iontorrent

RELEASE NOTES

Ion Reporter™ Software 5.10 Release Notes

Pub. No. MAN0017604 Rev. E.0

Contents

For Research Use Only. Not for use in diagnostic procedures.

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

Revision History

Revision	Date	Description

E.0	31 Jan. 2019	Update to release notes for Ion Reporter ™ Software 5.10.5. Issues found in Ion Reporter™ Software 5.10.3 and earlier include:
		• Fixed Issues:
		   o IR-37417
		   o IR-38076
		   o IR-37954
		• Known Issues:
		   o IR-37640
		   o IR-37643

D.0	19 Oct. 2018	Update to release notes for release of Ion Reporter™ Software 5.10.3. Issues found in Ion Reporter™ Software 5.10.2: • IR-36888 (Fixed in 5.10.2) • IR-36948 (Known Issue)
C.0	26 Sept. 2018	Update to release notes for release of Ion Reporter™ Software 5.10.2. Variant Matrix Summary filter chain added as new feature. Issues found in Ion Reporter™ Software 5.6, 5.10.0 or 5.10.1 and fixed: • IR-35997 • IR-35630 • IR-36125 • IR-35995
B.0	16 July 2018	Update to release notes for release of Ion Reporter ™ Software 5.10 for Ion Reporter ™ Server.
A.0	20 June 2018	New release notes for Ion Reporter™ Software 5.10 in the Thermo Fisher Cloud.

New Features in Ion Reporter™ Software 5.10

The Ion Reporter™ Software 5.10 release includes many new features and improvements.

Variant Matrix Summary filter chain for Ion Reporter 5.10 TagSeq and AmpliSeq HD analysis results

A new Filter Chain named "Variant Matrix Summary (5.10)" is now available in the software. When used in 5.10 software version TagSeq workflow and AmpliSeq HD workflows, this filter chain displays analysis results in the Analysis Results table that contain the same set of variants as those shown in the Variant Matrix tab's Summary display in the Analysis Visualization area of the software. This filter chain works *only* on analysis results generated with Ion Reporter ™ Software 5.10 workflows; it does not work with workflow analysis results from version 5.6 and earlier.

Updated hg19 Annotations

Hg19 annotation sources are updated and available in the annotation sets that are included with the latest predefined workflows in Ion Reporter™ Software 5.10. You can also add these updated annotation sources to custom annotation sets and custom analysis workflows.

Ion AmpliSeq™ HD Made-to-Order Panel Support

New workflow templates for use in the analysis of Ion AmpliSeq™ HD Made-to-Order panels are available. The workflow templates support SNV/Indel, CNV, and Fusion detection. Separate workflow templates with simplified visualizations include parameters for use with analysis of liquid biopsy samples, or tumor biopsy samples, for any of these panels. You can analyze DNA and Fusion analyses from separate DNA and RNA libraries, or from a single library preparation that contains total nucleic acid or cell-free DNA.

Mutation Load and Oncomine™ Tumor Mutation Load Assay Support

You can enable the calculation of Mutation Load (also known as Tumor Mutational Burden) in Mutations per Megabase (Mutations/Mb) if you enable a new workflow parameter — Mutation Load Calculation Filter Chain — for any DNA Single Sample workflow. Predefined workflows for the Oncomine™ Tumor Mutation Load Assay have the Mutation Load calculation turned on by default. New 5.10 workflows will be available after Ion Reporter ™ Software 5.10.2 is released.

Oncomine™ Childhood Cancer Research Assay Support

New workflows for analyzing Oncomine ™ Childhood Cancer Research Assay data are available that support SNV/Indel, CNV, and Fusion detection.

Oncomine™ TagSeq Pan-Cancer Research Assay Support

New workflows for analyzing Oncomine ™ TagSeq Pan-Cancer cell-free DNA Research Assay data are available that support SNV/Indel, CNV, and Fusion detection.

Oncomine™ Immune Repertoire TCRß-SR Assay Support

DNA and RNA workflows are now available for the analysis of human T-cell receptor beta chain CDR3 regions amplified with the Oncomine™ TCR**β**-SR Assay. Analysis results report the frequency and sequence features of clonotypes and provide secondary analyses of repertoire features. Data generated

by the Oncomine™ TCRβ-SR Assay can be compared to data generated by the Oncomine™ TCRβ-LR Assay in Ion Reporter™ Software 5.10.

Oncomine™ Immune Repertoire TCRβ-LR Assay Support

A workflow is now available for the analysis of human T-cell receptor beta chain CDR1, 2 and 3 regions amplified with the Oncomine™ TCRβ-LR Assay. Analysis results report the frequency and sequence features of clonotypes and provide secondary analyses of repertoire features. A plugin is also available to identify TCR beta variable gene alleles that are not present in the IMGT database. The plugin can be optionally run as part of an Immune Repertoire workflow.

Splicesite_5 and splicesite_3 refers to intron locations

Prior to Ion Reporter™ Software 5.10, we defined splicesite_5 and splicesite_3 as exon-centric. This was contrary to the common convention of splice site nomenclature that was intron-centric and would exchange the splicesite_5 and splicesite_3 designations. In Ion Reporter™ Software 5.10, splicesite_5 and splicesite_3 refers to the intron locations. In earlier releases of the software, you might have seen a 3' splice site in your results; you will now see a 5' splice site and vice versa.

Preimplantation Genetics Aneuploidy detection

A number of new improvements for Aneuploidy detection are in Ion Reporter™ Software 5.10.

