

Ion Reporter™ Software 5.22 Release Notes

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Contents

- Revision History 2
- New Features in Ion Reporter™ Software 5.22 3
- Important information about Ion Reporter™ Software 5.22 4
- Variation in calling behavior in older workflows with new Operating System (OS) versions 4
- Issues fixed in Ion Reporter™ Software 5.22 5
- Known issues in Ion Reporter™ Software 5.22 8
- Documentation 20
- Compatibility with Torrent Suite™ Software 20
- IonReporterUploader plugin 21
- Ion Reporter™ Software command-line utility (IRUCLI) 21
- IonReporterUploader plugin configuration 21

Revision History

Revision	Date	Description
A.0	May 21, 2026	New release notes for Ion Reporter™ Software 5.22.

New Features in Ion Reporter™ Software 5.22

Platform modernization and security enhancements

- Updated core technology stack components, including database and server frameworks
- Enhanced security measures including strengthened credential and password policies
- Ability to add new plugins is disabled to align with new security updates.

Analysis Workflow and Pipeline Updates

- Support for higher-throughput chips and assays kits
- Analysis workflows and templates that incorporate the latest algorithm improvements
- New aneuploidy score metric for arm-level CNV changes

Annotation and Content Updates

- Updated hg19 and GRCh38 annotation sources
- Updated cancer type terminology to align with latest standards
- Updated OncoPrint™ Variant Annotator classifications
- New variant classification terms: Oncogenic and Likely Oncogenic

Software assessment service

- Provides assessments to help optimize Ion Reporter™ Software analysis workflows for new and established assays on a new version of Ion Reporter™ Software. Contact your field service engineer (FSE) or field bioinformatics specialist (FBS) to learn more.

End of life for Ion Reporter™ Software 5.12 and 5.14 analysis workflows

Ion Reporter™ Software 5.12 and 5.14 analysis workflows are now retired from the Ion Reporter™ Software 5.22. Version 5.12 and 5.14 analysis workflows will also be unavailable after servers are upgraded to Ion Reporter™ Software 5.22. Analyses that are launched through analysis workflows from Ion Reporter™ Software 5.14 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.

Integrative Genomics Viewer (IGV) access now provided through ZIP file

The dependency on Java Web Start (JNLP) for access to the standalone version of the Broad Institute's Integrative Genomics Viewer (IGV) is removed due to enhanced software security. Enabled export for standalone IGV viewing. If the Account Preference is set to IGV, a ZIP file that contains files for upload to IGV is downloaded. Open IGV on your computer. Unzip the files, then open the session.xml file in IGV. For more information, see the Ion Reporter™ Software help system or the Ion Reporter™ Software 5.22 User Guide (Pub. No. MAN0029320).

Change to the TMB Non Germline Mutations Filter Chain

The TMB (Non-Germline Mutations) filter chain behavior has changed in Ion Reporter™ Software 5.22. CNVs are filtered out. This change does not impact TMB scores.

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 and later, 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 and later 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 the 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.

Important information about Ion Reporter™ Software 5.22

Variation in calling behavior in older workflows with new Operating System (OS) versions

The variant caller software module has been shown to exhibit the following expected behavior in Ion Reporter Software. When upgrading to Ion Reporter 5.22 with Operating System (OS) migration from Ubuntu™ 18.04 to Ubuntu™ 22.04, the variant caller may not reproduce exactly the same variant calling VCF files on these different versions of OS, even if other conditions (e.g., the input files, analysis workflow version) are identical. The small reproducibility differences are likely due to slightly different handling of floating-point arithmetic on the two different versions of OS. The discrepancies are usually insignificant and were found through extensive testing to be negligible most of the time.

