Alissa Interpret

Clinical decision support at your fingertips

Alissa Interpret Delivers

- Inherited and somatic sample workflows
- Molecular and structural variant classification and curation
- Clinical-grade standard operating procedure (SOP) implementation
- Access to knowledge bases and easy drafting of lab reports
- Team of experts as partners
- Seamless integration with lab systems

Make your variant assessment flow

Alissa Interpret allows clinical genetics and molecular pathology labs to efficiently triage, curate and report genomic variants. Whether from NGS or arrays, this genomics data management solution automates the lab's clinical workflow from variant filtration and annotation, through curation and classification, to draft lab report. In addition, Alissa Interpret can be seamlessly integrated with existing lab BioIT pipelines and LIMS systems. Users can also rely on support from a team of experts not just during setup, but also as the lab grows.

Designed for clinical diagnostics

Alissa Interpret provides access to clinical annotation sources and databases, both for inherited and somatic diseases, and supports ACMG guideline variant curation. It also features in-depth analytics tools for inheritance modes, variant effect prediction and variant review for the observed phenotype or tumor type.

A single platform for all clinical applications across NGS and CGH

Alissa Interpret combines CNVs, SNPs, indels, fusion genes and biomarkers (such as TMB and MSI) in an integrated workflow. On a single platform, Interpret supports workflows for both inherited and somatic disease, interpreting NGS and CGH derived variants—from filter trees through to the clinical-grade report (Figure 1).

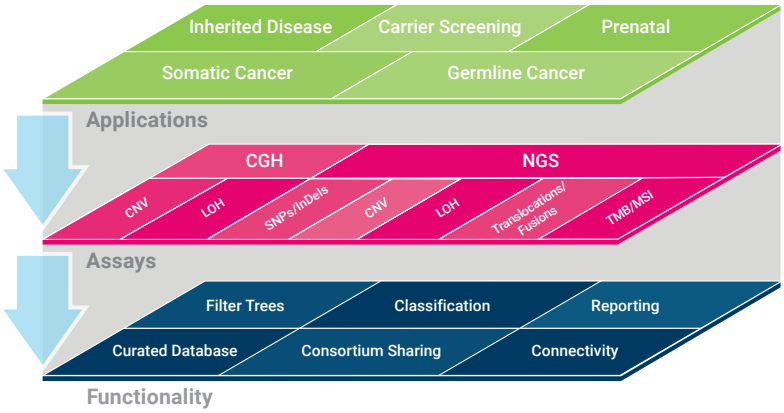

Figure 1. A 3D rendering illustrating how the tools and functionality provided by Alissa Interpret deliver clinically relevant variant assessment across different application areas and genomic events.

Agilent

Trusted Answers

Deploy new tests and scale to volume

Molecular diagnostic labs are implementing their standard operating procedures (SOPs) on Alissa Interpret to free up time for their clinical experts to focus on review and signing out cases. This fast and precise variant assessment and reporting solution allows clinical genetics and molecular pathology labs to run efficiently and scale to high throughput workflows across the menu of tests they offer. Interpret can also be seamlessly integrated with existing lab BioIT pipelines and LIMS systems for an even greater efficiency gain, either as a service or by using the available APIs.

Advanced decision tree based filtration system

Automate your lab's variant assessment workflow in configurable, versioned pipelines. Slice and dice to quickly drill down to your variants of interest for further manual review. Store and version your pipelines to support increasing volumes and scale your sample throughput with ease (Figure 2).

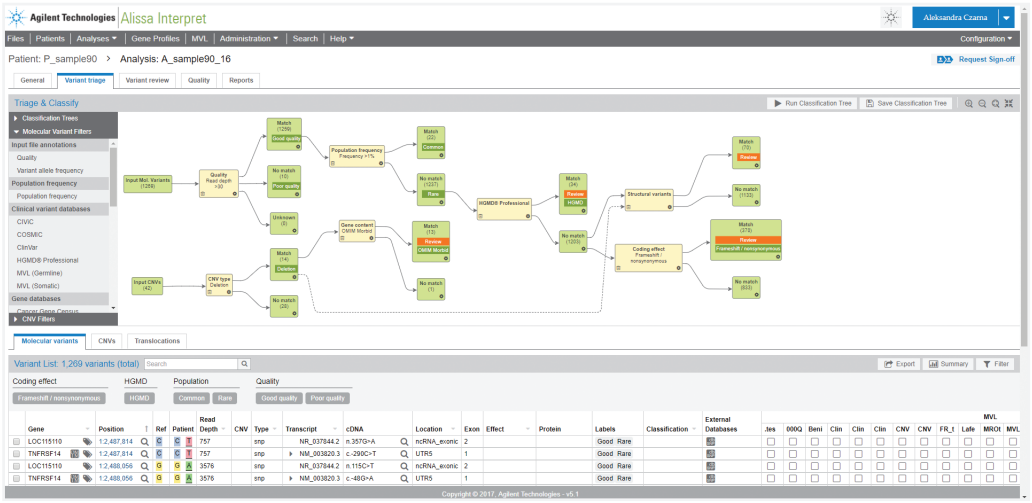

Figure 2. Classification tree with CNV integration.

