

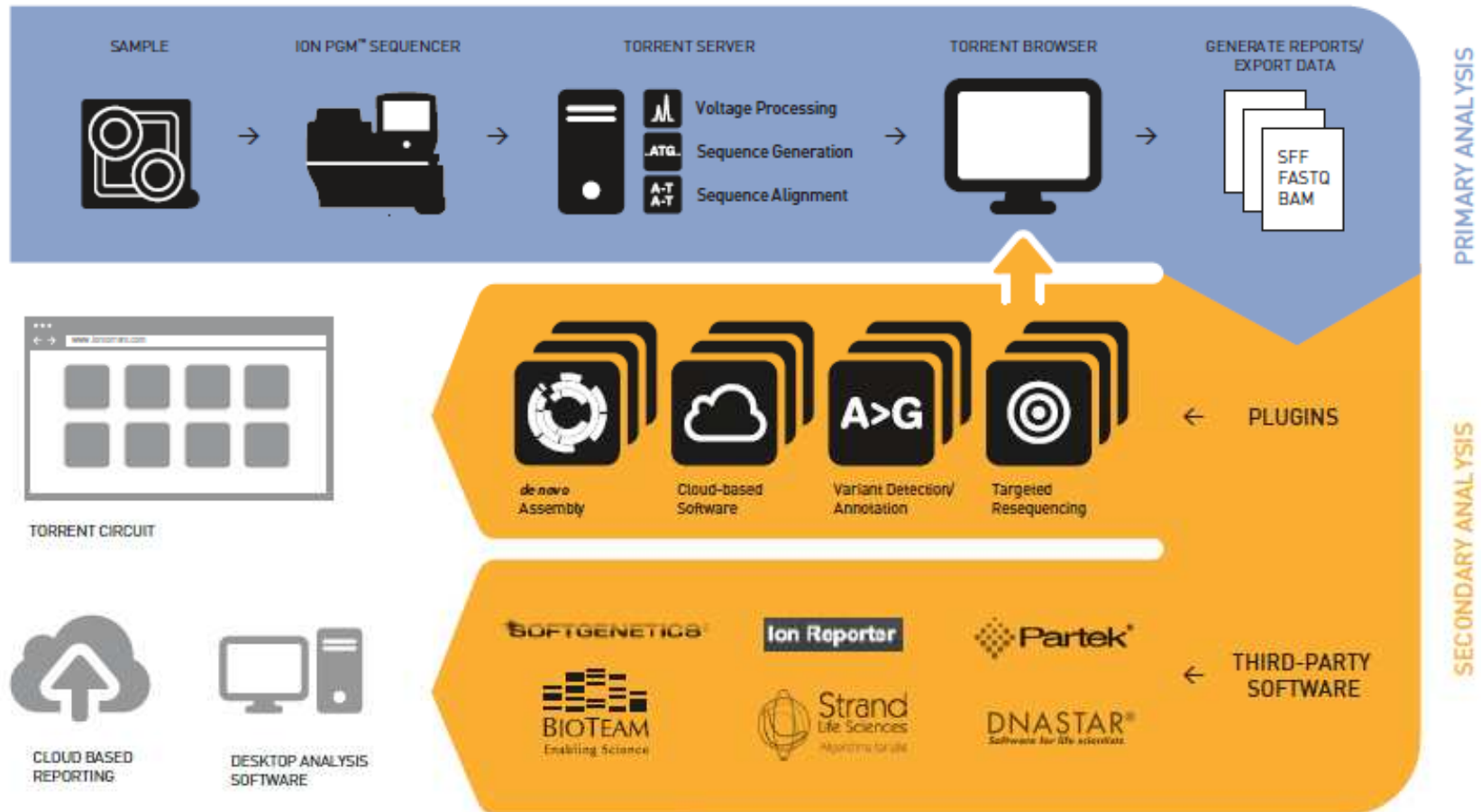


● Ion University: Data Analysis

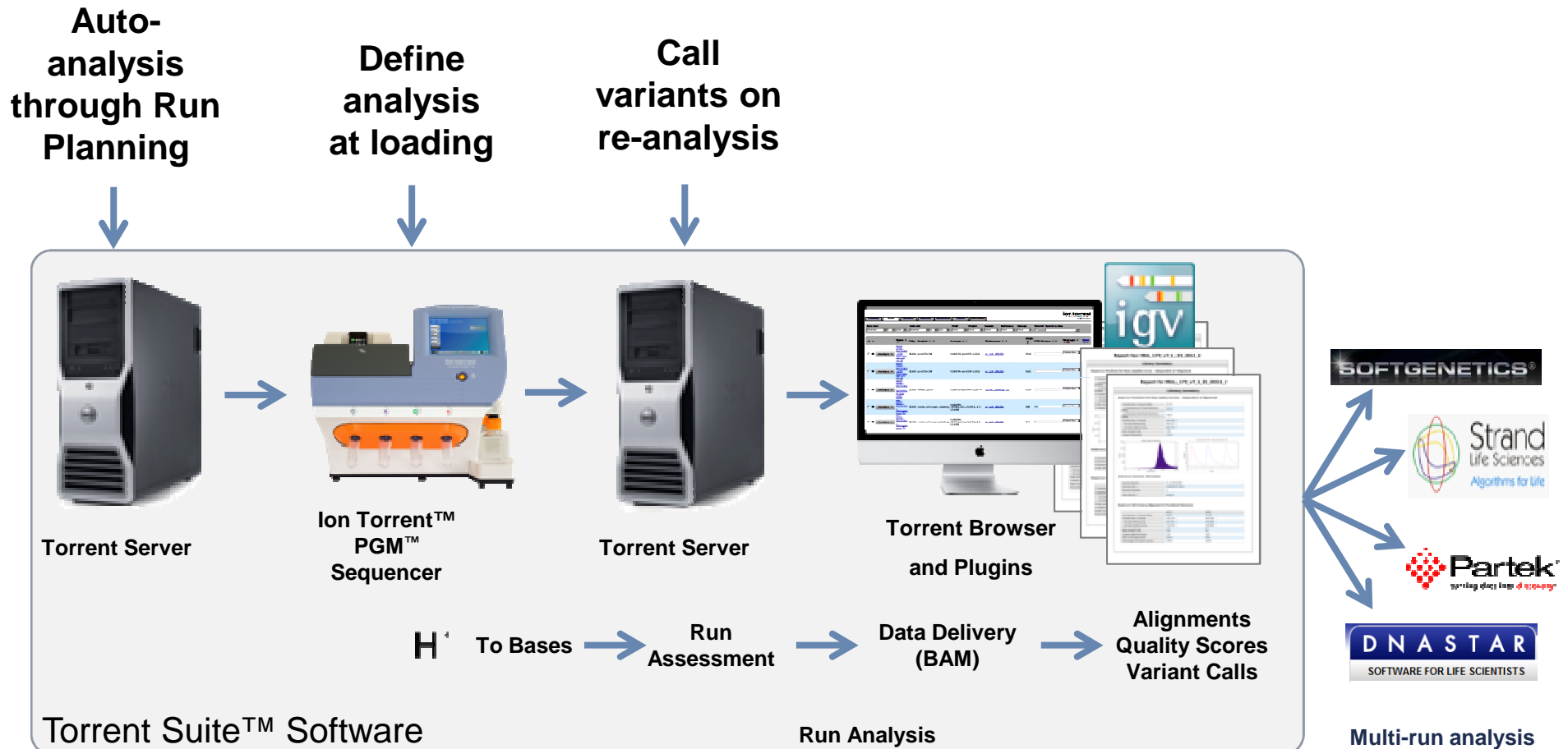
● The world leader in serving science

Torrent Server and Torrent Suite™ Software

Web-based data delivery with integrated alignment, variant calling, and data analysis plugins



