iontorrent

Ion Reporter™ Software 5.14 Release Notes

Pub. No. MAN0019037 Rev. D.0

Contents

Thermo Fisher
S C I E N T I F I C

Revision History

Revision	Date	Description
D.0	17 July 2020	Updated release notes for Ion Reporter Software 5.14 • Known issues added: IR-46103 and IR-46065
C.0	26 June 2020	Updated release notes for Ion Reporter™ Server 5.14 • Known issue IR-44969 added
B.0	19 June 2020	Updated release notes for Ion Reporter™ Software 5.14.1.
A.0	8 May 2020	New release notes for Ion Reporter™ Software 5.14.

New Features in Ion Reporter™ Software 5.14

The Ion Reporter™ Software 5.14 release includes many new features and improvements.

Time Series Visualization of Variants

You can track and visualize variants over time in samples from the same individual with time series visualizations. Create graphic plots to view metrics for variant frequency over time, and view trends and changes for variant alleles, copy number ratios, ploidy, fusions, SNVs, INDELs, and RNAExonVariants. Remove and restore variants dynamically in the graphs, and adjust how data are organized in the before you generate an image file of the chart. Customize the graphs to visualize the information that is most relevant to your research.

Updated Annotation Sources and Cancer Types

GRCh37 and GRCh38 annotation sources are updated in Ion Reporter™ Software 5.14. Additional cancer types have been added to the existing list of sample attribute values.

Support for Ion AmpliSeq™ Microbiome Health Research Kit

Ion Reporter Software 5.14 supports the new Ion AmpliSeq™ Microbiome Health Research Kit by detecting bacterial species through 16S rRNA gene and Target Species-specific amplicons. This analysis solution provides full taxonomic profiling as well as species level resolution for selected key microbes associated with human health. Single and multi-sample analysis comparisons are possible using a variety of common reference databases including SILVA and utilizing QIIME2 functionality.

Improved Archiving and Restoration of Samples and Analyses

The speed and reliability of sample and analysis archiving and restoration has been improved.

User-Selected Classification is added to VCF file

When users classify a variant in Ion Reporter™ Software, the classification value selected for that variant is written into the VCF file that is exported for the analysis.

Aneuploidy Detection and ReproSeq Analysis Workflow Improvements

- The Gains/Losses Details table in analyses launched with ReproSeq analysis workflows gives you the option to narrow or expand the list of events that were called. You can adjust the list of events to show only events that were filtered in for the analysis by the applied filter chain, or show both all CNVs that were called in the analysis.
- Y-axis values for the Whole Genome View are now shown on both the left and right side of the graph. The view provides a genome-wide perspective of the sample data for each barcode in the sample.
- Grey tiles in Analysis Results are darker and thicker for better visibility in the software and in report images.

Reporting Enhancements

- Visualization reports can now be used as a report template that you can save and use for future visualization reports. You can create a visualization report template when you open a visualization or apply a system-installed template or a custom template.
- You can add one or more images in PNG, GIF, JPG, or JPEG formats to reports. There is no limit on the number of images that can be added to a report.

Enhanced Filtering for Samples during Analysis Launches

Manual launches of analyses are made even easier by enhanced filtering for Samples by the sample attributes.

Exon Level CNV plots for Tumor Suppressor genes

Upcoming Oncomine™ Assays will be supported by new CNV algorithms and Exon-level CNV detection and graphical plotting.

End of life for Ion Reporter™ Software 5.2 analysis workflows.

Ion Reporter™ Software 5.2 analysis workflows are now retired from the Ion Reporter™ Software 5.14. Version 5.2 analysis workflows will also be unavailable after servers are upgraded Ion Reporter™ Software 5.14. Analyses that are launched through analysis workflows from Ion Reporter™ Software 5.2 and earlier will continue to be available to open and create reports for in the latest version of Ion Reporter™ Software. Each new version of Ion Reporter™ Software will continue to retire at least one of the earliest versions of the currently released Ion Reporter™ Software analysis workflows.

Java version required for the Integrative Genomics Viewer (IGV)

Java 8 is required to launch IGV from Ion Reporter Software. Java 8 is included with the software. If you are running Java 9 or later, you must have Java 8 also for JNLP to work correctly.

Ion AmpliSeq™ Designer access code is required to import panel designs

An AmpliSeq Designer access code has been added to enhance security for the import of panel designs from ampliseq.com. You must authenticate your account by providing ampliseq.com username and the access code to import panel designs for Ion AmpliSeq™ and Ion AmpliSeq™ HD Made-to-Order, On-Demand, or Ready-to-Use research panels from ampliseq.com into Ion Reporter™ Software. The imported files are used when you create an analysis workflow for use with the Ion AmpliSeq™ Designer panels.

You are required to generate an access code for your ampliseq.com account just one time, if you save the access code when it is generated. If you do not save the access code, you have the option to regenerate a new one when you sign in again on ampliseq.com. You will be required to set a new access code when the code expires.

