Thermo Fisher
SCIENTIFIC

Ion Torrent™ Technology

Run Validation and Introduction to the Torrent Browser

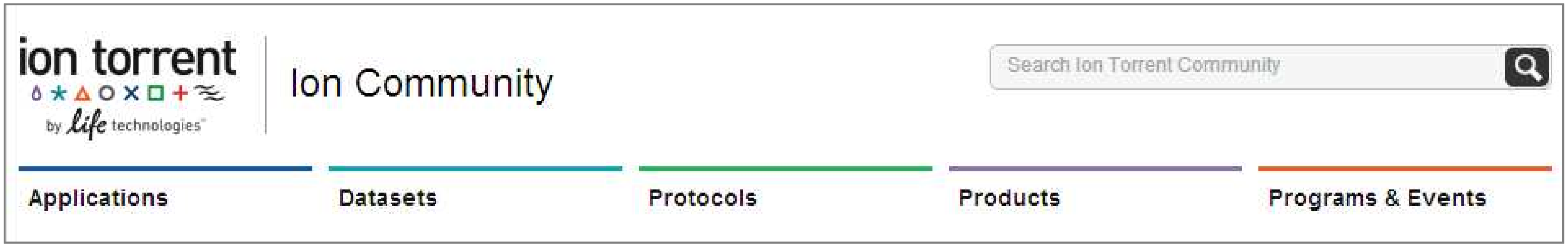
(Torrent Suite™ Software v4.0.2)

The world leader in serving science

Agenda

- Best places to find information
  - Ion Community
  - Torrent Browser
- Run report Analysis & validation
  - Live demo
  - Slides as reference

Ion Torrent^{TM} Community

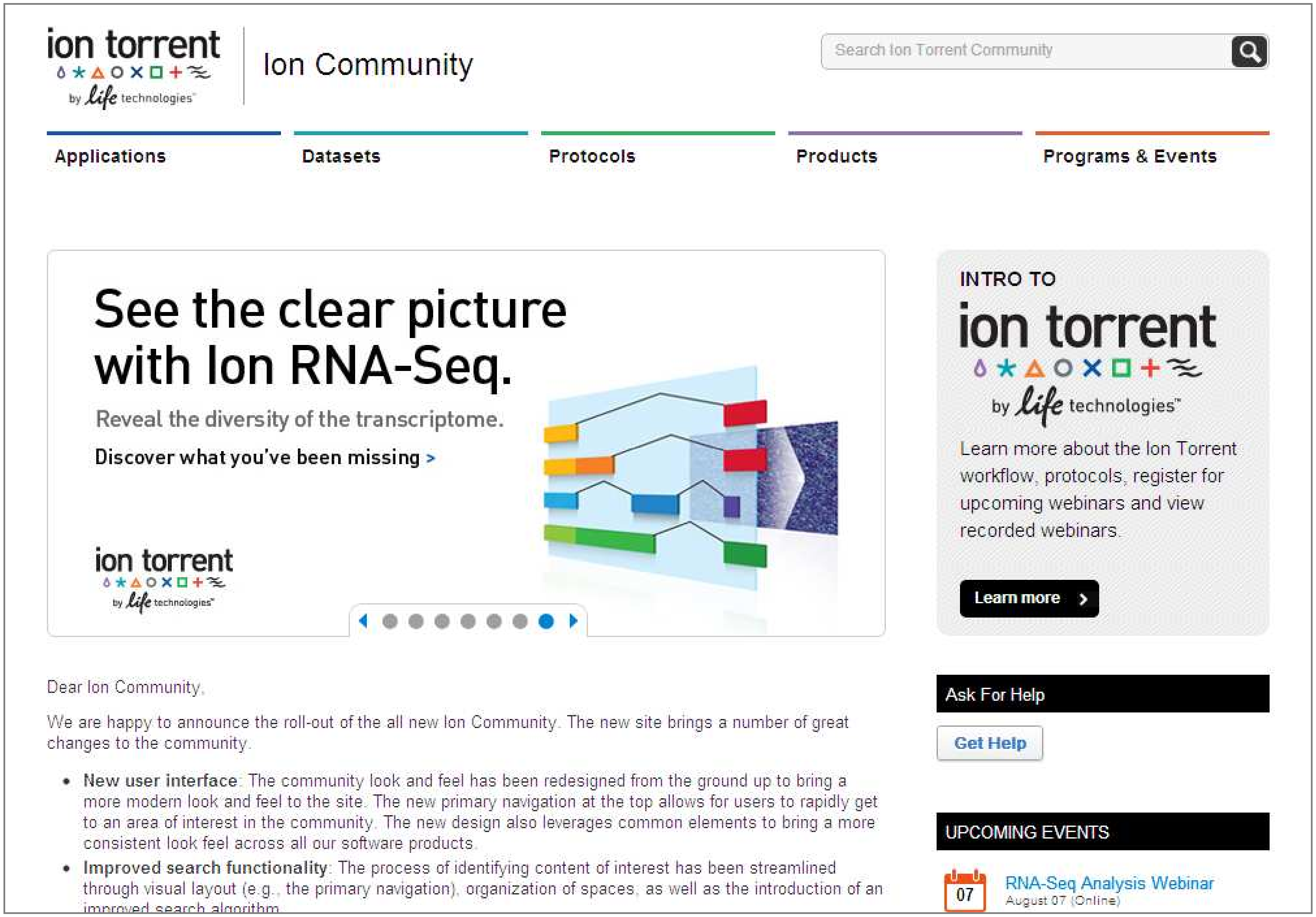

ion torrent
by life technologies
Search Ion Torrent Community

Ion Community

Applications
Datasets
Protocols
Products
Programs & Events

http://ioncommunity.lifetechnologies.com/welcome

Ion Torrent$^{\text{TM}}$ Community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Ion Community
Search Ion Torrent Community
Applications
Datasets
Protocols
Products
Programs & Events
See the clear picture with Ion RNA-Seq.
Reveal the diversity of the transcriptome.
Discover what you've been missing >
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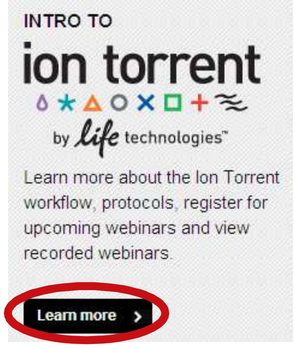
INTRO TO
ion torrent
by life technologies
Learn more about the Ion Torrent workflow, protocols, register for upcoming webinars and view recorded webinars.
Learn more
Ask For Help
Get Help
UPCOMING EVENTS
07
RNA-Seq Analysis Webinar
August 07 (Online)

Dear Ion Community,

We are happy to announce the roll-out of the all new Ion Community. The new site brings a number of great changes to the community.

- **New user interface**: The community look and feel has been redesigned from the ground up to bring a more modern look and feel to the site. The new primary navigation at the top allows for users to rapidly get to an area of interest in the community. The new design also leverages common elements to bring a more consistent look feel across all our software products.
- **Improved search functionality**: The process of identifying content of interest has been streamlined through visual layout (e.g., the primary navigation), organization of spaces, as well as the introduction of an improved search algorithm

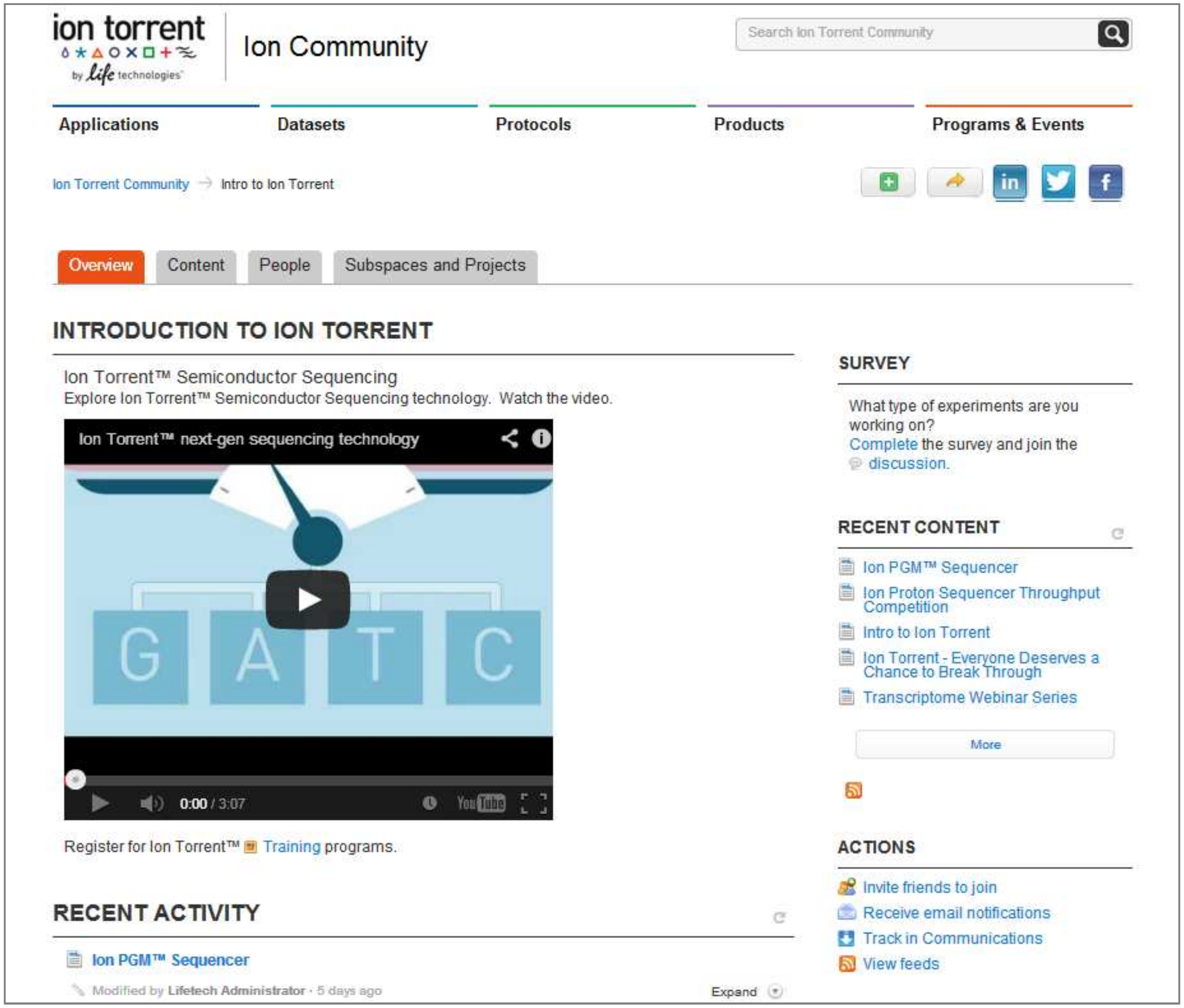
Ion Torrent^{TM} Community


INTRO TO

ion torrent

by life technologies™

Learn more about the Ion Torrent workflow, protocols, register for upcoming webinars and view recorded webinars.


ion torrent
by life technologies
Ion Community
Search Ion Torrent Community
Applications
Datasets
Protocols
Products
Programs & Events
Ion Torrent Community → Intro to Ion Torrent
Overview
Content
People
Subspaces and Projects

INTRODUCTION TO ION TORRENT

Ion Torrent™ Semiconductor Sequencing

Explore Ion Torrent™ Semiconductor Sequencing technology. Watch the video.

Ion Torrent™ next-gen sequencing technology
G
A
T
C
0:00 / 3:07

Register for Ion Torrent™ Training programs.

RECENT ACTIVITY

Ion PGM™ Sequencer

Modified by Lifetech Administrator · 5 days ago

Expand

SURVEY

What type of experiments are you working on? Complete the survey and join the discussion.

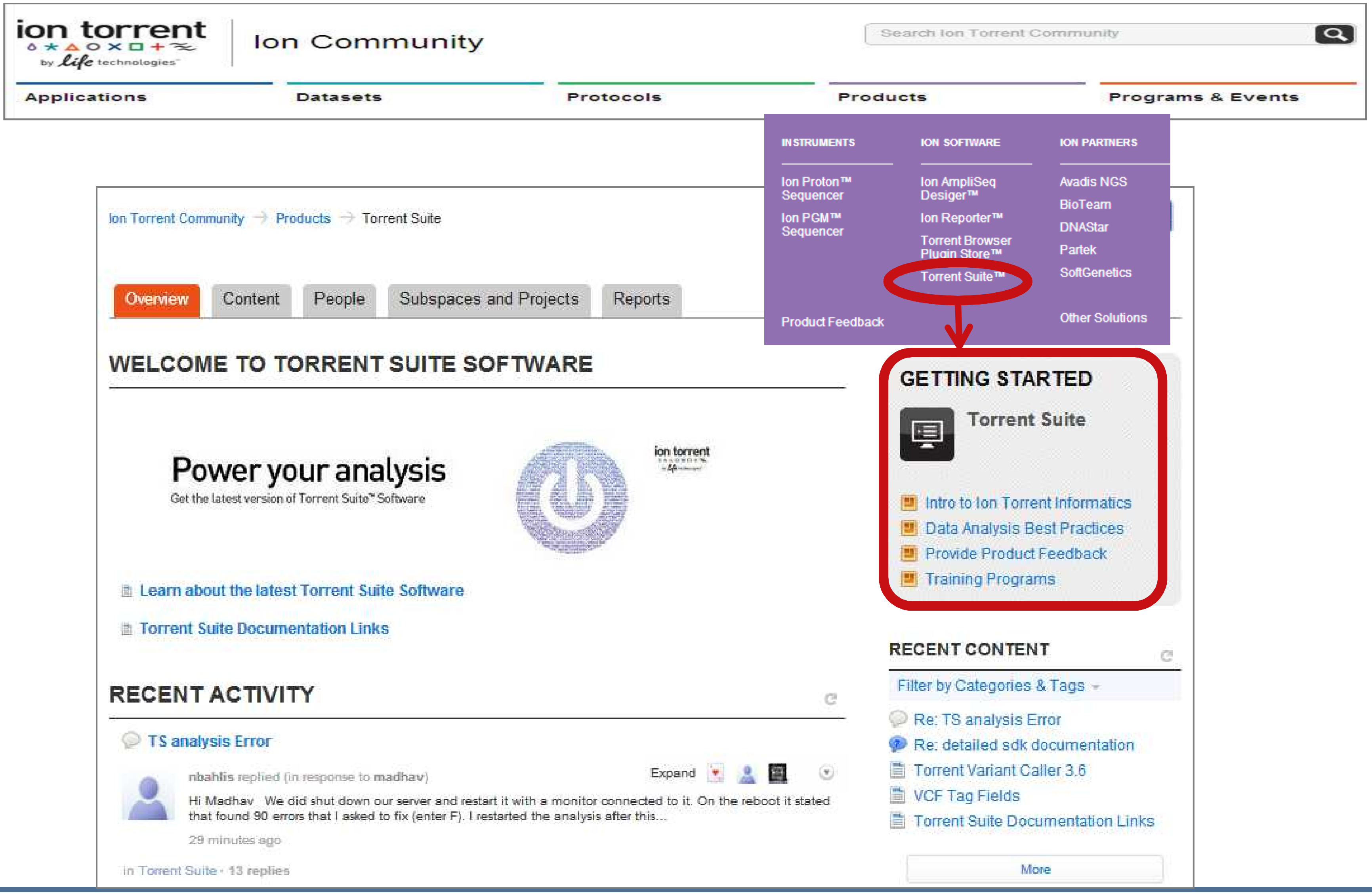
RECENT CONTENT

- Ion PGM™ Sequencer
- Ion Proton Sequencer Throughput Competition
- Intro to Ion Torrent
- Ion Torrent - Everyone Deserves a Chance to Break Through
- Transcriptome Webinar Series

ACTIONS

- Invite friends to join
- Receive email notifications
- Track in Communications
- View feeds

Ion Torrent^{TM} Community


ion torrent
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Ion Community
Search Ion Torrent Community
Applications
Datasets
Protocols
Products
Programs & Events
INSTRUMENTS
Ion Proton™ Sequencer
Ion PGM™ Sequencer
Product Feedback
ION SOFTWARE
Ion AmpliSeq Designer™
Ion Reporter™
Torrent Browser Plugin Store™
Torrent Suite™
ION PARTNERS
Avadis NGS
BioTeam
DNAStar
Partek
SoftGenetics
Other Solutions
Ion Torrent Community → Products → Torrent Suite
Overview
Content
People
Subspaces and Projects
Reports
Expand
More

WELCOME TO TORRENT SUITE SOFTWARE

Power your analysis

Get the latest version of Torrent Suite™ Software

Learn about the latest Torrent Suite Software

Torrent Suite Documentation Links

RECENT ACTIVITY

TS analysis Error

nbahlis replied (in response to madhav)

Hi Madhav We did shut down our server and restart it with a monitor connected to it. On the reboot it stated that found 90 errors that I asked to fix (enter F). I restarted the analysis after this...

29 minutes ago

in Torrent Suite · 13 replies

GETTING STARTED

Torrent Suite

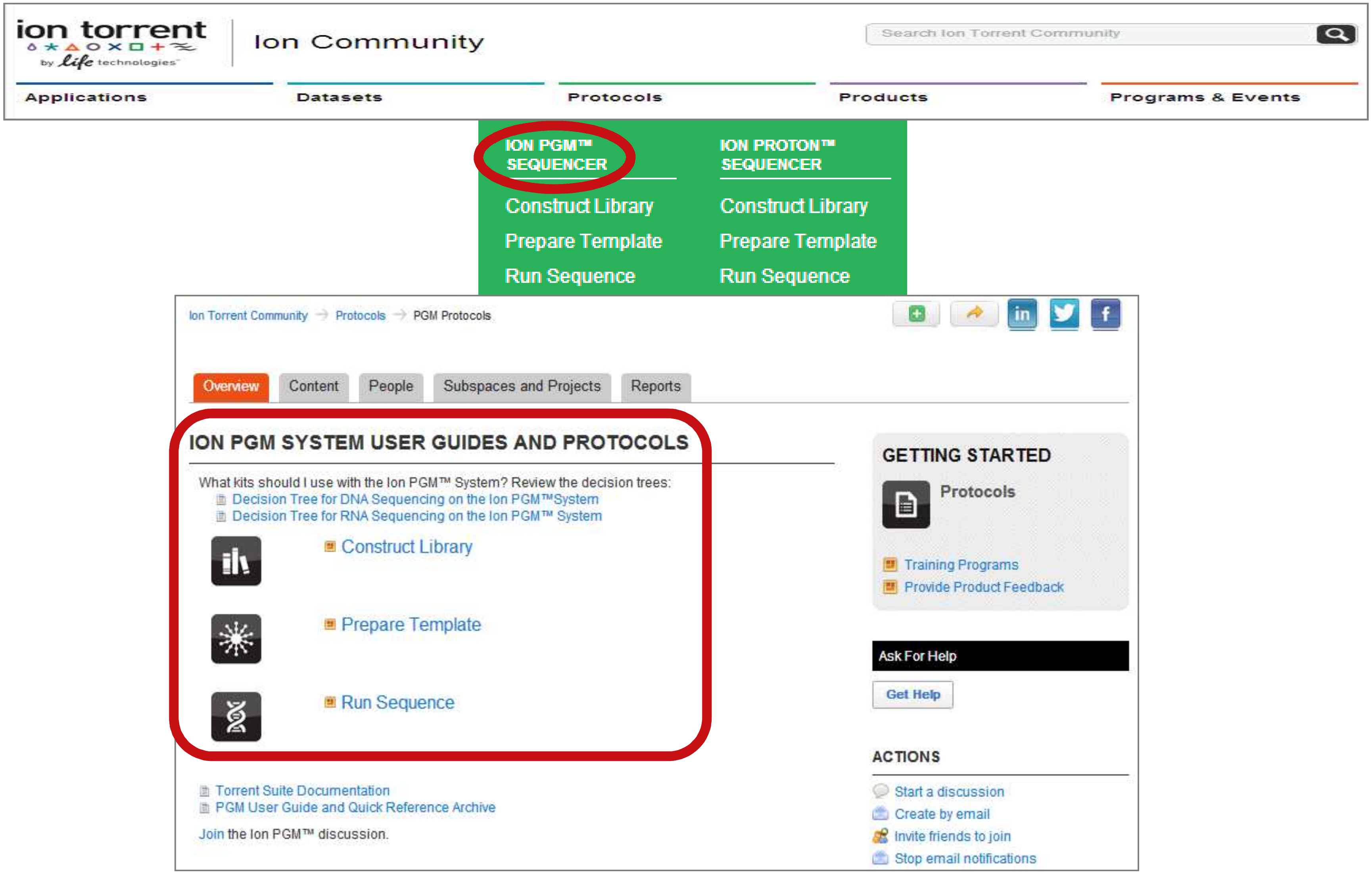
- Intro to Ion Torrent Informatics
- Data Analysis Best Practices
- Provide Product Feedback
- Training Programs

RECENT CONTENT

Filter by Categories & Tags

- Re: TS analysis Error
- Re: detailed sdk documentation
- Torrent Variant Caller 3.6
- VCF Tag Fields
- Torrent Suite Documentation Links

Ion Torrent^{TM} Community


ion torrent
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Ion Community
Search Ion Torrent Community
Applications
Datasets
Protocols
Products
Programs & Events
ION PGM™ SEQUENCER
Construct Library
Prepare Template
Run Sequence
ION PROTON™ SEQUENCER
Construct Library
Prepare Template
Run Sequence
Ion Torrent Community → Protocols → PGM Protocols
Overview
Content
People
Subspaces and Projects
Reports

ION PGM SYSTEM USER GUIDES AND PROTOCOLS

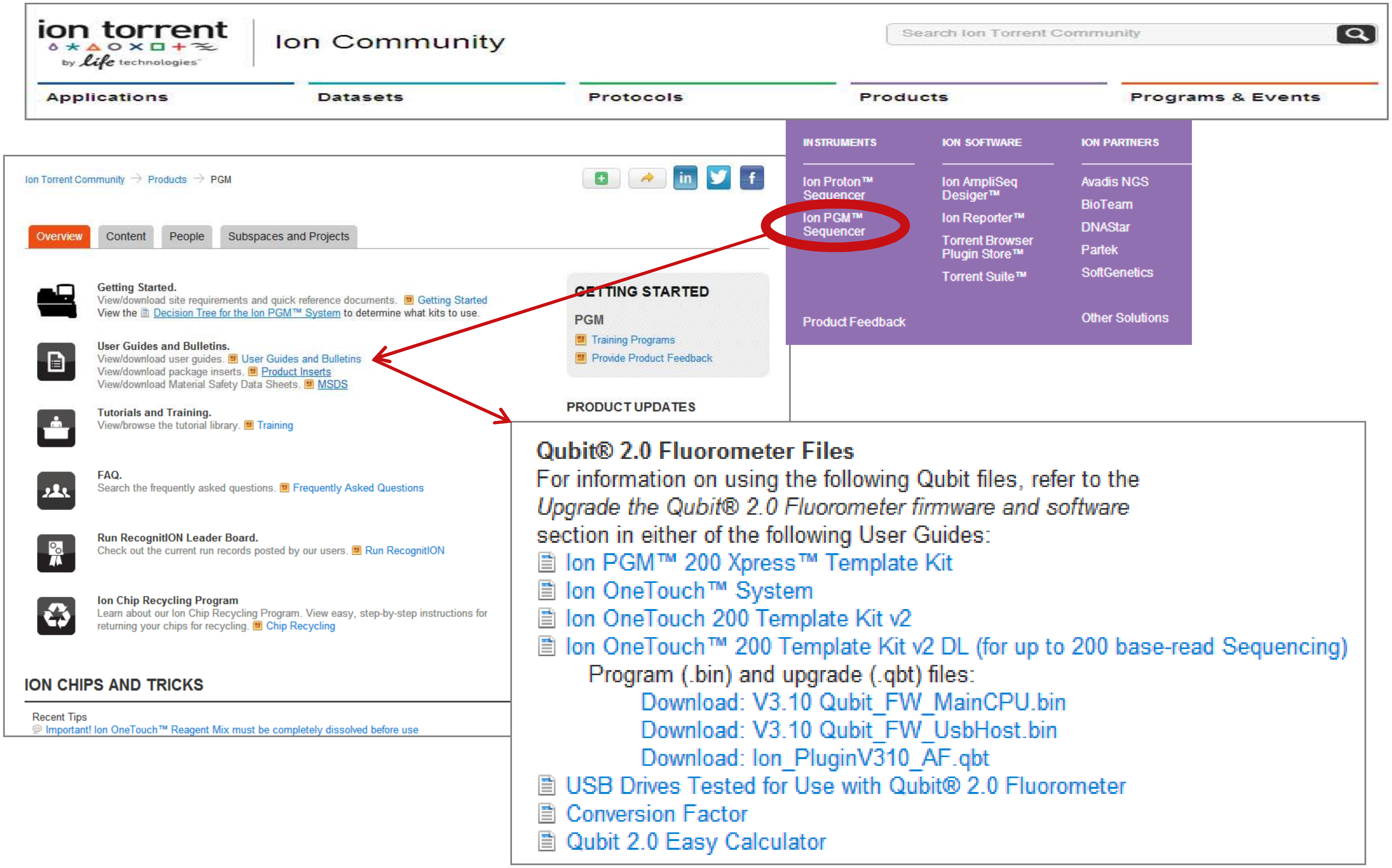
What kits should I use with the Ion PGM™ System? Review the decision trees:
- Decision Tree for DNA Sequencing on the Ion PGM™System
- Decision Tree for RNA Sequencing on the Ion PGM™ System

Construct Library
Prepare Template
Run Sequence
GETTING STARTED
Protocols
Training Programs
Provide Product Feedback
Ask For Help
Get Help
ACTIONS
Start a discussion
Create by email
Invite friends to join
Stop email notifications

- Torrent Suite Documentation
- PGM User Guide and Quick Reference Archive

Join the Ion PGM™ discussion.

Ion Torrent^{TM} Community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INSTRUMENTS
ION SOFTWARE
ION PARTNERS
Ion Proton™ Sequencer
Ion PGM™ Sequencer
Ion AmpliSeq Designer™
Ion Reporter™
Torrent Browser Plugin Store™
Torrent Suite™
Avadis NGS
BioTeam
DNAStar
Partek
SoftGenetics
Product Feedback
Other Solutions
Ion Torrent Community → Products → PGM
Overview
Content
People
Subspaces and Projects
GETTING STARTED
PGM
Training Programs
Provide Product Feedback
PRODUCT UPDATES

Getting Started.
View/download site requirements and quick reference documents. Getting Started
View the Decision Tree for the Ion PGM™ System to determine what kits to use.

User Guides and Bulletins.
View/download user guides. User Guides and Bulletins
View/download package inserts. Product Inserts
View/download Material Safety Data Sheets. MSDS

Tutorials and Training.
View/browse the tutorial library. Training

FAQ.
Search the frequently asked questions. Frequently Asked Questions

Run RecognitION Leader Board.
Check out the current run records posted by our users. Run RecognitION

Ion Chip Recycling Program
Learn about our Ion Chip Recycling Program. View easy, step-by-step instructions for returning your chips for recycling. Chip Recycling

ION CHIPS AND TRICKS

Recent Tips
Important! Ion OneTouch™ Reagent Mix must be completely dissolved before use

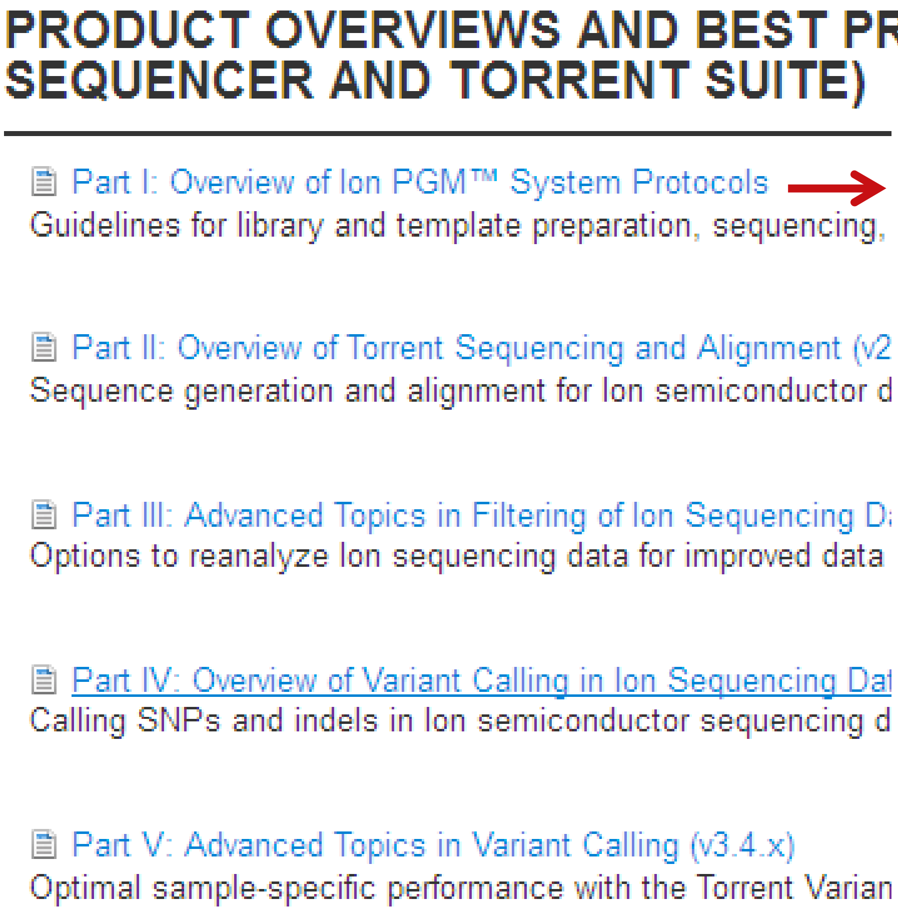
Qubit® 2.0 Fluorometer Files

For information on using the following Qubit files, refer to the *Upgrade the Qubit® 2.0 Fluorometer firmware and software* section in either of the following User Guides:

- Ion PGM™ 200 Xpress™ Template Kit
- Ion OneTouch™ System
- Ion OneTouch 200 Template Kit v2
- Ion OneTouch™ 200 Template Kit v2 DL (for up to 200 base-read Sequencing)
  - Program (.bin) and upgrade (.qbt) files:
    - Download: V3.10 Qubit_FW_MainCPU.bin
    - Download: V3.10 Qubit_FW_UsbHost.bin
    - Download: Ion_PluginV310_AF.qbt
- USB Drives Tested for Use with Qubit® 2.0 Fluorometer
- Conversion Factor
- Qubit 2.0 Easy Calculator

“Best Practices”, Ion Community

Check for updates!



PRODUCT OVERVIEWS AND BEST PRACTICES (ION PGM SEQUENCER AND TORRENT SUITE)

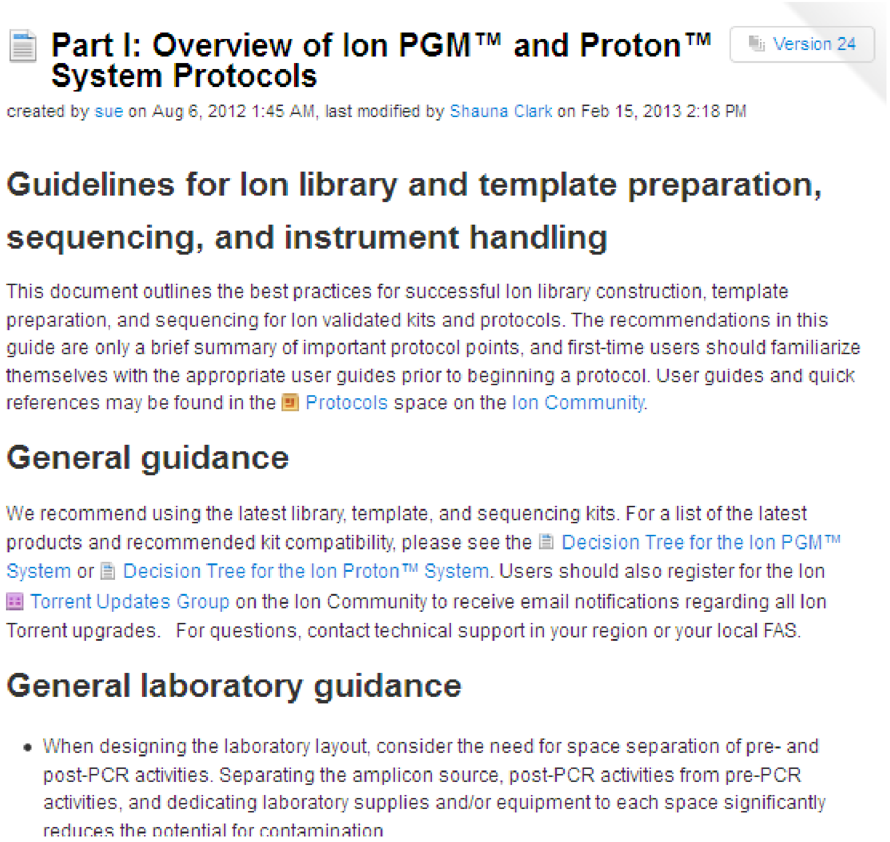
Part I: Overview of Ion PGM™ System Protocols
Guidelines for library and template preparation, sequencing,

Part II: Overview of Torrent Sequencing and Alignment (v2
Sequence generation and alignment for Ion semiconductor d

Part III: Advanced Topics in Filtering of Ion Sequencing D
Options to reanalyze Ion sequencing data for improved data

Part IV: Overview of Variant Calling in Ion Sequencing Dat
Calling SNPs and indels in Ion semiconductor sequencing d

Part V: Advanced Topics in Variant Calling (v3.4.x)
Optimal sample-specific performance with the Torrent Varian



Part I: Overview of Ion PGM™ and Proton™ System Protocols

Version 24

created by sue on Aug 6, 2012 1:45 AM, last modified by Shauna Clark on Feb 15, 2013 2:18 PM

Guidelines for Ion library and template preparation, sequencing, and instrument handling

This document outlines the best practices for successful Ion library construction, template preparation, and sequencing for Ion validated kits and protocols. The recommendations in this guide are only a brief summary of important protocol points, and first-time users should familiarize themselves with the appropriate user guides prior to beginning a protocol. User guides and quick references may be found in the Protocols space on the Ion Community.