Example Workflow: Variant Calling



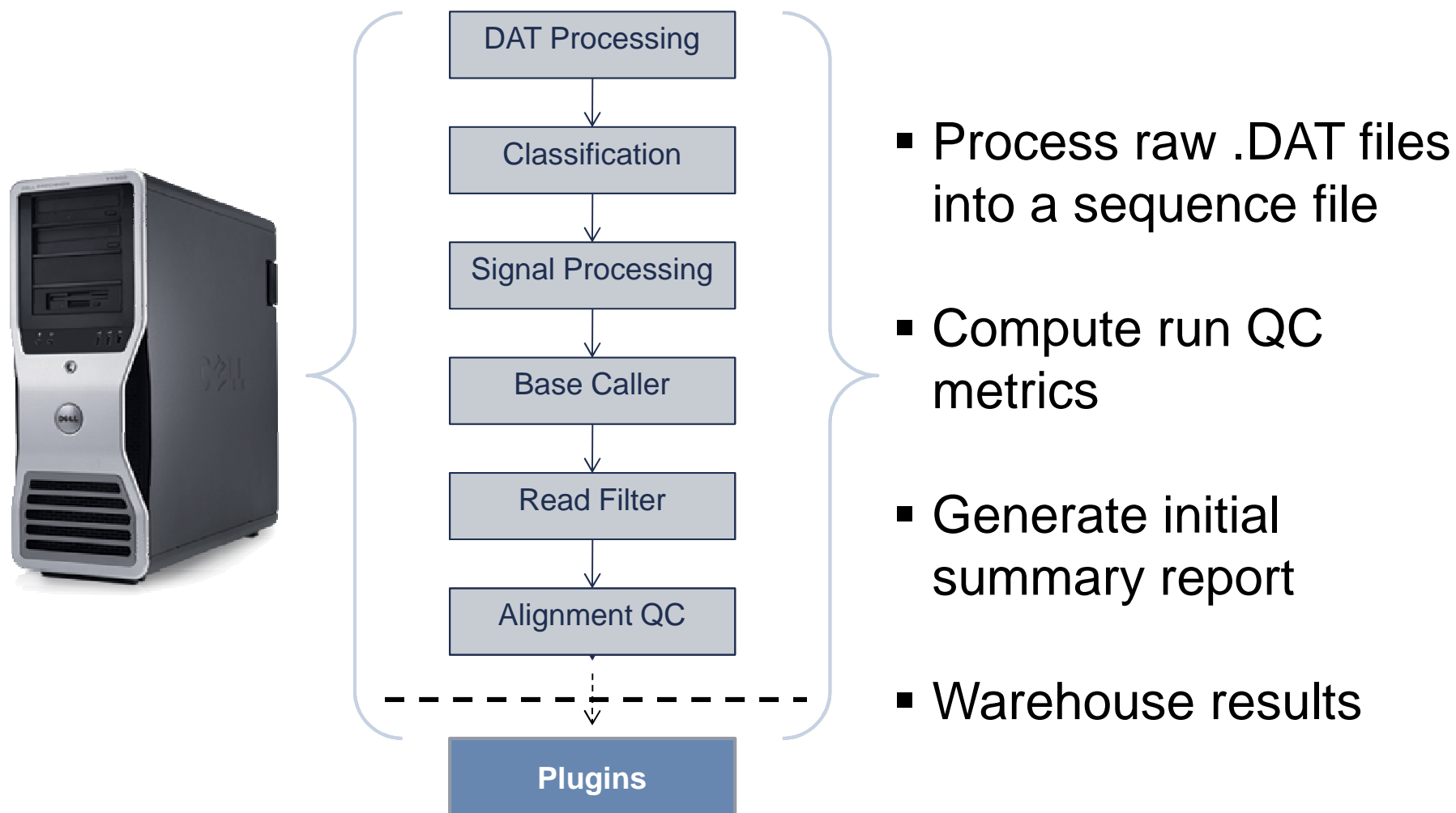
Preconfigured Torrent Server

- Preloaded with Torrent Suite™ Software
- Converts raw signal to base calls
- Performs preliminary alignment to a reference genome allowing run quality assessment
- Torrent Browser plugins
- Hosts web portal for data review and distribution to collaborators



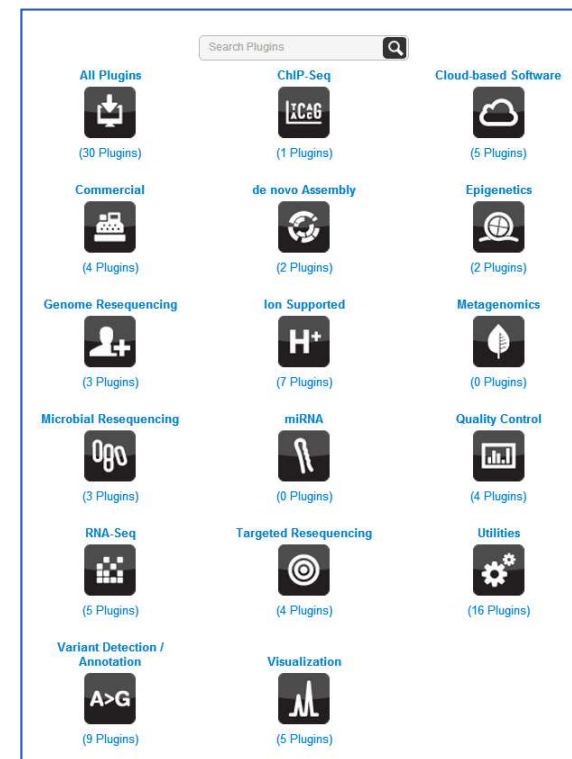
** Torrent Server is not designed to be a shared computing platform. It was engineered to be a **dedicated server** focused on the primary analysis of Ion Torrent™ data.

Torrent Server Analysis Pipeline



Torrent Browser Plugin Store & Torrent Suite™ Plugins

Your application. Your data. Your Plugin.



The App Store for Torrent Suite™ software

http://ioncommunity.lifetechnologies.com/community/products/torrent_browser_plugin_store

Torrent Pipeline – Approximate Data Sizes*

Process Description	File Types	Ion 314™ chip	Ion 316™ chip	Ion 318™ chip	Ion PI™ chip
Raw Voltage Data	DAT	28 GB	129 GB	242 GB	2 TB
Signal Processing	WELLS	1 GB	7-9 GB	12-15 GB	80-100 GB
Base Calls - Aligned	BAM	0.1 GB	1.7-2.0 GB	2.7-3.0 GB	40-60 GB
Base Calls - Flow	SFF	1 GB/	4.5-6.0 GB/	8-10 GB/	100-120GB
Base Calls - Base	FASTQ	0.2 GB	1-1.25 GB	1.8-2.25 GB	20-30 GB

**v3.0 250 bp run (500 flows) Sept2012. The information presented here is an approximation.
User experiences may vary.*

How many runs can be stored?

Process	Equipment	Ion 314™ chip	Ion 316™ chip	Ion 318™ chip
Data Acquisition	PGM™ Sequencer	40 runs	8 runs	5 runs
Raw Data	Torrent Server	300 runs	65 runs	40 runs
Archived Data	Torrent Server	4100 runs	880 runs	530 runs

File sizes for a typical run of 520 flows that enables 200 base pair read length.
The Torrent Server has 12 TB of space with n=2 redundancy.

**The information presented here is an approximation. User experiences may vary.*

Analyze twice the data in half the time

TSS 3.4

Total runtime ~ 21 hours with TSS 3.4

Ion Proton™ Run
(3.3 hrs)

(7G total throughput, 168 bp reads)

Data Processing (7.0 hrs) on Proton

Data Analysis (18 hrs) on Torrent Server

TSS 4.0

Total runtime ~ 8 hours with TSS 4.0

Ion Proton™
Run (2.4 hrs)

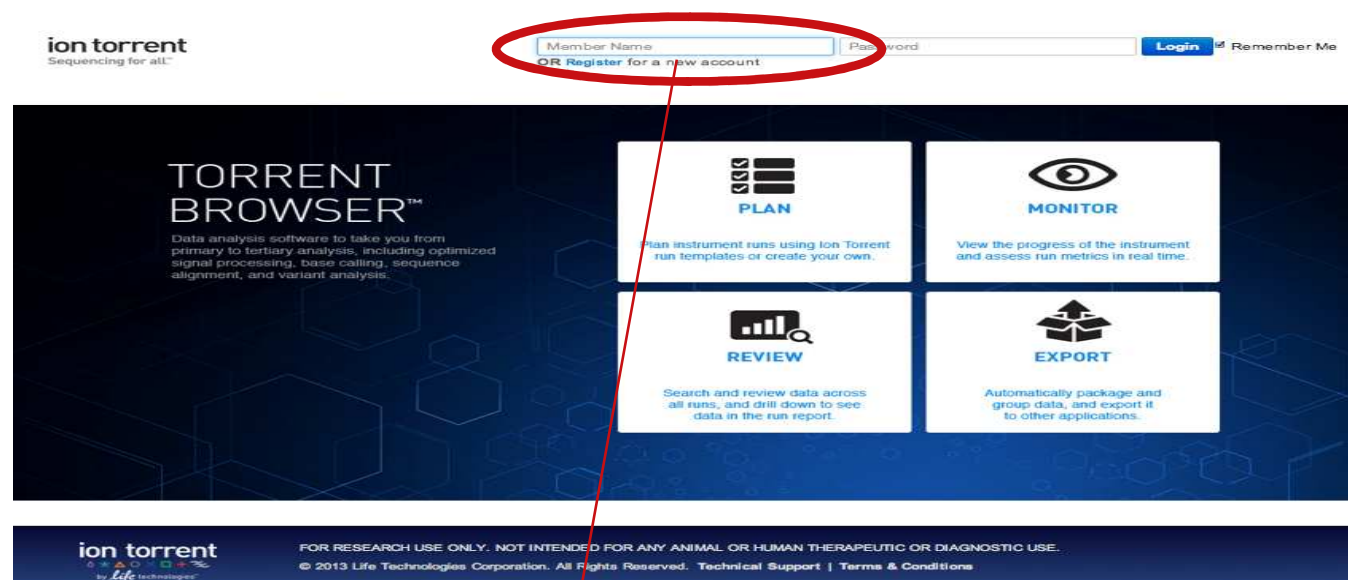
(14.5G total throughput, 200 bp reads)