1. Go to ampliseq.com and sign into your account.
2. Click **My Account > Manage Access Code**.
3. Generate an access code.
   a. In the Manage Access Code dialog box, select an Access Code Expiration in the dropdown menu.
   b. Click **Generate**.
   c. Click **Copy to Clipboard**.

   The access code is available for use on the clipboard.

   d. (Optional) Click **Save** to save the access code for use when you return to ampliseq.com.

You can now use the access code to import panel files or planned runs from ampliseq.com. For more information, see the Ion Reporter™ Software help system.

Issues fixed in Ion Reporter™ Software 5.14

Issue number	Description
IR-45651	In Ion Reporter™ Software 5.14.0, the MAF values were inadvertently omitted in both hg19 and GRCh38 DBSNP version 153 annotation sources. DBSNP version 153 annotation sources (both hg19 and GRCh38) are now updated with the correct MAF values in Ion Reporter™ Software 5.14.1. Using filter chains containing an MAF filter in Ion Reporter Software 5.14.0 returned incorrect results due to the annotation source issue in Ion Reporter™ Software 5.1.4.0. Now with the correction of the DBSNP version 153 annotation source in Ion Reporter™ Software 5.14.1, the use of a filter chain that includes the MAF filter works as in Ion Reporter™ Software 5.12.3.
IR-45636	In Ion Reporter™ Software 5.10 through 5.14.0, the FORMAT field for multiple variant types was inadvertently changed in the VCF results file due to the introduction of the FLT3ITD variant type, which resulted in missing information for some variant types. This issue is fixed in Ion Reporter™ Software 5.14.1.
IR-45576	Augmenting an existing custom CNV baseline with additional BAM files in Ion Reporter™ Software 5.12.3 and in Ion Reporter™ Software 5.14.0 on Connect could result in failure due to unsuccessful access to required baseline files. This issue is fixed in Ion Reporter™ Software 5.14.1.
IR-45466	BAM track loading and display fails for analysis results from Ion Reporter 5.6-versioned DNA and DNA and Fusions workflows, when visualizing the analysis results in Ion Reporter™ Software on Connect 5.14.0. This issue is fixed in Ion Reporter™ Software on Connect 5.14.1
IR-41102	In Sample presets, when preset of type Controlled Vocabulary is modified, the Name, Description and Encrypted fields will be audited. The Terms field was not audited for changes. This issue is fixed in Ion Reporter™ Software 5.14.
IR-37643	In rare cases, Ion Reporter™ Software filter chain filters that are based on matching genotype alleles to population variants did not work. This issue is fixed in Ion Reporter™ Software 5.14.
OFA-117	The reads mapping parameter "End Repair" was inadvertently set as 35 in Ion Reporter™ Software 5.14 Oncomine™ Focus analysis workflows. The correct value should have been 15 instead of 35. The incorrect value may cause slightly higher false positive rate especially with lower quality data near amplicon edges. This parameter value is planned to be corrected in the next version of the Oncomine™ Focus analysis workflows. **Workaround:** Users are encouraged to copy/edit the Oncomine™ Focus analysis workflows that include this setting, and change "End Repair" value to 15.
IR-40315	The Oncomine™ TCRB-SR DNA analysis workflow w1.2 corrects an issue that affected the reporting of unproductive rearrangements in the Oncomine™ TCRB-SR DNA assay, w1.0, released in Ion Reporter ™ Software 5.10. The issue led to a failure to report unproductive rearrangements that included an in-frame variable gene and joining gene. The issue is estimated to have prevented the reporting of ~10% of unproductive rearrangements. The impact was limited to applications of the TCRB-SR DNA assay that involve the analysis of unproductive rearrangements. You were encouraged to reanalyze data use the Oncomine™ TCRB-SR DNA analysis workflow w1.2 if you were affected by this issue. This issue is fixed in Ion Reporter™ Software 5.14.
IR-39761	In Ion Reporter ™ Software 5.4, 5.6 and 5.10 chrX calls could be incorrect. In Ion Reporter ™ Software 5.10, in samples with "male" gender chrX, the VCF INFO tag can be REF_CN=2, but should be REF_CN=1. Both RAW_CN and CN are affected by the incorrect REF_CN and are reported as one half of the value that it should be. In Ion Reporter ™ Software 5.4 and IR 5.6 there is also incorrect handling of chrX but it is more complex and is not fully characterized. This issue is fixed in Ion Reporter™ Software 5.14.

