



Appendix A Release 2.7

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Note: This Document may change slightly, and will be accompanied by snapshots providing an indication to real changes to the look of the system where applicable.

List of Primary Changes

(new functionality or large scale changes visible to the end user)

- Added shipping manifold for exporting plates or generating freezer content reports (with options to dump to an excel spreadsheet and/or include a full sample list)

Printable Page *(extracts only this table)*

Shipping Manifest

Date: 2009-07-06 11:03:20

Shipper: LabAdmin

To:
BC Generations Project
2775 Laurel St.,
Vancouver, BC
V5Z 1M9

From:
BC Generations Project
7.208 - 675 West 10th Ave,
Vancouver, BC
V5Z 1L3

Content Summary

Type: Human Blood Specimens

Subject Records: 22

First Subject: BC000110

Last Subject: BC000348

<u>Sample Type</u>	<u>Samples per Subject</u>	<u>Samples</u>	<u>Total Volume in mL</u>
Blood Plasma	8.18	180	720
Blood Serum	5.45	120	0.36
Red Blood Cells	2.73	60	240
Urine	3.00	66	264
White Blood Cells	2.73	60	240
Whole Blood	2.73	60	0.18
Totals (6 Records)	24.82	546.00	1464.54

- Added Shipment home page to view all details including content and upload information

Import Shipment

(No manifests found for Shipment 63)

Current Sources [49] linked to this Shipment

Define New Sources

Link to Existing Sources

Link to New Sources from Template File

Delimited input file:

Choose File

no file selected

Delimiter:

Tab

Comma

Upload

----- Select Template (optional) -----

Data from Shipment	
Shipment	[Edit] View Edits
Shipment ID	63
Shipment Sent	Oct-18-2010 00:00:00
Shipment Received	Oct-19-2010 00:00:00
Supplier_Organization	NWCH
Shipping Container	Cryoport
Recipient_Employee	Emp148: Darlene
Waybill Number	7963 5147 3398
Shipment Comments	Batch 73, Plate A103: 47 tumor RNA endometrial samples (UCEC) + 1 normal RNA endometrial sample (double normal) + 1 U87 control.
Received at Temp	-193
Container Status	Locked
Shipment Status	Received
Shipment Reference	DEL 1551
Shipment Type	Import
From_Site	External
Target_Site	Echelon

(excluded empty fields)

- $$\begin{pmatrix} \bullet \\ \bullet \\ \bullet \\ \bullet \\ \bullet \\ \bullet \end{pmatrix} \quad \mathbf{v}$$

Data from Starting Material, RNA_DNA_Source, Sample Origin, Patient	
Starting Material	[Edit] View History
Source ID	20565
Type	RNA_DNA_Source
Original Source	11035: JOC91
External Identifier	HuFCM-twinB-Tissue for RNA
Number	1.1
Source Label	
Received Date	Mar-03-2011
Current Amount	8
Original Amount	8
Amount Units	ul
Container Format	96-well ABGene
Received Employee	Emp233: Angela
Rack	Rac7: Garbage Rack
Status	Thrown Out
Barcode Label	No Barcode
Notes	
Parent Source	Src16519: RNA_DNA_Source-1
Source_Plate	Pla366791: A03500-1
Shipment	0
Reference_Project	REMC
RNA_DNA_Source	[Edit] View History
RNA_DNA_Source ID	16508
Starting Material	Src20565: RNA_DNA_Source-1.1
Sample Collection Date	0000-00-00
RNA_DNA_Isolation Date	0000-00-00
RNA_DNA_Isolation Method	
Nature	Tissue
Storage Medium	
Sample Origin	[Edit] View History
Original Source ID	11035
Starting Material supplied to the Lab?	Yes
Original Source Name	JOC91
Taxonomy	Homo sapiens - human [9606]
Original Source Type	Solid_Tissue
Tissue	Brain-Germinal Matrix
Stage	Fetal
Host	

- Added Employee Submission/Group Permission functionality for lab admins



User Emp221: Adrian belongs to:

- Gene Expression Production
- Gene Expression SAGE
- Microarray
- Receiving

Select Groups

Aly Karsan Lab
Bioinformatics
Bioinformatics Admin
BioSpecimens Core
BioSpecimens Core Admin
Brain Research
Cancer Genetics
Engineering
External
FG TechD
FG TechD Admin
Gastrointestinal Cancer (GI)
GE SAGE Admin
Gene Expression
Gene Expression Admin
Gene Expression Production
Gene Expression Project Admin
Gene Expression SAGE
Genomics
LIMS Admin
Mapping
Mapping Admin
Mapping Bioinformatics
Mapping Production
Mapping Project Admin
Mapping TechD
Marra
MGC_Closure
MGC_Closure Admin
MGC_TechD
Microarray
Microarray Admin
Programmed Cell Death (PCD)
Projects_Admin
Prostate
Prostate Lab
Prostate Lab Admin
Proteomics
QC
Randy Gascoyne Lab
Receiving
Sequencing
Sequencing Admin
Sequencing Bioinformatics
Sequencing Production
Sequencing Project Admin
Sequencing TechD
Systems
TCGA
Vectorology

Set Employee Groups

Reset

- Refactored Tissue, Histology information for Original Sources to enforce structured vocabulary and help ensure key information is tracked for all incoming samples.
- Added new functionality to download and preset standards templates into excel files

Download Excel File --- Select Template (optional) --- ☒ Add Row/Column Number of Rows to fill

