

Ion Reporter™ Software 5.16 Release Notes

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Revision History

Revision	Date	Description
C.0	12 March 2021	Additional information added to: Ion Reporter™ Server 5.16 new features: • Ion AmpliSeq™ CarrierSeq ECS Panel • OncoPrint™ Comprehensive Assay Plus Change in MAF filtering
B.0	17 December 2020	Updated release notes for Ion Reporter™ Server 5.16: • Fixed issues ○ IR-46893 ○ IR-46975 ○ IR-46988 ○ IR-46979 ○ IR-47057 • New feature: ○ Ion Reporter™ Server administrators now have more messaging and information on RAID status. • Feature removed – Myeloid Assay improvements
A.0	29 October 2020	New release notes for Ion Reporter™ Software 5.16.

New Features in Ion Reporter™ Software 5.16

Analysis workflow variant calling and annotation improvements and feature enhancements for assays and panels

- Ion AmpliSeq™ Microbiome Health Research Panel: detects microbial species via 16S and target species-specific amplicons with single and multi-analysis comparisons, using a variety of common databases and QIIME2 functionality
- OncoPrint™ tumor specific panels: analysis of focused, pre-designed or customized cancer panels relevant for clinical cancer research
- OncoPrint™ Comprehensive Assay Plus:
Comprehensive genomic profiling with analysis of low-frequency somatic variants (SNPs, Indels, CNVs) from over 500 genes, tumor mutation burden (TMB), Loss-Of-Heterozygosity, and microsatellite instability (MSI), and includes the following new features:
 - Exon-level Loss detection
 - %LOH and gene-level LOH detection
 - Automatically calculated tumor cellularity
 - Separate analysis workflows for samples prepared manually or on the Ion Chef instrument
 - Improvements in MSI detection
 - FusionSync technology covering >1300 isoforms with 49 fusion drivers, enabling: fusion detection from low input samples, detection of low level of fusion transcripts, and the ability to detect novel fusions for driver genes.
- Ion AmpliSeq™ CarrierSeq ECS Panel provides detection and analysis of single nucleotide variants (SNVs), insertion/deletions (INDELs), and copy number variants (CNVs) associated with 418 inherited disorders from a single assay. CarrierSeq ECS - 530 - w1.3 - Single Sample and CarrierSeq ECS - 540 - w1.3 - Single Sample workflows, released with Ion Reporter v5.16, contains the following improvements:
 - SNV/INDEL genotyping
 - Unified hotspot list of >36,000 SNVs and INDELs (combined a CarrierSeq hotspot list of >28,000 with a Igentify Curated hotspot list)
 - Parameter optimization, SVB Improvements, excluded high frequency NO CALL Hotspots, updated Hotspot Annotation
 - CNV calling
 - Confidence filtering (threshold of 6.9)
 - HMM sensitivity and specificity improvements
 - Improved baseline for gene conversion algorithm calling disorders from a single assay

Improved RAID status capabilities on Ion Reporter™ Server

Ion Reporter™ Server administrators now have more messaging and information on RAID status. To view the RAID status, in the Admin tab, click System Services, then click RAID Status.

Launch multiple Immune Repertoire workflows simultaneously for each sample

When you plan runs in Torrent Suite™ Software you can choose to select multiple immune repertoire analysis workflows to launch with each uploaded sample.

Change to MAF filter in Ion Reporter™ Software

In Ion Reporter™ Software 5.14 and earlier, the MAF filter searches MAFs of all alleles that are associated with a locus. Alleles at the locus found by the filter are returned as filtered results if they fall within the specified MAF range (except $rma=1$). In Ion Reporter™ Software 5.16, the MAF filter searches only the allele(s) that are specified by the genotype (excluding $rma=1$). The allele-based MAF filter results can be downloaded as Filtered Variants.

However, the Analysis Results screen in Ion Reporter™ Software 5.16 continues to show the locus-based MAF values when no MAF filter is applied. As a result, users may observe some variants which have displayed MAF values within the filtered in range are not returned by the new MAF filter on Analysis Result screen. To avoid the discrepancy, use allele view, which is not expected to have this issue because there is only one variant allele shown on each line.

New adjustable parameters to customize Immune Repertoire analysis workflows

You can customize immune repertoire analysis workflows with adjustable parameters.

