# Ion Reporter Software v5.0 Release Notes

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For Research Use Only. Not for use in diagnostic procedures.
New in this release

The Ion Reporter™ Software 5.0 release includes the following new features and improvements:

Ion Reporter™ Software v5.0 is now available in China
Ion Reporter™ Software v5.0 is now available in China on the China Thermo Fisher Cloud. Ion Reporter™ in China is a completely separate instance of the 5.0 software from Ion Reporter™ in the USA.

- Access via the IR App button on the China TFC:
  https://china.apps.thermofisher.com/apps/dashboard/#/

- Or via the direct China IR link: https://china.ionreporter.thermofisher.com/ir/

Because the new Ion Reporter™ software in China is a separate instance, all Organizations on IR China need to be created anew. All user roles will need to be assigned anew. Data and custom presets will not be migrated from the USA instance to the China instance of Ion Reporter. Current thermofisher.com customers can log in to both Thermo Fisher Cloud with the same login credentials.

Note: The Ion Reporter Uploader (IRU) is also a specific version for China. Please download IRU 5.0.4.32 from [http://iru.ionreporter.thermofisher.com](http://iru.ionreporter.thermofisher.com).

To add an IR Cloud-China account, enter the following IRU dataloader server information in IRU 5.0:

Protocol: https
Server: dataloader.china.ionreporter.thermofisher.com
Port: 443

Please see the Known Issues list for the China instance on page 10.

Full Support for Ion S5™ Sequencing Systems
Data from the new S5™ and S5™ XL sequencers, including all 5-series chips and kits, are supported by Ion Reporter workflows.

Integration into Thermo Fisher Cloud
Ion Reporter™ Software v5.0 integration with Thermo Fisher Cloud allows you to more easily share Ion Torrent data with collaborators and compare to Sanger sequencing data and TaqMan™ data. Ion Reporter User, Organization, and Storage space management are now incorporated into Thermo Fisher Cloud.
You can share files from Ion Reporter with Thermo Fisher Cloud collaborators by choosing to copy them to your Organization’s Thermo Fisher Cloud data folder. This new Organization folder was created upon the integration with ThermoFisherCloud. You can also continue to share entire analyses with other Ion Reporter™ Software users outside of your Organization just like you do today from within Ion Reporter™ Software. For more information, see the FAQs at www.thermofisher.com.

**Improved Flexible PDF reporting**

On the Report Live Preview page, you can choose which available sections to include in your report. The software allows increased flexibility in placement of report sections and the ability to save report templates to workflows. Go to Analyses Overview, select an analysis, and select variants. Then click Generate Report. Click and move sections of the report to your liking. Footers now show the analysis name and X of Y page numbering on every page.

**Aneuploidy Preimplantation Genetic Screening Display and Reporting**

Improved whole genome, multi-sample graphical and table displays for preimplantation genetic screening (PGS) are included in Ion Reporter v5.0. Customizable multi-sample reporting of PGS-specific sample attributes, such as gain and loss data filtering by Confidence score, are also added. These features are available for analysis results from the new aneuploidy workflow for the Ion ReproSeq™ Kit and from older aneuploidy workflows in Ion Reporter™ Software.

The Ion ReproSeq™ PGS (Pre-Implantation Genetic Screening) Kit with the Ion PGM™ System allows for rapid and affordable screening of aneuploidy in all 24 chromosomes. The Ion ReproSeq PGS Kit on the Ion PGM System provides throughput flexibility, enabling the cost-effective screening of 2 to 24 samples and minimizing the need to batch embryos and enabling same day transfer. Fastest benchtop NGS workflow for PGS — Users can go from single cell to answer in as little as 7.5 hours

**IGV Light**

New in Ion Reporter Software v5.0, you can visualize aneuploidy analyses with a streamlined IGV Light viewer. In addition, you can generate a PDF report with graphics
from the IGV Light viewer.

Also, you can see heatmaps showing cytoband coordinates, a details table for one sample, dna karyo selection and whole genome views, aneuploidy bars in karyo view, default CNV plot and table, plots and tables for groups of embryos, and metadata attributes such as ‘Couple ID’, ‘Embryo ID’, and ‘Biopsy Day’.