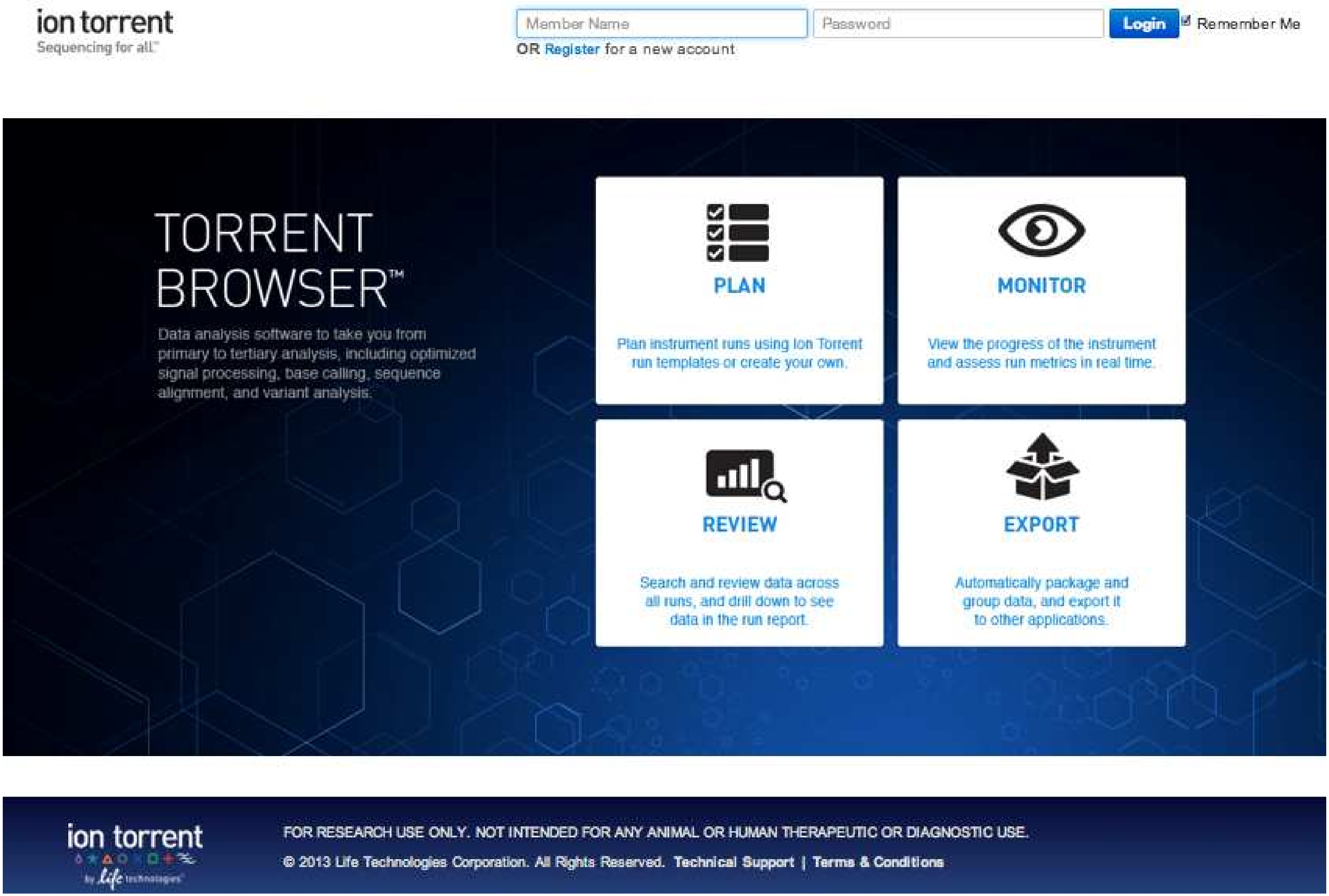
General guidance

We recommend using the latest library, template, and sequencing kits. For a list of the latest products and recommended kit compatibility, please see the Decision Tree for the Ion PGM™ System or Decision Tree for the Ion Proton™ System. Users should also register for the Ion Torrent Updates Group on the Ion Community to receive email notifications regarding all Ion Torrent upgrades. For questions, contact technical support in your region or your local FAS.

General laboratory guidance

- When designing the laboratory layout, consider the need for space separation of pre- and post-PCR activities. Separating the amplicon source, post-PCR activities from pre-PCR activities, and dedicating laboratory supplies and/or equipment to each space significantly reduces the potential for contamination

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


ion torrent
Sequencing for all™
Member Name
Password
Login
☑ Remember Me
OR Register for a new account
PLAN
MONITOR
REVIEW
EXPORT
ion torrent
by Life technologies™

TORRENT BROWSER™

Data analysis software to take you from primary to tertiary analysis, including optimized signal processing, base calling, sequence alignment, and variant analysis.

PLAN

Plan instrument runs using Ion Torrent run templates or create your own.

MONITOR

View the progress of the instrument and assess run metrics in real time.

REVIEW

Search and review data across all runs, and drill down to see data in the run report.

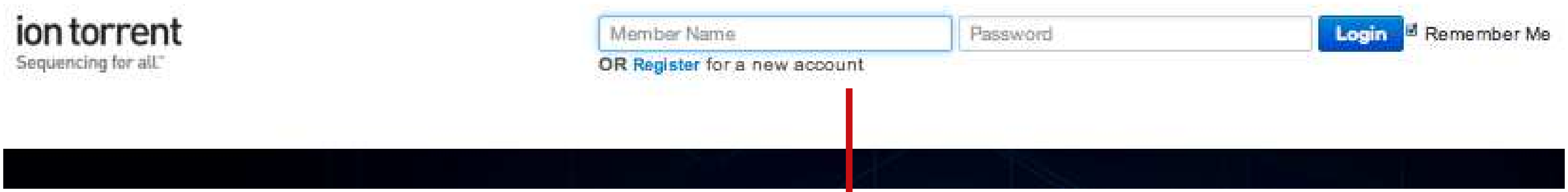
EXPORT

Automatically package and group data, and export it to other applications.

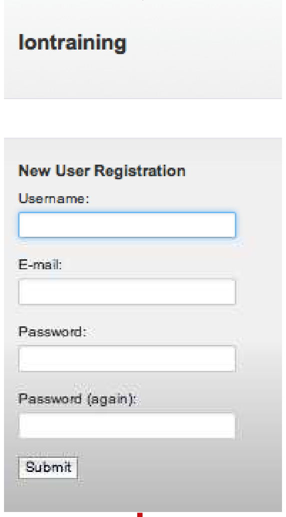
FOR RESEARCH USE ONLY. NOT INTENDED FOR ANY ANIMAL OR HUMAN THERAPEUTIC OR DIAGNOSTIC USE.

© 2013 Life Technologies Corporation. All Rights Reserved. **Technical Support** | **Terms & Conditions**

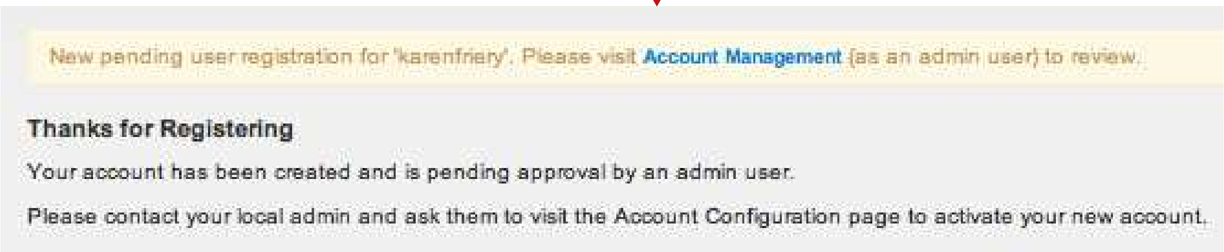
New Account Registration - Request


ion torrent
Sequencing for all
Member Name
Password
Login
☑ Remember Me

OR Register for a new account


Iontraining
New User Registration
Username:
E-mail:
Password:
Password (again):
Submit

1. Click Register
2. Fill out form
3. Submit
4. Approval



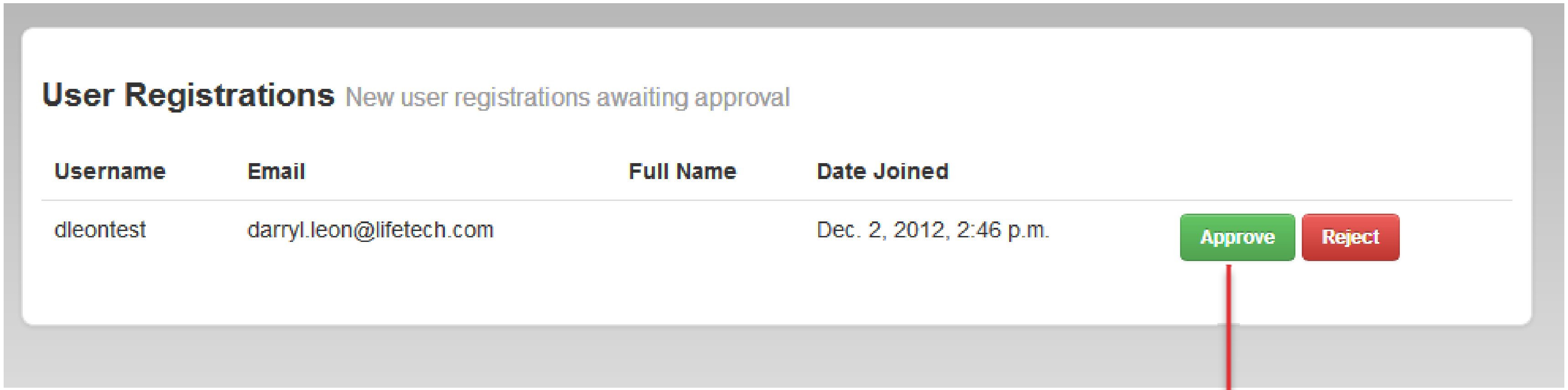
New pending user registration for 'karenfriery'. Please visit Account Management (as an admin user) to review.

Thanks for Registering

Your account has been created and is pending approval by an admin user.

Please contact your local admin and ask them to visit the Account Configuration page to activate your new account.

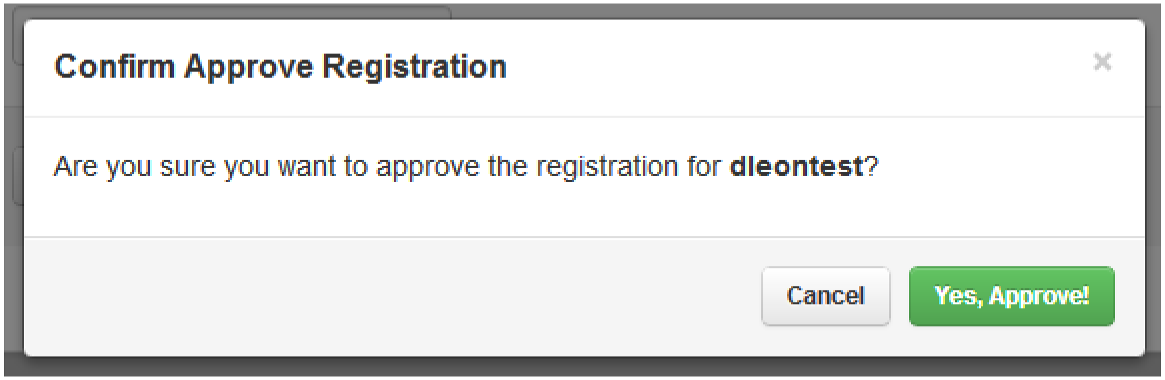
New Account Registration – Admin Approval



User Registrations New user registrations awaiting approval

Username	Email	Full Name	Date Joined
dleontest	darryl.leon@lifetech.com		Dec. 2, 2012, 2:46 p.m.

1. Login as Admin
2. Review request
3. Approve/Reject

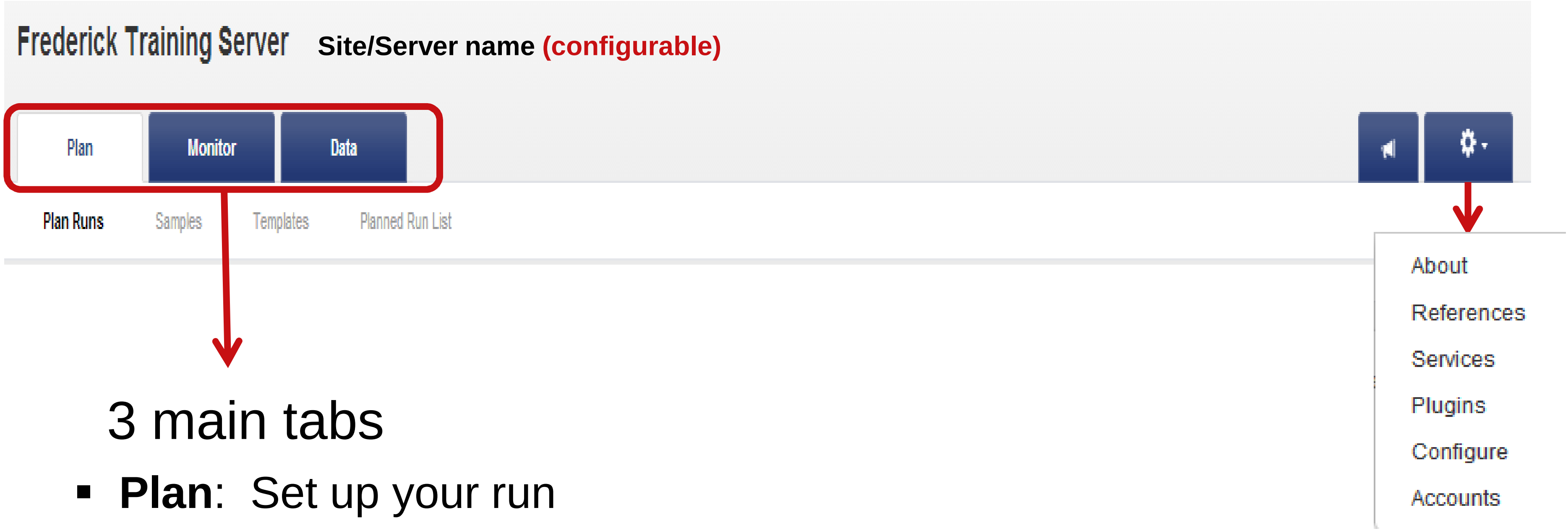


Confirm Approve Registration

Are you sure you want to approve the registration for **dleontest**?

*Note: Only administrators can reset user passwords.

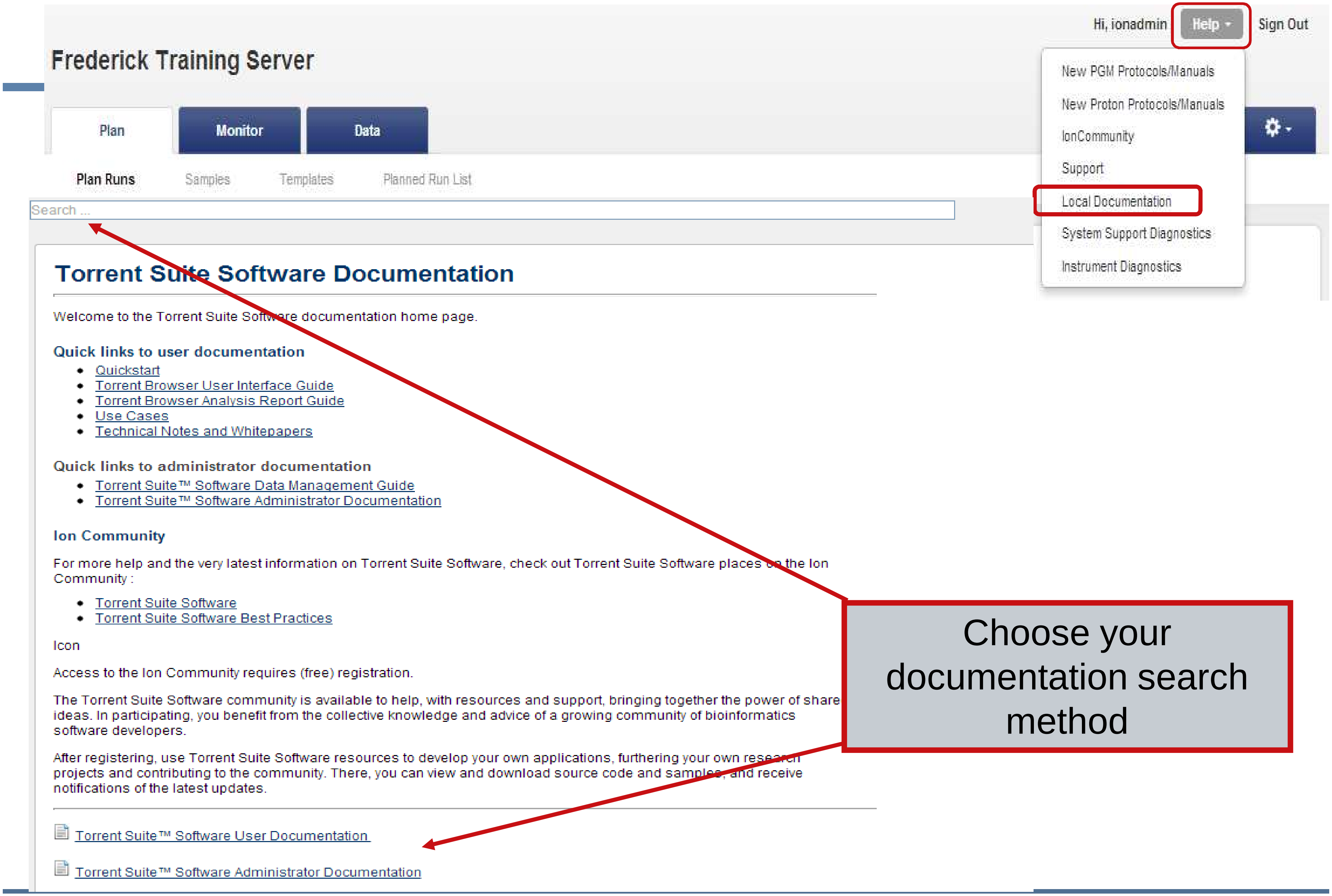
Log into Torrent browser


Frederick Training Server
Plan
Monitor
Data
Plan Runs
Samples
Templates
Planned Run List
About
References
Services
Plugins
Configure
Accounts

Site/Server name **(configurable)**

3 main tabs

- **Plan**: Set up your run
- **Monitor**: Check your run in real time
- **Data**: Analyze your run report(s)


Hi, ionadmin
Help
Sign Out
Frederick Training Server
Plan
Monitor
Data
Plan Runs
Samples
Templates
Planned Run List
Search ...
New PGM Protocols/Manuals
New Proton Protocols/Manuals
IonCommunity
Support
Local Documentation
System Support Diagnostics
Instrument Diagnostics

Torrent Suite Software Documentation

Welcome to the Torrent Suite Software documentation home page.

Quick links to user documentation

- Quickstart
- Torrent Browser User Interface Guide
- Torrent Browser Analysis Report Guide
- Use Cases
- Technical Notes and Whitepapers

Quick links to administrator documentation

- Torrent Suite™ Software Data Management Guide
- Torrent Suite™ Software Administrator Documentation

Ion Community

For more help and the very latest information on Torrent Suite Software, check out Torrent Suite Software places on the Ion Community :

- Torrent Suite Software
- Torrent Suite Software Best Practices

Icon

Access to the Ion Community requires (free) registration.

The Torrent Suite Software community is available to help, with resources and support, bringing together the power of share ideas. In participating, you benefit from the collective knowledge and advice of a growing community of bioinformatics software developers.

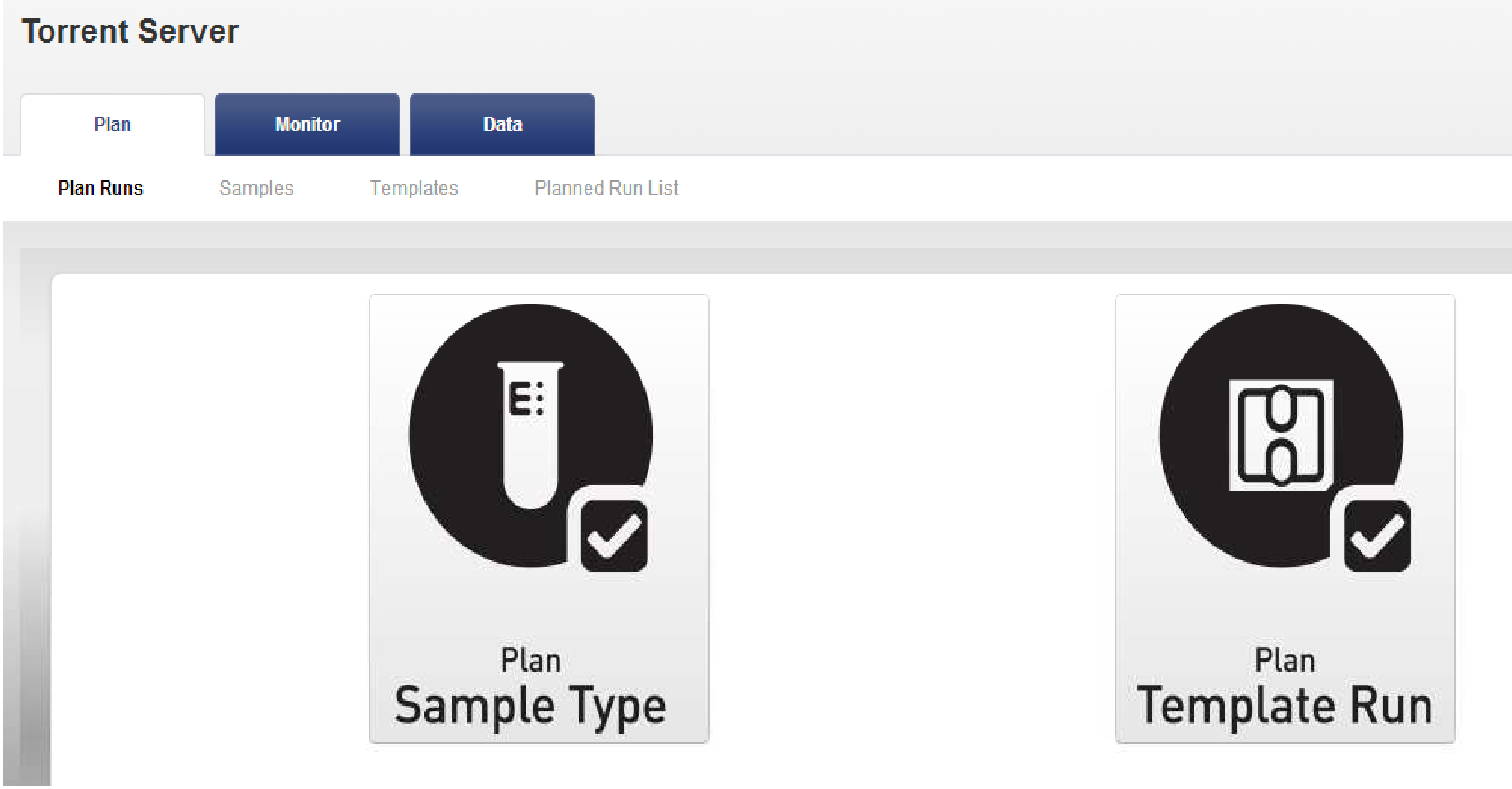
After registering, use Torrent Suite Software resources to develop your own applications, furthering your own research projects and contributing to the community. There, you can view and download source code and samples, and receive notifications of the latest updates.

Torrent Suite™ Software User Documentation

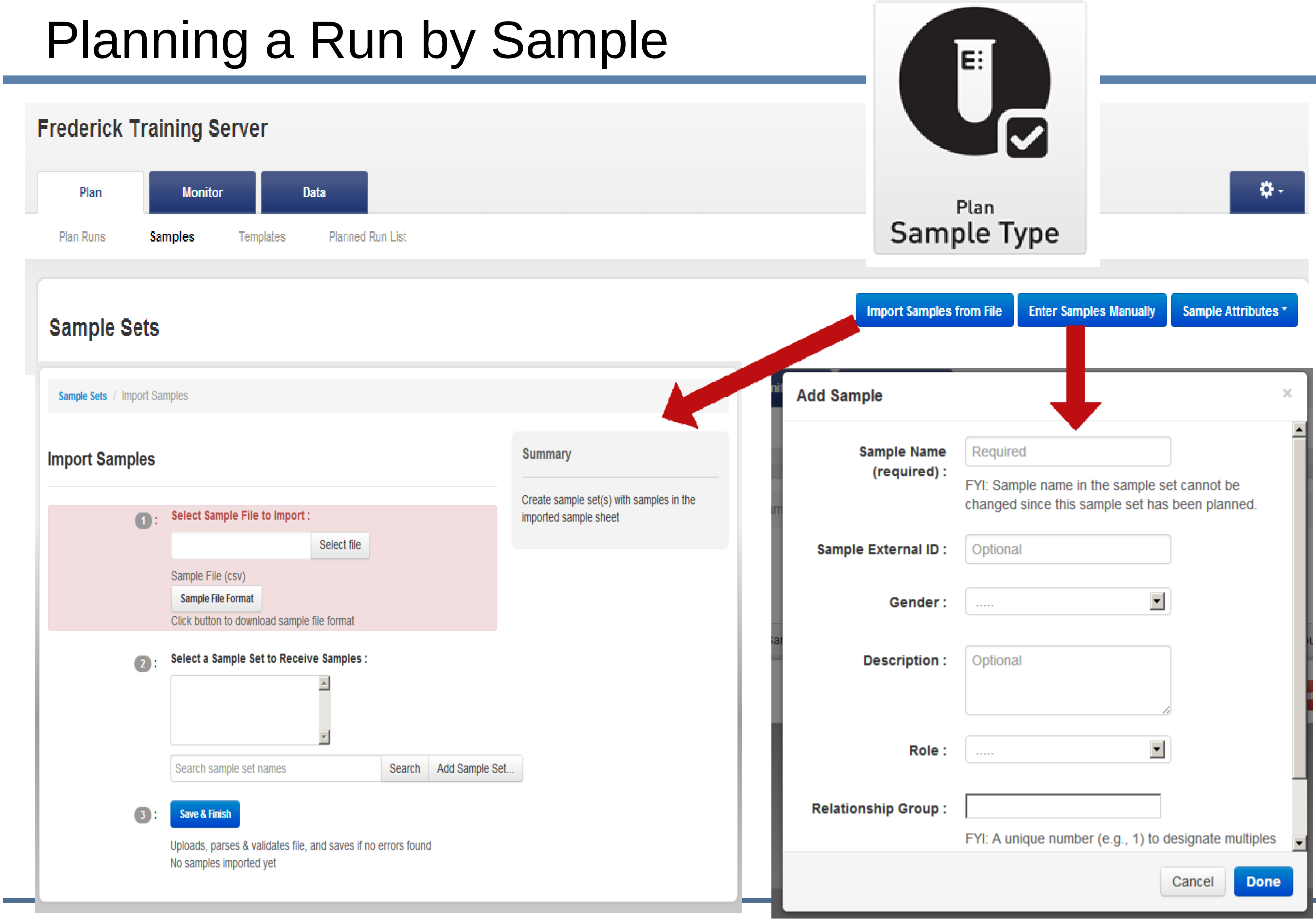
Torrent Suite™ Software Administrator Documentation

Choose your documentation search method

Planning a Run by Sample or Template


Torrent Server
Plan
Monitor
Data
Plan Runs
Samples
Templates
Planned Run List
Plan
Sample Type
Plan
Template Run

Planning a Run by Sample


Frederick Training Server
Plan
Monitor
Data
Plan Runs
Samples
Templates
Planned Run List
Plan
Sample Type
Import Samples from File
Enter Samples Manually
Sample Attributes
Sample Sets / Import Samples
Select file
Sample File Format
Search
Add Sample Set...
Save & Finish
Cancel
Done

Sample Sets

Import Samples

1 : **Select Sample File to Import :**

Sample File (csv)

Click button to download sample file format

2 : **Select a Sample Set to Receive Samples :**

Search sample set names

3 : 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

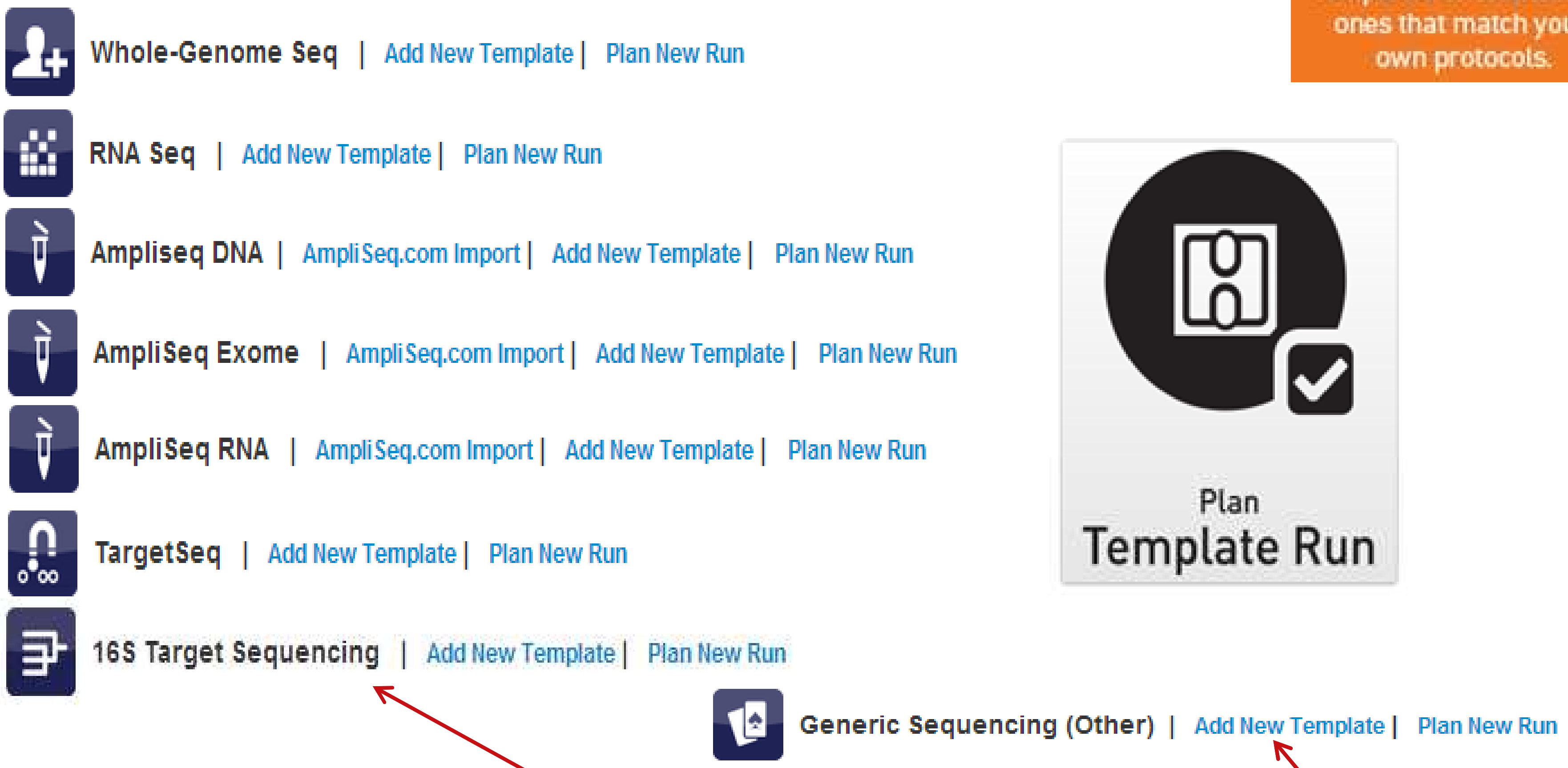
Role : .....

Relationship Group :

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

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

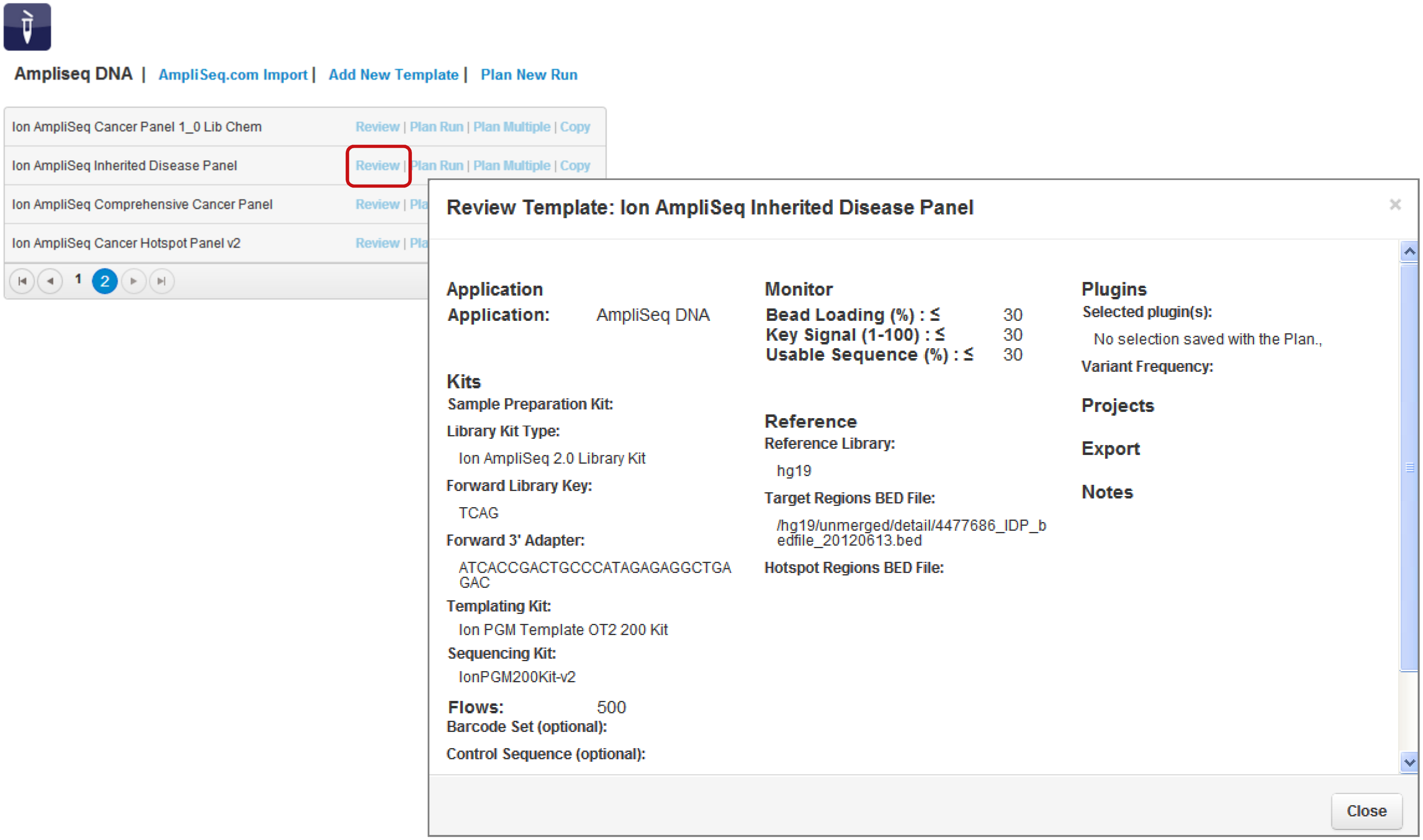
Generic Sequencing (Other) | Add New Template | Plan New Run

Plan
Template 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

Review Settings of Pre-installed Template



Ampliseq DNA | AmpliSeq.com Import | Add New Template | Plan New Run

Ion AmpliSeq Cancer Panel 1_0 Lib Chem	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Inherited Disease Panel	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Comprehensive Cancer Panel	Review | Pla
Ion AmpliSeq Cancer Hotspot Panel v2	Review | Pla

Review Template: Ion AmpliSeq Inherited Disease Panel

Application

Application: AmpliSeq DNA

Kits

Sample Preparation Kit:

Library Kit Type:
Ion AmpliSeq 2.0 Library Kit

Forward Library Key:
TCAG

Forward 3' Adapter:
ATCACCGACTGCCCATAGAGAGGCTGAGAC

Templating Kit:
Ion PGM Template OT2 200 Kit

Sequencing Kit:
IonPGM200Kit-v2

Flows: 500

Barcode Set (optional):

Control Sequence (optional):

Monitor

Bead Loading (%) : ≤ 30
Key Signal (1-100) : ≤ 30
Usable Sequence (%) : ≤ 30

Reference

Reference Library:
hg19

Target Regions BED File:
/hg19/unmerged/detail/4477686_IDP_bedfile_20120613.bed

Hotspot Regions BED File:

Plugins

Selected plugin(s):
No selection saved with the Plan.,

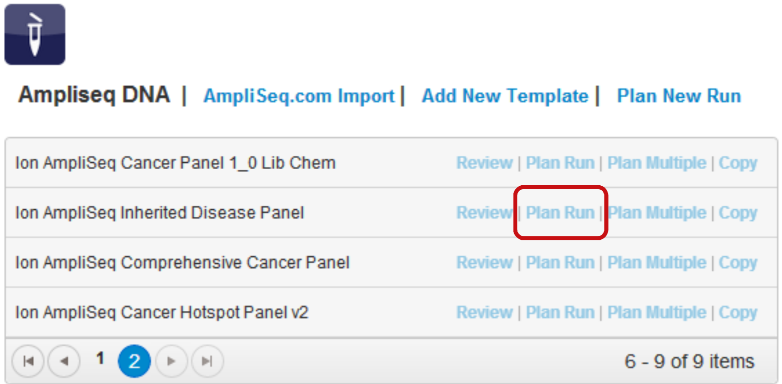
Variant Frequency:

Projects

Export

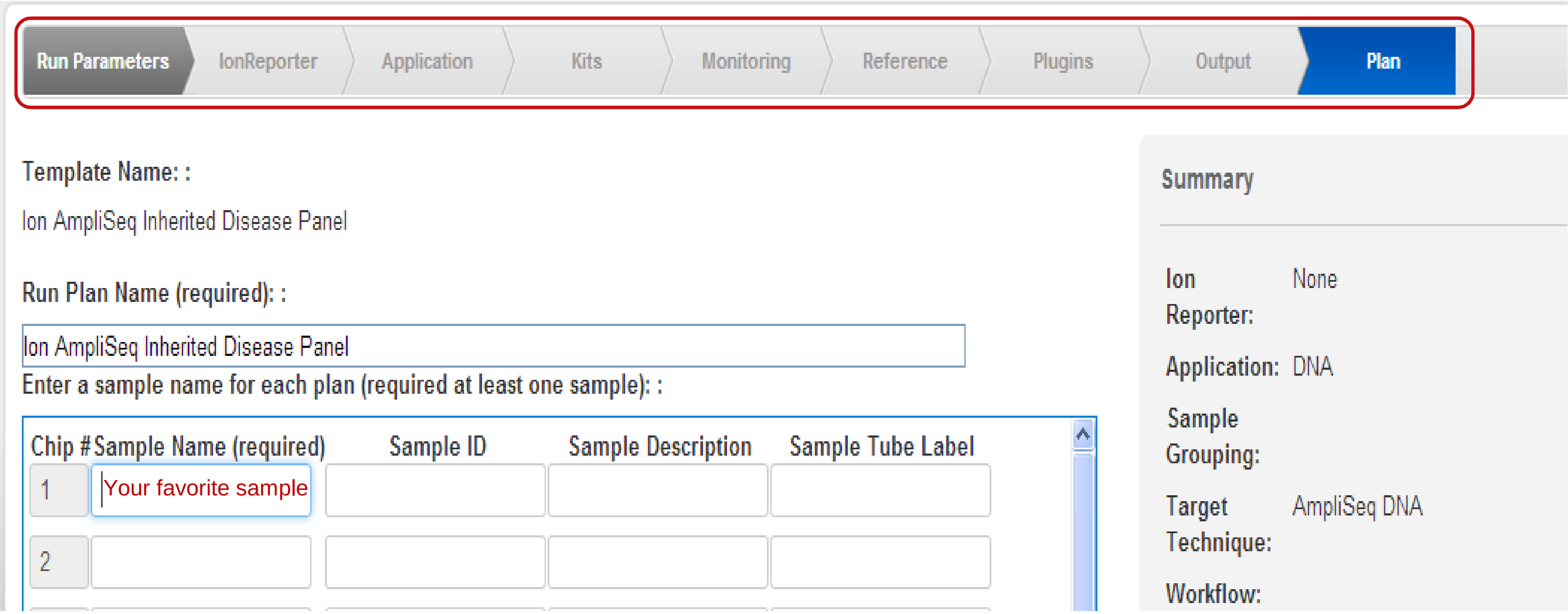
Notes

Plan Run from a Template


Ampliseq DNA | AmpliSeq.com Import | Add New Template | Plan New Run

Ion AmpliSeq Cancer Panel 1_0 Lib Chem	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Inherited Disease Panel	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Comprehensive Cancer Panel	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Cancer Hotspot Panel v2	Review | Plan Run | Plan Multiple | Copy

1
2
6 - 9 of 9 items


Run Parameters
IonReporter
Application
Kits
Monitoring
Reference
Plugins
Output
Plan

Template Name: :

Ion AmpliSeq Inherited Disease Panel

Run Plan Name (required): :

Ion AmpliSeq Inherited Disease Panel

Enter a sample name for each plan (required at least one sample): :

Chip #	Sample Name (required)	Sample ID	Sample Description	Sample Tube Label
1	Your favorite sample			
2				

Summary

Ion Reporter: None

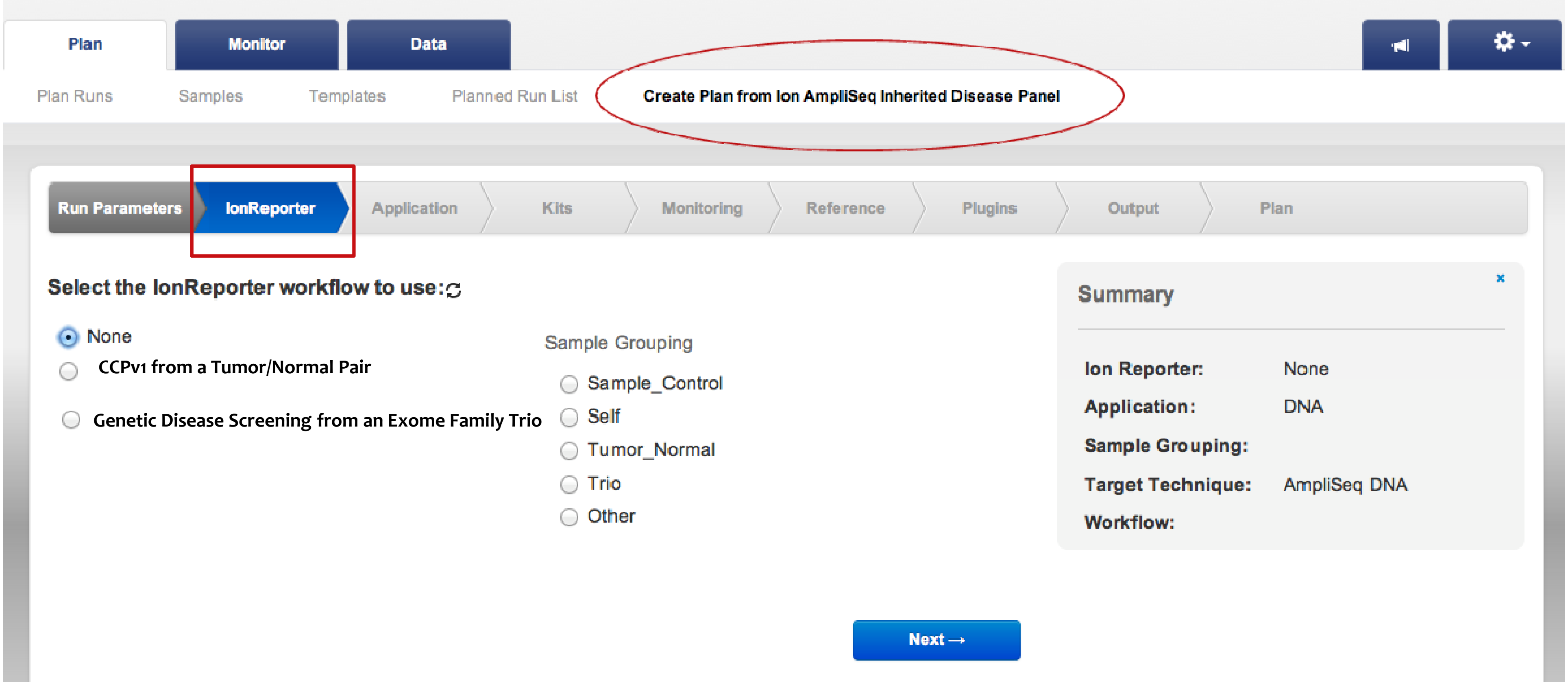
Application: DNA

Sample Grouping:

Target Technique: AmpliSeq DNA

Workflow:

Ion Reporter Integration



Plan
Monitor
Data
Plan Runs
Samples
Templates
Planned Run List
Create Plan from Ion AmpliSeq Inherited Disease Panel
Run Parameters
IonReporter
Application
Kits
Monitoring
Reference
Plugins
Output
Plan
Next →

Select the IonReporter workflow to use:

● None
○ CCPv1 from a Tumor/Normal Pair
○ Genetic Disease Screening from an Exome Family Trio

Sample Grouping

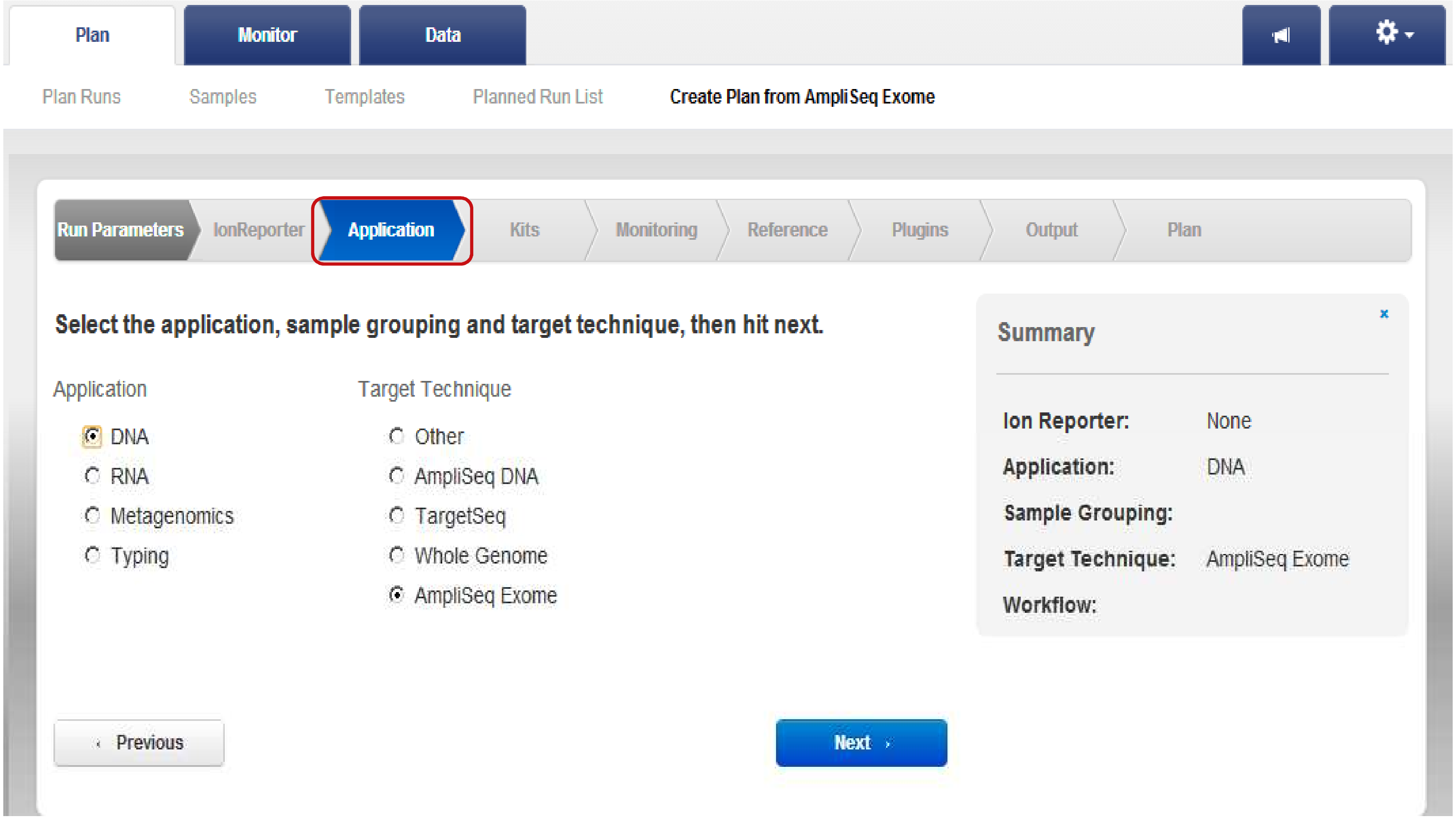
○ Sample_Control
○ Self
○ Tumor_Normal
○ Trio
○ Other

Summary

Ion Reporter:	None
Application:	DNA
Sample Grouping:	
Target Technique:	AmpliSeq DNA
Workflow:	

Select the IR Workflow and Sample Grouping

Template application


Plan
Monitor
Data
Plan Runs
Samples
Templates
Planned Run List
Create Plan from AmpliSeq Exome
Run Parameters
IonReporter
Application
Kits
Monitoring
Reference
Plugins
Output
Plan
‹ Previous
Next ›

Select the application, sample grouping and target technique, then hit next.

Application

- ● DNA
- ○ RNA
- ○ Metagenomics
- ○ Typing

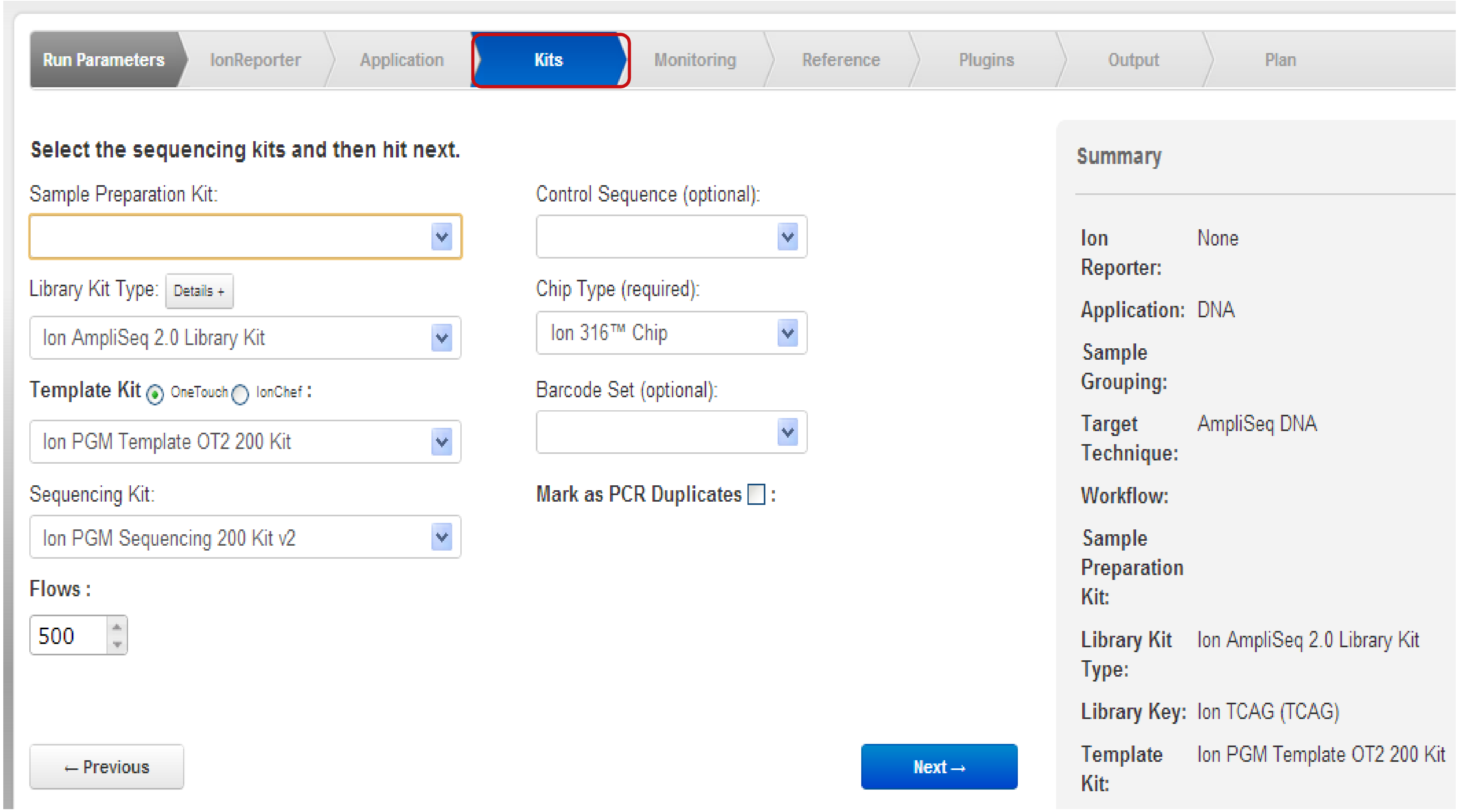
Target Technique

- ○ Other
- ○ AmpliSeq DNA
- ○ TargetSeq
- ○ Whole Genome
- ● AmpliSeq Exome

Summary

Ion Reporter:	None
Application:	DNA
Sample Grouping:	
Target Technique:	AmpliSeq Exome
Workflow:	

Plan Run from a Template - Kits


Run Parameters
IonReporter
Application
Kits
Monitoring
Reference
Plugins
Output
Plan
Details +
← Previous
Next →

Select the sequencing kits and then hit next.

Sample Preparation Kit:

Library Kit Type: Ion AmpliSeq 2.0 Library Kit

Template Kit ● OneTouch ○ IonChef **:** Ion PGM Template OT2 200 Kit

Sequencing Kit: Ion PGM Sequencing 200 Kit v2

Flows : 500

Control Sequence (optional):

Chip Type (required): Ion 316™ Chip

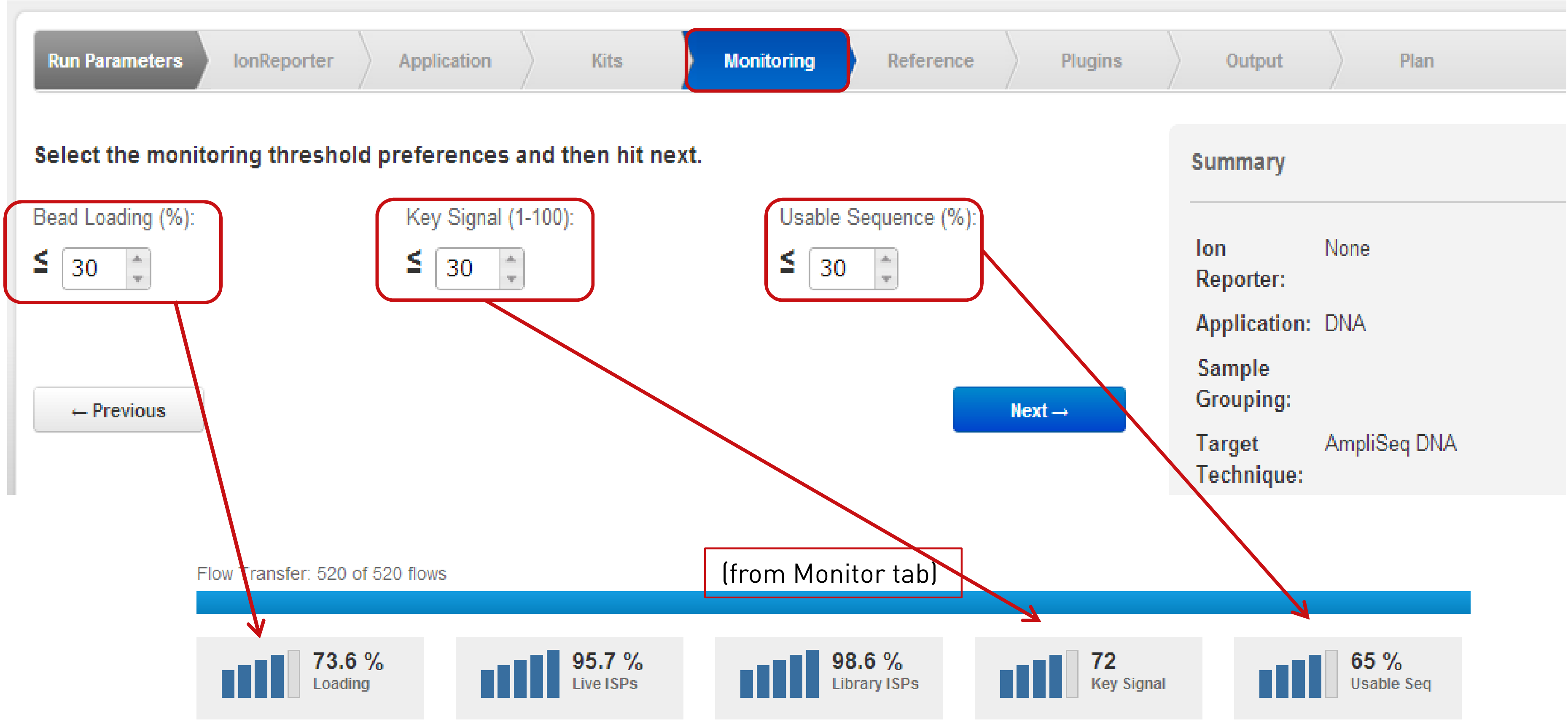
Barcode Set (optional):

Mark as PCR Duplicates ☐ **:**

Summary

Ion Reporter:	None
Application:	DNA
Sample Grouping:	
Target Technique:	AmpliSeq DNA
Workflow:	
Sample Preparation Kit:	
Library Kit Type:	Ion AmpliSeq 2.0 Library Kit
Library Key:	Ion TCAG (TCAG)
Template Kit:	Ion PGM Template OT2 200 Kit

Plan Run from a Template - Monitor


Run Parameters
IonReporter
Application
Kits
Monitoring
Reference
Plugins
Output
Plan
← Previous
Next →
(from Monitor tab)

Select the monitoring threshold preferences and then hit next.

Bead Loading (%): ≤ 30

Key Signal (1-100): ≤ 30

Usable Sequence (%): ≤ 30

Summary

Ion Reporter:	None
Application:	DNA
Sample Grouping:	
Target Technique:	AmpliSeq DNA

Flow Transfer: 520 of 520 flows

73.6 % Loading

95.7 % Live ISPs

98.6 % Library ISPs

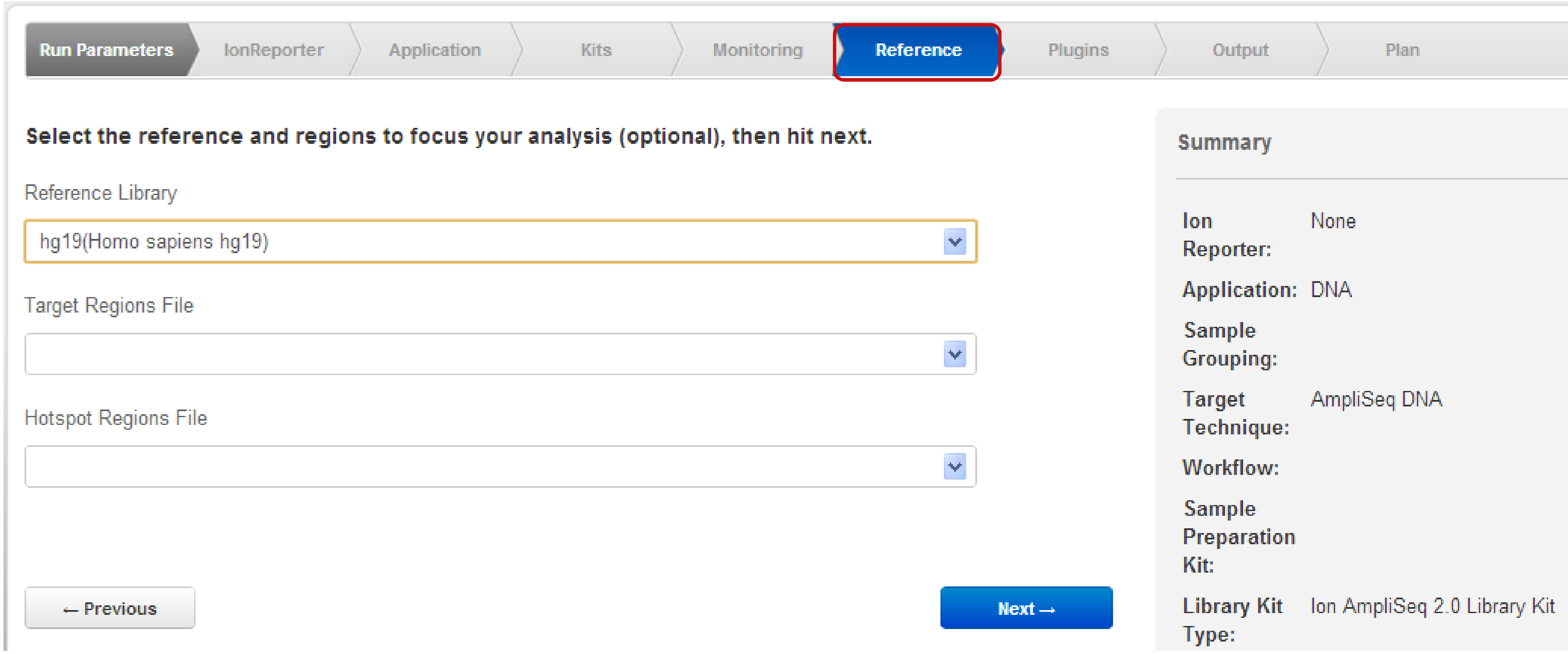
72 Key Signal

65 % Usable Seq

Set thresholds for run, view in Monitor Tab:

- Blue bar = greater than threshold set
- Red bar = less than threshold set

Plan a Run from a Template - Reference


Run Parameters
IonReporter
Application
Kits
Monitoring
Reference
Plugins
Output
Plan
← Previous
Next →

Select the reference and regions to focus your analysis (optional), then hit next.

Reference Library: hg19(Homo sapiens hg19)

Target Regions File:

Hotspot Regions File:

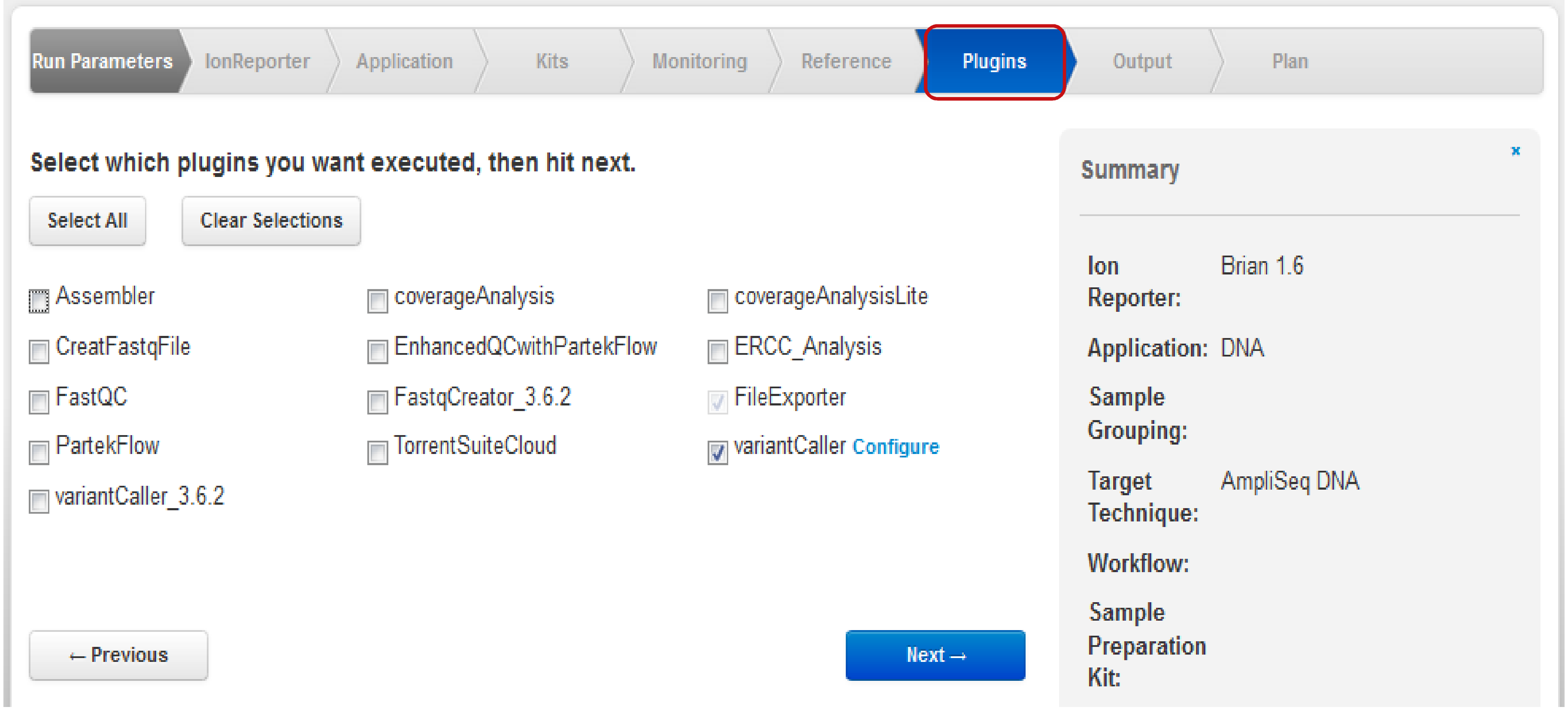
Summary

Ion Reporter:	None
Application:	DNA
Sample Grouping:	
Target Technique:	AmpliSeq DNA
Workflow:	
Sample Preparation Kit:	
Library Kit Type:	Ion AmpliSeq 2.0 Library Kit

References, sequences used in data analysis; Upload BED files

- Genome or other reference sequence
- Target Regions
- Hotspot Regions

Plan a Run from a Template - Plugins


Run Parameters
IonReporter
Application
Kits
Monitoring
Reference
Plugins
Output
Plan
Select All
Clear Selections
← Previous
Next →
Configure
×

Select which plugins you want executed, then hit next.

☐ Assembler
☐ coverageAnalysis
☐ coverageAnalysisLite
☐ CreatFastqFile
☐ EnhancedQCwithPartekFlow
☐ ERCC_Analysis
☐ FastQC
☐ FastqCreator_3.6.2
☑ FileExporter
☐ PartekFlow
☐ TorrentSuiteCloud
☑ variantCaller
☐ variantCaller_3.6.2

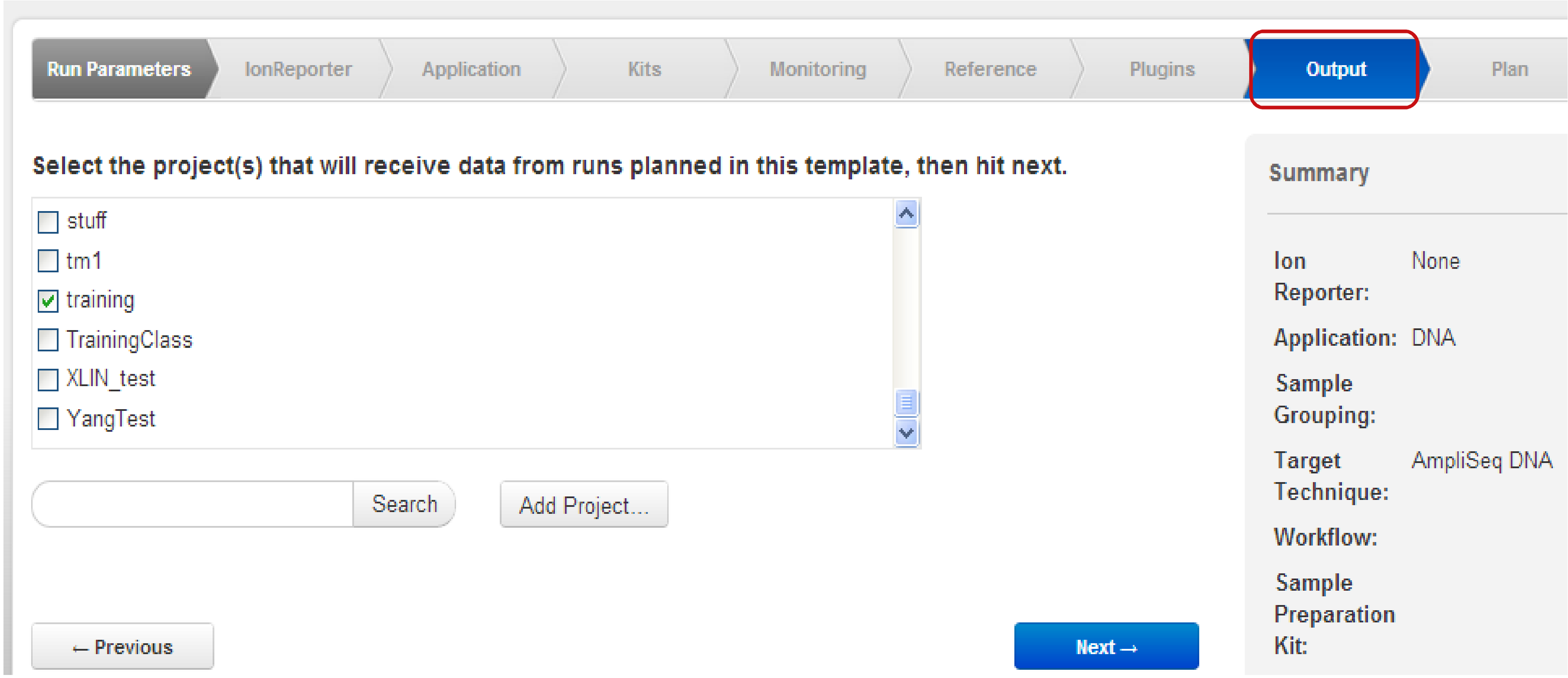
Summary

Ion Reporter: Brian 1.6
Application: DNA
Sample Grouping:
Target Technique: AmpliSeq DNA
Workflow:
Sample Preparation Kit:

Plugins, specific analysis invoked for this run

- Commercial plugins
- Customer plugins
- Plugins with parameter settings (somatic/germline)

Plan Run from a Template - Output


Run Parameters
IonReporter
Application
Kits
Monitoring
Reference
Plugins
Output
Plan

Select the project(s) that will receive data from runs planned in this template, then hit next.