Launch multiple Immune Repertoire workflows simultaneously for each sample

When you plan runs in Torrent Suite™ Software you can choose to select multiple immune repertoire analysis workflows to launch with each uploaded sample.

NCBI 16S sequence database included in Ion AmpliSeq™ Microbiome Health workflows

Ion AmpliSeq™ Microbiome Health Research Assay workflows now include the option to select the NCBI 16S sequence database for analysis.

Fusion calling parameter to allow potential increase in sensitivity

Fusion calling in analysis workflows for AmpliSeq HD and TagSeq panels and assays can now be done in one of two ways with a new optional fusion calling parameter. You now have the option to select how Present calls are made by: 1) using threshold settings for either molecular (family) counts or read counts, or 2) selecting a setting that requires the thresholds that you configure to be reached for both molecular and read counts. The default setting of this new parameter depends on the panel and analysis workflow but can now be edited to choose one or the other method. The types of counts used to call each fusion as Present are indicated in the analysis results. The impact of this parameter, when turned on to use either molecular counts or read counts, is the potential for increased fusion call sensitivity.

AmpliSeq™ Colon and Lung analysis workflow configuration settings have been updated

AmpliSeq™ Colon and Lung analysis workflow configuration settings have been updated to improve performance.

Ion AmpliSeq™ Microbiome Health Research Panel

- Data sorting is improved in the 16S rRNA Gene source data table in analysis results that use the Ion AmpliSeq™ Microbiome Health Research Panel and analysis workflows. By default, data is sorted with Family-level abundance results, descending, at the top, with the secondary sort by Genus-level abundance, descending, within Families. You can optionally choose to sort by Family name, with the secondary sort by Genus-level abundance, descending, within the alphabetically sorted Families.
- The species abundance bar graphs and heat maps now include a Phylum level data, in addition to Family and Genus.

BRCA analyses enhancements

- Oncomine BRCA troubleshooting: Gene_Deletions.xls file is now downloadable.
- Summary table included in BRCA visualizations provides access to more data

New data column for analysis results from AmpliSeq analysis workflows

- A Raw Coverage data column is now included in analysis results for AmpliSeq analysis workflows.

User experience improvement

- The “IRGV” tab has been renamed to “IRGV and Generate Report” tab. Users can visualize data in the IRGV data and generate a report that contains the data from the same tab.

Data and annotation source updates

- Updated controlled vocabulary for cancer types
- Updated hg19 and GRCh38 annotation sources

End of life for Ion Reporter™ Software 5.4 analysis workflows

Ion Reporter™ Software 5.4 analysis workflows are now retired from the Ion Reporter™ Software 5.16. Version 5.4 analysis workflows will also be unavailable after servers are upgraded Ion Reporter™ Software 5.16. Analyses that are launched through analysis workflows from Ion Reporter™ Software 5.4 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.

Software assessment service

Assessment to help optimize Ion Reporter(TM) workflows for new and established assays on a new version of Ion Reporter™ Software. Contact your bioinformatics support team to learn more.