Issue number	Description
IR-41847	When you visualize multiple Fusion analyses, which differed in their FASTA reference, only the FASTA reference of the first selected analysis data was loaded into the IRGV viewer. This could have resulted in some fusion events, which had a different FASTA file than the first selected analysis, to not be correctly displayed. A workaround was to select the analysis first in which a particular fusion record of interest is present. This issue is fixed in Ion Reporter™ Software 5.14.
IR-41818	To ensure that archives and samples are successful, it was recommended that you increase the session timeout value. You could change the value in the **Admin** tab, under **System Services**, in the **Configure Services against Session Timeout (Minutes)** field. The recommendation was to set 1400 minutes (that is, 24 hours). The maximum limit is 3600 minutes. After the archive process is complete, the recommendation was to set the timeout value back to the default value. This issue is fixed in Ion Reporter™ Software 5.14.
IR-37255	The on-screen preview of a visualization report could be blank if the size of the data that you added to the report exceeds the memory allocation for the browser. A PDF version of the report was not affected. The PDF report included the visualization files that were not visible in the preview. This issue is fixed in Ion Reporter™ Software 5.14.
IR-31031	The Details section for the Immune Repertoire analysis workflow contained some analysis workflow components that were not applicable to the analysis workflow and resulting analyses: Annotation set, report template, parameters. This issue is fixed in Ion Reporter™ Software 5.14.
IR-30937	The Liquid Biopsy analysis Results data columns Mol Depth, Mol Counts, Mol Freq and Detection Limit were not populated in the Liquid Biopsy tab of the Analysis Results for CNV variant rows. This issue is fixed in Ion Reporter™ Software 5.14.
IR-24539	When you refresh an Ion Reporter™ Genomic Viewer window, a blank page appeared. This issue is fixed in Ion Reporter™ Software 5.14.
IR-23854	A male or female gender must be specified for each sample in a trio analysis in Torrent Suite™ Software. Validation was not performed on sample genders when the trio analysis workflow was automatically launched in Ion Reporter™ Software after it was transferred from Torrent Suite™ Software. This issue is fixed in Ion Reporter™ Software 5.14.
IR-41223	In Ion Reporter™ Software 5.4 and 5.6, incorrect copy numbers could be reported in targeted panels that used a VCIB copy number baseline and include chrX genes in the Pseudo-Autosomal Region (PAR,) such as AR. The copy number RAW_CN Genes could be erroneously doubled in male samples that use male baselines with REF_CN=1. This affected final copy number after any correction to tumor cellularity. The issue is fixed in Ion Reporter ™ Software 5.12.

Known issues and limitations in Ion Reporter™ Software 5.14

Issue number	Description
IR-46065	In Ion Reporter™ Software 5.14, the use of 5.0 to 5.10 versions of the filter chain **Confident Somatic CNVs - CNVs Only** will return all variants (no filtering is applied) due to a change in variant filtering logic. **Workaround:** Use the **Confident Somatic CNVs - CNVs Only** filter chain from Ion Reporter™ Software 5.12 or 5.14 to achieve the same filtered results that were returned with the filter chain in the earlier versions of Ion Reporter™ Software.
IR-46103	In Ion Reporter™ Software 5.14, an issue was observed only for the Fusions Sample QC Test=Warning metric. The **QC Test** column in the Fusion section of the results table in the Summary view of the **Variant Matrix** tab incorrectly shows a Fusion QC Warning as a check mark, rather than the correct exclamation mark. The correct Warning symbol is shown in the Fusion view in of the **Variant Matrix** tab for all analysis results. The Fusions QC Test=PASS/FAIL metrics all give the correct symbols in the Summary view of the Variant Matrix tab and Fusion view in of the **Variant Matrix** tab for all analysis results.

Issue number	Description
IR-44969	If an analysis is shared with an organization, the analysis can be archived only in the source organization. Samples in the analysis will be not be archived because samples remain common between the source and target organization. To archive samples, first unshare the analysis.
IR-44964	When a user clicks on the Locus link from the Fusion details table in the Variant Matrix Summary tab, data from the reference FASTA file of the first selected analysis is opened in Ion Reporter Genomic Viewer (IRGV). If the non-targeted fusion is contained in any analyses other than the first analysis, IRGV will not display that data when the Locus link is used to start IRGV.
IR-41058	When using the option to download variants as a current results TSV file from the Analysis Results screen, the column order and variants that are exported in the TSV file are the same as the variants shown in the table of analysis results in Ion Reporter™ Software. However, due to the way data is stored and then sorted in the software, the sort order between the screen and the TSV file might be different. The variants in the TSV file are always sorted by the Locus column.
IR-44334	In audit records, all actions performed by the user are categorized as **Add** or **Modification**. Audit Records that include records of a deletion are captured as a **Modification**. **Workaround:** Users can view the status of the deleted record as part of the audit record details. To find the record of a deletion, look at the **Status** field in the audit details. If a record has been deleted, the status will be **Deleted**.
IR-42886	When a CNV record from MyVariants is exported, the export might contain comma-separated ploidy values. When importing the record back into Ion Reporter ™ Software, after making edits to the file, the **Copy Number** field is not imported if the CNV record includes multiple copy number values. **Workaround:** For a successful import, edit the file to either 1) remove all ploidy values or 2) keep a single ploidy value in the column.
IR-45279	When uploading BAM files into Ion Reporter Software 5.14 and earlier, the characters that are used in uploaded filenames can be any combination of alphanumeric characters (A-Z, a-z, 0-9) plus spaces, periods (.), dashes (-), and underscores (_). If unsupported characters are entered, the file will get uploaded without any errors but, the analysis run with the sample will fail.
IR-45381	The analysis name is incorporated into Immune Repertoire output files. Long sample names, and/or analyses names which are based on long sample names, can prevent some PDF output files from being generated by the Immune Repertoire analysis workflows. The issue is due to limitations on the number of characters that can be used in file names. To resolve this issue, reduce the length of the analysis name, then re-launch the analysis, or reduce the length of the sample name in Ion Reporter™ Software, then reanalyze the sample.
IR-45168	An issue with the Torrent Variant Caller module could cause false negative calls. This issue is fixed in Ion Reporter Software 5.14. As a result of correcting the issue, slightly different variant calling results are expected in Ion Reporter™ Software 5.14 compared with previous versions. The software update primarily affects homopolymer InDel calling in certain circumstances such as a variant that is close to the edge of the amplicon, or a large group of alternative alleles that is evaluated jointly. In general, better sensitivity is anticipated. In rare incidents, the software can produce false positive or false negative calls that were not reported by the software in the previous version.
IR-41021	The list of filters for some filter chains that appear in the Filter Options section of the Analysis Results screen are not ordered consistently. However, the results of the filtering for the variants will appear the same each time that a filter chain is applied. This does not affect how filter chains function.
IR-36949	When you download Ion Reporter ™ Software logs on a Microsoft Windows™ operating system, the Microsoft™ Windows 7-Zip File Manager or WinRAR software are the recommended tools to extract the downloaded ZIP files.
IR-44743	The BAM file named "Demo AmpliSeq Exome CNV case" that is included with Ion Reporter™ Server is corrupted and will fail when used with workflows. **Workaround:** Select another Exome BAM file to demonstrate workflows until the file is updated in a later version.

