Introduction to MiSeq Data Analysis and BaseSpace genomics cloud computing

Eri Kibukawa
Bioinformatics Support Scientist
APAC Technical Support
Agenda

MiSeq Reporter

- What is MSR?
- MSR Workflows
- MSR User Interface

BaseSpace

- Value of BaseSpace
- Key features of BaseSpace
- BaseSpace User Interface
What is MiSeq Reporter?

- A software service for the MiSeq that performs on-instrument data analysis
- Performs an analysis workflow as specified by the user
- Launches automatically after RTA completes primary analysis
- Can be accessed via a web-based interface from any computer networked to the MiSeq
- Can also be installed on a separate PC (stand-alone)
- Allows re-analysis of the sequencing run off-instrument
What is MiSeq Reporter?

- Software conducts secondary analysis in MiSeq sequencing pipeline.

![Diagram showing the workflow of MiSeq Reporter](image)

1. **Image capture**
2. **Analyze image**
3. **Basecalling**
4. **Converting basecalled files into FASTQ**
5. **Analysis specified by workflow**
6. **Report**

---

**MiSeq Control Software (MCS)**
- Real Time Analysis (RTA)
  - *primary analysis*

**MiSeq Reporter (MSR)**
- *secondary analysis and visualization*
MiSeq Reporter Web-based interface

http://localhost:8042

http://IP address:8042

**Supported Web browser**

MSRv2.0 updated the user interface to Silverlight to improve performance and support use on a Mac.

* The UI has been tested on the following web browsers:

<table>
<thead>
<tr>
<th>Browser</th>
<th>Version</th>
<th>OS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chrome</td>
<td>20.0</td>
<td>Windows</td>
</tr>
<tr>
<td>Firefox</td>
<td>13.0</td>
<td>Windows</td>
</tr>
<tr>
<td>IE</td>
<td>IE 8 and IE 9</td>
<td>Windows</td>
</tr>
<tr>
<td>Safari</td>
<td>5.1.7</td>
<td>MacOS</td>
</tr>
</tbody>
</table>
Applications?

- Amplicon Sequencing
- Custom Amplicon
- Targeted Resequencing
- Custom Enrichment
- Small RNA sequencing
- Clone checking
- ChIP-Seq
- Library QC
- Plasmid
- RNA-Seq
- De novo sequencing
- Resequencing
- Small genome
- RNA sequencing
- 16S Metagenomics
What applications to apply?

**DNA**
- Small Genome Sequencing
- Targeted Resequencing
- Assembly
- Resequencing
- Plasmids
- Custom Enrichment
- Custom Amplicon
- PCR Amplicon
- Clone Checking
- Metagenomics 16S, rRNA
- Other
- ChIP-Seq
- Library QC
- FASTQ Only

**RNA**
- RNA Sequencing
- RNA-Seq
- Small RNA
MiSeq Reporter Workflows

- Resequencing
- Custom Amplicon
- De novo assembly
- Generate FASTQ
- Library QC
- 16S Metagenomics
- PCR Amplicon
- Small RNA

Standard formatted output files!
- FASTQ
- BAM
- VCF
- TXT
- HTML
<table>
<thead>
<tr>
<th>Workflow</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Resequencing</strong></td>
<td>Performs alignment to a ref genome, and performs variant calling for sequence from a small genome.</td>
</tr>
<tr>
<td><strong>Library QC</strong></td>
<td>Fast resequencing of a ref genome to QC the DNA library. No variant calling. Provides per-sample summary statistics.</td>
</tr>
<tr>
<td><strong>Custom Amplicon</strong></td>
<td>Performs alignment and variant calling for a TSCA library against its manifest file/sequence. Provides somatic variant caller option.</td>
</tr>
<tr>
<td><strong>PCR Amplicon</strong></td>
<td>Sequencing of Nextera-fragmented PCR amplicons and performs alignment, and variant analysis for amplicon regions.</td>
</tr>
<tr>
<td><strong>de novo Assembly</strong></td>
<td>Assembles small (&lt;20 Mb) genomes from reads. No genomic reference needed.</td>
</tr>
<tr>
<td><strong>16S Metagenomics</strong></td>
<td>Performs 16S rRNA bacterial metagenomic analysis of a mixed population.</td>
</tr>
<tr>
<td><strong>Small RNA</strong></td>
<td>Provides counts of mature miRNA sequences from human. Adapter sequences are also masked automatically.</td>
</tr>
<tr>
<td><strong>GenerateFASTQ</strong></td>
<td>Demultiplex and output FASTQ files, but perform no other processing.</td>
</tr>
</tbody>
</table>
### Output Files per Workflow (used to show Reports etc.)