Issues fixed in Ion Reporter™ Software 5.16

Issue number	Description
IR-47057	Users of the Ion Reporter™ Software API can get analysis details and links to download a Quality Control (QC) report, final report, and compressed archive (ZIP format) of unfiltered and filtered variants files with the <code>/api/v1/analysis</code> call. The name parameter is required if the type parameter is "sample". However, if users do not provide a name argument, a 400 - Bad Request error is returned. Workaround: Include the name argument for all cases with the <code>/api/v1/analysis</code> call.
IR-46893	When using the IonReporterUploader command-line utility, users were able to upload a BAM file and define samples although an identical same sample name existed in the Ion Reporter™ Software organization. However, analyses that were configured to automatically launch did not work properly when such a BAM file was uploaded. This issue is fixed in Ion Reporter™ Software 5.16.0.2. IonReporterUploader command-line utility now automatically appends existing samples with a suffix, for example <code>_v1</code> , then uses the new sample name to launch analysis.
IR-46975	Due to upgrade from Java 8 to 11, Ion Reporter™ Servers that were configured with HTTP proxy settings were not able to configure the Ion Reporter™ Software account on a Torrent Server. This is fixed in Ion Reporter™ Software 5.16.0.2.
IR-46988	In previous versions of Ion Reporter™ Software, if a modified or edited variant ID or OID (Observed ID) was an integer, analyses failed because the VCF record could not be imported. This is fixed in Ion Reporter™ Server 5.16.
IR-46979	Previously, in Ion Reporter™ Software 5.16 on Connect, a user who accepted an invitation from an administrator was unable to sign into the software and the new user was not displayed in the administration screen in Ion Reporter™ Software 5.16 on Connect. In Ion Reporter™ Software 5.16.0.2, new users are created correctly by the software.
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 returned all variants (no filtering is applied) due to a change in variant filtering logic. This is fixed in Ion Reporter™ Software 5.16.
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. This is fixed in Ion Reporter™ Software 5.16.
IR-44969	If an analysis was shared with an organization, the analysis was archived only in the source organization. Samples in the analysis were not archived because samples remained common between the source and target organization. This is fixed in Ion Reporter™ Software 5.16.
IR-44964	When a user clicked on the Locus link from the Fusion details table in the Variant Matrix Summary tab in Ion Reporter™ Software 5.14, data from the reference FASTA file of the first selected analysis was opened in Ion Reporter Genomic Viewer (IRGV). If the non-targeted fusion was contained in any analyses other than the first analysis, IRGV did not display that data when the Locus link was used to start IRGV. This is fixed in Ion Reporter™ Software 5.16.
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 returned all variants (no filtering is applied) due to a change in variant filtering logic. This is fixed in Ion Reporter™ Software 5.16.
IR-45279	When uploading BAM files into Ion Reporter™ Software, 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 were entered in Ion Reporter™ Software 5.14 and earlier, the file was uploaded without any errors but, the analysis run with the sample failed. An error appears if incorrect errors are entered into the name field for BAM file uploads in Ion Reporter™ Software 5.16.

Issue number	Description
IR-45168	An issue with the Torrent Variant Caller module caused false negative calls. This issue was fixed in Ion Reporter Software 5.14, and, as a result of correcting the issue, slightly different variant calling results were expected in Ion Reporter™ Software 5.14 compared with previous versions. The software update primarily affected 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 rare incidents, the software produced false positive or false negative calls that were not reported by the software in the previous version. This is fixed in Ion Reporter™ Software 5.16.
IR-42804	In Ion Reporter Software 5.14 and earlier, Analysis Visualization Reports could only be created from the Generate Report button that was available in the IRGV tab in the Analysis Visualization screen. Other tabs in the Analysis Visualization screen contained graphs and table contents, however, an inactive Generate Report button prevented reports generation from those tabs. Users were required to first click on the IRGV tab to generate the report. This is fixed in Ion Reporter™ Software 5.16. The IRGV tab is renamed to IRGV and Generate Reports and the Generate Report button is available only in the newly renamed tab.

Known issues and limitations in Ion Reporter™ Software 5.16

Issue number	Description
IR-46733	When fusion variants are detected as NOCALL, the No Call Reason column in the Analysis Results table does not represent the reason for no call. However, the No Call Reason information for fusion variants is available if you download all variants. The non-Filtered VCF file that is included in the ZIP file for the All Variants download includes all variants for an analysis. Review the "NOCALL_REASON" field for fusion variants to get the value for NOCALL fusion variants. This issue does not affect No Call Reason results for other types of variants.
IR-46683	If you launch an analysis workflow that includes multiple barcodes and different analysis workflows selected for each barcode, the following error message appears: "lonReporter:ERROR:Row2:Selected workflow name does not match a previous sample with the same SetID, with workflow name in row 1." You can resolve this issue in one of two ways. 1) Change the analysis workflow to which the error refers to match the previous analysis workflow selection for the this SetID. 2) Or, change the SetID to a new value if you intend this sample to be used in a different Ion Reporter™ Software analysis. The issue does not affect immune repertoire analyses as launches of multiple immune repertoire analyses at the same time is supported in Ion Reporter™ Software 5.16.
IR- 45389	If exon-levels CNVs are detected in a panel, not all of the CNVs may be represented for that gene in CNV heatmaps. This occurs due to how the software identifies CNVs. In the CNV heatmap for a set of CNVs, for a specific genomic segment, ploidy for variants is analyzed in the ascending order of the variant positions based on the following rules: • If a single variant with the highest ploidy is identified, the software analysis will 1) begin with one variant before the segment, and 2) include all of the variants after the segment that have the highest ploidy, and 3) include the single variant that was identified as having the highest ploidy variant. • If there are multiple variants identified as having the highest ploidy, the following variants are included in the analysis: 1) the last identified variant that has the highest ploidy, and 2) one variant before the multiple variants and, 3) all variants after the multiple variants. NOCALL variants are not counted.
IR-31124	When visualizing REFERENCE calls for hotspot alleles in the Liquid Biopsy tab of Analysis Results, some records might have empty values in Mol Counts, Mol Freq, Detection Limits. This happens when consecutive REF calls occur. The empty values are equivalent to values reported in the first record of the group of consecutive REF calls that are found in the genome, and shown in the BED file, or as sorted by the software in consecutive rows of the Analysis Results table.
IR-46824	Restoration of archived analyses that originally contained sample(s) that are deleted from the system at the time of restoration is not allowed. An error message indicates that VCF or BAM sample files are missing. Workaround: Upload the original samples to Ion Reporter™ Software and re-launch the analysis of the samples through the same analysis workflow.
IR-46380	In Immune Repertoire Result, the date and time shown in the Sequenced On column is not correctly displayed. Workaround: The sequencing date and time are shown correctly in the Torrent Suite™ Software and in sequencing run information in the QC Report for the sample that is uploaded.
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 .