Issue number	Description
IR-44642	In Chrome™ browser version 80 and later, an analysis or sample becomes uneditable for other users in the organization if one user starts an edit process, then closes the browser and exits Ion Reporter™ Software before an edit action is complete. The issue occurs when these actions are done in the following screens. • **Analysis Results screen** – If a user clicks a link to open an analysis, clicks **Edit**, or clicks **Actions > Edit** in the Analysis screen, then closes the Analysis Results screen before they save edits • **Generate Report screen** – If a user clicks **Generate Report** from the Analysis Results screen, then closes the Generate Report wizard before the final report generation is cancelled or published. • **Define Samples screen** – In the Samples tab, if a user clicks a sample link (or clicks **Define Sample > Manual)**, to open the Define Samples page, then closes the screen before the Review step is complete and edits are saved In each case, a Chrome™ browser dialog box prompts to the user to click **Leave** or **Cancel** when they click to close the screen. The same prompt might open when a user navigates to the **Notification** screen or **Admin** screen from any of the affected screens (**Analysis Results screen, Generate Report screen and Define Samples screen)** Ion Reporter™ Software functionality is not affected if **Leave** is selected**.** If however, **Cancel** is clicked, then the open screen might not close. To resolve this issue, the user who closed the screen must sign into Ion Reporter™ Software, using the same browser without clearing the local storage of the browser. Other users who refresh the affected screens can then make edits.
IR-42804	Analysis Visualization Reports can only be created from the **Generate Report** button that is available in the IRGV tab in the Analysis Visualization screen. Other tabs in the Analysis Visualization screen in which that button is inactivated can have graph and table contents that might be able to be added to those reports, even though the **Generate Report** button in those tabs remains inactive. Click on the IRGV tab to generate the report.
IR-33625	For Oncomine™ BRCA analysis workflows, the default canonical transcript has been changed from NM_007300.3 to NM_007294.3. If a custom transcript set is selected when the preferred BRCA1 transcript is NM_007300.3, the exon numbering for BigDup and BigDel CNV variants are still based on the numbering that is in the NM_007294.3 transcript. As a result, Exon 13 in transcript NM_007300.3 is not used in Exon Deletion/Duplication variant calling.
IR-41252	While viewing a specific chromosomal region, if you zoom in on the VCF track in Ion Reporter Genomic Viewer (IRGV), the drawing that represents the CNV can disappear from the screen. This is due to a calculation in the software of the offset for drawing representations of SNVs, CNVs, MNVs, and so on. The CNV is visible again when you zoom in to a point where the retrieved data block of data from the index file is different from the previous block of data.
IR-33725	Column sorting for the "Mol Counts" and "Mol Freq" columns is not correct for ascending sort in the LOD view for liquid biopsy analyses. This is due to the way the data is stored in the internal database.
IR-40286	Quality control for CNV calling of BAM files can fail in several ways. When CNV calling fails, analyses will complete but all CNV hotspots will be NOCALLs and no de-novo CNV calling will occur. One or more of the following can cause the CNV calling to fail: MAPD value is greater than "MAPD threshold," aligned reads less are than "min-read-count," percentage of amplicons with no reads assigned greater than "min-non-zero-amplicons-percent," percentage of reads assigned to amplicons less than "min-aligned-read-percent", or the median read count across amplicons is less than "-min-median-reads-per-amplicon."