Phenotype-driven variant prioritization

Alissa Interpret provides a variant prioritization feature using patient phenotypical traits, phenotype-genotype association data and other variant annotations to propose a set of potentially relevant variants to the user, ranked by estimated relevance for the analysis at hand.

Building and accessing curated variant databases

Collaboratively curate your internal knowledgebase while also tapping into an expansive array of public databases, including variant adaptations and effect annotations, frequency databases, clinically relevant peer reviewed findings, and many others (Figure 3A).

A)

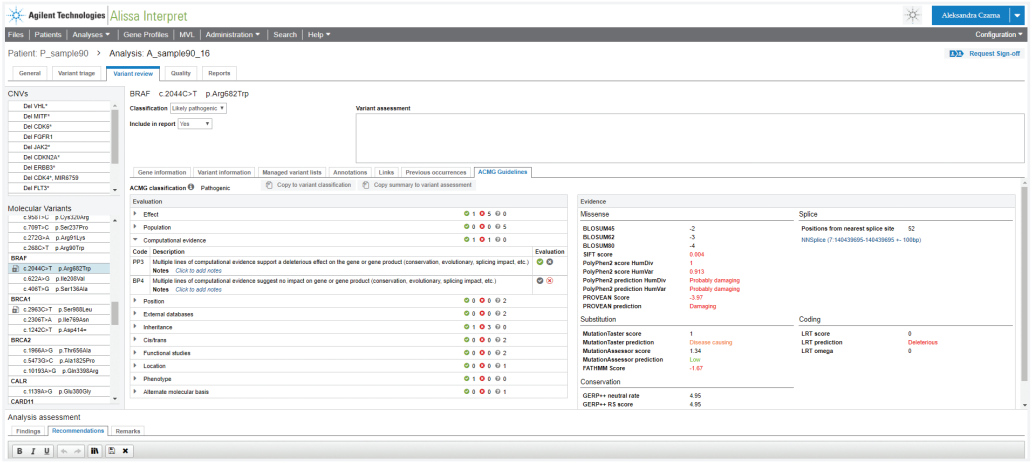

Figure 3A. Variant curation using the ACMG guidelines made easy, with all relevant evidence at your fingertips. In this example the 'Evidence' section includes the relevant computational evidence for the detected BRAF gene mutation.

For molecular pathology specifically (Figure 3B), Interpret also integrates direct access to up-to-date actionable knowledge on efficacy of therapies and clinical trials available in both community driven database like CIViC and COSMiC and the third party curated information maintained in JAX-CKB.*

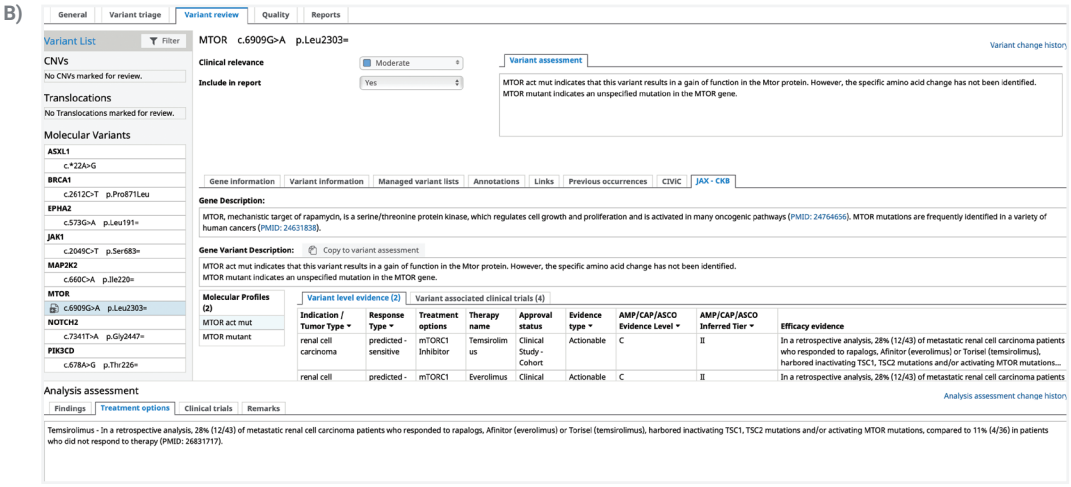

Figure 3B. Direct access to up-to-date clinically actionable variant information for variants in cancer—including therapy and clinical trial information—speeds up variant review and reporting, powered by CIViC and JAX-CKB.

