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SMRT Link and Analysis Tools for PacBio Data

SMRT Informatics Developers Conference - January 17, 2018

AGENDA

- 5.1.0 release goals
- New features
 - Support for key analysis applications
 - Multiplexed microbial assembly
 - Structural variant calling
 - De novo assembly
 - Barcoding workflow redesign
 - Sample Setup redesign
 - Data Management and SMRT Analysis usability improvements
 - Release of Iso-Seq 2 [Beta]
 - Minor Variants support for custom target configs



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Release Goals

HIGH-LEVEL GOALS

- Increased system throughput
 - Support for longer movies
 - Chemistry improvements
- End to end support for high-priority applications
- Focus on usability aspects of SMRT Link
- Preliminary R&D work on
 - Building out No-Amp targeted pulldown (Cas9) solution
 - Diploid consensus

SMRT TOOLS - NEW FEATURES

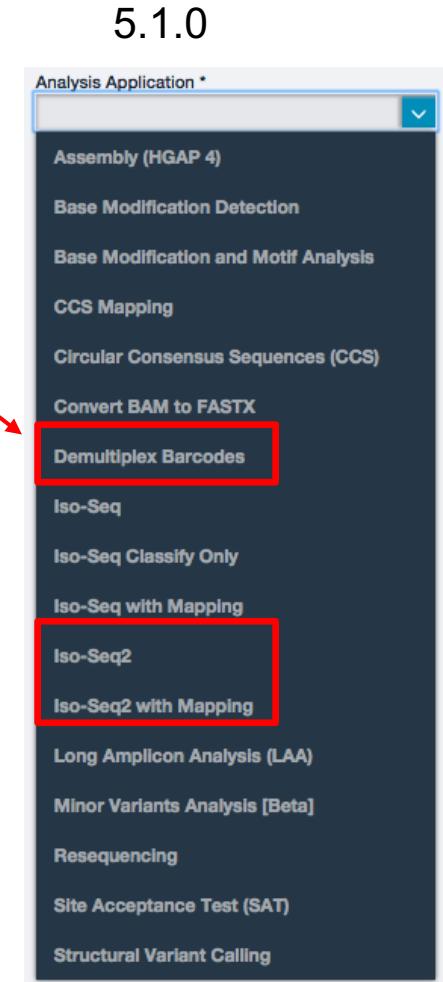
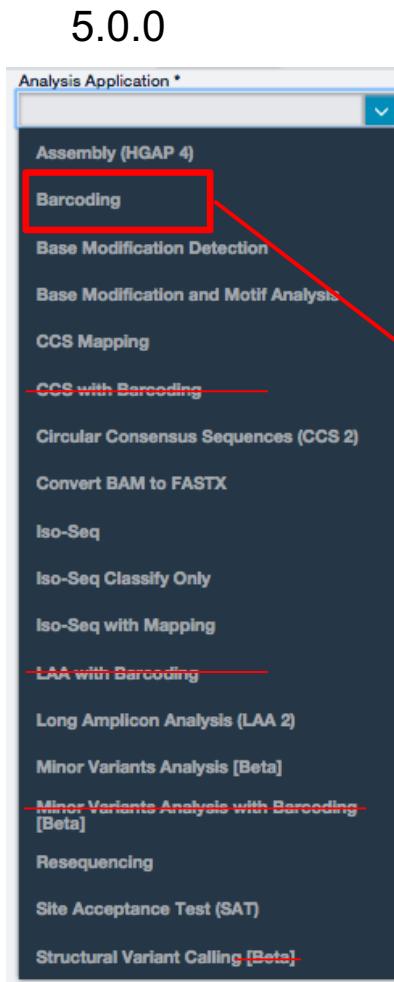
Applications

- Multiplexed Microbial Assembly
 - Completely redesigned barcode workflow
 - New barcode calling software
- Structural Variation
 - Support for multi-sample (joint) calling
 - Moved out of Beta status
- De Novo Assembly
 - Support for running unzip after HGAP.4
 - Support for generating GFA output
 - Binary release now available
- Iso-Seq
 - Address scalability issues
- Minor Variants
 - Support for adding custom target configurations (gene annotations)

SMRT LINK – NEW FEATURES

SMRT Link

- Barcoding workflow redesign
- Redesign of Sample Setup
- Usability improvements
 - Data Management
 - SMRT Analysis
- Analysis import/export





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Multiplexed Microbial Assembly

