SeqOne GENOMICS

Connect to a source of deeper genomic insights

SeqOne platform in Oncology

- A comprehensive software solution for analyzing somatic variants based on DNA, RNA or ctDNA
- To provide support for diagnosis and therapeutic decision, SeqOne platform detects several types of somatic variants including:
  - Single Nucleotide Variant (SNV), Multi Nucleotide Variant (MNV), and short indels
  - Splicing event and gene fusion for RNA sequencing

Data-specific solutions

RNA solution for splicing events, SeqOne platform provides functional analysis of the impact of splicing in the new protein

ctDNA Bioinformatics pipeline have been tuned to be able to detect very low variant allele frequency

DNA

- MSI and TMB Computation of biomarkers to determine
- patients eligible to targeted drugs including Tumor Mutational Burden (TMB) and Microsatellite instability (MSI)
- CNV Call of Copy Number variation (CNV) when cohorts of individuals are available
- ALU insertion Detection of ALU insertion, medium-size deletions and duplications (<300 bp) including FLT3-ITD variation

Advantages of SeqOne platform for Oncology

- Compatibility SeqOne bioinformatic pipelines are compatible with most gene panels and have been designed to be agnostic to specificities of the wet lab
- Annotation Fusion, splicing events & SNV are enriched with annotations arising from several knowledge databases including CIVIC, OMIM, CLINVAR, GNOMAD and COSMIC
- Pooled analysis in which SeqOne platform computes variant frequency for a sample of individuals to detect sequencing artifacts
- Drug and trial recommendation provided for each variant based on the Molecular Match knowledge database
- Pathogenicity prediction provided with ACMG classes using ComPerMed framework, which is a technical guideline to harmonize clinical interpretation of variants
- UMI adapters SeqOne platform implements dedicated platform to account for UMI adapters:
  - UMI-specific pipeline increase variant detection sensitivity
  - UMI-specific pipeline is critical to improve SNV calling precision for samples with very low tumoral content and ctDNA

10 reasons to consider SeqOne GENOMICS

1

From FastQ to final report

A true end-to-end solution for efficiency and traceability from raw data (FastQ or Dragen VCF) to easily understandable and actionable clinical report.

2

Supports both somatic and constitutional analysis

SeqOne supports both somatic and constitutional analysis on a unified platform

3

Bioinformatic excellence

SeqOne's platform offers advanced bioinformatics that detect complex variants and support all the important usages including UMIs for liquid biopsy analysis, noise and artefact reduction for a lower false positive rate

4

Easy-to-use interpretation environment

An intuitive visual environment providing tools to boost interpretation efficiency. SeqOne's platform offers specific applications to address the requirements of each genomic test

5

ML driven variant classification

Biological and clinical pre-classification based on European International Guidelines (ACMG, AMP, ComPerMed) and on machine learning systems

6

Quality control

QC base-per-base coverage ensuring true negative assertion

7

World-class support

Qualified support team of genomic specialists Method validation for accreditation bodies

8

Certification

A platform built for clinical diagnostic routine: CE-IVD, HDS and ISO27001 certified

9

Data security

SeqOne stores data on an ISO27001 compliant platform and offers additional user-specific data encryption to ensure data stays safe

10

Up-to-date knowledge

Regularly updated molecular and clinical knowledge bases (biological, clinical and therapeutic) with update notification to enable retrospective analysis of variants, treatments and clinical trials.