

Ion Reporter™ Software 5.2.1 Release Notes

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New in 5.2.1

The Ion Reporter™ Software 5.2.1 release includes all the features of Ion Reporter™ Software 5.2 and the following bug fixes and improvements.

Intermediate Filter Chain results (IR-26067)

In Ion Reporter™ Software 5.2, intermediate values for filtered variants in a Filter Chain were erroneously identical to the final results of the entire Filter Chain. This is corrected in Ion Reporter™ Software 5.2.1; the number of variants and the number of genes are now correct at each step in the Filter Chain.

TVC duplicate hotspot alleles (TS-13996)

In the Torrent Variant Caller (TVC) in Ion Reporter™ Software 5.2, Hotspot files with duplicate alleles were not being consolidated into a single entry, causing multiple issues downstream. This is corrected in Ion Reporter™ Software 5.2.1.

Unique entries in variants database (IR-27446/FST-8451)

In Ion Reporter™ Software 5.2 during import of VCF sample files, an additional field was used to add granularity to add records to the mongoDB database. Due to the way variant ids are compared when a VCF file is loaded into the Ion Reporter™ software database, some entries of the VCF file were not loaded into mongoDB. This occurred only in version 5.2 when the VCF file contained multiple variants with an identical locus and different genotypes. As a result, fewer variants were imported from the VCF file in Ion Reporter™ Software 5.2 than in Ion Reporter™ Software 5.0. This is corrected in Ion Reporter™ Software 5.2.1.

Final PDF report generation (IR-26889)

In Ion Reporter™ Software 5.2 the generation of multiple PDF reports occasionally caused the software to stop working and give an error. The issue was found and corrected in Ion Reporter™ Software 5.2.1.

Fusion algorithm intermediate files (IR-27841)

In Ion Reporter™ Software 5.2, intermediate temporary files were deleted and were not part of the analysis results. By request from customers, these files are now retained in Ion Reporter™ Software 5.2.1.

Allele view showing multiple COSMIC IDs (IR-25826/FST-8221)

In Ion Reporter™ Software 5.2 the ID field in the variant review table contains all of the IDs for all of the alternate alleles for the same position in the per allele (Proper) view, rather than breaking out the particular ID corresponding only to the corresponding individual alternate allele. This issue is now corrected in Ion Reporter™ Software 5.2.1. Typically, these IDs correspond to COSMIC IDs provided by variant caller VCF file output in the third column of the VCF file. (For a small portion of the variants in the VCF file, the number of COSMIC IDs may differ from the number of alternate alleles. For such variants, all of the COSMIC IDs will be listed in per allele view).

New Features in 5.2

The Ion Reporter™ Software 5.2 release includes many new features and improvements. All of these features are also supported in Ion Reporter™ Software 5.2.1.

Adjustment of hit level allowed for each VariantDB independently

In Ion Reporter™ Software, you can create custom annotation sources for each VariantDB with a different "VariantDB Hit Level". You can add these custom VariantDBs to an annotation set, each controlled by its own "VariantDB Hit Level" independently.

To enable the VariantDB Hit Level, add one of the following lines to your VCF file header from which the VariantDB custom annotation sources are created:

- ##HITLEVEL=locus
- ##HITLEVEL=allele
- ##HITLEVEL=genotype
- ##HITLEVEL=overlap
- ##HITLEVEL=auto

GRCh38 Human Reference support

The new GRCh38 Reference Genome in Ion Reporter™ Software is based on the latest GRC human reference assembly and is the first major update since 2009. Highlights include:

- Changes to chromosome coordinates
- Fixed errors in the former sequence
- Multiple loci for some highly variable genes
- Creation of custom workflows in Ion Reporter™ Software using this reference genome to support custom panel and future Ion catalog and community panel analyses.

All annotation sources are now available as updated GRCh38-based sources, including:

DB table name	Description
GRCh38_clinvar_20160203	GRCh38 CLINVAR version 20160203
GRCh38_cosmic_75	GRCh38 COSMIC version 75
GRCh38_dbsnp_146	GRCh38 DBSNP version 146
GRCh38_dgv_20150723	GRCh38 DGV version 20150723
GRCh38_ensgeneScores_5	GRCh38 Ensembl Gene Functional canonical transcripts scores version 5
GRCh38_ensgene_79	GRCh38 ENSEMBL version 79 gene model
GRCh38_esp6500_20151203	GRCh38 5000 EXOMES version 20151203
GRCh38_namedVariants_20151113	GRCh38 Named Variants version 20151113
GRCh38_pfam_29	GRCh38 PFAM version 29
GRCh38_phylop_20151118	GRCh38 PHYLOP version 20151118
GRCh38_refgeneScores_5	GRCh38 Refgene Functional canonical transcripts scores version 5
GRCh38_refgene_72	GRCh38 REFSEQ version 72 gene model
drugbank_20150107	DrugBank version 20150107
go_20151216	GENE ONTOLOGY version 20151216
omim_20160128	OMIM version 20160128

You can create GRCh38 custom panels and analyses at AmpliSeq.com or through the assistance of the Ion Torrent™ White Glove program. Workflows and Filter Chains for GRC38 reference genome are supported in Ion Reporter™ Software 5.2.