<table>
<thead>
<tr>
<th>Workflow</th>
<th>Output Files</th>
</tr>
</thead>
</table>
| All                  | • DemultiplexComplete.txt  
|                      | • DemultiplexSummaryF*L*.txt  
|                      | • Logging¥*  
|                      | • DataAccessFiles¥*  
|                      | • Plots¥*  
|                      | • AdapterTrimming.txt (if applicable)                                        |
| Custom Amplicon      | • AmpliconRunStatistics.xml  
|                      | • .bam and .bai files per Sample  
|                      | • .vcf files per Sample  
|                      | • Summary.xml / .htm  
|                      | • Mismatch.htm  
|                      | • ErrorsAndNoCallsByLaneTileReadCycle.csv                                   |
| Resequencing         | • ResequencingRunStatistics.xml  
|                      | • Mismatch.htm  
|                      | • .bam and .bai files per Sample  
|                      | • .vcf files per Sample  
|                      | • Summary.xml / .htm  
|                      | • Mismatch.htm  
|                      | • ErrorsAndNoCallsByLaneTileReadCycle.csv                                   |
| Library QC           | • ResequencingRunStatistics.xml  
|                      | • .bam and .bai files per Sample  
|                      | • Summary.xml / .htm  
|                      | • Mismatch.htm  
|                      | • ErrorsAndNoCallsByLaneTileReadCycle.csv                                   |
| PCR Amplicon         | • ResequencingRunStatistics.xml  
|                      | • .bam and .bai files per Sample  
|                      | • .vcf files per Sample  
|                      | • Summary.xml / .htm  
|                      | • Mismatch.htm  
|                      | • ErrorsAndNoCallsByLaneTileReadCycle.csv                                   |
| Assembly             | • AssemblyRunStatistics.xml  
|                      | • Contigs.fa per Sample  
|                      | • DotPlot.png per Sample (Sample with Reference genome)  
|                      | • Summary.xml / .htm  
|                      | • Assembly*¥configs.fa  
|                      | • Assembly*¥Log                                                           |
| Metagenomics         | • MetagenomicsRunStatistics.xml  
|                      | • Classification.txt  
|                      | • .txt.gz file per sample                                                   |
| Small RNA            | • SmallRNARunStatistics.xml  
|                      | • TrimmerHistogram.txt  
|                      | • .contam per Sample  
|                      | • .export.contam per Sample  
|                      | • .export.genome per Sample  
|                      | • .export.mirna per Sample  
|                      | • .export.rna per Sample  
|                      | • .genome per Sample  
|                      | • .mirna per Sample  
|                      | • .rna per Sample                                                           |
| Generate FASTQ       | • ResequencingRunStatistics.xml  
|                      | • Fastq.gz per sample                                                       |

*¥ indicates files that are optional and may not always be generated.*
New default aligners & variant callers

MSR v2.0 added/updated new standard aligners & variant callers!

<table>
<thead>
<tr>
<th>Workflow</th>
<th>Default Aligner</th>
<th>Default Variant Caller</th>
</tr>
</thead>
<tbody>
<tr>
<td>Resequencing</td>
<td>BWA</td>
<td>GATK</td>
</tr>
<tr>
<td>Custom Amplicon (TSCA)</td>
<td>Banded Smith-Waterman</td>
<td>GATK</td>
</tr>
<tr>
<td>PCR Amplicon (Nextera)</td>
<td>BWA</td>
<td>GATK</td>
</tr>
<tr>
<td>Library QC</td>
<td>BWA</td>
<td>N/A</td>
</tr>
</tbody>
</table>

*Can switch back to old Eland/Starling through config setting.

