Oncomine Reporter

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 the initial sequence analysis of many variants to the annotation of relevant cancer drivers and a final report by Ion Torrent™ Oncomine™ Reporter. This creates a simple, streamlined solution that doesn't require any specialized bioinformatics expertise.

An NGS reporting solution for everybody

Oncomine Reporter is a curated knowledgebase and reporting software solution developed with a streamlined three-step workflow. It delivers easy access to vital information (including tumor mutational burden annotations), which enables the contextual investigation of sample-specific variants with respect to labels, guidelines, current clinical trials, and peer-reviewed literature (Figure 1). To help ensure quality, it integrates industry standards such as the four-tiered system from a joint consensus of AMP, ASCO, and CAP.[1]

Data are meticulously curated and updated monthly. 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.

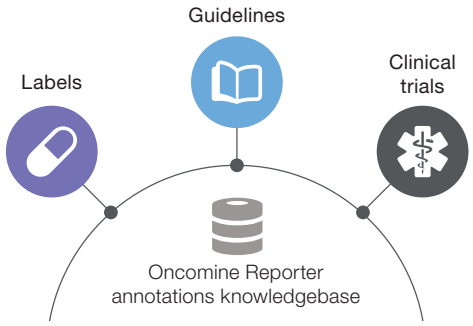

Figure 1. This curated knowledgebase and reporting software links biomarkers to labels, guidelines, clinical trials, and peer-reviewed literature and enables custom reporting.

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 is 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

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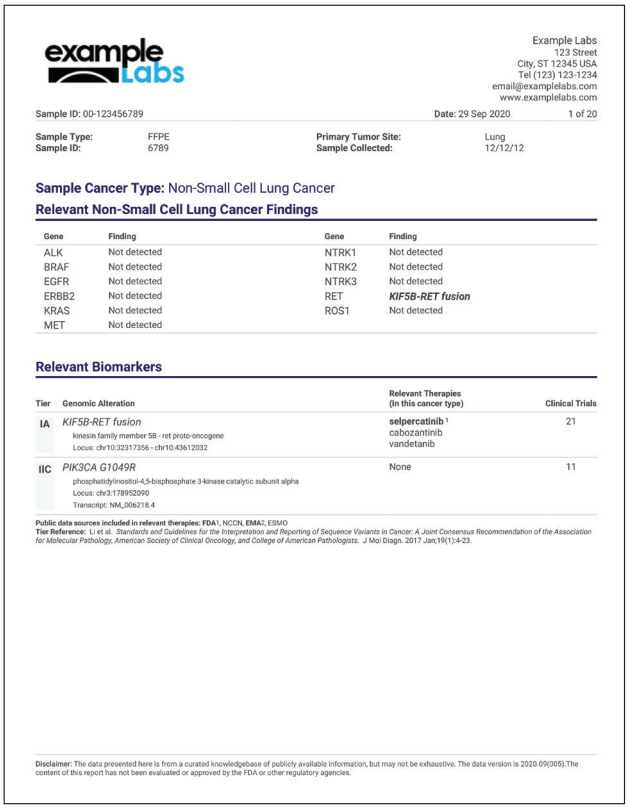
Custom reporting—make it your own

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 (Figure 2). 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.

Figure 2. The Oncomine Reporter workflow is streamlined into three easy steps, so that reports can be created in minutes.

The report builder enables you to select and order the sections of the report. This flexibility lets you create reports that contain only summary information or as much detail as you need (Figure 3). Additionally, you can choose from templates available in several languages other than English, including Chinese (traditional and simplified), 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.



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Sample ID: 00-123456789 Date: 29 Sep 2020 1 of 20

Sample Type: FFPE
Sample ID: 6789
Primary Tumor Site: Lung
Sample Collected: 12/12/12

Sample Cancer Type: Non-Small Cell Lung Cancer

Relevant Non-Small Cell Lung Cancer Findings

Gene	Finding	Gene	Finding
ALK	Not detected	NTRK1	Not detected
BRAF	Not detected	NTRK2	Not detected
EGFR	Not detected	NTRK3	Not detected
ERBB2	Not detected	RET	***KIF5B-RET fusion***
KRAS	Not detected	ROS1	Not detected
MET	Not detected		

Relevant Biomarkers

Tier	Genomic Alteration	Relevant Therapies (In this cancer type)	Clinical Trials
IA	*KIF5B-RET fusion* kinesin family member 5B - ret proto-oncogene Locus: chr10:32317356 - chr10:43612032	**selpercatinib** [1] cabozantinib vandetanib	21
IIC	*PIK3CA G1049R* phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha Locus: chr3:178952090 Transcript: NM_006218.4	None	11

Public data sources included in relevant therapies: FDA[1], NCCN, **EMA**[2], ESMO
Tier 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.

Disclaimer: The data presented here is from a curated knowledgebase of publicly available information, but may not be exhaustive. The data version is 2020.09(005).The content of this report has not been evaluated or approved by the FDA or other regulatory agencies.

Figure 3. The report builder allows customization of templates, layout, and content.

Oncomine Reporter combines curation and informatics into a powerful knowledgebase to help cancer researchers link biomarkers to labels, guidelines, clinical trials, and peer-reviewed literature.

1. Li et al. (2017) 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* 19(1):4-23.

Ordering information

Product		Cat. No.
Oncomine Reporter	One-year license	A33109
Oncomine Reporter (accessed via the Thermo Fisher™ Connect Platform)	One credit	A34298

Find out more at
thermofisher.com/oncomine-reporter

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