Data Processing (6.4 hrs) on Proton

Data Analysis (5.6 hrs) on
Torrent Server

440 flow TargetSeq exome run
Start: Ion Proton™ instrument run starts
End: Availability of complete sequence and mapping data

Torrent Browser

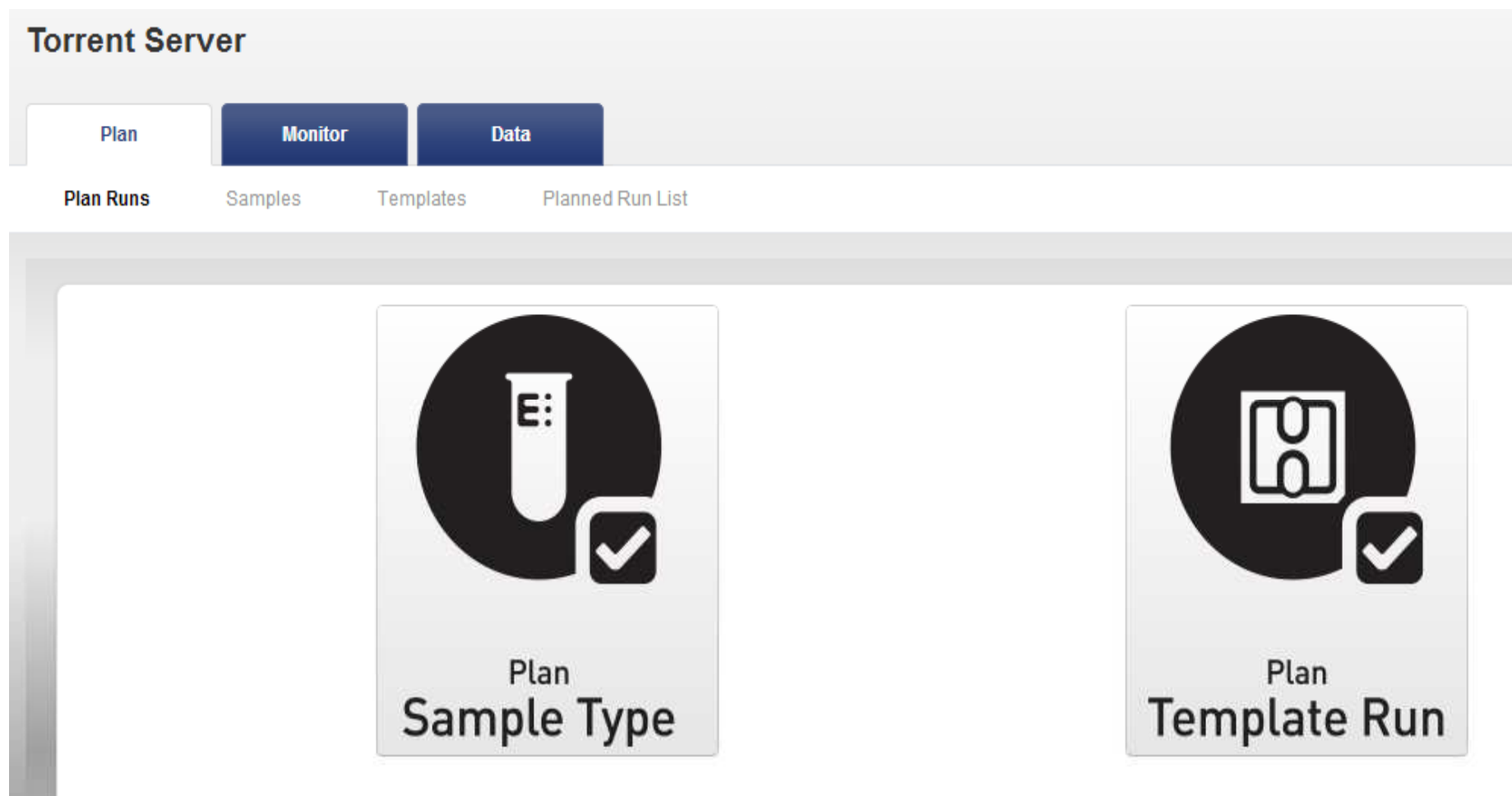


- Plan run
- Monitor run
- Access data
- Export data

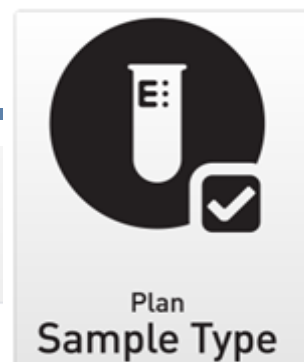
[Login](#)

Support for all Ion instruments

Planning a Run by Sample or Template



Planning a Run by Sample



Frederick Training Server

Plan

Monitor

Data

Plan Runs

Samples

Templates

Planned Run List



Sample Sets

Import Samples from File

Enter Samples Manually

Sample Attributes ▾

Sample Sets / Import Samples

Import Samples

1 : Select Sample File to Import :

Select file

Sample File (csv)

Sample File Format

Click button to download sample file format

2 : Select a Sample Set to Receive Samples :

Search sample set names

Search

Add Sample Set...

3 : Save & Finish

Uploads, parses & validates file, and saves if no errors found
No samples imported yet

Summary

Create sample set(s) with samples in the imported sample sheet

Add Sample

Sample Name (required) : Required

FYI: Sample name in the sample set cannot be changed since this sample set has been planned.

Sample External ID : Optional

Gender :

Description : Optional

Role :

Relationship Group :

FYI: A unique number (e.g., 1) to designate multiples

Cancel

Done

Planning a Template Run

Create new run templates and plan instrument runs. You can use Ion Torrent templates or create new ones that match your own protocols.



Whole-Genome Seq | [Add New Template](#) | [Plan New Run](#)



RNA Seq | [Add New Template](#) | [Plan New Run](#)



AmpliSeq DNA | [AmpliSeq.com Import](#) | [Add New Template](#) | [Plan New Run](#)



AmpliSeq Exome | [AmpliSeq.com Import](#) | [Add New Template](#) | [Plan New Run](#)



AmpliSeq RNA | [AmpliSeq.com Import](#) | [Add New Template](#) | [Plan New Run](#)



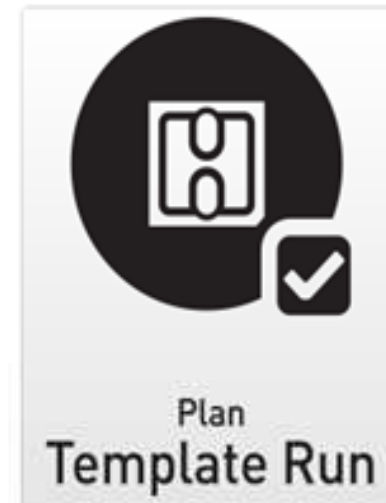
TargetSeq | [Add New Template](#) | [Plan New Run](#)



16S Target Sequencing | [Add New Template](#) | [Plan New Run](#)



Generic Sequencing (Other) | [Add New Template](#) | [Plan New Run](#)



Set up a run

- Use pre-installed template (application/product-based) or Create your own
- Start run on PGM™ sequencer using run code of planned run