*Switched the default aligner to BWA, and switched variant caller from Starling to GATK.

* For the Custom Amplicon workflow, you can choose variant caller between GATK (the default), Somatic (for tumor samples), or Starling (legacy variant caller, for backward-compatibility) specifying by the “samplesheet”
MSR Top - First Look at the Interface

List of past runs

Type of runs

Run completion status
Important Functions in this window

1. Check runfolder to requeue

2. Press REQUEUE button

Settings

Help Page
The Help Page is a good first place to look for answers!

http://www.illumina.com/help/miseq_reporter/
Typical interface – General Summary Report
Resequencing/Amplicon

- Coverage and error
- Samples table
- Q score
- Targets table
- SNP/indel + annotation
- Table of samples/variants
Resequencing/Amplicon

- Scope of view ruler
- Zoom in/out
- Export Table as csv file
- Search/filter
De Novo Assembly Display (Contigs)

* Dot plot is included only if you provide a reference sequence for the assembly
Small RNA Workflow Sample Tab

Tabular information

Distribution of RNA species

Top 10 most abundant species
### Metagenomics Workflow Details Tab

#### Tabular Information

<table>
<thead>
<tr>
<th>Sample ID</th>
<th>Sample Name</th>
<th>Cluster Raw</th>
<th>Cluster PF</th>
<th>Taxonomic Level</th>
</tr>
</thead>
<tbody>
<tr>
<td>UK_Test</td>
<td>UK_Test</td>
<td>5491024</td>
<td>4476722</td>
<td>Kingdom</td>
</tr>
<tr>
<td>UK_Test</td>
<td>UK_Test</td>
<td>5491024</td>
<td>4476722</td>
<td>Phylum</td>
</tr>
<tr>
<td>UK_Test</td>
<td>UK_Test</td>
<td>5491024</td>
<td>4476722</td>
<td>Class</td>
</tr>
<tr>
<td>UK_Test</td>
<td>UK_Test</td>
<td>5491024</td>
<td>4476722</td>
<td>Order</td>
</tr>
<tr>
<td>UK_Test</td>
<td>UK_Test</td>
<td>5491024</td>
<td>4476722</td>
<td>Family</td>
</tr>
</tbody>
</table>

#### Classification

- **Unclassified**: 34.71%
- **Deltaproteobacteria**: 13.22%
- **Obovibacteriia**: 5.89%
- **Cetobacteriia**: 17.26%
- **Acidobacteria (class)**: 3.01%
- **Bacteroidetes**: 0.11%
- **Flavobacteria (class)**: 0.04%
- **Bacillales**: 8.77%
- **Methanobacteriia**: 0.72%
- **Kryptotricha**: 0.75%
- **Alphaproteobacteria**: 0.11%
- **Clostridiales (class)**: 0.04%
- **Sphingobacteria**: 0.03%
- **Thermotogae (class)**: 0%
- **Thermoprotei**: 0%
- **Flavobacteria**: 0%
- **Mollicutes**: 0%
- **Koribacteraceae**: 0%
- **Halobacteria**: 0%
- **Chloroeeae (class)**: 0%
- **Deltaproteobacteria**: 0%
- **Anaerivibacteria**: 0%
- **Actinomycetales**: 0%
- **Verrucomicrobia**: 0%
- **Thermotogae**: 0%

**Total**: 100%
General Run Status button & tabs

- Great Source of information about the run including: Status
Run Status Button

- Great Source of information about the run including: Status; Sample Sheet; Logs
Run Status Button

- Great Source of information about the run including: Status; Sample Sheet; Logs; and Errors
Run Status Button

- Great Source of information about the run including: Status; Sample Sheet
How to control Workflows?