Customize Template Preset Template

Generate Standard Template for Table

- Added upload and mapping of data directly from excel files

Delimited input file: no file selected

Delimiter: ☒ Tab ☐ Comma

--- Select Template (optional) ---

- Improved attribute functionality to use lookup tables and enums. Also improved editing and duplicate issues (also in protocols)

Define Source Attributes			
ID	Label	Submitted_Concentration (Source)	Submitted_Concentration_Measured_by (Source)
20565	Src20565: RNA_DNA_Source-1.1	<input type="text"/>	<input type="text"/>
20566	Src20566: RNA_DNA_Source-1.1	<input type="text"/>	<input type="text"/>
20567	Src20567: RNA_DNA_Source-1 TCGA-BC-4073-01B-02R-A130-13	0.16	<input type="text"/>

- Sets all " cells with value above it (to prevent rows below from being filled, si

- ✓ External
- External-Bioanalyzer
- External-Nanodrop
- External-Qubit
- External-Picogreen
- Internal-Nanodrop
- Internal-Qubit
- Internal-Picogreen
- Internal

- Improved Rack home page
- Added minimum standards for user passwords
- Enhanced view module to enable more powerful generation of customized reports
- Added basic graphing functionality to query and views
- Added Patient tracking
- Added capability of tracking information specific to xenograft samples
- Added Run_Analysis, an automated analysis framework to standardize analysis for different types of runs/analyses. For each individual step of an analysis, information such as start/finish or which software version is used is tracked. Both the BWA alignment and BioScope alignment pipeline run under Run_Analysis for this release.
- Added Multiplex_Run_Analysis to track the index and sample info of a pooled samples run

- Added API support for the new Run_Analysis and Multiplex_Run_Analysis tracking [hotfixed]
- Added Queueing system for managing Illumina scheduling priorities [hotfixed]
- Automated validation of Primers based upon Vector Sequences (removing need for admins to do this, and enabling instant access to all 'valid' primers)
- Added distinct Department Tab for QC group [hotfixed]
- Added QC_Batch functionality to track batches of items for QC'ing (including report pages and history views) [hotfixed]

- Added ability to add and display edit changes for any fields that Change_History is tracked [hotfixed]

table 1																			
	run status	run time	pipeline finished	pipeline	table id	table number	pipeline	run initiated by	forced code	line	forced code	pipeline type	run comments	table edit comments	test status	protected	run GC status	run GC status edit comments	full run path
Analyzed	Jan-11-2011 09:42:16	Jan-15-2011 01:00:11	HISep-4	SLX NOI SAIC DLBOL	34920	AO1872	1	PET SLX-PET	Corey	117944830	1	A	Paired	mrm set to Approved (2011-01-17);	Row	No	Passed	Jan-17-2011: (N/A -> Passed)	Quality Graph View Assoc Call Summary
Analyzed	Jan-11-2011 09:42:17	Jan-15-2011 01:00:12	HISep-4	SLX NOI SAIC DLBOL	34921	AO1872	1	PET SLX-PET	Corey	117944830	2	A	Paired	mrm set to Approved (2011-01-17);	Row	No	Passed	Jan-17-2011: (N/A -> Passed)	Quality Graph View Assoc Call Summary
Analyzed	Jan-11-2011 09:42:18	Jan-15-2011 01:00:13	HISep-4	SLX NOI SAIC DLBOL	34922	AO1872	1	PET SLX-PET	Corey	117944830	3	A	Paired	mrm set to Approved (2011-01-17); Jan-17-2011: (Yes -> No) non-billable as per R2 slightly poor quality	Row	No	Passed	Jan-17-2011: (N/A -> Passed)	Quality Graph View Assoc Call Summary
Analyzed	Jan-11-2011 09:42:19	Jan-15-2011 01:00:14	HISep-4	SLX NOI SAIC DLBOL	34923	AO1872	1	PET SLX-PET	Corey	117944830	4	A	Paired	mrm set to Approved (2011-01-17);	Row	No	Passed	Jan-17-2011: (N/A -> Passed)	Quality Graph View Assoc Call Summary
Analyzed	Jan-11-2011 09:42:20	Jan-15-2011 01:00:15	HISep-4	SLX NOI SAIC DLBOL	34924	AO1872	1	PET SLX-PET	Corey	117944830	5	A	Paired	mrm set to Approved (2011-01-17);	Row	No	Passed	Jan-17-2011: (N/A -> Passed)	Quality Graph View Assoc Call Summary
Analyzed	Jan-11-2011 09:42:21	Jan-15-2011 01:00:16	HISep-4	SLX NOI SAIC DLBOL	34925	AO1872	1	PET SLX-PET	Corey	117944830	6	A	Paired	mrm set to Approved (2011-01-17);	Row	No	Passed	Jan-17-2011: (N/A -> Passed)	Quality Graph View Assoc Call Summary

- Added Adapter_Index_Sequence tracking in database to track the index used in index pooling [hotfixed]

- Added ability to create tray of tubes and ability to use tray of tubes to go through protocol and maintain as tray of tubes [hotfixed]
- Added ability to aliquot tube and existing tray into a new tray [hotfixed]
- Added capability for primer plate to be able to apply to tray of tubes [hotfixed]
- Added interface and ability to create sample pool rearrays using, `library_plates`, `tubes`, or `trays` [hotfixed]