If you use the automatic variant search between Ion Reporter™ Software and the CE Primer design or qPCR Assay design web tools, differences in GRCh38 support timelines can have the following impact:

Before August 26:

- If you submit Hg19 coordinates from IR to CE/qPCR, there are no errors.
- If you submit GRCh38 coordinates from IR to CE/qPCR, there can be errors. Even if the web software does not show errors, incorrect CE/qPCR primer results can occur if incorrect coordinates are transferred from the Ion Reporter™ Software to CE/qPCR tool.

After August 26, but before October 21:

- If you submit Hg19 coordinates from IR to CE/qPCR, there are no errors.
- If you submit GRCh38 coordinates from IR to CE/qPCR, a message describing incapability appears.

After October 21:

- If you submit Hg19 coordinates from IR to CE/qPCR, a message describing incapability appears.
- If you submit GRCh38 coordinates from IR to CE/qPCR, from IR to CE/qPCR tool, there are no errors.

New Amplicon Coverage Report Available

You can now generate a per-amplicon coverage report in Ion Reporter™ Software 5.2. You can see a panel of the amplicons that fall below a certain level of read coverage, for which you set a threshold. Metrics for total % amplicons and % BED regions covered are given and can be added to the QC report.

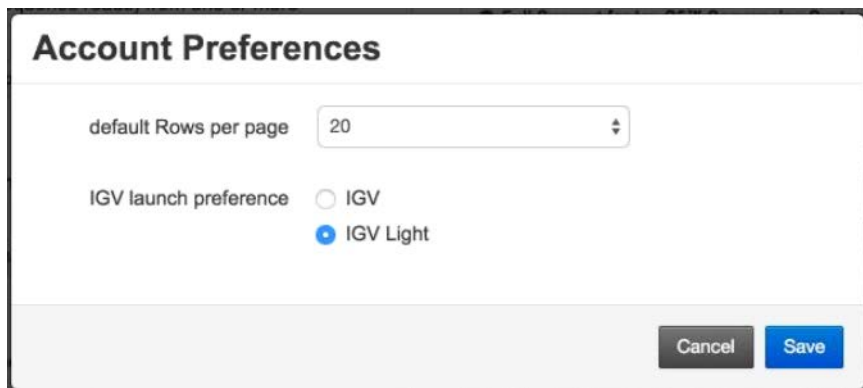
IGV Light viewer displays multiple types of analyses

New in Ion Reporter™ Software 5.2, you can visualize any human DNA or RNA analysis type with IGV Light viewer. Highlights include:

- The Chromosome bar shows the variant location on the chromosome.
- DNA and RNA coverage bars show coverage for the region.
- Annotations show annotation source results.
- Chart view allows you to toggle between DNA and RNA view.
- Sample/Analysis summary allows you to sort by analysis number.
- Search allows you to enter a chromosome range in which to search for variants.
- Confidence filter allows you to filter for CNV calls; MAPD filter allows identifying samples that may have too much noise to provide robust CNV detection.

User Account Preferences for table grid and IGV viewer

You can select the number of rows displayed in tables and whether to open either IGV Light or the full IGV Viewer by selecting a variant's Locus, from Account Preferences. Twenty rows per table and IGV Light are the default settings.

The image shows a dialog box titled "Account Preferences". It contains two settings: "default Rows per page" with a dropdown menu set to "20", and "IGV launch preference" with two radio buttons: "IGV" (unselected) and "IGV Light" (selected). At the bottom right, there are "Cancel" and "Save" buttons.

Multiple databases

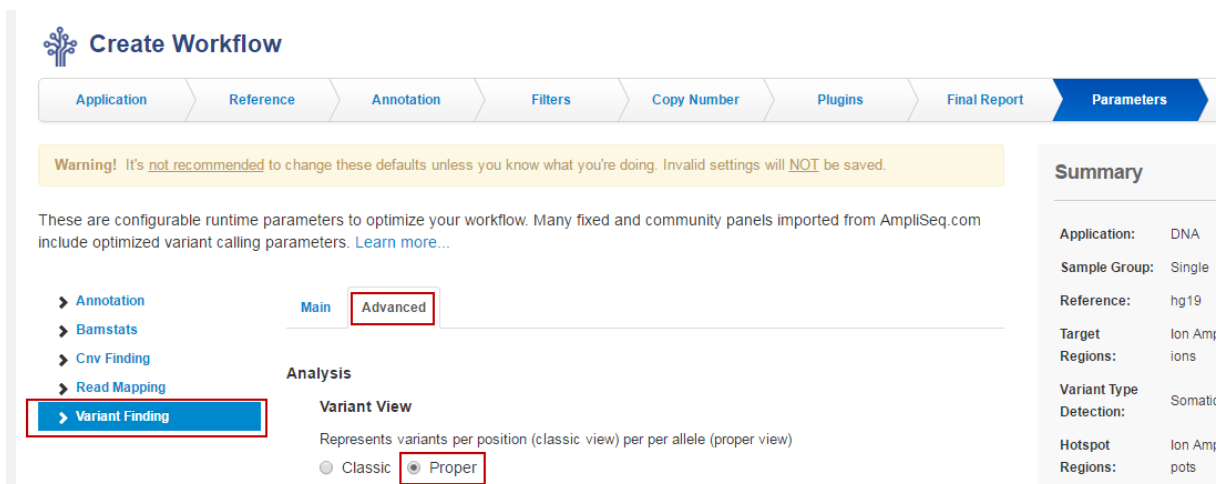
You can now track different sets of favored variants and store these sets in different MyVariants databases that you can create. You can do this by assigning any custom MyVariants database to a specific workflow. You can now also import Variant DBs into MyVariants.