**16S alpha-diversity and beta-diversity calculations across multiple samples**

Harnessing the power of Quantitative Insights Into Microbial Ecology (QIIME) algorithms, alpha diversity rarefaction curves and beta diversity calculations highlighting differences between multiple samples are automatically performed and displayed. The Metagenomics workflow in Ion Reporter™ Software v5.0 features two additions: alpha diversity results and beta diversity results.

Alpha diversity results are the differences among species (or genus, or families) for one sample. Beta diversity results are the differences among species/genus/families of multiple samples. If you only run one sample, Ion Reporter software will only return alpha diversity results.

**Expanded filter creation**

New filter chain flexibility allows you to construct customized, nested filter chains in a new user interface. Using filter names and AND and OR modifiers and parentheses, you can now construct precise custom queries to filter your variant data.
Three new shipped filters

Three new filters are added to Ion Reporter Software v5.0: Homopolymer Length, Variant Classification, and CNV Somatic Confidence.

Homopolymer Length – a range filter that only applies to indels.
**Variant Classification** – filters on user classification options: unclassified, unknown, benign, suspected benign, suspected deleterious, deleterious.

**CNV Somatic Confidence** – includes 5% Confidence Interval Range and 95% Confidence Interval Range (for Oncomine™ Focus and Oncomine™ Comprehensive Assay data).
Import VariantDB or other VCF files into My Variants and improved display
Now you can import VariantDB files into your My Variants list, sort the My Variants table, expand or collapse variant rows, and edit within the My Variants table itself.

A Classification column is now included on the My Variants page. You can add flags in this column to indicate if a variant is Unclassified, Unknown, Benign, Suspected Benign, Deleterious, or Suspected Deleterious. These flags are visible across analyses and are denoted with a comment icon.

Archive and Restore Samples and Analyses from Ion Reporter™ Server System
From the Ion Reporter Local Server you can now archive and restore Samples and Analyses to a Torrent Storage device. Once the storage device is set up, you simply select samples on the Sample page, then click Actions > Archive. Batch archiving and restoring files is also enabled.

Create Multiple Organizations on the Ion Reporter™ Server System
Create additional independent Organizations on your Ion Reporter Server with the same security and isolation of data as in the cloud Ion Reporter.

Improve Fusion Calling
Improvements include:

- A “Fusion Overall Call” summarizes each sample’s fusion results
- Fusions’ Present/Absent/No Call is based on isoform presence or absence and on 3’/5’ imbalance values
- Reason for any No Calls is provided in the Detection column
- Ability to sort by TYPE column
- Display QC pass/fail for total mapped fusion panel reads
- Configure the Total Mapped Fusion Panel Reads threshold
- Display QC statistics for RNA fusion samples
- Main and advanced algorithm parameters are now configurable
- Nomenclature change: ‘Novel’ to ‘non-targeted’
Customize Analysis Results Table and Samples Table with “Table Preferences”
You can now make changes to the Analysis Results and Samples tables’ columns. Add, Hide, adjust width, and drag-and-drop columns to suit any application. Easily switch between your saved Table Preferences. The last used preference is persisted for future analyses run through the same workflow, and the named Table Preferences and their persistence is specific for each user.

After you choose an analysis and are on the Analysis Results page, click the Actions button and Select Columns to begin the Add/Hide column customization. When finished, you can save the table preference, give it a name (such as “Genotype Project”), and then apply it to future Analysis Results tables.

Organize Samples and Analyses by “Project”
If you selected a Project for your samples in Torrent Suite™ Software, you can now choose to display a “Project” column on the Samples and Analyses tables in Ion Reporter™ Software. Go to Actions > Select Columns > Project for both pages.

Splice Site Size Parameter
The Splice Site Size annotation parameter is back in Ion Reporter™ Software versions 4.6 and 5.0. It erroneously disappeared in v4.4. There are no plans to discontinue this parameter in the future.

Tumor-Normal algorithm improvement
The Tumor-Normal algorithm now includes a default filter for Flowspace Alternate (FAO) allele depth at position.