- Sample sheet is required
- MSR will demultiplex reads based upon the sample sheet
- Can be created by the Illumina Experiment Manager software (IEM – available from MyIllumina)
- Tells the MSR software how to demultiplex
- Tells the MSR software which analysis workflow to do on the data
MiSeq Reporter can be run in several ways

- **on-instrument** (MiSeq)
  installed as default
  automatically starts while MiSeq run

- **off-instrument** (on another Windows PC)
  user can download MSR from MyIllumina and install
  into own Windows PC.
  so-called ‘standalone’ MSR

- **upon cloud!**
  MSR features (+SAV and more) after basecall
  are there on BaseSpace

- supported on 64-bit Windows (Vista, Windows 7)
- Installation Guide could be downloaded from MyIllumina
BaseSpace

genomics cloud computing

Eri Kibukawa

Bioinformatics Support Scientist

APAC Technical Support
Agenda

MiSeq Reporter

- What is MSR ?
- MSR Workflows
- MSR User Interface

BaseSpace

- Value of BaseSpace
- Key features of BaseSpace
- BaseSpace User Interface
Building Solutions Around our Instruments
Informatics at Illumina
A Simple Path to Biological Understanding
In the future most end users will touch our software, not our hardware
Why use “the cloud” for sequencing?
...it meets the needs of the evolving user base

<table>
<thead>
<tr>
<th></th>
<th>Genome center</th>
<th>Biologist</th>
<th>Clinician</th>
</tr>
</thead>
<tbody>
<tr>
<td>Throughput</td>
<td>✔️</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Customization</td>
<td>✔️</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Simplicity</td>
<td></td>
<td>✔️</td>
<td>✔️</td>
</tr>
<tr>
<td>Stability</td>
<td></td>
<td>✔️</td>
<td>✔️</td>
</tr>
<tr>
<td>Low capital</td>
<td></td>
<td>✔️</td>
<td>✔️</td>
</tr>
<tr>
<td>Low labor</td>
<td></td>
<td>✔️</td>
<td>✔️</td>
</tr>
</tbody>
</table>

Cloud-enabled
Building “It Just Works” Software

Tools: App Store
- Choice
- Competition
- Click-to-buy
- Trust

Platform: Cloud
- Plug and play
- Community
- Secure
- Scalable
BaseSpace™

Cloud + Apps

Plug and play
Community
Secure
Scalable

Choice
Competition
Click-to-buy
Trust
BaseSpace: First Half 2012

MiSeq plug-and-play
Offsite backup
Full menu of workflows
Instant sharing
Direct Integration of BaseSpace

MiSeq users have the option to “push” data to BaseSpace
## Replicating Data Analysis Locally on MiSeq Reporter

### MiSeq Control Software

<table>
<thead>
<tr>
<th>Setting</th>
<th>Path</th>
</tr>
</thead>
<tbody>
<tr>
<td>Recipe Folder</td>
<td>C:\Illumina\MiSeq Control Software\CustomRecipe</td>
</tr>
<tr>
<td>Sample Sheet Folder</td>
<td>C:\Illumina\MiSeq Control Software\SampleSheets</td>
</tr>
<tr>
<td>Manifest Folder</td>
<td>C:\Illumina\MiSeq Control Software\Manifests</td>
</tr>
<tr>
<td>Output Folder</td>
<td>D:\Illumina\MiSeqOutput</td>
</tr>
</tbody>
</table>

- **Send instrument health information to Illumina to aid customer support.**
- **When using BaseSpace, replicate analysis locally on MiSeq.**

**Agreement**

**Save and Continue**
MiSeq Pushes Data to BaseSpace

![MiSeq Control Software](image)
Primary Analysis Summary
Easy to Use
Seamless upload, analysis, storage, and collaboration

Share data with the colleagues you choose, build your research community online, and manage who does and does not have access to your data.
BaseSpace Apps
App Store Developers

Illumina (iSAAC, SAV, Strelka, Grouper, …)
Open Source (GATK, BWA, Tophat+Cufflinks, …)
Individuals (professors, grad students)
Commercial partners (initial app partners, coming more)

Several different models to deploy software (free, pay for compute only, buy commercial software etc.)
Base Space storage

Buying Storage

FREE
1 Terabyte Storage for ILMN data

Plus One
+1 Terabyte Storage
Add Plus One

Plus Ten
+10 Terabytes Storage
Add Plus Ten

* Please contact your local sales person for pricing!