Plan Tab

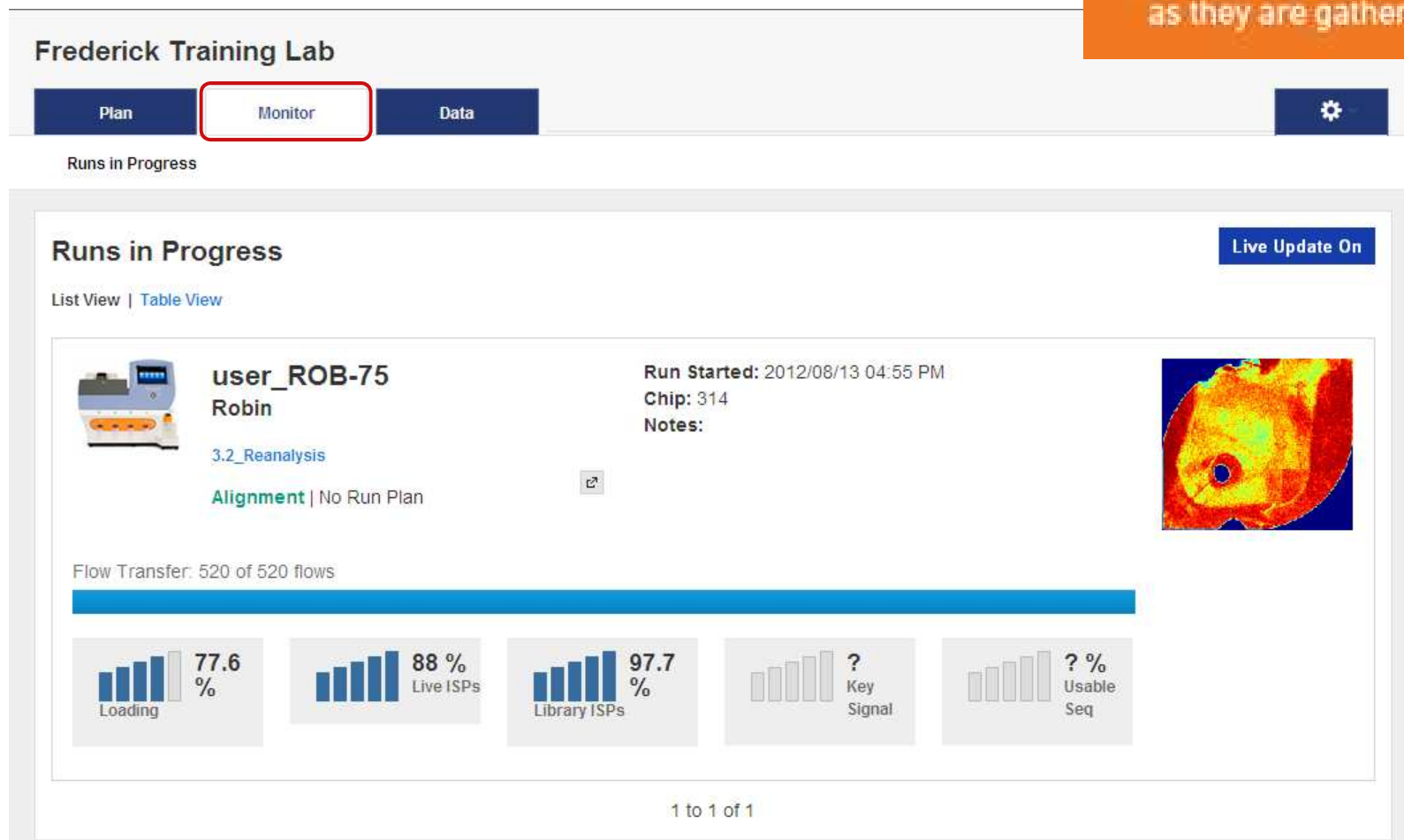


Sample or Template Run Planning

- Reusable experimental designs,
 - Run Parameters
 - Ion Reporter (Integrate IR workflow & sample grouping selection)
 - Application (Whole genome, Ion Ampliseq™, Targeted Seq, RNA Seq, Generic sequencing)
 - Kits (Ion kit, Barcode kit...)
 - Monitor thresholds (Bead Loading, Usable Sequence, Key Signal)
 - Reference (Fasta and BED files)
 - Plugins
 - Output
 - Plan

Monitoring a Run

View the progress of the instrument in real time and assess the run metrics as they are gathered.



Track your run in progress

Reviewing Data - Run Reports

Search and review across all of your runs and drill down to see your data in the run report. View your data grouped into projects.

Frederick Training Server

Plan Monitor **Data**

Completed Runs & Results Projects

Completed Runs & Results

List View | Table View

Page is static until refreshed Auto Update

Filter Data

List of runs

Run Name	Sample	Sample Set	App.	Run	Analysis	Status	Chip	Report Name	Reference	Barcode	Flows	Total Reads	Mean Read Len.	Q20 Bases	Output
☆ AmpliCancer_8_Crop200			05/04/12	12/05/13	Completed	316	AmpliCancer_8_Crop200...	hg19	IonXpress		520	13.1 k	136	1.38 M	1.79 M
☆ R_2013_08_29_23_36_01_u...			08/29/13	11/16/13	Completed	318	Auto_user_CAT-39-ECBC...	PRRS	RNA_Barcode_None		500	1.68 M	87.0	124 M	147 M
☆ R_2013_10_23_18_08_58_u...			10/23/13	11/16/13	Completed	314	Auto_user_CAT-40_463	e_coli_d...			500	419 k	227	86.2 M	95.2 M
☆ AmpliCancer_8			05/04/12	11/16/13	Completed	316	Auto_AmpliCancer_8_462	hg19	IonXpress		520	2.95 M	79.0	210 M	235 M
☆ R_2013_11_15_17_10_17_u...	PC		11/15/13	11/15/13	Completed	314	Auto_user_CAT-42_460								
☆ R_2013_11_15_14_32_54_u...	MICHELLE		11/15/13	11/15/13	Completed	314	Auto_user_BAT-121_459								
☆ R_2013_11_15_14_22_18_u...	SAL		11/15/13	11/15/13	Completed	314	Auto_user_CAT-41_458								
☆ R_2013_11_15_09_36_24_u...	e.coli		11/15/13	11/15/13	Completed	314	Auto_user_BAT-120_456								