Issues fixed in Ion Reporter™ Software 5.22

Issue number	Description
Analysis workflows	
IR-55967	Improvements to algorithms in the CFTR analysis workflows in Ion Reporter™ Software 5.22 allow long deletions to be called more reliably leading to more “PRECISE” calls when compared with Ion Reporter™ Software 5.20 and earlier.
IR-49290	In Ion Reporter™ Software 5.20, some analysis workflows such as those for OncoPrint™ Comprehensive Assay Plus, might take 5 minutes or more to import into Ion Reporter™ Software. Most analysis workflows take approximately 1 minute to import.
IR-49407	When you copied, or edited, any analysis workflow and uploaded one of the following target regions BED files, the plan.json file that was associated with the panel did not update the TVC parameter settings if the panel was downloaded to a local computer from AmpliSeq.com . <ul style="list-style-type: none"> · Ion AmpliSeq™ TP53 Panel · CFTR NxGenMDX Panel · Ion AmpliSeq™ Pharmacogenomics Panel · WG00527
IR-49423	Errors occurred when results of multiple completed analysis results that used Microbiome, Metagenomics, or Immune Repertoire analysis workflows were downloaded.
IR-49397	If an analysis that used an OCA Plus analysis workflow contained samples with extreme ploidy, for example, ploidy that is greater than or equal to 11, the analysis might have failed.
IR-49379	In a small number of cases, if a new target regions BED file that was imported from AmpliSeq.com was selected when an analysis workflow was copied from any analysis workflow, the TVC parameters were set based on the values that are contained in the imported files.
Variant calling	
IR-57556	False positive FLT3-ITD variants (specifically for CCATT insertions) were shown in some sample results that used the OncoPrint Myeloid MRD (RUO) workflow due to an issue that automatically generated combined variant entries.
IR-55540	False positive FLT3-ITD variants (specifically for CCATT insertions) were shown in some sample results that used the OncoPrint Myeloid MRD (RUO) workflow due to incorrect minimum insertion size parameter.
IR-49497	The sequence of the FLT3ITD insertion/duplication could, in some cases, deviate from the actual duplicated sequence. The position and length of the FLT3ITD insertion/duplication were reported correctly.
Filters and Filter Chains	
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™ Software 5.4 and later, some edits could persist if a user canceled changes made in filter-chain dialog box.

IR-44638	In Ion Reporter™ Software 5.14 and later, a software update to the Minor Allele Frequency filter which allowed users to select the Include Unannotated Variants option caused a discrepancy between the total number of variant rows shown in the table and the counts given in the software for the total number of Filtered In and Filtered Out variants.
Annotations	
IR-42277	<p>Ion Reporter 5.22 includes updates to improve HGVS-compliant annotation of duplication variants. Annotation of single-base duplications has been corrected.</p> <p>In some cases, annotation may still depend on how the variant is represented in the input data (e.g., alignment position), which can lead to differences in whether a variant is described as a duplication or insertion. Multi-base duplications may still be annotated as ins and not dup if they are not left-aligned in the VCF.</p> <p>Protein (amino acid) duplications function correctly and the dup/ins difference in annotation has no functional difference. To find a variant named as cDNA dup, you may need to look for insertions (ins) with similar positions as the dup, and check Ion Reporter™ Genomic Viewer (IRGV) or Integrative Genomics Viewer (IGV) for nearby sequences to match the dup with the ins variant. It is also recommended that users should rely on protein annotation to identify variants if available.</p>
IR-49275	PFAM annotations included links to the website for the PFAM database. Due to URL changes made by the PFAM website, when you clicked on an annotation in the PFAM column in Ion Reporter™ Software, the current PFAM website opened and redirected to the new PFAM website at https://www.ebi.ac.uk/interpro/entry/pfam .
IR-49244	A rare issue could occur for analysis results that used the COSMIC annotation source that is included in Ion Reporter™ Software and contained a reference sequence with multiple base pairs. During the Annotation step of the software analysis, when such called variants were annotated by the COSMIC annotation source that is in the software, the software was unable to fully match and annotate these called variants with COSMIC variant, if the option to include locus, allele or genotype hit level matches was used.
Analysis Results	
IR-42886	When a CNV record from MyVariants was 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 was not imported if the CNV record included multiple copy number values.
IR-45381	The analysis name is incorporated into Immune Repertoire output files. Long sample names, and/or analysis names which were based on long sample names, could prevent some PDF output files from being generated by the Immune Repertoire analysis workflows.
IR-33725	Column sorting for the "Mol Counts" and "Mol Freq" columns was not correct for ascending sort in the LOD view for liquid biopsy analyses.