☐ stuff
☐ tm1
☑ training
☐ TrainingClass
☐ XLIN_test
☐ YangTest

Search
Add Project...
← Previous
Next →

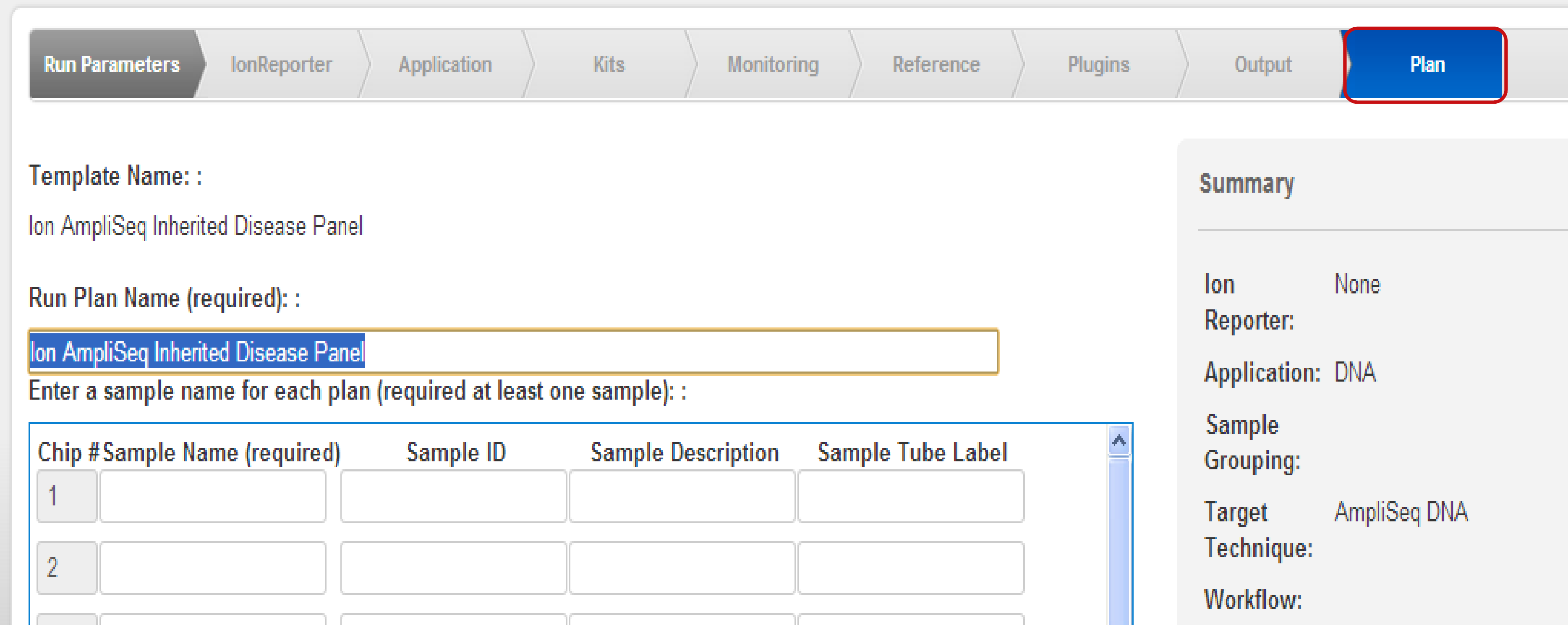
Summary

Ion Reporter:	None
Application:	DNA
Sample Grouping:	
Target Technique:	AmpliSeq DNA
Workflow:	
Sample Preparation Kit:	

Projects, ways to mark data into groups

- Data sets can be in many projects
- Can group data from a cohort together
- Data in projects can be combined

Plan Run from a Template


Run Parameters
IonReporter
Application
Kits
Monitoring
Reference
Plugins
Output
Plan

Template Name: :

Ion AmpliSeq Inherited Disease Panel

Run Plan Name (required): :

Ion AmpliSeq Inherited Disease Panel

Enter a sample name for each plan (required at least one sample): :

Chip #	Sample Name (required)	Sample ID	Sample Description	Sample Tube Label
1				
2				

Summary

Ion Reporter: None

Application: DNA

Sample Grouping:

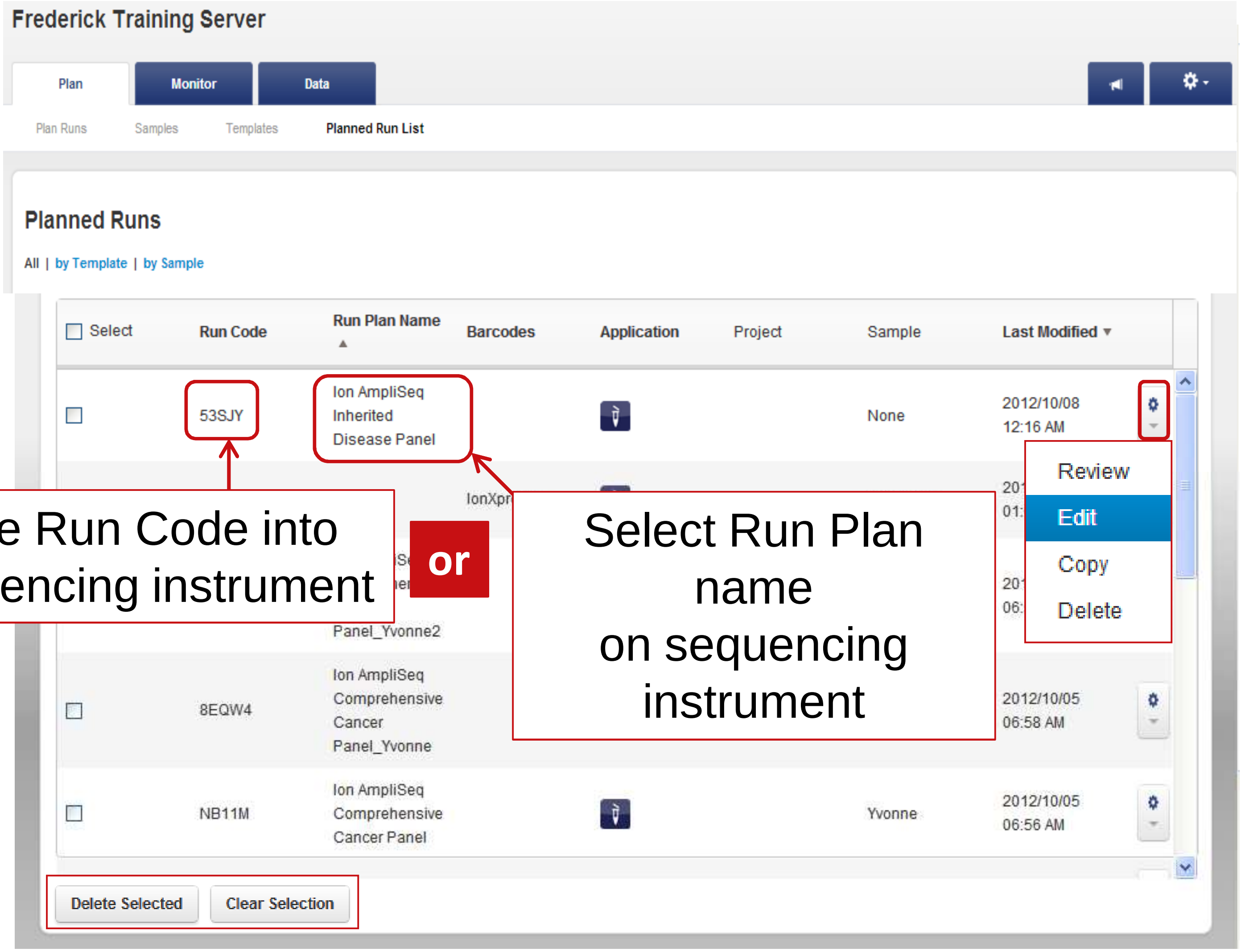
Target Technique: AmpliSeq DNA

Workflow:

Plan Runs

- Accept template defaults and plan in seconds
- Add sample names to barcodes
- Plan for a group in one action

Planned Runs List


Frederick Training Server
Plan
Monitor
Data
Plan Runs
Samples
Templates
Planned Run List
Review
Edit
Copy
Delete
Delete Selected
Clear Selection

Planned Runs

All | by Template | by Sample

☐ Select	Run Code	Run Plan Name	Barcodes	Application	Project	Sample	Last Modified
☐	53SJY	Ion AmpliSeq Inherited Disease Panel				None	2012/10/08 12:16 AM
			IonXpr				
		Panel_Yvonne2					
☐	8EQW4	Ion AmpliSeq Comprehensive Cancer Panel_Yvonne					2012/10/05 06:58 AM
☐	NB11M	Ion AmpliSeq Comprehensive Cancer Panel				Yvonne	2012/10/05 06:56 AM

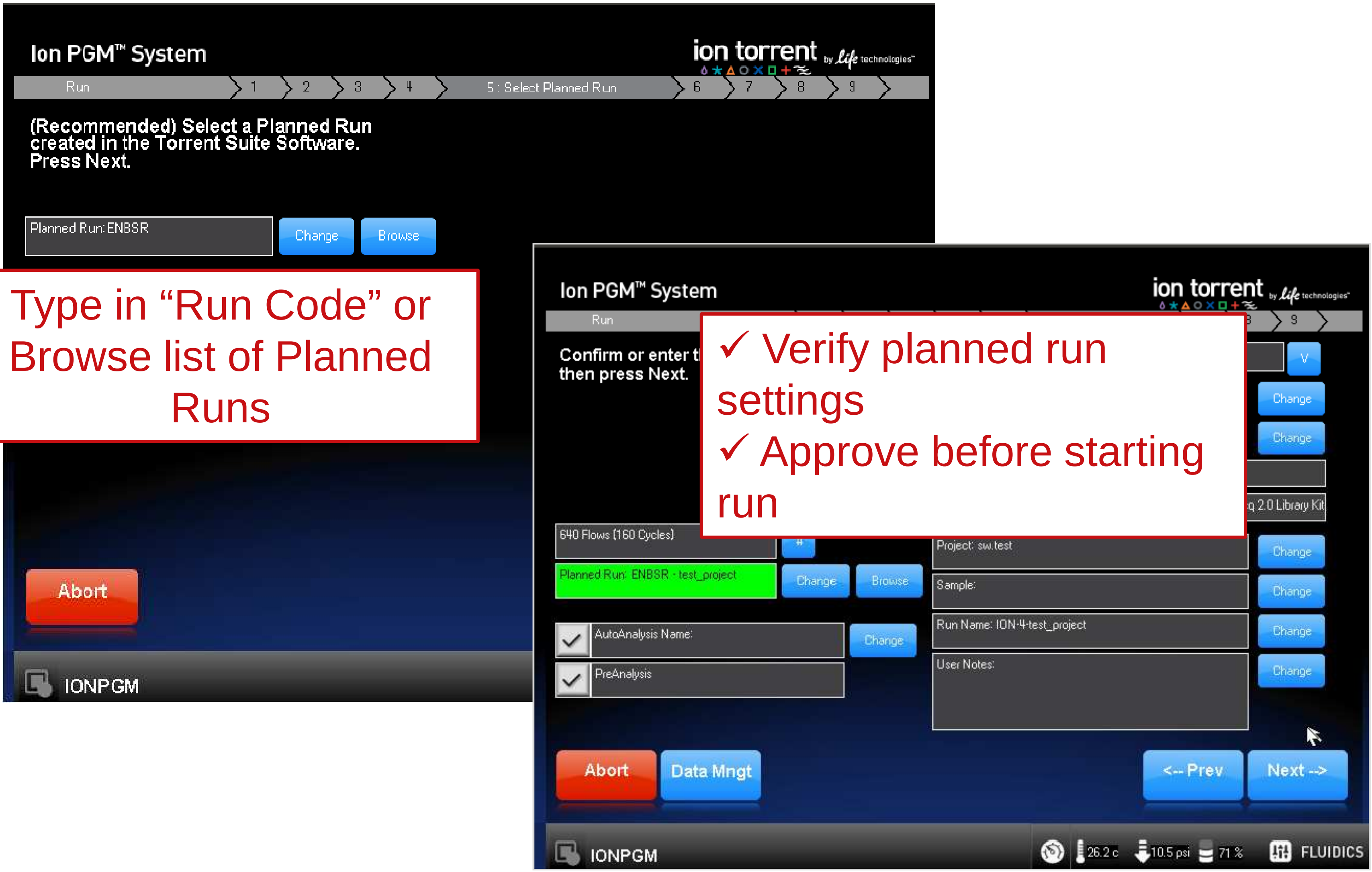
Type Run Code into sequencing instrument

or

Select Run Plan name on sequencing instrument

ThermoFisher SCIENTIFIC

Pulling in a Planned Run to the PGM™ Sequencer


Ion PGM™ System
ion torrent by Life technologies
Run
1
2
3
4
5 : Select Planned Run
6
7
8
9
Change
Browse
Abort
IONPGM

(Recommended) Select a Planned Run created in the Torrent Suite Software. Press Next.

Planned Run: ENBSR

Ion PGM™ System
ion torrent by Life technologies
Run
9
V
Change
Change
Change
Browse
Change
Change
Change
Change
Change
Abort
Data Mngt
<-- Prev
Next -->
IONPGM
26.2 c
10.5 psi
71 %
FLUIDICS

Confirm or enter t then press Next.

q 2.0 Library Kit

640 Flows (160 Cycles)

Planned Run: ENBSR - test_project

Project: sw.test

Sample:

Run Name: ION-4-test_project

User Notes:

☑ AutoAnalysis Name:

☑ PreAnalysis

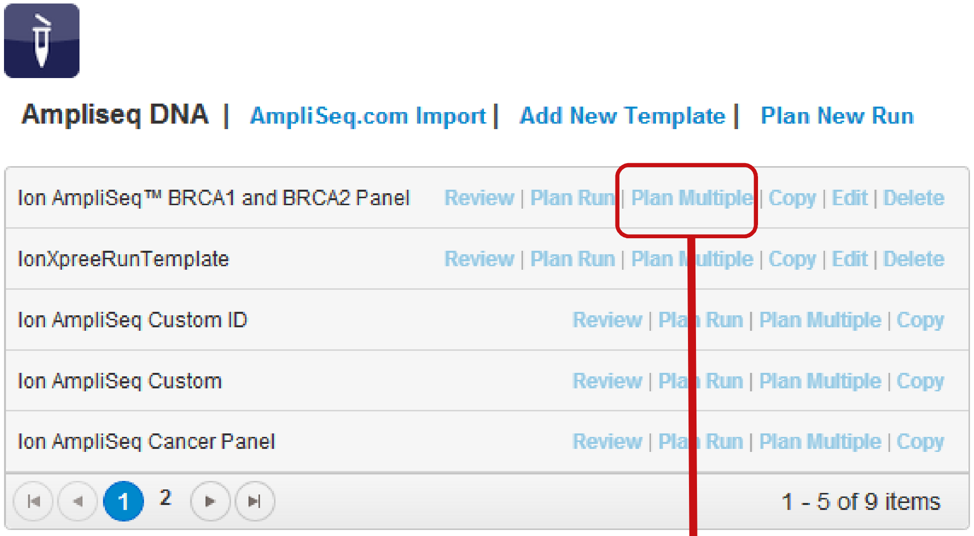
Type in "Run Code" or Browse list of Planned Runs

✓ Verify planned run settings

✓ Approve before starting run

Easily Upload Multiple Plans - Overview

Download Plan Multiple Runs File

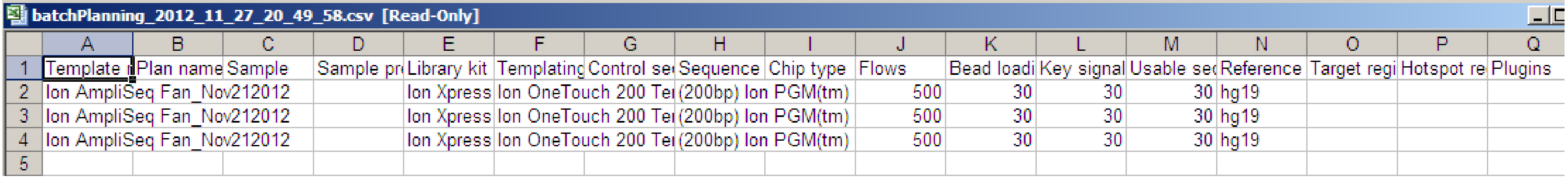


Ampliseq DNA | AmpliSeq.com Import | Add New Template | Plan New Run

Ion AmpliSeq™ BRCA1 and BRCA2 Panel	Review | Plan Run | Plan Multiple | Copy | Edit | Delete
IonXpreeRunTemplate	Review | Plan Run | Plan Multiple | Copy | Edit | Delete
Ion AmpliSeq Custom ID	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Custom	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Cancer Panel	Review | Plan Run | Plan Multiple | Copy

1 - 5 of 9 items

Review Uploaded Planned Runs

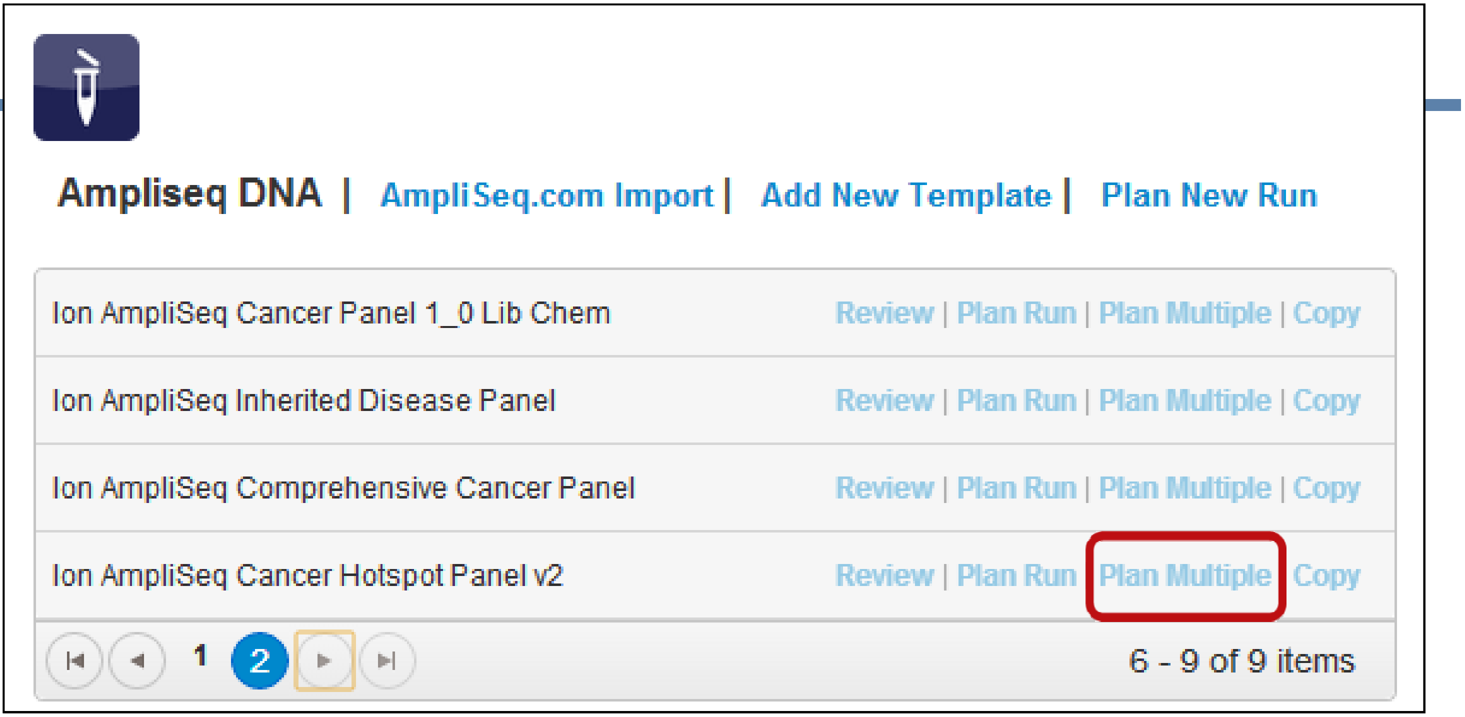


batchPlanning_2012_11_27_20_49_58.csv [Read-Only]

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	Template	Plan name	Sample	Sample pr	Library kit	Templating	Control se	Sequence	Chip type	Flows	Bead loadi	Key signal	Usable se	Reference	Target regi	Hotspot re	Plugins
2	Ion AmpliSeq Fan_Nov212012				Ion Xpress	Ion OneTouch 200 Tei		(200bp) Ion PGM(tm)		500	30	30	30	hg19			
3	Ion AmpliSeq Fan_Nov212012				Ion Xpress	Ion OneTouch 200 Tei		(200bp) Ion PGM(tm)		500	30	30	30	hg19			
4	Ion AmpliSeq Fan_Nov212012				Ion Xpress	Ion OneTouch 200 Tei		(200bp) Ion PGM(tm)		500	30	30	30	hg19			
5																	

Modify File for Planning Multiple Runs

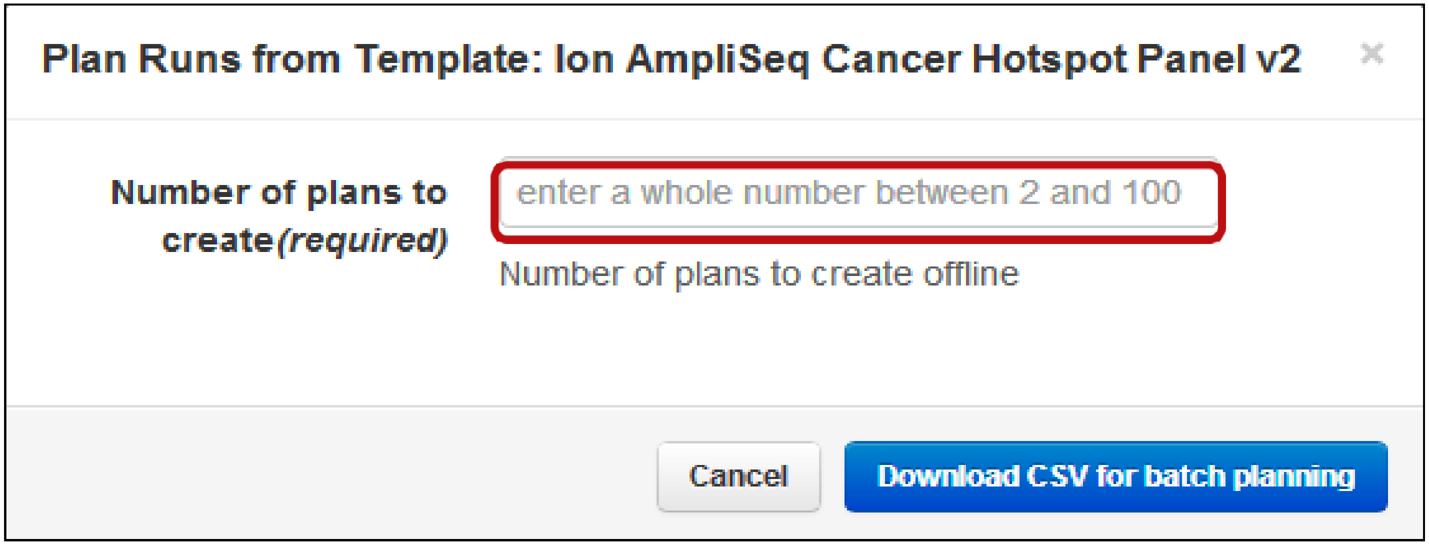
Select Plan Multiple



Ampliseq DNA | AmpliSeq.com Import | Add New Template | Plan New Run

Ion AmpliSeq Cancer Panel 1_0 Lib Chem	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Inherited Disease Panel	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Comprehensive Cancer Panel	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Cancer Hotspot Panel v2	Review | Plan Run | Plan Multiple | Copy

Enter Number of Plans to Create

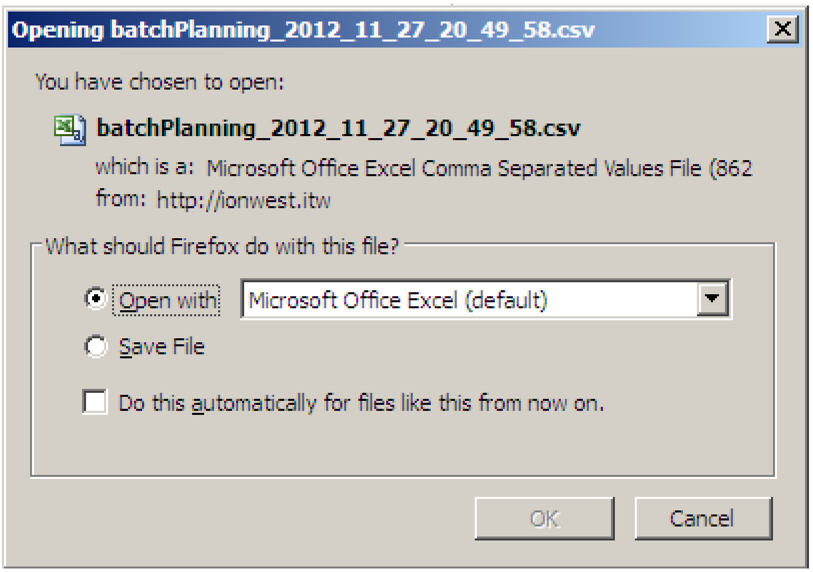


Plan Runs from Template: Ion AmpliSeq Cancer Hotspot Panel v2

Number of plans to create ***(required)***: enter a whole number between 2 and 100

Number of plans to create offline

Save CSV File and Edit



Opening batchPlanning_2012_11_27_20_49_58.csv

You have chosen to open:

batchPlanning_2012_11_27_20_49_58.csv

which is a: Microsoft Office Excel Comma Separated Values File (862

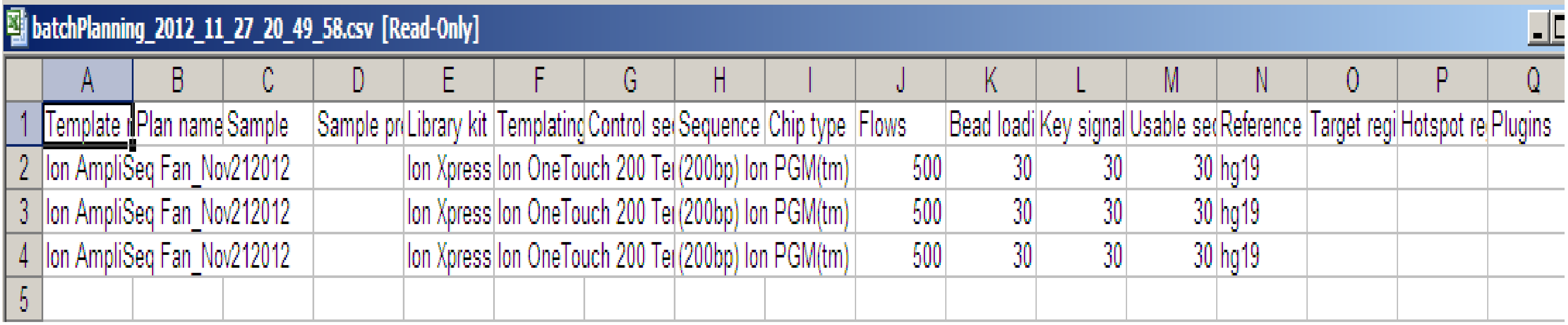
from: http://ionwest.itw

What should Firefox do with this file?

● Open with Microsoft Office Excel (default)

○ Save File

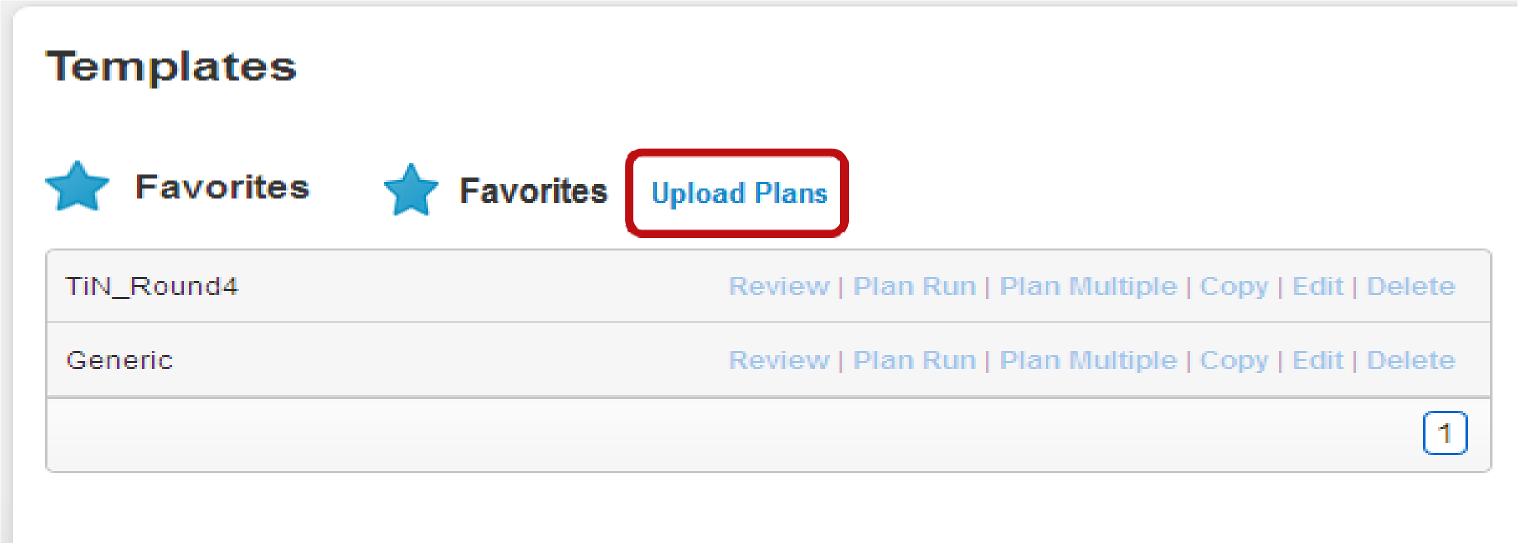
☐ Do this automatically for files like this from now on.

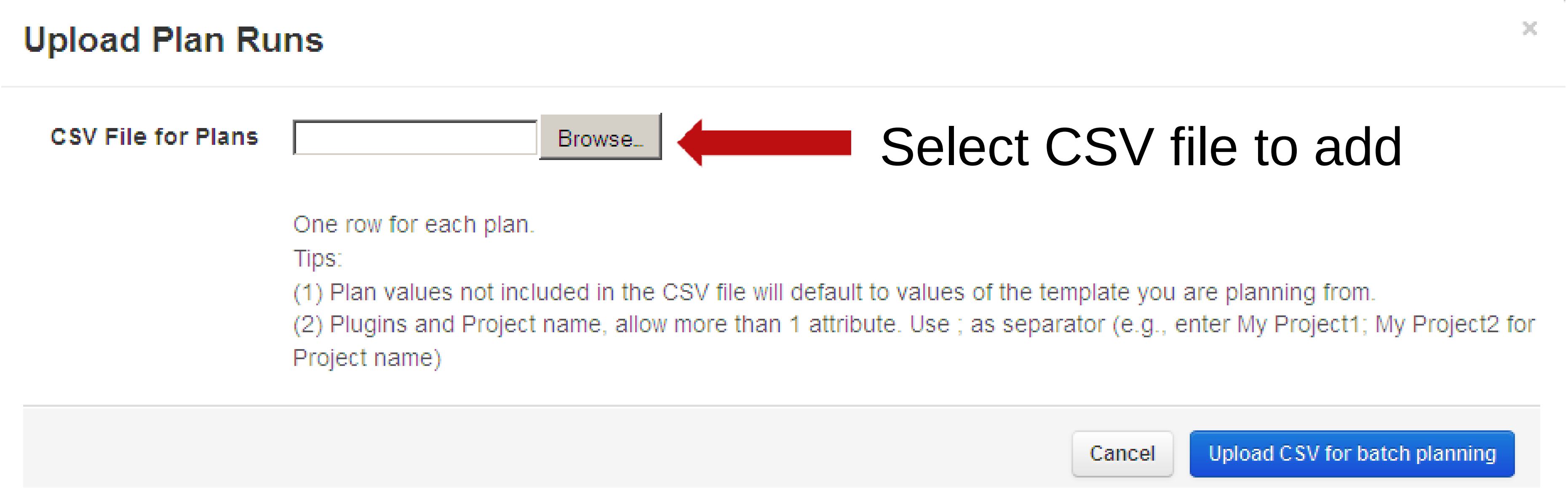


batchPlanning_2012_11_27_20_49_58.csv [Read-Only]

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	Template	Plan name	Sample	Sample pr	Library kit	Templating	Control se	Sequence	Chip type	Flows	Bead loadi	Key signal	Usable se	Reference	Target regi	Hotspot re	Plugins
2	Ion AmpliSeq Fan_Nov212012				Ion Xpress	Ion OneTouch 200 Te		(200bp) Ion PGM(tm)		500	30	30	30	hg19			
3	Ion AmpliSeq Fan_Nov212012				Ion Xpress	Ion OneTouch 200 Te		(200bp) Ion PGM(tm)		500	30	30	30	hg19			
4	Ion AmpliSeq Fan_Nov212012				Ion Xpress	Ion OneTouch 200 Te		(200bp) Ion PGM(tm)		500	30	30	30	hg19			
5																	

Upload Plans

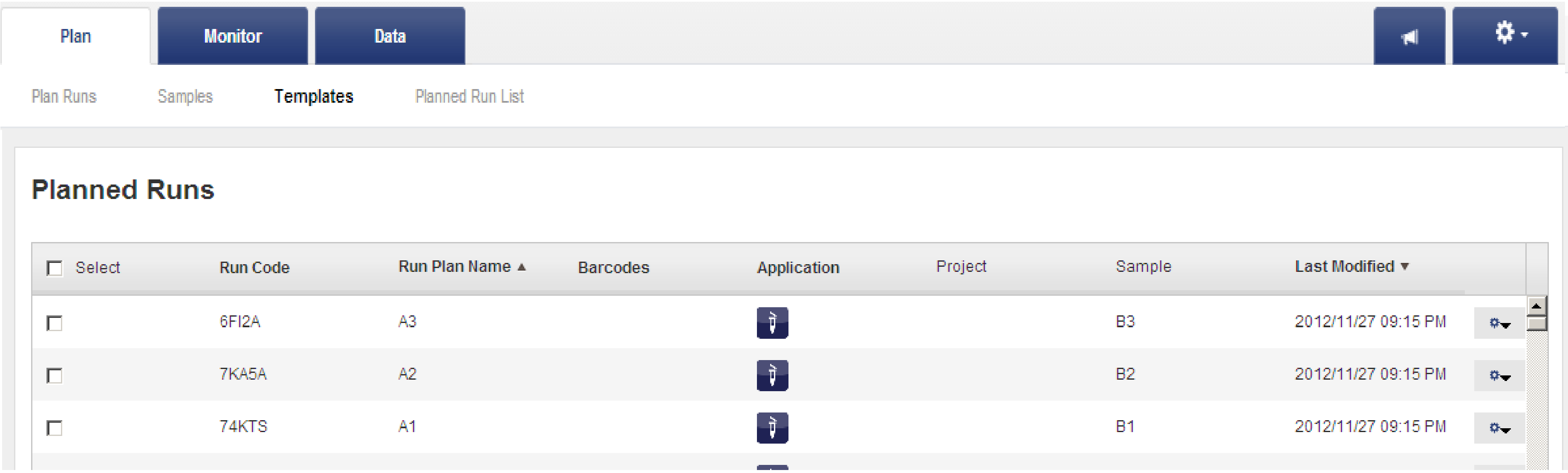

Templates
Favorites
Favorites
Upload Plans
TiN_Round4
Review | Plan Run | Plan Multiple | Copy | Edit | Delete
Generic
Review | Plan Run | Plan Multiple | Copy | Edit | Delete
1


Upload Plan Runs
×
CSV File for Plans
Browse...
Cancel
Upload CSV for batch planning

One row for each plan.
Tips:
(1) Plan values not included in the CSV file will default to values of the template you are planning from.
(2) Plugins and Project name, allow more than 1 attribute. Use ; as separator (e.g., enter My Project1; My Project2 for Project name)

