Proactive Health SINGLE-GENE RISK™ 84 GENES

TEST CODE: PR22020

Overview

MyOme Proactive Health Single-Gene risk report uses a Blended Genome-Exome (BGE) backbone built from whole exome sequencing and low coverage whole genome sequencing to identify a range of variant types. This allows MyOme to re-query a patient's data as healthcare needs change and new information about the genome is discovered.

Clinical Use

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. Genetic testing may provide information about an individual's disease risk, support a clinical diagnosis, and assist with the development of a personalized treatment and management strategy in conjunction with standard clinical assessment.

Method

PCR-free whole genome library is constructed and a sub-aliquot is taken through PCR amplification and exome selection. The blended genome and 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 allows identification of single-nucleotide variants (SNVs) and small insertions and deletions (indels). Variant interpretation by qualified scientists based on guidelines by the ACMG.

Sample Types

- Blood (2 EDTA tubes)
- Saliva (2 tubes)
- Buccal (3 swabs)

Turn Around Time

- From initial sample received, approximately 6 to 8 weeks
- For previously processed sample, approximately 2 to 4 weeks

Included

- Analysis of SNVs and small insertions and deletions
- Confirmation of Pathogenic/Likely Pathogenic variants by orthogonal method (e.g., Sanger sequencing)
- Cohesive report with actionable recommendations
- **84 Genes included:** *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, TNNI3, TNNC1, TNNT2, TP53, TPM1,TRDN, TSC1, TSC2, TTN, TTR, VHL, WT1*

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 small insertions/deletions

1. American College of Medical Genetics and Genomics. SF v3.2 list for reporting of secondary findings in clinical exome and genome sequencing: A policy statement of the ACMG. *Genet Med.* June 22, 2023. doi: 10.1016/j.gim.2023.100866.
2. MyOme Inc, Data on File.

CONDITION-GENE RELATIONSHIP

The genes listed below are analyzed in this report. MyOme selected them based on our Gene Inclusion Framework Guidelines. Genes are prioritized based on clinical validity, actionability, penetrance/prevalence, and feasibility.

Cardiovascular	
Condition	**Gene(s)**
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, SCN5A, TNNC1, TNNI3, TNNT2, TPM1, TTN, RBM20*
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	*TGFBR1, TGFBR2, SMAD3*
Long QT syndrome	*CALM1, CALM2, CALM3, KCNH2, KCNQ1, SCN5A, TRDN*
Marfan syndrome	*FBN1*
Myofibrillar myopathy	*BAG3, DES, FLNC*
Short QT syndrome	*KCNH2, KCNQ1*

Other	
Condition	**Gene(s)**
Biotinidase deficiency	*BTD*
Hereditary hemochromatosis	*HFE*
Hereditary hemorrhagic telangiectasia	*ACVRL1, ENG, SMAD4*
Malignant hyperthemia	*CACNA1S, RYR1*
Monogenic diabetes	*HNF1A*
Ornithine transcarbamylase deficiency	*OTC*
RPE65-related retinopathy	*RPE65*
Wilson disease	*ATP7B*

Cancer	
Condition	**Gene(s)**
Familial adenomatous polyposis	*APC*
Familial ovarian cancer	*PALB2*
Gastrointestinal stromal tumor	*KIT*
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*