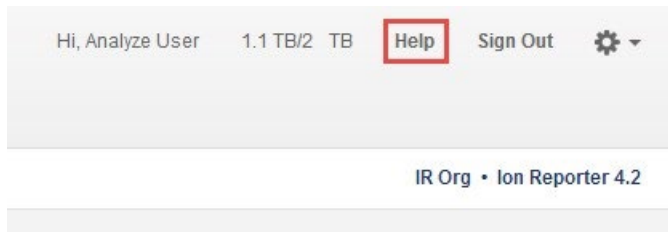| Issue number	Description
IR-41823	In Ion Reporter ™ Software, p-values in Analysis Results in the Summary view in the column named "p-value" are rounded to 5 decimal places (between 0.00001-0.99999) when displayed on the screen. Very small p-values that are less than 0.00001 are rounded to 0.00001 by default when displayed on screen. Very large p-values that are greater than 0.99999 are rounded to 0.99999 by default when displayed on screen.
IR-39002	Variant calling in Ion Reporter ™ Software enables specifying minimum callable probability parameter for Limit of Detection calculation. For all DNA-detecting Ion AmpliSeq ™ HD and TagSeq analysis workflows, the variant calling now enables users to specify the minimum detachable probability for the calculation of Limit Of Detection (LOD) through the "min_callable_prob" parameter. LOD is defined to be the lowest possible allele frequency in the sample such that the variant is callable with probability higher than the "min_callable_prob" value, when molecular depth is given. In Ion Reporter™ Software 5.10, the values of "min_callable_prob" in the default parameter sets for all DNA-detecting Ion AmpliSeq ™ HD and TagSeq analysis workflows were set to be 0.98. In Ion Reporter ™ Software 5.12, the values of "min_callable_prob" in the default parameter sets for all DNA-detecting Ion AmpliSeq ™ HD and TagSeq analysis workflows are changed to be 0.95 and 0.8, respectively. As a consequence, variant calling in Ion Reporter ™ Software might report lower values of LOD than does variant calling in Ion Reporter™ Software 5.10, when the same dataset that uses the default parameter settings is analyzed.
IR-39523	Differences in the predefined filter chains and similar custom filter chains can occur if both gene models (refGene and ensGene) are not taken into account. The gene model used in the analysis must match the gene model that is used by the filter chain.
IR-36948	LOD reporting for TagSeq and Ion AmpliSeq ™ HD assays is improved in Ion Reporter ™ Software 5.10 and later. The new definition of LOD is as follows: Given the molecular depth at the locus, LOD is the lowest possible variant frequency in the sample that can be detected by the system with a true positive rate greater than 98%. Compared with Ion Reporter ™ Software 5.6 and earlier, higher values of LOD are expected in Ion Reporter ™ Software 5.10. By definition, given the molecular depth, a variant of a frequency that is less than LOD in the sample might still be called by the variant caller, however the variant call might not be detectable in a repeated manner with a probability greater than 98%. In general, the change on the LOD calculation and reporting does not affect the variant calling results. In future releases, the target value of true positive rate used in the LOD calculation and reflected in analysis results will be adjustable to align with requirements for specific applications. Please contact your local Field Bioinformatics Support team with any questions.
IR-34781	The non-targeted fusion detection is not fully supported for Ion AmpliSeq ™ HD and TagSeq fusions analysis workflows. The molecular family counts for any non-targeted fusion candidates that are observed in the sample are not computed. The molecular family count is reported as 0, and the Detection call is made based on only the read counts, such as is the case with Ion AmpliSeq™ fusions analysis workflows.
IR-35322	The variantCaller plugin for Torrent Suite ™ Software 5.10 includes the use_fd_param=1 for default Ion AmpliSeq ™ HD somatic and germline settings. The parameter, when set to true, uses the new FD parameters. Ion Reporter ™ Software 5.10 has partial support for FD parameters with the following limitations: • The use_fd_param parameter is not visible in the Ion Reporter ™ Software, but it can be enabled with the import of a variant calling JSON file that includes use_fd_param=1. 2. The related min_ratio_for_fd parameter (default 0.1) is not available in Ion Reporter ™ Software, and it cannot be set or changed in Ion Reporter ™ Software 5.10.