They include:

- Smaller genomic tile size: genomic tile size is now adjustable to facilitate increased resolution of sub-chromosomal germline and mosaic aneuploidy event detection. New pre-built CNV baselines that correspond to smaller tiles sizes are included in the software and are ready for use in any customized Aneuploidy analysis workflows. For best results, ensure the custom baseline tile size matches the tile size that is specified by the workflow into which you add the custom baseline.
- Expected Normal Ploidy Buffer: The expected normal ploidy buffer filter chain (and all other filter chains) are now available in the Ion Reporter™ Genomic Viewer (IRGV) tab. Previously, this filter chain was only available in the Analysis Results table for single analyses. The Expected Normal Ploidy Buffer is used to filter out false positive mosaic results that occur very close to expected normal ploidy. Users can adjust the ploidy values encompassed by the buffer.
- Enhanced whole genome view graphics and data: a new "Productive Reads" metric, improved coloring and dot size, and fixed ploidy lines in the display make the Whole Genome View in IRGV even easier to interpret.

Improvements in LOD calculation for TagSeq and in Ion AmpliSeq HD assays

The LOD reporting for TagSeq and AmpliSeq HD assays in Ion Reporter ™ Software 5.10 is a new design that function more sensibly and conservatively than in previous releases. Compared with Ion Reporter 5.6 and earlier, higher values of LOD reported in Ion Reporter™ Software 5.10 are expected. In general, the change on the LOD reporting does not affect the variant calling results.

Ion Reporter ™ Software 5.10 Release Notes   4

FLT3-ITD detection for the Oncomine™ Myeloid Research Assay

A new algorithm detects Internal Tandem Duplications in the FLT3 gene, which are displayed as a new variant type – FLT3ITD – in samples analyzed with the Ion Reporter™ Software 5.10 Oncomine Myeloid Research Assay workflows.

Ion 550 chip support

Ion 550 chip support will be available for select assays with analysis workflows at both the launch of Ion Reporter™ Software 5.10 and after the software is released.

Copy/Edit older workflows

Ion Reporter™ Software 5.10 allows you to copy Ion Reporter™ Software 5.6 and earlier workflows. This can make it easier to edit those workflows with existing parameters and presets, after you upgrade to Ion Reporter™ Software 5.10. Beginning with this release, you will be able to add future off-cycle packages into the Ion Reporter™ Software even after the software has been upgraded to a version that is later than the version of the off-cycle software package.

Automatically add Notes and Classification to variants in MyVariants database

As new instances of variants that are flagged as Important or Ignore are added automatically to a MyVariants database, you can now choose a setting that automatically adds to the variant the Note that was last added and the Classification that was last given to that variant. This setting automates the annotation of known MyVariants.

Additional audit tracking

As an administrator, you can track many types of user activity within your organization in Ion Reporter™ Software. For example, you can see who created analyses and who modified or deleted Samples, variant Notes, variant Classifications, and other activity.

Get BAM files from Ion Reporter Server

A new API call named getAssociatedBamfiles allows Ion Reporter™ Server customers to automate the retrieval and export of BAM files that have been uploaded to their Ion Reporter™ Server System.

End of life for Ion Reporter™ Software 4.6 workflows on Thermo Fisher Connect and Ion Reporter™ Servers in 5.10.

Ion Reporter™ Software 4.6 workflows are now retired from the Ion Reporter™ Software 5.10 on Thermo Fisher Connect. Version 4.6 workflows will also be unavailable after servers are upgraded Ion Reporter™ Software 5.10. In the future, each new version of Ion Reporter™ Software will retire at least one of the earliest versions of the currently released Ion Reporter™ Software analysis workflows.

Variant calling changes between Ion Reporter™ Software 5.6 and 5.10 workflows

As we are constantly striving to improve our algorithmic pipelines, you will notice differences between the results of Ion Reporter™ Software 5.6 workflows and their Ion Reporter™ Software 5.4 counterparts. You may potentially see more differences in Ion Reporter ™ Software 5.10 than in other prior releases, due to the significance and number of improvements and bug fixes that are included in Ion Reporter™ Software 5.10.

Tab and Column name changes

The cfDNA tab in the Analysis Visualization screens used by TagSeq workflow analyses has been relabeled as "Variant Matrix". This tab can also be used to visualize Ion AmpliSeq™ HD analysis results. Use of the term "Depth":

DP is defined as the count of chip-level reads aligned at this locus that participate in variant calling. Columns that always give only DP as the VCF key value (FDP is never given, nor is other logic ever used) are labeled "Depth", in Ion Reporter™ Software.

In the Variant Matrix>SNV/Indel detail table, the "Amplicon Coverage" column has been relabeled "Depth" in the software.

In the LOD tab of the Analysis Results table, the "Coverage" column (which uses DP value, only) has been relabeled "Depth" in the software.

Allele Subset information

There is a new data column called "Subset Of" (or subset) that can be used to help clarify alleles at a variant locus in either Allele View or Locus View results.

The following information applies to Locus View only:

The subset column indicates that an allele is part of a larger variant that has been called is present (the superset). The format is subset index (superset index). The larger variant can be found by using the value of the superset index counting into the alleles listed in the "Observed Allele" column. The subset id can be a hotspot id or a number. If it is a number and not a hotspot id then it is also an index counting in the alleles listed in the "Observed Allele" column. The subset allele always will match one of alleles without a genotype. A special case is that two superset indices may be present in which case both are displayed with a "/" between them.