REDESIGN OF BARCODING WORKFLOW



- Specify sample names of individual barcodes

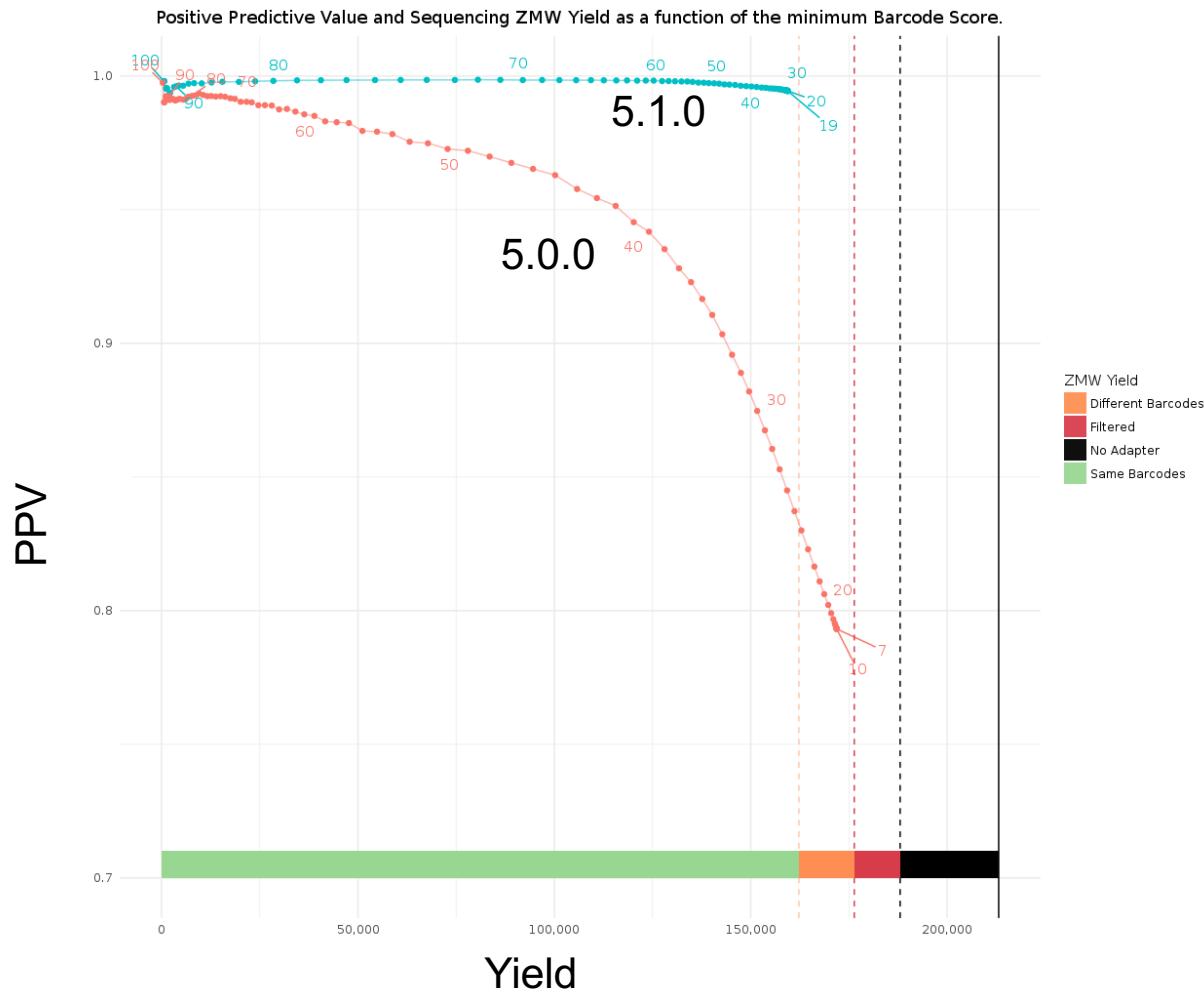


- Better assignment of reads to barcodes
- New, more efficient demultiplexing algorithm
- Extensive new QC metrics



- Flexibility to launch analyses on a single barcode or as a batch with custom parameters

DE-MULTIPLEXING PERFORMANCE – 5.0.0 VS 5.1.0



RUN DESIGN: NEW SECTION FOR BARCODES

The screenshot shows the SMRT Link software interface for 'Run Design'. The top navigation bar includes the SMRT Link logo, a 'Not Secure' warning, and the URL <https://smrtlink-bihourly.nanofluidics.com:8243/sl/#/run-design/new>. The top right corner shows the user 'mbudagyan' and 'Admin' status. The main title 'Run Design' is centered above the form.

New Run Design

Run Information

- Run Name: Run 11.10.2017 17:17
- Run Comments: (empty)
- Experiment Name: (empty)
- Experiment Id: (empty)
- Estimated Run Duration (mins): 540

Run Reagents / Consumables

- 1 SMRT cell
- 1 sequencing reagent plate
- 1 OS enzyme tube
- 1 mineral oil tube
- 3 boxes of tips
- 1 mixing plate
- 1 sample plate

Sample Information

- Binding Kit: (dropdown menu)
- Sequencing Kit: (dropdown menu)
- DNA Control Complex: (dropdown menu)
- Insert Size (bp): 10000
- Movie Time per SMRT Cell (mins): 360

Advanced Options

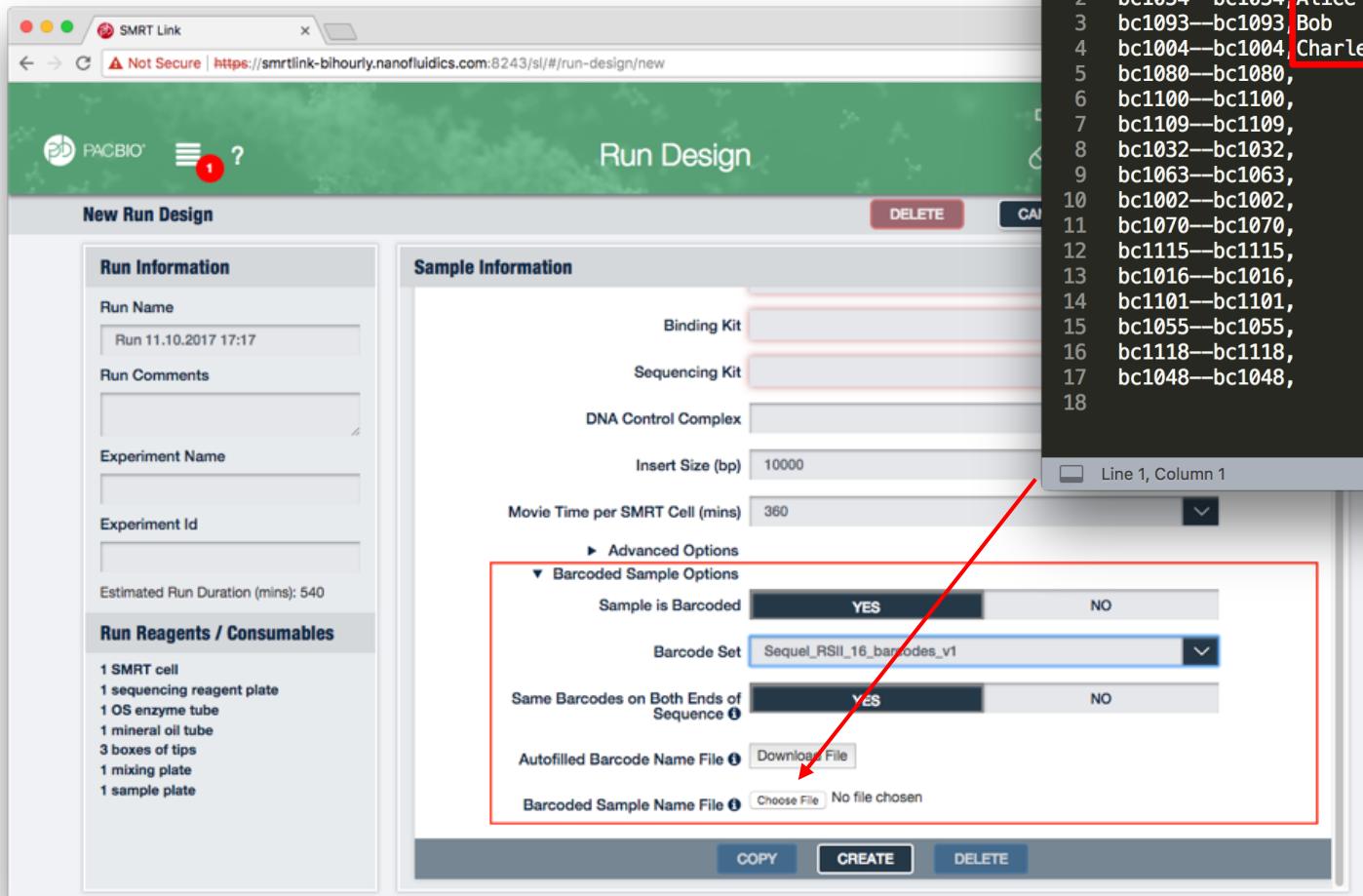
Barcoded Sample Options

- Sample is Barcoded: YES (selected)
- Barcode Set: Sequel_RSII_16_barcodes_v1 (dropdown menu)
- Same Barcodes on Both Ends of Sequence: YES (selected)
- Autofilled Barcode Name File: Download File
- Barcoded Sample Name File: Choose File No file chosen

