ion torrent

# Oncomine Reporter

## Powerful informatics tool for cancer research

Managing, and ultimately interpreting, the significant quantities of variant data produced by next-generation sequencing (NGS) presents a formidable challenge. The Ion Torrent™ Oncomine™ informatics workflow presents a sample-to-report solution for data analysis, from initial sequence analysis of many variants to annotation of relevant cancer drivers and final report by Ion Torrent™ Oncomine™ Reporter. This creates a simple, streamlined solution that doesn't require any specialized bioinformatics expertise.

## Robust, curated, and validated knowledgebase

Oncomine Reporter is a decision support tool developed specifically to enable streamlined access to a final report in three easy steps. It delivers easy access to vital information (including tumor mutational burden annotations), which enables the contextual investigation of sample-specific variants to understand their use with respect to labels, guidelines, and current clinical trials (Figure 1). To help ensure quality reporting, it integrates industry standards such as the four-tiered system from a joint consensus of AMP, ASCO, and CAP.*

Oncomine Knowledgebase data are meticulously curated and updated quarterly. After data are collected from various global data sources, a team of professional curation scientists manually reviews all candidate evidence. Two independent reviewers examine each piece of candidate evidence for context and standardization. The process has QC steps built in at various stages. Oncomine Reporter provides global clinical trial information for >60 countries with summary information, including contact information for enrollment.

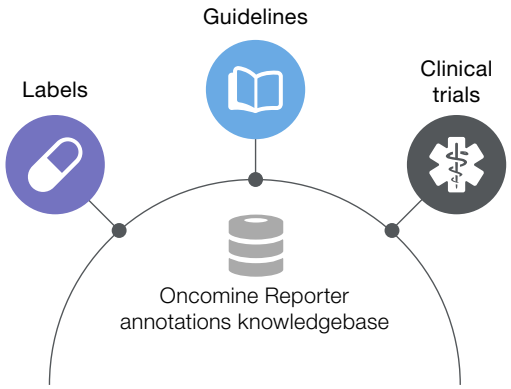


**Figure 1. This decision support tool links variants to labels, guidelines, and clinical trials and enables custom reporting.**

## Relevant content

Oncomine Reporter provides two key forms of relevance content that, depending on the strength of evidence and correspondence to the data source, can be used toward the research and development of future companion diagnostics. The types of relevance content provided include:

- Clinical consensus information that's provided for research and reflects published therapies and current labeling guidelines based on genetic event status, collected from US and European sources
- Global clinical trials with open enrollment in which genetic events are used as enrollment criteria

ThermoFisher SCIENTIFIC

ion torrent

## Custom reporting—make it your own

Oncomine Reporter has an easy-to-use interface with filtering options based on data source, cancer type, and clinical trial location. Role-based user profiles provide the flexibility to standardize workflows for operators in laboratory environments.

Workflow templates enable streamlined access to a final report in three easy steps: analysis, filter, and report. In order to fit the branding needs of your lab, the report is customizable with options for a logo, location, and operator, in addition to other custom fields for specific information about the sample.

The report builder enables you to select and order the report sections. This flexibility lets you create reports that contain only summary information or as much detail as you need (Figure 2). Additionally, you can choose from templates available in several languages other than English, including Chinese, French, German, Italian, Japanese, Korean, Portuguese, Spanish, and Russian. The template components, custom fields, and descriptors reflect the language of choice, while the curated content remains in English.

Oncomine Reporter combines curation and informatics into a powerful decision support tool to help cancer researchers link variants to labels, guidelines, and clinical trials.

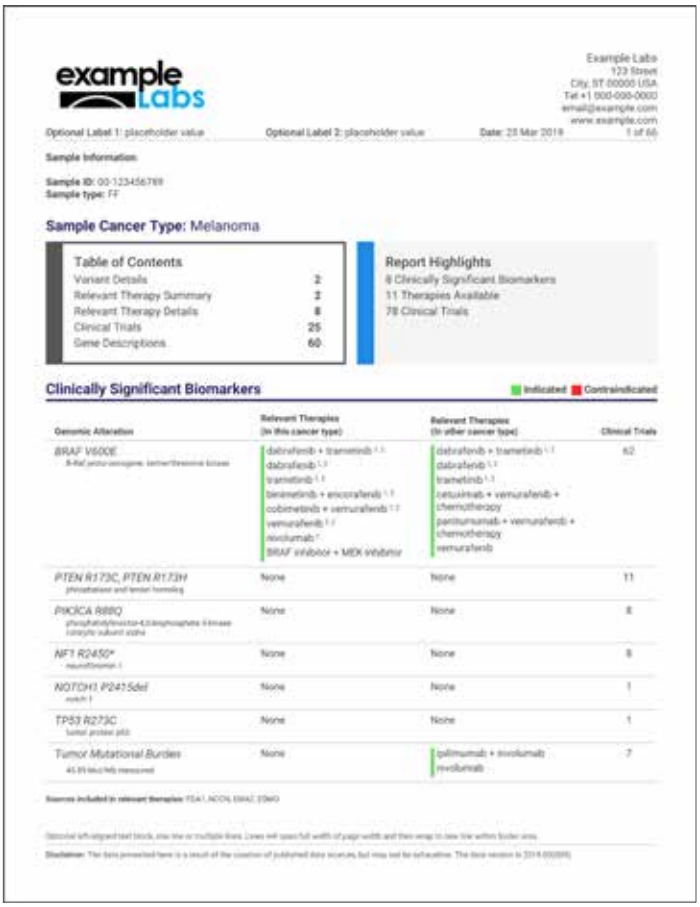


**Figure 2. The report builder allows customization of templates, layout, and content.** Integrated cytogenetics reporting enables a simple workflow for myeloid cancer. **Note:** Availability of a single-page report depends on the number of variants in the sample.

* Reference: Li et al. Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists. *J Mol Diagn.* 2017 Jan;19(1):4-23.

Find out more at
**thermofisher.com/oncomine-informatics**

ThermoFisher SCIENTIFIC