The following applies to Allele View only:

The subset column indicates that an allele is part of a larger variant that has been called present (the superset). The format is "SupersetID" which will be a name for the superset variant. A special case is that two superset indices may be present in which case both are displayed with a "/" between them.

Flow disruption parameters

The variantCaller plugin in Torrent Suite ™ Software 5.10 includes a parameter named use_fd_param=1 for use with the default Ion AmpliSeq ™ HD somatic and germline settings. The parameter, when set to true, uses Flow Disruptiveness (FD) parameters instead of allele types (INDEL, SNP, MNP) as the criterion to select the parameter set. If enabled for Torrent Suite ™ Software Planned Runs that use the variantCaller plugin, the (non-FD, weak FD, strong FD) allele applies the (INDEL, SNP, MNP) parameters, respectively.

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 tvc json file that includes use_fd_param=1.

- 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.

Issues fixed in Ion Reporter™ Software 5.10

Issue number	Description
IR-38076	An issue was found in Ion Reporter ™ Software 5.6 and 5.10 involving the import of workflows with customized algorithm parameters, which was followed by subsequent workflow creation using the Create Workflow process. The new Create Workflow-created workflows used the imported workflow's algorithm parameters, rather than the workflow's default parameters. None of the pre-defined (Ion) workflows that are shipped with the software, pre-defined (Ion) workflows installed on- or off-cycle to Ion Reporter ™ Servers, or custom workflows copied and edited from these pre-defined "Ion" workflows on either Ion Reporter ™ on Thermo Fisher Cloud or Ion Reporter ™ Server, are impacted. This issue is fixed in Ion Reporter ™ Software 5.10.5, and the Ion Reporter ™ on Thermo Fisher Cloud 5.10.5 software was deployed with corrected algorithm parameters. The details are as follows: The issue caused a resetting of the default algorithm parameters to those parameters of the imported workflow, for subsequently-created Create Workflow-created workflows that used the same workflow template as the imported workflow (a workflow template is defined by a combination of the Application Type, Grouping, Panel Amplicon Technology, and Variant Detection Type). Seven workflow templates were impacted in Ion Reporter™ Cloud 5.6, and seven workflow templates were impacted in Ion Reporter ™ Cloud 5.10 until 5.10.5 was launched. The following version 5.6 and 5.10 workflows on Ion Reporter ™ on Thermo Fisher Cloud which were impacted have now been corrected in Ion Reporter ™ on Thermo Fisher Cloud: IR 5.6 1. TumorNormal workflow(s) 2. AmpliSeq Somatic workflow(s) 3. Tag Sequencing workflow(s) 4. AmpliSeq Germline workflow(s) 5. Annotate Variants workflow(s) 6. Aneuploidy workflow(s) 7. Metagenomics workflow(s) IR 5.10 1. TumorNormal workflow(s) 2. AmpliSeq Exome Genetic Disease Screening workflow(s) 3. AmpliSeq Somatic workflow(s) 4. Tag Sequencing workflow(s) 5. AmpliSeq Germline workflow(s) 6. TargetSeq Genetic Disease Screening workflow(s) 7. AmpliSeq Genetic Disease Screening workflow(s) The workaround for Ion Reporter ™ Server 5.6. and Ion Reporter ™ Server 5.10 customers who may have been impacted is to use the Copy Workflow functionality to create custom workflows, and not use the Create Workflow method. This issue does not impact other workflows with different template configurations, and does not impact copy/edited workflows in the same Ion Reporter ™ Organization even of the same template configuration. This issue is fixed in Ion Reporter ™ Software 5.10.5.
IR-37954	An issue was found in Ion Reporter 5.10 with MyVariants database flagging. A variant in an analysis that should have been automatically flagged as an addition to a MyVariants database was neither recognized nor added. The issue was due to an unintended consequence of a performance improvement that sorts MyVariants during the flagging process of variants from new analyses. During the sort of the MyVariants in the MyVariants database, MyVariants with

