

**enGenome provides innovative software technology and bioinformatics services for the interpretation of sequencing data in clinical and research settings.**

*"We are passionate about delivering the most accurate genomic interpretation and bringing hope to millions of patients with rare genetic diseases"*

## Variant Interpretation from VCF

eVai is a CE-IVD software that provides expert interpretation of germline variants to assist the geneticist in the diagnosis of rare disease.

**eVai**



Classification of SNVs/INDELS and CNVs according to ACMG/ClinGen guidelines



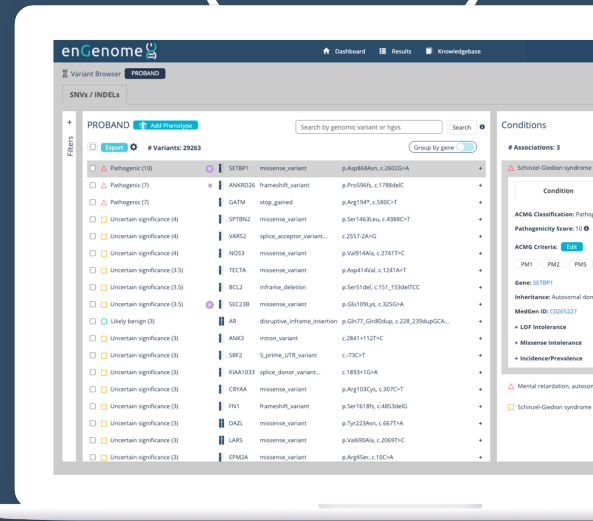
Prioritization of variants based on pathogenicity



Family analysis up to 7 members and inference of inheritance patterns



Analysis of variants from gene panels, WES and WGS



**Request a Demo**

## Secondary Analysis from FastQ

enGenome's pipelines process data from DNA-Seq, RNA-Seq and others.

We develop custom, accurate and reproducible bioinformatics workflows combining AI, Bioinformatics and High Performance Computing.