Note: Amazon’s new archiving service announced last week will give us 10X cost savings and so enable even lower pricing.
combination choice to deploy

**Free**
- It just works
- 1TB of storage
- Includes alignment

**Plus**
- Additional storage on demand

**Apps**
- Developer priced
  - Per use or subscription
API & Developer Portal

- API in Early Access now
- API available in July
- Developer Registration is Live
- Registration of App(s).
- Management of user’s apps and account
- Access to API documentation and tutorials
- Access to App analytics and statistics
- A showcase/app gallery of current apps in BaseSpace
- Access to billing and metering functionality and documentation

developer.basespace.illumina.com
API DETAILS

- RESTful based API
  - a simple web service implemented using HTTP and the principles of REST. It is a collection of resources, with four defined aspects:
    - the base URI for the web service, such as http://example.com/resources/
    - the Internet media type of the data supported by the web service. This is often JSON, XML or YAML but can be any other valid Internet media type.
    - the set of operations supported by the web service using HTTP methods (e.g., GET, PUT, POST, or DELETE).
    - The API must be hypertext driven

- Currently JSON format only
- Authorization is implemented with Oauth V2 standard protocol

- SSL Required
- App Registration via Developer Portal
Signing into BaseSpace: basespace.illumina.com
BaseSpace Interface Dashboard

Provides access to all BaseSpace features

Latest Runs:
• Displays most recent runs uploaded to BaseSpace
  Your run or a shared run from another user
• Designed to provide a quick glance at the status of the run

Project base icons and items that finished analysis
FAQ

How does Illumina protect my data?
We protect your data through various technical, electronic, and administrative measures. Your instrument data will be transmitted using industry-standard encryption (SSL).

We restrict access to your data to individuals at Illumina who need to know the information in accordance with their job responsibilities. Your data will be hosted on Amazon Web Services (AWS), which is compliant with a wide variety of industry-accepted security standards. More information can be found at [http://aws.amazon.com/security/](http://aws.amazon.com/security/).

Please note that it is your responsibility to select and protect an appropriately secure password. A poor password can negate the protection offered by even the highest level of computer security.

Does Illumina access my data?
Data uploaded to and produced on BaseSpace remains your property, and Illumina will not access your data for research purposes, nor claim any Intellectual property rights to your data. Illumina does collect information about your data, in order to improve BaseSpace and our other products and services as well as to provide you with support.

Will Illumina share or publish my data?
Data you share with Illumina technical support personnel will not be further distributed.

Where is my data hosted?
Data is currently stored using Amazon Web Services. We currently use Amazon’s U.S. based facilities.

Illumina use my personal information?
We may use your personal information to contact you in connection with the services. Unless you tell Illumina otherwise, we may contact you about other Illumina products and services.
The New BaseSpace

Something important is about to happen in BaseSpace. It’s really the beginning of a transformation that will be happening over the rest of the year turning BaseSpace into an informatics application platform. In the coming days, we will be releasing a completely redesigned user experience with better data management and sharing. Important new features like a fully integrated BAV, and a whole new look and feel. The data you already have in BaseSpace is still there, as is all the security and reliability you depend on us for. In this post we’ll walk through a number of the new features so you understand what’s new and how to use it.

How We Think of Data

We always knew that we would be expanding our data model to include things like projects, but we wanted to get some real world feedback before we went through that transformation. Last spring we went back to the drawing board and completely re-architected the data model to work the way our end-users—biologists, lab managers, clinicians—want to manage their data. Essentially what we have now are two areas focused on different types of users. These two areas are “Runs” and “Projects”. The diagram below shows how data flows from an individual Run into these areas.
Runs Tab

Provides access to a number of lists that allow you to view your data in greater detail

**Runs:**
- Displays a list of your runs
- Allows you to sort your runs by different parameters
Run Details Page

Downloads: Allows you to save files on your local computer

overview

Run Details:
• Displays panes of information:
  • Run Summary
  • Primary Analysis Summary
  • Secondary Analysis Summary
Download options
Sharing feature

Sharing with Others:

[Image of BaseSpace interface showing sharing settings dialog]

Sharing a run entry shares the run itself. Projects must be shared individually.