Buttons at the bottom:

- COPY
- CREATE
- DELETE

BARCODED SAMPLE NAME FILE



The screenshot shows the SMRT Link software interface for 'Run Design'. On the left, there's a sidebar with 'Run Information' (Run Name: Run 11.10.2017 17:17, Run Comments: empty, Experiment Name: empty, Experiment Id: empty, Estimated Run Duration (mins): 540), 'Run Reagents / Consumables' (1 SMRT cell, 1 sequencing reagent plate, 1 OS enzyme tube, 1 mineral oil tube, 3 boxes of tips, 1 mixing plate, 1 sample plate), and a 'Sample Information' section with fields for Binding Kit, Sequencing Kit, and DNA Control Complex, all currently empty. In the 'Advanced Options' section, under 'Barcoded Sample Options', there are three dropdowns: 'Sample is Barcoded' (YES selected), 'Barcode Set' (Sequel_RSII_16_barcodes_v1 selected), and 'Same Barcodes on Both Ends of Sequence' (YES selected). Below these, there's a 'Autofilled Barcode Name File' button with a download icon, which is highlighted by a red box and a red arrow pointing from it to a CSV file in the background.

Barcode_Names (6).csv	
1	Barcode Name,Bio Sample Name (allowed characters: alphanumeric; space; dot; underscore; hyphen)
2	bc1054--bc1054,Alice
3	bc1093--bc1093,Bob
4	bc1004--bc1004,Charles
5	bc1080--bc1080,
6	bc1100--bc1100,
7	bc1109--bc1109,
8	bc1032--bc1032,
9	bc1063--bc1063,
10	bc1002--bc1002,
11	bc1070--bc1070,
12	bc1115--bc1115,
13	bc1016--bc1016,
14	bc1101--bc1101,
15	bc1055--bc1055,
16	bc1118--bc1118,
17	bc1048--bc1048,
18	

- Fill in the sample names for the barcodes used
- Upload the file

QC METRICS IN RESULTS OF DEMULTIPLEX BARCODES

SMRT Link SMRT Link SMRT Link

Secure | https://smrtlink-sms.nanofluidics.com:8243/sl/#/analysis/job/1039;report=barcode

PACBIO mbudagyan Admin

Project: All My Projects

SUCCESSFUL COPY DELETE

Analysis Results - janet demux test

► Analysis Overview

▼ Barcodes

Summary Metrics

Barcode Data	Value	Analysis Metric
472,948	95	Unique Barcodes
181,179	472,948	Barcode Reads
Barcoded Read Statistics	181,179	Unbarcoded Reads
Barcode Quality Scores	4,972	Mean Reads
Barcoded Read Binned Histograms	7,655	Max. Reads
	2,036	Min. Reads
	80,527	Mean Read Length
	35,376	Mean Longest Subread Length

► Data

Barcodes

Number Of Reads Per Barcode

Barcode Frequency Distribution

Mean Read Length Distribution

Barcode Quality Score Distribution

Read Length Distribution By Barcode

Barcode Quality Distribution By Barcode

The screenshot shows the SMRT Analysis software interface. At the top, there are three tabs labeled 'SMRT Link'. Below them is a header with the user 'mbudagyan' and an 'Admin' button. The main area is titled 'Analysis Results - janet demux test'. It features a 'SUCCESSFUL' status message with 'COPY' and 'DELETE' buttons. On the left, there's a sidebar with sections like 'Analysis Overview', 'Barcodes' (which is expanded), 'Summary Metrics' (which is also expanded and highlighted with a red box), and 'Data'. The 'Summary Metrics' section contains tables of QC metrics. To the right of the sidebar are several charts: 'Number Of Reads Per Barcode', 'Barcode Frequency Distribution', 'Mean Read Length Distribution', 'Barcode Quality Score Distribution', 'Read Length Distribution By Barcode', and 'Barcode Quality Distribution By Barcode'. Each chart has a dashed arrow pointing from its title to the corresponding row in the 'Summary Metrics' table.

ONE DATASET GENERATED PER BARCODE IN HIERARCHICAL DISPLAY

The screenshot shows the SMRT Link Data Management interface. At the top, there's a purple header bar with the PACBIO logo, a user icon for 'mbudagyan' (Admin), and a 'Data Management' title. Below the header is a dark navigation bar with buttons for 'CREATE DATA SET', 'CREATE PROJECT', 'VIEW OR IMPORT SEQUENCE DATA', and 'EXPORT DATA SETS'. A dropdown menu labeled 'View: BAM Data' is open. The main area is titled 'Data Sets' and contains a table with columns: Data Set Name, Well Sample Name, Bio Sample Name, Barcode Name, Run Name, Date Created, and Created By. The table lists several entries, with the first four entries ('Re-barcode Alice/Bob/Charles' and its three sub-entries) highlighted by a red box. The last entry is '54029_SAT_1Cell_20160219'.