Custom TVC parameters enabled

If you ran the Torrent Variant Caller plugin in Torrent Suite™ Software, you can now upload the TVC parameters JSON file into Ion Reporter™ Software 5.2 and use your custom settings. When building your custom workflow in Ion Reporter™ Software, upload your JSON file on the Parameters screen. The values uploaded replace the default values in Ion Reporter™ Software.

Allele-specific (Proper) view of variants

When setting workflow parameters, you can now choose between Classic (variants per position), and Proper (variants per allele); these choices are similar to those available in Torrent Suite™ Software. When creating or modifying a workflow, on the Parameters screen, select Variant Finding, Advanced, and under Variant View, select Proper.



Create Workflow

Application Reference Annotation Filters Copy Number Plugins Final Report **Parameters**

Warning! It's not recommended to change these defaults unless you know what you're doing. Invalid settings will NOT be saved.

These are configurable runtime parameters to optimize your workflow. Many fixed and community panels imported from AmpliSeq.com include optimized variant calling parameters. [Learn more...](#)

> Annotation
 > Bamstats
 > Cnv Finding
 > Read Mapping
 > **Variant Finding**

Main **Advanced**

Analysis

Variant View

Represents variants per position (classic view) per per allele (proper view)

☐ Classic
 ☒ **Proper**

Summary

Application: DNA
 Sample Group: Single
 Reference: hg19
 Target Regions: Ion Amp
 Variant Type Detection: Somatic
 Hotspot Regions: Ion Amp
 pots

Ubuntu™ 14.04 operating system compatibility

Ion Reporter™ Software 5.2 in the USA Cloud is now running on Ubuntu 14.04 operating system. Ion Reporter™ Software 5.2 runs on an Ion Reporter™ Server that uses Ubuntu™ 14.04 and is backward compatible with Ubuntu™ 12.04, the version that is currently installed.

You can choose to update your Ubuntu operating system now, before you upgrade to Ion Reporter™ Software 5.2, or, you can wait until the next release of Ion Reporter™ Software (version 5.4). The Ubuntu™ 14.04 operating system will be required for Ion Reporter™ Software 5.4. Please contact your local bioinformatics support representative for help with the Ubuntu 12.04 to 14.04 upgrade processes for Ion Reporter™ Software 5.2 Local Server.

End of life for Ion Reporter™ Software 4.0 workflows on the Thermo Fisher Cloud and Server in 5.2.

Ion Reporter™ Software 4.0 workflows are now retired from the Thermo Fisher Cloud version 5.2 of the software. If your work requires you to use the older workflows, contact sales about the purchase of an Ion Reporter™ Server. Owning a server allows you to continue work on the older workflows if you decide not to upgrade to 5.2 or any future versions. In the future, each new version of Ion Reporter™ Software will retire at least one oldest version of Ion Reporter™ Software analysis workflows.

Run results review before auto upload to Ion Reporter™ Software

New in Torrent Suite™ Software 5.2, you can review run results and decide whether to upload them to Ion Reporter™ Software for further analysis. You can set this quality check pause when setting up your run plan template or when editing a planned run.

Sample transfer between accounts in different Organizations

You can now transfer samples to another user in a different Organization. You can delete the data once the recipient(s) accept the file. This feature can be helpful to Core labs when they complete sequencing and analysis work for clients and want to transfer the sample and then delete the data from their Ion Reporter™ Software account in the cloud or on local servers.

Asynchronous Download enabled

Asynchronous downloading is now available. You can start a download and resume work in other areas of the application, instead of waiting for download to complete. Go to the new “Notifications” sub tab of the Home tab to find downloads.

Archival location specified

If you are a new Ion Reporter™ Server customer and select samples or analyses to archive, Ion Reporter™ Software 5.2 prompts you to specify a storage location. If you are an existing customer upgrading to Ion Reporter™ Software 5.2 and you specified your archive storage location in Reporter™ Software 5.0 you do not need to re-enter the storage location. If you are an existing 5.0 customer upgrading to version 5.2 and you have not specified your archive storage location in 5.0, specify the storage location by changing archivalMountPath=/tmp/ to archivalMountPath=/storage IP address/ in ionreportermanager/server/server.properties file and restart the Tomcat server.

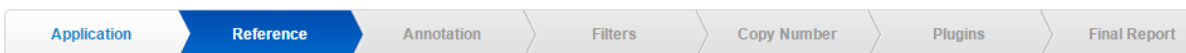
Report Logo file Remove button

If you uploaded an organization logo to your report template, you can now remove that logo by pressing the Remove button. You can then upload the new logo.

Factory workflows and files flagged with Ion Torrent icon

An Ion Torrent™ symbol is visible for factory workflows, MyVariants databases, filter chains, and target, hotspot and fusions files so that you can differentiate factory versus custom entities. In exported files, a string is appended to the entity name.