Query by Sample Name API
You can now query by sample name using this API:

/webservices_42/rest/api/analysis?format=json&Name&type=sample

This returns a list of analysis names performed on the sample, ordered by start date.
Tag Workflows for inclusion in Torrent Suite workflow list

You can now reduce the number of Ion Reporter™ workflows that appear on the drop-down menu on the Ion Reporter chevron during planned run creation in Torrent Suite™ Software.

This is achieved by applying “Tag for IRU” in Ion Reporter™ Software. IRU stands for Ion Reporter Uploader and it is the plugin that transfers Torrent Suite run data to Ion Reporter, but it can also tag the Ion Reporter workflows that you want to see in Torrent Suite.

1. Log into Ion Reporter.
2. Go to Workflows > Overview.
3. Select a workflow, then click Actions > Tag for IRU. Repeat for each workflow of interest.

Only the tagged for IRU workflows will now show up when planning your runs in Torrent Suite.

To undo, select Untag for IRU.
# Known issues and limitations in IR 5.0-China

This table lists known issues and limitations with the Ion Reporter™ Software 5.0-China release.

<table>
<thead>
<tr>
<th>Issue number</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>IR-22780</td>
<td>Users must specify sample type “RNA” for RNA samples when using the Ion Reporter Uploader plugin or IRUCLI (IRU command line), otherwise the software labels them as DNA and the RNA fusion analysis will fail.</td>
</tr>
<tr>
<td>IR-22839</td>
<td>To retrieve final or QC reports in the JSON format using APIs, you must specify the start_date and end_date. For example: <a href="https://china.ionreporter.thermofisher.com/webservices_42/rest/api/finalreport?format=json&amp;name=">https://china.ionreporter.thermofisher.com/webservices_42/rest/api/finalreport?format=json&amp;name=</a>&lt;name&gt;&amp;start_date=2016-04-01&amp;end_date=2016-05-01.</td>
</tr>
<tr>
<td>IR-22921</td>
<td>If you are uploading a folder with IRUCLI, note that the folder must not contain file types other than BAM. Non-BAM files will not load via the command line IRU.</td>
</tr>
<tr>
<td></td>
<td>IRU 5.0.4.32 is the only compatible IRU plugin. Please download IRU 5.0.4.32 from <a href="http://iru.ionreporter.thermofisher.com">http://iru.ionreporter.thermofisher.com</a>.</td>
</tr>
</tbody>
</table>
# Known issues and limitations in IR 5.0

This table lists known issues and limitations with the Ion Reporter™ Software 5.0 release.

<table>
<thead>
<tr>
<th>Issue number</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Gene fusions</strong></td>
<td></td>
</tr>
<tr>
<td>IR-18398</td>
<td>Total number of present/reported fusions are not displayed in the QC Report of older versions of the software. In fusion-detecting workflows versioned 4.x, the QC Report will list the ‘Number of Fusions’ assayed, while in 5.0, the ‘Number of Fusions’ value will be the number of ‘Present Fusions’ in the sample.</td>
</tr>
<tr>
<td>IR-18664</td>
<td>A bug causes the Fusions tab not to display variants after navigating from the Summary tab when on a page number higher than the Fusions tab will have. The work around is to go to page 1 of a non-fusion tab before switching to the Fusions tab, since that tab contains different and often less data rows. If switching to the Fusions tab from another tab where the page number is higher than the number of pages that the new tab has, you may see a blank page.</td>
</tr>
<tr>
<td>IR-16258</td>
<td>Due to changes in the Ion Reporter™ Uploader to normalize outcomes of fusion-detecting workflows, the results may be slightly different from Ion Reporter™ 4.4 workflows run in the Ion Reporter™ v4.4 and v4.6 software versions. This is because in the Ion Reporter™ v4.4 software, 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™ v4.4 version of the Fusion workflow used in the v4.4 and v4.6 software versions should still give the same results if unmapped BAMs were used in both software versions for those 4.4-versioned workflows.</td>
</tr>
<tr>
<td>IR-19344</td>
<td>When archiving samples and analyses, no warning/error message is displayed when archiving a sample along with an analysis when the sample is either already archived or deleted.</td>
</tr>
<tr>
<td><strong>Archiving Samples and Analyses</strong></td>
<td></td>
</tr>
<tr>
<td><strong>Ion Reporter Uploader (IRU) Plugin</strong></td>
<td></td>
</tr>
<tr>
<td>IR-12770</td>
<td>Visualizing Fusions in IGV must be done independently from visualizing DNA variants in IGV, due to the distinct genomic mapping required for each type of data set.</td>
</tr>
<tr>
<td>IR-18723</td>
<td>The IRU that comes in Torrent Suite Software v5.0, (IRU5.0.0.21) contained errors that prevented users from adding a new Ion Reporter account against instances of Ion Reporter Software v5.0. The workaround, is for Ion Reporter on Thermo Fisher Cloud users, who also use Torrent</td>
</tr>
</tbody>
</table>
Suite Software v5.0, to update the IRU plugin from Ion Reporter Software v5.0. This will resolve the problem.