- Added interface for batch pool rearray of the same rearray specification [hotfixed]

- Index9_LigateAdapter : ((A*TV) Wells) : ((A*TV) (DV/TV) (TV-DNA) BrewSourceWells) : ((A*TV) Wells) : ((A*TV) (DV/TV) (TV-DNA) BrewSourceWells) : ((CV100)
- ((A* 50) Wells) : ((A* 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : ((A* 50) Wells) : ((A* 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : ((10 /100)
- Eg. with 384 samples: City = ((A* 50) 384) : ((A* 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : ((A* 50) 384) : ((A* 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : ((10 /100)
- **5X Quick Ligase Buffer** : ((0.2 * 50) 384) : (((0.2 * 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : (((0.2 * 50) 384) : (((0.2 * 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : ((10 /100) ul = **4242.98 uL**
 - **Quick T4 DNA Ligase 2000ea**uL : (((0.134 * 50) 384) : (((0.134 * 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : (((0.134 * 50) 384) : (((0.134 * 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : ((10 /100) ul = **2642.80 uL**
 - **PE Adapter 1uM** : (((0.02 * 50) 384) : (((0.02 * 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : (((0.02 * 50) 384) : (((0.02 * 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : ((10 /100) ul = **424.30 uL**
 - **Ultrapure dH2O** : (((0.341384615384615 * 50) 384) : (((0.341384615384615 * 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : (((0.341384615384615 * 50) 384) : (((0.341384615384615 * 50) (5 / 50) (50 / (50 - 15.2307692307692)) 12) : ((10 /100) ul = **7242.44 uL**
- Brew Volume = BrewVolume, DNA_volume = DNA
- Eg. Brew Volume = 34.77 ul = 34.77 ul DNA_volume = 15.23 ul = 15.23 ul

[Save As New Chemistry](#)

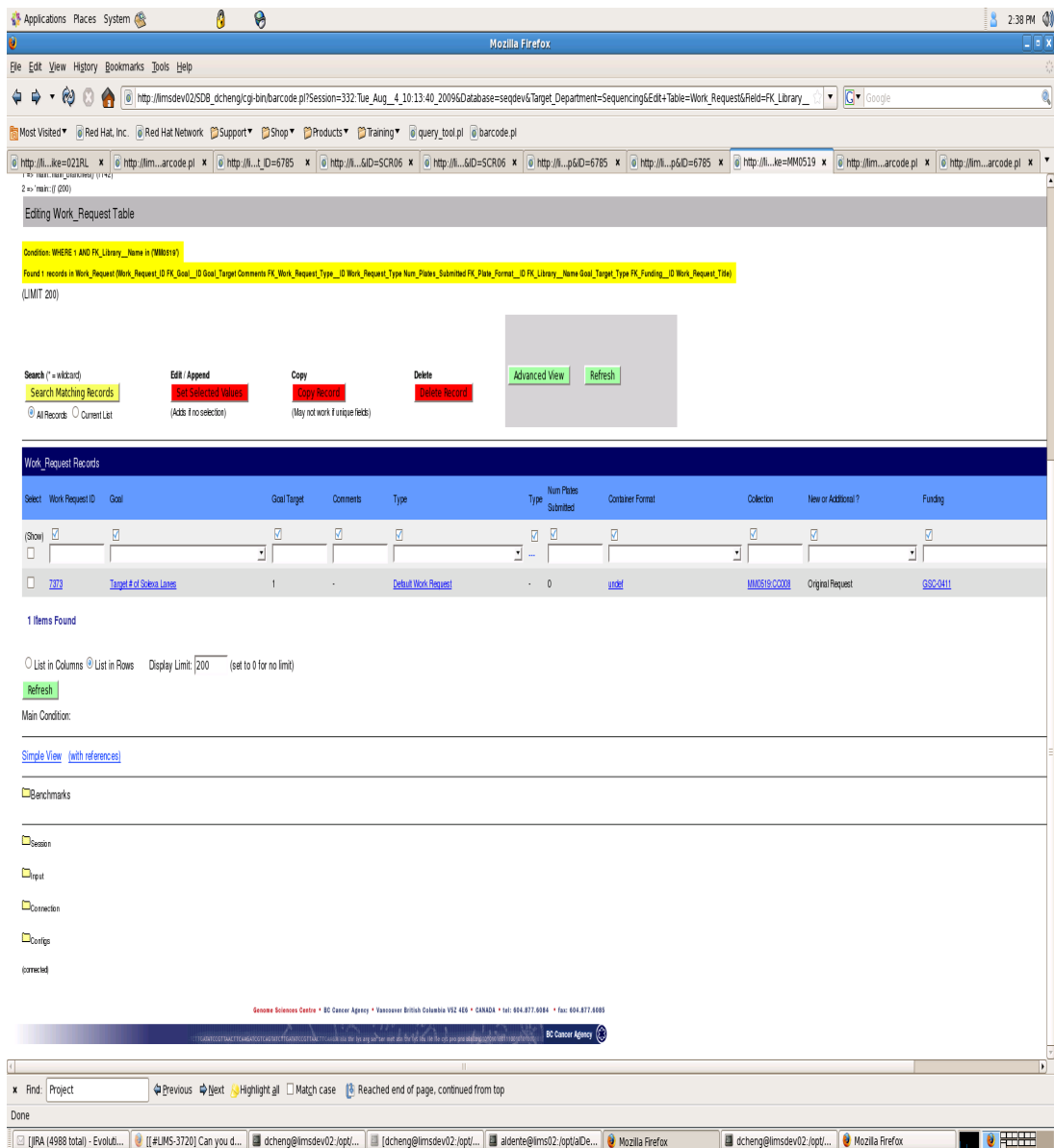
xii Appendix A

Minor Changes

(improvements to existing core functionality visible to the end user)