Issue number	Description
	identical chromosome, reference alleles, observed alleles, but different genotypes, are not distinguished from each other, and one genotype is recognized and the other genotype is not. Ion Reporter ™ Software now includes genotype comparison as part of the MyVariants sort. This is fixed as part of Ion Reporter ™ Software 5.10.5.
IR-37417	A very rare edge case scenario was identified in Ion Reporter Software 5.10 which can cause incorrect flagging of a variant when synching an analysis to MyVariants, and incorrect placement of the variant in the MyVariants table. The issue only occurs if two sets of variants have the same locus, reference allele, observed allele and different Variant Type; then while syncing an analysis to MyVariants, the Variant Type comparison is not handled properly, and the variant and its analysis gets synced to the MyVariants database with a possibly incorrect MyVariants Flag shown in the Edit Variants screen of analyses results, but not the MyVariants screen. The required prerequisite for this issue to occur is: There are two different called variants, for example one REF and one SNV, with their locus, reference and observed allele being identical. The REF is a hotspot where the observed allele is the same for both the variants There is another variant whose locus is downstream in genomic coordinates from the affected variant and whose GT matches the affected variant. The result is that the SNV variant is wrongly displayed together in the same entry with the REF variant and the MyVariants flagging match in the Edit Variants screen of analyses results is made against that next variant downstream where the genotype matches. For the affected SNV the Classification attribute is not able to be successfully updated from the MyVariants screen and variant notes associated with the variant will not be displayed in the MyVariants screen. This issue does not impact any other aspects of the variant data in any analyses, and is fixed in Ion Reporter ™ Software.
IR-36888	In Ion Reporter ™ Software 5.10.2, the fix for issue IR-35997 inadvertently caused the values for SNVs and Indels in the "Mut Molecular Cov" column to show incorrectly. The values were incorrectly multiplied by 100 when viewed in the Variant Matrix section of the Analysis Visualization screen, in the 5.10.2 software. This has been corrected in Ion Reporter 5.10.3.
IR-35997	In Ion Reporter™ Software 5.10.0 and 5.10.1, in analyses that used the TagSeq and AmpliSeq HD workflows, the Analysis Visualization's 'Variant Matrix' tab showed an LOD value in the column "QC Test (LOD) %" that was not a percentage; the value shown was instead the calculated LOD value itself. This has been corrected in Ion Reporter 5.10.2. The "QC Test (LOD) %" value is now a percentage value. This value is displayed correctly in the "Detection Limit %" column of the Analysis Results' 'LOD' tab in Ion Reporter™ Software 5.10.0, 5.10.1, and 5.10.2.
IR-35630	An issue with CNV baseline creation for AmpliSeq panels and Whole Genome Low Pass (any non-VCIB) custom workflows was discovered in Ion Reporter ™ Software 5.10.0 and 5.10.1. The issue caused CNV baseline creation to possibly generate incorrect values in the output baseline, leading to incorrect CNV calls when the baseline is used in workflows. This issue has been fixed in Ion Reporter Software 5.10.2. Recommendations: We recommend that you recreate in the 5.10.2 and later software any custom non-VCIB CNV baselines that were created in 5.10.0 and 5.10.1 version software using the CNV baseline creation workflow. We also recommend that you do not launch two CNV baseline creation workflows concurrently which use the same set of input samples, until the first baseline creation workflow has finished.
IR-36125	An issue was found in Ion Reporter™ Software 5.10 that caused the SmallVariants.vcf and SmallVariants.filtered.vcf files to be missing from the downloaded results compressed directory, if analysis results were visualized in Ion Reporter Genomic Viewer (IRGV) before the directory of variants data was downloaded. In Ion Reporter 5.10.2 this has been corrected so

Issue number	Description
	that these files are always included in the appropriate downloaded results compressed directories.
IR-35995	In Ion Reporter ™ Software 5.6 a downloaded CSV file, of analysis results that used the AmpliSeq Immune Repertoire Plus - TCR beta chain - w1.0 - Single Sample workflow, included some clones that showed inconsistencies between the Total Counts and the sum of Plus and Minus counts. This issue was due to a bug in the reporting of the Plus and Minus counts; the Total Counts were correct. Typically only a small number of clones were affected. This is fixed in Ion Reporter ™ Software 5.10.
IR-34934	Metagenomics analysis results for Ion Reporter ™ Software organizations that used spaces in the organization name did not open successfully. This is fixed in Ion Reporter ™ Software 5.10.1.
IR-34935	Mosaic aneuploidy copy number data segments near expected normal ploidy values from analyses run in Ion Reporter ™ Software 5.10 may differ in their filtered-in and filtered-out segments from analysis results that were run with the same workflows in Ion Reporter ™ Software 5.4 and 5.6. This can occur with the use of the Aneuploidy Mosaicism filter chain, or any filter chain that contains the Expected Normal Ploidy Buffer (ENPB) filter. The issue occurs in Ion Reporter ™ Software 5.4 and 5.6 because the values stored and retrieved for filtering could be stored as a Java float value that is slightly above or slightly below the called value. This issue is corrected in Ion Reporter ™ Software 5.10.1. The exact values are stored in Ion Reporter ™ Software 5.10.1 and the filter chains that use the ENPB filter perform as expected.
IR-35185	When a parameters JSON file was imported into a workflow that had never been saved the software would go back to the Research Application step and the parameters would not be imported; default parameters would be instead present in the unsaved workflow. The suggested workaround was to save the workflow before the import. This is fixed in Ion Reporter ™ Software 5.10.1.
IR-31912	In Ion Reporter ™ Software 5.6, the date that is included in the footer of published final reports, audit reports, and Quality Control (QC) reports does not match the date that is listed in the reporter header as the "Report generated on" date. The issue also occurred in visualizations. This issue is fixed for all reports and visualizations in Ion Reporter ™ Software 5.10.
IR-33812	In IR5.6, for cfDNA Liquid Biopsy results, MAF (Mol Freq) in the visualization page was incorrectly displayed as 1 when the allele ratio was 1 (100%). The correct display is 100. This issue is fixed in Ion Reporter™ Software 5.10.
IR-34700	Ion Reporter ™ Software RNA Fusions and DNA and RNA Fusions workflows do not support input of Samples with multiple BAM files. To process such samples with the current version of the software, merge the reads from the multiple BAM files into a single BAM file, and then use this BAM file as input to get the Fusions results in the analysis.
IR-31190	Ion Reporter™ Software 5.4 and 5.6 cannot properly call variants on a sample that uses multiple Ion Reporter™ BAM files. This issue affects samples that are manually defined in Ion Reporter™ Software and include multiple BAM files. It also affects proton samples that are analyzed and uploaded to Ion Reporter™ Software, with Torrent Suite™ Software version 5.0 and earlier. This issue is fixed for DNA analyses in Ion Reporter ™ Software 5.10.
IR-34091	When you click a row in the Summary table in the Ion Reporter ™ Genomic Viewer (IRGV) Analysis Results screen to visualize a specific sample, the VCF for the clinvar track does not display in the Reference section. This is due to an issue with the loading of the genome data loads in the sample-specific IRGV Analysis Results screen. Workaround: Review the VCF track data from the IRGV tab in the IRGV Analysis Results screen.
IR-34638	A known bug that affected variant calling results caused Ion Reporter ™ Software 5.6 to fail to reproduce exactly the same VCF records for TagSeq workflows, although input parameters for