Data Set Name	Well Sample Name	Bio Sample Name	Barcode Name	Run Name	Date Created	Created By
Re-barcode Alice/Bob/Charles	T0213_384-plex_barcode... [multiple]	[multiple]	m54008_1602...	11/10/2017, 4:19:1...	secondarytest	
Re-barcode Alice/Bob/Charles (Alice)	T0213_384-plex_barcode... Alice	lbc1-lbc1	m54008_1602...	11/10/2017, 4:20:3...	secondarytest	
Re-barcode Alice/Bob/Charles (Bob)	T0213_384-plex_barcode... Bob	lbc2-lbc2	m54008_1602...	11/10/2017, 4:20:3...	secondarytest	
Re-barcode Alice/Bob/Charles (Charles)	T0213_384-plex_barcode... Charles	lbc3-lbc3	m54008_1602...	11/10/2017, 4:20:3...	secondarytest	
54029_SAT_1Cell_20160219	Lambda_A01	unknown	tiny_54029_S...	11/10/2017, 4:19:0...	String	

- Bio Sample Name assigned by Barcode Name if not provided
 - CSV is optional
- Ability to modify Bio Sample Name and demux parameters

ANALYZE EACH BARCODED DATASET WITH CUSTOM PARAMETERS

The screenshot shows the SMRT Analysis software interface. At the top, there's a navigation bar with the SMRT Link logo, a 'Not Secure' warning, and a URL. On the right, a user profile for 'mbudagyan' (Admin) is shown. Below the header, a project dropdown is set to 'All My Projects'. The main area is titled 'Create New Analysis - Settings'. It includes fields for 'Analysis Application *' (set to 'Assembly (HGAP 4)'), 'Name *' (empty), and 'View:' (set to 'BAM Data'). A dropdown menu for 'Analysis Type' is open, showing options: 'One Analysis on All Data Sets' (selected), 'One Analysis per Data Set - Identical Parameters', and 'One Analysis per Data Set - Custom Parameters'. The 'Custom Parameters' option is highlighted with a blue background. Below this is a section for 'ADVANCED ANALYSIS PARAMETERS'. To the right, a 'Data Sets' table lists various datasets with columns for 'Data Set Name', 'Well Sample Name', and 'Bio Sample Name'. Some rows have checkboxes and dropdown menus for barcode selection.

	Data Set Name	Well Sample Name	Bio Sample Name
<input type="checkbox"/> ↗ Re-barcode Alice/Bob/Charles [All] [None]	T0213_384-plex_barcode...	[multiple]	
<input checked="" type="checkbox"/> Re-barcode Alice/Bob/Charles (Alice)	T0213_384-plex_barcode...	Alice	
<input checked="" type="checkbox"/> Re-barcode Alice/Bob/Charles (Bob)	T0213_384-plex_barcode...	Bob	
<input checked="" type="checkbox"/> Re-barcode Alice/Bob/Charles (Charles)	T0213_384-plex_barcode...	Charles	
<input type="checkbox"/> 54029_SAT_1Cell_20160219	Lambda_A01	unknown	
<input type="checkbox"/> ↗ Run_02.19.2016 00:27 384-plex barcode AB [All] [None]	T0213_384-plex_barcode...	[multiple]	
<input type="checkbox"/> Run_02.19.2016 00:27 384-plex barcode AB	T0213_384-plex_barcode...	unknown	
<input type="checkbox"/> Run_20160304_SQ02_Run0753_PB1052	PB1052_A01	unknown	
<input type="checkbox"/> pacbio_dataset_subreadset-170531_223853351	20170525_A12_IguanaSA...	unknown	
<input type="checkbox"/> pacbio dataset subreadset-160216 202541225	unknown	unknown	

EDIT PARAMETERS FOR EACH DATASET, THEN LAUNCH

The screenshot shows the SMRT Link software interface. At the top, there's a navigation bar with icons for back, forward, search, and help, followed by the 'SMRT Link' logo and a URL 'Not Secure | https://smrtlink-bihourly.nanofluidics.com:8243/sl/#/analysis/settings'. On the right of the header is a user profile 'mbudagyan' with an 'Admin' role. Below the header, the main title is 'SMRT Analysis'. A 'Project' dropdown shows 'All My Projects'. The main content area is titled 'Create New Analysis - Settings'. It includes fields for 'Analysis Application' (set to 'Assembly (HGAP 4)'), 'Name' (containing 'Mary's custom assembly' and '_Re-barcode Alice/Bob/Charles (Alice)'), 'View' (set to 'BAM Data'), and a 'Data Sets' table. The table has columns for 'Data Set Name', 'Well Sample Name', and 'Bio Sample Name'. It lists several datasets, with one row highlighted in yellow: 'Re-barcode Alice/Bob/Charles (Alice)' with Well Sample Name 'T0213_384-plex_barcode...' and Bio Sample Name 'Alice'. Other rows include 'Re-barcode Alice/Bob/Charles (Bob)' (Well Sample Name 'T0213_384-plex_barcode...', Bio Sample Name 'Bob') and 'Re-barcode Alice/Bob/Charles (Charles)' (Well Sample Name 'T0213_384-plex_barcode...', Bio Sample Name 'Charles'). There are also other entries like '54029_SAT_1Cell_20160219' (Well Sample Name 'Lambda_A01', Bio Sample Name 'unknown') and 'Run_02.19.2016 00:27 384-plex barcode A8' (Well Sample Name 'T0213_384-plex_barcode...', Bio Sample Name 'unknown'). At the bottom left is a button for 'ADVANCED ANALYSIS PARAMETERS'. At the top right of the main content area are 'CANCEL' and 'START AND CREATE NEXT' buttons.

	Data Set Name	Well Sample Name	Bio Sample Name
<input type="checkbox"/>	Re-barcode Alice/Bob/Charles (All) [None]	T0213_384-plex_barcode... [multiple]	
<input checked="" type="checkbox"/>	Re-barcode Alice/Bob/Charles (Alice)	T0213_384-plex_barcode... Alice	
<input checked="" type="checkbox"/>	Re-barcode Alice/Bob/Charles (Bob)	T0213_384-plex_barcode... Bob	
<input checked="" type="checkbox"/>	Re-barcode Alice/Bob/Charles (Charles)	T0213_384-plex_barcode... Charles	
<input type="checkbox"/>	54029_SAT_1Cell_20160219	Lambda_A01	unknown
<input type="checkbox"/>	> Run_02.19.2016 00:27 384-plex barcode A8 (All) [None]	T0213_384-plex_barcode... [multiple]	
<input type="checkbox"/>	Run_02.19.2016 00:27 384-plex barcode A8	T0213_384-plex_barcode... unknown	
<input type="checkbox"/>	Run_20160304_SQ02_Run0753_PB1052	PB1052_A01	unknown
<input type="checkbox"/>	pacblio_dataset_subreadset-170531_223853351	20170525_A12_IguanaSA...	unknown

- SMRT Link highlights the current input dataset in yellow
- Autopopulates the dataset name to the (editable) analysis name