Issue number	Description
IR-34013	One of the output files of the CNV VCIB output is a tab-delimited text file with column headers: "gene_cn.txt." Ion Reporter ™ Software 5.6 and earlier included a column labeled "chr" with entries in each CNV_ID region that use the following rule: take the corresponding contig for the hg19.fasta file and remove the prefix "chr." This would not be robust against other FASTA files, for example, assemblies that do not use "chr." Therefore, in Ion Reporter ™ Software 5.10 and later this entry now uses the full contig name, for example "chr1," and so on. The order of the entries in the "Chrom"[?] column is defined by the order in which the contig names are found in the fasta.fai index file. This might break scripts that depend on this column. For example a script that includes entries with the format used in Ion Reporter ™ Software 5.10 or earlier, such as "11" will match "chr11" in the FASTA file but in Ion Reporter ™ Software 5.10 or later this entry will be the same as the FASTA file. That is, "chr11."
IR-33433	In Ion Reporter ™ Software, both the Allele View VCF file and the Locus View VCF file includes values in the FDP and DP fields that are the same; however, each allele is displayed as a single line of record in the Allele View VCF file.
IR-34146	VCF files that contain information for more than one sample are currently not supported using Allele (Proper) view. For example, the VCF output files for tumor-normal analysis workflows contain genotype information for both normal and tumor samples. As a result, the analysis is expected to fail, if the Allele view option is enabled in a custom Ion Reporter ™ Software analysis workflow.
IR-34768	If user-created Custom sample attributes share the same name as predefined Ion Reporter ™ Software sample attributes, the import of samples might use either the custom or predefined attribute, depending on which attribute type is encountered first by the software. This issue is present in Ion Reporter ™ Software 5.6 and later5.10.
	Workarounds: The workaround for this issue is to, ideally, not create custom sample attributes for which an Ion predefined attribute is available. Alternatively, if using custom attributes with the same name as an Ion predefined attribute, you can confirm that the attribute values for the samples use the correct attribute after upload, or you can choose to add the values for those attributes after the samples are successfully uploaded.
IR-34789	When files or reports are downloaded from the Ion Reporter™ software, there will be a mismatch in time stamp data between what is shown on the screens in the software and in the downloaded file. This is due to the difference in user and server time zones. The data shown on the software screens will match the client's time zone and the data shown on the downloaded files will match the server's time zone. One exception to this difference is the visualization report where the downloaded PDF will show client time stamp under the 'launched on' field.
IR-30952	The period character (.) is not allowed at the start of the names of various elements in Ion Reporter ™ Software. The following elements are not allowed to have a period at the beginning of their name: Project name, Workflow name, Sample name, any analysis Workflow Preset name, Analysis name, CNV baseline name. Originally, this was documented for Project name, only: "If the value of the Project attribute in your sample starts with a period (.), the list of analyses in the Analyses tab will be empty. The workaround is to create a Table Preference that does not include the Project column, and then apply that to your table. See the topic "Set table preferences" in the Ion Reporter™ Software Help for details.
IR-30955	In Ion Reporter™ Software, the allele grouping (including grouping of hotspots) algorithm was improved to reduce the filtering of true variants. This can sometimes lead to some NOCALLs, due to the way alleles are grouped for evaluation. Variant detection will continue to improve in future Ion Reporter™ Software versions, as new data is gathered and analysis is performed.
IR-30957	In the results for TagSeq Liquid Biopsy analyses, CNVs contain only the start coordinate position of the variant in the 5.6 version of software. The Details section for the Immune Repertoire analysis workflow contains some components that are not applicable to the analysis workflow and resulting analyses: Annotation set, report template, parameters.

Issue number	Description
IR-30985	TagSeq Liquid Biopsy analysis workflows, which detect CNVs, give a p-value but not a "Confidence Score" or "Confidence Interval" for each called CNV. In the Ion Reporter™ Software 5.6 IRGV, the Confidence filter setting (for example, Confidence=10.0) is displayed in the Whole Genome View, but this information not relevant to the data from these analyses using TagSeq Liquid Biopsy CNV-detecting analysis workflows. Note: The Confidence filter setting has been replaced by a filter chain that can apply a confidence score based on a threshold that is set in the filter chain.
IR-30676	You can use Analysis name, Sample name, and Project when you search for Immune Repertoire visualizations. You cannot use barcode names for searches of Immune Repertoire visualization results.
IR-30650	CNV Baseline Creation for TagSeq analysis workflows is not possible if you use the existing target regions BED file in Ion Reporter™ Software 5.6 or later5.10. The BED files for TagSeq analysis workflows in the software do not contain CNV amplicons, and therefore should not be used to create a new CNV baseline.
IR-29790	If you create Table Preferences to add sample attribute columns in the Samples tab with Ion Reporter™ Software 5.4 or earlier, and you want to access those preferences in Ion Reporter™ Software 5.4 or later, you must do one of the following: If you are using version 5.6, delete the entire Table Preference, then recreate it. If you are using version 5.4, recreate the Table Preference by 1) Remove the added columns. 2) Re-add the columns through the "Select Columns" dialog box.
IR-29352	In Torrent Suite™ Software 5.4, variantCaller plugin checks the TMAP parameters used in the mapping step and if the initial TMAP program does not have the parameters "-J 25 --end-repair 15 --do-repeat-clip --context", mapping will be re-run before variant calling is invoked. However, these parameters are not used for TMAP program in Ion Reporter™ Software for non-Oncomine™ Assay and non-Hi-Q Exome analysis workflows. As a result of these differences, variants called in the Torrent Suite™ Software variantCaller plugin and variants called in Ion Reporter™ Software might not reach parity for some Ion AmpliSeq™ panels, such as CCP, CHPv2, CFTR, AML, Colon-Lung, IDP, non-Oncomine™ BRCA and non-Hi-Q Exome panels.
IR-29159	When creating a new annotation-only analysis workflow, Oncomine™ customers with analysis workflows available to their Ion Reporter ™ Software organization will see the availability of the OVAT plugin. Functionality for the OVAT plugin is highly dependent upon the panel used for the assay, so only data from supported panels should be run through analysis workflows containing the OVAT plugin.
IR-24941	When editing a filter chain, canceling during the edit should bring the user back to the filter chain, as it was before the edit with no changes. In Ion Reporter™ 5.4 Software, some edits might persist if a user cancels changes made in filter-chain dialog box. To get back to the same state before edits were made, the page needs to be reloaded to clear all edits made before the cancel.
IR-29709	In some older versions of the Firefox and Safari browsers, the choice of a filter chain will successfully filter the data and list the correct number of variants, but a statement "No Filters Selected" will be present where the filters in the filter chain and their individual filtering results should be listed. A workaround is to use the Chrome browser.
IR-24657	IGV does not load the reads & read coverage track as many times as the number of analyses you select. For example, when you select five analyses with the same input BAM file, then the reads & read coverage track loads only the first one, not all of them.
IR-24080	When setting "UCSC COMMON SNPs" filter to "In", only filters in SNPs that have the "UCSC COMMON SNPs" annotation are filtered, although other variant types are contained in the full database.
IR-23462	Currently, Ion Reporter™ Software 5.2 does not require you to specify the sample types for RNA/Fusions samples. However, if you do not specify RNA samples as RNA type, you do not get correct results.

