

Genetic testing for predisposition to cancer



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The benefits of our applications for hereditary cancer predispositions

Automated analysis of hereditary cancer predispositions

MH Guide/BRCA and MH Guide/Mendel for hereditary cancer predispositions are optimized for automated identification of clinically-significant germline variants associated with hereditary breast and ovarian cancers (HBOC), and other hereditary cancer predispositions, respectively.

How your laboratory benefits from our solutions:

- Approved for diagnostic use**
Our applications for HBOC and other hereditary cancers are modules of MH Guide. MH Guide is a software application approved in Europe as an IVD medical device according to (EU) 2017/746 (IVDR).
- Customizable evaluation**
The filtering and editing options allow quick access to the most important information as well as the integration of proprietary databases.
- Faster results**
Automatic access to relevant databases, as well as variant pre-classification according to ACMG criteria and genotype-phenotype correlations.
- Audited quality**
Molecular Health's quality management system (QMS) is certified according to EN ISO 13485, for the design and manufacture of medical devices. Users benefit from the safety and reliability of MH software applications.
- Easy to integrate**
Flexible interfaces make it possible to analyze standard data formats from the sequencing of commercially-available or proprietary gene panels, independent of the platform used.

Identify hereditary cancer predispositions – quickly, accurately, and efficiently

Our software applications analyze gene variants in comparison with data from Dataome, one of the world's largest knowledge bases for biomedical information. The software provides annotation data from recognized databases such as ClinVar, BRCA Exchange, and LOVD, which are updated regularly.

You can use any commercially available or custom gene panels and have the data analyzed in VCF format with our applications.

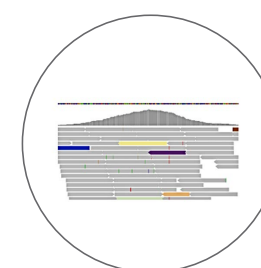
The software summarizes all of the relevant results in individual reports that provide users with clear, specific information on possible pathogenic gene mutations associated with HBOC and other hereditary cancers.



2

The analyses process

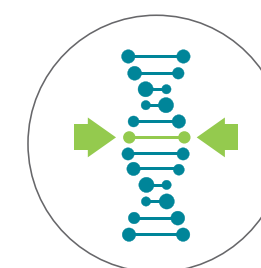
Genomic data from a blood sample



Technology-independent data upload:

- VCF files
- Commercial panels
- Custom panels

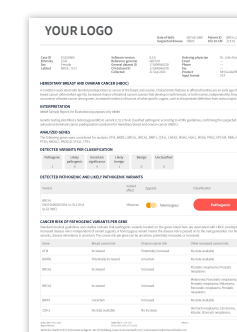
Interpretation of genetic variants



Automated knowledgebase comparison and classification

- Public databases
- MH database
- ACMG classification
Richards S et al., Genet Med 2015

Reporting



Standardized, customizable report

- Your summary
- Summary of pathogenic variants
- All reported variants with classification

3

Integration in lab workflows

Flexibility and data security in one

The web-based software applications can be easily integrated in the laboratory. They enable the annotation and interpretation of genetic variants from common NGS or other analysis platforms.



Approved for clinical use

Our applications for HBOC, and other hereditary cancers are modules of MH Guide, a software application approved in Europe as an IVD medical device according to (EU) 2017/746 (IVDR).



SaaS – individually scalable

Our applications are offered as scalable SaaS (Software as a Service) to suit small and large institutions alike.



Secure data transmission

Molecular Helath employs advanced encryption standards (SSL/TLS, AES-256) to safeguard patient data and stores it with controlled access authorization.



Guaranteed security of patient data

MH Guide meets the requirements of:

- General Data Protection Regulation (GDPR) in Europe.
- Health Insurance Portability and Accountability Act (HIPAA) in the USA.
- Genetic Diagnostics Act (GenDG) in Germany.



Customizable patient reports

The design, content, and format of analysis reports can be adapted to individual needs on request.



Flexible input and output formats

Our applications process the standard data format VCF. Output formats are PDF, and JSON. Structured export of all variant information is available in CSV format for single and multi case analysis.



Efficient workflows in your lab

Our applications let you optimize your everyday processes. The cloud-based software automates the interpretation of germline variants and delivers high-quality analyses.



Data center architecture

Molecular Health utilizes data centers certified according to international security standards, including Trusted Site Infrastructure (TSI) and ISO 27001.

Molecular Health performs third-party penetration tests and maintains a continuous process for vulnerability scanning and handling.