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Structural Variation

Joint calling

MULTI-SAMPLE SELECTION FOR STRUCTURAL VARIATION

SMRT Link | https://smrtlink-alpha.nanofluidics.com:8243/sl/#/analysis/settings

PACBIO mbudagyan Admin Project: All My Projects CANCEL START

Create New Analysis - Settings

Analysis Application * Structural Variant Calling

Analysis Name * Multi-sample SV Demo

View: BAM Data

Analysis of Multiple Datasets

Analysis Type * One Analysis on All Data Sets

Associated Inputs Reference * Hg19

Structural Variants

Minimum Length of Structural Variant (bp) 50

Minimum Reads That Support Variant (Count) 2

Minimum Percentage of Reads That Support Variant (%) 20

Data Sets

	Data Set Name	Well Sample Name	Bio Sample Name	Barcode Name
<input checked="" type="checkbox"/>	HG00731-5-fold J V&V	[multiple]	HG00731	
<input checked="" type="checkbox"/>	HG00732-5-fold J V&V	[multiple]	HG00732	
<input checked="" type="checkbox"/>	HG00733-5-fold J V&V	[multiple]	HG00733	
<input type="checkbox"/>	AW Merge Test	[multiple]	Testing	
<input type="checkbox"/>	HG00733_Jaguar_10hx3_20hx2	unknown	unknown	
<input type="checkbox"/>	HG00731 5-fold JV&V	unknown	unknown	
<input type="checkbox"/>	HG00733 10-fold JV&V	unknown	unknown	
<input type="checkbox"/>	HG00732 5-fold JV&V	unknown	unknown	
<input type="checkbox"/>	HG00733 5-fold JV&V	unknown	unknown	
<input type="checkbox"/>	Jaguar SV VV 5cells_10hx3_20hx2	[multiple]	HG00733_Jaguar_10hx3...	

MULTI-SAMPLE SUPPORT

The screenshot shows the SMRT Analysis software interface. At the top, there are three tabs labeled "SMRT Link". The main header includes the "PACBIO" logo, a user icon for "mbudagyan", and an "Admin" link. A navigation bar below the header includes "Project: All My Projects" and buttons for "COPY" and "DELETE".

The main content area displays "Analysis Results - Puerto Rican Trio 3x5-fold J V&V SV Calling #01". The status is "SUCCESSFUL".

A sidebar on the left has sections for "Analysis Overview", "Report" (which is expanded to show "Count by Sample", "Count by Annotation", and "Structural Variants"), and "Data".

The "Count by Sample" table provides the following data:

		Insertions (total bp)	Deletions (total bp)	Homozygous Variants	Heterozygous Variants	Total Variants (total bp)
Count by Sample	HG00731	13,684 (5,389,546)	8,589 (5,113,599)	4,383	17,890	22,273 (10,503,145)
Count by Annotation	HG00732	12,859 (4,968,941)	8,124 (4,341,261)	4,259	16,724	20,983 (9,310,202)
Structural Variants	HG00733	13,299 (5,595,503)	8,716 (5,194,418)	4,735	17,280	22,015 (10,789,921)

INFORMATION BROKEN UP BY SAMPLE

The image displays two screenshots of the SMRT Analysis software interface, showing results for a Puerto Rican Trio 3x5-fold J V&V SV Calling analysis.

Left Screenshot (Analysis Results):

- Project:** All My Projects
- Status:** SUCCESSFUL
- Analysis Overview:** Puerto Rican Trio 3x5-fold J V&V SV Calling #01
- Report:** Count by Sample, Count by Annotation, Structural Variants
- Data:** HG00731, HG00732, HG00733
- Length Histogram:** Variants < 1 kb and Variants ≥ 1 kb for each sample. The histograms show the count of variants versus their length in bp (base pairs).

Right Screenshot (File Downloads):

- Project:** All My Projects
- Status:** SUCCESSFUL
- Analysis Overview:** Puerto Rican Trio 3x5-fold J V&V SV Calling #01
- Report:**
- Data:**
 - File Downloads:**

File	Size	Type
Aligned reads (HG00733)	9,433,744,160 bytes	bam
Aligned reads (HG00731)	9,277,861,072 bytes	bam
Aligned reads (HG00732)	9,495,217,252 bytes	bam
 - File Downloads:**

File	Size	Type
Analysis Log	59,225 bytes	log
Master Log	237,570 bytes	log
Analysis Log	17,311,275 bytes	vcf
Structural variants	11,446,870 bytes	bed
Aligned reads	28,187,169,721 bytes	bam

BIOSAMPLE NAME

Dataset HG00732

Editable Dataset Attributes

Biological Sample Name
HG00732

Project: All My Projects

EDIT COPY ANALYZE... DELETE

CANCEL SAVE

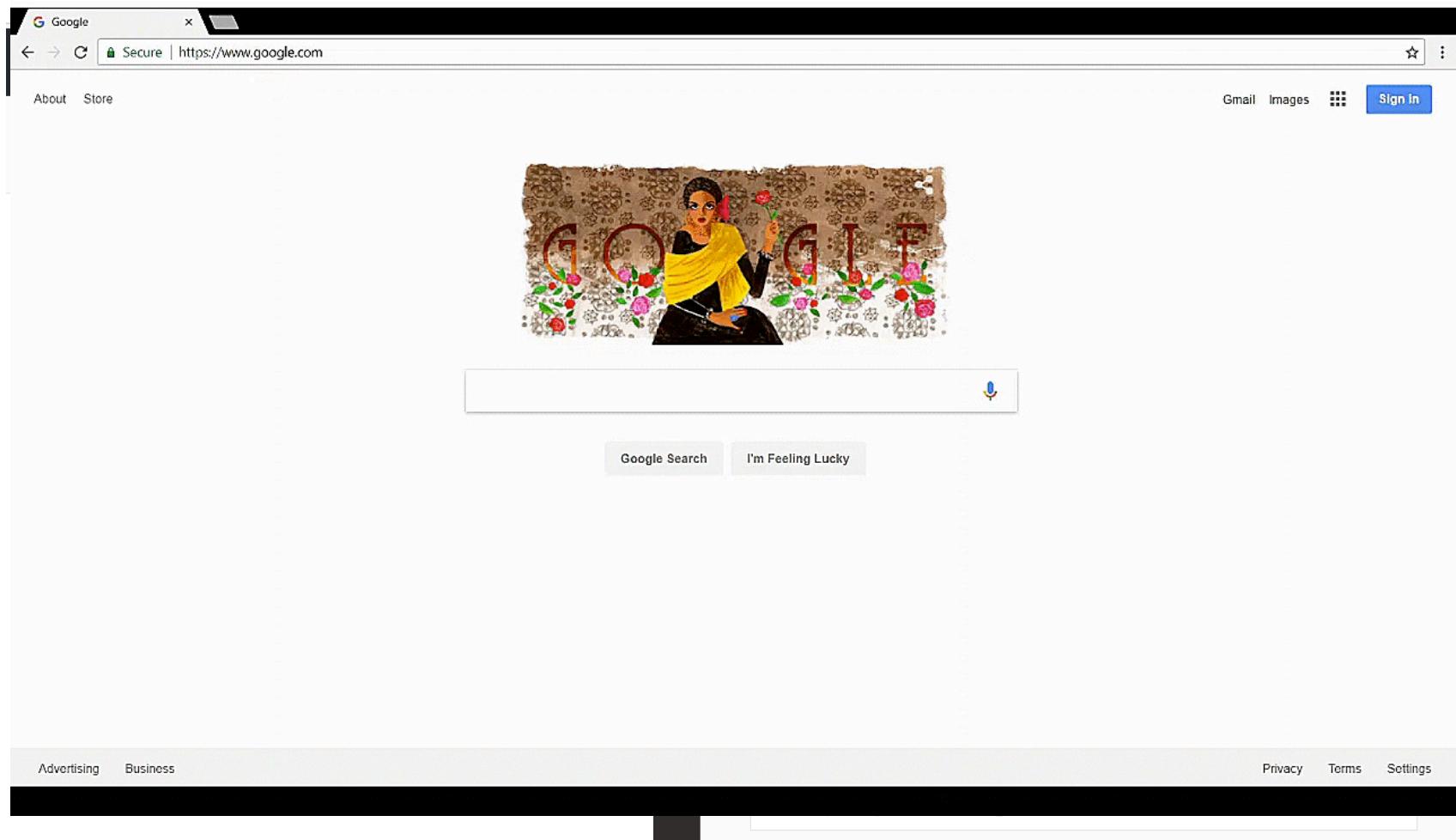
Data Set Id	56462
Well Sample Name	[multiple]
Biological Sample Name	HG00732
Description	
Number of Subreads	1,852,006
Total Length of Subreads (bp)	15,883,219,136