Run Summary: R_2013_11_15_14_32_54_user_BAT-121

Read Summary: Unaligned

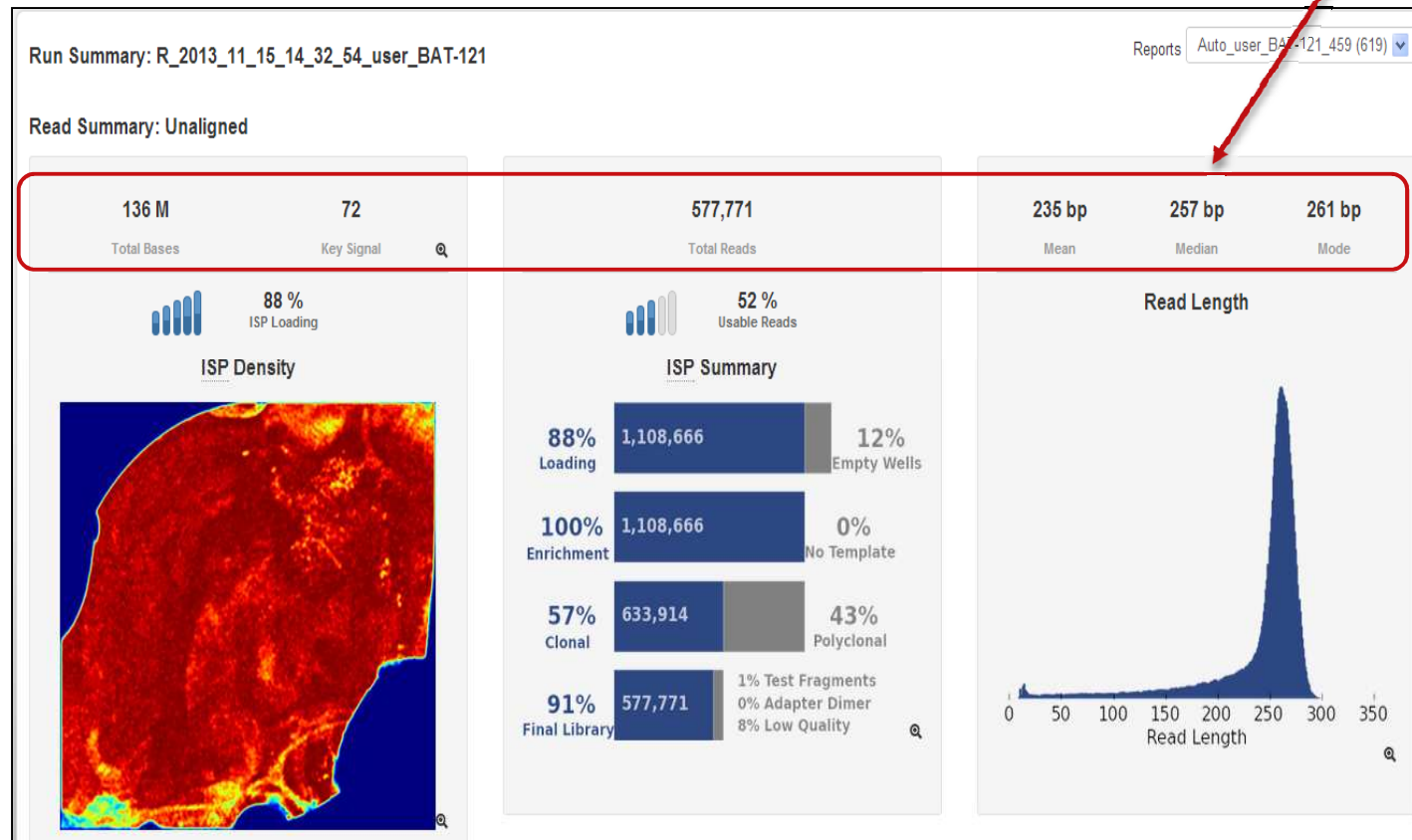
ISP Density

ISP Summary

Read Length

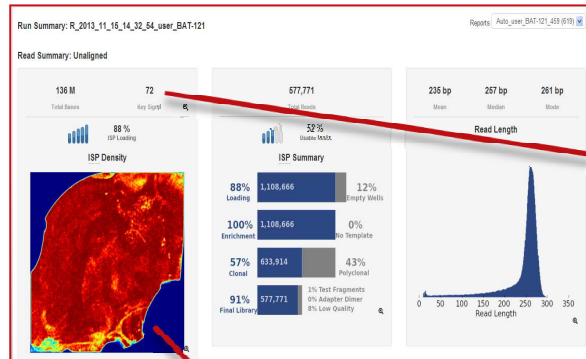
Run Report – Summary of Unaligned reads

New Median and Mode metrics added

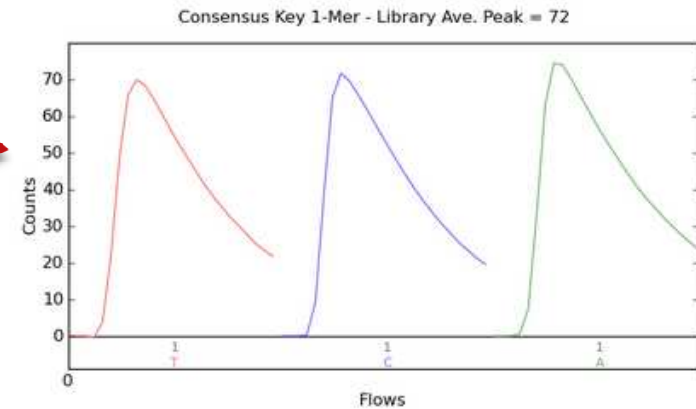


Click for details of each section

Run Report – Chip Loading & Key Signal



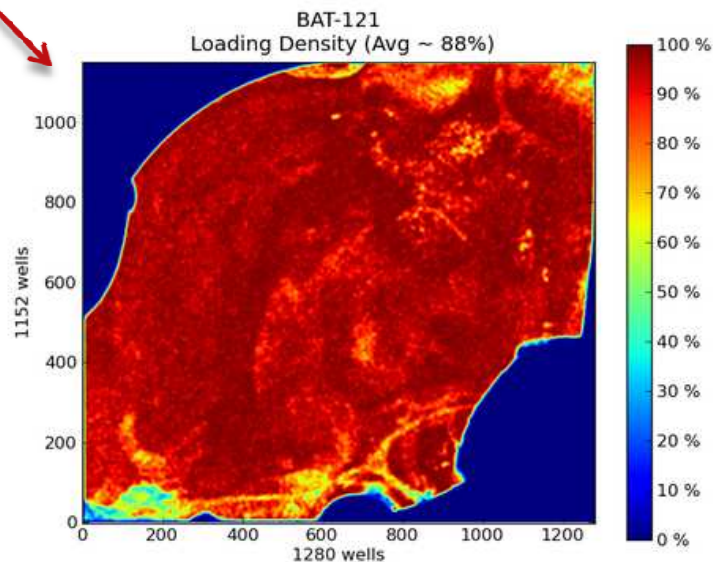
Key Incorporation Traces



Consensus Key 1-mer Graph

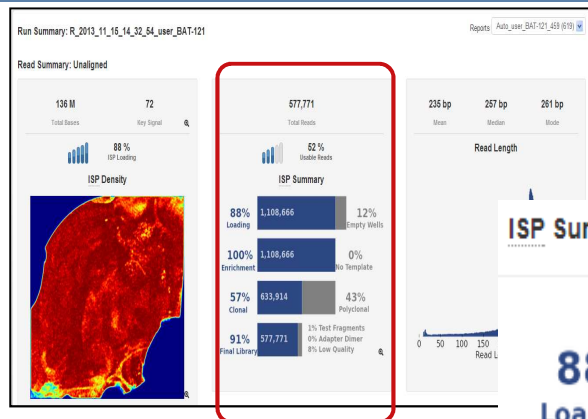
Signal strength of the first three bases of the key

ISP Density

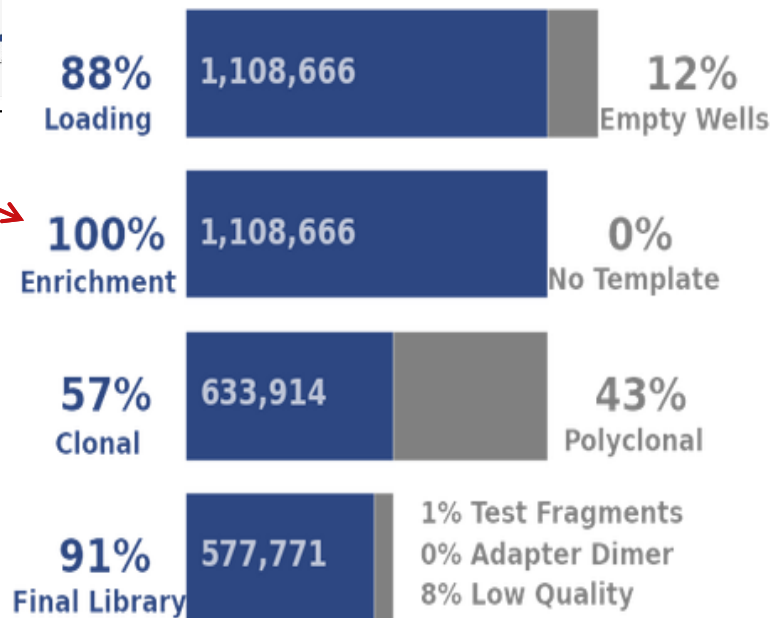


Visualization of loading density

Run Report – Chip Well Details



ISP Summary



Chip well details

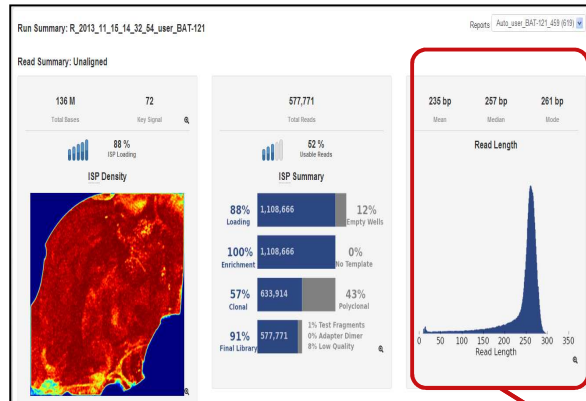
Addressable Wells	1,262,519	
With ISPs	1,108,666	87.8%
Live	1,108,666	100.0%
Test Fragment	6,167	00.6%
Library	1,102,499	99.4%

Library ISP details

Library ISPs	1,102,499	
Filtered: Polyclonal	474,752	43.1%
Filtered: Low Quality	49,862	04.5%
Filtered: Primer Dimer	114	00.0%
Final Library ISPs	577,771	52.4%

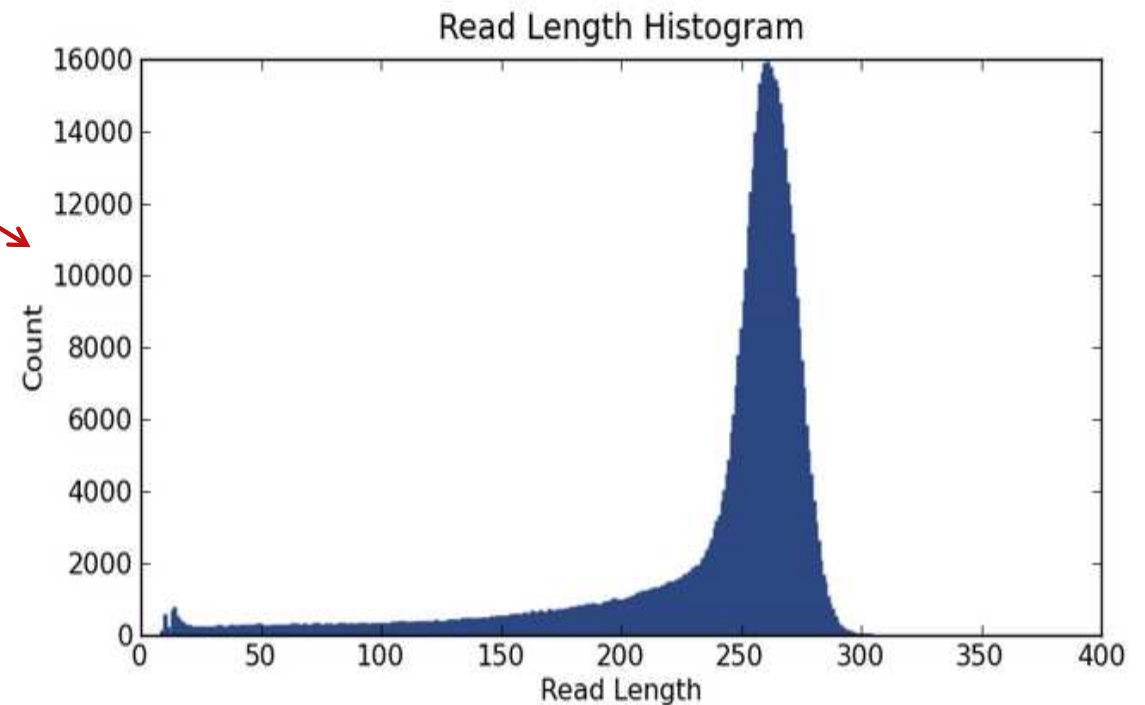
- Measure loading performance and enrichment efficiency
- Quantify read filter metrics: assess polyclonality and low quality reads