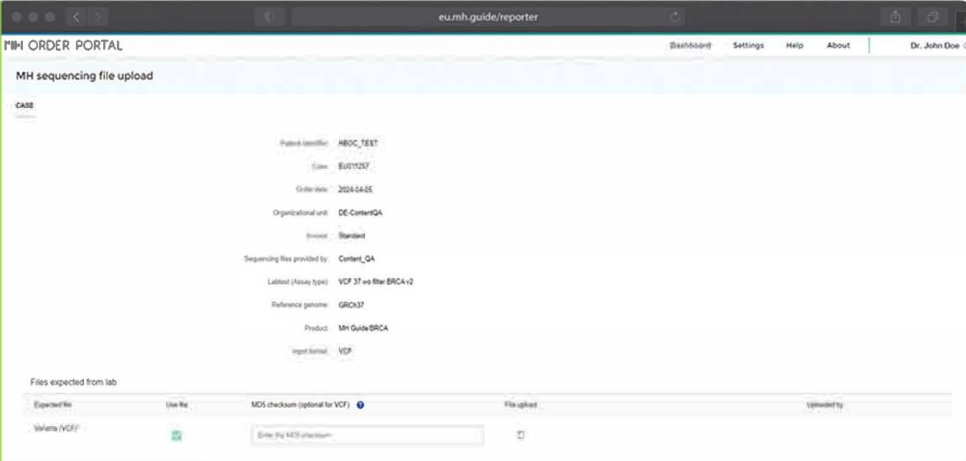
4

Generate the report: just a few, intuitive steps

How it looks on your screen: from raw data upload
to final patient report

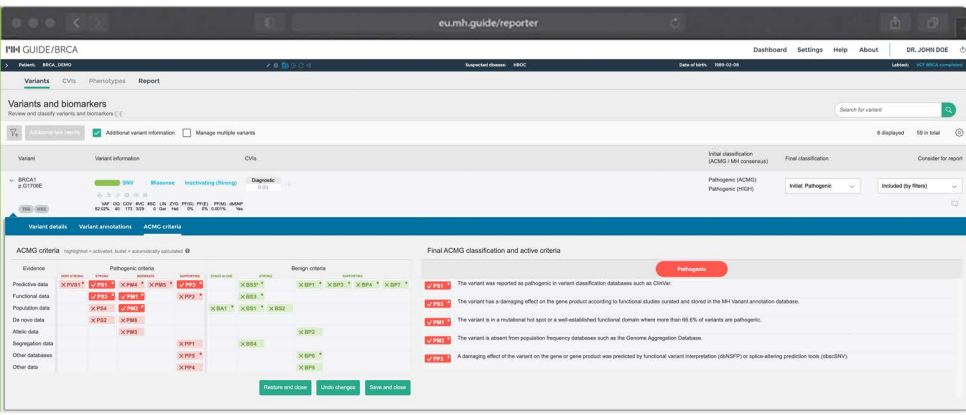
1

Upload sequence data easily, via the MH Order Portal



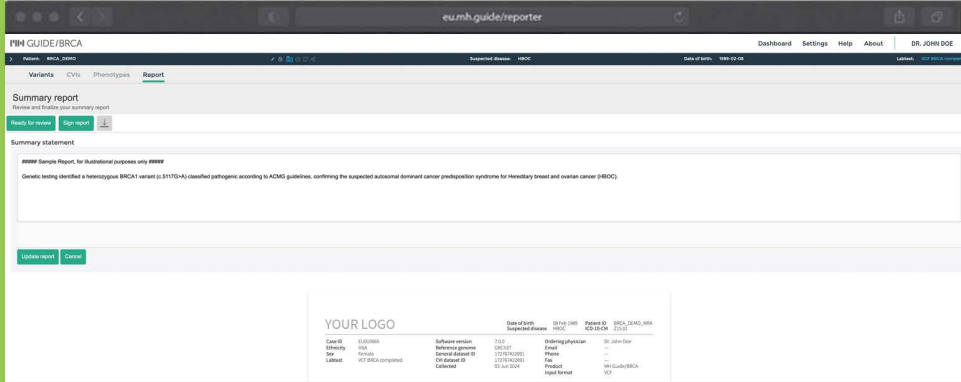
2

Automatic variant classification



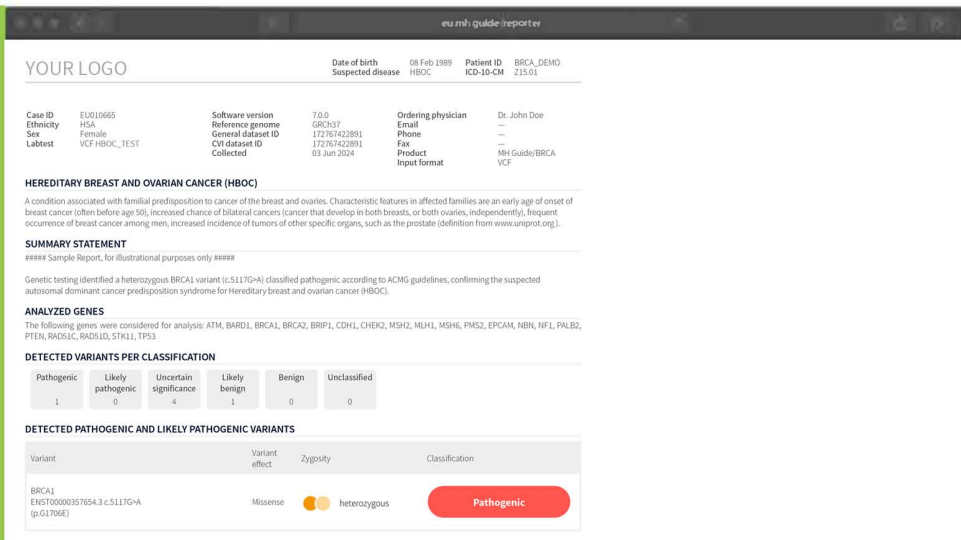
3

Generate the report



4

Export the report (detailed description on following page)