- Add ability to Transfer/Aliquot samples 'out' to a new container without shifting focus from current containers.
- Adjust Split function to prompt for split number for **each** container. (ie if splitting 8 tubes into 16, users specify **Split each container into: 2** rather than (previously) 'Split into: 16'). This is more intuitive and removes the chance of 'invalid' numbers being chosen. (hotfixed)
- Prompt enabling users to change the Pipeline during a transfer step within a protocol will only appear if multiple applicable Pipelines include the current Lab Protocol
- Enable movement of items into multiple boxes at one time (<items_for_box_1><box_1><items_for_box_2><box_2> ... etc)
- Added functionality to move contents of two racks of the same type by scanning them together
- Enable loading of slots in boxes in ascending or descending order for columns and/or rows.
- Enabled user to pick the type of label to print when re-printing source barcodes.
- Enable bulk sample redistribution across boxes (enabling users to scan N boxes and extract all samples of a particular type into one or more target boxes)
- Smarter sample relocation into slotted boxes. Confirmation step auto-fills target slots (by row or column; asc or desc order) , and providing feedback wrt first slot used, last slot used & occupied slots that were skipped.

- When only editing a single record that went through the multi-page edit form, it will now go to the single page edit form by default.
Before:



After:

The screenshot shows a Mozilla Firefox browser window with the following elements:

- Header:** Applications, Places, System, 2:35 PM.
- Address Bar:** http://lmsdev02SD8_dcheng/cg-bin/barcode.pl?Session=332 Tue_Aug_4_10_13_40_2009&Database=seqdev&Target_Department=Sequencing&Edit+Table=Work_Request&Field=FK_Library_...
- Navigation Bar:** File, Edit, View, History, Bookmarks, Tools, Help.
- Search Bar:** Google.
- Most Visited:** Red Hat, Inc., Red Hat Network, Support, Shop, Products, Training, query_tool.pl, barcode.pl.
- Tab Bar:** Multiple tabs open, including http://lmsdev02SD8_dcheng/cg-bin/barcode.pl?Session=332 Tue_Aug_4_10_13_40_2009&Database=seqdev&Target_Department=Sequencing&Edit+Table=Work_Request&Field=FK_Library_...
- Main Content Area:**
 - [View/Edit Multiple Records at one time](#)
 - [Search results for Work_Request](#)
 - 7373**
 - Edit Work_Request Form**
 - (Mouse over fields for tooltips)**
 - Goal:** Target # of So
 - Goal Target:** 1
 - Comments:** [Text Area]
 - Type:** [Dropdown Menu] Search Filter
 - Num Plates Submitted:** 0
 - Container Format:** [Dropdown Menu] Search Filter
 - Collection:** MM0519 CC008 (Auto Completed)
 - New or Additional?:** Original Request
 - Finding:** SSC-0411 Search Filter
 - Work Request Title:** [Text Field]
 - Referenced By:** [Material Transfer Plate](#)
 - New Search:** [Button] Multi-Record
 - Update Work_Request:** [Button]
 - Save as New Work_Request Record:** [Button]
 - Benchmarks:** [Section Header]
 - Sequencing:** [Section Header]
 - Input:** [Section Header]
 - Connection:** [Section Header]
 - Config:** [Section Header]
- Footer:** Find: Project Previous Next Highlight all Match case Reached end of page, continued from top
- Taskbar:** [Taskbar with multiple open applications]

- More transparent ancestry information supplied on main pages for Library, Original_Source, Source records

- Improved get_Primer_data API to figure out tube/plate primer on its own [hotfixed]
- Added get_bcr_data to API [hotfixed]
- Added interface for Bioinformatics to delete the primer plate that they order themselves [hotfixed]



- Allowed lab admins to delete plates with prep records [hotfixed]

- For library_plate that's involved in a rearray, a link will show up to give the option to view all plates in the ancestry box

Pla292229 INX022-1

DNA
96-well ABGene
Original Plate
Library: Index pool 022
From OS: 93 patient gDNA tumour
Made: Oct-28-2009, TZ
Current Pipeline: AMP

Schedule: ([Edit](#) [Batch Edit](#))
Location: [Rac25504: F20-59 \(-20 Degrees\) S4-R2](#)

Starting Material: [Src7634: RNA DNA Source-1](#)

Re-Print Container Barcode -Select-

Attributes: [Set Attribute](#) or [Add New](#)

Save Plate Set

QC: ☒ Start QC ☐ QC Gel ☒ QC Monitoring

Actions **Start Protocol** **Summaries** **Data** **Attribute** **Links** **Links** **Wells** **Ancestry**

Choose Set: Protocol Tracking

☒ Save NEW set **Protocol:**

View All (Including Rearrays and Pools)

Ancestry of Library_Plate 292229

Siblings	Children
current gen	+1 gen
96-well ABGene	1.50 mL Tube, 96-well ABGene
	MicroAmp
	Pla293926
	Pla294452
	Pla294453
	Pla294454
	Pla293889
	Pla293890

[Edit this record](#)

