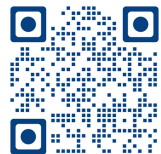


CONTACT US

www.seqone.com
contact@seqone.com



CONFIDENTLY PERFORM NGS DATA ANALYSIS

Regulatory Compliance

CE-IVD platform, ISO-13485 certified

Cyber Security

ISO-27001 certified hosting environment
Health Data Storage (HDS) certified
Patented Genomic Data Double Encryption

Data Privacy

Data not shared or commercialized
Variant knowledge base remains fully private

SEQONE genomeAlert!



Automated variant reevaluation agent developed in collaboration with geneticists



Monthly reanalysis of all historical cases (ClinVar latest updates)



Time-saving report (highlight new candidates or revoke diagnoses)

SeqOne

FROM GENOME TO PERSONALIZED MEDICINE

FOR RARE & INHERITED DISEASES



Web-based
User-friendly interface



One-stop shop
germline and somatic



Powered by
explainable AI

DIAG. AI	ACMG	VKB	PATIENT GT VAF	GENE	TRANSCRIPT	HGVS	EXON	EFFECT	CLINVAR
96%	5	5	50.8%	SLC25A22	NM_024698.6	c.813_814del p.A272QfsTer144	9/10	High Frameshift	3 LP Mucopolysaccharidosis VI
90%	5	5	46.9%	SLC25A22	NM_024698.6	c.818G>A p.R273K	9/10	Moderate Missense	
85%	5	5	100%	BCAP31	NM_001139441.1	c.-45+1_-45+2d --	N/A	High Splice Donor	7 VUS
75%	5	5	0%	OCLN	NM_002538.4	c.1037+1G>A --	N/A	High Stop Gained	
71%	5	5	44.8%	SLC3A1	NM_000341.4	c.1084C>T p.R396W	6/10	Moderate Stop Gained	8 P Prinzmetal's angina
71%	5	5	88.2%	MEFV	NM_000243.3	c.169_17@2del p.A744S	3/5	High Frameshift	
70%	5	5	43.8%	METTL23	NM_001080510.5	c.413A>G p.G303R	3/3	High Stop Gained	
52%	5	5	56%	TLR7	NM_004333.6	c.907G>A p.R396W	5/12	Moderate Stop Gained	3 LP Mucopolysaccharidosis VI
51%	New	5	44.6%	DHCR7	NM_004333.6	c.2102G>A p.R86Ter	8/9	High Stop Gained	
50%	New	5	50%	CYP24A1	NM_016562.4	c.2144-10delinsTT --	9/12	High Frameshift	2 B 1 P Bicuspid aortic valve
50%	New	5	54%	CEP55	NM_000552.5	c.991C>T p.P301LfsTer139	9/9	Moderate Stop Gained	8 P Prinzmetal's angina
23%	New	5	50.6%	RAB3GAP1	NM_004333.6	c.163del p.R1046C	1/16	Moderate Frameshift	
22%	New	5	52.7%	VWF	NM_152641.4	c.5237G>A p.P705S	5/12	Moderate Stop Gained	
14%	New	5	51.5%	JPH3	NM_004333.6	c.2107C>T p.R1746K	4/9	Low Stop Gained	5 P Congenital long QT syndrome
11%	New	5	51.5%	JPH3	NM_004333.6	c.2107C>T p.R1746K	4/9	Low Stop Gained	5 P Congenital long QT syndrome
11%	New	5	51.5%	OTOG1	NM_173591.7	c.5237G>A	4/9	High	3 LP Mucopolysaccharidosis VI



© SeqOne 2024 - All rights reserved

SM-2024072

SeqOne Platform is a CE-IVD certified in vitro diagnostic medical device, designed to perform bioinformatics analysis of raw high-throughput sequencing data to help diagnosis. Manufacturer: SeqOne Genomics (France). Please read the instructions provided in the user manual carefully.

www.seqone.com - contact@seqone.com

WHO WE ARE



OUR VISION

Founded in 2017, SeqOne develops state-of-the-art genomics analysis tools for clinical applications in oncology and rare diseases. **Our vision is to make personalized healthcare a reality** for all by democratizing access to **advanced genomic insights**, enabling every lab to offer **affordable** precision medicine solutions to patients **at scale**.

OUR SOLUTION

Our **CE-IVD** platform provides **time-saving, flexible, and cost-effective** decision support, **empowering decentralized laboratories** worldwide to deliver precision diagnostics. We integrate **cutting-edge AI and big data technologies** to redefine genetic data analysis.

70+

SeqOne employees



1000+ routine users



Fast-growing, present in 10 countries

THE SEQONE PLATFORM

Complete germline pipelines for **DNA** analysis, tailored for **targeted panels, exome, genome and aCGH arrays** to provide support for diagnosis and therapeutic decisions.

Hereditary Cancers

Rare & Inherited Diseases

GermVar (from FASTQ file)

In-house / Third-party secondary analysis

GermVar Tertiary (VCF from Dragen, Epi2ME, Alissa Reporter or XLS file)

ALL-IN-ONE NGS DATA ANALYSIS SOLUTION

For Solo & Family Analyses



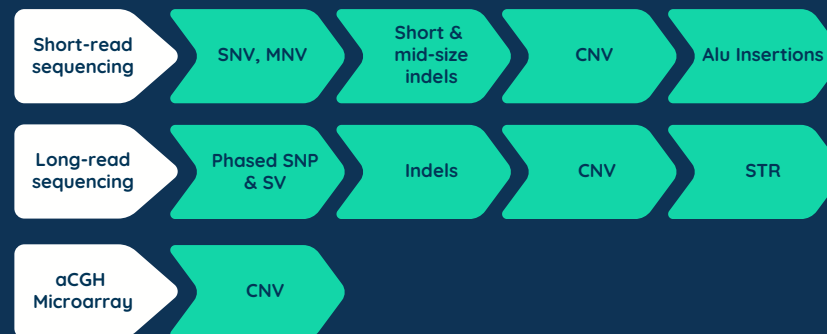
Maximize your workflow efficiency

- **SeqOne SDS** automates data and metadata upload from the sequencer, autorun analysis, and bi-directional communication with the LIMS system
- **DiagAI machine learning assistance** to rank, shortlist and suggest causal variants
- **Advanced & customizable filtering and reporting** to fit with lab workflow
- **Private and secure Variant Knowledge Base (VKB)** to keep track of past evaluations



Ensure accurate identification of your variants

- **Automated classification** based on ACMG/ClinGen
- **Premium annotation data sources:** ClinVar, gnomAD V4, OMIM
- **Scoring integration:** REVEL, CI-SpliceAI
- **Pathogenicity prediction** with an in-house, AI-powered score
- **Precise variant detection** on Hg19/Hg38 reference genome



Benefit from a flexible and future-proof platform

- **Wet-lab agnostic** (Illumina, Agilent, Twist, Roche, etc.)
- **Sequencer compatibility** (Illumina, MGI, Element, ONT, etc.)
- **Monthly updates** to keep pace with scientific discoveries