Create Workflow



Select a reference, region file and optionally a hotspot file you wish to use in this analysis. Select whether you wish to detect somatic (low frequency) or germline mutations. [Learn more...](#)

Reference

- ☐ GRCh38
- ☒ hg19

Focus Analysis

Target Regions:

- ☒ Ion AmpliSeq AML Regions
- ☒ Ion AmpliSeq BRCA Regions
- ☒ Ion AmpliSeq CCP Regions
- ☒ Ion AmpliSeq CFTR Regions
- ☒ Ion AmpliSeq CHPv1 Regions
- ☒ Ion AmpliSeq CHPv2 Regions

Variant Type Detection:

Hotspot Regions:

[← Previous](#) [Cancel](#)

[Next →](#)

UTF8 characters enabled in Organization names

You can now use UTF8 characters (including Chinese and Japanese characters) in user first and last names and in organization names.

Date Range search added to My Variants page

You can now search by date range on the My Variants overview page. Enter earliest and latest possible dates and click **Search**. The utility will display analyses that occurred during this date range.

Ion Reporter

Hi, Ion User 227.9 GB/20 TB Help Sign Out ⚙

[Home](#) [Samples](#) [Analyses](#) [Workflows](#) [Admin](#)

Overview Launch **My Variants** IR Org • Ion Reporter 5.2

My Variants

My Variants hg19 MyVariantDefaultDb_hg19

3/10/2016 3/16/2016 Search

		Locus	Classification	Gene(s)	GenoType	Ref	Type	Analysis Name	Sample Name
▶	📄	chr1:874820	BENIGN	SAMD11	C/T	C	SNV	Demo AmpliSeq Exome VCF_c313_2016-03-14-11-00-710	Demo AmpliSeq Exome VCF
▶	📄	chr1:874821	SUSPECTED_BENIGN	SAMD11	T/C	T	SNV	Demo AmpliSeq Exome VCF_c343_2016-03-12-17-21-416...(2)	Demo AmpliSeq Exome VCF
▶	📄	chr1:876499	DELETERIOUS_UNCLASSIFIED	SAMD11	G/G	A	SNV	Demo AmpliSeq Exome VCF_c343_2016-03-12-17-21-416...(2)	Demo AmpliSeq Exome VCF

Duplicate analysis name changes during CSV upload

If you are uploading multiple analyses by CSV upload and you have duplicate analysis names, the software stacks the duplicate analyses at the top of the table and highlights the duplicate in red text. You can now edit the red text to make the names unique, click Enter, and proceed with your CSV upload.

Web Services API

The Web Services API has expanded functionality. You can now:

- upload a sample (BAM or VCF)
- launch a workflow

See the Web services API chapter of Ion Reporter™ Software Help.

Saved Search and Filter Results of Samples, Workflows, and Analyses pages

Results of searches and filtering on Samples, Analyses, and Workflows pages are now saved as cookies. As a result, when you navigate away from and back to those pages, you will see the searched-for and/or filtered results if you return to the page during the same browser session while within the same browser window.

Improvements in Aneuploidy analysis workflow algorithm

In Ion Reporter™ Software 5.2, a “Remove Duplicates” parameter was added in Parameters>>CNV finding>>Advanced for the Aneuploidy workflows to allow removal of duplicate reads which can occur during the template creation. In the “ReproSeq Low-pass whole-genome aneuploidy” workflow in version 5.2 of Ion Reporter™ Software, this parameter is enabled by default. Removing these duplicates has been shown to improve (lower) MAPD values and can remove some calls which have a strong likelihood of having been false positives when called in the 5.0 version of the ReproSeq analysis pipeline.

Other Algorithmic improvements

Aneuploidy algorithms include updates that account for the probability of a sample being called as a male or female, or calling the sample gender unknown, when the number of total reads is low and the number of reads from the Y chromosome is 0.

In the new "Metagenomics 16S w1.1" workflow, the "Slash ID Reporting range" default value is changed from 0.8 to 0.2. In addition, the "Primer(s) Detected" default value is changed to "Both Ends". These new values of "Both Ends" and "0.2", together, gives more accurate species diversity with minimal number of slash calls to get to genus and species level.

The previous defaults of "Single End" and "0.8" can give better Family level calls.

Bug fix correction of amino acid reporting error

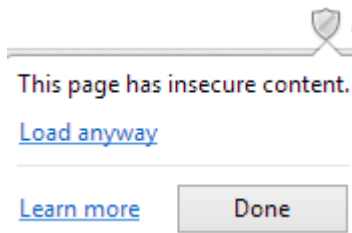
A bug fix corrected amino acid change positions that were previously incorrectly reported.

On the forward strand, amino acid change positions were previously reported incorrectly if the anchor base of a deletion is the last base of the previous codon. An example of this is the following:

A bug in Ion Reporter™ Software 5.0 that caused an incorrect amino acid change to be reported for a single base T deletion at chr11:108117732 is fixed in 5.2. For cDNA, TTATAT was reported with the first or second T deleted depending on left or right alignment. TTA codon is Leu and TAT codon is Tyr. Amino acid positions are Leu-315 and Tyr-316. Ion Reporter™ Software 5.0 was annotating the amino acid change as p.Tyr316sf instead of p.L315fs. This is corrected Ion Reporter™ Software 5.2.