Data from Container, Library_Plate

Container	[Edit] [View]
Edit	Storage History
Plate ID	292229
Library	INX022: Index pool 022
Number	1
Pipeline	AMP: Amplicon
Created	Oct-28-2009 15:13:10
Employee	Emp164: Thomas
Container Format	96-well ABGene
Size	96-well
Status	Active
Rack	Rac25504: F20-59 (-20 Degrees) S4-R2
Current Volume	5
Current Volume Units	ul
Test Status	Production

- Views grouped by visibility (Public, Employee, Group, Other)
- The auto-complete field changed from a single value selection into a dropdown box with multiple value selection
- View's output options can contain a group by checkbox
- View's input options can contain attribute search fields

Group Specific Improvements

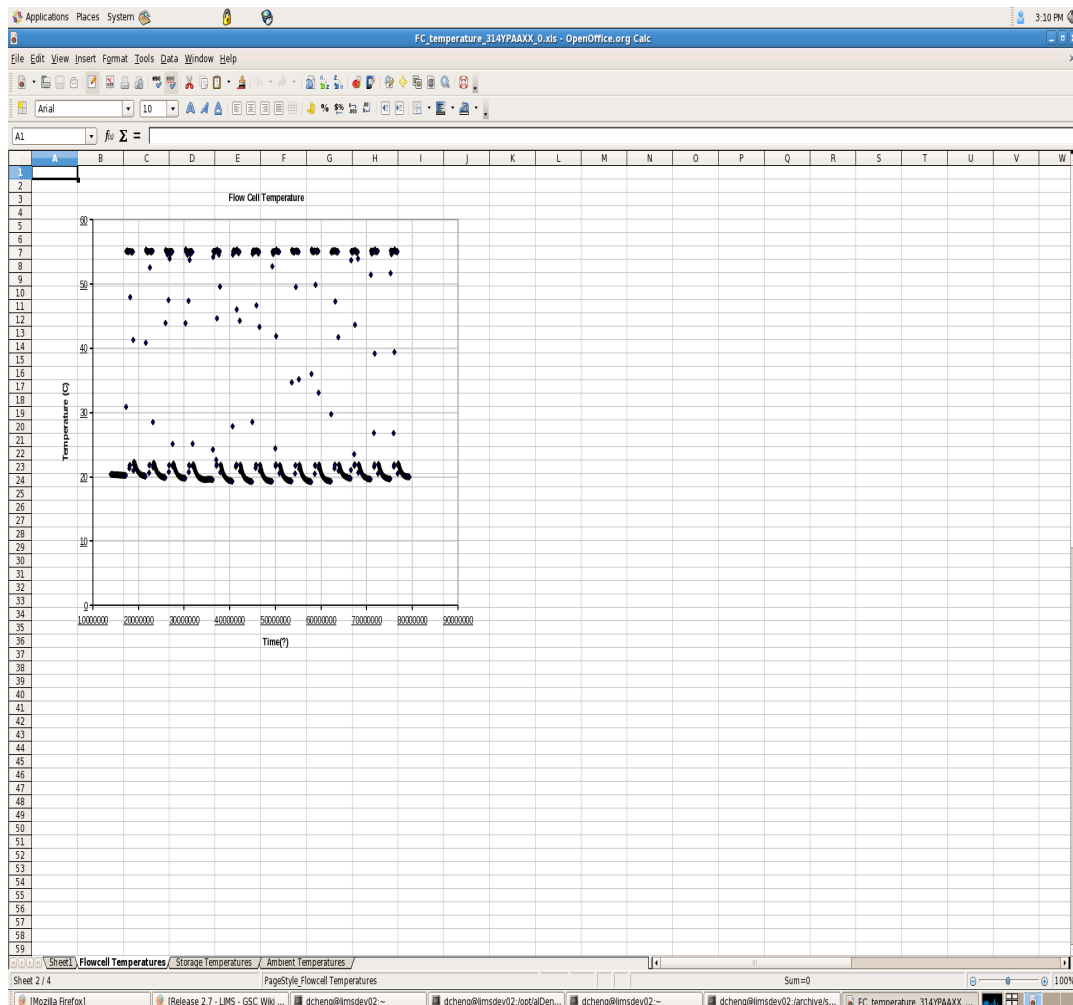
(Changes applicable only to specific groups)

- Added plugin for SOLID run analysis along with views to monitor SOLID data
- Added automate checking and linking of data directory to individual solid runs
- Added support for BioScope analysis pipeline for solid runs. The pipeline is completely automated using Run_Analysis. Support single end fragment solid runs, pair end fragment solid runs and miRNA barcode solid runs.
- Steps for single end fragment pipeline: SOLID-4, BioScope-1.2.1 Mapping, BioScope-1.2.1 Mapping Small Indel Frag, BioScope-1.2.1 MaToBam, BioScope-1.2.1 Position Error, SOLID Rsync Analysis Result
- Steps for pair end pipeline: SOLID-4, BioScope-1.2.1 Pair End Mapping, BioScope-1.2.1 Pair End Pairing, BioScope-1.2.1 Pair End Position Error, SOLID Rsync Analysis Result
- Steps for miRNA barcode pipeline: SOLID-4, SOLID Replace First Base, SOLID Adapter Trim, BioScope-1.2.1 Mirna Barcode Mapping, BioScope-1.2.1 Mirna Barcode MaToBam, SOLID Rsync Analysis Result