INVITE A COLLABORATOR

Email address

[Field for email address]

Send this e-mail

[Button to send e-mail]

COlLABORATORS (1)

proberts@illumina.com

pending

Read Only

[Option to make collaborator read-only]

[Options to cancel or save settings]
Secondary Analysis Summary

App Settings:
Details of analysis settings
Sample Details
## Run Summary

<table>
<thead>
<tr>
<th>Level</th>
<th>Yield Total</th>
<th>Projected Total Yield</th>
<th>Yield Perfect</th>
<th>Yield &lt;= 3 errors</th>
<th>Aligned (%)</th>
<th>% Perfect (Num Cycles)</th>
<th>% &lt;= 3 errors (Num Cycles)</th>
<th>Error Rate (%)</th>
<th>Intensity Cycle 1</th>
<th>% Intensity Cycle 20</th>
<th>% &gt;= Q30</th>
</tr>
</thead>
<tbody>
<tr>
<td>Read 1</td>
<td>950.4 M</td>
<td>950.4 M</td>
<td>0.0</td>
<td>0.0</td>
<td>0.00</td>
<td>0.0 [150]</td>
<td>0.0 [150]</td>
<td>0.00</td>
<td>900</td>
<td>85.9</td>
<td>93.1</td>
</tr>
<tr>
<td>Read 2</td>
<td>31.7 M</td>
<td>31.7 M</td>
<td>0.0</td>
<td>0.0</td>
<td>0.00</td>
<td>0.0 [5]</td>
<td>0.0 [5]</td>
<td>0.00</td>
<td>1047</td>
<td>0.0</td>
<td>97.2</td>
</tr>
<tr>
<td>Read 3</td>
<td>800.7 M</td>
<td>800.7 M</td>
<td>0.0</td>
<td>0.0</td>
<td>0.00</td>
<td>0.0 [139]</td>
<td>0.0 [139]</td>
<td>0.00</td>
<td>889</td>
<td>81.8</td>
<td>90.3</td>
</tr>
<tr>
<td>Total</td>
<td>1,092.7 M</td>
<td>1,092.7 M</td>
<td>0.0</td>
<td>0.0</td>
<td>0.00</td>
<td>0.0 [139]</td>
<td>0.0 [139]</td>
<td>0.00</td>
<td>985</td>
<td>84.3</td>
<td>91.9</td>
</tr>
</tbody>
</table>

### Read 1

<table>
<thead>
<tr>
<th>Lane</th>
<th>Yields</th>
<th>Density (Kbase/mm²)</th>
<th>Cluster PF (%)</th>
<th>PhysPropFlas (%)</th>
<th>Reads (M)</th>
<th>Reads PF (M)</th>
<th>% &gt; G30</th>
<th>Yield</th>
<th>Cycles Err Rated</th>
<th>Aligned (%)</th>
<th>Error Rate (%)</th>
<th>Error Rate 35 cycle (%)</th>
<th>Error Rate 75 cycle (%)</th>
<th>Error Rate 100 cycle (%)</th>
<th>Intensity Cycle 1</th>
<th>% Intensity Cycle 20</th>
<th>% &gt;= Q30</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>12</td>
<td>774 +/- 18</td>
<td>98.06 +/- 0.35</td>
<td>0.161 / 0.280</td>
<td>6.60</td>
<td>6.34</td>
<td>93.1</td>
<td>950.4 M</td>
<td>0</td>
<td>0.0 +/- 0.0</td>
<td>0.00 +/- 0.00</td>
<td>0.00 +/- 0.00</td>
<td>0.00 +/- 0.00</td>
<td>950 +/- 212</td>
<td>86.9 +/- 1.7</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Read 2