Run Report – Read Length Details



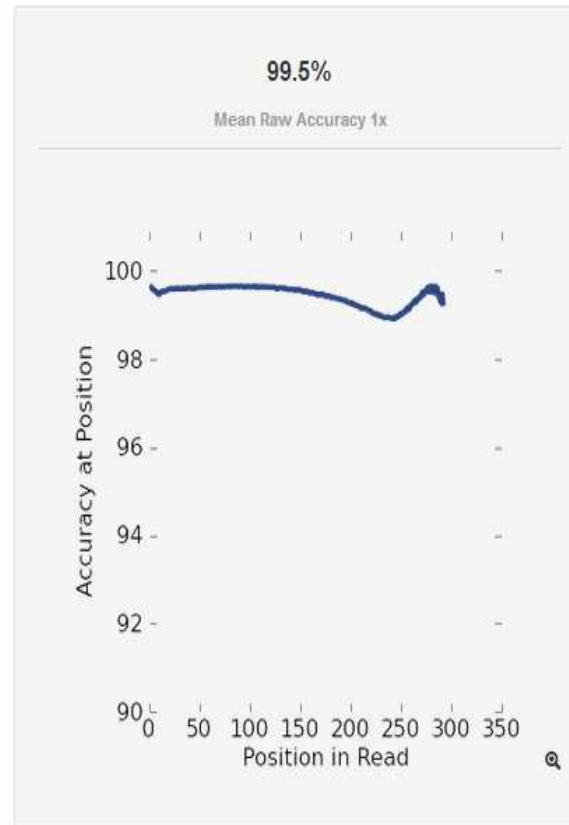
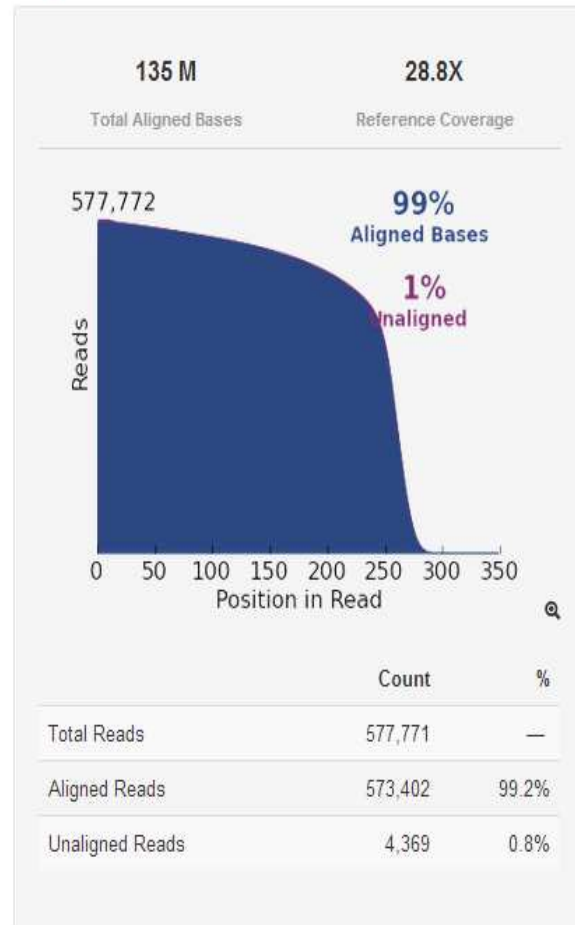
Histogram of read length for all reads in output files

Read Length Details



Run Report – Reads Aligned to Reference

Aligned to E. coli DH10B



131 M
AQ17 Total Bases

	AQ17	AQ20	Perfect
Total Number of Bases [bp]	131 M	126 M	103 M
Mean Length [bp]	237	231	195
Longest Alignment [bp]	325	322	320
Mean Coverage Depth [x]	28.1	27.0	22.1

Run Report – Output Files

Hi, ionuser Help Sign Out

Reanalyze Summary PDF Plugins PDF Classic Report

Reports 3.2_Re-analysis (241)

3.0_Re-analysis | Frederick Training Lab - Torrent Browser Page 1 of 5

Run: R_2012_09_13_12_29_55_user_CAT-11

Run Summary

Unaligned

155M 71 660

86% Read Loading

ISP Density

3.0_Re-analysis | Frederick Training Lab - Torrent Browser Page 2 of 5

Aligned to E. coli DH10B

155M 33.2X 99.1%

Plugin Output

Test Fragments

File format of older

Output Files

File Type	Unaligned Reads	Aligned Reads
Library	BAM SFF FASTQ	BAM BAI
Barcodes	BAM SFF FASTQ	BAM BAI

Barcode Name	Sample	Bases	>=Q20 Bases	Reads	Mean Read Length	Read Length Histogram	Files
No barcode	None	3,919,092	3,098,417	42,495	92 bp		BAM BAI
IonXpress_007	None	809,623,089	671,266,731	4,673,571	173 bp		BAM BAI

10 items per page 1 - 2 of 2 items

File formats produced for extensive data analysis via third party software packages (offered on Webstore) or other bioinformatics tools.

Plugins

Output Files

File Type	Unaligned Reads	Aligned Reads
Library	BAM	BAM BAI

Plugin Summary

Test Fragments

Analysis Details

Support

Software Version

Select plugins to run

Select a plugin

[Alignment](#) — v4.0-r77189

[coverageAnalysis](#) — v4.0-r78587

[coverageAnalysisLite](#) — v4.0.71113

[CreatFastqFile](#) — v3.6.63335

[EnhancedQCwithPartekFlow](#) — v1.9

[ERCC_Analysis](#) — v4.0-r76483

[FastQC](#) — v3.4.1.1

[FastqCreator_3.6.2](#) — v3.6.0-r57238

[FileExporter](#) — v4.0-r76310

[IonReporterUploader](#) — v4.0-r77705

[PartekFlow](#) — v1

[TorrentSuiteCloud](#) — v4.0-r72612


Close

Reviewing Data - Projects

Search and review across all of your runs and drill down to see your data in the run report. View your data grouped into projects.

Frederick Training Lab

Hi, iona

Plan Monitor **Data** 

Completed Runs & Results **Projects**

Projects

[Create a New Project](#)

Date: 2005-07-16 - 2012-10-03 Search Names: [Clear](#) [Go](#)

Action	Name	Results	Last Modified
edit delete log	PGM_training	7	2012/10/01 12:38 PM
edit delete log	class		
edit delete log	training		
edit delete log	maseq-inhouse		
edit delete log	sales		
edit delete log	project1		
edit delete log	Florida		

[Delete Project](#)

Result Sets in class

Date: 2005-07-16 - 2012-10-03 [Go](#)

Selected	Name	Status	Reference	Date
<input type="checkbox"/>	Auto_BAT-65_125	Completed	e_coli_dh10b	2012/04/20 05:47 PM
<input type="checkbox"/>	Auto_BAT-66_127	Completed	e_coli_dh10b	2012/05/02 10:05 PM
<input type="checkbox"/>	Auto_BAT-64_124	Completed	e_coli_dh10b	2012/04/19 10:54 PM
<input type="checkbox"/>	Auto_BAT-67_129	Completed	e_coli_dh10b	2012/05/03 05:51 PM
<input type="checkbox"/>	Bat-67-TS2.2	Completed	e_coli_dh10b	2012/05/16 01:30 PM

Project = set of runs

Filtering – Which reads make it to alignment?

For a read to be represented, the following must be achieved:



- Well is "positive" for an Ion Sphere™ Particle (determined by the Ion Sphere™ Location Solution)
- Well produced strong signal across each of the first three key nucleotides
- Read contains a minimum of 8 bases
- The key of the read is an **exact** match to the defined library key
- Remove polyclonal reads with mixed read filter
- The read fits the “expected signal model”

<http://ioncommunity.lifetechnologies.com/docs/DOC-7011> (p. 327)

Read Trimming

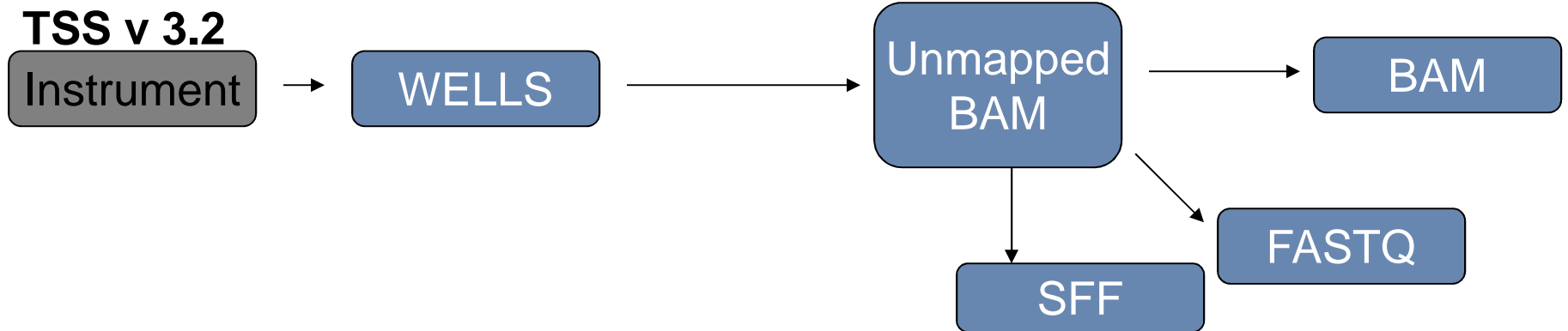
Each reported read is subject to removing lower quality bases according to the following rules:



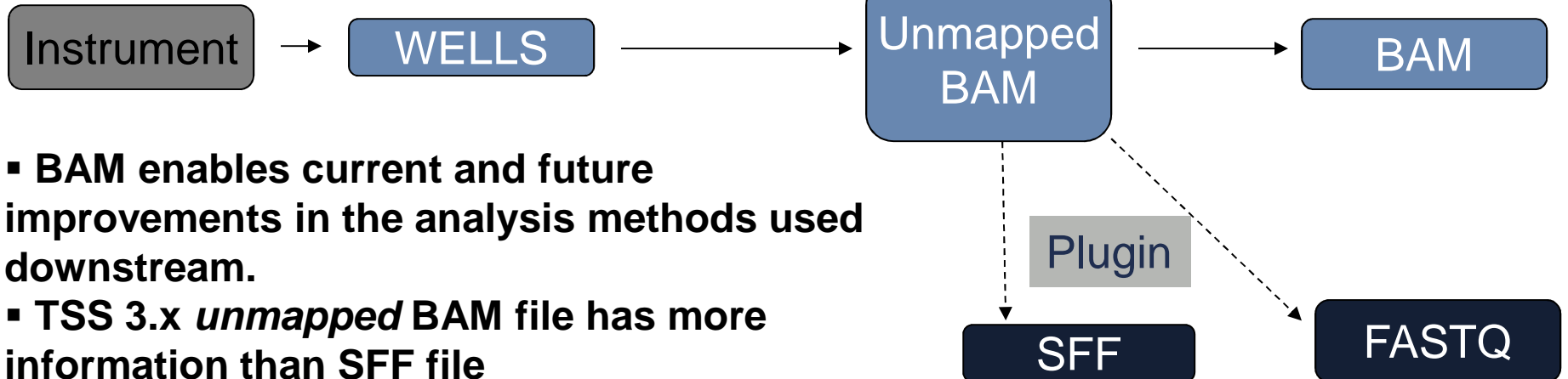
- First four bases of the 5' end that contain the key are removed.
- No quality trimming occurs at the 5' end.
- At the 3' end, if sequencing occurs through the insert to the P1 adapter, then the P1 adapter is removed.
- Remove lower quality base calls based on signal intensities
- The 3' end of the read is trimmed to the point where the average quality score is at least Q15 across a moving 30 bp window

<http://ioncommunity.lifetechnologies.com/docs/DOC-7011> (p. 326)

Transition from SFF to BAM for Torrent Suite™ Software 3.4 and later




TSS v 3.4 and later



- BAM enables current and future improvements in the analysis methods used downstream.
- TSS 3.x *unmapped* BAM file has more information than SFF file
- TSS 3.x *unmapped* BAM file typically less than half the size of the corresponding SFF file.

SFFCreator and FASTQCreator Plugins


- FastqCreator — v3.4.48073

Completed 

To download: "Right Click" -> "Save Link As..."

[R_2012_11_15_11_09_14_user_B32-299--R160826-B32_HSMnonBC_314_R1-CF_Auto_user_B32-299--R160826-B32_HSMnonBC_314_R1-CF_2.fastq](#) 132636K

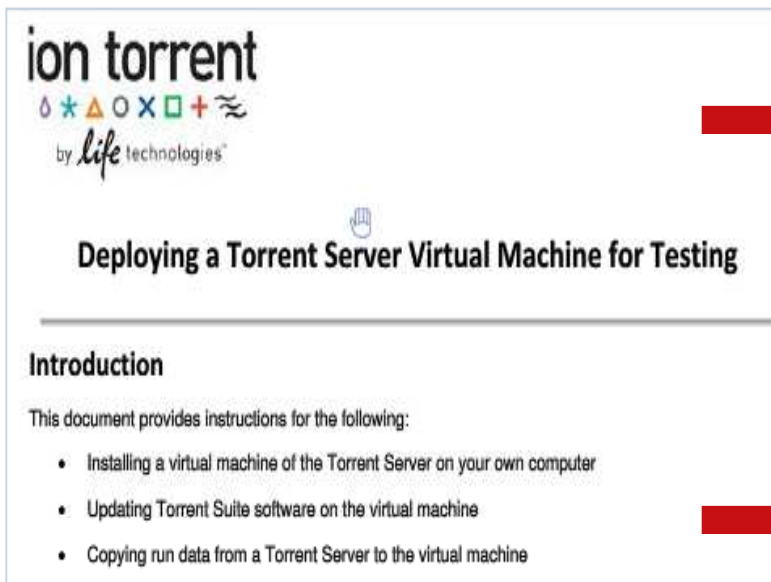
- SFFCreator — v3.4.48073

Completed 

To download: "Right Click" -> "Save Link As..."

[R_2012_11_15_11_09_14_user_B32-299--R160826-B32_HSMnonBC_314_R1-CF_Auto_user_B32-299--R160826-B32_HSMnonBC_314_R1-CF_2.sff](#) 730970K

Testing Software Updates



ion torrent
by *life* technologies

Deploying a Torrent Server Virtual Machine for Testing

Introduction





This document provides instructions for the following:

- Installing a virtual machine of the Torrent Server on your own computer
- Updating Torrent Suite software on the virtual machine
- Copying run data from a Torrent Server to the virtual machine



Try Torrent Browser on the cloud

We recommend reviewing this new software on the cloud prior to download


1. Please watch this video, which shows how to use the cloud instance, **first**.
The link is here  [How To Set Up A Torrent Suite Cloud Account](#)
2. If you are running version TB 2.2, or earlier, on your local server please also watch this video showing how to modify your server to run the cloud plugin
 [Setting Up Your Torrent Server for the Torrent Suite Cloud Plugin](#)
3. Link for cloud registration is here <https://torrentsuite.lifetechnologies.com/>
4. Link for Plugin Store is here  [Torrent Browser Plugin Store](#)
5. For any technical issues use this e-mail address  pod@penguincomputing.com

<http://ioncommunity.lifetechnologies.com/docs/DOC-6825>



Experience the new version using a virtual machine

Download the VM for 3.0 [HERE](#)

The Instructions are here  [Torrent Server Virtual Machine](#)

Watch this [Video showing how to set up a VM](#) for complete instructions around this process

Torrent Server Virtual Machine

*Safe environment for testing,
i.e., plugins, software updates*



Watch the Torrent Browser 3.0 Videos (also applicable to Torrent Browser 3.2)

We have prepared several videos that review how the new Torrent Browser Software user interface works and we also have provided an HTML model which allows you to review the design of the new software; please review and let us know what you think:

Below are a set of videos to introduce you to the streamlined user interface of Torrent Browser 3.0

-  [Planning a Run in Torrent Browser 3.0](#)
-  [Monitoring in Torrent Browser 3.0](#)
-  [Data in Torrent Browser 3.0](#)

You can review the upcoming version of Torrent Browser Software that was shown in the videos above using the [clickable HTML model](#) (recommended browsers Firefox or Chrome).

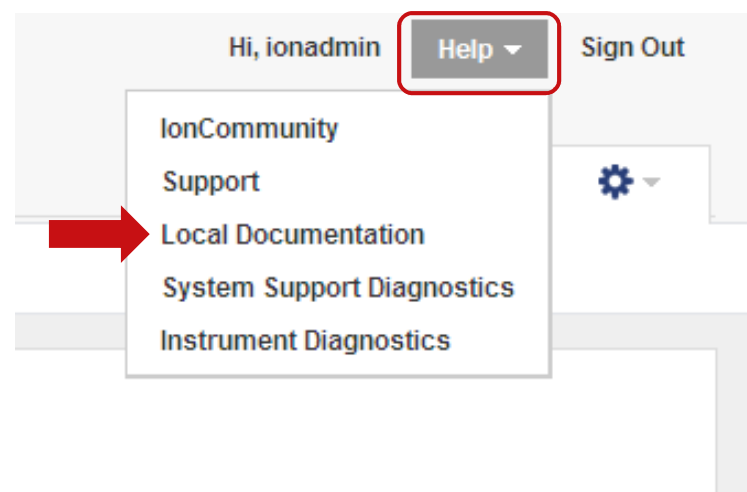
<http://ioncommunity.lifetechnologies.com/docs/DOC-1921>