IR-47706	For Fusion isoforms such as MTAP-CDKN2B_AS1_004.M7C5, some fusion panels used a "Do Not Report" flag internally to suppress false calls caused by background coverage. The final VCF file correctly excluded the output for the call. However, the "Fusion Overall Call" in the top of the Analysis Results screen reported the call.
IR-40286	Quality control for CNV calling of BAM files could fail in several ways. When CNV calling failed, analyses completed but all CNV hotspots were NOCALLs and no de-novo CNV calling occurred.
IR-23462	For some older analyses, when the BAI file was missing from the input BAM folder, the BAM and Reads Coverage tracks did not load in IGV or Ion Reporter™ Genomic Viewer screens.
IR-47689	When a user clicked on a link for a specific annotation on the DRA column in Ion Reporter™ Software analysis results, a MESH web page for DRA (Disease Research Area) annotations opened instead of the direct link to the page with details for an annotation.
Software	
IR-47612	The preview for visualization reports and final reports preview were not available if you used version 14 of the Safari® browser on macOS® Big Sur.
IR-47647	When using Microsoft™ Internet Explorer browser version 20H2, the status of all accounts on the IonReporterUploader plugin configuration screen were red or 'waiting', even though some of the accounts were available to select in the screen.
IR-29709	In some older versions of the Firefox and Safari browsers, the choice of a filter chain successfully filtered the data and listed the correct number of variants, but a statement "No Filters Selected" was present where the filters in the filter chain and their individual filtering results should have been listed.
IR-47983	IonReporterUploader Command-line Utility failed for transfers of BAM files which contained read groups with different flow orders.
Server Administration	
IR-51583	Spare hard drives in RAID array produced a warning state in the RAID status for Ion Reporter™ Server and generated an email warning.
Archive/Restore	
IR-49288	When the bulk archival/restore process was aborted, all of the entities except for the last one that is in the queue were aborted.

Known issues in Ion Reporter™ Software 5.22

Issue number	Issue Summary	Impact and Workaround
Analysis Workflows		
IR-65113	Analyses using the “Demo AmpliSeq Exome CNV case” sample will fail.	Contact your Field Bioinformatics Scientist (FBS) or Field Support Engineer (FSE) for assistance.
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 analysis workflows until the file is updated in a later version.
IR-49458	Unproductive reads can be incorrectly reported as productive in the OncoPrint BCR IGH Leader-J analysis workflows.	N/A
IR-56195	Parameter values in non-allowed ranges can be saved to user-defined analysis workflows. A warning message is shown but can be ignored. When the analysis workflow is saved, invalid parameter values are automatically reverted to default values without clear notification.	Ensure that you enter allowed ranges for parameter values that you change when creating or editing an analysis workflow. Ranges for allowed values are shown on the software screen when you place the pointer over the parameter name. If you see a warning message about parameter value, ensure that you edit parameters in the analysis workflow to be within allowed value ranges.
IR-56774	When using a trio analysis workflow, the order of sample columns in the annotation view changes each time the same variants are selected. That is, the order of Mother, Father, and Daughter columns changes positions in the analysis results.	This issue affects trio analysis results with Mother and Father columns for trio analyses and Case and Control columns for paired analyses. Only the column order is affected; the data in each column is accurate.
IR-62987	When an analysis workflow that includes the No Report Template setting is launched by a user with the Analyze role and then the analysis results are transferred to a user with Report role user, using the option "Send to Report Role", the Report role user cannot generate a report. The user receives an error that access is denied.	This issue prevents Report role users from generating a report for transferring analyses that do not use report templates. Complete the following steps to resolve this issue. <ol style="list-style-type: none"> 1) Send the transferred analysis back to the Analyze role. 2) Ask an administrator to publish the report. After completing the steps, the Report role user should be able to successfully generate reports from the transferred analysis results.