<table>
<thead>
<tr>
<th>Lane</th>
<th>Yields</th>
<th>Density (Kbase/mm²)</th>
<th>Cluster PF (%)</th>
<th>PhysPropFlas (%)</th>
<th>Reads (M)</th>
<th>Reads PF (M)</th>
<th>% &gt; G30</th>
<th>Yield</th>
<th>Cycles Err Rated</th>
<th>Aligned (%)</th>
<th>Error Rate (%)</th>
<th>Error Rate 35 cycle (%)</th>
<th>Error Rate 75 cycle (%)</th>
<th>Error Rate 100 cycle (%)</th>
<th>Intensity Cycle 1</th>
<th>% Intensity Cycle 20</th>
<th>% &gt;= Q30</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>12</td>
<td>774 +/- 18</td>
<td>98.06 +/- 0.35</td>
<td>0.000 / 0.000</td>
<td>6.60</td>
<td>6.34</td>
<td>97.2</td>
<td>31.7 M</td>
<td>0</td>
<td>0.0 +/- 0.0</td>
<td>0.00 +/- 0.00</td>
<td>0.00 +/- 0.00</td>
<td>0.00 +/- 0.00</td>
<td>1047 +/- 231</td>
<td>0.0 +/- 0.0</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Read 3

<table>
<thead>
<tr>
<th>Lane</th>
<th>Yields</th>
<th>Density (Kbase/mm²)</th>
<th>Cluster PF (%)</th>
<th>PhysPropFlas (%)</th>
<th>Reads (M)</th>
<th>Reads PF (M)</th>
<th>% &gt; G30</th>
<th>Yield</th>
<th>Cycles Err Rated</th>
<th>Aligned (%)</th>
<th>Error Rate (%)</th>
<th>Error Rate 35 cycle (%)</th>
<th>Error Rate 75 cycle (%)</th>
<th>Error Rate 100 cycle (%)</th>
<th>Intensity Cycle 1</th>
<th>% Intensity Cycle 20</th>
<th>% &gt;= Q30</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>12</td>
<td>774 +/- 18</td>
<td>98.06 +/- 0.35</td>
<td>0.164 / 0.280</td>
<td>6.60</td>
<td>6.34</td>
<td>90.3</td>
<td>800.7 M</td>
<td>0</td>
<td>0.0 +/- 0.0</td>
<td>0.00 +/- 0.00</td>
<td>0.00 +/- 0.00</td>
<td>0.00 +/- 0.00</td>
<td>889 +/- 191</td>
<td>81.8 +/- 3.6</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Indexing QC

![BaseSpace screenshot showing indexing QC results]

- **M1 Reads**: Percentage of reads identified (PF)
- **PF Reads**: Percentage of reads identified (PF)
- **Max**: Maximum value

<table>
<thead>
<tr>
<th>Index Number</th>
<th>Sample ID</th>
<th>Project</th>
<th>Index 1</th>
<th>Index 2</th>
<th>Reads Identified (PF)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>120320-14</td>
<td>Falcon</td>
<td>T02A2G</td>
<td>T02B2C</td>
<td>11,623</td>
</tr>
<tr>
<td>2</td>
<td>120320-13</td>
<td>Falcon</td>
<td>T02C2D</td>
<td>C02T2E</td>
<td>15,2453</td>
</tr>
<tr>
<td>3</td>
<td>120320-17</td>
<td>Falcon</td>
<td>T02C2F</td>
<td>T02S2G</td>
<td>34,500</td>
</tr>
<tr>
<td>4</td>
<td>120320-3B</td>
<td>Falcon</td>
<td>T02C2G</td>
<td>T02C2H</td>
<td>20,0262</td>
</tr>
</tbody>
</table>
Sample Sheet
Contact feature
Please join & give us your idea! comments! and votes!!
Sharing = Collaboration = Community
Thank You!

Eri Kibukawa
Bioinformatics Support Scientist
Technical Support
Illumina