Known issues and limitations in Ion Reporter™ Software 5.2 and 5.2.1

Issue number	Description
Gene fusions	
IR-16258	Due to changes in the Ion Reporter™ Uploader (IRU) to normalize outcomes of fusion-detecting workflows, the results may be slightly different from Ion Reporter™ Software 4.4 workflows run in the Ion Reporter™ Software versions 4.4 and 4.6. This is because in the Ion Reporter™ Software 4.4, either mapped or unmapped BAM files for Fusions could have been uploaded. Only where mapped and unmapped results are compared for the exact same workflow would any change in results be expected. The Ion Reporter™ Software 4.4 Fusion workflow used in the 4.4 and 4.6 software versions should still give the same results if unmapped BAMs were used in both software versions for those 4.4 workflows.
Workflow creation	
IR-18951	To create an Ion Reporter™ Software workflow for the Cloud from the Plan template page in Torrent Suite™ Software (using Create New Workflow), you must be logged in to the Ion Reporter™ Software.
IR-25087	In order for Biopsy runs to be successful, IR Organization names for Liquid Biopsy must use only the first 128 characters in the UTF-8 ASCII character set. In addition, the characters used to name the IR Organization must pass standard Ion Reporter Organization name validation. Attempts to create IR Organization names that use characters outside of these requirements receive validation errors immediately.
TVC Parameters for AmpliSeq Exome Hi-Q Panel	
IR-24611	If you upload a Custom TVC JSON parameter file, no error message appears for a Boolean parameter with a non-Boolean value.
IR-24035	TVC parity results do not match when you use an AS-Exome HiQ panel for 540 chip data.
IGV and IGV Light	
IR-24903	MyVariants added in previous versions of the Ion Reporter™ Software are not able to be (re)classified (Benign, Deleterious, etc.) directly from on the MyVariants page, but can be classified from the individual analyses' Analysis Variants Review table.
IR-24731	If you first annotate a variant workflow and run the attached VCF file, and then open an analysis and click on the variant, the VCF track is empty and the chromosome ID in the bar above track view is not correct.
IR-24730	Some GRCh38 version annotation sources (DGV, Cytoband, Clinvar, dbsnp, etc.) support a special type of variant called random (e.g. "chr15_KI270727v1_random:17624"). When you select such a variant from a successful analysis, a new IGV Light window opens that shows an incorrect chromosome ID display above the track. The chromosome ID display differs from the one you selected.
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.

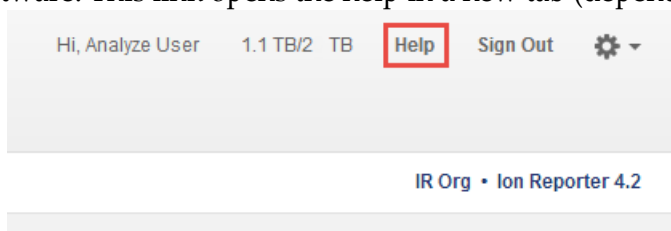
Issue number	Description
IR-24540	When you visualize a very large number of analyses or multiple analyses from larger targeted panels, the following message can appear: "Request to retrieve variants timed out" when loading Variant Impact and Gene Fusion tabs. Workaround: Load fewer analyses at a time for visualization.
IR-24478	Long custom annotation sets are truncated in the last column on the right in the Custom window. Workaround: Move the column to the left of the rightmost position, and optionally save this as a table preference.
IR-24606	The coverage track is not shown for other amplicons on download of IGV when you drag the track view to another location to avoid an overlap instead of entering that specific location or clicking at that location. Workaround: Close the current session and open another JNLP session for the new locus. The issue is due to the cache maintained for display.
IR-24551	When there is already an IGV window open and you click on another locus, a new IGV window opens. Workaround: Use the Chrome browser and "insecure content". When you visit a secure page with insecure content, a shield icon appears at the right edge. Click on the shield icon, and then click Load anyway, and the insecure content will be loaded. 
IR-23464	When you search for amplicons by gene name, IGV Light displays only one amplicon for that gene even though there are other amplicons in the .bed file that fall on that same gene.
IR-19012	Ion Reporter™ Software 5.2 reports an incorrect amino acid change position. The amino acid shift is different from the one shown in IGV.
MyVariants	
IR-22843	On the MyVariants page, when you search for variants by sample name or analysis name, the search does not find all the associated variants.
New issues for the Ion Reporter™ Software 5.2	
IR-24831	In user-created workflows that use the default MyVariant database, you will see the name of MyVariant database in the following format in the downloaded TSV file: for example, MyVariants_8a9148ef3a948140013a948436aa0529. However, if you create and name a custom MyVariant database, you will see exactly the same MyVariant database name in the downloaded TSV file.
IR-24760	A new custom-created database is not selected by default in the VariantDB dropdown, it must be chosen from the list after creation.