Select CSV file to add

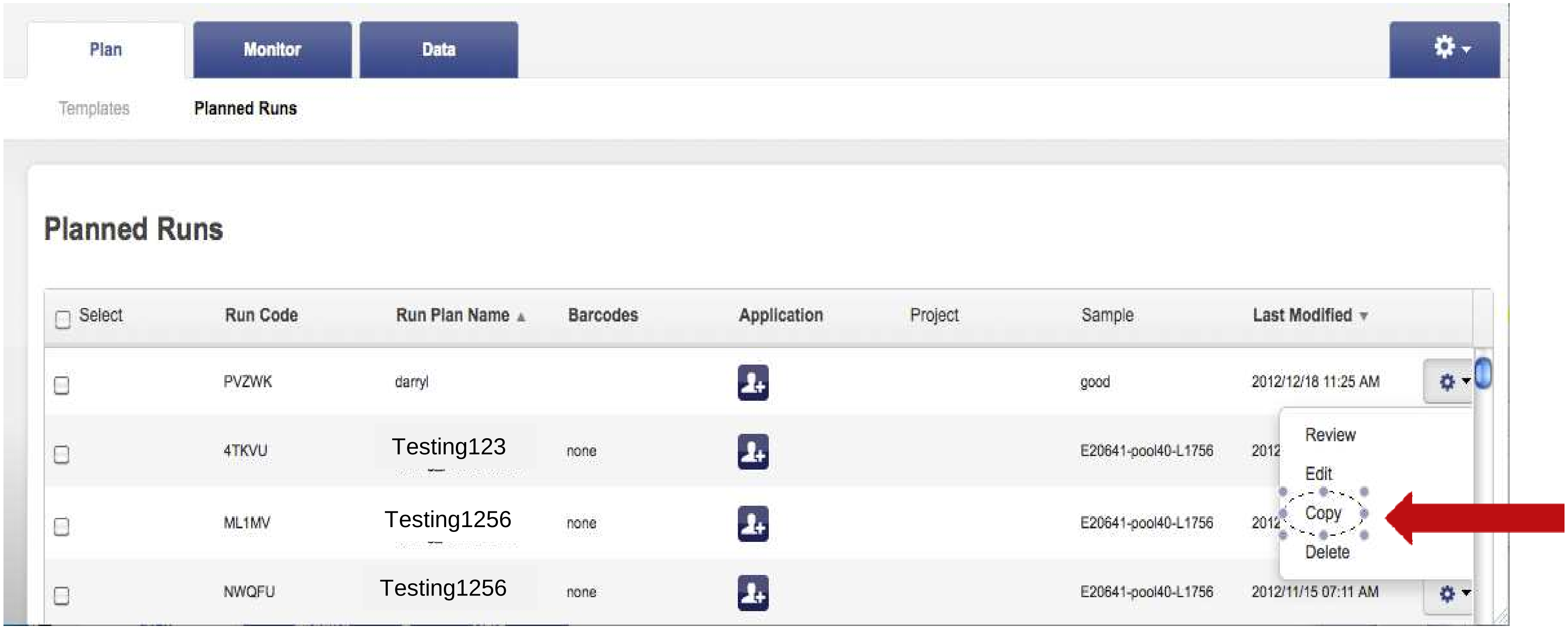
Review uploaded Planned Runs


Plan
Monitor
Data
Plan Runs
Samples
Templates
Planned Run List

Planned Runs

☐ Select	Run Code	Run Plan Name ▲	Barcodes	Application	Project	Sample	Last Modified ▼
☐	6FI2A	A3				B3	2012/11/27 09:15 PM
☐	7KA5A	A2				B2	2012/11/27 09:15 PM
☐	74KTS	A1				B1	2012/11/27 09:15 PM

Plan cloning: Copy

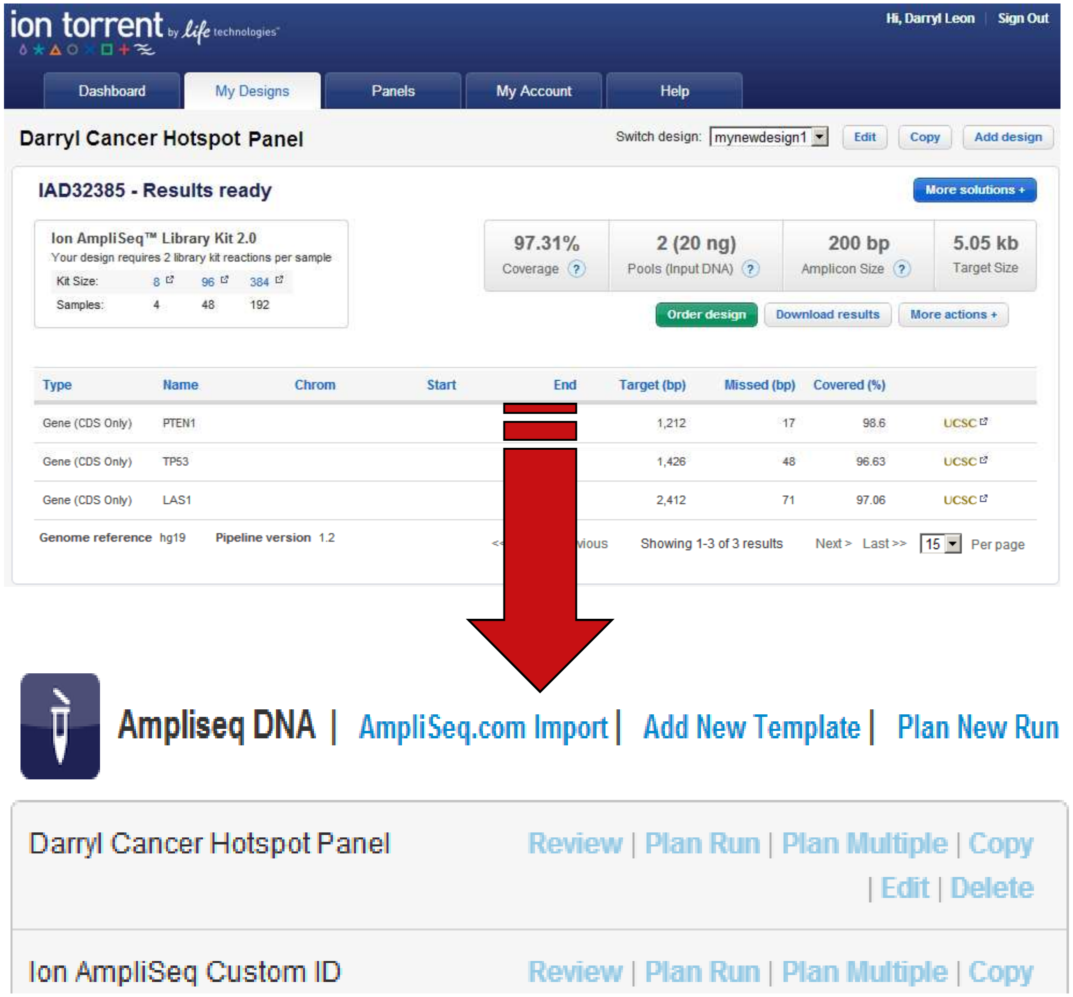

Plan
Monitor
Data
Templates
Planned Runs
Review
Edit
Copy
Delete

Planned Runs

☐ Select	Run Code	Run Plan Name ▲	Barcodes	Application	Project	Sample	Last Modified ▼
☐	PVZWK	darryl				good	2012/12/18 11:25 AM
☐	4TKVU	Testing123	none			E20641-pool40-L1756	2012
☐	ML1MV	Testing1256	none			E20641-pool40-L1756	2012
☐	NWQFU	Testing1256	none			E20641-pool40-L1756	2012/11/15 07:11 AM

Easily Create Run Template from Ion AmpliSeq™ Designer downloaded files

Ion AmpliSeq™ Designer


ion torrent by life technologies
Hi, Darryl Leon | Sign Out
Dashboard
My Designs
Panels
My Account
Help

Darryl Cancer Hotspot Panel

Switch design: mynewdesign1

Edit
Copy
Add design

IAD32385 - Results ready

More solutions +

Ion AmpliSeq™ Library Kit 2.0

Your design requires 2 library kit reactions per sample

Kit Size:	8	96	384
Samples:	4	48	192

97.31% Coverage

2 (20 ng) Pools (Input DNA)

200 bp Amplicon Size

5.05 kb Target Size

Order design
Download results
More actions +

Type	Name	Chrom	Start	End	Target (bp)	Missed (bp)	Covered (%)	
Gene (CDS Only)	PTEN1				1,212	17	98.6	UCSC
Gene (CDS Only)	TP53				1,426	48	96.63	UCSC
Gene (CDS Only)	LAS1				2,412	71	97.06	UCSC

Genome reference hg19 **Pipeline version** 1.2

<< vious Showing 1-3 of 3 results Next > Last >> 15 Per page

Torrent Browser

Ampliseq DNA | AmpliSeq.com Import | Add New Template | Plan New Run

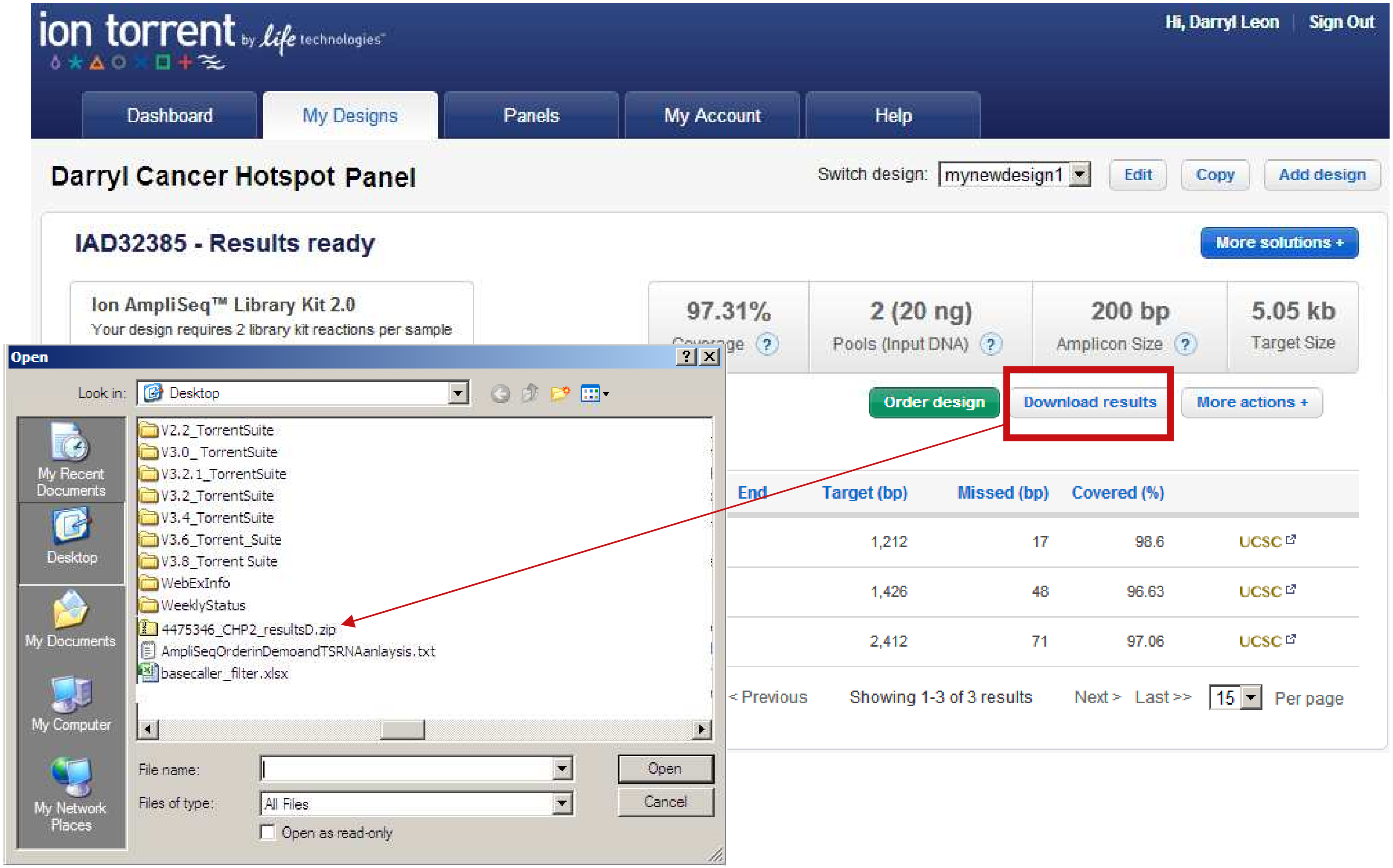
Darryl Cancer Hotspot Panel

Review | Plan Run | Plan Multiple | Copy | Edit | Delete

Ion AmpliSeq Custom ID

Review | Plan Run | Plan Multiple | Copy

Download zip file from Ion AmpliSeq™ Designer to local computer


ion torrent by life technologies
Hi, Darryl Leon
Sign Out
Dashboard
My Designs
Panels
My Account
Help
Switch design:
Edit
Copy
Add design
More solutions +
Order design
Download results
More actions +
UCSC
< Previous
Next >
Last >>
Per page
Open
Look in:
My Recent Documents
Desktop
My Documents
My Computer
My Network Places
Open
Cancel

Darryl Cancer Hotspot Panel

Switch design: mynewdesign1

IAD32385 - Results ready

Ion AmpliSeq™ Library Kit 2.0

Your design requires 2 library kit reactions per sample

97.31%	2 (20 ng)	200 bp	5.05 kb
Coverage	Pools (Input DNA)	Amplicon Size	Target Size

End	Target (bp)	Missed (bp)	Covered (%)	
	1,212	17	98.6	UCSC
	1,426	48	96.63	UCSC
	2,412	71	97.06	UCSC

Showing 1-3 of 3 results — 15 Per page

Open

Look in: Desktop

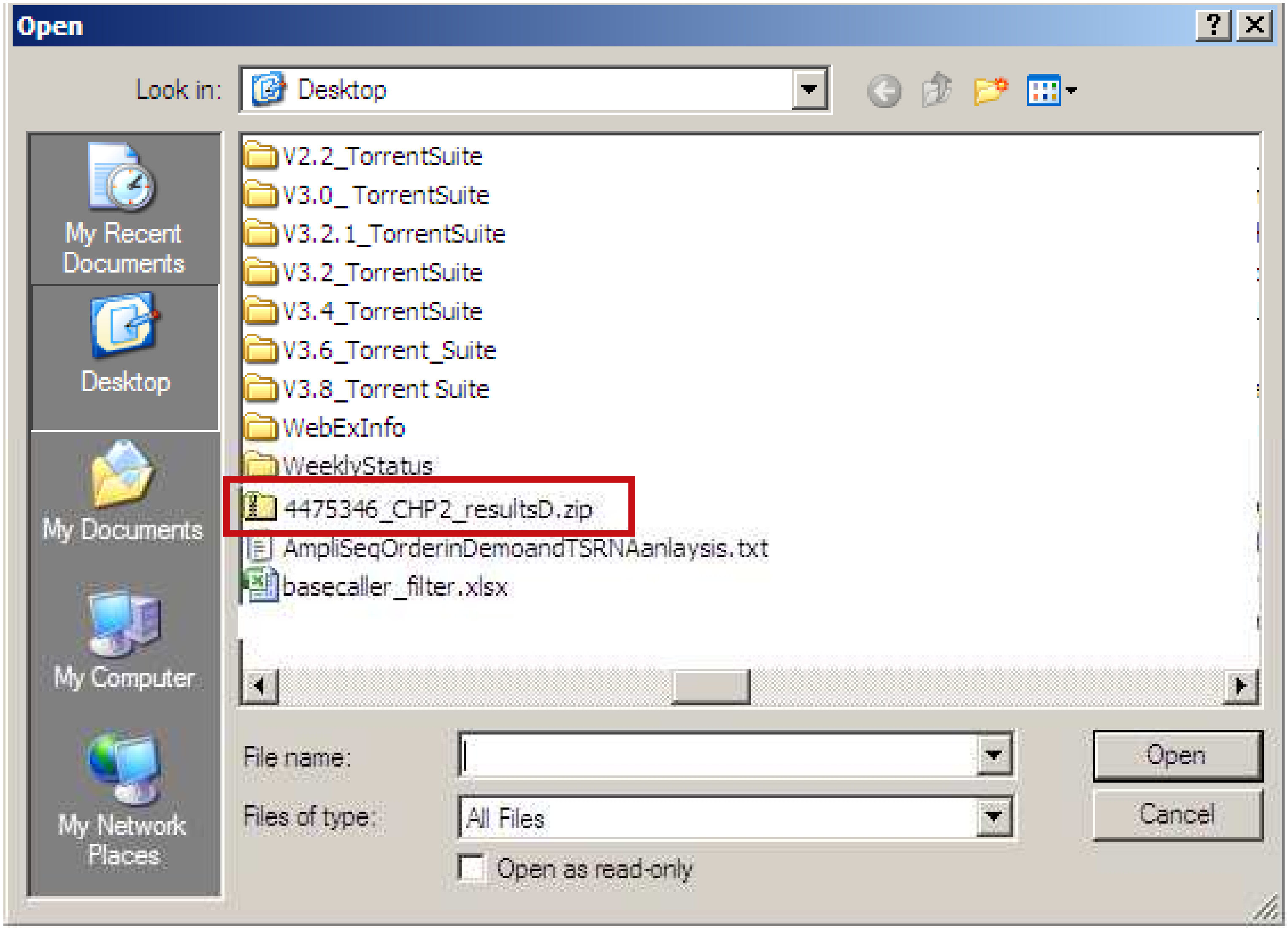
- V2.2_TorrentSuite
- V3.0_ TorrentSuite
- V3.2.1_TorrentSuite
- V3.2_TorrentSuite
- V3.4_TorrentSuite
- V3.6_Torrent_Suite
- V3.8_Torrent Suite
- WebExInfo
- WeeklyStatus
- 4475346_CHP2_resultsD.zip
- AmpliSeqOrderinDemoandTSRNAanlaysis.txt
- basecaller_filter.xlsx

File name:

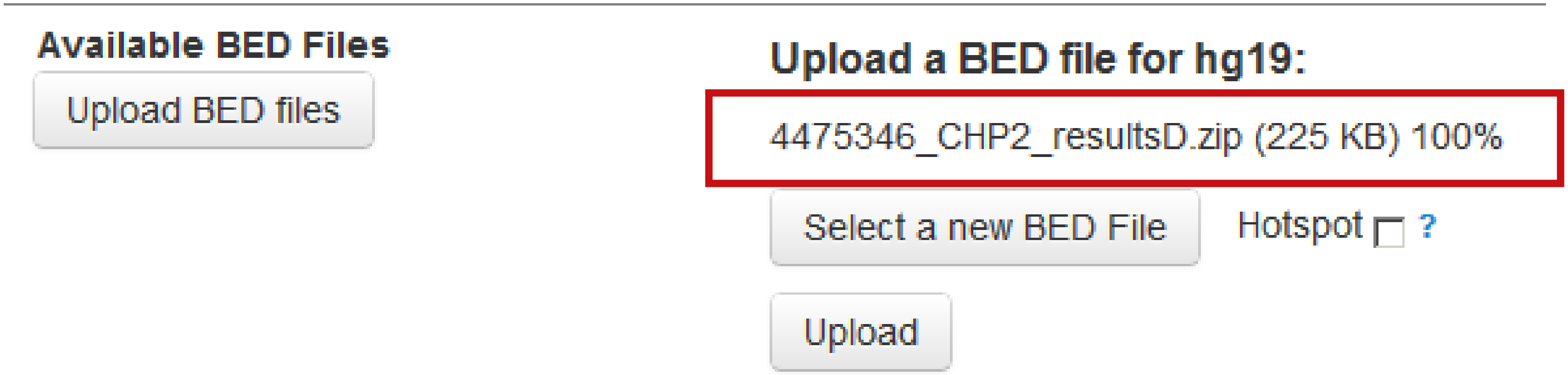
Files of type: All Files

☐ Open as read-only

Navigate to Ion AmpliSeq™ Designer Zipped file and Upload

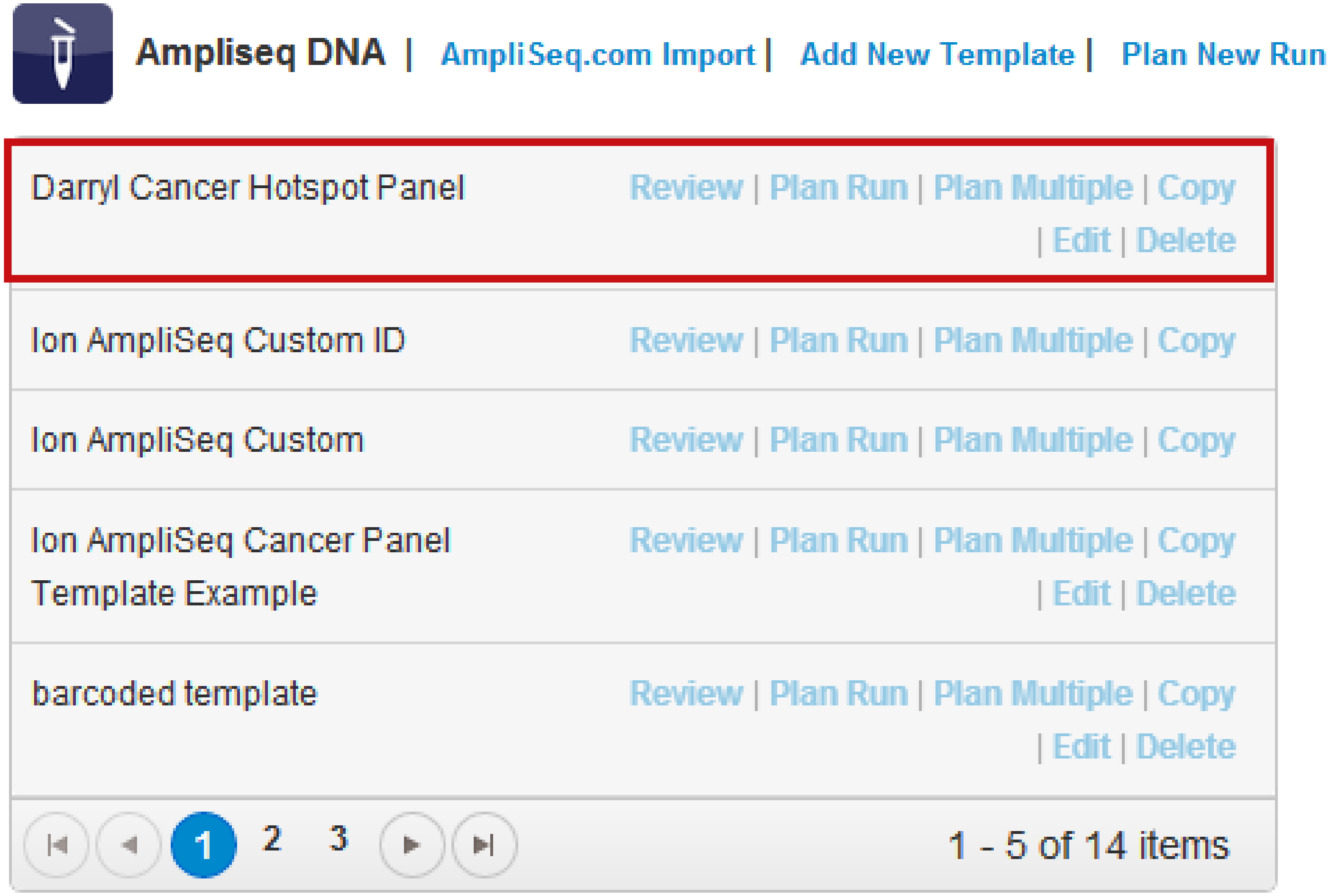

Open
Look in: Desktop
My Recent Documents
Desktop
My Documents
My Computer
My Network Places
V2.2_TorrentSuite
V3.0_ TorrentSuite
V3.2.1_TorrentSuite
V3.2_TorrentSuite
V3.4_TorrentSuite
V3.6_Torrent_Suite
V3.8_Torrent Suite
WebExInfo
WeeklyStatus
4475346_CHP2_resultsD.zip
AmpliSeqOrderinDemoandTSRNAanlaysis.txt
basecaller_filter.xlsx
File name:
Files of type: All Files
☐ Open as read-only
Open
Cancel

Verify Zipped BED File is Added


Available BED Files
Upload BED files
Upload a BED file for hg19:
Select a new BED File
Hotspot ☐ ?
Upload

4475346_CHP2_resultsD.zip (225 KB) 100%

Verify Template is Automatically Generated

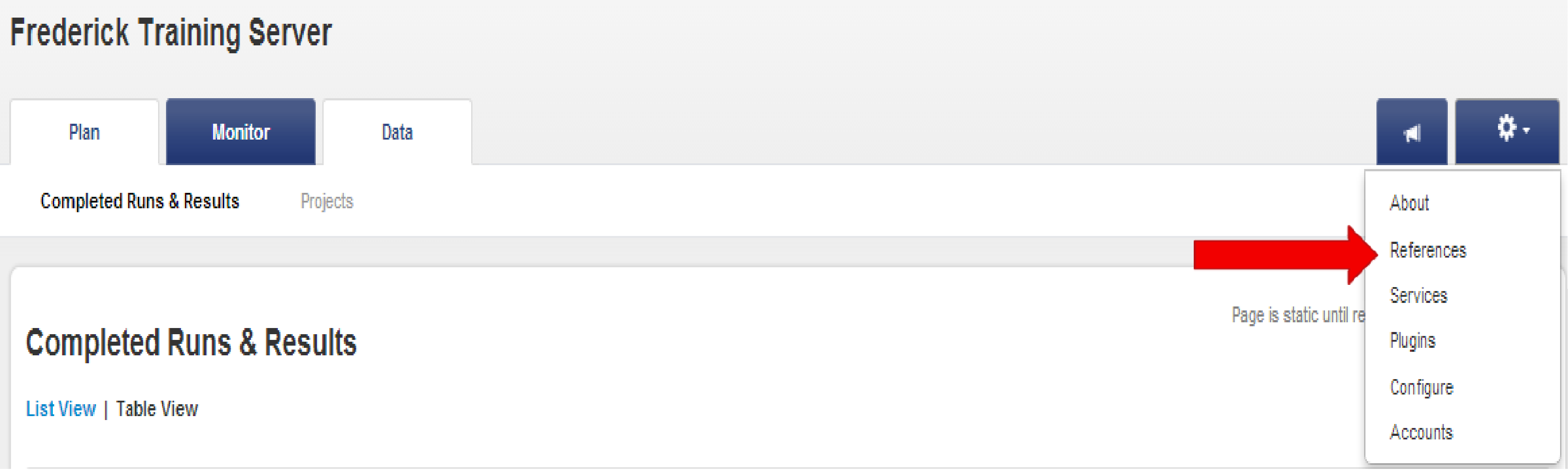


Ampliseq DNA | AmpliSeq.com Import | Add New Template | Plan New Run

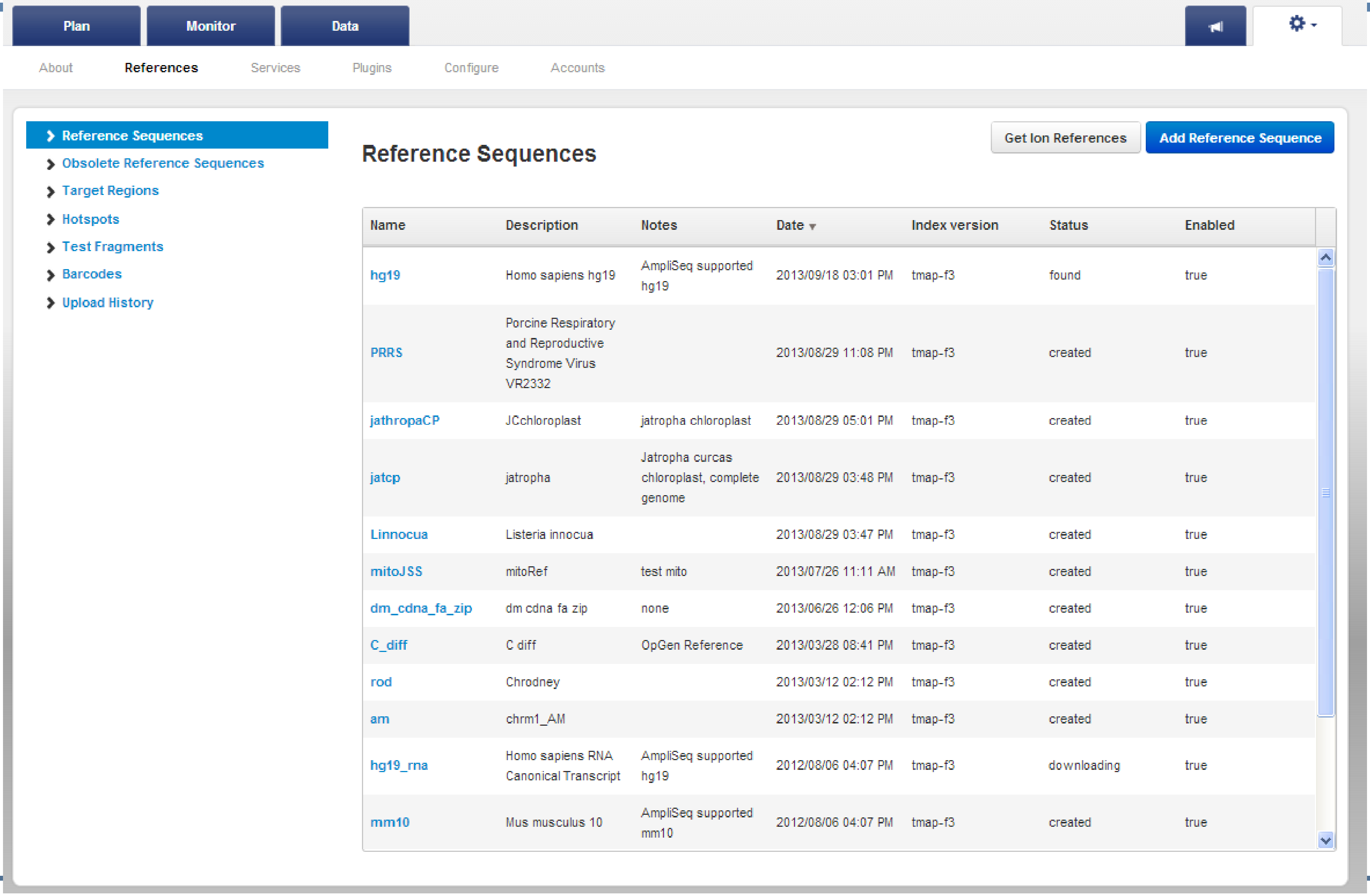
Darryl Cancer Hotspot Panel	Review | Plan Run | Plan Multiple | Copy | Edit | Delete
Ion AmpliSeq Custom ID	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Custom	Review | Plan Run | Plan Multiple | Copy
Ion AmpliSeq Cancer Panel Template Example	Review | Plan Run | Plan Multiple | Copy | Edit | Delete
barcoded template	Review | Plan Run | Plan Multiple | Copy | Edit | Delete

1 - 5 of 14 items

Select References in Torrent Browser


Frederick Training Server
Plan
Monitor
Data
Completed Runs & Results
Projects
About
References
Services
Plugins
Configure
Accounts
Page is static until re
Completed Runs & Results
List View | Table View

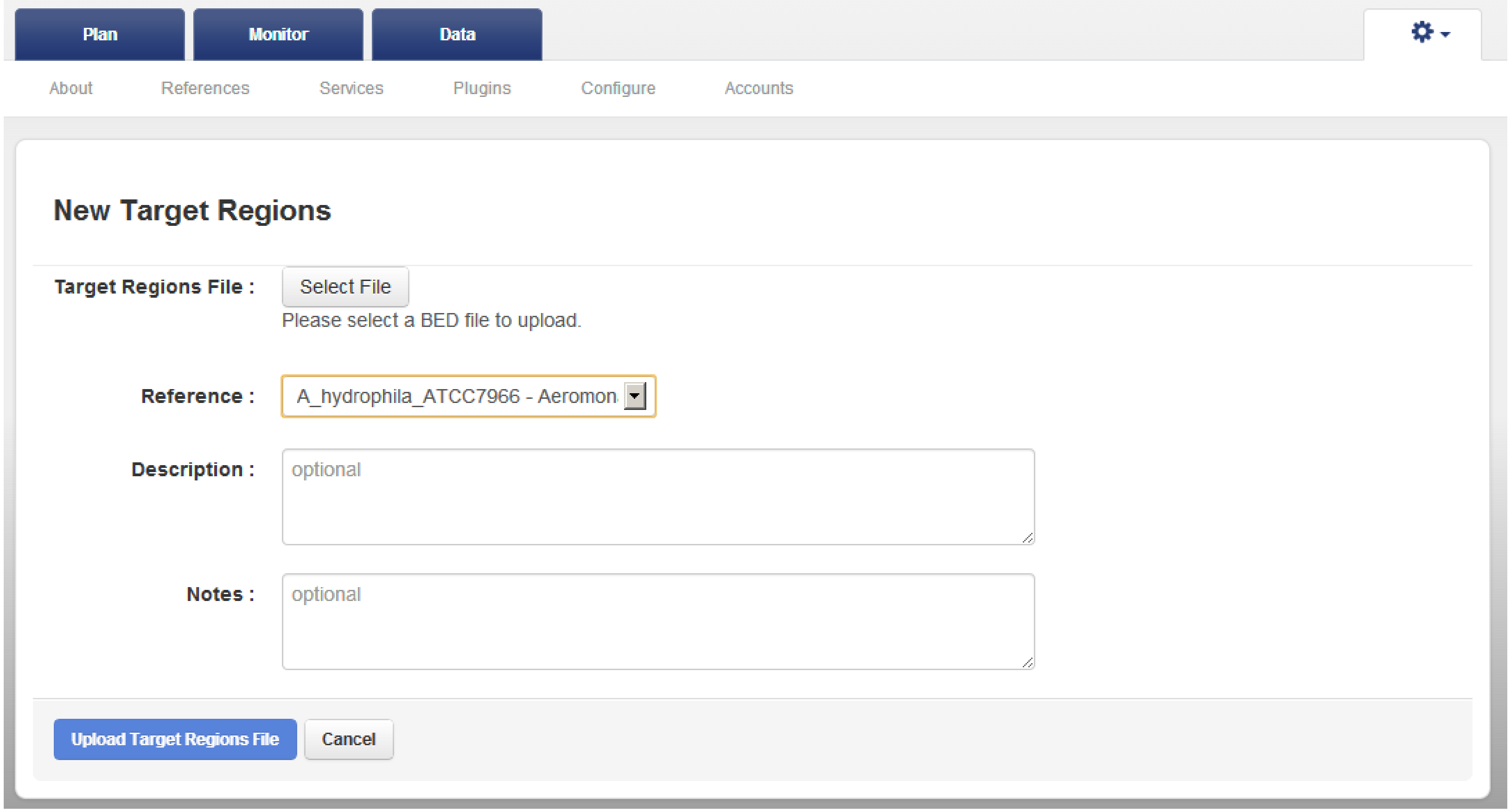
Select Reference Genome


Plan
Monitor
Data
About
References
Services
Plugins
Configure
Accounts
Reference Sequences
Obsolete Reference Sequences
Target Regions
Hotspots
Test Fragments
Barcodes
Upload History
Get Ion References
Add Reference Sequence

Reference Sequences

Name	Description	Notes	Date ▾	Index version	Status	Enabled
hg19	Homo sapiens hg19	AmpliSeq supported hg19	2013/09/18 03:01 PM	tmap-f3	found	true
PRRS	Porcine Respiratory and Reproductive Syndrome Virus VR2332		2013/08/29 11:08 PM	tmap-f3	created	true
jathropaCP	JCchloroplast	jatropha chloroplast	2013/08/29 05:01 PM	tmap-f3	created	true
jatcp	jatropha	Jatropha curcas chloroplast, complete genome	2013/08/29 03:48 PM	tmap-f3	created	true
Linnocua	Listeria innocua		2013/08/29 03:47 PM	tmap-f3	created	true
mitoJSS	mitoRef	test mito	2013/07/26 11:11 AM	tmap-f3	created	true
dm_cdna_fa_zip	dm cdna fa zip	none	2013/06/26 12:06 PM	tmap-f3	created	true
C_diff	C diff	OpGen Reference	2013/03/28 08:41 PM	tmap-f3	created	true
rod	Chrodney		2013/03/12 02:12 PM	tmap-f3	created	true
am	chrm1_AM		2013/03/12 02:12 PM	tmap-f3	created	true
hg19_rna	Homo sapiens RNA Canonical Transcript	AmpliSeq supported hg19	2012/08/06 04:07 PM	tmap-f3	downloading	true
mm10	Mus musculus 10	AmpliSeq supported mm10	2012/08/06 04:07 PM	tmap-f3	created	true

Target File Selection


Plan
Monitor
Data
About
References
Services
Plugins
Configure
Accounts

New Target Regions

Target Regions File : Select File
Please select a BED file to upload.

