



Proactive Health Plus

SINGLE-GENE RISK™

151 GENES

TEST CODE: PR21037

Overview

MyOme Proactive Health Plus Single-Gene Risk™ report, 151 Genes uses a PCR-free whole-genome backbone that allows identification of a range of variant types. Whole-genome sequencing (WGS) allows MyOme to re-query a patient's genome as healthcare needs change and new information about the genome is discovered.

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) guidelines¹, and reports pathogenic or likely pathogenic variants. Genetic testing may provide information to assess individual 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 library prep followed by 2x150 bp paired-end whole-genome sequencing is the backbone for this test. In-house pipeline analysis allows identification of single-nucleotide variants (SNVs), small insertions and deletions (indels) and copy number variants (CNVs). Variant interpretation is conducted by qualified scientists based on guidelines by the ACMG.

Sample Types

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

Turnaround Times

- From sample received, most results are delivered in 5–6 weeks.*
- Follow-up testing or re-requisitions are typically completed in under 2 weeks, often within just a few days.

*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.

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

This test was developed, and its 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. This test has 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.

Included

- Analysis of SNVs, indels, and CNVs (deletions and duplications)
- Confirmation of Pathogenic/Likely Pathogenic variants by orthogonal method (e.g., Sanger sequencing)
- Cohesive report with actionable recommendations
- 151 genes included: *ABCD1, ACTA2, ACTC1, ACTN2, ACVRL1, APC, APOB, ATM, ATP7B, BAG3, BAP1, BARD1, BMPR1A, BMPR2, BRCA1, BRCA2, BRIP1, BTD, 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, MITF, 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, SDHA2, SDHB, SDHC, SDHD, SERPINA1, SERPINC1, SLC40A1, SMAD3, SMAD4, SMAD9, STK11, TFR2, TGFB2, TGFB3, TGFB1, TGFB2, TMEM127, TMEM43, TNNC1, TNNI3, TNNT2, TP53, TPM1, TRDN, TSC1, TSC2, TTN, TTR, VCL, VHL, WT1*

Test Performance²

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

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		Other (Cont.)	
Condition	Gene(s)	Condition	Gene(s)
Arrhythmogenic right ventricular cardiomyopathy	DES, DSC2, DSG2, DSP, JUP, PKP2, PLN, TMEM43	Malignant hyperthermia	CACNA1S, RYR1
Brugada syndrome	SCN5A	Monogenic diabetes	HNF1A, HNF1B
CACNA1C-related disorders	CACNA1C	Ornithine transcarbamylase deficiency	OTC
Catecholaminergic polymorphic ventricular tachycardia	CALM1, CALM2, CALM3, CASQ2, RYR2, TRDN	Pompe disease	GAA
Danon disease	LAMP2	Pulmonary arterial hypertension	BMPR2, CAV1, GDF2, SMAD9
Dilated cardiomyopathy	ACTC1, BAG3, DES, FLNC, LMNA, MYH7, SCN5A, TNNC1, TNNI3, TNNT2, TPM1, TTN, VCL, RBM20	RPE65-related retinopathy	RPE65
Ehlers-Danlos syndrome, vascular type	COL3A1	Thrombophilia	F2, F5
Emery-Dreifuss muscular dystrophy	EMD, FHL1, LMNA	Wilson disease	ATP7B
Fabry disease	GLA	Cancer	
Familial hypercholesterolemia	APOB, LDLR, LDLRAP1, PCSK9	BAP1-related tumor predisposition syndrome	BAP1
Familial thoracic aortic aneurysm and dissection	ACTA2, MYH11, MYLK, PRKG1, SMAD3, TGFB2, TGFB3	Birt-Hogg-Dube syndrome	FLCN
Hereditary transthyretin-related amyloidosis	TTR	CDH1-related diffuse gastric and lobular breast cancer syndrome	CDH1
Hypertrophic cardiomyopathy	ACTC1, CSRP3, MYBPC3, MYH7, MYL2, MYL3, PRKAG2, TNNC1, TNNI3, TNNT2, TPM1	DICER1-related tumor predisposition	DICER1
Intrinsic Cardiomyopathy	ACTN2, PLN	Familial adenomatous polyposis	APC, MSH3
Loeys-Dietz syndrome	TGFB2, TGFB3, TGFBR1, TGFBR2, SMAD3	Familial ovarian cancer	BRIP1, PALB2, RAD51C, RAD51D
Long QT syndrome	CALM1, CALM2, CALM3, KCNH2, KCNQ1, SCN5A, TRDN	Gastrointestinal stromal tumor	KIT, PDGFRA
Long QT syndrome, acquired	KCNE1	Hereditary breast cancer	BARD1, ATM, CHEK2, PALB2
Marfan syndrome	FBN1	Hereditary breast and ovarian cancer	BRCA1, BRCA2
Myofibrillar myopathy	BAG3, CRYAB, DES, FLNC	Hereditary leiomyomatosis and renal cell cancer	FH
Progressive muscular dystrophy	DMD	Hereditary Mixed Polyposis Syndrome (HMPS)	GREM1
Short QT syndrome	KCNH2, KCNJ2, KCNQ1	Hereditary nonpolyposis colon cancer	ATM
Other		Hereditary paraganglioma-pheochromocytoma syndrome	MAX, SDHA2, SDHB, SDHC, SDHD, TMEM127
Condition	Gene(s)	Juvenile polyposis syndrome	BMPR1A
Acute intermittent porphyria	HMBS	Juvenile polyposis with hereditary hemorrhagic telangiectasia	SMAD4
Adrenoleukodystrophy	ABCD1	Li-Fraumeni syndrome	TP53
Alpha-1 antitrypsin deficiency	SERPINA1	Lynch syndrome	EPCAM, MLH1, MSH2, MSH6, PMS2
Biotinidase deficiency	BTD	Melanoma	CDK4, MITF
Ehlers-Danlos syndrome, classic type	COL5A1, COL5A2	Melanoma-pancreatic cancer syndrome	CDKN2A
Familial Mediterranean fever	MEFV	Multiple endocrine neoplasia	CDKN1B, MEN1, RET
G6PD deficiency	G6PD	MUTYH-associated polyposis	MUTYH
GTP cyclohydrolase I deficiency	GCH1	Neurofibromatosis type 1	NF1
Hemophilia B	F9	Neurofibromatosis type 2	NF2
Hereditary antithrombin deficiency	SERPINC1	Non-small cell lung carcinoma	EGFR
Hereditary hemochromatosis	HAMP, HFE, HJV, SLC40A1, TFR2	NTHL1-deficiency tumor predisposition syndrome	NTHL1
Hereditary hemorrhagic telangiectasia	ACVR1L, ENG, GDF2, SMAD4	Papillary renal cell carcinoma	MET
Hereditary thrombophilia due to congenital protein C deficiency	PROC	Peutz-Jeghers syndrome	STK11
Hereditary thrombophilia due to congenital protein S deficiency	PROS1	Polyposis and colorectal cancer	POLD1, POLE
Pompe disease	GAA	POT1 Tumor predisposition	POT1
		Prostate cancer	HOXB13
		PTEN hamartoma tumor syndrome	PTEN
		Retinoblastoma	RB1
		Schwannomatosis	LZTR1
		Tuberous sclerosis complex	TSC1, TSC2
		Von Hippel-Lindau syndrome	VHL