Issue number	Description
IR-24741	Ion Reporter™ Software must reference the report.pdf URL in the POST run level. Otherwise, an incomplete report.pdf is uploaded to Ion Reporter™ Software. Workaround: You can manually upload the samples again to get the complete report.pdf file in Ion Reporter™ Software.
IR-24736	The Venn diagram data in visualization tabs is updated with variant impact data after about ten seconds when you apply a filter chain. When you switch tabs, the diagram goes back to the default.
IR-24680	After you sort the genes column, the number of variants increases for AmpliSeq Exome paired sample workflow analysis.
IR-24669	In the MultiAnalysis Visualization display, when you do one of the following, the score changes back to "Variant Impact": Select SIFT score as a scoring option and then filter by the numbers in the Venn diagram. Change the Chromosome selection. Change the Filter Chain selection.
IR-24668	Gene names and reference alleles in TSV files are not imported into the MyVariant database.
IR-24643	The advanced searching query "location:exonic,intronic" is not yet supported under multi-visualization.
IR-24633	You cannot visualize a single analysis with the Report (only) role. Workaround: Add a role or roles that allow you to adjust filters, such as the Analyze role.
IR-24610	To edit a workflow created in an older (prior to 5.2) version of Ion Reporter™ Software, you must select a MyVariants database in the Annotation chevron to proceed.
IR-24576	Sometimes your email format is not validated properly while sharing analyses. Workaround: Ensure that your email is valid before you share analyses or you cannot proceed. (There is no message telling you this).
IR-24539	When you refresh an IGV Light window, a blank page appears.
IR-24419	Spaces or special characters are not supported as separators when constructing a genomic range filter. You can only use "comma" and "or" as a separator.
IR-24080	When setting "UCSC COMMON SNPs" filter to "In", it implicitly only filters in SNPs that have the "UCSC COMMON SNPs" annotation, even though 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 auto-launched in Ion Reporter™ Software from Torrent Suite™ Software.
IR-23801	A search for variant types works only for the following Fusions tab variant types: EXPR_CONTROL, ASSAYS_5P_3P, RNA_HOTSPOT, GENE_EXPRESSION
IR-23490	There is no 540 AmpliSeq Exome Hi-Q workflow in Ion Reporter™ Software 5.2. However, you can import 540-specific parameter files from AmpliSeq.com or Torrent Suite™ Software and set up custom workflows using the 540-specific TVC parameter files.

Issue number	Description
IR-23462	Currently, Ion Reporter™ Software 5.2 does not require you to specify the sample type to be RNA. However, if you do not specify RNA samples as RNA type, you do not get correct results.
IR-23379	In DNA and Fusions workflow, cellularity is not required for NTC RNA samples, but is still required for NTC DNA Sample.
IR-22848	In the GRCh38 genome reference, there exist alternate loci which are not part of the 1-22, X,Y chromosome contigs, and so are not annotated by the software (by design), for example chr22_K1270879v1_alt. IMPORTANT NOTE: The software does, however, annotate the GSTT1 gene which is also located on an alternate loci.
IR-24430	For some older analyses when bai file is missing from the input bam folder, then bam and Reads Coverage tracks do not load in IGV or IGV Light windows. 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-24955	IGV Light: bam and Read coverage tracks are repeated in IGV Light when using TS plugin version of Ion Reporter™ Uploader (IRU) plugin to upload data from multi-sample analyses. Paired and Tumor/Normal analyses have each sample's bam and read coverage tracks loaded twice, and Trio analyses have each sample (Mother, Child, Father) loaded three times each. This issue does not occur in IGV, only in the IGV Light browser within the Ion Reporter™ Software.
IR-25249	When a complex filter chain with "OR" is applied, the filtered variant count is correct, however, the filtered gene count may be incorrect.
IR-25095	Due to a design change to improve MyVariants filtering in IR 5.2, for IR 4.0-run analyses (only), All flagged MyVariants in IR v4.0 analysis will show up in Ion Reporter™ Software 5.2 when filtering for either IMPORTANT or IGNORE. MyVariants filtering works correctly for analyses run from IR 4.2-5.2 workflows.
IR-25252	When creating an hg19 Annotation set, do not use the annotation source DrugBank of version 20150107, please use the annotation source DrugBank of version 1. If you use the DrugBank of version 20150107 in an hg19 annotation set, you will not be able to create filter chain of DrugBank for any analysis that uses the annotation set.
IR-25485	Each filter in the filter chain should only report variants remaining after applying that specific filter. Instead, the number of variants resulting after applying all filters is written against each interim filter in the filter chain. The result of this is that the final number of variants is correct, while the intermediate steps can have incorrect numbers of variants filtered at that step.

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 on thermofisher.com. Search for Ion Reporter™ Software to locate the product page that contains links to the software documentation.

Compatibility with Torrent Suite™ Software

The Ion Reporter™ Uploader (IRU) plugin versions are compatible with the Torrent Suite™ Software and Ion Reporter™ Software versions listed here:

Version Compatibility Matrix		
Ion Reporter™ Uploader plugin	Compatibility on Torrent Suite™ Software	Compatibility on Ion Reporter
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)

Ion Reporter™ Uploader (IRU) plugin Release Notes

A new version of the IRU plugin is available on Thermo Fisher Cloud US, Ion Reporter™ Uploader 5.2.1.2. You can download it from <http://iru.ionreporter.thermofisher.com>. This web page replaces the Ion Community plugin store as the download location for the latest version of Ion Reporter™ Uploader.

From Torrent Suite™ Software, the plugin version format is “plugin_name p.q.r.s”, where “p.q” represents the major/minor version number of Torrent Suite™/Ion Reporter™ Software for which the plugin uses. The next number “r”, represents the patch number and “s” represents the number of builds done on this patch.