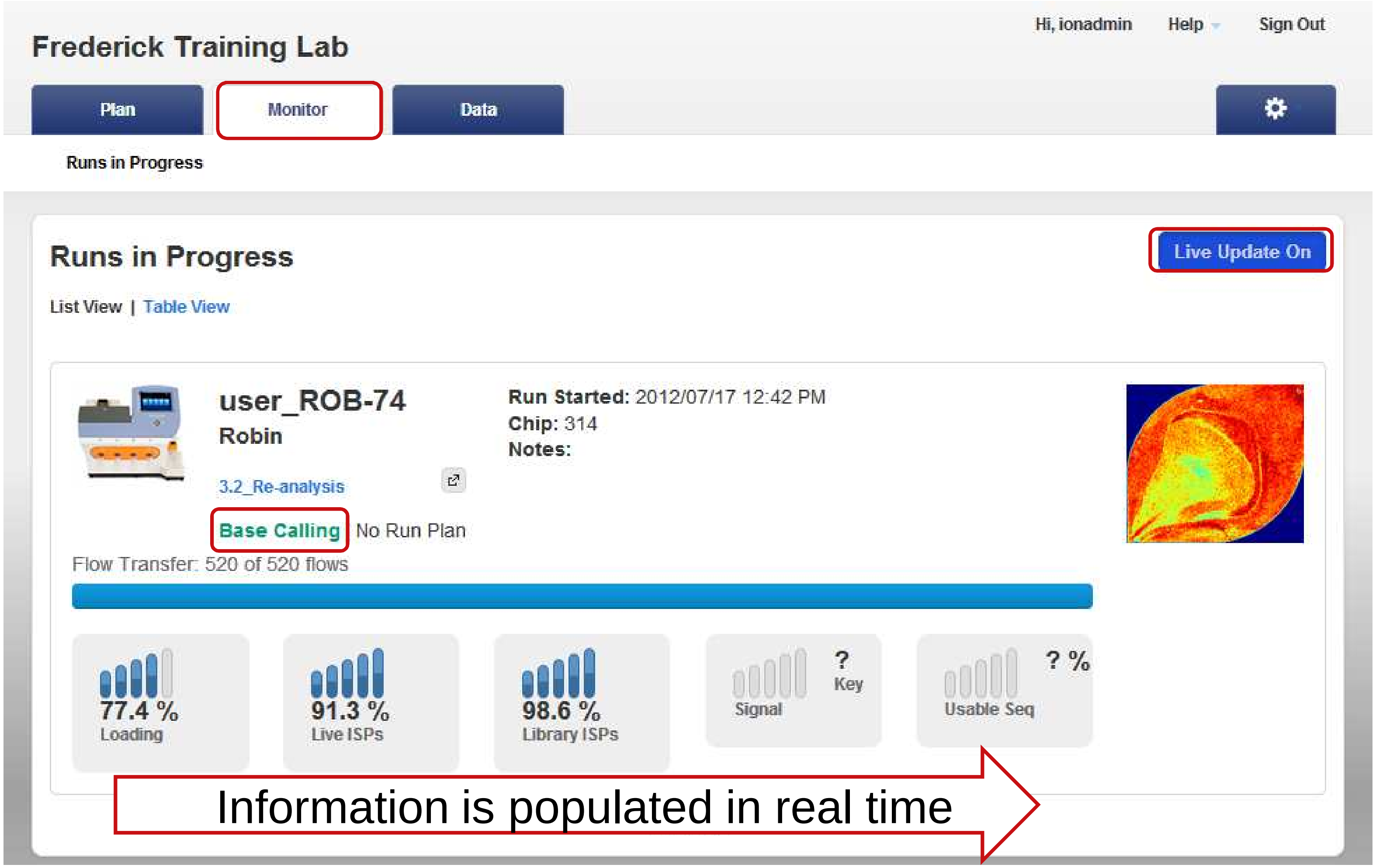
Reference : A_hydrophila_ATCC7966 - Aeromon

Description : optional

Notes : optional

Upload Target Regions File
Cancel

Monitor Tab



Frederick Training Lab

Hi, ionadmin
Help
Sign Out

Runs in Progress

Runs in Progress

List View | Table View

user_ROB-74

Robin

3.2_Re-analysis

Run Started: 2012/07/17 12:42 PM
Chip: 314
Notes:

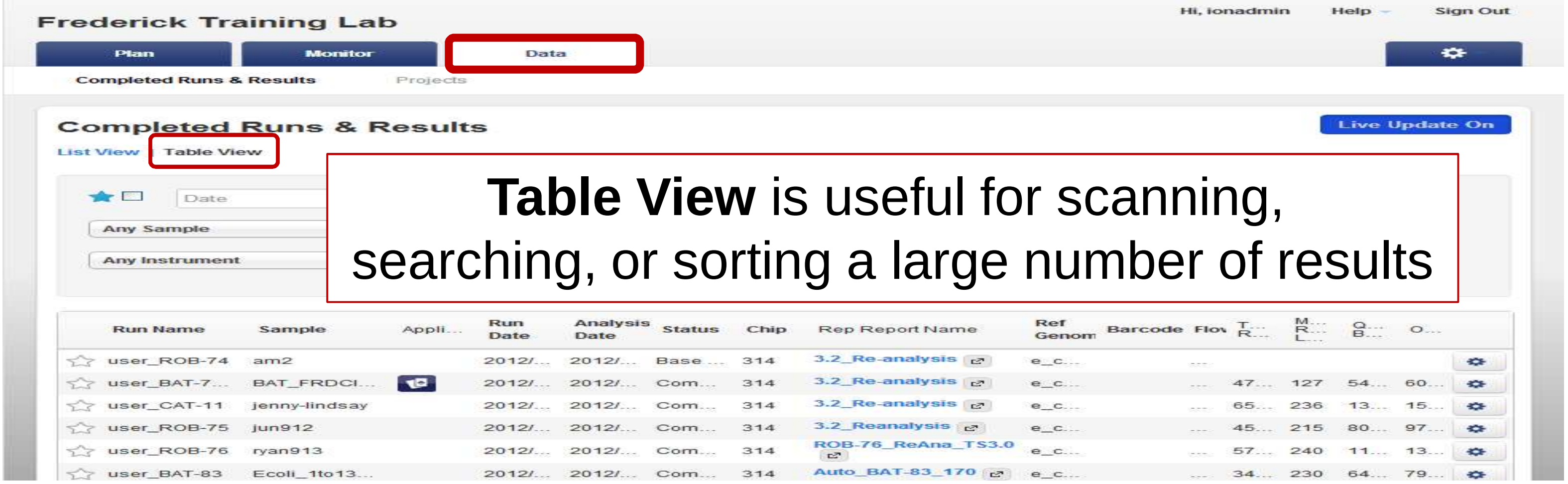
Base Calling No Run Plan

Flow Transfer: 520 of 520 flows

77.4 %	91.3 %	98.6 %	? Key	? %
Loading	Live ISPs	Library ISPs	Signal	Usable Seq

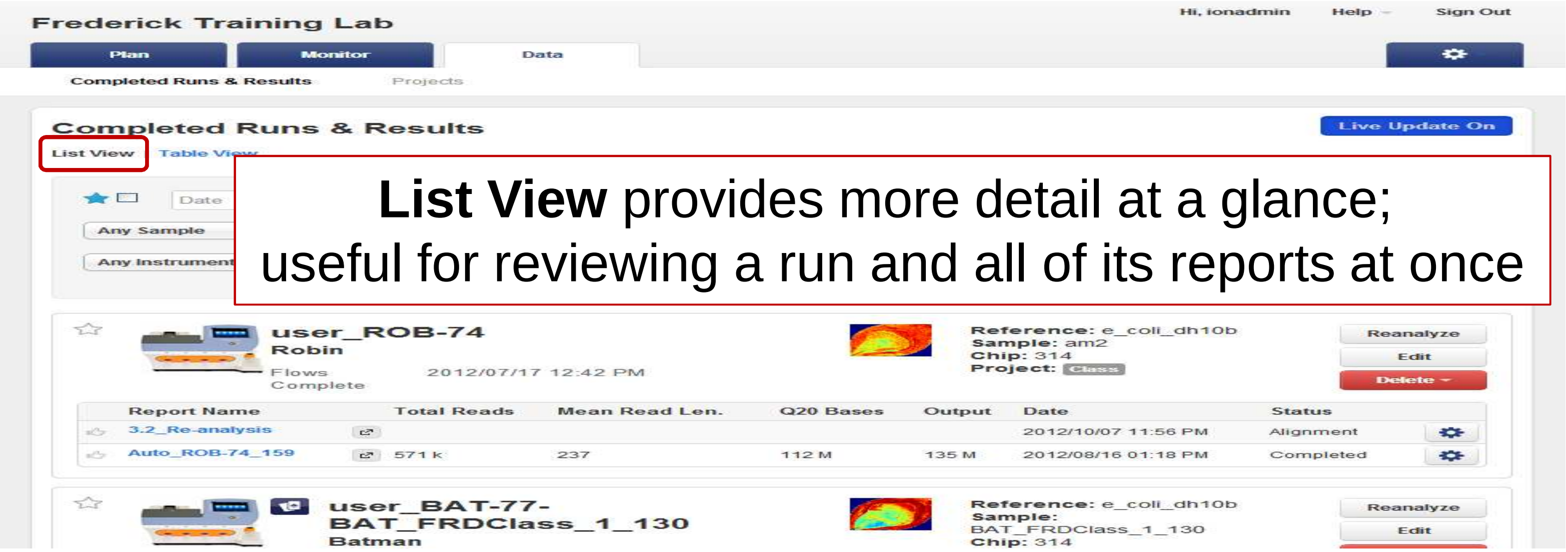
Information is populated in real time

Data Tab – Table View & List View


Frederick Training Lab
Hi, ionadmin
Help
Sign Out
Plan
Monitor
Data
Completed Runs & Results
Projects
Completed Runs & Results
Live Update On
List View
Table View
Date
Any Sample
Any Instrument

	Run Name	Sample	Appli...	Run Date	Analysis Date	Status	Chip	Rep Report Name	Ref Genom	Barcode	Flow	T... R...	M... R... L...	Q... B...	O...
☆	user_ROB-74	am2		2012/...	2012/...	Base ...	314	3.2_Re-analysis	e_c...		...				
☆	user_BAT-7...	BAT_FRDCl...		2012/...	2012/...	Com...	314	3.2_Re-analysis	e_c...		...	47...	127	54...	60...
☆	user_CAT-11	jenny-lindsay		2012/...	2012/...	Com...	314	3.2_Re-analysis	e_c...		...	65...	236	13...	15...
☆	user_ROB-75	jun912		2012/...	2012/...	Com...	314	3.2_Reanalysis	e_c...		...	45...	215	80...	97...
☆	user_ROB-76	ryan913		2012/...	2012/...	Com...	314	ROB-76_ReAna_TS3.0	e_c...		...	57...	240	11...	13...
☆	user_BAT-83	Ecoli_1to13...		2012/...	2012/...	Com...	314	Auto_BAT-83_170	e_c...		...	34...	230	64...	79...

Table View is useful for scanning, searching, or sorting a large number of results


Frederick Training Lab
Hi, ionadmin
Help
Sign Out
Plan
Monitor
Data
Completed Runs & Results
Projects
Completed Runs & Results
Live Update On
List View
Table View
Date
Any Sample
Any Instrument
Reanalyze
Edit
Delete
Reanalyze
Edit

user_ROB-74
Robin
Flows Complete 2012/07/17 12:42 PM
Reference: e_coli_dh10b
Sample: am2
Chip: 314
Project: Class

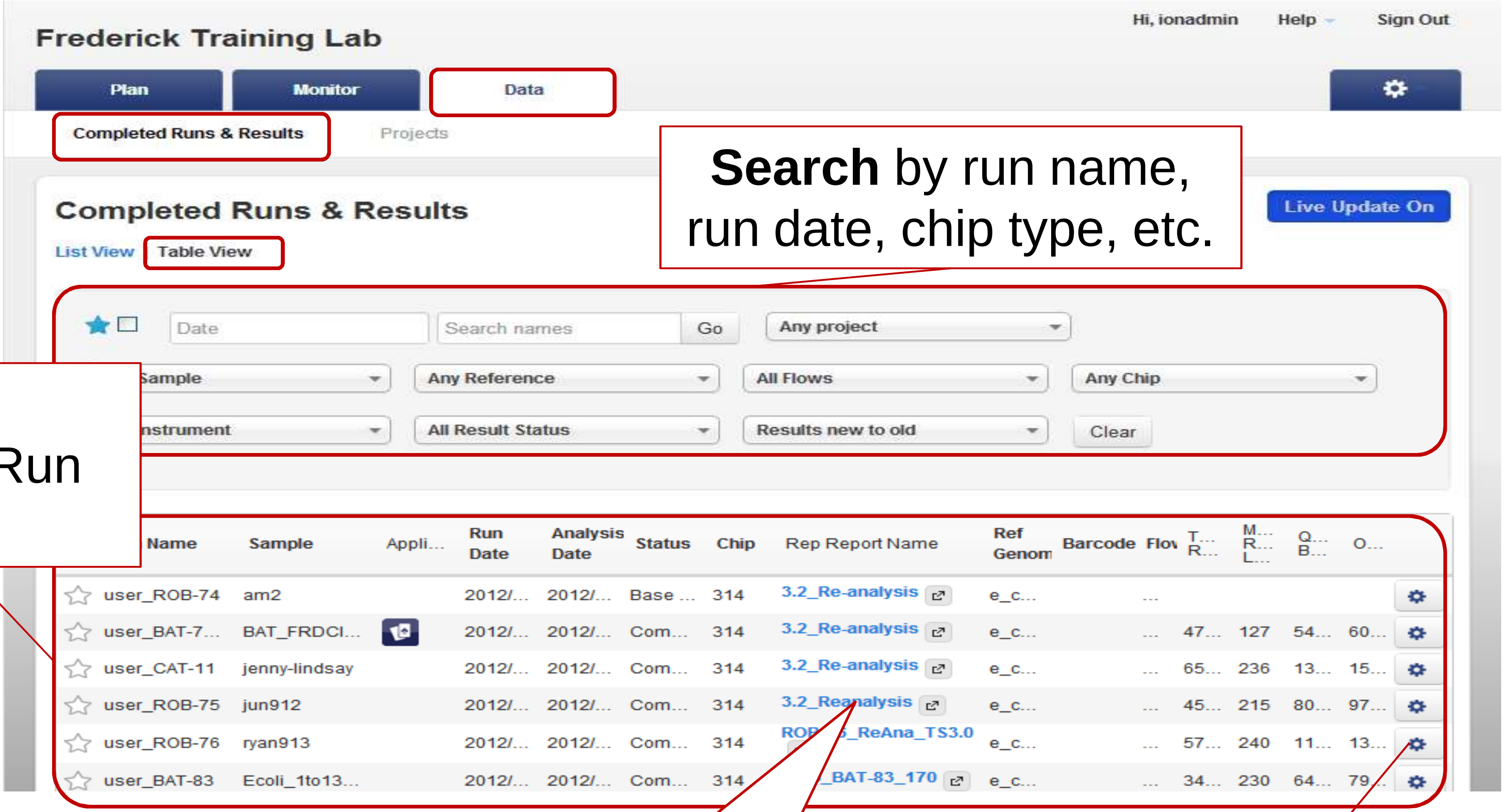
Report Name	Total Reads	Mean Read Len.	Q20 Bases	Output	Date	Status
3.2_Re-analysis					2012/10/07 11:56 PM	Alignment
Auto_ROB-74_159	571 k	237	112 M	135 M	2012/08/16 01:18 PM	Completed

user_BAT-77-BAT_FRDClass_1_130
Batman
Reference: e_coli_dh10b
Sample: BAT_FRDClass_1_130
Chip: 314

List View provides more detail at a glance; useful for reviewing a run and all of its reports at once

Screen shot is from TS 3.2; other versions may vary.

Data Tab

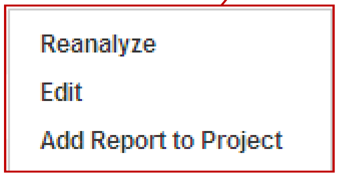

Frederick Training Lab
Hi, ionadmin
Help
Sign Out
Plan
Monitor
Data
Completed Runs & Results
Projects
Completed Runs & Results
List View
Table View
Live Update On
Date
Search names
Go
Any project
Sample
Any Reference
All Flows
Any Chip
nstrument
All Result Status
Results new to old
Clear

Name	Sample	Appli…	Run Date	Analysis Date	Status	Chip	Rep Report Name	Ref Genom	Barcode	Flov	T… R…	M… R… L…	Q… B…	O…
☆ user_ROB-74	am2		2012/…	2012/…	Base …	314	3.2_Re-analysis	e_c…		…				
☆ user_BAT-7…	BAT_FRDCI…		2012/…	2012/…	Com…	314	3.2_Re-analysis	e_c…		…	47…	127	54…	60…
☆ user_CAT-11	jenny-lindsay		2012/…	2012/…	Com…	314	3.2_Re-analysis	e_c…		…	65…	236	13…	15…
☆ user_ROB-75	jun912		2012/…	2012/…	Com…	314	3.2_Reanalysis	e_c…		…	45…	215	80…	97…
☆ user_ROB-76	ryan913		2012/…	2012/…	Com…	314	ROB_5_ReAna_TS3.0	e_c…		…	57…	240	11…	13…
☆ user_BAT-83	Ecoli_1to13…		2012/…	2012/…	Com…	314	_BAT-83_170	e_c…		…	34…	230	64…	79…

Search by run name, run date, chip type, etc.

Table of Runs & Run Reports

Click to see run report


Reanalyze
Edit
Add Report to Project

Open a report

Run Report - Overview

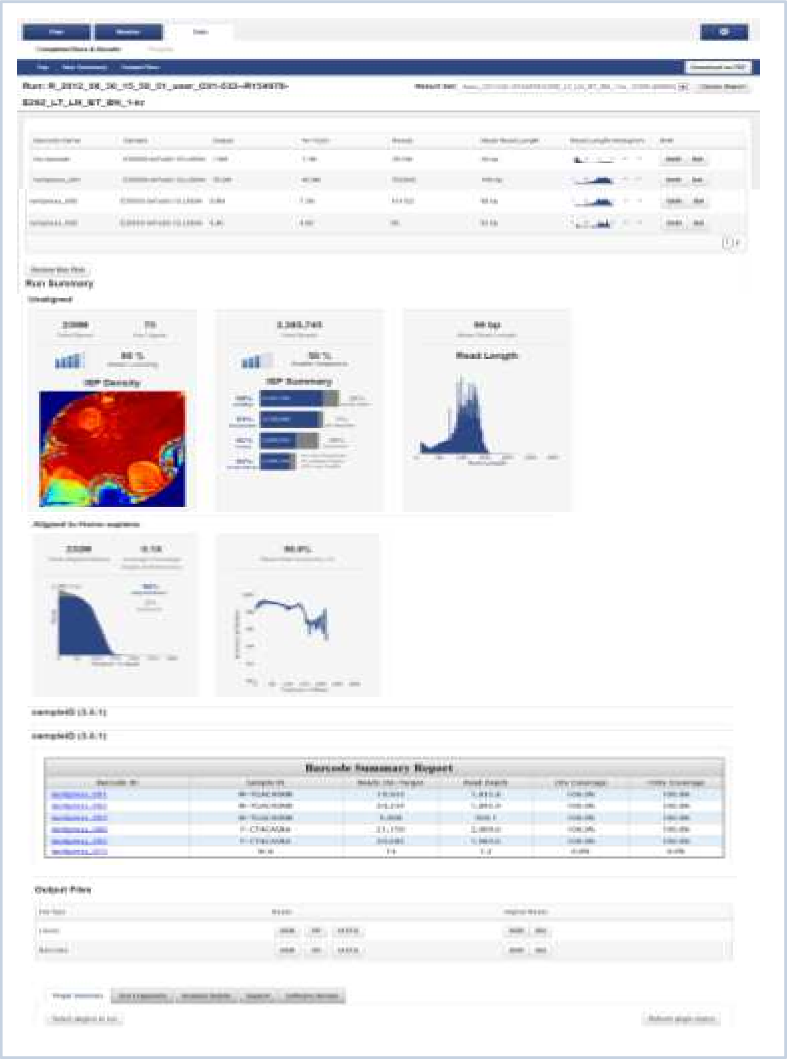
Navigation bar

Barcoding table (if applicable)

Unaligned/ Aligned metrics

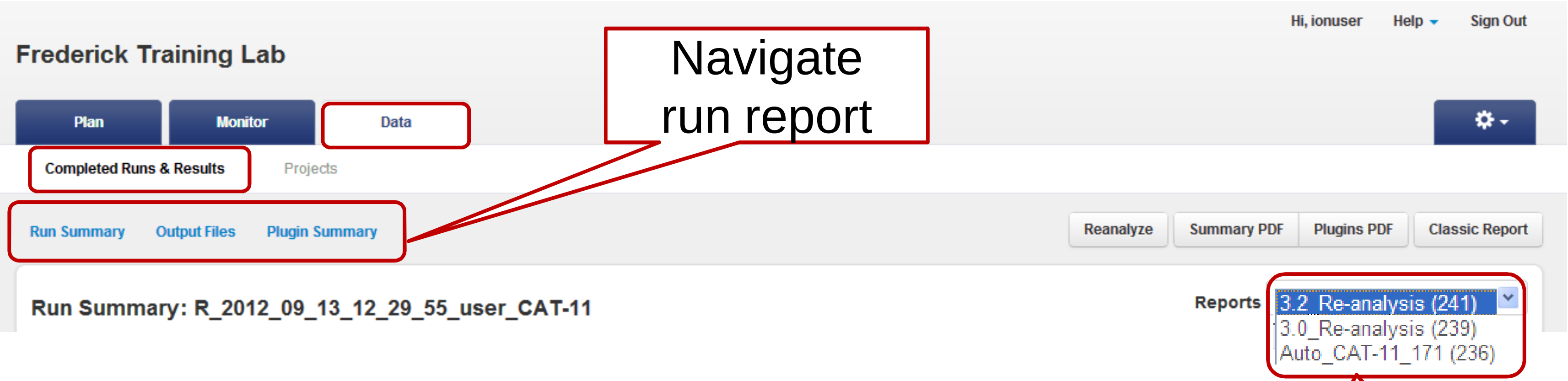
Plugin summaries

Output files



Screen shot is from TS 3.2; other versions may vary.

Run Report – Top

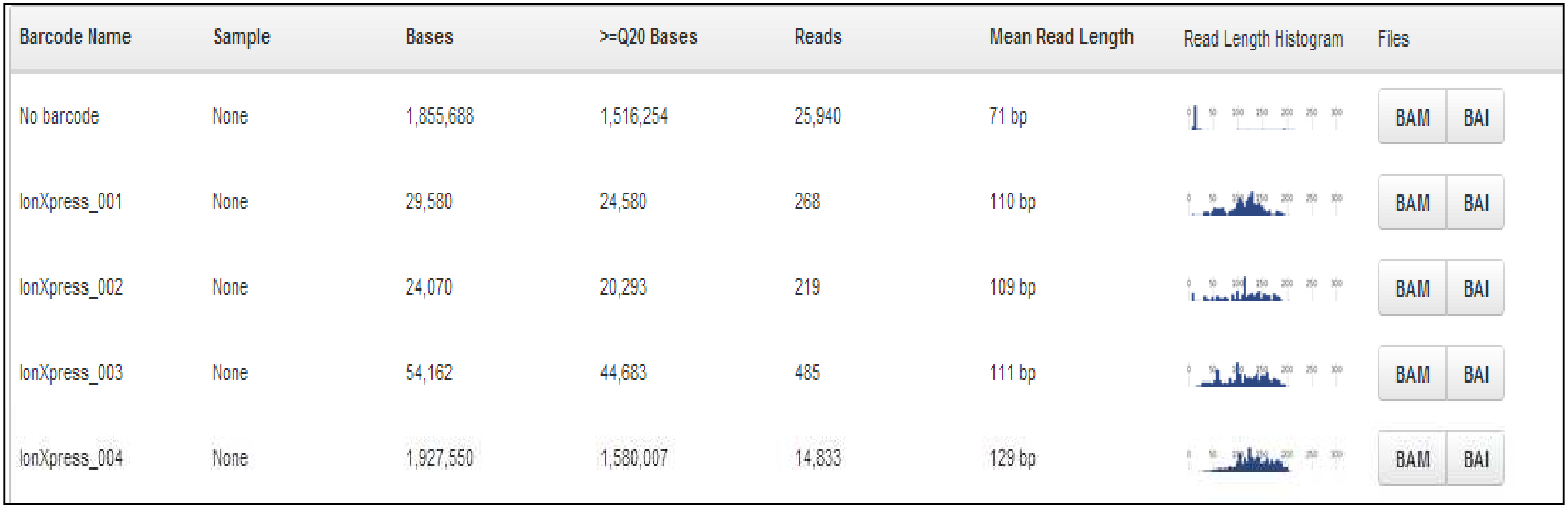

Frederick Training Lab
Hi, ionuser
Help
Sign Out
Plan
Monitor
Data
Completed Runs & Results
Projects
Run Summary
Output Files
Plugin Summary
Reanalyze
Summary PDF
Plugins PDF
Classic Report
Run Summary: R_2012_09_13_12_29_55_user_CAT-11
Reports
3.2_Re-analysis (241)
3.0_Re-analysis (239)
Auto_CAT-11_171 (236)

Navigate run report

See other run reports for this run*

* Most recent analysis defaults as representative run report. User can change representative run report.

Run Report – Barcoding information (if used)

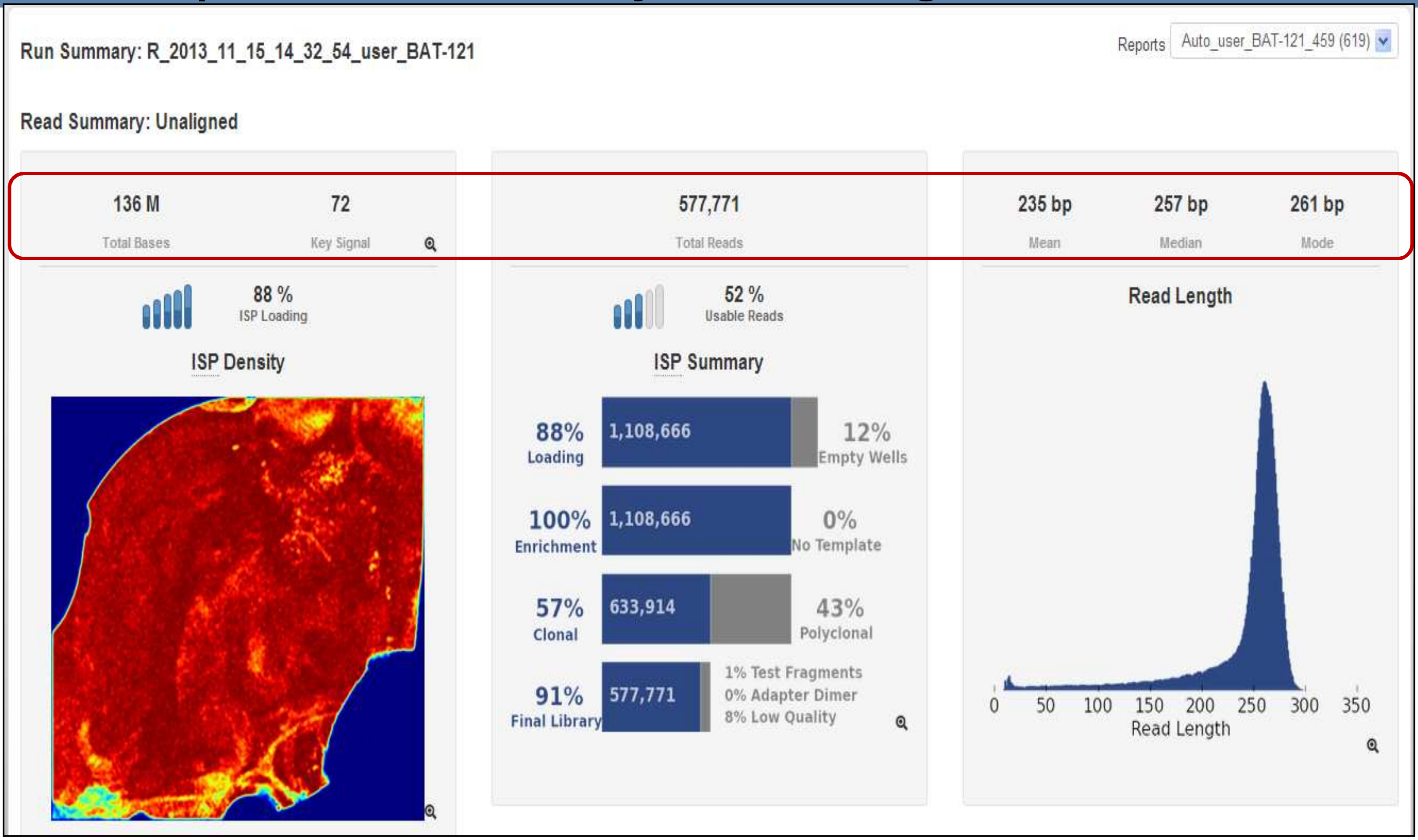


Barcode Name	Sample	Bases	>=Q20 Bases	Reads	Mean Read Length	Read Length Histogram	Files
No barcode	None	1,855,688	1,516,254	25,940	71 bp		BAM BAI
IonXpress_001	None	29,580	24,580	268	110 bp		BAM BAI
IonXpress_002	None	24,070	20,293	219	109 bp		BAM BAI
IonXpress_003	None	54,162	44,683	485	111 bp		BAM BAI
IonXpress_004	None	1,927,550	1,580,007	14,833	129 bp		BAM BAI

For each Barcode, we show…

- Total output (bases)
- AQ20 Bases
- AQ20 reads
- Mean AQ20 read length

Run Report – Summary of Unaligned reads



Run Summary: R_2013_11_15_14_32_54_user_BAT-121

Reports: Auto_user_BAT-121_459 (619)

Read Summary: Unaligned

136 M Total Bases

72 Key Signal

577,771 Total Reads

235 bp Mean

257 bp Median

261 bp Mode

88 % ISP Loading

52 % Usable Reads

ISP Density
ISP Summary
88% Loading
1,108,666
12% Empty Wells
100% Enrichment
1,108,666
0% No Template
57% Clonal
633,914
43% Polyclonal
91% Final Library
577,771
1% Test Fragments
0% Adapter Dimer
8% Low Quality
Read Length
0
50
100
150
200
250
300
350
Read Length

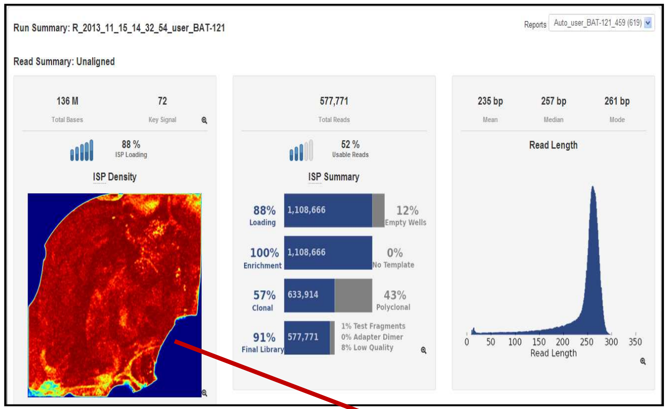
Efficiency of chip loading

Percentage of wells that generated reads that passed filtering

Average read lengths

Information about bases and reads *before* mapping

Chip Loading Image: Very Good Loading Example



Run Summary: R_2013_11_15_14_32_54_user_BAT-121

Reports Auto_user_BAT-121_459 (619)

Read Summary: Unaligned

136 M Total Bases
72 Key Signal
88 % ISP Loading

ISP Density

577,771 Total Reads
52 % Usable Reads

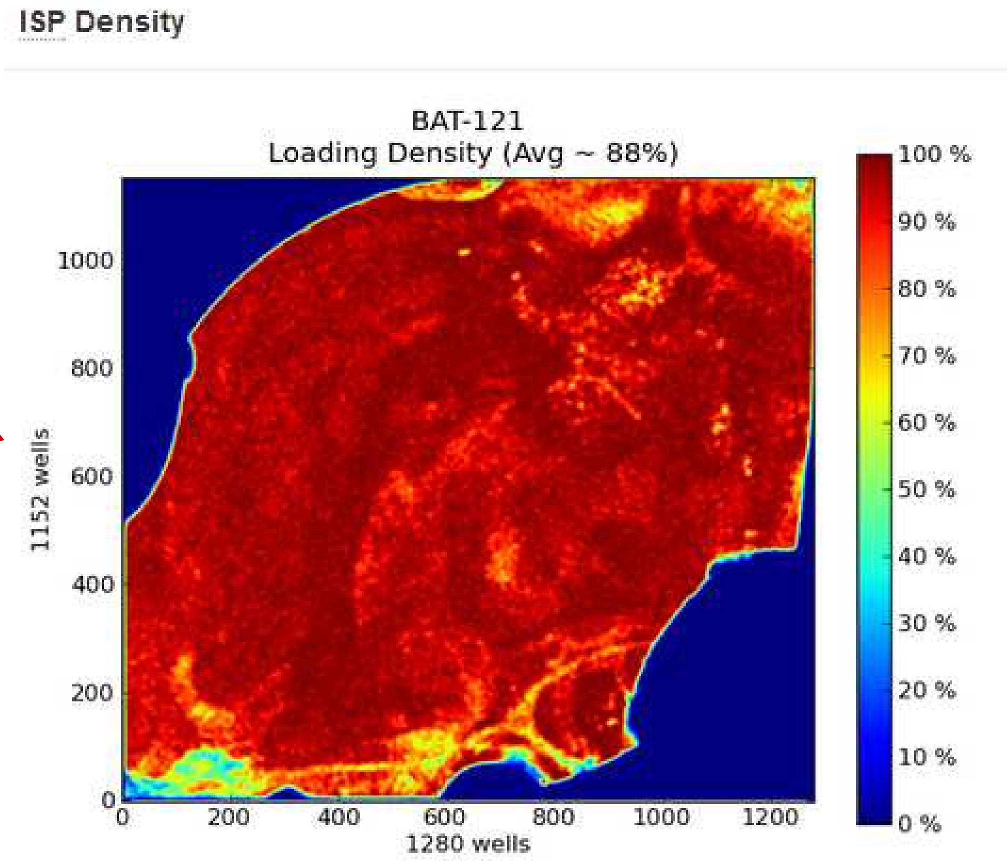
ISP Summary

88% Loading	1,108,666	12% Empty Wells
100% Enrichment	1,108,666	0% No Template
57% Clonal	633,914	43% Polyclonal
91% Final Library	577,771	1% Test Fragments 0% Adapter Dimer 8% Low Quality

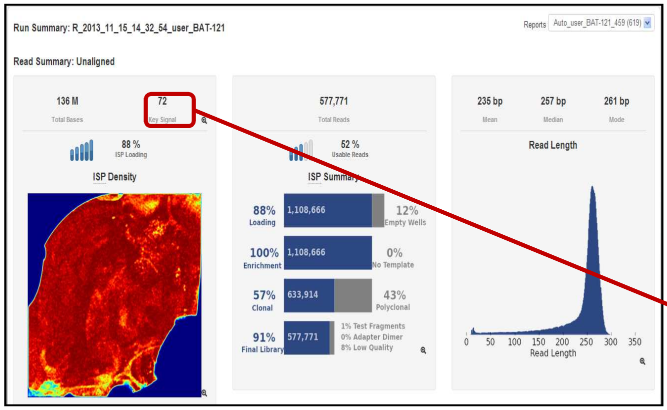
235 bp Mean
257 bp Median
261 bp Mode

Read Length

Ion 314™v2 chip heat map, indicating percent loading across the physical surface



Run Report validation – Key Signal



Run Summary: R_2013_11_15_14_32_54_user_BAT-121

Reports: Auto_user_BAT-121_459 (619)