Issue number	Description
	the software and input data were identical. The issue occurred opportunistically and primarily affected the VCF fields RO, SRR and SRF. In most cases, the issue did not affect any other values of the VCF records, including the variant evaluation results. In rare cases, the issue caused different candidates to be generated and impacted allele grouping and evaluation. The issue is fixed in Ion Reporter ™ Software 5.10.
IR-34814	After applying a custom Table Preference, some data columns of Father and Mother information in the Analysis Results screen shows incorrect data (proband data is instead shown). The affected columns include: Father Genotype, Mother Genotype, Father Allele Coverage, Mother Allele Coverage, Father Coverage and Mother Coverage. When viewing the data using the default table columns (no custom Table Preferences selected) the issue does not occur. This issue is fixed in Ion Reporter™ Software 5.10.
IR-31663	For Tumor Mutation Load workflow analyses in 5.6, sample names must not contain space characters, even though the space character is allowed to create sample names for other types of analyses. Sample names with spaces for Tumor Mutation Load workflow analysis are now supported for the 5.10 version of Ion Reporter™ Software.
IR-31656	In Ion Reporter™ Software 5.6, variants flagged for the first time as Important or Ignore for a MyVariants database, do not cause older analyses, when opened, to get updated with the same variant getting added in those older analyses to the MyVariants database. Variants flagged in pre-5.6 analyses do cause the same variant to be automatically flagged in Ion Reporter™ Software 5.6 analyses when the version 5.6 analysis is opened, as expected.
IR-30941	In Ion Reporter™ Software 5.6, if you created a Table Preference while you viewed the analysis results that do not include fusions, and then applied that Table Preference while you viewed analysis results that do include fusions, the Genes column only reported the first gene that is mentioned as part of the fusion pair. This issue is fixed; the correct fusions gene and exon annotations will be shown in the Genes column in Ion Reporter ™ Software 5.10.
IR-30931	In Ion Reporter ™ Software 5.6, when two or more analyses which use the same input sample are launched concurrently, there is a possibility that the second and subsequent analyses will fail, because it has not found the sample still in use by the first analysis. Workaround: If you run multiple analyses that use the same sample, launch the analyses at least one minute or more apart from each other. This issue is fixed in the 5.10 software.
IR-30824	For analyses using samples with multiple BAM files, only the first BAM file was being loaded into IRGV for visualization. This issue is fixed in Ion Reporter™ Software 5.10
IR-30585	In the Ion Reporter ™ Software 5.6, IRGV Visualization tab, TagSeq Liquid Biopsy Assay CNV results are not displayed in the Whole Genome View or in the Proband Coverage Ratio (seg) track or in the Karyo view next to the chromosome ideograms as blue bars for GAIN and red bars for LOSS. This is due to differences in the analysis data outputs of the TagSeq Liquid Biopsy workflows. Workaround: CNVs can be confirmed by hovering the cursor over data tracks in the Selected Chromosome View and looking at data where Filter=Gain and SVTYPE=CNV, for example. This issue is fixed in Ion Reporter™ Software 5.10
IR-29734	After publishing a PDF report, changes are not allowed to the Classification column for variants in the Analysis Results. The dropdown lists for Classification should be disabled. However, in Ion Reporter™ Software 5.6 they are not disabled. Therefore, when users try to change the Classification of a variant in an analysis with a report that has been published, an error occurs. This issue is fixed in Ion Reporter ™ Software 5.10.
IR-28787	In the 5.6 version of Ion Reporter ™ Software, when you created or edited an Aneuploidy NoGender workflow, and set Display sex chromosomes parameter "Plot Y chromosome for Female or Unknown Gender" to 1/True, the sex chromosome tile data will be shown and the software may show the X and Y data as a gain (blue bar). This gain information on the sex

Issue number	Description
	chromosomes under these workflow settings should be ignored, or evaluated carefully. This issue has been fixed in Ion Reporter ™ Software 5.10.
IR-30601	In Ion Reporter™ Software 5.6, after you sort the Genes column the Analysis Results screen, the number of variants increases for Ion AmpliSeq™Exome paired sample workflow analysis.

Allele-specific (Proper) view of variants: When you set workflow parameters, you can select variants per position, Classic, or variants per allele, Proper. The default variant output in Ion Reporter™ Software is a Classic view (locus-centric), with each line of the VCF file corresponding to one line of Ion Reporter™ Software variant output. In Classic view, there can be multiple alternate alleles for a given locus. Ion Reporter™ Software also offers a Proper view output feature, which is "allele-centric" with each allele displayed as a single line of record in the output (Per-allele view). The VCF file that is generated by Classic view is called "Classic VCF". The VCF file that is generated by the Per allele view is called "proper VCF". The FDP (Flow Evaluator read depth at the locus) and DP (Total read depth at the locus) are subfields inside the INFO field of the VCF file. Within each classic VCF line, FDP and DP are based on the TOTAL SUM of ALL the FAO (Flow Evaluator Alternate allele observations) and AO (Alternate allele observations) fields, which are based on the following formulas:

"FDP=SUM(FAO)+FRO or DP=SUM(AO)+RO"

Multiple alleles from a single classic VCF are spread between multiple proper VCF lines. Each of these split lines contains the same FDP/DP values but different FAO/AO values, yet with the same VCFPOS value which can be traced back to the same classic VCF line. As a result, someone will need to collect all the FAO/AO values from multiple lines of proper VCF with the same VCFPOS to in order to apply to the same formulas.

