Make your Variant Assessment Flow

Alissa Interpret allows clinical research labs to efficiently triage, curate and report genomic variants. Whether from NGS or arrays, this genomics data management solution automates the lab’s workflow from variant filtration and annotation, over curation and classification, to draft lab report. Rely on a team of experts to deploy new assays quickly and ramp up your research as your lab grows.

**Designed for Clinical Research**

Alissa Interpret is built with the clinical research lab in mind. The software provides access to a wealth of annotation sources and databases, supports building a bespoke curated variant database, and features a wide range of in-depth analytic tools for inheritance modes, phenotype context, and reviewing variant effect.

**A Single Platform for all Applications across NGS and CGH**

Imagine identifying a deletion or LOH region that spans a recessive variant. Alissa Interpret combines CNVs, SNPs, indels and fusion genes in an integrated workflow. Alissa integrates your application workflows from somatic to inherited disease, your variants from molecular to structural, and your data from secondary to tertiary analysis—all flowing on a single platform.

**Alissa Interpret Delivers**

- Inherited and somatic sample workflows
- Molecular and structural variant classification and curation
- Clinical-grade standard operating procedure (SOP) implementation
- Database access and lab report drafting with ease
- Team of experts as partners

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

Labs that implement their standard operating procedures on Alissa Interpret free up time for their for clinical researchers to focus on curating variants and checking hypotheses. This fast and precise variant assessment and reporting solution allows labs to run efficiently and scale to high throughput across different research applications.

Advancing Filtration System Decision Trees

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.

![Classification tree with CNV integration.](image)

**Figure 2.** Classification tree with CNV integration.

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.

![Variant curation using ACMG guideline automation.](image)

**Figure 3.** Variant curation using ACMG guideline automation. In this case, the “affected gene information” heading automatically includes a section on the BRAF gene, because that variant is reported.
Powerful Cohort Analysis

With Alissa Interpret, you can easily group a set of cases according to phenotype, assay characteristics, affected vs. non-affected status, and more. The platform allows you to compare these groups, and to annotate and compare all variants in the cohort with the full suite of tools also available for index, trio and single sample analyses.

A Fully Traceable Environment

The Alissa Interpret platform supports full traceability of all versions of databases, pipelines, and workflows. Keep track of what databases are used, follow up on which research scientist annotates what information to which specific variants, and build a truly reproducible variant assessment pipeline.

Figure 4. An example of a cohort analysis report. The insert demonstrates the overview of gene mutational burden in the cohort.
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