Issue number	Issue Summary	Impact and Workaround
IR-47510	<p>Upon launching the AmpliSeq™ Microbiome Health analysis workflows for the same sample, the abundances calculated and reported on the 16S rRNA Gene tab in Ion Reporter™ Software 5.18 and later (Family Relative Abundance% and Gene Relative Abundance% columns in the visualization) might show some minor variation from one run to another.</p>	<p>This occurs when there are reads that have multiple best hits upon mapping to the reference; the mapping method used by the software picks any one target at random, which leads to different estimations. 16S regions are very similar to each other, so it is very likely that a given read is equidistant from several reference sequences. As a result, such results are expected. These variations in analysis results do not impact the overall quality of the results.</p>
IR-48754	<p>If multiple Immune Repertoire analysis workflows are launched at the same time, one or more analyses may stall or make the server inaccessible temporarily. To avoid this issue, do not launch multiple Immune Repertoire analysis workflows. The Ion Reporter™ Server may become unavailable for up to 24 hours before automatically.</p>	<p>Contact your Field Support Engineer (FSE) if the server does not come back up automatically after 24 hours.</p>
IR-35322	<p>The variantCaller plugin for Torrent Suite™ Software 5.10 and later includes the use_fd_param=1 for default AmpliSeq™ HD somatic and germline settings. The parameter, when set to true, uses the new FD parameters. Ion Reporter™ Software 5.12 and later has partial support for FD parameters with the following limitations:</p> <ul style="list-style-type: none"> <li data-bbox="402 1262 833 1493">• 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. <p>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 5.12 and later analysis workflows.</p>	<p>Contact your Field Bioinformatics Scientist (FBS) for further assistance if you would like to change these parameters in Ion Reporter™ Software.</p>

Issue number	Issue Summary	Impact and Workaround
IR-33625	<p>For OncoPrint™ BRCA analysis workflows, the default canonical transcript has been changed from NM_007300.3 to NM_007294.4. 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_007294.4 transcript. As a result, Exon 13 in transcript NM_007300.3 is not used in Exon Deletion/Duplication variant calling.</p>	<p>It is recommended that the default canonical transcript (NM_007294.4) be used for OncoPrint™ BRCA workflows to help ensure that exon numbering in charts and CNV calling remains consistent.</p> <p>If a custom transcript must be used, check reference- reported exon numbers against the default NM_007294.4 transcript to help ensure accurate interpretation of deletion or duplication event.</p>
Variant calling		
IR-45389	<p>If exon-levels CNVs are detected in a panel, not all CNVs may be represented for that gene in CNV heatmaps.</p>	<p>This occurs due to how the software identifies CNVs.</p> <p>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:</p> <ul style="list-style-type: none"> • If a single variant with the highest ploidy is identified, the software analysis will: <ul style="list-style-type: none"> ○ begin with one variant before the segment ○ include all the variants after the segment with the highest ploidy ○ include the single variant 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: <ul style="list-style-type: none"> ○ the last identified variant with the highest ploidy ○ one variant before the multiple variants ○ all variants after the multiple variants. NOCALL variants are not counted.