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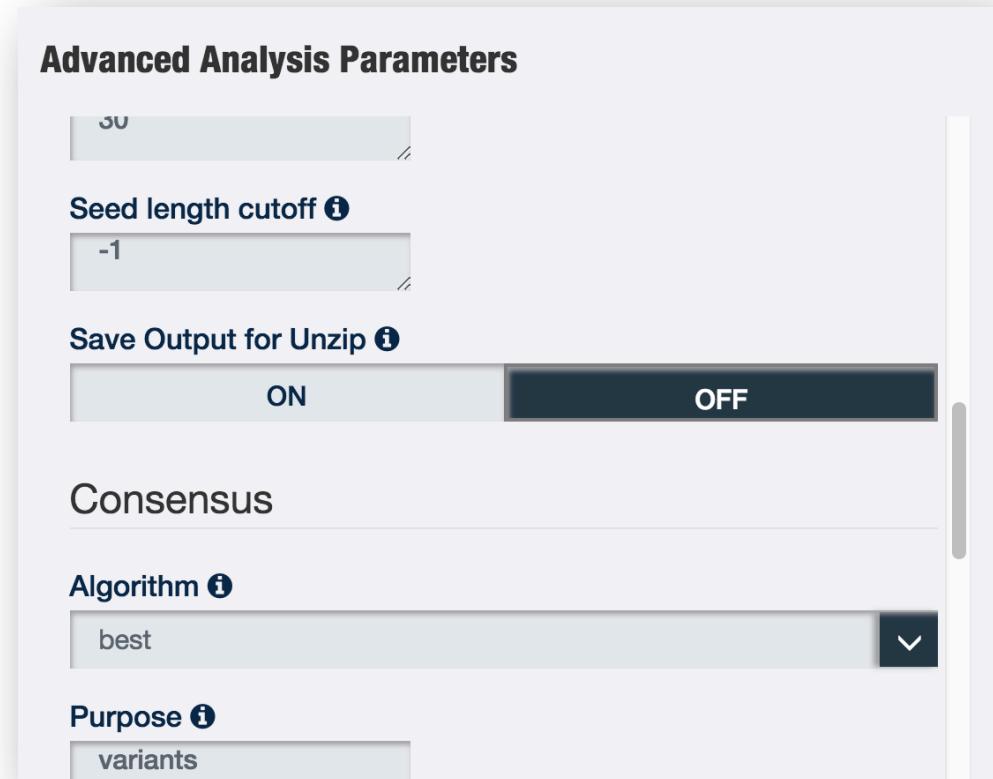
De Novo Assembly

BINARY RELEASE – FALCON/UNZIP

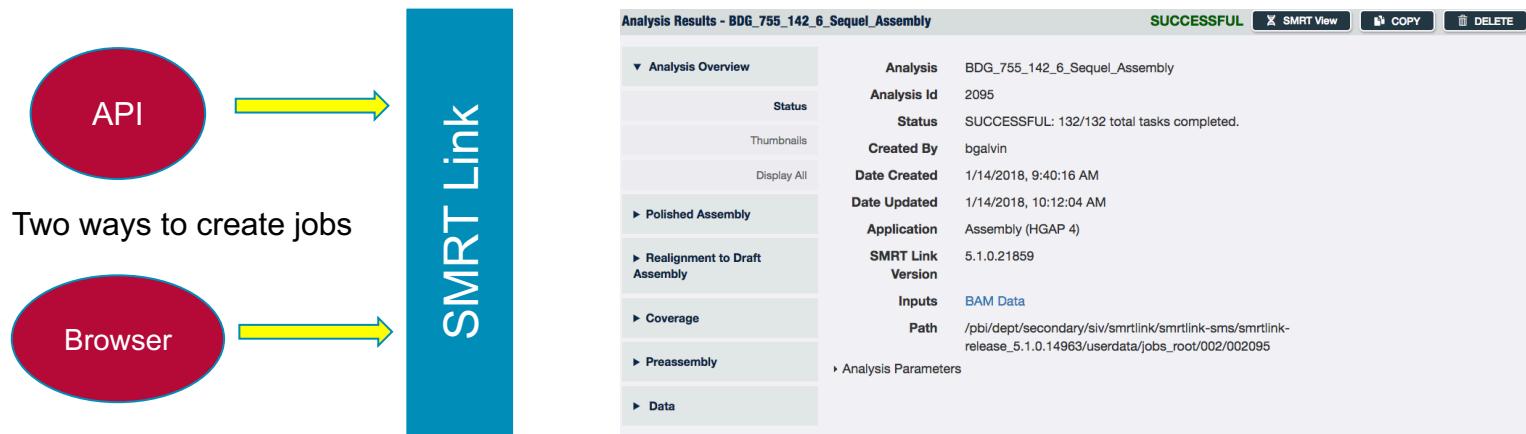


RUNNING UNZIP ON HGAP.4 OUTPUT

- HGAP 4 advanced parameter
Save Output for Unzip, **off** by default
- Optionally retain the final set of `*.las` files after overlapping raw reads, which can consume large amounts of disk space, especially for larger genomes
- Unnecessary when assembling haploid genomes, e.g., bacteria or when there is no intention to unzip