The IRU plugin is available upon Torrent Suite™ Software installation or upgrade and by download from the corresponding major/minor version of the Ion Reporter™ Software. At any point in time, Torrent Suite™ Software or Ion Reporter™ can have the IRU plugin available in the software. However, the software applications may have releases later or earlier depending on the product schedules. The most current IRU plugin is always available for download from <http://iru.ionreporter.thermofisher.com>. However, IRUCLI 5.2 now 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 to 5.2 first, 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 only need 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 5.2.1.2 may be:

```
/results/plugins/IonReporterUploader/java/jre/openjdk-7-jre-headless/usr/lib/jvm/java-7-openjdk-amd64/jre/bin/
```

or, on a TS that is installed with IRU 5.2.1.2 may be:

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

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

A manual installation using an IRU.zip file was allowed for Torrent Suite™ Software 5.0 and earlier. Beginning with Torrent Suite™ Software 5.2, zip files are replaced with debian packages. For a Torrent Suite™ Server 5.2 connected to the internet, the IRU plugin can be updated through the off-cycle mechanism as detailed in the Torrent Suite™ Software User Guide. For a Torrent Suite™ Server 5.2 not connected to the internet, the IRU 5.2 debian package is available for a manual update at <http://iru.ionreporter.thermofisher.com/>. For customers who require version 5.2 of the IRU, but prefer to continue using Torrent Suite™ Software 5.0 and earlier, an IRU 5.2 zip file is available on this page.

Installation Packages				
IRU plugin Version	.zip available	.deb available	zip installable	deb installable
IRU 5.2	yes	yes	5.0 and earlier	5.2 and later
IRU 5.0	yes	no	5.0 and earlier	
IRU 4.4	yes	no	Torrent Suite™ Software 4.6 and earlier	

Ion Reporter™ Uploader plugin configuration

Use the following Ion Reporter™ Uploader configuration setting to transfer to 5.2.x:

Server: dataloader.ionreporter.thermofisher.com

Note: The old, previous server address, 40.dataloader.ionreporter.lifetechnologies.com, will continue to work for the 5.2.x release, but please use the new address going forward.

Ion Reporter™ Server: Update to 5.2.1

Note: To optionally upgrade the Ubuntu™ Operating System software from 12.04 to 14.04 on your Ion Reporter™ Server System, contact your FBS/FSE/FAS for assistance.

Take note of which version of Ion Reporter™ Software you are currently using. Use the 4.6 to 5.2.1 instructions if you are upgrading from 4.6. Use the 5.0 to 5.2.1 instructions if you are upgrading from 5.0. Use the 5.2 to 5.2.1 instruction if you are upgrading from Ion Reporter™ Software 5.2 to version 5.2.1.

The sections that follow have instructions on how to update Ion Reporter™ Software Server System to 5.2.1. Use the command line interface with a connection to the Internet to complete the instructions.

The Ion Reporter™ Server Software 5.2 is designed to work with the Ubuntu™ operating system versions 12.04 and 14.04. 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.

Please contact your local Ion Torrent™ bioinformatics representative for specific instructions and help upgrading the Ubuntu™ operating system of your Ion Reporter™ Server Software. Do NOT update the Ubuntu™ operating system of your Ion Reporter™ Server System 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 4.6 to 5.2.1

To upgrade from Ion Reporter™ Software 4.6 to 5.2.1, you must first upgrade to 5.0, then 5.2.. This can take up to five hours to complete. To update the ionreporter-irconfig, enter the following into your command line interface:

Step	Command
1	<code>sudo apt-get update</code>
2	<code>sudo apt-get install ionreporter-irconfig</code>
3	<code>sudo IRconfig --update-to-5.0</code>
4	<code>sudo apt-get update</code>
5	<code>sudo apt-get install ionreporter-irconfig</code>
6	<code>sudo IRconfig -s</code> Check that Ion Reporter™ Software 5.0 installed correctly
7	Check that IR Server has the correct version (1.5.0) of matplotlib: 7.1. Log into console with username ionadmin 7.2. Check the matplotlib version <code>\$ python -c "import matplotlib as mpl; print mpl.__version__"</code> 7.3. If the printout is 1.5.0, then do not perform the next two matplotlib commands; If the printout is higher than 1.5.0 (for example 2.0.x), run following 2 matplotlib-related commands to rollback the matplotlib to version 1.5.0: <code>\$ sudo pip uninstall matplotlib</code> <code>\$ sudo pip install matplotlib==1.5.0</code>
8	<code>sudo IRconfig --update-to-5.2</code>
9	<code>sudo apt-get update</code>
10	<code>sudo apt-get install ionreporter-irconfig</code>
11	<code>sudo IRconfig -s</code>

Steps 1, 2, and 3 give you the latest Ion Reporter™ Software 5.0 IRconfig scripts and modify the repository to Ion Reporter™ 5.0. Steps 4, 5, 6, and 7 download Ion Reporter™ 5.0 Software to Ion Reporter™ Server. Steps 8, 9, 10, and 11 give the steps to change the repository to Ion Reporter™ Software 5.2. and then install Ion Reporter™ 5.2.1 Software.

If your downstream speed is around 2M/s, you can expect three-plus hours to finish.

Update 5.0 to 5.2.1

You can upgrade Ion Reporter™ Software 5.0 directly to Ion Reporter™ 5.2.1 Software without any intermediate stage. In the following table, steps 2, 3, and 4 give users the latest Ion Reporter™ Software 5.2.1 IRconfig scripts and modify the repository to Ion Reporter™ Software 5.2.1. Steps 5, 6, and 7 install Ion Reporter™ Software 5.2.1.