Issue number	Issue Summary	Impact and Workaround
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 zero, and the Detection call is made based on only the read counts, such as is the case with Ion AmpliSeq™ fusions analysis workflows.	N/A
Filters and Filter Chains		
IR-64072	When the dbSNP Minor Allele Frequency (MAF) filter is used with Include unannotated = true, reference minor alleles (RMA=1) are treated as unannotated and are always filtered in regardless of their MAF values.	To filter out RMA=1 alleles with Include unannotated = true, the Not In and dbSNP common filter should be used in combination for their removal.
IR-60588	Some variants in Ion AmpliSeq™ custom panels are filtered out when the ExAC filter is used in a filter chain.	If you use ExAC filters to create filter chains, it is recommended that you set the Variant View parameter to Allele View.
IR-49401	Filtering results might differ when you use the Minor Allele Frequency (MAF) filter in Ion Reporter Software 5.20 and later compared to filtering results in Ion Reporter™ Software 5.18 and earlier.	To obtain similar results from the MAF filter as in Ion Reporter™ Software 5.18, deselect the "Include unannotated variants" checkbox when you create a filter chain that includes a MAF filter with Ion Reporter™ Software 5.20.
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 the operation of filter chains.
IR-39523	Differences in the predefined filter chains and similar user-defined filter chains can occur if both gene models (RefGene GeneModel and Ensembl GeneModel) are not considered.	The gene model used in the analysis must match the gene model that is used by the filter chain.

Annotations		
IR-62938 (related to IR-42277)	HGVS guidelines require cDNA level duplication to be annotated as dup (i.e. c.1934dup) instead of ins (i.e., c.1934_1935insG). In Ion Reporter™ Software 5.22, cDNA duplications (dup) annotation implementation is incomplete. In some cases, annotation may still depend on how the variant is represented in the input data (e.g., alignment position), which can lead to differences in whether a variant is described as a duplication or insertion. Multi-base duplications may still be annotated as ins and not dup if they are not left-aligned in the VCF.	Annotations for protein (amino acid) duplications function correctly and the dup/ins difference in annotation has no functional difference. To find a variant named as cDNA dup, you may need to look for insertions (ins) with similar positions as the dup, and check Ion Reporter™ Genomic Viewer (IRGV) or Integrative Genomics Viewer (IGV) for nearby sequences to match the dup with the ins variant. It is also recommended that users should rely on protein annotation to identify variants if available.
IR-49228	dbSNP annotations include links to the external home page for the dbSNP database. Due to recent URL changes made by the dbSNP website, when you click on a specific annotation in the dbSNP column in Ion Reporter™ Software, a dbSNP website opens to a 404 page error.	Workaround: To open the direct link for the annotation, edit the URL of the main dbSNP web page that is opened for a variant, as shown in this example. If the URL is for example: https://www.ncbi.nlm.nih.gov/SNP/snp_ref.cgi?rs=rs974924 . Change the URL as shown in this example: https://www.ncbi.nlm.nih.gov/snp/rs974924 .
Analysis Results		
IR-65553	Indels near the 3' end of reads are causing MAPQ (mapping quality) scores to drop to very low values, even when the read is perfectly and uniquely mapped.	Contact your Field Bioinformatics Scientist (FBS) or Field Support Engineer (FSE) for assistance.
IR-57608	In rare cases, a reported fusion with good reads count, might show zero or a very few number of reads with the Broad Institute's Integrated Viewer (IGV), which are much less than the number of reads reported in the Ion Reporter™ Software Analyses Results screen. This could be caused by an additional exon that is amplified and sequenced by existing primers, which becomes unmapped due to the presence of a large insertion. There could also be other technical or biological reasons.	Contact your Field Bioinformatics Scientist (FBS) or Field Support Engineer (FSE) for assistance.

