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.

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
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.

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.

Ordering information

<table>
<thead>
<tr>
<th>Product</th>
<th>Cat. No.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oncomine Reporter</td>
<td>A33109</td>
</tr>
<tr>
<td>Oncomine Reporter (accessed via the Thermo Fisher™ Connect Platform)</td>
<td>A34298</td>
</tr>
</tbody>
</table>

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

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.