To update the ionreporter-irconfig, enter the following into your command line interface:

Step	Command
1	<p>Check that IR Server has the correct version (1.5.0) of matplotlib:</p> <ol style="list-style-type: none">1. Log into console with username ionadmin2. Check the matplotlib version <pre>\$ python -c "import matplotlib as mpl; print mpl.__version__"</pre> <p>3. If the printout is 1.5.0, then do not perform the next two commands; If the printout is higher than 1.5.0 (for example 2.0.x), run following 2 commands to rollback the matplotlib to version 1.5.0:</p> <pre>\$ sudo pip uninstall matplotlib \$ sudo pip install matplotlib==1.5.0</pre>
2	<pre>sudo apt-get update</pre>
3	<pre>sudo apt-get install ionreporter-irconfig</pre>
4	<pre>sudo IRconfig --update-to-5.2</pre>
5	<pre>sudo apt-get update</pre>
6	<pre>sudo apt-get install ionreporter-irconfig</pre>
7	<pre>sudo IRconfig -s</pre>

If your downstream speed is around 2M/s, you can expect three-plus hours to finish.

Update 5.2 to 5.2.1

If you have Internet access and have Ion Reporter™ Software 5.2, enter the following into your command line interface to update to version 5.2.1:

Step	Command
1	Log into console with username ionadmin
2	<code>sudo apt-get update</code>
3	<code>sudo apt-get install ionreporter-irconfig</code>
4	<code>sudo IRconfig -s</code>

If your downstream speed is around 2M/s, you can expect three-plus hours to finish.

Verify software versions with the following command:

```
dpkg -l ionreporter*
```

The following package information appears:

Name	Version	Description
ii ionreporter-activemq	5.10.0-11	Ion Reporter activemq
ii ionreporter-analysis	5.2.40	Ion Reporter analysis
ii ionreporter-annotdelta	4.4.2	Ion Reporter AnnotationSource Delta
ii ionreporter-annotgrch38delta1	5.2.31	Ion Reporter AnnotationSource GRCh38 Delta 1
ii ionreporter-annotgrch38delta2	5.2.31	Ion Reporter AnnotationSource GRCh38 Delta 2
ii ionreporter-annotgrch38delta3	5.2.31	Ion Reporter AnnotationSource GRCh38 Delta 3
ii ionreporter-annothg19delta	5.2.0	Ion Reporter AnnotationSource hg19 Delta
ii ionreporter-axeda	5.2.0	Ion Reporter Axeda
ii ionreporter-dbsnp146delta1	5.2.2	Ion Reporter AnnotationSource dbsnp146 Delta 1
ii ionreporter-dbsnp146delta2	5.2.2	Ion Reporter AnnotationSource dbsnp146 Delta 2
ii ionreporter-dbsnpdelta	4.2.173	Ion Reporter AnnotationSource dbsnp138 Delta
ii ionreporter-grch38ref	5.2.0	Ion Reporter GRCh38 reference
ii ionreporter-grch38ref1	5.2.0	Ion Reporter GRCh38 reference
ii ionreporter-grch38ref2	5.2.0	Ion Reporter GRCh38 reference
ii ionreporter-helpdoc	5.2.3	Ion Reporter Help Doc
ii ionreporter-igvlight	5.2.1	Ion Reporter igv light
ii ionreporter-igvlightgrch38	5.2.5	Ion Reporter igv light grch38
ii ionreporter-igvservlet	5.2.67	Ion Reporter IgvServlet

ii ionreporter-irconfig	5.2.13	Ion Reporter IRconfig
ii ionreporter-iru-server	5.2.1.2	Ion Reporter IRU server
ii ionreporter-manager	5.2.40	Ion Reporter Manager
ii ionreporter-mongobin	5.2.40	Ion Reporter mongo binaries
ii ionreporter-mongoconf	5.2.5	Ion Reporter mongo configuration
ii ionreporter-mvarviz	5.2.60	Ion Reporter
ii ionreporter-python-drmaa	4.2.206	Ion Reporter python drmaa
ii ionreporter-ref	5.2.31	Ion Reporter reference
ii ionreporter-server	5.2.40	Ion Reporter
ii ionreporter-tomcat8	8.0.20-12	tomcat
ii ionreporter-ui	5.2.40	Ion Reporter UI

Post-Update Steps

Complete the following operations to confirm the functionality of the updated software:

- Log in as default user name: ion.reporter@lifetech.com with password: **123456**
- Accept the End User License Agreement (EULA).
- Start an annotation-only workflow with built-in demo data.
- Set up your Torrent Browser with this Ion Reporter™ Server.
- Upload your data to the Ion Reporter™ Server.

Revision History

Revision	Date	Description
A.0	01 December 2016	Technical updates to Release Notes for Ion Reporter 5.2 <ul style="list-style-type: none">• New Known issue: IR-25087• Added new features:<ul style="list-style-type: none">• Saved Search and Filter Results• Improvements in Aneuploidy analysis workflow algorithm
B.0	21 February 2017	Release Notes for Ion Reporter™ Software 5.2.1 Patch <ul style="list-style-type: none">• Bug fixes and improvements:<ul style="list-style-type: none">○ Intermediate Filter Chain results○ TVC duplicate hotspot alleles○ Unique entries in variants databases○ Final PDF report generation○ Fusion algorithm intermediate files○ Allele view showing multiple COSMIC IDs• Update to installation instructions

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