HGAP.4 TO UNZIP



```
# From the falcon code base
(venv) % python -m falcon_kit.mains.hgap4_adapt --help
usage: hgap4_adapt.py [-h] [--job-output-dir JOB_OUTPUT_DIR]
```

Given a full HGAP4 run, generate directories and symlinks to make it look like a pypeflow run.

optional arguments:

- h, --help show this help message and exit
- job-output-dir JOB_OUTPUT_DIR
 Directory of HGAP4 job_output. (A symlink or relative path is fine.) Task-dirs are under here in "tasks/" (de

Typically:

```
mkdir mydir/
cd mydir/
python -m falcon_kit.mains.hgap4_adapt --job-output-dir=../job_output/
```

GFA OUTPUT – ASSEMBLY DEBUGGING

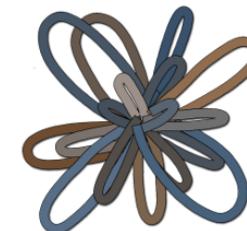
Script available in both SMRT Tools and GitHub



```
% python ./falcon_kit/mains/gen_gfa_v1.py -h
```

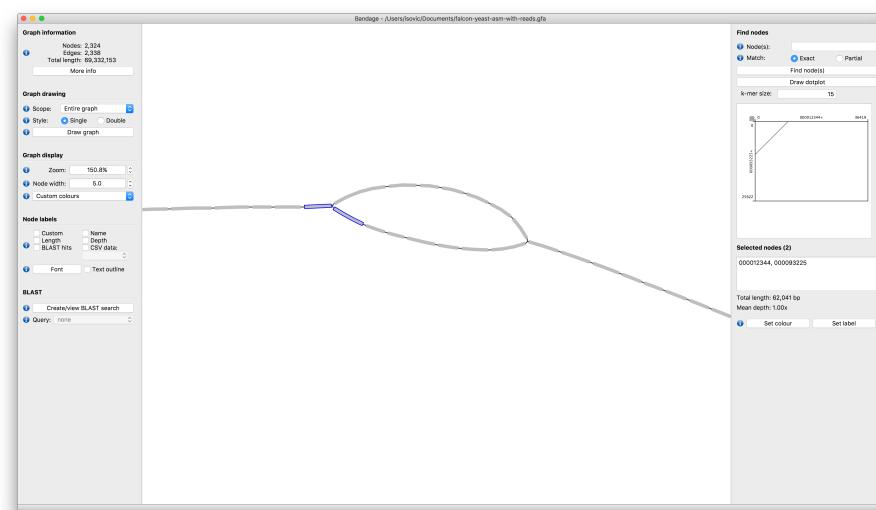
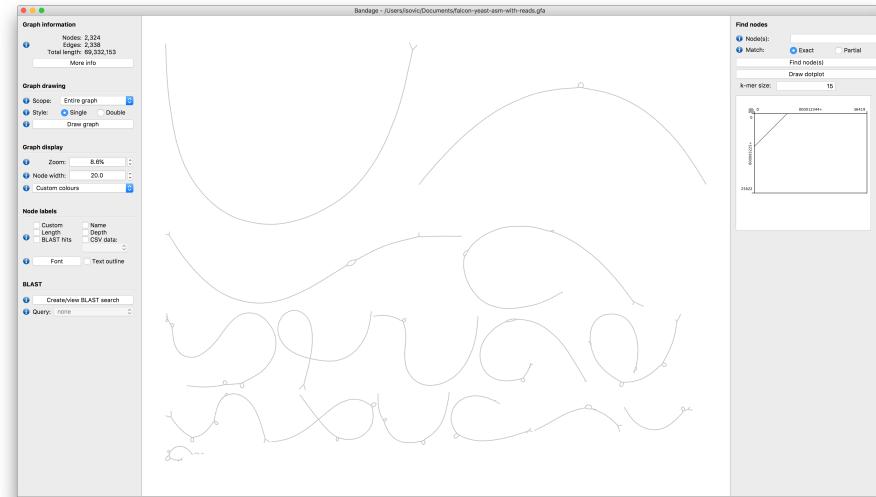
```
usage: gen_gfa_v1.py [-h] [--p-ctg-tiling-path P_CTG_TILING_PATH]
                     [--a-ctg-tiling-path A_CTG_TILING_PATH]
                     [--preads-fasta PREADS_FASTA] [--p-ctg-fasta P_CTG_FASTA]
                     [--a-ctg-fasta A_CTG_FASTA]
                     [--sg-edges-list SG_EDGES_LIST] [--utg-data UTG_DATA]
                     [--ctg-paths CTG_PATHS] [--add-string-graph]
                     [--write-reads] [--write-contigs] [--min-p-len MIN_P_LEN]
                     [--min-a-len MIN_A_LEN]
```

Generates GFA output (on stdout) from FALCON's assembly.



Bandage

<https://github.com/rrwick>





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Usability Improvements

Data Management and SMRT Analysis

COPY AND RELAUNCH ANALYSIS

The following screenshots demonstrate the process of copying an analysis job and relaunching it.

Analysis Results - Demo SV

Status: FAILED

Analysis Overview:

- Analysis: Demo SV
- Analysis Id: 28612
- Status: FAILED: Task pbsvtools.tasks.align-18 FAILED in 295.08 sec.
- Created By: mbudagyan

Data:

- Date Created: 12/12/2017, 10:47:31 AM
- Date Updated: 12/12/2017, 10:55:59 AM
- Application: Structural Variant Calling
- SMRT Link Version: 5.1.0.20106
- Inputs: BAM Data Reference

Copy Button: A red box highlights the "COPY" button.