**Trio Analyses**

<table>
<thead>
<tr>
<th>IR-18535</th>
<th>When you add one variant of an older version (Ion Reporter v4.4/4.6) Trio analysis, a bug in the software causes the variant to be added twice in expanded mode.</th>
</tr>
</thead>
<tbody>
<tr>
<td>IR-17735</td>
<td>In a Trio analysis single analysis visualization, table rows do not match the default filter condition. This is due to the fact that disease attribute is only present in the proband, not the father or mother variomes. When opening a trio analysis in Visualize mode and applying the Genetic Disease category filter, you need to explicitly filter proband variants by clicking the proband circle.</td>
</tr>
</tbody>
</table>

**Annotations**

| IR-13201 | The exon number should be 7 for TPM3 gene for fusion variant of TPM3-ROS1. T7R35, however, the gene column displays TPM3(8)-ROS1(35). The correct display should be TPM3(7)-ROS1(35). |

**Analysis results**

<table>
<thead>
<tr>
<th>IR-15587</th>
<th>In testing, we found the manual launch of 96 samples would occasionally either not start or not show progress on the graphic user interface. If this happens to you, check the Analysis Overview screen and see if the job has started, or re-launch fewer samples at a time. If you abort/delete any pending analyses on the Analyses Overview page, the analyses will still run on the backend. In order to completely delete them, log in as iruser and type qdel -u * in the command-line before you re-launch any analyses.</th>
</tr>
</thead>
<tbody>
<tr>
<td>IR-18951</td>
<td>Unable to create an Ion Reporter workflow from Torrent Suite Plan template page using the Create New Workflow button. Server is going to Thermofisher ordering page instead of create workflow page. The workaround is to create the Ion Reporter Workflow in Ion Reporter.</td>
</tr>
<tr>
<td>IR-18589</td>
<td>Multi-analysis visualization variant review table does not display a genotype for Probands in IDP trio analyses after applying Genetic Disease variants filter. If you are reviewing a single trio in multi-analysis, you can select the proband circle in the Venn and then you can see the proband results.</td>
</tr>
</tbody>
</table>

**CNV**

| IR-19024 | CNV Heat map Excel export file has “Genes” column incorrectly labeled “ploidy”. |

**Filtering**

<table>
<thead>
<tr>
<th>IR-18893</th>
<th>A bug causes an error on Variant Impact heatmap after failure of an advanced query filter with three segments and one of the segments in parentheses (). Workaround: remove parentheses. This problem is slated to be fixed in v5.2.</th>
</tr>
</thead>
<tbody>
<tr>
<td>IR-16921</td>
<td>A bug prevents users from accessing custom Variant DBs with the same name, but different versions. The work around is to give versions of a filter slightly different names. This is slated to be fixed in a future release.</td>
</tr>
<tr>
<td>IR-18852</td>
<td>An “Invalid filter chain query expression” error is returned when using gene panel filters with brackets in their names.</td>
</tr>
<tr>
<td>IR-18856, IR-18414</td>
<td>When building a filter chain query, if you decide to remove a filter after you have applied it by using the trash can icon, you must delete it manually from the filter chain description string directly above the filters list, in order to create a valid filter</td>
</tr>
</tbody>
</table>
When a chromosome filter and filter chain are both applied on variant impact page, the filter results displayed in Venn is correct. Upon switching the filter chain on and off, the displayed number in Venn becomes inconsistent. In this case, switching to the Variant table and then switching back to Variant Impact tab will reset the numbers correctly.