Note: In Ion Reporter™ Software 5.6, proper view (proper VCF) should be considered a beta feature. After you sort the Genes column the Analysis Results screen, the number of variants increases for Ion AmpliSeq™Exome paired sample workflow analysis. In Ion Reporter™ Software 5.10, Proper view has been renamed to Allele View and Classic View has been renamed to Locus view. |

Known issues and limitations in Ion Reporter™ Software 5.10

Issue number	Description
IR-37640	Variability Correction Information Baseline (VCIB) CNV baseline has a known issue in Ion Reporter ™ Software 5.10. The issue affects panels that include genes on Chromosome X. For genes on Chromosome X only, samples marked as "male" have Copy Number values equal to half of the value that they should be if the baseline is "female" (the default). However, if the sample is marked as "unknown" or "female", the issue will not be triggered, but the GAIN calls for samples previously marked "male" but now marked "female" or "unknown" are not consistent between Ion Reporter ™ Software 5.10 and earlier releases. The reason: "gain-threshold-xy" is ignored in samples marked as "unknown" or "female" and "gain-threshold" is used instead for genes in Chromosome X. There is no good workaround to restore exactly the same behavior that was available in Ion Reporter ™ Software 5.6 and earlier.
IR-37643	An issue was found in Ion Reporter ™ Software 5.10 that causes filter chains to not function correctly in the case of multi-allelic variants. If a variant is heterozygous with non-reference alleles in its genotype, or a variant has multiple alleles in its genotype or an annotation source database has multiple alleles at the same locus, the filtering is performed on only one allele. This allele may not be the most relevant allele to the variant call, and therefore cause variants to be filtered in or out incorrectly. For example, if a dbSNP Minor Allele Frequency (MAF) filter of $0.0 < MAF < 0.01$ is applied to a variant which has a called allele with MAF=0.141 but dbSNP contains another allele with MAF=0.001 at the same locus, then the filter may use the MAF=0.001 value rather than MAF=0.141 to incorrectly filter out the variant.
IR-36948	LOD reporting for Tag Seq and AmpliSeq HD assays is improved in Ion Reporter ™ Software 5.10. 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 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 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 tvc 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

Issue number	Description
	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 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 customer scripts that depend on this column.
IR-34815	Results shown in the Variant Matrix tab may not be visible in the Analysis Results table when the Variant Matrix Summary filter chain is used for the same analysis. This discrepancy is due to a difference in the rules that causes multi-allele variants that are present in the Variant Matrix tab to be filtered out by the Variant Matrix Summary filter chain when not all alleles pass the filter criteria used by the filter chain.
IR-35192	The Snapshot button in the Krona view of 16S Metagenomics results does not work in some Web browser versions. This is a known issue with Krona: https://github.com/marbl/Krona/issues/83. Workarounds: Take a screen capture of the Krona diagram image and save it. Alternatively, use an earlier version of browsers to export the SVG snapshot images, such as Firefox 58.0.1., available here: https://ftp.mozilla.org/pub/firefox/releases/58.0.1/.
IR-34778	The accuracy of fusion assay annotation is improved in Ion Reporter ™ Software 5.10, and includes a modification of fusion reference files in AmpliSeq Lung Fusion workflows. Details: A number of fusion annotation discrepancies were identified in the AmpliSeq Colon Lung v2 with RNA Lung Fusion single sample workflow and AmpliSeq RNA Lung Fusion single sample workflows. New Ion Reporter ™ Software 5.10 versions of these Lung Fusion workflows containing the changes listed below can be identified as they have "w1.1" in their name. Summary of changes: In particular, the fusion assay labeled EML4-ALK.E13A20.AB462411 was found to be inconsistent with the genbank sequence AB462411, but is more consistent with the breakpoint reported in the literature for COSMIC fusion ID COSF408, so this has been relabeled EML4-ALK.E13A20.COSF408.1. Fusion target sequences for EML4-ALK.E13A20.COSF1062.1, EML4-ALK.E14A20.COSF1064, EML4-ALK.E17A20.COSF1366.1, and EML4-ALK.E17A20.COSF1367.1 have been slightly modified to more accurately reflect the breakpoints reported in the literature citations associated with their COSMIC fusion IDs. These updated sequences have been labeled EML4-ALK.E13A20.COSF1062.2, EML4-ALK.E14A20.COSF1064.1, EML4-ALK.E17A20.COSF1366.2, and EML4-ALK.E17A20.COSF1367.2, respectively. The following assays have been removed: (EML4-ALK.E20A20.COSF409, EML4-ALK.E6aA20.COSF411, EML4-ALK.E6bA20.COSF412, EML4-ALK.E6bA20.COSF412.1, EML4-ALK.E15A20.COSF413, EML4-ALK.E14A20.COSF477, EML4-ALK.E2A20.COSF478, EML4-ALK.E2A20.COSF479, EML4-ALK.E18A20.COSF487, EML4-ALK.E20A20.COSF730, KIF5B-RET.K15R11.COSF1255, EML4-ALK.E6A19.COSF1296, EML4-ALK.E17A20.COSF1366, EML4-ALK.E17A20.COSF1367). For the majority of these assays, a suffixed fusion assay on the panel (for example, ALK.E2A20.COSF478.1 in place of ALK.E2A20.COSF478) more closely matches the breakpoint cited in the literature associated with the COSMIC fusion identifier. The assays EML4-ALK.E6aA20.AB374361 and EML4-ALK.E6bA20.AB374362 match the COSF411 and COSF412 literature breakpoints.
IR-33667	By default, columns that contain large amounts of information are truncated in the Analysis Results screen to save visual space. There is an issue that when one of these columns is moved to the very last column location in the table, the full data is shown. The recommended workaround is to move the column to any other location that is not the last column in the table.
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.

