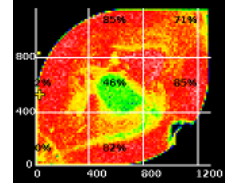


Torrent Scout

Torrent Scout Light

Torrent Scout Light is a Web based interactive tool, which provides users access to raw data generated by the Ion Torrent Personal Genome Machine(TM). It allows users to navigate and view data all the way from the raw signal to the final alignment. Torrent Scout Light is based on the Google Web Toolkit and VAADIN/Java. It uses the Torrent Scout application as a library on the server side. Functionality includes:



- Viewing ionograms and alignments
- Viewing raw traces of multiple flows of one well, or of multiple wells and one flow
- Export both raw and NN subtracted data of one of multiple flows, and of an entire area on the chip (optionally filtered by a mask)
- Find reads based on alignment (indels for instance), both via the interactive plugin (suggested if you are running multiple searches), and also via the TSL application
- View regional empty traces (if data is available)
- View XYZ charts of any read property (such as bead find metric versus Q20 values)
- Load and save your searches (stored as heat maps)
- Find/filter reads based on scores (such as % identity, Q lengths etc)
- Compute the mean signal of an area of multiple flows
- Find reads based on genome position
- Calculate your own masks using the dropdown and command line mask calculator (allows saving/loading of masks)
- Compute your own masks based on the raw data and using various histogram functions

Installation Instructions:

Install via Debian package

```
sudo apt-get install ion-torrentscout-light
```

Manual Installation

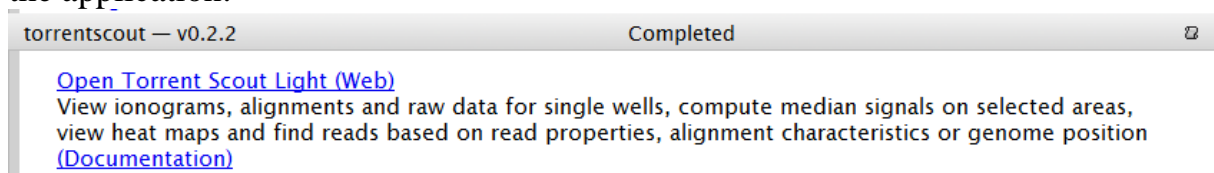
- `sudo apt-get install tomcat6 tomcat6-admin tomcat6-common`
- `sudo nano /etc/default/tomcat6`
change line with JAVA_OPTS to:
`JAVA_OPTS="-Djava.awt.headless=true -server -Xms2048m -Xmx8000m -XX:MaxPermSize=512M"`
(to allow for more concurrent users, increase -Xmx setting. One user requires about 3-4 GB at peak time, such as when loading raw data)

- `sudo nano /etc/tomcat6/tomcat-users.xml`
Uncomment user section so that it contains:
`<user username="tomcat" password="tomcat" roles="admin, manager, manager-gui"/>`
- `sudo nano /var/lib/tomcat6/conf/logging.properties`
In there, change all the log levels to SEVERE to reduce log output – or else the log file can get quite large
- `cp TSL.war /var/lib/tomcat6/webapps`
- To use the desktop Torrent Scout version: `cp torrentscout.war /var/lib/tomcat6/webapps`
- `sudo /etc/init.d tomcat6 restart`
- To start TSL : <http://yourserver.com:8080/TSL>
- To restart TSL : `http://yourserver.com:8080/TSL?restartApplication`
- To download the desktop version of TS : `http://yourserver.com:8080/torrentscout`