Downloaded filtered variant results for older version (4.2,4.4,4.6) trio analyses can be random: sometimes correct, but sometimes no variants or all variants. A workaround is to download multiple times and the filtered results will be generated in one of those attempts.

**Export Heatmap**

Export Heatmap does not work directly in Internet Explorer 9, but there is a workaround. It first opens up an HTML page and you can save the file as a .txt file, then save it as a .csv file. Then, open with Microsoft® Excel and select **Delimited**, then **Next**.

![Image of text import wizard](image)

Then select **Tab** and **Comma**. Then click **Finish**.
Or, copy the text from the browser, and paste into Excel using the text import wizard. Use a semicolon (;) as a separator.

**IGV and IGV Light**

Depending on security settings, the error message "igv.jnlp cannot be opened because it is from an unidentified developer" can be seen on Macintosh® computers when attempting to open IGV.

To avoid this error, change either your Macintosh® security preferences or your browser settings to allow apps from unidentified developers.

**IR-13145** If using IGV with Firefox browser, you must unblock the page if your browser settings are blocking mixed content.
| IR-18033 | The graphical chromosome view is not completely shown on the Aneuploidy report when track height is set above 300. Set track height below 300 to avoid this issue. |
| IR-19016 | Aneuploidy analyses run on older versions of Ion Reporter cannot be displayed as multi-sample aneuploidy visualizations in IGV light. |
| IR-18031 | For three or more aneuploidy analyses, Whole Genome Karyoview display of gain and loss segments is not available due to space limitations. |
| IR-18935 | For CNV heatmaps, when all the sample names are the same, the gender is shown as unknown for all analyses other than the first one checked. |
| IR-21257 | In IGV Light for Ion Reporter v5.0, Karyo view does not show all amplification and deletions correctly. If there are hidden ploidy lines (with expected value) in the data before unexpected data, it sometimes does not show the lines. Hidden ploidy lines are ploidy lines with value 2 for expected value 2 that are in the data, but are never drawn (this is by design). The bug occurs when the software decides to use, for example, 3 ploidy lines in the summary. The software does not use the 3 ploidy lines from the summary, but the 3 ploidy lines from the original data including the hidden ones. Therefore, if there were 2 hidden lines and 1 to be shown it was just drawing 1 in that summary. This is fixed for version 5.2. |

**Variant Calling Parameters**

| IR-15419 | When creating a custom AmpliSeq workflow for a panel that already has the panel files present in the Ion Reporter Software as part of a factory workflow, do not re-import the target regions BED file from AmpliSeq.com or else Torrent Variant Calling parameters will not be optimal for the workflows due to the accompanying files that come with it. To avoid this, copy the respective factory workflows and customize the parameters them, if desired. This will ensure the best and most recent Torrent Variant Calling parameters are used. |
| IR-19341 | Calls at hotspot locations are reported with left-aligned positions in the VCF file and in the variant tables. In previous versions of the software, such calls were reported with their original hotspot positions. |