Issue number	Description
IR-23379	In DNA and Fusions analysis workflows, cellularity is not required for NTC RNA samples, but is still required for NTC DNA samples.
IR-24430	For some older analyses when the BAI file is missing from the input BAM folder, then BAM and Reads Coverage tracks do not load in IGV or Ion Reporter™ Genomic Viewer screens. The workaround is to re-run the analyses, which will generate the BAI file and cause successful loading of both the BAM and Reads Coverage tracks.
IR-25252	When you create an hg19 annotation set, do not use the annotation source DrugBank version 20150107. Use instead annotation source DrugBank version 1 or DrugBank version 20161212. If you use the DrugBank version 20150107 in an hg19 annotation set, you will not be able to create filter chain of DrugBank for any analysis.
IR-31487	A known bug that affected the variant calling module in Ion Reporter™ Software 5.4 caused the results for variants with a very long (>1024 bytes) variant_ID to not be recorded in the VCF file. The variant_ID is a unique key for a variant that, due to improvements to ensure uniqueness for any variant in a sample, was constructed using additional variant data fields in Ion Reporter™ Software 5.2 and 5.4 compared to variant IDs from earlier software versions, which used fewer fields to construct a variant's variant_ID. Rare variants with extremely long (>1024 bytes) variant_IDs were excluded due to exceeding the byte length limit of the variant ID field. The bug was fixed in Ion Reporter™ Software 5.6. Due to this fix, if there is variant in the analysis with a variant_ID length >1024 bytes, then running version 5.2 or 5.4 analysis workflows in Ion Reporter™ Software 5.6 results in the presence of more variants than when the analysis workflows are run in Ion Reporter™ Software 5.2 or Ion Reporter™ Software 5.4. However, if there is no variant with variant_ID length >1024, the number of variants will be the same for the different analysis workflow versions.

Documentation

You can access product documentation through the help link at the top right of Ion Reporter™ Software. This link opens the help in a new tab (depending on your browser settings).

Software documentation is also available at

https://www.thermofisher.com/us/en/home/technical-resources/technical-referencelibrary/next-generation-sequencing-support-center/ngs-software-support.html.

Compatibility with Torrent Suite™ Software

In Ion Reporter ™ Software on Connect requires an access code is required to configure user accounts for the IonReporterUploader plugin and to use Ion Reporter™ Software command-line utility (IRUCLI).

To create an access code for use with the IonReporterUploader plugin setup and to use Ion Reporter™ Software command-line utility (IRUCLI):

1. Sign into Ion Reporter™ Software.
2. Click ⚙ **(Settings) > Manage Tokens**.
3. Click **Set New Access Code**, then enter an access code in the New Access code field.

   The access code must contain at least 6 characters. The maximum length of the access code is 50 characters.

4. Select an expiration time in the Access code Age dropdown menu, then click Save and Generate.

   Note: The IRU token is for use with the IonReporterUploader command-line utility and is not required for this procedure.

   The access code that you must use to set up the IonReporterUploader is shown in the **Manage Tokens** dialog box, and is available on the clipboard. Save this access code for use in future account setups. Alternatively, you can reset the access code as needed.

The IonReporterUploader plugin versions are compatible with the following Torrent Suite™ Software and Ion Reporter™ Software versions.