Issue number	Description
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 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 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 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-34604	There is an issue with sample information displayed in the Summary table when you select multiple analyses that use different Research Application types, if you select DNA, then select a Fusions Only analysis, and another DNA analysis, and Visualize the results. The sample information is displayed correctly when you visualize the results in the Ion Reporter™ Genomic Viewer (IRGV) for an analysis. However, if you open the results of an individual analysis by clicking on a row in the Summary table, the resulting Summary table of the individual analysis can show incorrect information on the right, compared to the graphics shown on the left. If you select the fusion analysis last, the visual display is correct.
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 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-31043	Custom CNV baseline creation is not supported for TagSeq-based Liquid Biopsy workflows in Ion Reporter™ Software.
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	The Details section for the Immune Repertoire workflow contains some workflow components that are not applicable to the workflow and resulting analyses: Annotation set, report template, parameters.
IR-31031	Firefox browser version 4.7 and later is required for visualization support in Ion Reporter™ Software 5.6 and Ion Reporter™ Software 5.10.
IR-31022	When visualizing analyses and exporting as SVG, some browsers such as Chrome and Safari may not successfully download the requested file. Workaround: Firefox browser may be used to download CNV Heatmap SVG files successfully.

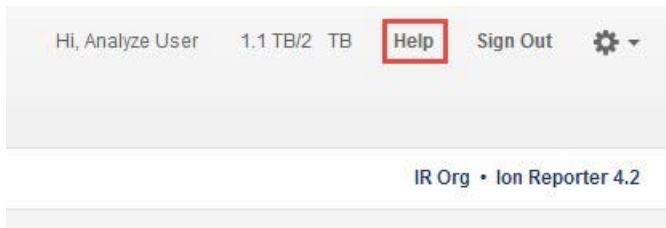| Issue number	Description
IR-30985	TagSeq Liquid Biopsy workflows, which detect CNVs, give a p-value but not a "Confidence Score" or "Confidence Interval" for each called CNV. In the Ion Reporter™ Software 5.6 IRGV, the Confidence filter setting (for example, Confidence=10.0) is displayed in the Whole Genome View, but this information not relevant to the data from these analyses using TagSeq Liquid Biopsy CNV-detecting 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-30616	If a hotspot allele X is haplotyped with another allele Y, the variantCaller plugin may call the long haplotyped allele Z that consists of X and Y. As a result, Ion Reporter™ Software will report and annotate the hotspot allele X as negative, although allele X is present as part of the allele Z. For example, if X is an SNP that is haplotyped with another SNP Y, the MNP (Z) that consists of the two SNPs might be called. If you believe this has occurred, check the SUBSET file in the VCF record to determine whether an allele is a subset of a called allele. When this occurs, X will be found as a SUBSET entry in the FORMAT field in the VCF record that called Z.
IR-30650	CNV Baseline Creation for TagSeq workflows is not possible if you use the existing target regions BED file in Ion Reporter™ Software 5.6 or 5.10. The BED files for TagSeq workflows in the software do not contain CNV amplicons, and therefore should not be used to create a new CNV baseline.
IR-30937	The Liquid Biopsy analysis Results data columns Mol Depth, Mol Counts, Mol Freq and Detection Limit are not populated in the Liquid Biopsy tab of the Analysis Results for CNV variant rows.
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-27786	HP-DEL is classified incorrectly by TVC evaluator: The indel_as_hpindel parameter controls whether SNP filtering parameters should be applied to non-homopolymer (HP) indels (when disabled, or set to 0) rather than indel filtering parameters. In prior releases to Torrent Suite™ Software 5.4 indel classification as HP-indel, or non-HP indel, had a bug where some HP-indel deletions were incorrectly characterized as non-HP indels. This bug is fixed in Torrent Suite™ Software 5.4 but it affects filtering of affected indels when indel_as_hpindel is disabled. The parameter indel_as_hpindel is enabled by default in Ion 540™/Ion Proton™ germline parameter files and indel filtering is applied to all indels, so this fix will not affect the generic version of this panel. It will also not affect any other panel where this parameter is enabled (for example, AmpliseqExome). In all other generic panels, indel_as_hpindel is disabled by default, as indel filtering is more stringent than SNP filtering, and we expect a possible improvement in sensitivity with a possible increase in false positives. However, in testing somatic panels toggling indel_as_hpindel has no effect on indel calling. A change is seen in Ion 520™/Ion 530™ or Ion 318™ chips that have indel_as_hpindel disabled by default with germline calling. The indel False Positive rate increases and is offset by an increase in sensitivity. Panels that use this parameter in indel germline calling may be affected. A full return to the prior behavior of Torrent Suite™ Software 5.4 is not possible without