**MyVariants**

<p>| IR-18286 | On the MyVariants table, reported analyses number is not updated in real-time and is inconsistent with the analysis number displayed in expanded mode. Updating in real-time is not possible due to the high performance hit of the query. Therefore, the summary line shows the last cached information about the number of analyses. Expanding the information refreshes the info and triggers a deep query. |</p>
<table>
<thead>
<tr>
<th>IR-18275</th>
<th>For entries in MyVariants table coming from IR 4.0/4.2 analyses, the analysis name column will remain blank, and if multiple analyses were generated using same samples, they will appear as apparently duplicate rows in My Variant table in expanded mode. Also, the Notes of each of these analyses will contain the text &quot;Analysis name is unavailable&quot; in place of the Analysis name.</th>
</tr>
</thead>
<tbody>
<tr>
<td>IR-18117</td>
<td>Do not edit comments in a 4.0 or 4.2 analysis for flagged variants as this will change the common comments for this variant throughout the versions.</td>
</tr>
<tr>
<td>IR-18180</td>
<td>Notes added to 4.0 and 4.2 analyses are not preserved on My Variants page. Only v4.4 onwards analysis comments are shown on My Variants page.</td>
</tr>
<tr>
<td>IR-18180</td>
<td>When the Gene column is sorted on the My Variants table, the sorting result can appear sometimes to be random. However, the sort order of the genes in one row (variant) is by chromosomal order, not alphabetical order, which is used by the search to order the rows.</td>
</tr>
<tr>
<td>IR-18934</td>
<td>A software bug prevents users from adding multiple CNV or Fusion variants with the same starting location in same analysis to their My Variants. When attempted, the result is multiple CNV or fusion variants with the same chromosome and starting location (but different ending location) are shown only once, with the variants displayed in a random manner.</td>
</tr>
<tr>
<td>IR-18878</td>
<td>Sample names are blank for flagged variants in 4.6 single and paired analyses. This is a bug that is expected to be fixed in next release.</td>
</tr>
<tr>
<td>IR-18937</td>
<td>Variant Notes do not refresh automatically. If you add comments to a variant, you should refresh the page in order to see them on the screen.</td>
</tr>
<tr>
<td>IR-18327</td>
<td>A bug is causing incorrect Genotypes to be shown on My Variants page, as 1/1 or 0/1 for example, for 4.2 and 4.0 My Variants. This is due to a data model change that has occurred over time.</td>
</tr>
<tr>
<td>IR-18197</td>
<td>When importing a TSV file for My Variants, some variants that are not flagged actually get uploaded into My Variants. Essentially, those variants with all valid fields in the TSV file are uploaded.</td>
</tr>
</tbody>
</table>

## Reports

| IR-19004 | In testing we found the Audit Log and View QC Report PDFs are missing from exported files when Safari browser. The workaround is to use Chrome browser. |

### Documentation

Access product documentation through the help link at the top right of Ion Reporter™ Software product pages. This link opens the help in a new tab (depending on your browser settings):
Documentation links are posted in the Ion Reporter™ Software space in the Ion Community. Help text (without images) is also posted in the Ion Reporter™ Software space in the Ion Community. See also the Ion Reporter™ Software FAQ on the Ion Community.

Compatibility with Torrent Suite™ Software

The Ion Reporter™ Uploader (IRU) plugin requires Torrent Suite™ Software 5.x (5.0 or higher) in order to upload results to Ion Reporter™ Software 5.x. For best results, use the latest version of the Ion Reporter Plugin, available within the Ion Reporter™ software, or from the Ion Community Plugin Store http://ioncommunity.lifetechnologies.com/docs/DOC-7645.

Ion Reporter™ Uploader plugin Release Notes

A new version of the Ion Reporter™ Uploader (IRU) is available on Thermo Fisher Cloud US 5.0.0.25-jre8. This can be downloaded from http://iru.ionreporter.thermofisher.com. Download any updates to the plugin from this link in the future. Additional information is available on Ion Community: https://ioncommunity.thermofisher.com/docs/DOC-9098 and https://ioncommunity.thermofisher.com/docs/DOC-9571.

From Torrent Suite, 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 this plugin is intended to be used with. The next number “r”, represents the patch number and “s” represents the number of builds done on this patch.

However, IRUCLI 5.0 now requires a Java version of 1.7 or higher to function, therefore IRUCLI installed on an older Torrent Server running Java 1.6 will not work anymore unless an additional setup step is performed.