- | | | | | | | | | | | | | | | | | |
|---|------------------------|------------------------------|------------------------|-----------------------------|----------|----------|---------------------|--------------------------------|--------|-------|-----------|-----------|-------|-------|---------|---------|
| SOLID - Run Statistics | | | | | | | | | | | | | | | | |
| <div> <div>Configure Input Options</div> <div>Configure Output Options</div> </div> | | | | | | | | | | | | | | | | |
| <div> <div>Generate Results</div> <div>Max Number of Results</div> <div></div> </div> | | | | | | | | | | | | | | | | |
| <div> <div>Printable Page</div> <div>(extracts only this table)</div> </div> | | | | | | | | | | | | | | | | |
| <div> <div>Excel File</div> <div>(extracts only this table)</div> </div> | | | | | | | | | | | | | | | | |
| <div> <div>CSV File</div> <div>(extracts only this table)</div> </div> | | | | | | | | | | | | | | | | |
| SOLID - Run Statistics | | | | | | | | | | | | | | | | |
| <div> <div>Select</div> <div>Run ID</div> <div>Collection</div> <div>Plate ID</div> <div>Project</div> <div>Run Status</div> <div>Run Validation</div> <div>Run Date</div> <div>Equipment ID</div> <div>SOLID Run Type</div> <div>End Read Type</div> <div>Number Reads</div> <div>Number Aligned Reads</div> <div>Percent Map</div> <div>Zero Mismatches</div> <div>Megabases Of Coverage</div> <div>Reads Per Spot</div> </div> | | | | | | | | | | | | | | | | |
| <div> <div>Toggle</div> </div> | | | | | | | | | | | | | | | | |
| <input type="checkbox"/> | 117894 | HS2957.SA233 | 350847 | Sam Aericio | Analyzed | Pending | 2011-01-20 12:20:10 | SH-8 - EQU238 | Paired | PET 2 | 541705939 | 178705522 | 32.99 | 4.31 | 5787.88 | 1.09772 |
| <input type="checkbox"/> | 117894 | HS2957.SA233 | 350847 | Sam Aericio | Analyzed | Pending | 2011-01-20 12:20:10 | SH-8 - EQU238 | Paired | PET 1 | 541692202 | 402585167 | 74.32 | 25.48 | 18085.8 | 1.16426 |
| <input type="checkbox"/> | 117474 | HS2953.SA231 | 348950 | Sam Aericio | Analyzed | Approved | 2011-01-06 14:30:27 | SH-5 - EQU231 | Paired | PET 2 | 555756610 | 122548367 | 22.05 | 2.27 | 3956.01 | 1.09189 |
| <input type="checkbox"/> | 117474 | HS2953.SA231 | 348950 | Sam Aericio | Analyzed | Approved | 2011-01-06 14:30:27 | SH-5 - EQU231 | Paired | PET 1 | 555756610 | 396338792 | 71.71 | 24.69 | 17750.2 | 1.13385 |
| <input type="checkbox"/> | 117473 | HS2953.SA231 | 348949 | Sam Aericio | Analyzed | Approved | 2011-01-06 14:29:47 | SH-5 - EQU231 | Paired | PET 1 | 520606279 | 400073500 | 76.85 | 27.72 | 18023.7 | 1.15342 |
| <input type="checkbox"/> | 117473 | HS2953.SA231 | 348949 | Sam Aericio | Analyzed | Approved | 2011-01-06 14:29:47 | SH-5 - EQU231 | Paired | PET 2 | 520606279 | 146046481 | 28.05 | 3.09 | 4709.03 | 1.10327 |
| <input type="checkbox"/> | 117441 | A01470.SA227 | 348638 | Sam Aericio | Analyzed | Approved | 2011-01-05 12:17:16 | SH-10 - EQU220 | Paired | PET 1 | 584156017 | 476865967 | 81.60 | 32.07 | 21686.1 | 1.20501 |
| <input type="checkbox"/> | 117441 | A01470.SA227 | 348638 | Sam Aericio | Analyzed | Approved | 2011-01-05 12:17:16 | SH-10 - EQU220 | Paired | PET 2 | 584156017 | 244863886 | 41.89 | 6.68 | 7945.04 | 1.14174 |
| <input type="checkbox"/> | 117440 | HS2951.SA227 | 348637 | Sam Aericio | Analyzed | Approved | 2011-01-05 12:15:41 | SH-10 - EQU220 | Paired | PET 1 | 587224531 | 465130893 | 79.21 | 34.96 | 21288.6 | 1.15219 |
| <input type="checkbox"/> | 117440 | HS2951.SA227 | 348637 | Sam Aericio | Analyzed | Approved | 2011-01-05 12:15:41 | SH-10 - EQU220 | Paired | PET 2 | 587224531 | 243820579 | 41.37 | 7.23 | 7887.56 | 1.10123 |
| <input type="checkbox"/> | 117381 | HS2950.SA229 | 348153 | Sam Aericio | Analyzed | Approved | 2010-12-24 12:30:32 | SH-11 - EQU221 | Paired | PET 2 | 635966360 | 251268111 | 39.5 | | | |