Comprehensive report templates

With Alissa Interpret, reports can be fully configured towards lab needs, both in content as well as layout. For comprehensive report templates, you can include information on your sample, findings, public information, databases, and literature annotations.

Additionally, easy-to-read overviews of variants are provided with their various characteristics, such as read depth, nomenclature, transcripts, gene definitions, and classification. Automatically generated text can be included in a context-sensitive way.

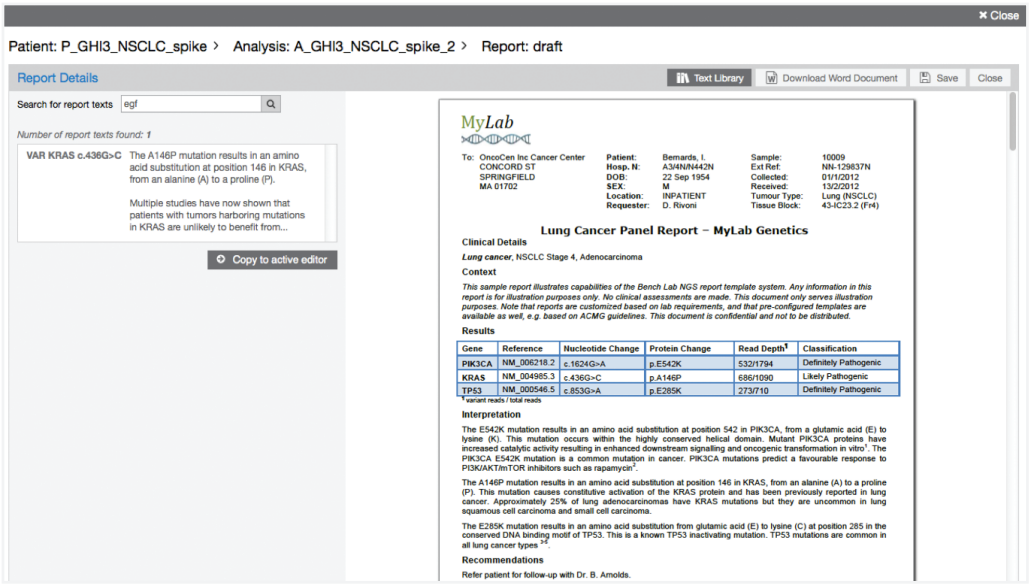

Figure 4. Example of an automated clinical-grade draft report based on convenient report templates.

*Somatic gene variant annotations and related content have been powered by Interpret's JAX-CKB, a database of The Jackson Laboratory Clinical Knowledgebase (JAX-CKB™).

A clinical-grade environment

HIPAA compliant and manufactured in an ISO13485 certified facility, Alissa Interpret supports the lab's accreditation and compliance with features like database versioning and audit trails. Organize your lab's workflow by having experts review and sign off on cases collaboratively.

One source—The Agilent advantage

Agilent promises to deliver trusted answers to your critical questions and challenges—helping achieve excellent outcomes in your laboratory, clinic, organization, and in the world we seek to improve.

Streamlined	Complete	Trusted

- Inventory management
- End-to-end ordering
- Cost savings with bulk purchases
- Troubleshooting and support

Intended Use Statement

Alissa Interpret software is intended for variant storage, visualization, and annotation using public, commercial and customer internal data sources. It allows end users to set up pipelines to perform or automate the triage and classification of genetic variants. It provides features for recording variant assessments and the drafting of variant analysis reports. The integration capabilities allow for the automated exchange of variant and report information with external software systems.

Alissa Interpret software is intended to be used by trained lab professionals, clinical geneticists and molecular pathologists as a decision-support software platform for the analysis and interpretation of genetic variants identified in human samples in the context of clinical information recorded for a sample.

www.agilent.com

Alissa Interpret is a USA Class I Exempt Medical Device, Europe CE IVD, Canada and Australia Class I IVD Device.

This information is subject to change without notice.

PR7000-2103

Printed in the USA, May 16, 2022
5991-8498EN

Agilent
Trusted Answers