Create New Analysis - Settings

Analysis Application: Structural Variant Calling

Analysis Name: Copy of Demo SV

Associated Inputs:

Reference: Hg19

Structural Variants:

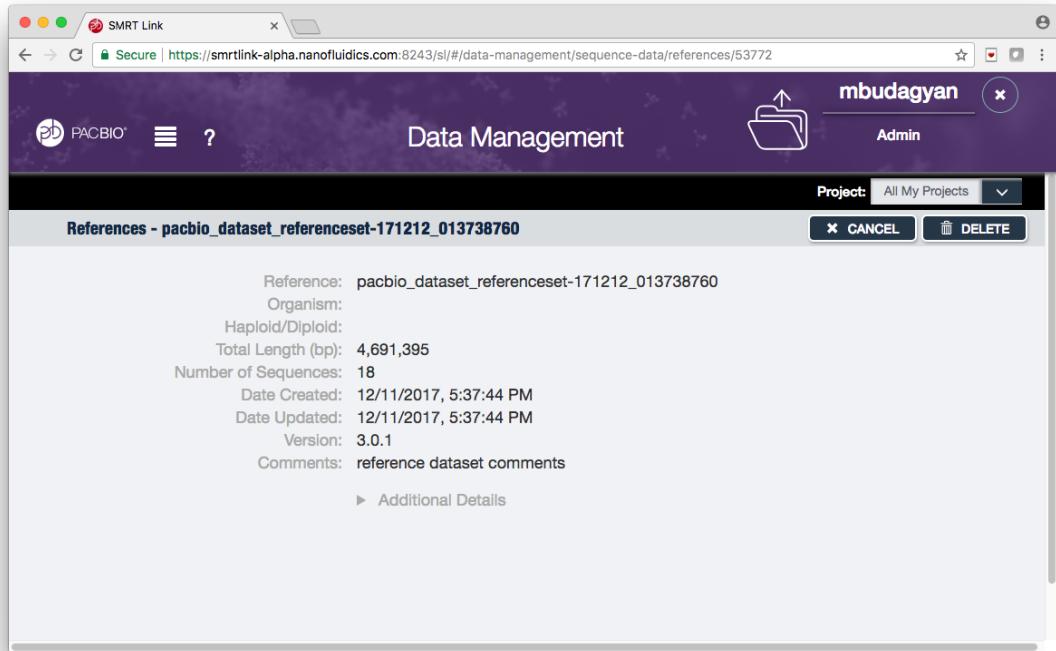
- Minimum Length of Structural Variant (bp): 50
- Minimum Reads That Support Variant (Count): 2
- Minimum Percentage of Reads That Support Variant (%): 20

Data Sets:

	Data Set Name	Well Sample Name
<input type="checkbox"/>	zpm1-Cell1	zpm1
<input type="checkbox"/>	BYU_Turneri-Cell5	BYU_Turneri
<input checked="" type="checkbox"/>	HG00733 Sequel	unknown
<input type="checkbox"/>	3_Cell-1_Workflow_Diffusion.py-Cell8	3_Cell-1_Workflow_Diffusi...
<input type="checkbox"/>	15kb_Column Cleanup_5pM-Cell6	15kb_Column Cleanup_5pM 15
<input type="checkbox"/>	2_Cell-1_Workflow_Diffusion.py-Cell7	2_Cell-1_Workflow_Diffusi... 2
<input type="checkbox"/>	BYU_Turneri-Cell4	BYU_Turneri
<input type="checkbox"/>	M1028-8pM-Cell4	M1028-8pM

DATA MANAGEMENT – REMOVING THE UNWANTED

- Deletes from the UI only
 - Collections
 - References
 - Barcode sets
- Helps reduce clutter
- UI responsiveness



CREATE ANALYSIS - NEW LAYOUT

SMRT Link

Not Secure | https://smrtlink-bihourly.nanofluidics.com:8243/sl/#/analysis/settings

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Project: All My Projects

Create New Analysis - Settings

X CANCEL ▶ START

Analysis Application *

- Assembly (HGAP 4)
- Base Modification Detection
- Base Modification and Motif Analysis
- CCS Mapping
- Circular Consensus Sequences (CCS)
- Convert BAM to FASTX
- Demultiplex Barcodes
- Iso-Seq

Analysis Name *

View: BAM Data

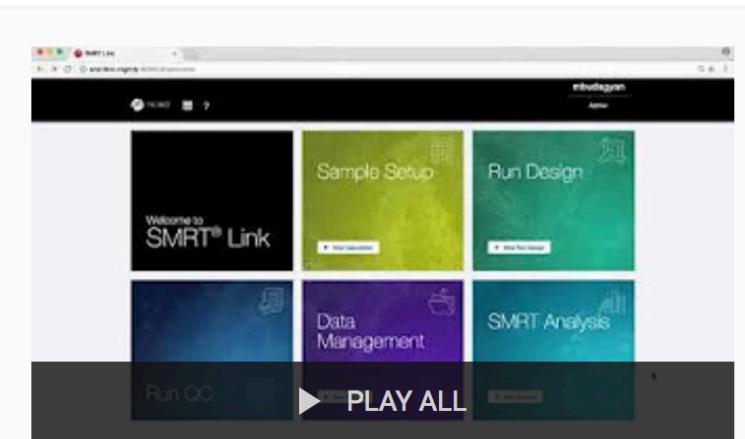
Data Sets

	Data Set Name	Well Sample Name	E
<input type="checkbox"/>	hdfsubreads	unknown	un
<input type="checkbox"/>	Output-dataset-for-protractor-barcoding-test	All None	BCS23 diffusion 70pM P6... un
<input type="checkbox"/>	Auto-merged subreads @ 1513096418273	[multiple]	un
<input type="checkbox"/>	pacbio_dataset_subreadset-171114_215558341	10-10-2017_14hr_Lambd...	un
<input type="checkbox"/>	lambda/0007_tiny	Inst42267-040315-SAT-10...	un
<input type="checkbox"/>	pacbio_dataset_subreadset-170313_050639539	unknown	un
<input type="checkbox"/>	LVP2_D09-5253_BA008270-1st_4hrs_PkmidC525	"LVP2_D09-5253_BA0082... un	un
<input type="checkbox"/>	Re barcode Alice/Bob/Charles	All None	T0212_384_plex_barcode... un

SMRT LINK REFERENCE MATERIALS

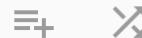
pacb.com > Support > Software Downloads

- SMRT Link Documentation
 - Release Notes
 - Installation Instructions
 - SMRT Link User Guide
 - Barcoding Overview
- Developer Documentation
 - SMRT Tools Reference Guide
 - SMRT Link APIs
- Training materials
 - SMRT Link and SMRT Analysis Tutorials



PacBio SMRT Link Training Series

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