Ion Torrent™ Software Support Policies

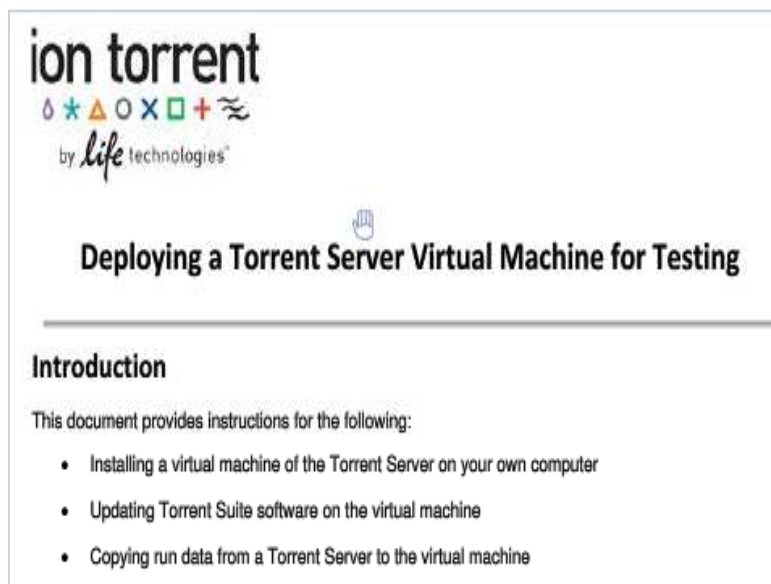
Available Help Documents



- Torrent Suite™ Software User Documentation
 - Torrent Browser User Interface Guide (aka tab guide)
 - Torrent Browser Analysis Report Guide
- Torrent Suite™ Software Administrator Documentation
 - Developing Your System
 - Maintaining Your System
 - Administration
 - Troubleshooting
- Release Notes



Available Resources



Torrent Server Virtual Machine

*Safe environment for testing,
i.e., plugins, software updates*

<http://ioncommunity.lifetechnologies.com/docs/DOC-1921>

The screenshot shows the 'HIGHLIGHTED DATASETS' section of the Ion Community website. It includes a table with columns: Name, Application Type, Chip Type, and Date Posted. The table lists several datasets, including E. coli DH10B and E. coli EHEC runs.

Name	Application Type	Chip Type	Date Posted
E. coli DH10B - 400bp Mode w/ >99% Per Base Accuracy	Resequencing	316	June 1, 2012
E. coli DH10B - May 2012 Grand Challenge Paired-End Dataset	Resequencing	318	May 1, 2012
E. coli EHEC - 300bp Run	Resequencing	318	May 1, 2012
E. coli EHEC - May 2012 Kits and Chemistry	Resequencing	318	May 1, 2012
E. coli DH10B - >900Mb AQ17 w/ 99.999% Consensus Accuracy	Resequencing	316	March 1, 2012

[Show More](#)

Example data sets

**Ion Community > Datasets >
Datasets by Chip**

Included Torrent Server / Torrent Suite™ Software Support

Torrent Suite™ Software is open source software

- Ion Torrent Field Bioinformatics Specialists will support Torrent Suite™ software, but *not* source code
- Source code is available on Ion Community, Torrent Dev section
- If working on source code, must install on platform other than Torrent Server



Ion Trainings

[Ion Torrent Community](#) → [Programs & Events](#) → [Training](#)

WELCOME TO ION TORRENT TRAINING!

Welcome to the Ion Community Training Page!

We recommend you start with the new Training Decision Tree to determine what training path is best for you: [Ion Torrent Training Decision Tree](#)

ION INTRODUCTORY TRAINING: FOR NEW USERS



Self-paced Training

[Ion Torrent Workflow Tutorials](#)

[How to get started with Torrent Suite Software](#)



Instructor-led Training

PGM™ System Operational Training US/CAN, [register >](#) EU, [register >](#)

NEW! Ion Data Analysis Essentials US/CAN, [register >](#)

Introduction to Torrent Suite Software Web Course US/CAN, [register >](#) EU, [register >](#)

http://ioncommunity.lifetechnologies.com/community/programs_and_events/training

Bioinformatics Training and Services

lifetechnologies.com/biofxservices

Item	Bioinformatics data analysis	Time (hrs)
1	Targeted Resequencing	3
2	Amplicon Sequencing	3
3	Exome Sequencing	3
4	Whole Genome*	3
5	AmpliSeq	3

Item	IT professional services	Time (hrs)
18	IT Consulting Services	1
19	Remote Software Updates for Torrent Server	1

20 hours to use—however you choose

Ordering information
SKU: ZGPCSCIONBFX

Item	Bioinformatics training	Time (hrs)
6	Ion Data Analysis Essentials (Life Technologies site) ↗	14
7	Intro to Torrent Suite™ Software ↗	3
8	Ion Variant Calling Data Analysis*** ↗	3
9	Ion AmpliSeq™ DNA Data Analysis ↗	3
10	Ion AmpliSeq™ RNA Data Analysis ↗	3
11	Ion Reporter™ Software Workflow ↗	3
12	Variant Calling Analysis & Interpretation ↗	2
13	RNA-Seq Data Analysis** ↗	2
14	smRNA Data Analysis** ↗	1
15	De novo Assembly* ↗	1
16	Targeted Sequencing Introduction / Overview** ↗	1
17	Linux Basics ↗	3

Introduction to Torrent Suite™ Software: An Interactive Web Course

Who Should Attend?

- 3 hour interactive, online session
 - Instructor led
 - Practice with data sets
- Ion PGM™ or Proton™ Users with no previous experience with Torrent Suite™ Software and are interested in a data and software-focused class with hands-on experience with Torrent Suite™ Software
 - New Ion Users who have taken the Ion PGM™ or Proton™ Systems Course and would like a refresher and the opportunity to for additional hands-on experience with the Torrent Suite Software

Prerequisites:

Ownership of a Ion PGM™ or Proton™ System or affiliation with a laboratory that has purchased a system. Browser Requirements for interactivity: Firefox or Google Chrome

Course Description:

Jump-start your Ion Torrent data analysis with this interactive web course which will introduce and provide hands-on training for the Torrent Suite™ Software. Each attendee will be given access to the Torrent Suite™ Software and data sets with exercises to guide them through hands-on scenarios.

Time Zone Conversion: Not located in the US/Pacific time zone? See what time it is in your [local time zone](#).

[Click here for current training promotions>>](#)

Tell a colleague about this course. Copy the following URL:
<https://learn.lifetechnologies.com/courses/view/id/303>






Torrent Server IT Service Contract

- Using Torrent Suite Software is as simple as using any web interface
- Keeping it updated and managing the data requires some Linux® software experience.
- If you don't have it, the BioTeam can help.
- Order it from the Web Store.

Product	Part #
3 month support contract	4465993
12 month support contract	4465994



Bioinformatics Services

Service Product	Description	Part Number
Variant Caller Annotation 	Data analysis for enhanced variant annotation	4473258
IT cluster install (new) 	High Perf Cluster Install Svc	SV000212
Bioinformatics Consulting (new) 	Remote or on-site service for data analysis and troubleshooting	SV000211
IT professional services 	Consulting for software installation	SV000206
On-site software upgrades for Torrent Server 	Service for Torrent Server software upgrades	SV000010

- Provided by Field Bioinformatics Specialists or Field Service Engineers
- Contact your sales representative

Ion Community - Torrent Suite™ Software

http://ioncommunity.lifetechnologies.com/community/products/torrent_suite

Ion Torrent Community → Products → Torrent Suite

Overview Content People Subspaces and Projects Reports

RECENT ACTIVITY

"Error: publisher failed" when trying to upload a hotspot file
jditts replied (in response to Alex ~)
Thanks Everyone!
6 hours ago
in Torrent Suite · 9 replies

Paired-end inputs into newbler not outputting 454ContigGraph.txt
fixlex replied (in response to benwoodcroft)
What do you mean with 'recreate it'? Using your data? I checked one of our assemblies with 2.6 (multiple PE and shotgun aff files) and it nicely shows a 454ContigGraph.txt file.
1 day ago
in Torrent Suite · 3 replies

Running the barcode splitter from the command line
Mary Pacold replied (in response to emilyteravest)
Yes, in the current 2.2 release, there is a standalone utility for barcode classification. The pipeline invokes it in the following way from the report directory: `barcodeSplit -s -l ./rawlib.sff-b...`
2 days ago
in Torrent Suite · 1 reply

Getting all the data off the server
Mary Pacold replied (in response to Jeremiah Minich)
After you log into your torrent server, navigate to this path: `/results/analysis/output/Homely/your_report_name` And you should see the "unfiltered" subfolder inside.
2 days ago
in Torrent Suite · 4 replies

Annotate plugin
roys commented
Hi Lek, Just checking if there is still any update on using this plugin to use with barcoded samples on the Torrent Suite v2.2? Thanks roys
2 days ago
in Torrent Suite · 21 comments

Automatic variant caller execution on AmpliSeq runs
andrea_mafficini replied (in response to casplan)
Thanks for the reply, I will follow your suggestion until the next update of the torrent suite. Best regards Andrea
2 days ago

GETTING STARTED

Torrent Suite

- Ion Applications
- Ion Datasets
- Getting Started With Torrent Suite Software
- Getting Started With Torrent Variant Caller
- Getting Started With Torrent Suite Development

RECENT CONTENT

Filter by Categories & Tags

- Re: "Error: publisher failed" when trying to upload a hotspot file
- Re: How do I make TMAP more stringent in the VariantCaller plugin?
- Changed out hotspot file, but variantCaller will not find it as an option
- How does the variantCaller find indels? (indel_variants.vcf)
- Re: Data storage

More

ACTIONS

- Start a discussion
- Create by email
- Invite friends to join
- Receive email notifications**
- Track in Communications
- View feeds

- Sign up to receive automatic update notifications
- Monitor discussion threads
- Monitor new content

ion torrent



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