Everything at a glance:*

Patient data and suspected diagnosis

Summary of the disease, your interpretation
of the findings, and analyzed genes

Number of detected variants
per classification

Summary of detected
pathogenic variants

Zygosity

Variant classification according
to ACMG

List of analyzed genes and inferred
pathogenicity of the variant

Electronic signature of the
human geneticist in charge

YOUR LOGO

Date of birth
Suspected disease
08 Feb 1989
HBOC
Patient ID
ICD-10-CM
BRCA_DEMO
Z15.01

Case ID	EU010665	Software version	7.0.0	Ordering physician	Dr. John Doe
Ethnicity	HSA	Reference genome	GRCh37	Email	—
Sex	Female	General dataset ID	172569309751	Phone	—
Labtest	VCF BRCA completed	CVI dataset ID	172569309751	Fax	—
		Collected	03 Jun 2024	Product	MH Guide/BRCA
				Input format	VCF

HEREDITARY BREAST AND OVARIAN CANCER (HBOC)

A condition associated with familial predisposition to cancer of the breast and ovaries. Characteristic features in affected families are an early age of onset of breast cancer (often before age 50), increased chance of bilateral cancers (cancer that develop in both breasts, or both ovaries, independently), frequent occurrence of breast cancer among men, increased incidence of tumors of other specific organs, such as the prostate (definition from www.uniprot.org).

SUMMARY STATEMENT

Sample Report, for illustrational purposes only

Genetic testing identified a heterozygous BRCA1 variant (c.5117G>A) classified pathogenic according to ACMG guidelines, confirming the suspected autosomal dominant cancer predisposition syndrome for Hereditary breast and ovarian cancer (HBOC).


ANALYZED GENES

The following genes were considered for analysis: ATM, BARD1, BRCA1, BRCA2, BRIP1, CDH1, CHEK2, MSH2, MLH1, MSH6, PMS2, EPCAM, NBN, NF1, PALB2, PTEN, RAD51C, RAD51D, STK11, TP53

DETECTED VARIANTS PER CLASSIFICATION

Pathogenic	Likely pathogenic	Uncertain significance	Likely benign	Benign	Unclassified
1	0	4	1	0	0

DETECTED PATHOGENIC AND LIKELY PATHOGENIC VARIANTS

Variant	Variant effect	Zygosity	Classification
BRCA1 ENST00000357654.3 c.5117G>A (p.G1706E)	Missense	 heterozygous	Pathogenic

CANCER RISK OF PATHOGENIC VARIANTS PER GENE

Standard medical guidelines and studies indicate that pathogenic variants located on the genes listed here are associated with HBOC predisposition. The increased disease risk is independent of variant zygosity. A homozygous variant means the disease risk is passed on to the next generation. For heterozygous variants, disease inheritance is uncertain. The cancer risk per gene can be uncertain, potentially increased, or increased.

Gene	Breast cancer risk	Ovarian cancer risk	Other increased cancer risks
ATM	Increased	Potentially increased	No data available
BARD1	Potentially increased	Uncertain	No data available
BRCA1	Increased	Increased	Prostatic neoplasms; Prostatic neoplasms
BRCA2	Increased	Increased	Melanoma; Pancreatic neoplasms; Prostatic neoplasms; Melanoma; Pancreatic neoplasms; Prostatic neoplasms
BRIP1	Uncertain	Increased	No data available
CDH1	No data available	No increase	Stomach neoplasms; Stomach neoplasms; Carcinoma, lobular;

Order date 27 Nov 2023
Report Version 2

Signed by Dr. John Doe
09 Aug 2024 11:30 (UTC+02:00)

Phone —

*MH Guide/BRCA sample report of an HBOC predisposition analysis

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How to reach Molecular Health



Molecular Health GmbH
Kurfuersten-Anlage 21
69115 Heidelberg, Germany
(GER): +49 6221 43851-150

CustomerService@molecularhealth.com

We develop and deliver innovative technologies
for in silico medicine and precision medicine

Our solutions enable the conversion of large amounts of data into evidence-based, medically relevant results for the actors in the healthcare sector. Therewith, we provide molecular pathologists, geneticists, physicians, and patients with better information

on diagnoses and therapy options. We support pharmaceutical and health organizations by optimizing clinical studies in the development of promising active ingredients and meaningful disease models.

[Request a demo](#)



[Learn more about our certifications](#)