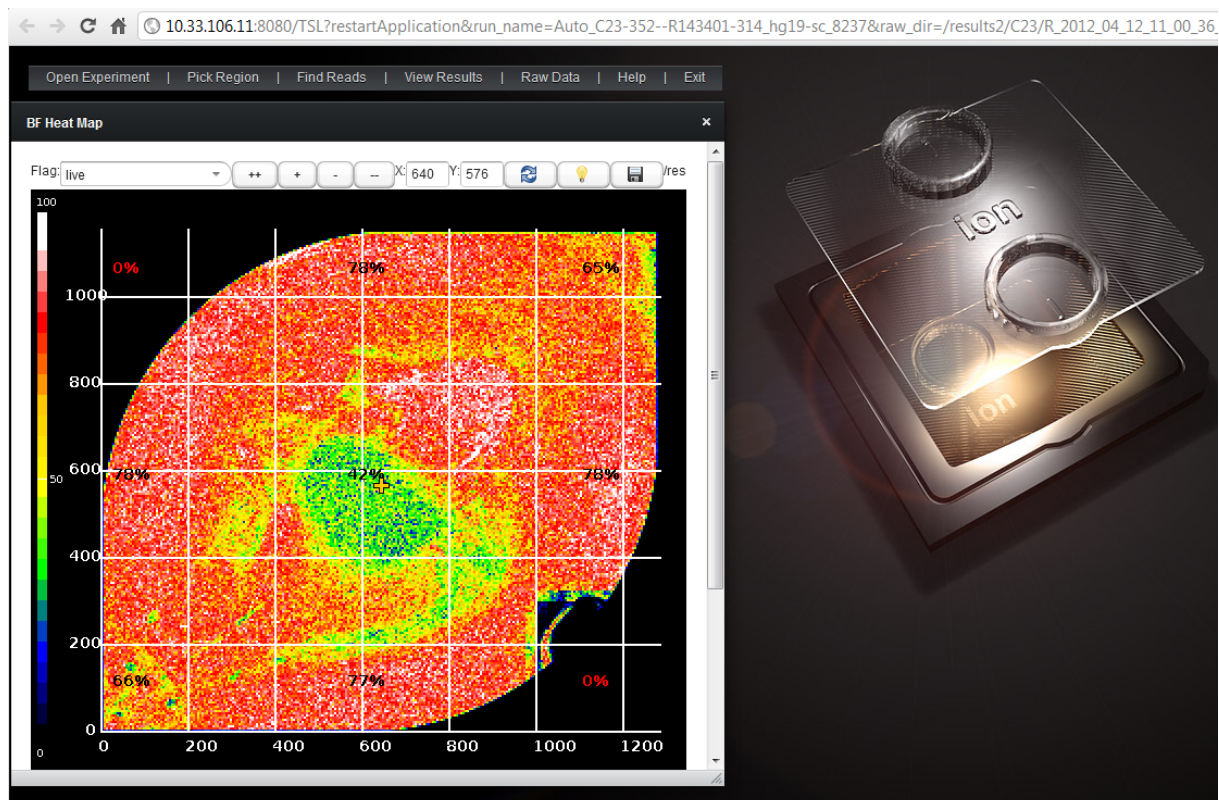
Torrent Scout Plugin

The **Torrent Scout Plugin** prepares the results data for viewing by creating index files on the .sff and .BAM file, by computing various heat maps and by pre-computing alignments searches when the plugin is used interactively. The plugin should always be run (ideally automatically) before launching the viewer so that the viewer does not have to do all the calculations on the head node.

By default the plugin computes those index files and presents the user with a link to the application:



The link both launches the application and loads the data set for the particular run:



In some cases, if a lot of alignment searches are to be done, the plugin also has an interactive part that allows a user to precompute the alignment searches. Simply select the plugin to run (again) and it will prompt you with a form where you can have up to 20 alignment searches done all at once:

TorrentScout Alignment Search Parameters

Search for alignment patterns for the following flows (end=0 means all):
 Start flow: End flow:

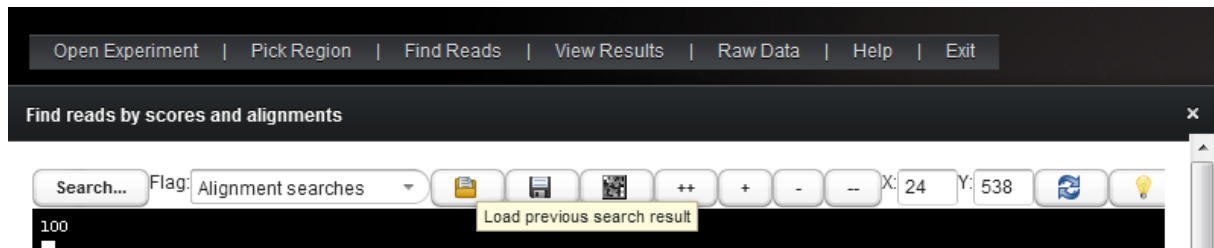
Read sequence (eg TT_) (X = 4 searches with G/A/T/C)	Alignment sequence (eg TTT) (? = any base or gap, _ = gap)	Name of heat map (X will be replaced with G/A/T/C)
<input type="text" value="TT_"/>	<input type="text" value="TTT"/>	<input type="text" value="missed_T"/>
<input type="text" value="XX_"/>	<input type="text" value="XXX"/>	<input type="text" value="missed_X"/>
<input type="text"/>	<input type="text"/>	<input type="text"/>
<input type="text"/>	<input type="text"/>	<input type="text"/>
<input type="text"/>	<input type="text"/>	<input type="text"/>

The following special characters are used:

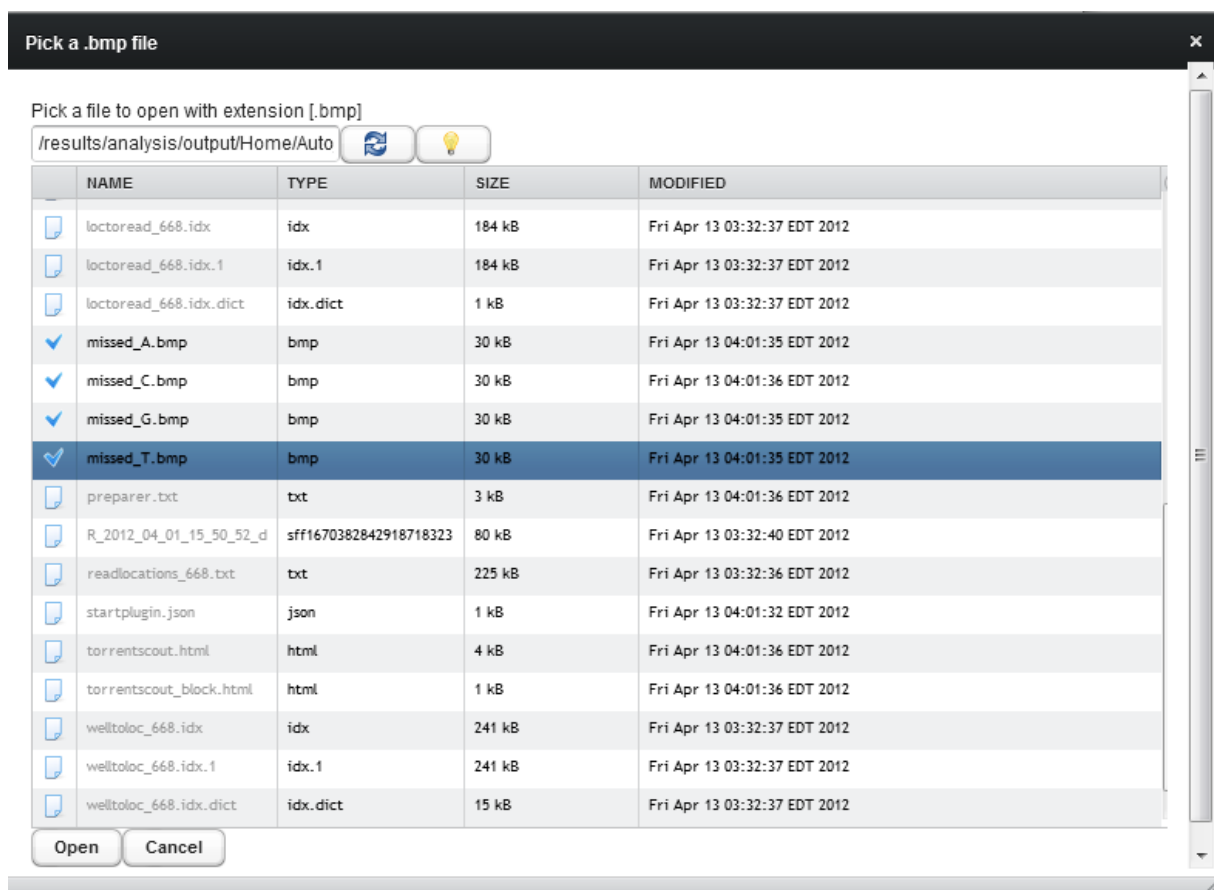
- X denotes a G, A, T or C. Whenever an X appears in a search, this will correspond to 4 searches, for X=G, X=A, X=T and X=C (including in the name of the heat map)
- ? denotes any base or a gap. Each ? will match a G, A, T, C or a _ character