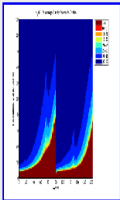
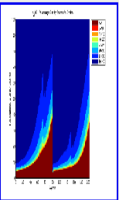
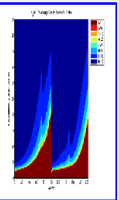
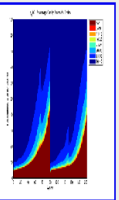
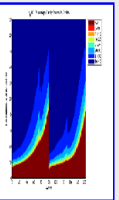
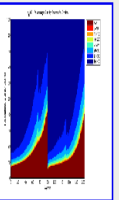
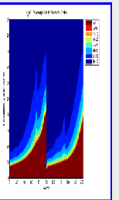
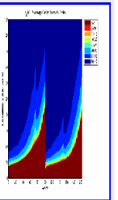
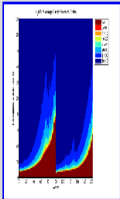
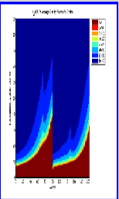
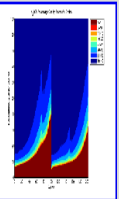
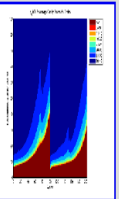
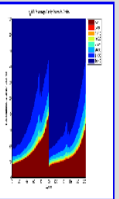
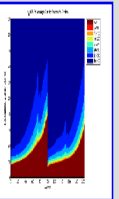
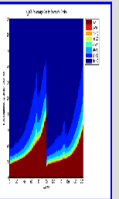
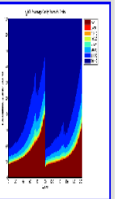
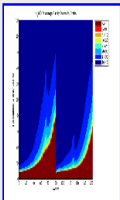
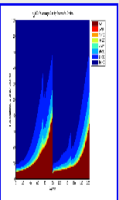
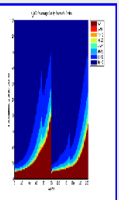
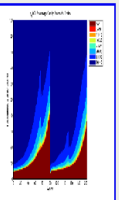
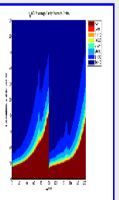
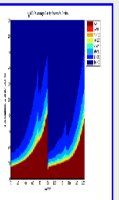
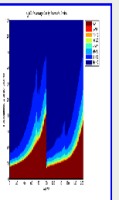
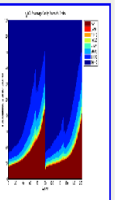








- Release 2.7

- Added SOLID - Ready for emulsion PCR view and SOLID - Libraries Ready for Sequencing view for SOLID runs scheduling [hotfixed]
- Added get_SOLID_run_data API support for Bioinformatics [hotfixed]
- Added plugin for LS_454 data (to enable tracking of externally generated data of this format)
- Automated the process to generate flowcell temperature plot and quality graph.



Alignment Independent Quality Summary

Popup W

Tile	Lane 1	Lane 2	Lane 3	Lane 4	Lane 5	Lane 6	Lane 7	Lane 8
0001								
0002	s_1_0002.png	s_2_0002.png	s_3_0002.png	s_4_0002.png	s_5_0002.png	s_6_0002.png	s_7_0002.png	s_8_0002.png
0003	s_1_0003.png	s_2_0003.png	s_3_0003.png	s_4_0003.png	s_5_0003.png	s_6_0003.png	s_7_0003.png	s_8_0003.png
0004	s_1_0004.png	s_2_0004.png	s_3_0004.png	s_4_0004.png	s_5_0004.png	s_6_0004.png	s_7_0004.png	s_8_0004.png
0005	s_1_0005.png	s_2_0005.png	s_3_0005.png	s_4_0005.png	s_5_0005.png	s_6_0005.png	s_7_0005.png	s_8_0005.png
0006								
0007	s_1_0007.png	s_2_0007.png	s_3_0007.png	s_4_0007.png	s_5_0007.png	s_6_0007.png	s_7_0007.png	s_8_0007.png
0008	s_1_0008.png	s_2_0008.png	s_3_0008.png	s_4_0008.png	s_5_0008.png	s_6_0008.png	s_7_0008.png	s_8_0008.png
0021	s_1_0021.png	s_2_0021.png	s_3_0021.png	s_4_0021.png	s_5_0021.png	s_6_0021.png	s_7_0021.png	s_8_0021.png
0022	s_1_0022.png	s_2_0022.png	s_3_0022.png	s_4_0022.png	s_5_0022.png	s_6_0022.png	s_7_0022.png	s_8_0022.png
0023								
0024	s_1_0024.png	s_2_0024.png	s_3_0024.png	s_4_0024.png	s_5_0024.png	s_6_0024.png	s_7_0024.png	s_8_0024.png
0025	s_1_0025.png	s_2_0025.png	s_3_0025.png	s_4_0025.png	s_5_0025.png	s_6_0025.png	s_7_0025.png	s_8_0025.png
0026	s_1_0026.png	s_2_0026.png	s_3_0026.png	s_4_0026.png	s_5_0026.png	s_6_0026.png	s_7_0026.png	s_8_0026.png
0027	s_1_0027.png	s_2_0027.png	s_3_0027.png	s_4_0027.png	s_5_0027.png	s_6_0027.png	s_7_0027.png	s_8_0027.png
								