Issue number	Description
	adjusting indel-filtering parameters. Guidance would be to adjust parameters for indel calling to be more stringent.
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 workflows. As a result of these differences, variants called in the Torrent Suite™ Software variantCaller plugin and variants called in Ion Reporter™ Software may 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 workflow, Oncomine™ customers with 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 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 may 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-23464	Searching by Gene name in IRGV shows only the first amplicon targeted to the requested Gene though other amplicons may be present for that gene. The workaround is to adjust the zoom settings to view the entire Gene region to examine all corresponding amplicons.
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-24539	When you refresh an Ion Reporter™ Genomic Viewer window, a blank page appears.
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-23854	A male or female gender must be specified for each sample in a trio analysis in Torrent Suite™ Software. Validation is not performed on sample genders when the trio workflow is automatically launched in Ion Reporter™ Software after it is transferred from Torrent Suite™ Software.
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.
IR-23379	In DNA and Fusions 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-25095	Due to a design change to improve MyVariants filtering in Ion Reporter™ Software 5.2, for Ion Reporter™ Software 4.0-run analyses (only), All flagged MyVariants in Ion Reporter™ Software 4.0 analyses will appear in Ion Reporter™ Software 5.2 when filtering for either IMPORTANT or IGNORE. MyVariants filtering works correctly for analyses that are run with workflows from Ion Reporter™ Software 4.2 to Ion Reporter™ Software 5.2.

Issue number	Description
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 workflows in Ion Reporter™ Software 5.6 results in the presence of more variants than when the 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 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

The Ion Reporter™ Uploader (IRU) 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
IRU plugin 5.10.0.32	Torrent Suite™ Software 5.10 and earlier	Ion Reporter™ Software 5.10 and earlier (including Ion Reporter™ Software 5.0 – China, Ion Reporter™ Software 5.2 – China in the future)
IRU plugin 5.6.0.41	Torrent Suite™ Software 5.6 and earlier	Ion Reporter™ Software 5.6 and earlier (including Ion Reporter™ Software 5.0 – China, Ion Reporter™ Software 5.2 – China in the future)
IRU plugin 5.4.0.44	Torrent Suite™ Software 5.4 and earlier	Ion Reporter™ Software 5.4 and earlier (including Ion Reporter™ Software 5.0 – China, Ion Reporter™ Software 5.2 – China in the future)
IRU plugin 5.2.1.2	Torrent Suite™ Software 5.2 and earlier	Ion Reporter™ Software 5.2 and earlier (including Ion Reporter™ Software 5.0 – China, Ion Reporter™ Software 5.2 – China in the future)
IRU plugin 5.0.4.36	Torrent Suite™ Software 5.0 and earlier	Ion Reporter™ Software 5.0 and earlier, Ion Reporter™ Software 5.0 – China
IRU plugin 4.6.x.y	Torrent Suite™ Software 4.4.3.x and earlier	Ion Reporter™ Software 4.6 and earlier (no Ion Reporter™ Software – China)

IonReporterUploader (IRU) plugin

A new version of the IonReporterUploader (IRU) plugin is available: Ion Reporter™ Uploader 5.10.0.32 or later. This version of the IRU plugin is already installed when Torrent Suite™ Software 5.10 is installed or upgraded.

New IRU plugin versions may become available between released of Torrent Suite™ Software or Ion Reporter™ Software. If you need to upgrade the IRU plugin on a Torrent Server of version 5.2 or higher that is connected to the Internet, you can use the off-cycle upgrades 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 IRU 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 IRU plugin for customers who want to continue using Torrent Suite™ Software 5.0 and earlier but want to upgrade IRU.

In addition, there is a ZIP file of the IRU plugin command line version (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 under the Settings > Ion Reporter Uploader in the Ion Reporter™ Software.

The most current IRU plugin is 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.

Note that IRUCLI 5.2 and above 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.

If you have Torrent Suite™ Software 4.6 or lower running on Ubuntu™ 10.04 operating system and want to use IRUCLI on this machine, you need to update your IRU plugin first, and then execute your irucli.sh with this special command:

$ export PATH=/results/plugins/IonReporterUploader/java/_jre_location_/bin:$PATH

and then enter the usual irucli.sh command:

$ ./irucli.sh -c myconnectionfile.txt -s a.csv

You are only required to do this path-setting step once per UNIX terminal session.

Note: The _jre_location_ in the above path may slightly change depending on which version of java was embedded in the IRU plugin that was installed, which in turn depends on the version of the IRU plugin. A typical Path for jre on a Torrent Server installed with IRU 5.10.0.32 might be:

/results/plugins/IonReporterUploader/java/jre/openjdk-7-jre-headless/usr/lib/jvm/java-7-openjdkamd64/jre/bin/

Alternatively, on Torrent Suite™ Software that is installed with IRU 5.10.0.32, the path could be:

/results/plugins/IonReporterUploader/java/jre/jre1.8.0_45/bin/

This issue does not affect newer Torrent Suite™ Servers that run the Ubuntu™ 14.04 operating system.

Ion Reporter™ Uploader plugin configuration

Use the following Ion Reporter™ Uploader configuration setting to transfer to Ion Reporter™ Cloud:

Server: 40.dataloader.ionreporter.thermofisher.com

This is the default shown when configuring an Ion Reporter™ Cloud 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 12.04 to 14.04 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 5.6 and Ion Reporter™ Software 5.10 are designed to work with the Ubuntu™ operating system version 14.04, and is not compatible with version 12.04. Messages may 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 your Ion Reporter™ Local Server, contact your local FBS.

Update Ion Reporter™ Server Software to 5.10

To upgrade Ion Reporter™ Software to 5.10, you must have an up-to-date software license.

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.