IR-65942	PDF files are intermittently missing when analysis results are downloaded from sequencing run that use the ImmuneRep analysis workflow.	To resolve this issue, recreate the sample, using a shorter sample name, then launch the analysis workflow with the new sample name.
IR-65054	The MSI QC column in the downloaded Summary.tsv file is empty although the column in the software correctly shows "PASS" for the same sample.	A blank value in the Summary.tsv file can be considered a "PASS". Other values are shown correctly in the file.
IR-61921	The CNV Confidence Interval (CI) is not shown in analysis results screen for CNVs in HRR genes if when segmentation fails but VCIB calling is successful.	The Confidence Interval is available in the VCF results file.
IR-60466	Allele frequency data shown in ExAC columns in analysis results in the Population tab does not show information about specific alleles.	To determine the frequency of an allele, you can click a link of interest in the ExAC columns section to open the gnomAD browser and find the Other Alternate Alleles section. Then, compare the observed allele to the allele frequency to match the corresponding allele frequency of the allele.
IR-56118	In rare cases, when using the OncoPrint Focus Assay analysis workflow on Ion Reporter™ Software on Connect, some analyses are launched without the qcinfo file, which can result in false positive variants in analysis results.	The qcinfo file is available when you download detailed analysis logs.
IR-57600	In some cases, if a REF or NOCALL matches the allele of an entry in the dbSNP or gnomAD population databases, the match may not be properly recognized when a filter chain is applied.	This could potentially result in such a REF or NOCALL record not being filtered properly. To suppress REF and NOCALL records, create and use a filter chain that excludes REF and NOCALL variants from the allowed Variant Type values to prevent this issue.
IR-60432	Inconsistent values are sometimes generated for the TMB somatic mutation substitution plots for homozygous calls.	The discrepancy only affects the accuracy of TMB visualization bar plots and pie charts and does not impact TMB calculation.
IR-60471	Some links to the ExAC database may no longer open detailed variant pages on the gnomAD website. Links might redirect to the incorrect page, or show an error such as: "An error prevented this page from being displayed."	This issue occurs because the ExAC dataset is superseded by the gnomAD database, and some legacy ExAC variant identifiers are no longer fully supported. When reviewing results from ExAC-based filter chains, ExAC filters may not meet your expectations of which variants are shown or hidden.

IR-62576	Exported VCF files for analysis results that use a filter chain that includes both the FATHMM Score(97) and COSMIC v97 filters contain variants that are not annotated with FATHMM scores.	Mitigation: To continue using a VCF file, do one of the following. Open the analysis results in the software, then remove the FATHMM Score(97) filter from the filter chain, save and apply the filter chain, and then export the VCF file again.
IR-49355	If Allele View is used when you view variants in the analysis results table, the Allele Ratio column refers to the ratio between <i>one</i> ALT allele and the REF allele, rather than the ratio between <i>all</i> ALT alleles to the REF allele. As a result, when multiple alleles are present at a location, it can be difficult to determine if multiple Present alleles are grouped together in Locus View. Note: The Allele Ratio column also refers to ratio between <i>all</i> ALT alleles to the REF allele when Locus View is used.	Workaround: Disregard the Allele Ratio column in the Analysis Results screen, and instead use the Allele Frequency% column to evaluate the prevalence of variants.
IR-47734	In Ion Reporter™ Software 5.14, changes were made to genotype parsing that impacted some valid VCF files with a genotype that includes a single allele such as those on the Y chromosome, male nonpseudoautosomal regions of X, or mitochondrion.	The issue impacts only VCF files that are not generated by Torrent Suite™ Software, Ion Reporter™ Software, or Genexus™ Software. This issue does not impact VCFs generated by these Thermo Fisher Scientific software products.
IR-47610	While uploading a large number of multiple VCF files with the IonReporterUploader command-line utility on a windows computer, uploads may stop.	Workaround: Add a maximum of 5 VCF files for each file upload.
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.	N/A

