, BAG3, BMPR1A, BRCA1, BRCA2, BTD, CACNA1S, CALM1, CALM2, CALM3, CASQ2, CHEK2, COL3A1, DES, DSC2, DSG2, DSP, ENG, FBN1, FLNC, GAA, GLA, HFE, HNF1A, KCNH2, KCNQ1, LDLR, LDLRAP1, LMNA, MAX, MEN1, MLH1, MSH2, MSH6, MUTYH, MYBPC3, MYH11, MYH7, MYL2, MYL3, NF2, OTC, PALB2, PCSK9, PKP2, PMS2, PRKAG2, PTEN, RB1, RBM20, RET, RPE65, RYR1, RYR2, SCN5A, SDHAF2, SDHB, SDHC, SDHD, SMAD3, SMAD4, STK11, TGFBR1, TGFBR2, TMEM127, TMEM43, TNNC1, TNNI3, TNNT2, TP53, TPM1, TRDN, TSC1, TSC2, TTN, TTR, VHL, WT1

Condition-Gene Relationship Table

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Test Performance[2]

- ≥60x average exome-wide coverage
- ≥1x average genome-wide coverage
- ≥90% of exonic regions at ≥20x depth
- >99.5% sensitivity for SNVs
- >97.5% sensitivity for indels

Included in Report

- Analysis of SNVs and indels
- 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.gim.2023.100866. 2. MyOme Inc. Data on file.

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Condition–Gene Relationship Table

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Cardiovascular Conditions

CONDITION	GENE
Arrhythmogenic right ventricular cardiomyopathy	*DES, DSC2, DSG2, DSP, PKP2, TMEM43*
Brugada syndrome	*SCN5A*
Catecholaminergic polymorphic ventricular tachycardia	*CALM1, CALM2, CALM3, CASQ2, RYR2, TRDN*
Dilated cardiomyopathy	*ACTC1, BAG3, DES, FLNC, LMNA, MYH7, RBM20, SCN5A, TNNC1, TNNI3, TNNT2, TPM1, TTN*
Ehlers–Danlos syndrome, vascular type	*COL3A1*
Emery–Dreifuss muscular dystrophy	*LMNA*
Fabry disease	*GLA*
Familial hypercholesterolemia	*APOB, LDLR, LDLRAP1, PCSK9*
Familial thoracic aortic aneurysm and dissection	*ACTA2, MYH11, SMAD3*
Hereditary transthyretin–related amyloidosis	*TTR*
Hypertrophic cardiomyopathy	*ACTC1, MYBPC3, MYH7, MYL2, MYL3, PRKAG2, TNNC1, TNNI3, TNNT2, TPM1*
Loeys–Dietz syndrome	*SMAD3, TGFBR1, TGFBR2*
Long QT syndrome	*CALM1, CALM2, CALM3, KCNH2, KCNQ1, SCN5A, TRDN*
Marfan syndrome	*FBN1*
Myofibrillar myopathy	*BAG3, DES, FLNC*
Short QT syndrome	*KCNH2, KCNQ1*

Cancer

CONDITION	GENE
Familial adenomatous polyposis	*APC*
Familial ovarian cancer	*PALB2*
Hereditary breast cancer	*ATM, CHEK2, PALB2*
Hereditary breast and ovarian cancer	*BRCA1, BRCA2*
Hereditary nonpolyposis colon cancer	*ATM*
Hereditary paraganglioma–pheochromocytoma syndrome	*MAX, SDHAF2, SDHB, SDHC, SDHD, TMEM127*
Juvenile polyposis syndrome	*BMPR1A*
Juvenile polyposis with hereditary hemorrhagic telangiectasia	*SMAD4*
Li–Fraumeni syndrome	*TP53*
Lynch syndrome	*MLH1, MSH2, MSH6, PMS2*
Multiple endocrine neoplasia	*MEN1, RET*
MUTYH–associated polyposis	*MUTYH*
Neurofibromatosis type 2	*NF2*
Peutz–Jeghers syndrome	*STK11*
PTEN hamartoma tumor syndrome	*PTEN*
Retinoblastoma	*RB1*
Tuberous sclerosis complex	*TSC1, TSC2*
Von Hippel–Lindau syndrome	*VHL*
WT1–related Wilms tumor	*WT1*

Other Conditions

CONDITION	GENE
Biotinidase deficiency	*BTD*
Hereditary hemochromatosis	*HFE*
Hereditary hemorrhagic telangiectasia	*ACVRL1, ENG, SMAD4*
Malignant hyperthermia	*CACNA1S, RYR1*
Monogenic diabetes	*HNF1A*
Ornithine transcarbamylase deficiency	*OTC*
Pompe disease	*GAA*
RPE65–related retinopathy	*RPE65*
Wilson disease	*ATP7B*

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.