Read Summary: Unaligned

136 M Total Bases

72 Key Signal

88 % ISP Loading

577,771 Total Reads

52 % Usable Reads

235 bp Mean

257 bp Median

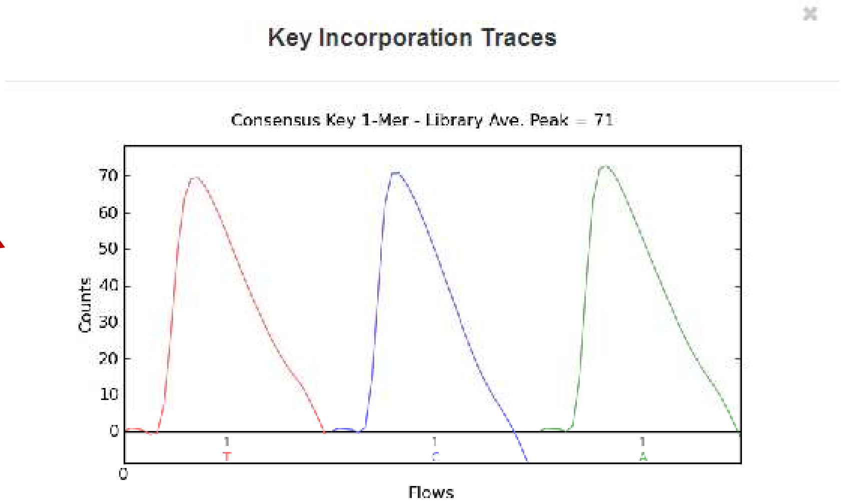
261 bp Mode

88% Loading: 1,108,666; 12% Empty Wells

100% Enrichment: 1,108,666; 0% No Template

57% Clonal: 633,914; 43% Polyclonal

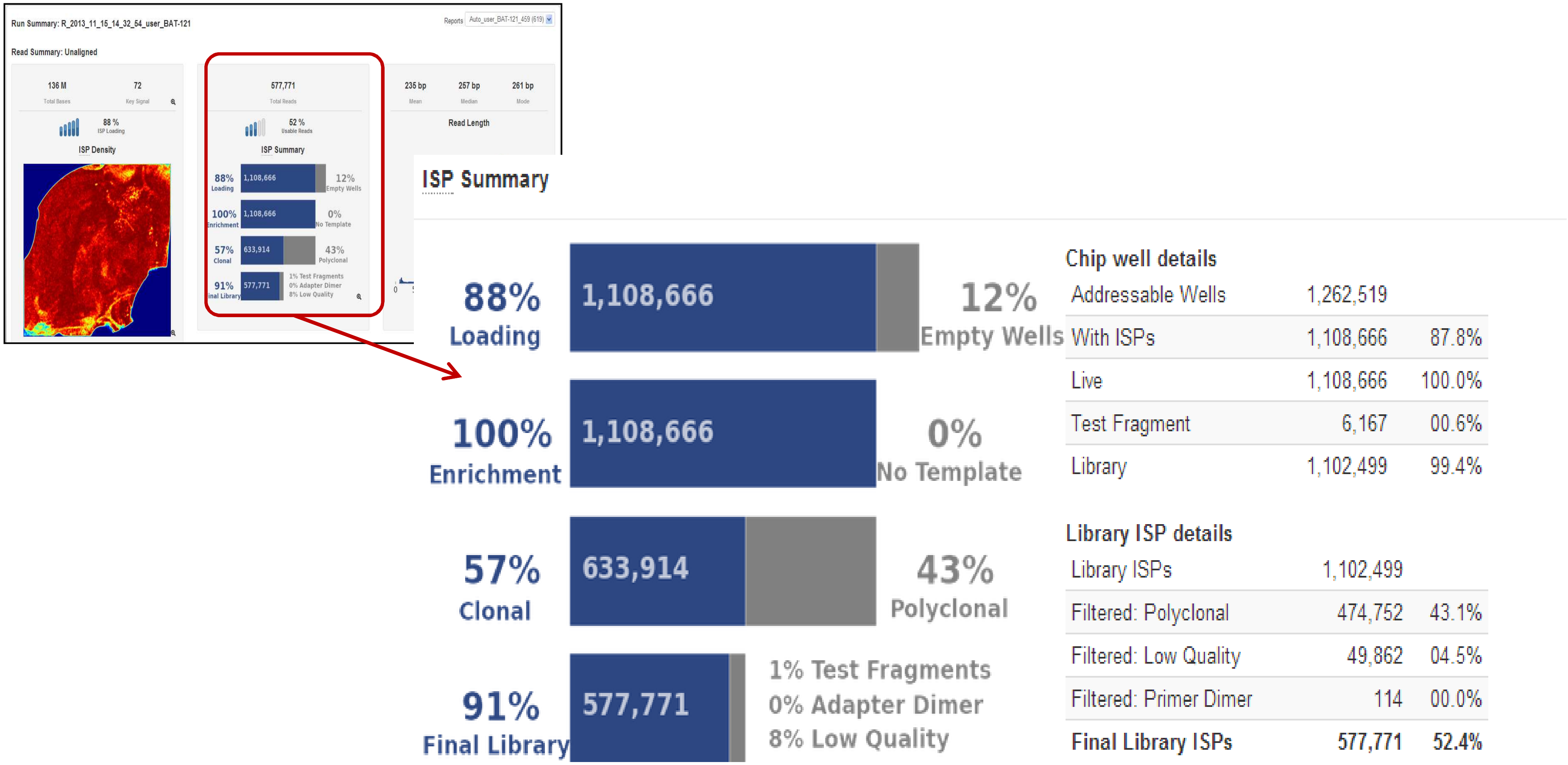
91% Final Library: 577,771; 1% Test Fragments, 0% Adapter Dimer, 8% Low Quality



Key Incorporation Traces

The **Consensus Key 1-Mer** graph shows the strength of the signal from the first three one-mer bases of the library key. This graph represents the consensus signal measurement of release of H+ during nucleotide incorporation. The y-axis shows signal strength, measured in **Counts**, which is an arbitrary but consistent unit of measure. The x-axis shows time as nucleotide **Flows** over the chip.

Run Report – Chip Well Details



Run Summary: R_2013_11_15_14_32_54_user_BAT-121

Reports: Auto_user_BAT-121_459 (619)

Read Summary: Unaligned

Total Bases: 136 M

Key Signal: 72

ISP Loading: 88 %

Total Reads: 577,771

Usable Reads: 52 %

Mean: 235 bp

Median: 257 bp

Mode: 261 bp

ISP Density
ISP Summary
Read Length
88%
Loading
1,108,666
12%
Empty Wells
100%
Enrichment
1,108,666
0%
No Template
57%
Clonal
633,914
43%
Polyclonal
91%
Final Library
577,771
1% Test Fragments
0% Adapter Dimer
8% Low Quality

Chip well details

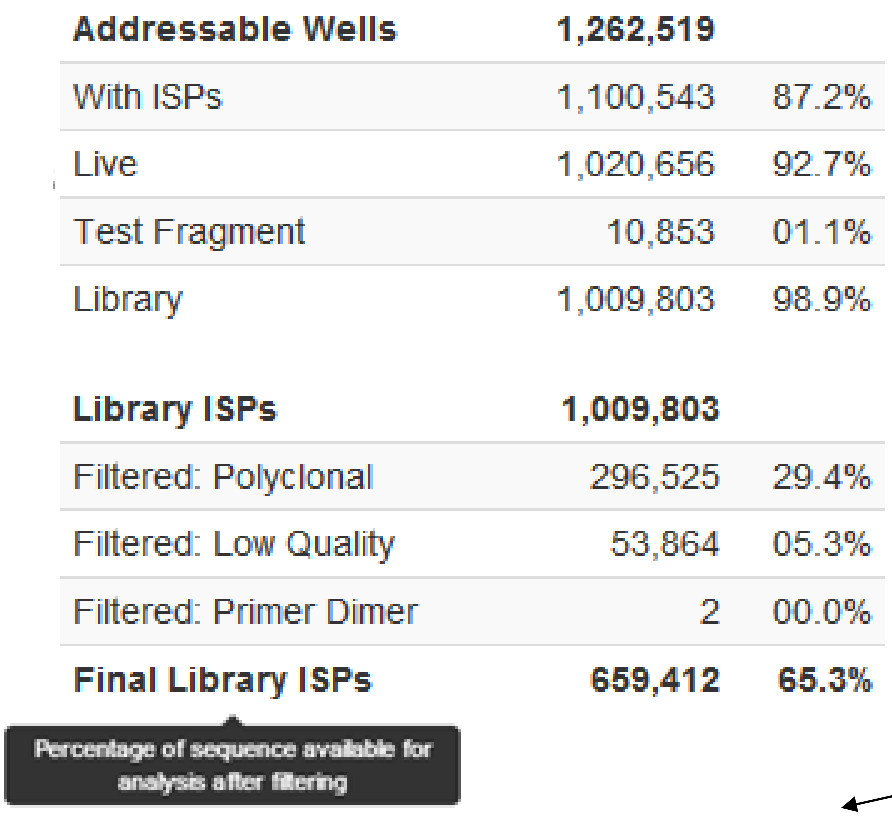
Addressable Wells	1,262,519	
With ISPs	1,108,666	87.8%
Live	1,108,666	100.0%
Test Fragment	6,167	00.6%
Library	1,102,499	99.4%

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

Ion Sphere™ Particle (ISP) Identification Summary

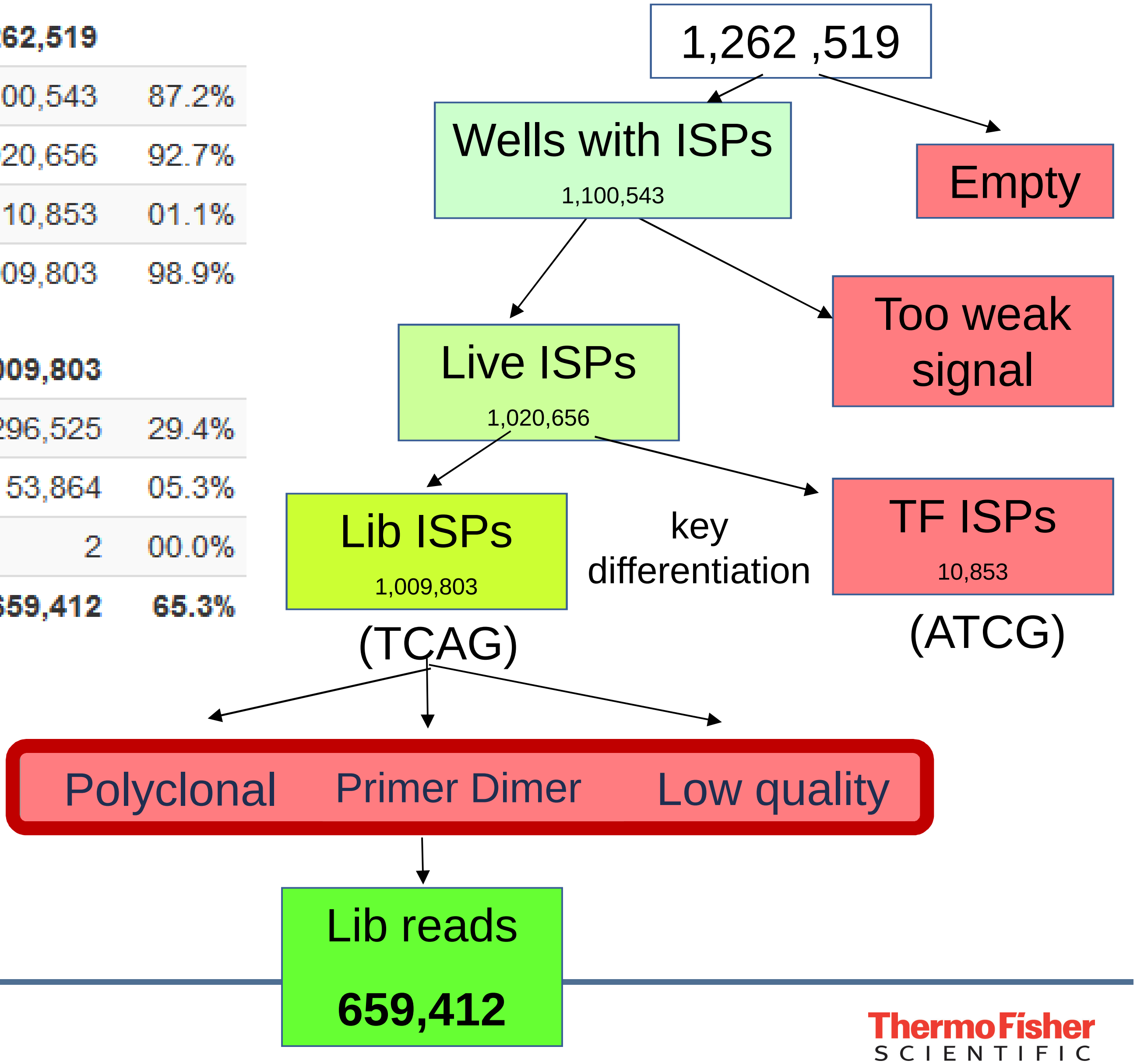


Addressable Wells	**1,262,519**	
With ISPs	1,100,543	87.2%
Live	1,020,656	92.7%
Test Fragment	10,853	01.1%
Library	1,009,803	98.9%

Library ISPs	**1,009,803**	
Filtered: Polyclonal	296,525	29.4%
Filtered: Low Quality	53,864	05.3%
Filtered: Primer Dimer	2	00.0%
Final Library ISPs	**659,412**	**65.3%**

Percentage of sequence available for analysis after filtering

Mouse over for help



1,262 ,519

Wells with ISPs
1,100,543

Empty

Live ISPs
1,020,656

Too weak signal

Lib ISPs
1,009,803

(TCAG)

key differentiation

TF ISPs
10,853

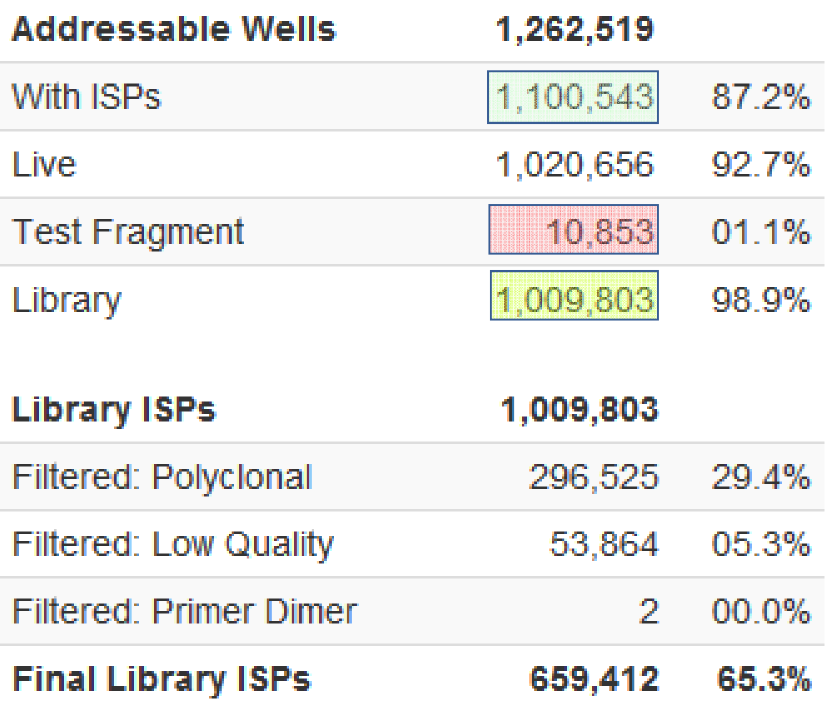
(ATCG)

Polyclonal Primer Dimer Low quality

Lib reads

659,412

Ion Sphere™ Particle (ISP) Identification Enrichment Calculation

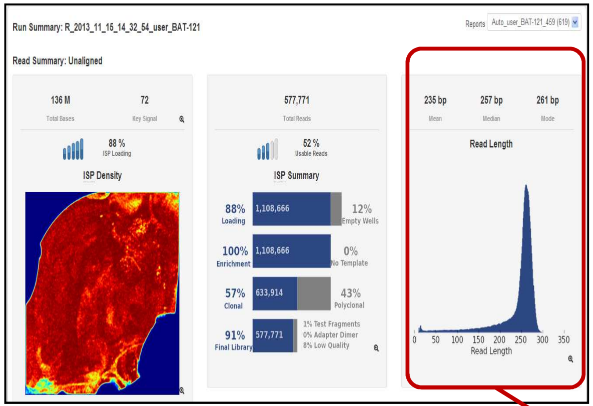


Addressable Wells	**1,262,519**	
With ISPs	1,100,543	87.2%
Live	1,020,656	92.7%
Test Fragment	10,853	01.1%
Library	1,009,803	98.9%

Library ISPs	**1,009,803**	
Filtered: Polyclonal	296,525	29.4%
Filtered: Low Quality	53,864	05.3%
Filtered: Primer Dimer	2	00.0%
Final Library ISPs	**659,412**	**65.3%**

$$\%\ \text{enrich} = \frac{\text{Lib ISPs}\ \ 1{,}009{,}803}{\left(\text{Wells with ISPs}\ \ 1{,}100{,}543 - \text{TF ISPs}\ \ 10{,}853\right)}$$

Run Report – Read Length Details



Run Summary: R_2013_11_15_14_32_54_user_BAT-121

Reports Auto_user_BAT-121_459 (619)

Read Summary: Unaligned

136 M Total Bases

72 Key Signal

88 % ISP Loading

ISP Density

577,771 Total Reads

52 % Usable Reads

ISP Summary

88% Loading 1,108,666 12% Empty Wells

100% Enrichment 1,108,666 0% No Template

57% Clonal 633,914 43% Polyclonal

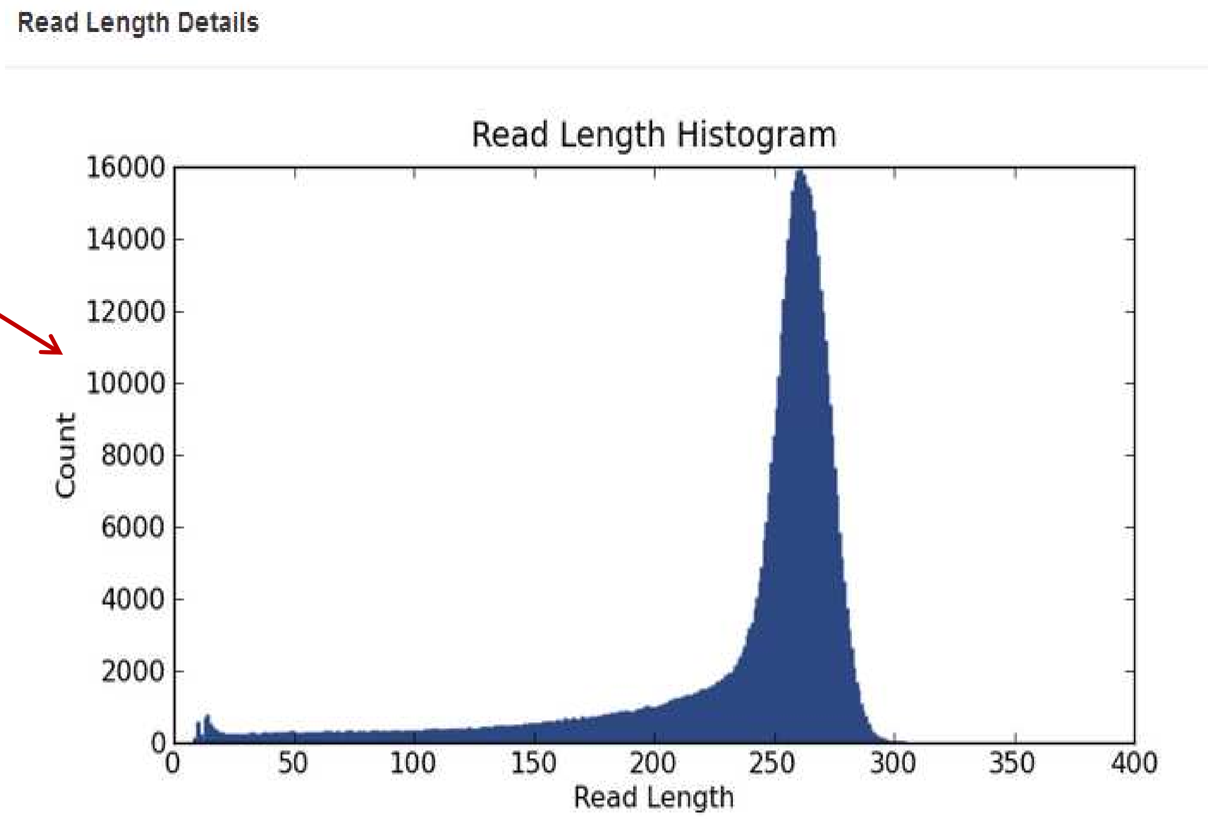
91% Final Library 577,771 1% Test Fragments 0% Adapter Dimer 8% Low Quality

235 bp Mean

257 bp Median

261 bp Mode

Read Length

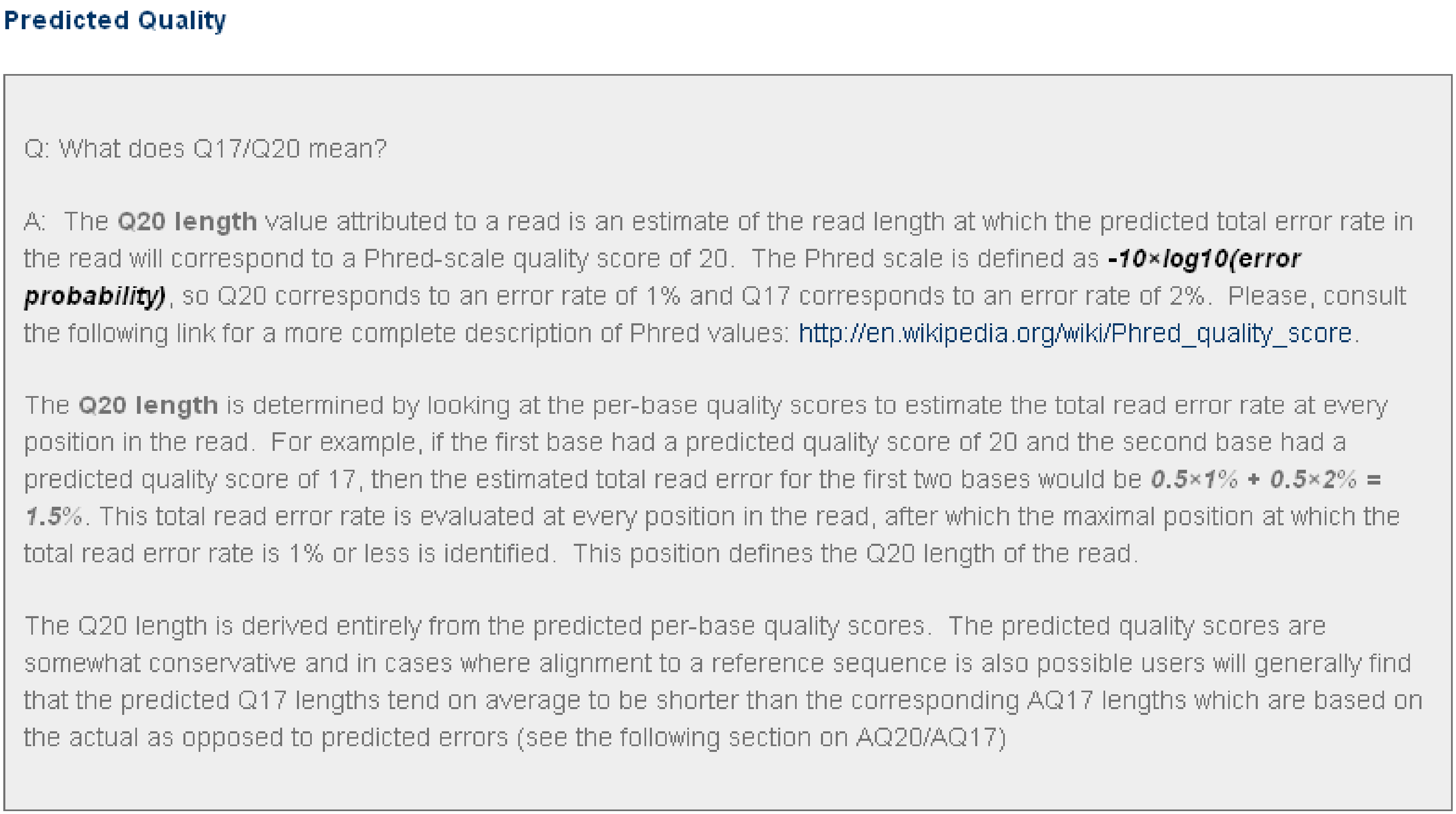


Read Length Details

Read Length Histogram

Histogram of read length for all reads in output files

What does Q20 mean?



Predicted Quality

Q: What does Q17/Q20 mean?

A: The **Q20 length** value attributed to a read is an estimate of the read length at which the predicted total error rate in the read will correspond to a Phred-scale quality score of 20. The Phred scale is defined as ***-10×log10(error probability)***, so Q20 corresponds to an error rate of 1% and Q17 corresponds to an error rate of 2%. Please, consult the following link for a more complete description of Phred values: http://en.wikipedia.org/wiki/Phred_quality_score.

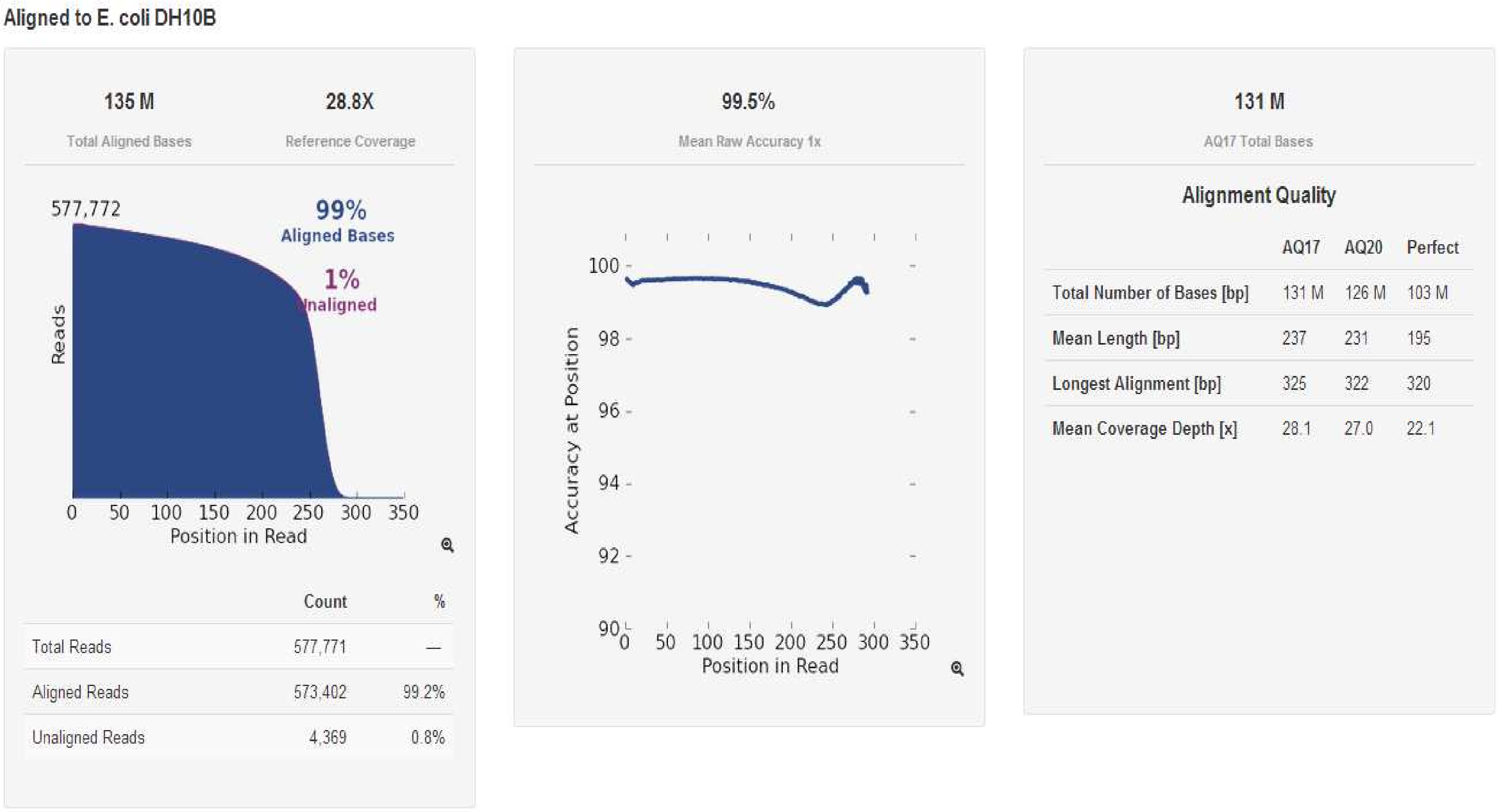
The **Q20 length** is determined by looking at the per-base quality scores to estimate the total read error rate at every position in the read. For example, if the first base had a predicted quality score of 20 and the second base had a predicted quality score of 17, then the estimated total read error for the first two bases would be ***0.5×1% + 0.5×2% = 1.5%***. This total read error rate is evaluated at every position in the read, after which the maximal position at which the total read error rate is 1% or less is identified. This position defines the Q20 length of the read.

The Q20 length is derived entirely from the predicted per-base quality scores. The predicted quality scores are somewhat conservative and in cases where alignment to a reference sequence is also possible users will generally find that the predicted Q17 lengths tend on average to be shorter than the corresponding AQ17 lengths which are based on the actual as opposed to predicted errors (see the following section on AQ20/AQ17)

What does AQ20 mean?

- Alignment of reads is a process to map the read to a reference
- Any discrepancy in alignment to a reference is listed as a mismatch, and described by a mapping quality score
- In Torrent Browser, throughput reads are >= AQ20 reads
- AQ20 length of a read is the longest length at which the aligned read has a mismatch rate of 1% or less
- AQ20 content is the sum of all the AQ20 lengths

Run Report – Reads Aligned to Reference



Aligned to E. coli DH10B

135 M
Total Aligned Bases

28.8X
Reference Coverage

577,772
99%
Aligned Bases
1%
Unaligned
Reads
0
50
100
150
200
250
300
350
Position in Read

	Count	%
Total Reads	577,771	—
Aligned Reads	573,402	99.2%
Unaligned Reads	4,369	0.8%

99.5%
Mean Raw Accuracy 1x

Accuracy at Position
100
98
96
94
92
90
0
50
100
150
200
250
300
350
Position in Read

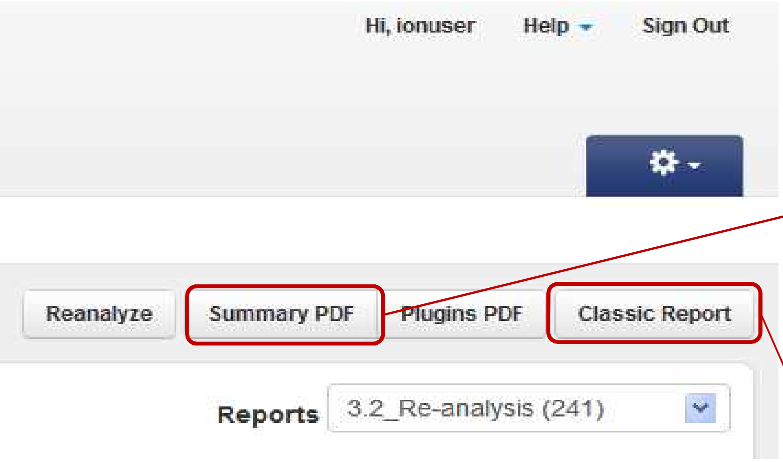
131 M
AQ17 Total Bases

Alignment Quality

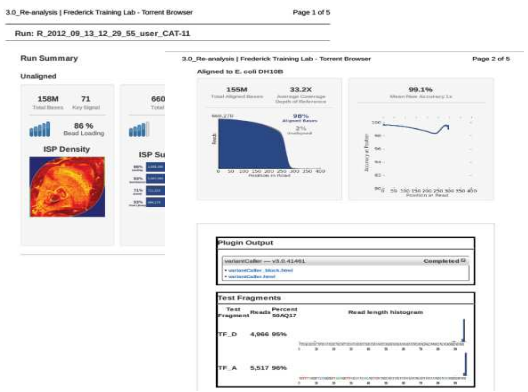
	AQ17	AQ20	Perfect
Total Number of Bases [bp]	131 M	126 M	103 M
Mean Length [bp]	237	231	195
Longest Alignment [bp]	325	322	320
Mean Coverage Depth [x]	28.1	27.0	22.1

Shows metrics gathered *after* mapping to reference.