IR-49191	<p>If you use some custom scripts to process the VCF file that is downloaded from Ion Reporter™ Software, the VCF file generated by DNA and Fusions analysis workflows for use with the OncoPrint™ Myeloid Assay can contain the two following headers: <pre>##INFO=<ID=SVTYPE,Number=1,Type=String,Description="Type of structural variant"> ##INFO=<ID=SVTYPE,Number=A,Type=String,Description="Type of structural variant"></pre> This is an incorrect VCF file type and will result in an error message.</p>	<p>Workaround: Remove the following line from the header and re-run the script that generated the error message to correct the VCF format of the file: <pre>##INFO=<ID=SVTYPE,Number=A,Type=String,Description="Type of structural variant"></pre></p>
IR-48096	<p>Although you can download results files for metagenomics analyses from the Analyses screen with the Actions> Download menu, the downloaded results will include only the following single plots: Chao1.txt, Shanon.txt, Simpson.txt and observed Species.txt.</p>	<p>The content of these files is calculated by from alpha diversity results by using all of the genus, species, and family data combined, and therefore does not match the results shown in the Visualization/Downloads section of the metagenomics analysis results. To download all results files for metagenomics analyses, use the Download results files for all samples link, shown in the Visualization/Downloads section of the metagenomics analysis results.</p>
IR-34146	<p>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 user-defined Ion Reporter™ Software analysis workflow.</p>	N/A
IR-48185	<p>In rare cases when barcoded and non-barcoded samples are combined in the same sequencing run, a NullPointerException error is received when downloading variant files in Ion Reporter™ Software.</p>	<p>Workarounds: 1) Delete coverageAnalysis plugin output in Torrent Suite™ Software, then re-upload samples using the IRU plugin and complete the analysis on Ion Reporter™ Software. 2) Upload the BAM file using IRUCLI command-line utility by downloading it from Torrent Suite™ Software, then complete the analysis in Ion Reporter™ Software.</p>

Visualizations		
IR-65168	When generating IGV files for multiple analyses in Ion Reporter™ Software and opening them in the Broad Institute's Integrated Viewer (IGV) desktop application, annotation tracks are displayed multiple times instead of appearing once per analysis. This occurs when selecting 2 or more completed analyses for visualization and exporting IGV files.	N/A
IR-56693	Visualizations for analysis results that use ReproSeq™ analysis workflows in Ion Reporter™ Software 5.18 and 5.20 are missing a coverage line for chromosomes when a user-defined workflow is used with baseline tile sizes of 0.1 Mbp or smaller.	In order to help ensure the coverage line for chromosomes is shown, it is recommended that baseline tile sizes greater than 0.1 Mbp be used with a user-defined or system-installed ReproSeq™ analysis workflow.
IR-49325	Data that is downloaded from visualizations for which filter chains are used contain data from the filter chain that is applied in the Analysis Results screen, instead of the filter chain that is applied in the Visualization screen.	<p>Workaround: To download a ZIP file that contains filtered variants for the filter chain that is applied in the Visualization screen, you must first apply and save the filter chain on the Analysis Results screen for each individual analysis, then complete one of the following options.</p> <ul style="list-style-type: none"> • Select the analyses in Analyses table, then click Visualize. In the Visualization screen, click Download > Filtered Variants. The ZIP file that is downloaded will contain the expected data. • Select the analysis or analyses in the Analyses table and then click Actions>Export Filtered. <p>Alternatively, you can click Download>Current Results TSV to download a TSV file that contains data from the Visualization screen.</p>
IR-44509	You can use the visualizations in the software to confirm deletions and duplications. Whole gene deletion or duplication results can be confirmed in the pre-corrected view.	<p>Workaround: Whole gene deletion or duplication results can be confirmed only in the pre-corrected view. That is, if a BRCA1 deletion or duplication (BRCA1DEL or BRCA1DUP) or a BRCA2 deletion or duplication (BRCA2DEL or BRCA2DUP) for a GeneCNV subtype is shown in the Call Details of the CNV variants table, review the visualization to verify the direction of the GENE CNV subtype. Click Pre-corrected and Compare the SampleID (sid) amplicons to the BRCA1 or BRCA2 genes.</p>

