

Empowering people to use genetic testing for their health and well-being

Whole Exome Sequencing Decode&Discover

WHAT IS WHOLE EXOME SEQUENCING?

Whole exome sequencing (WES) is a **comprehensive genetic test which analyzes the protein-coding regions (exons) of all human genes (~20,000 genes)**. The sum of all the exons is called an exome. The human exome contains ~85% of known disease-related variants. The remaining 15% of disease-causing variants are located within introns (non-coding regions). **Decode&Discover** is designed to detect the exome variants, as well as the intronic variants. All of these variants can change the function of the underlying DNA sequence, thereby causing disease.

WHY PERFORM WHOLE EXOME SEQUENCING?

WES offers a simultaneous analysis of a large number of genes. **It substantially increases the chances of finding the genetic cause of diseases with complex and non-specific symptoms.** WES reduces the time and cost from symptom presentation to diagnosis, and has an increased diagnostic yield. The results may provide information about the recurrence risk (chance of having another child with a similar condition) and may also be useful for other family members.

WHO CAN BENEFIT FROM WHOLE EXOME DECODE&DISCOVER?



Patients with a complicated medical history that affects many organs



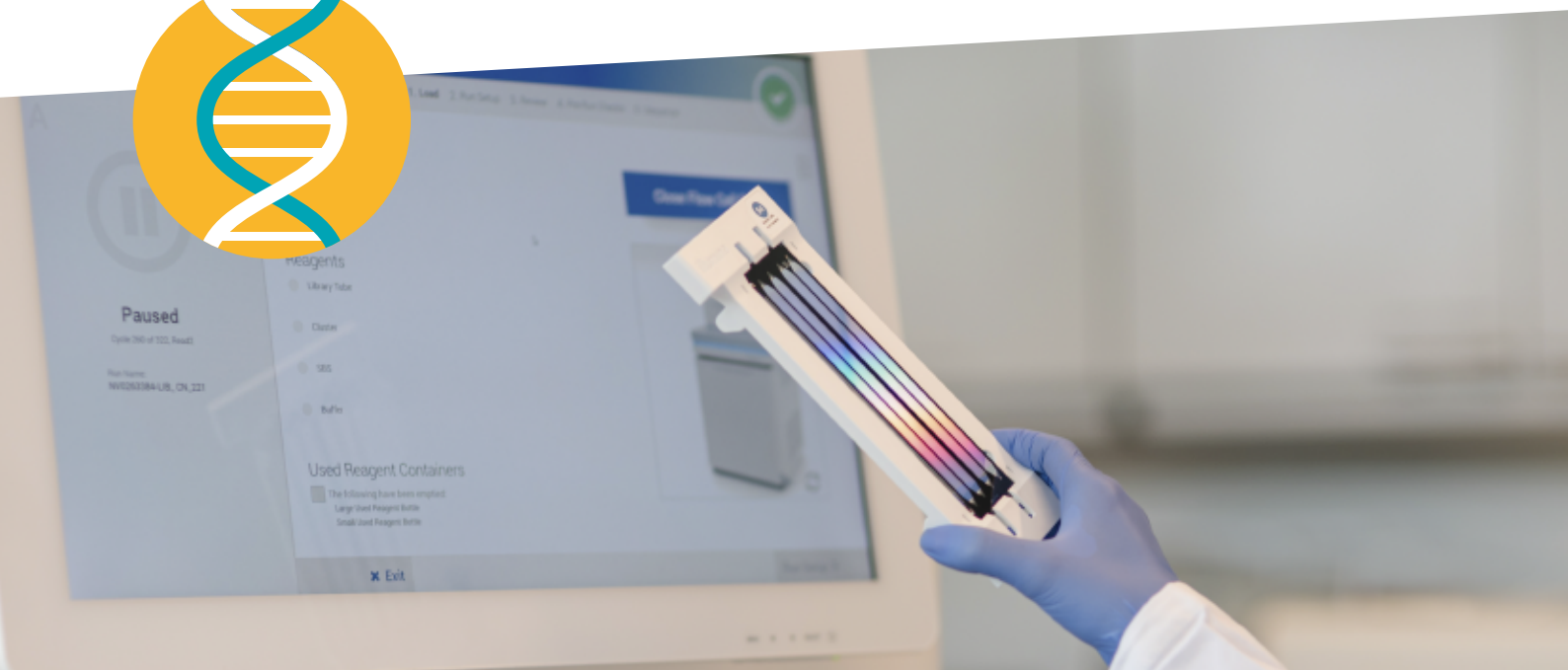
Patients who have undergone previous genetic testing with inconclusive results



Patients with complex, non-specific symptoms with multiple differential diagnoses



Patients with a severe presentation in the neonatal or childhood period



OUR TEST OPTIONS

Single WES

Only the patient is tested

Duo WES

Patient and one biological parent are tested

Trio WES

Patient and both biological parents are tested

Trio WES is the most commonly performed analysis providing comprehensive results with the highest diagnostic yield. In cases where only one or no biological parent is available for testing, we can perform Duo WES or Single WES respectively. Trio WES allows simultaneous analysis for all modes of inheritance and can ascertain the significance of clinically relevant variants.

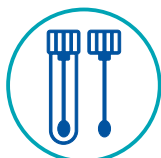
HOW TO ORDER DECODE&DISCOVER



Pre-Test
GENETIC
COUNSELLING



STEP 1
TEST
ORDERED



STEP 2
SAMPLE
COLLECTED



STEP 3
SAMPLE
PROCESSED



STEP 4
RESULTS
DELIVERED



Post-Test
GENETIC
COUNSELLING

POSSIBLE OUTCOMES OF THE TEST

Pathogenic and likely pathogenic variants: the genetic cause of the observed symptoms has been identified and may help determine the right treatment and management plan.

Variants of unknown significance (VUS): there was not enough evidence to classify the variant as either pathogenic or neutral. However, future information may connect the variant with the patient's symptoms. If new information becomes available, the meaning of the results may change for the patient and their relatives (and they will be notified). Annual variant reclassification and testing family members is recommended.

Incidental findings: genetic changes that are not associated with the patient's current condition may be discovered which may be medically important and will be automatically included in the report unless they are associated with adult-onset disorders for which there are no interventions available.

Secondary findings: genetic changes that are not associated with the patient's current condition, which have been defined by the American College of Medical Genetics as medically important. The patient or legal guardian must consent to the reporting of these results.

It is important to note that a negative result does not guarantee the absence of a disorder or that the disorder does not have a genetic cause. Additional knowledge may become available that could explain the underlying cause of the symptoms.

ABOUT US

Medicover Genetics supports you throughout your diagnostic journey with reliable testing and genetic counselling.



German leader in
genetic testing



>20 years
of experience



Up-to-date
diagnostic algorithm



Strong clinical
team of scientists
and physicians



Accredited
laboratories