Known issues and limitations in Ion Reporter™ Software 5.16

Issue number	Description
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-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-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-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.
IR-44642	In Chrome™ browser version 80 and later, an analysis or sample cannot be edited by 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.

Known issues and limitations in Ion Reporter™ Software 5.16

Issue number	Description
IR-33625	For OncoPrint™ 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."
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. Therefore, 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 considered. The gene model used in the analysis must match the gene model that is used by the filter chain.

Known issues and limitations in Ion Reporter™ Software 5.16

Issue number	Description
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.
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.

Known issues and limitations in Ion Reporter™ Software 5.16

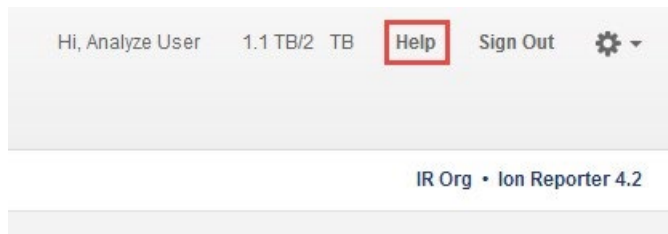
Issue number	Description
IR-34768	If user-created Custom sample attributes share the same name as predefined Ion Reporter™ Software sample attributes, the import of samples might use either the custom or predefined attribute, depending on which attribute type is encountered first by the software. This issue is present in Ion Reporter™ Software 5.6 and later 5.10. 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.
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-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 later. 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 use Table Preferences to add sample attribute columns in the Samples tab that were created in Ion Reporter™ Software 5.4 or earlier, in order to access those preferences in Ion Reporter™ Software 5.6 or later, you must delete the entire Table Preference, then recreate it.

Known issues and limitations in Ion Reporter™ Software 5.16

Issue number	Description
IR-29159	When creating a new annotation-only analysis workflow, OncoPrint™ 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 and later, 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 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. 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.
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, 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 5.16.0.27	Torrent Suite™ Software 5.16 and earlier	Ion Reporter™ Software 5.16 and earlier
Ion Reporter™ Uploader plugin 5.14.0.6	Torrent Suite™ Software 5.14 and earlier	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™ Uploader plugin 5.6.0.41	Torrent Suite™ Software 5.8 and earlier	Ion Reporter™ Software 5.6 and earlier

IonReporterUploader plugin

A new version of the IonReporterUploader plugin is available: Ion Reporter™ Uploader plugin 5.1.0.20 or later. This version of the plugin is already installed when Torrent Suite™ Software 5.16 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 5.8 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 5.8 and later.

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 “r” represents the patch number and “s” represents the number of builds done on this patch.

IRUCLI 5.6 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

Ion Reporter™ Software 5.16 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.

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.

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 an Ion Reporter™ Local Server, contact your local FBS.

Update Ion Reporter™ Server Software to 5.16

To upgrade Ion Reporter™ Software to 5.16, 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.

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