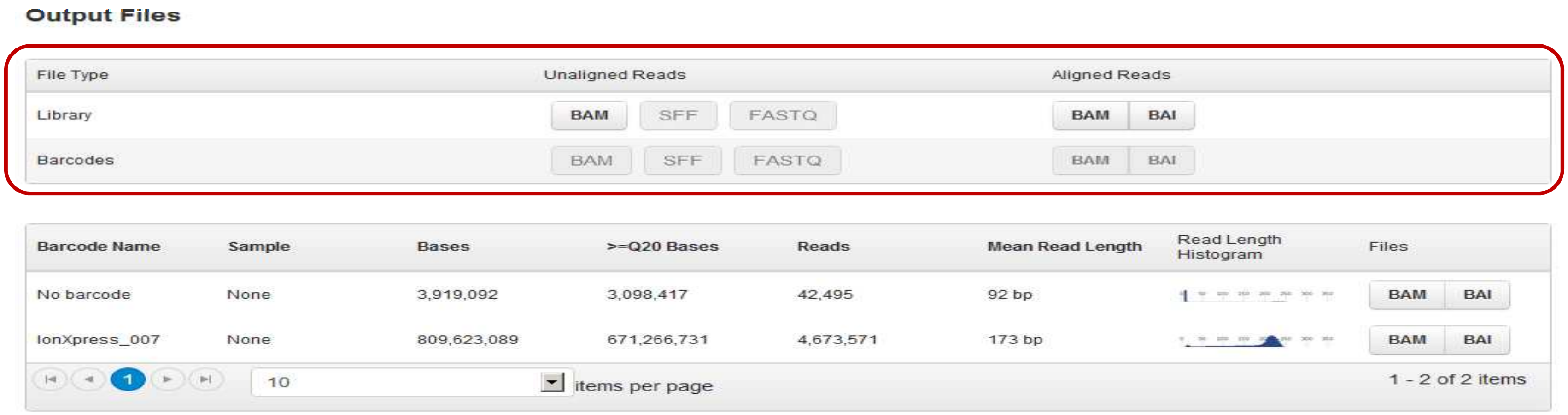
Run Report – Output Files


Hi, ionuser
Help
Sign Out
Reanalyze
Summary PDF
Plugins PDF
Classic Report

Reports: 3.2_Re-analysis (241)



File format of older version



Output Files

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

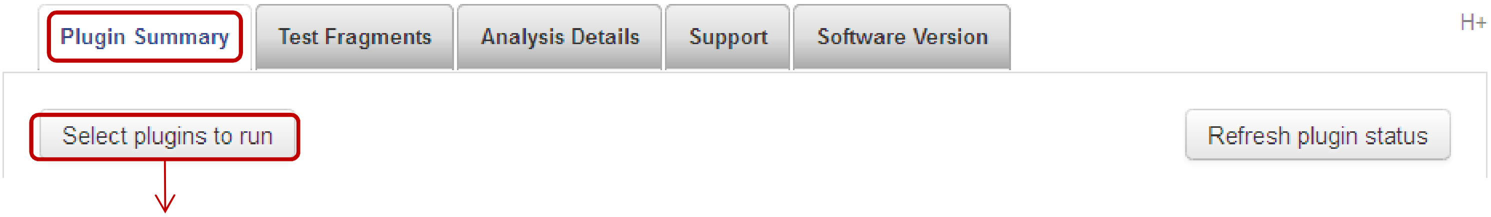
Barcode Name	Sample	Bases	>=Q20 Bases	Reads	Mean Read Length	Read Length Histogram	Files
No barcode	None	3,919,092	3,098,417	42,495	92 bp		BAM BAI
IonXpress_007	None	809,623,089	671,266,731	4,673,571	173 bp		BAM BAI

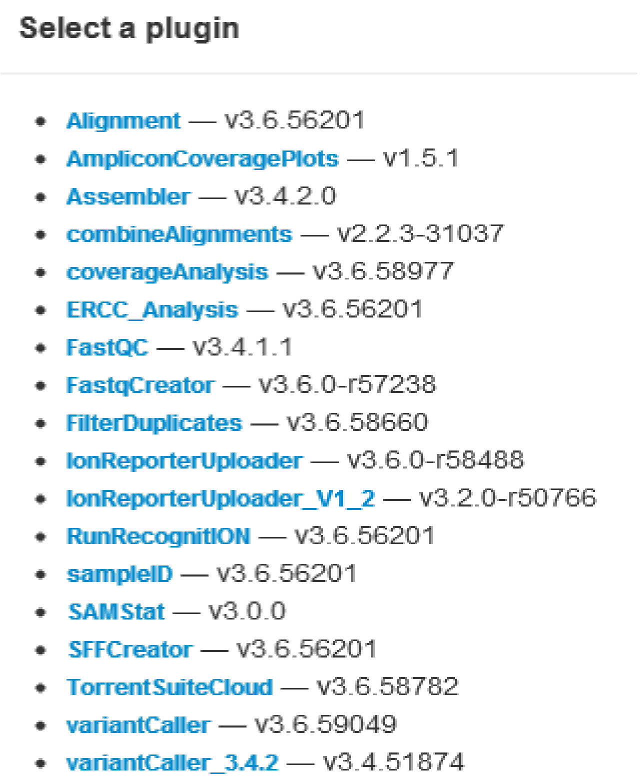
10 items per page

1 - 2 of 2 items

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

Plugin Summary


Plugin Summary
Test Fragments
Analysis Details
Support
Software Version
H+
Select plugins to run
Refresh plugin status

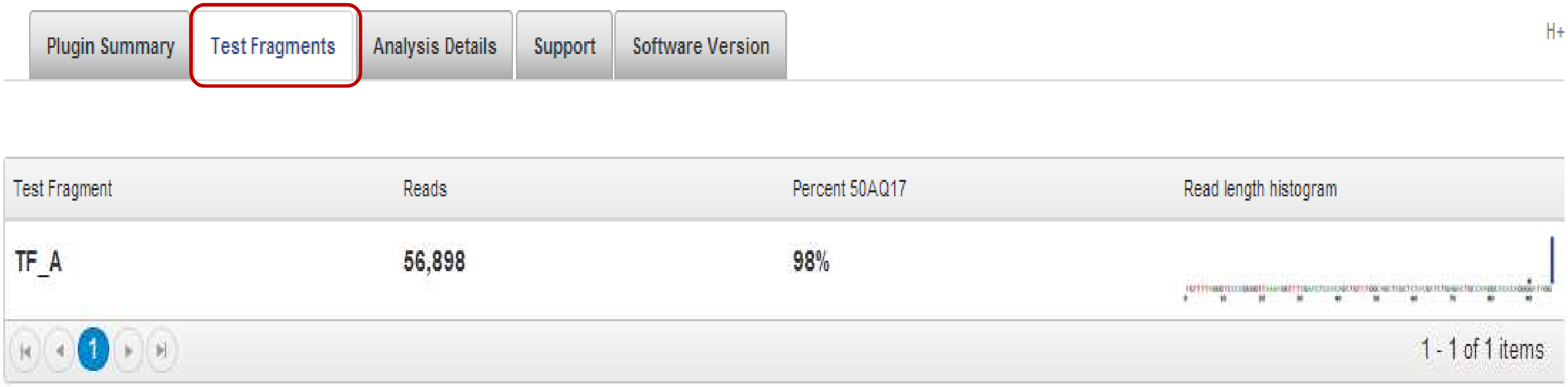


Select a plugin

- **Alignment** — v3.6.56201
- **AmpliconCoveragePlots** — v1.5.1
- **Assembler** — v3.4.2.0
- **combineAlignments** — v2.2.3-31037
- **coverageAnalysis** — v3.6.58977
- **ERCC_Analysis** — v3.6.56201
- **FastQC** — v3.4.1.1
- **FastqCreator** — v3.6.0-r57238
- **FilterDuplicates** — v3.6.58660
- **IonReporterUploader** — v3.6.0-r58488
- **IonReporterUploader_V1_2** — v3.2.0-r50766
- **RunRecognitION** — v3.6.56201
- **sampleID** — v3.6.56201
- **SAMStat** — v3.0.0
- **SFFCreator** — v3.6.56201
- **TorrentSuiteCloud** — v3.6.58782
- **variantCaller** — v3.6.59049
- **variantCaller_3.4.2** — v3.4.51874

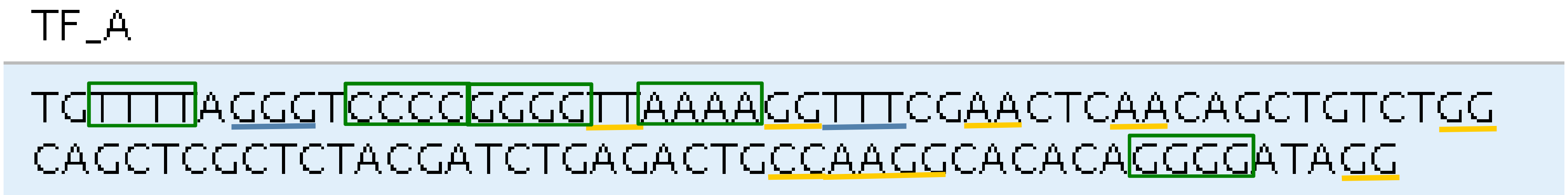
variantCaller Features
Supports TargetSeq™, Ion AmpliSeq™, & whole genome applications • Each may be run as Germ Line or Somatic
Enables calling for all custom products • Supports any genome or custom BED file
Summarizes statistics for barcodes, coverage, chromosomes, variants & hotspots
Calls at 5% or 50%
Compatible with barcoded samples
Planning page for automatic variant calling

Test Fragment Summary


Plugin Summary
Test Fragments
Analysis Details
Support
Software Version
H+
1
1 - 1 of 1 items

Test Fragment	Reads	Percent 50AQ17	Read length histogram
TF_A	56,898	98%	

Run Report Validation: Test fragment Summary

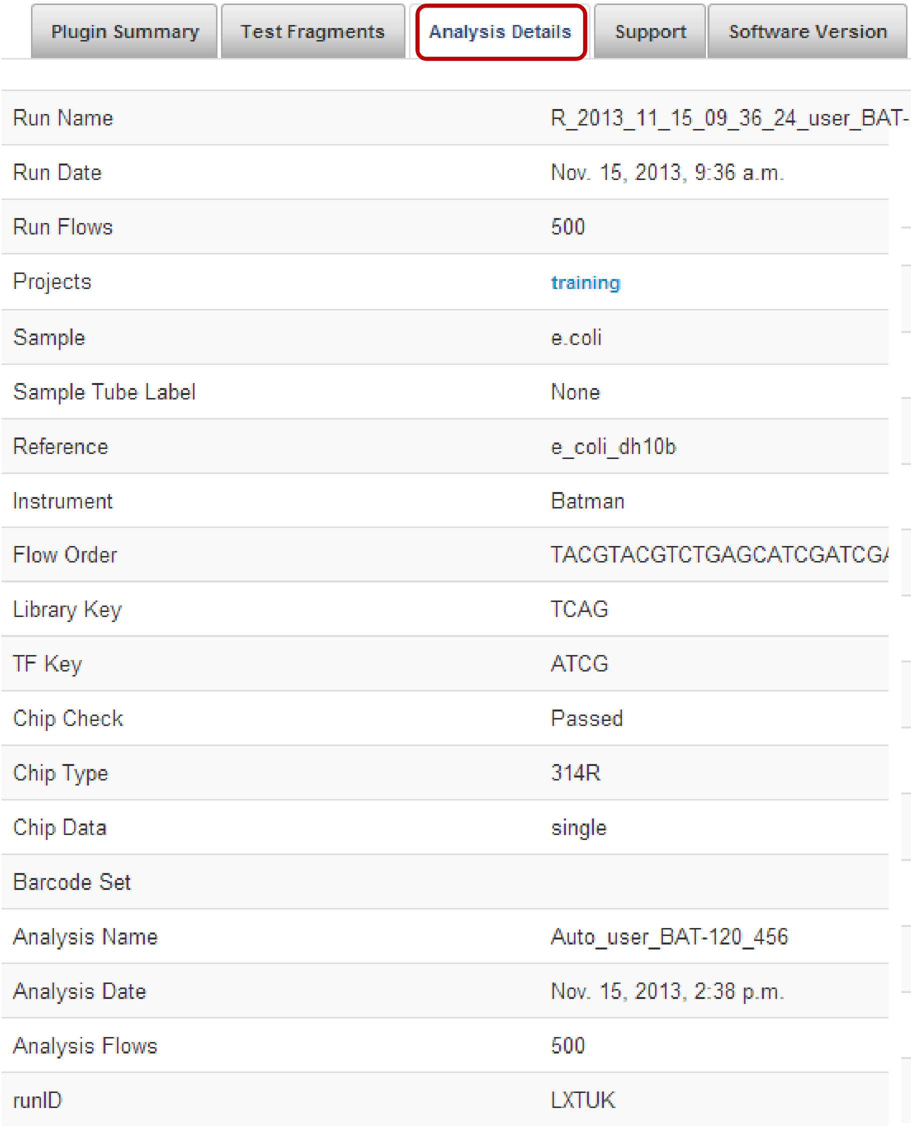


TF_A

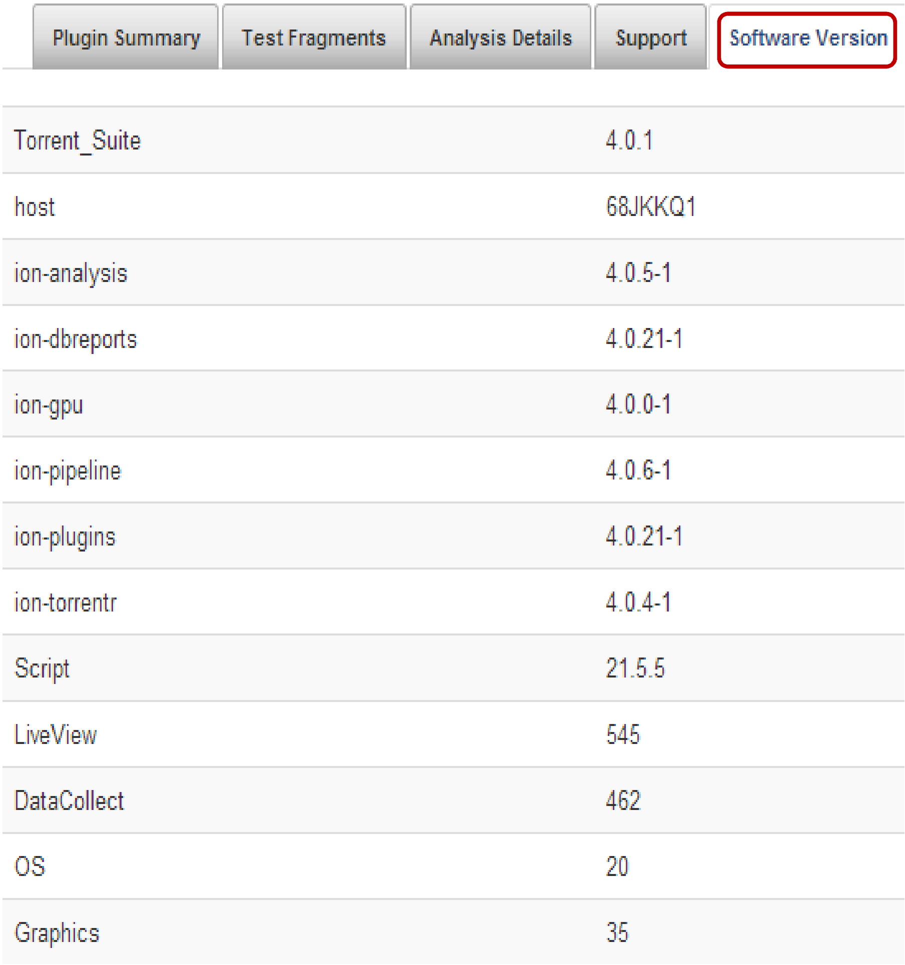
TGTTTTAGGGTCCCCGGGGTTAAAAGGTTTCGAACTCAACAGCTGTCTGG
CAGCTCGCTCTACGATCTGAGACTGCCAAGGCACACAGGGGATAGG

- Test Fragment designed with variable homopolymeric challenges (2mer, 3mer and 4mer)
- TFs are used for install validation
- TFs are spiked into sample for run validation
- No specification on test fragment sequencing performance
- Specific kit type may have different TFs

Report Information

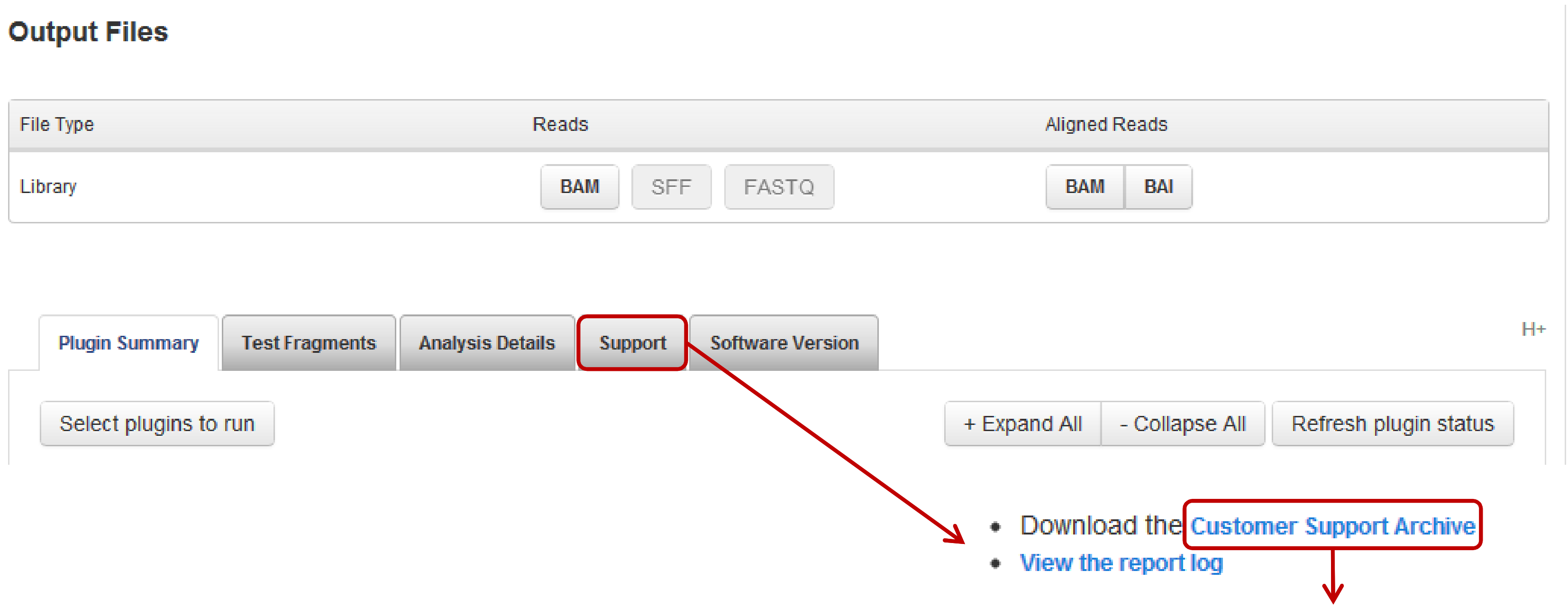

Plugin Summary
Test Fragments
Analysis Details
Support
Software Version

Run Name	R_2013_11_15_09_36_24_user_BAT-120
Run Date	Nov. 15, 2013, 9:36 a.m.
Run Flows	500
Projects	training
Sample	e.coli
Sample Tube Label	None
Reference	e_coli_dh10b
Instrument	Batman
Flow Order	TACGTACGTCTGAGCATCGATCG
Library Key	TCAG
TF Key	ATCG
Chip Check	Passed
Chip Type	314R
Chip Data	single
Barcode Set	
Analysis Name	Auto_user_BAT-120_456
Analysis Date	Nov. 15, 2013, 2:38 p.m.
Analysis Flows	500
runID	LXTUK


Plugin Summary
Test Fragments
Analysis Details
Support
Software Version

Torrent_Suite	4.0.1
host	68JKKQ1
ion-analysis	4.0.5-1
ion-dbreports	4.0.21-1
ion-gpu	4.0.0-1
ion-pipeline	4.0.6-1
ion-plugins	4.0.21-1
ion-torrentr	4.0.4-1
Script	21.5.5
LiveView	545
DataCollect	462
OS	20
Graphics	35

Customer Support Archive (CSA)



Output Files

File Type	Reads	Aligned Reads
Library	BAM SFF FASTQ	BAM BAI

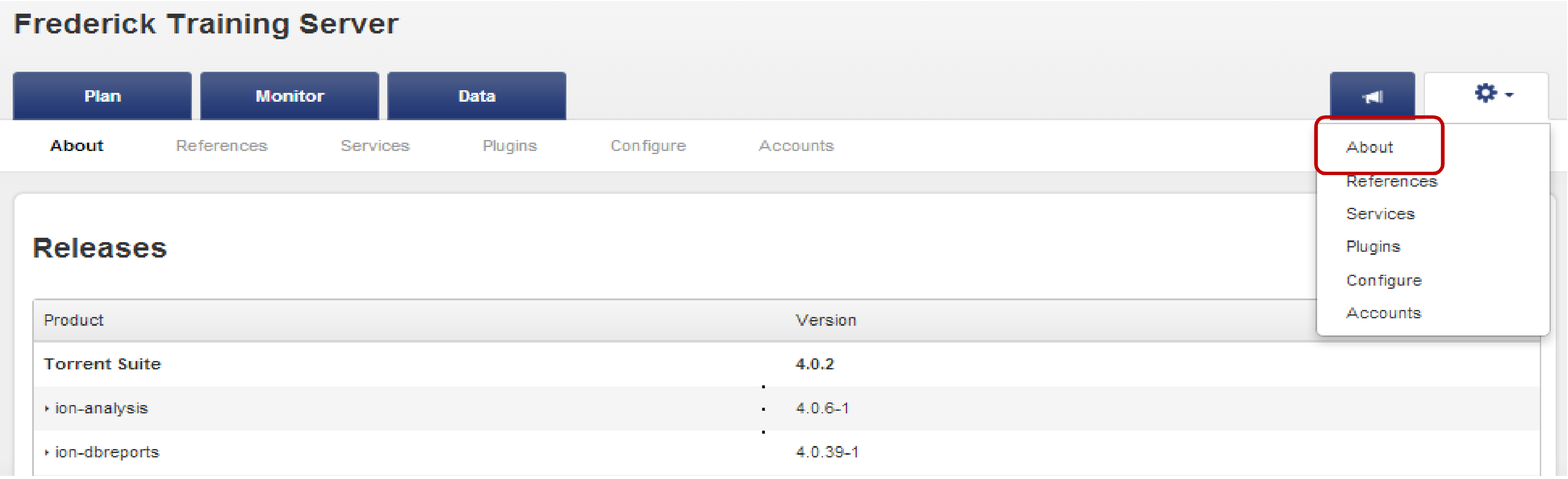
Plugin Summary
Test Fragments
Analysis Details
Support
Software Version
H+
Select plugins to run
+ Expand All
- Collapse All
Refresh plugin status

- Download the Customer Support Archive
- View the report log

Files for Troubleshooting; useful for Technical Support

If you need troubleshooting /support, send in your CSA file (have it ready!)

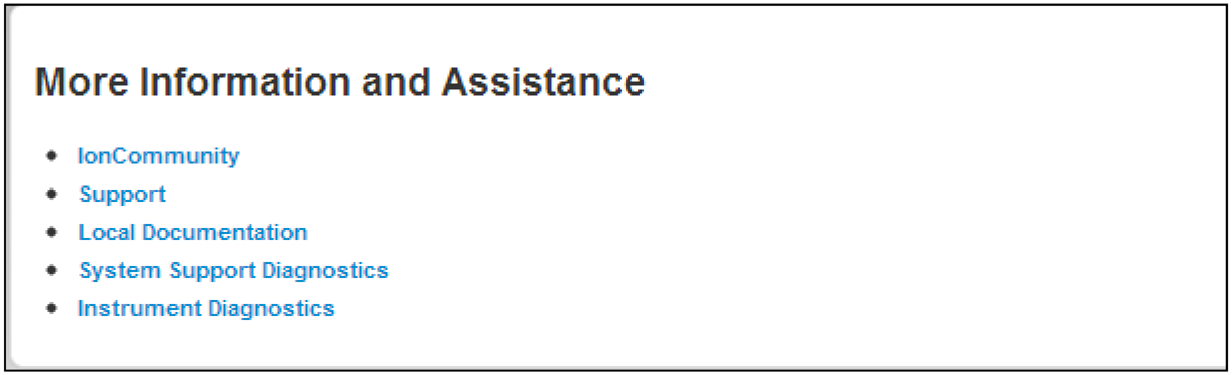
About Link


Plan
Monitor
Data
About
References
Services
Plugins
Configure
Accounts
About
References
Services
Plugins
Configure
Accounts

Frederick Training Server

Releases

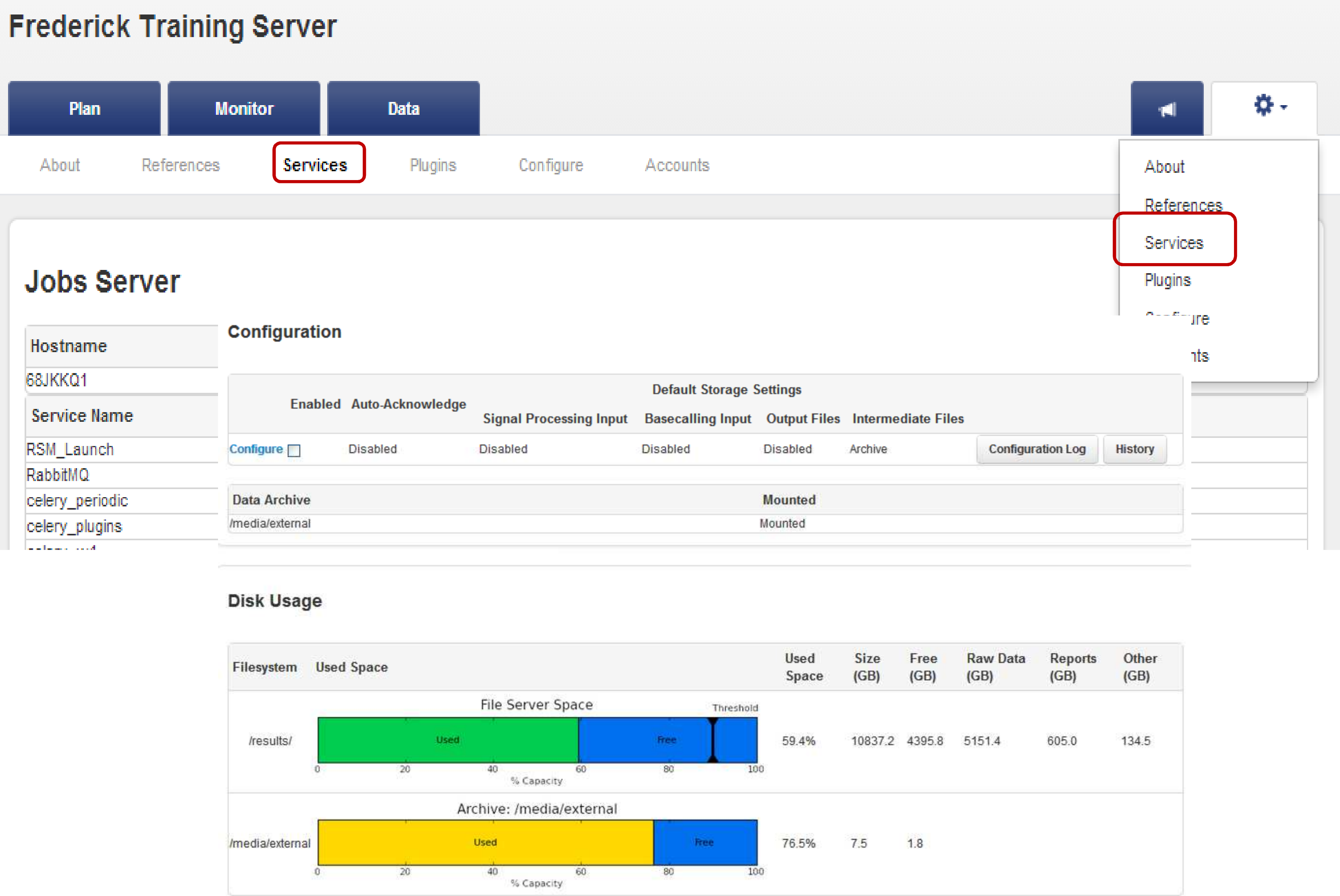
Product	Version
Torrent Suite	**4.0.2**
‣ ion-analysis	4.0.6-1
‣ ion-dbreports	4.0.39-1



More Information and Assistance

- IonCommunity
- Support
- Local Documentation
- System Support Diagnostics
- Instrument Diagnostics

Services Link


Frederick Training Server
Plan
Monitor
Data
About
References
Services
Plugins
Configure
Accounts
About
References
Services
Plugins
File Server Space
Threshold
Used
Free
0
20
40
60
80
100
% Capacity
Archive: /media/external
Used
Free
0
20
40
60
80
100
% Capacity

Jobs Server

Hostname
68JKKQ1

Service Name
RSM_Launch
RabbitMQ
celery_periodic
celery_plugins

Configuration

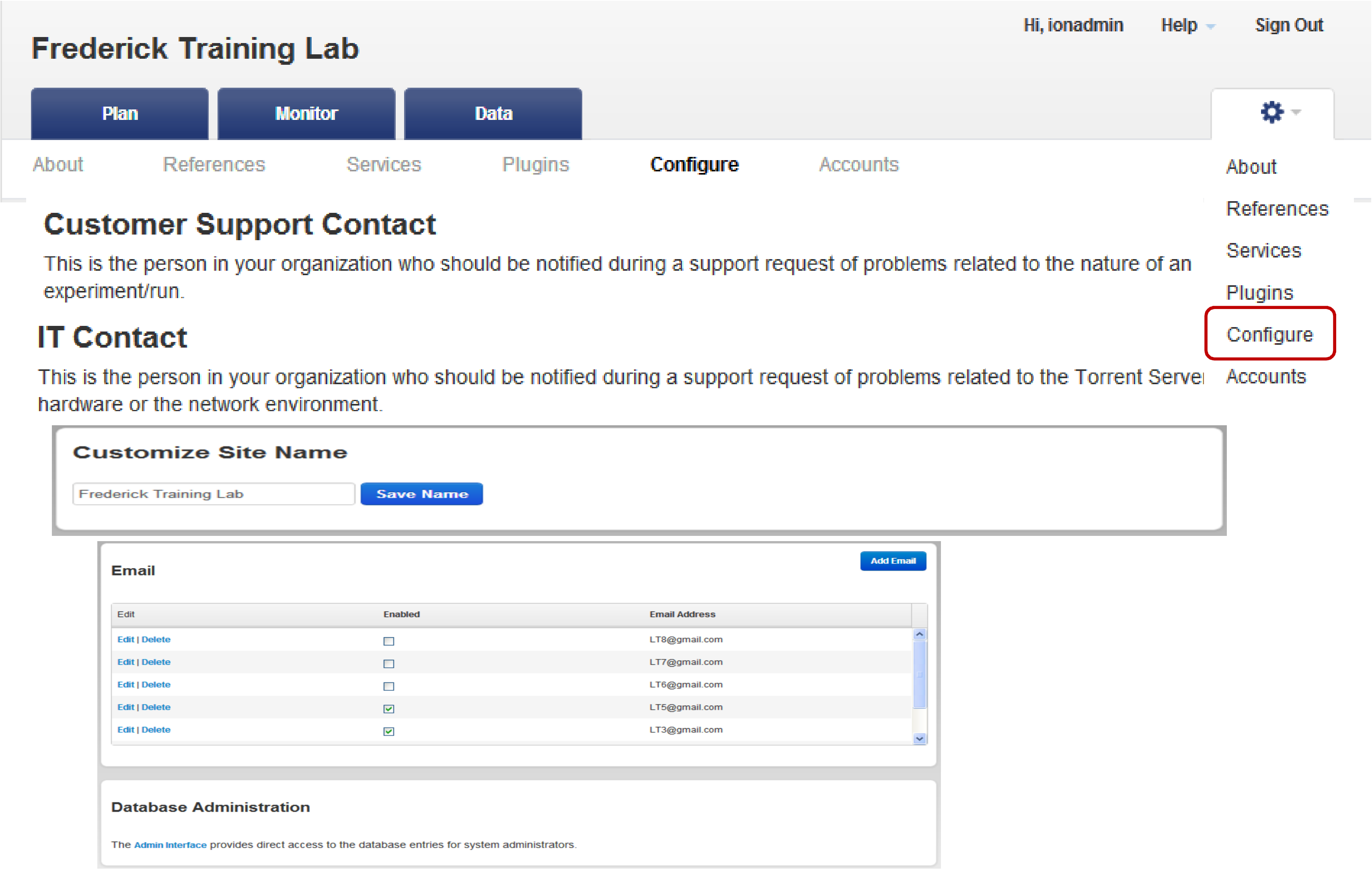
			Default Storage Settings					
	Enabled	Auto-Acknowledge	Signal Processing Input	Basecalling Input	Output Files	Intermediate Files		
Configure	☐	Disabled	Disabled	Disabled	Disabled	Archive	Configuration Log	History

Data Archive	Mounted
/media/external	Mounted

Disk Usage

Filesystem	Used Space	Used Space	Size (GB)	Free (GB)	Raw Data (GB)	Reports (GB)	Other (GB)
/results/		59.4%	10837.2	4395.8	5151.4	605.0	134.5
/media/external		76.5%	7.5	1.8			

Configure Link


Frederick Training Lab
Hi, ionadmin
Help
Sign Out
Plan
Monitor
Data
About
References
Services
Plugins
Configure
Accounts
About
References
Services
Plugins
Configure
Accounts

Customer Support Contact

This is the person in your organization who should be notified during a support request of problems related to the nature of an experiment/run.

IT Contact

This is the person in your organization who should be notified during a support request of problems related to the Torrent Server hardware or the network environment.

Customize Site Name

Frederick Training Lab

Email

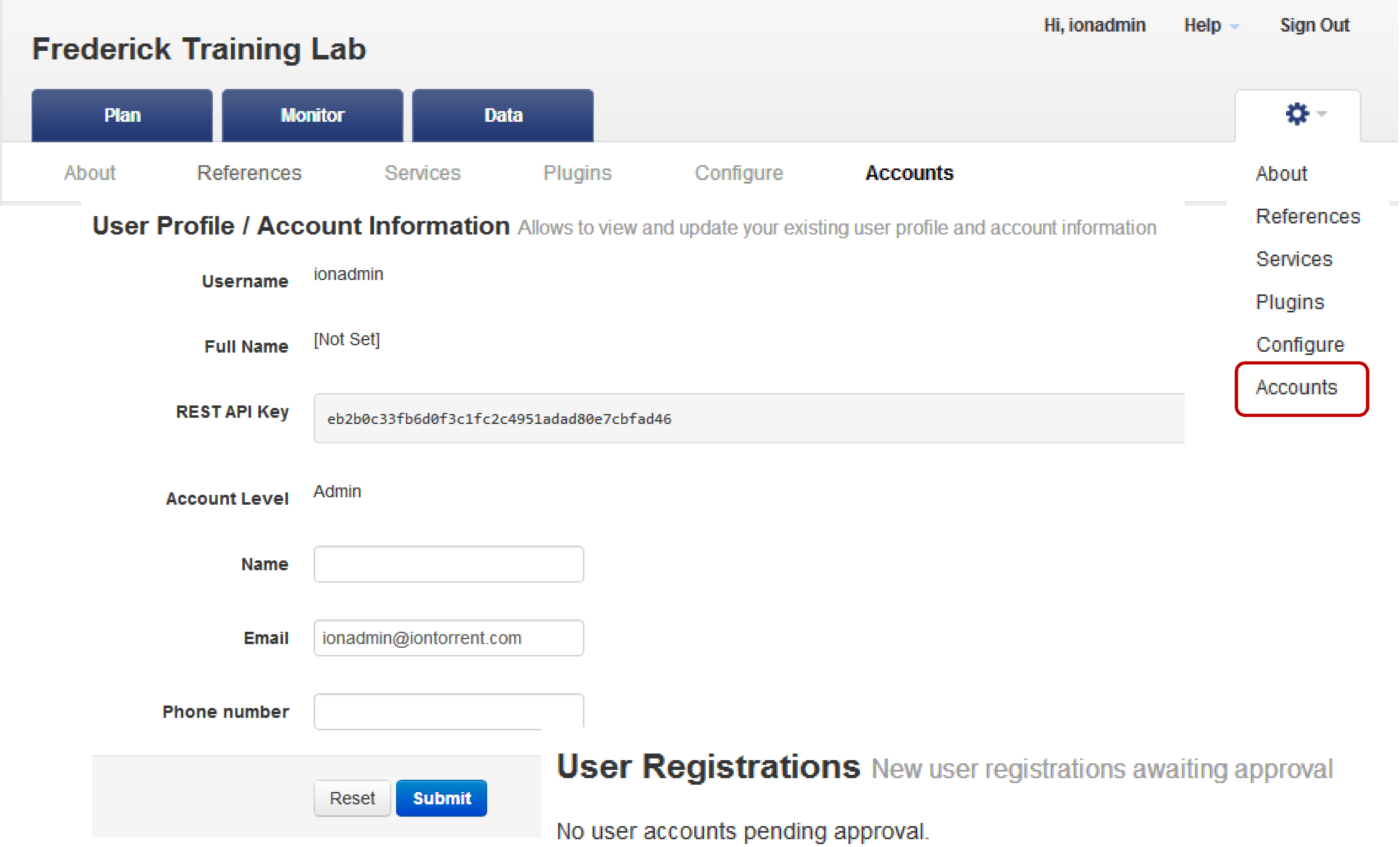
Edit	Enabled	Email Address
Edit | Delete	☐	LT8@gmail.com
Edit | Delete	☐	LT7@gmail.com
Edit | Delete	☐	LT6@gmail.com
Edit | Delete	☑	LT5@gmail.com
Edit | Delete	☑	LT3@gmail.com

Database Administration

The Admin Interface provides direct access to the database entries for system administrators.

Screen shot is from TS 3.6; other versions may vary.

Accounts Link


Frederick Training Lab
Hi, ionadmin
Help
Sign Out
Plan
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About
References
Services
Plugins
Configure
Accounts
About
References
Services
Plugins
Configure
Accounts
Reset
Submit

User Profile / Account Information Allows to view and update your existing user profile and account information

Username	ionadmin
Full Name	[Not Set]
REST API Key	eb2b0c33fb6d0f3c1fc2c4951adad80e7cbfad46
Account Level	Admin
Name	
Email	ionadmin@iontorrent.com
Phone number	

User Registrations New user registrations awaiting approval

No user accounts pending approval.

ion torrent

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