- ‘_’ is a gap (as in the .BAM alignment)

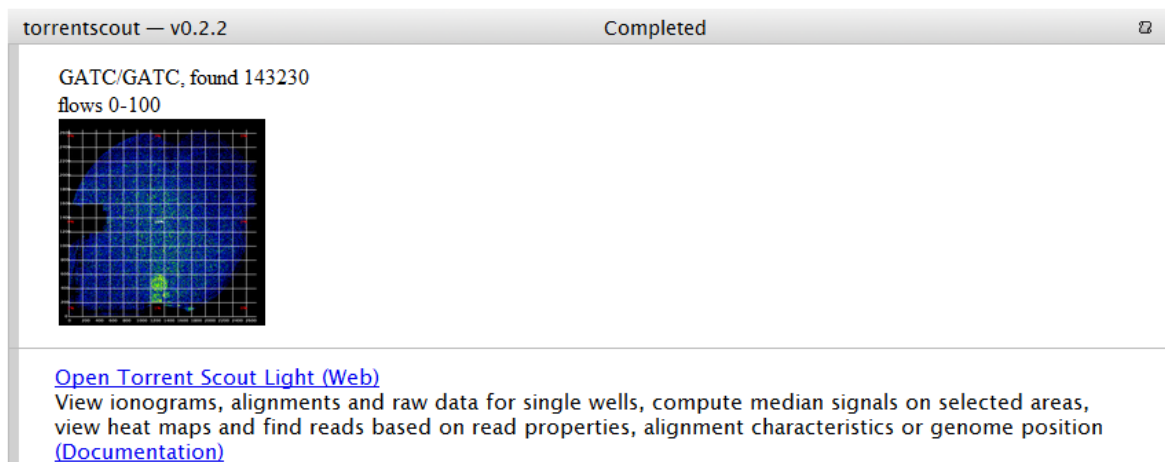
The alignment searches are stored as a heat map similar to the image above and can be loaded in the application under “Find Reads by Scores and Alignments”. Click on the “Load previous search results” and pick a .bmp file that is stored in the plugin_out/torrentscout_out folder of your run:



A file explorer will prompt you to pick a .bmp file that contains the search result. The names of the files are what you entered in the alignment search form (followed by .bmp)



The search results are also displayed as thumbnail images in the plugin page:



Proton Experiments

The plugin works on any chip, including proton chips. For Proton experiments, the plugin will compute the index files and heat maps for all blocks. It will also compute an overview heat map for the entire Proton experiment.

Alignment searches are done on all blocks, and each block will contain a corresponding heatmap results file.

Please go to the [LifeTech Community](#) or [GitHub](#) page for more documentation and source code, or send an email to [Chantal Roth](#) for help or feedback.