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-41252	In the IRGV & Generate Report tab, if you zoom in on the VCF track while viewing a specific chromosomal region 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.
Reports		
IR-65000	The QC Report shown in the Report Preview pane fails to display any data when accessed from the Generate Report screen.	Access the QC Report in the software in the Analyses screen.
IR-64999	When a section for BRCA results is included in report being generated from the Analysis Visualization screen, the report preview tab and report generation fails to load and shows an error message "We can't open this file. Something went wrong. Refresh." This occurs if the section for BRCA results is empty.	Remove the BRCA section from the report generation screen in the software, then generate the report.
IR-64150	During organization creation in Ion Reporter™ Software on Connect, a failure message indicating 503 Service Unavailable errors can occur, although the organization is created successfully in the backend and users can log in normally later.	Sign out and sign back into Ion Reporter™ Software on Connect to verify that the new organization exists.
IR-62983	Images uploaded into Image Sections on the Configuration page of Generate Report are not shown in Preview and are missing from the Downloaded PDF. The issue occurs when image filenames contain spaces.	To prevent this issue, do not upload images with filenames that contain spaces. You can rename the image before you upload the image. For example, use "tumor_panel_v1.png" instead of "tumor panel v1.png".
Software		
IR-65950	The ion icon that identifies system-installed sample attributes is missing from the column filters on in the Samples screen.	When you click on More Filters, you can see the ion icon to view which samples attributes are system-installed.
IR-65601	The Analysis Overview screen is experiencing significantly longer loading times, depending on which columns are included in the screen.	Decrease the number of rows shown or reduce the number of columns shown in the screen. If a timeout occurs, remove the Copy Number Baseline column to review the screen.

IR-65532	In very rare cases, MSI Status is incorrectly shown as QCFail for OCAPlus w 2.1 analysis workflows.	This issue affects only Ion Reporter™ Software on connect. If this issue occurs, create a new analysis workflow then relaunch the analysis.
IR-65262	The rank column sorting in Clone Summary for the Immune Repertoire results clears all table data when sorting in ascending or descending order.	If this issue occurs, refresh the screen. Do not use the ascending or descending sort order when viewing the Clone Summary.
IR-65169	Filters on the Analysis Overview screen are not shown for selected values when navigating back from another screen. Although the filter selection is not shown the filtered results are shown in the screen.	Reapplying any new filter should update the filtered results to show the correct filter selection.
IR-41823	In Ion Reporter™ Software, p-values in Analysis Results in the Summary view in the column named "p-value" are rounded to five 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.	N/A
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.	

Archive/Restore		
IR-64123	The Abort action for Archive and Restore operations in Ion Reporter™ Software does not show "Archive Aborted" or "Restore Aborted" statuses and banner messages until the operations are completed.	The status updates when the operations are complete.
Auditing and audit records		
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 .

Samples and sample attributes		
IR-34768	If user-defined sample attributes have the same name as predefined Ion Reporter™ Software sample attributes, the import of samples might use either the user-defined or the predefined attribute, depending on which attribute type is encountered first by the software.	Workarounds: It is recommended that you do not create user-defined sample attributes that use the same names as Ion predefined sample attributes. Alternatively, if you do use a user-defined sample 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 uploading samples, or you can choose to add the values for those attributes after the samples are successfully uploaded.
Exon tile baseline creation		
IR-48306	Exon Tile baseline creation is failing with error "Segmentation fault (core dumped)" in rare cases. In tests, this failure occurs once in 150 baseline creation attempts.	Workaround: A relaunch of the baseline creation will likely resolve the failure since this issue rarely occurs.
Ion Reporter Command-Line Utility		
IR-47896	If large numbers of VCF or BAM files are uploaded with the IonReporterUploader command-line utility on a Microsoft™ Windows computer, uploads may stop.	Workaround: Add a maximum of five files each time that files are uploaded.

Documentation

You can access product documentation through the help link at the top right of Ion Reporter™ Software. This link opens the help system in a new tab, based 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, 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 six 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.


IonReporterUploader plugin

A new version of the IonReporterUploader plugin is available: Ion Reporter™ Uploader plugin 5.22 or later.

New plugin versions might become available between releases of Torrent Suite™ Software or Ion Reporter™ Software. If you need to upgrade IonReporterUploader plugin on an Ion™ 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.

Ion Reporter™ Software command-line utility (IRUCLI)

A ZIP file of the Ion Reporter™ Software command-line utility (IRUCLI) is available that 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 is no longer supported 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 the new address should now be used.

The information in this guide is subject to change without notice.

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