If you have Torrent Suite v4.6 or lower running on Ubuntu 10.04 and want to use IRUCLI on this machine, you need to update your IRU plugin to 5.0 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
```

This path setting step only needs to be done once per UNIX terminal session.

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

```
/results/plugins/IonReporterUploader/java/jre/jre1.8.0_45/bin/
```
This matter does not impact newer Torrent Servers running the Ubuntu 14.04 operating system.
**IonReporterUploader plugin Configuration**

Use the following IonReporterUploader configuration setting to transfer to 5.0.x:

Server: 40.dataloader.ionreporter.lifetechnologies.com

**Note:** The “40” prefix is still used for the 5.0.x release.

**Ion Reporter Server: Update to version 5.0**

Please take note of which version of Ion Reporter Software you are currently using. Please use the 4.4-5.0 instructions if you are upgrading from 4.4. Please use the 4.6 to 5.0 instructions if you are upgrading from 4.6.

The following are directions to update Ion Reporter Servers to the 5.0 version of software, and they can be performed using the command line interface with a connection to the Internet.

The Ion Reporter™ Server Software versions 4.0-5.0 are designed to work with the Ubuntu Operating System 12.0.4 that comes with the Ion Reporter™ Server. While you may periodically see messages asking if you want to update your Ubuntu software, doing so will cause the Ion Reporter™ Software on the Server to stop working correctly due to changes between Ubuntu versions over which we do not have control.

Please do NOT update your Ubuntu OS, if prompted to do so.

We plan to make available future Ion Reporter™ Server Software versions which are compatible with more recent Ubuntu versions, and will provide documentation on how to update at that time. Until then, please do NOT update the Ubuntu 12.0.4 OS of your Ion Reporter Server System without our guidance and assistance.

For other options and assistance with updating your Ion Reporter Local Server, please contact your local FBS.

**4.4 to 5.0**

To upgrade from Ion Reporter Software v4.2 to v4.6, you must first upgrade to 4.4, then 4.6. This may take up to five hours to complete.

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

```
1  sudo apt-get update
2  sudo apt-get install ionreporter-irconfig
3  sudo IRconfig --update-to-4.6
4  sudo apt-get update
5  sudo apt-get install ionreporter-irconfig
6  sudo IRconfig -s
```

Check that Ion Reporter 4.4 installed correctly

```
7  sudo IRconfig --update-to-5.0
8  sudo apt-get update
9  sudo apt-get install ionreporter-irconfig
   sudo IRconfig -s
```
Ion Reporter™ v4.4 users need to go through Ion Reporter™ v4.6 to upgrade their servers to Ion Reporter™ v5.0 software. Steps 1, 2, and 3 give users the latest Ion Reporter v4.6 IRconfig scripts and modify the repository to Ion Reporter™ v4.6. Steps 4, 5, 6, and 7 install Ion Reporter™ v4.6 software to Ion Reporter™ server and change the repository to Ion Reporter™ v5.0. Steps 8, 9, and 10 finally install Ion Reporter™ v5.0 software.

4.6 to 5.0

To upgrade from Ion Reporter™ Software v4.6 to v5.0, follow the instructions below. This may take up to two hours to complete.

Note: During the upgrade from Ion Reporter Software v4.6 to 5.0, a message will appear that an update of mysql is available and will be automatically updated to the new mysql version. This happens regardless of the choice you make.

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

1. sudo apt-get update
2. sudo apt-get install ionreporter-irconfig
3. sudo IRconfig --update-to-5.0
4. sudo apt-get update
5. Sudo apt-get install ionreporter-irconfig
6. sudo IRconfig -s

Ion Reporter™ v4.6 software users can directly upgrade to Ion Reporter™ v5.0 software without any intermediate stage. Steps 1, 2, and 3 give users the latest Ion Reporter™ v5.0 IRconfig scripts and modify the repository to Ion Reporter™ v5.0. Steps 4, 5, and 6 install Ion Reporter™ v5.0 software.

Update Ion Reporter™ software. If your downstream speed is around 2M/s, you should expect 3+ hours to finish.

Verify software versions using following command.

dpkg -l ionreporter*  

You should see following package information:


Post-Update Steps
Please 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
- EULA should be accepted by customer.
- Start an annotation-only workflow with built-in demo data.
- Set up IonReporterUploader customer's Torrent Browser with this Ion Reporter Server
- Upload customer's data to the Ion Reporter Server.
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