Version Compatibility Matrix		
Ion Reporter™ Uploader plugin	Compatibility with Torrent Suite™ Software	Compatibility with Ion Reporter™ Software
Ion Reporter™ Uploader plugin 5.14.0.6	Torrent Suite™ Software	Ion Reporter™ Software 5.14 and earlier
Ion Reporter™ Uploader plugin 5.12.0.38	Torrent Suite™ Software 5.12 and earlier	Ion Reporter™ Software 5.12 and earlier
Ion Reporter™ Uploader plugin 5.10.0.32	Torrent Suite™ Software 5.10 and earlier	Ion Reporter™ Software 5.10 and earlier

		Ion Reporter™ Software 5.6 and earlier
Ion Reporter™ Uploader plugin 5.6.0.41	Torrent Suite™ Software 5.6 and earlier	
Ion Reporter™ Uploader plugin 5.4.0.44	Torrent Suite™ Software 5.4	Ion Reporter™ Software 5.4

IonReporterUploader plugin

A new version of the IonReporterUploader plugin is available: Ion Reporter™ Uploader plugin 5.14.0.6 or later. This version of the plugin is already installed when Torrent Suite™ Software 5.14 is installed or upgraded.

New plugin versions might become available between released of Torrent Suite™ Software or Ion Reporter™ Software. If you need to upgrade IonReporterUploader plugin on a Torrent Server of version 5.4 or later that is connected to the Internet, you can use the off-cycle upgrade procedures described in the Torrent Suite™ Software User Guide.
If your Torrent Server is not connected to the internet, a debian (.deb) package is available from http://iru.ionreporter.thermofisher.com. Use of the debian (.deb) package is the only option to update IonReporterUploader plugin in Torrent Suite™ Software 5.2 and above.

Also available on http://iru.ionreporter.thermofisher.com is a compressed directory (ZIP format) version of the IonReporterUploader plugin for customers who want to continue using Torrent Suite™ Software 5.0 and earlier but want to upgrade IonReporterUploader plugin.

Ion Reporter™ Software command-line utility (IRUCLI)

A ZIP file of the Ion Reporter™ Software command-line utility (IRUCLI). This allows you to upload files to Ion Reporter™ Software from a computer other than the Torrent Server. You can also reach http://iru.ionreporter.thermofisher.com through the **Download Ion Reporter™ Uploader** link that is in Ion Reporter™ Software when you click ⚙ **Settings > Ion Reporter Uploader**.

The most current IonReporterUploader plugin and Ion Reporter™ Software command-line utility (IRUCLI) are always available for download from http://iru.ionreporter.thermofisher.com.

Further information
The plugin version format is "plugin_name p.q.r.s", where "p.q" represents the major/minor version number of the Torrent Suite™/Ion Reporter™ Software with which the plugin is used. The next number "r", represents the patch number and "s" represents the number of builds done on this patch.

IRUCLI 5.4 and later requires a Java version of 1.7 or higher to function. Therefore, IRUCLI installed on an older Torrent Server running Java 1.6 does not work anymore unless you perform an additional setup.

IonReporterUploader plugin configuration

Use the following IonReporterUploader plugin configuration setting for Ion Reporter™ Software accounts to transfer data to Ion Reporter™ Software on Connect:

Server: 40.dataloader.ionreporter.thermofisher.com

This is the default shown when configuring an Ion Reporter™ Software on Connect account in the Torrent Suite™ Software.

Note: The previous server address, 40.dataloader.ionreporter.lifetechnologies.com, will continue to work, but please use the new address going forward.

Ion Reporter™ Server: Update Operating System

To upgrade the Ubuntu™ Operating System software from 14.04 to 18.04 on your Ion Reporter™ Server, contact your Field Bioinformatics Specialist (FBS), Field Support Engineer (FSE), or Field Application Scientist (FAS) for assistance.

Ion Reporter™ Software 5.14 is designed to work with the Ubuntu™ operating system version 18.04, and is not compatible with version 14.04 or 16.04. Messages can periodically appear asking if you want to update your Ubuntu™ software. Do NOT update your Ubuntu™ operating system, if prompted to do so. Doing so without help from support or the Ion Reporter™ Server-specific instructions causes the Ion Reporter™ Software on the server to stop working correctly due to changes between Ubuntu™ versions.

Contact your local Ion Torrent™ Field Bioinformatics Specialist (FBS) for specific instructions and help to upgrade the Ubuntu™ operating system of your Ion Reporter™ Server. Do NOT update the Ubuntu™ operating system of your Ion Reporter™ Server without the guidance and assistance of an Ion Torrent™ bioinformatics representative. For other options and assistance with updating a Ion Reporter™ Local Server, contact your local FBS.

Update Ion Reporter™ Server Software to 5.14

To upgrade Ion Reporter™ Software to 5.14, you must have an up-to-date software license. Upgrades of the Ubuntu ™ operating system is part of a separate server support contract.

The first year of software license and hardware support comes with the purchase of the Ion Reporter™ Server (4487118). In subsequent years, a combined Ion Reporter™ Software license and Hardware support contract (ZG10SCIONSERVER) is required to update the Ion Reporter™ Software through the online command line process, or as part of an on-site visit from a support representative to upgrade the software. This yearly license allows upgrading as many times as desired to as many Ion Reporter™ Software versions as are released during that year. Contact your local FBS, FSE or other service representative for online instructions to update Ion Reporter™ Software or to schedule an onsite visit.

thermofisher.com/support | thermofisher.com/askaquestion
thermofisher.com

27 July 2020