- Automated the process to generate basecall summary

819P2ABXX Base Calling Summary

Lane Base Calling Results									
Lane	Read	Lane Yield (KB)	Raw Clusters (per tile)	PF Clusters (per tile)	PF Clusters Percent	1st Cycle Int (PF)	% intensity after 20 cycles (PF)	Phasing	Prephasing
1	1	3257856	1078178	1008000	93.48	1023 +/- 88	86.18 +/- 1.65	0.5357	0.3461
1	2	3257856	1078178	1008000	93.48	761 +/- 67	86.51 +/- 1.53	0.2691	0.3396
2	1	4036800	1372213	1249010	91.36	1074 +/- 101	86.17 +/- 0.99	0.5382	0.3228
2	2	4036800	1372213	1249010	91.36	803 +/- 79	85.73 +/- 1.42	0.2652	0.3270
3	1	3848949	1299377	1190887	91.93	1071 +/- 95	86.17 +/- 1.17	0.5454	0.3240
3	2	3848949	1299377	1190887	91.93	803 +/- 68	84.98 +/- 5.21	0.2703	0.3230
4	1	3969561	1349524	1228205	91.32	1061 +/- 97	85.72 +/- 1.47	0.5431	0.3384
4	2	3969561	1349524	1228205	91.32	799 +/- 72	85.40 +/- 1.68	0.2669	0.3478
5	1	6200777	2185063	1918557	87.90	1109 +/- 97	85.45 +/- 1.04	0.5131	0.3096
5	2	6200777	2185063	1918557	87.90	817 +/- 72	85.48 +/- 1.28	0.2556	0.3204
6	1	6242210	2183827	1931377	88.53	1075 +/- 103	85.79 +/- 1.05	0.5133	0.3043
6	2	6242210	2183827	1931377	88.53	804 +/- 77	85.08 +/- 1.54	0.2525	0.3021
7	1	6169310	2163025	1908821	88.34	1096 +/- 104	85.66 +/- 1.12	0.5127	0.2975
7	2	6169310	2163025	1908821	88.34	822 +/- 84	85.29 +/- 1.83	0.2526	0.2859
8	1	6307425	2213786	1951555	88.24	1068 +/- 112	85.71 +/- 1.09	0.5090	0.3250
8	2	6307425	2213786	1951555	88.24	798 +/- 82	85.38 +/- 1.71	0.2523	0.3207

[IVC](#)

[All](#)

Raw Results

Lane	Read	Lane Mean	Lane Std Dev	Lane Median	Q20 Bases	Q20 Percent	Q30 Bases	Q30 Percent	Total Bases
1	1	31.80	4.55	37.00	2989564667	85.79	2797785747	80.29	3484674225
1	2	32.73	4.13	39.00	3126144984	89.71	2975041111	85.38	3484674225
2	1	30.96	4.37	37.00	3703703010	83.51	3452924713	77.86	4434994537
2	2	31.80	4.00	38.00	3864138253	87.13	3647790503	82.25	4434994537
3	1	31.08	4.48	37.00	3521368487	83.85	3283767590	78.19	4199587272
3	2	31.90	4.11	38.00	3668421351	87.35	3465458683	82.52	4199587272
4	1	30.81	4.54	37.00	3628489235	83.19	3376150926	77.41	4361663285
4	2	31.67	4.14	38.00	3790973196	86.92	3575256437	81.97	4361663285
5	1	29.77	4.21	37.00	5679327646	80.42	5251147375	74.36	7062125434

- Automated the process to produce concat qseq
- Automated data compression for Illumina data after alignment is done
- Automated the process to run BCL converter to generate qseq files from bcl files

New Departments

- Set up BioSpecimen Core Department with responsibility to receive & enter imported sample information.
- Set up TCGA Department to enable easy access to project specific views for administrators

Set up Prostate_Lab department and additional tracking for CLIPR data (as a new Run Type).

Deferred Requests

(Improvement requests that we are aware of, but which are being deferred due to relatively lower priority)

Future Development

(larger scale improvements which would require implementation only at release time, but which may not be available in the near future)

Hotfix Patches since previous release

(list of patches that have been implemented as upgrades from the prior release. These may or may not have been applied prior to the new release)

Hotfixed:

- Installation.pat
Upgrades to the installation process.
- Queue_Core.pat
Set up a queueing system for prioritizing runs
- upgrade_Core_2_6.pat
- add_Equipment_Attribute.pat
- add_Study_Attribute.pat

- add_Analysis_Software_Attribute.pat
- add_fields_to_SolexaAnalysis.pat
- require Reference Code (SOW) for all submissions
- added optional link between SOW (Funding) and Jira Tickets
- added links to more easily add collaborators to Projects via Project, Work_Request, Funding pages
- added tooltip to show when links are redirecting to home pages
- included Attribute values in search (for Plate, Sample, Original_Source, Library, Source)
- Add_Adapter_Index_Sequence.pat
- Run_Analysis.pat
- Run_Analysis_upgrade.pat
- Run_Analysis_Current_Analysis.pat
- Run_Analysis_Attribute.pat
- Multiplex_Run_Analysis.pat
- Multiplex_Run_Analysis_Update.pat
- Multiplex_Run_Analysis_Attribute.pat
- SOLID_Run_Analysis.pat
- Add_Genome_to_SOLID_Run_Analysis.pat
- Add_Sample_ID_to_SOLID_Run_Analysis.pat
- Multiplex_SOLID_Run_Analysis.pat
- Multiplex_SolexaRun_Analysis.pat
- install_CLIPR_Run_Analysis_2_6.pat
- install Multiplex CLIPR Run Analysis 2 6.pat

Not Hotfixed:

- `move_plate_class_plus.pat`
Move Plate Class attribute to the Plate table and other changes

