



EasyGenomics

Next Generation Bioinformatics
on the Cloud

<http://www.easygenomics.com>

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Xing Xu, Ph.D

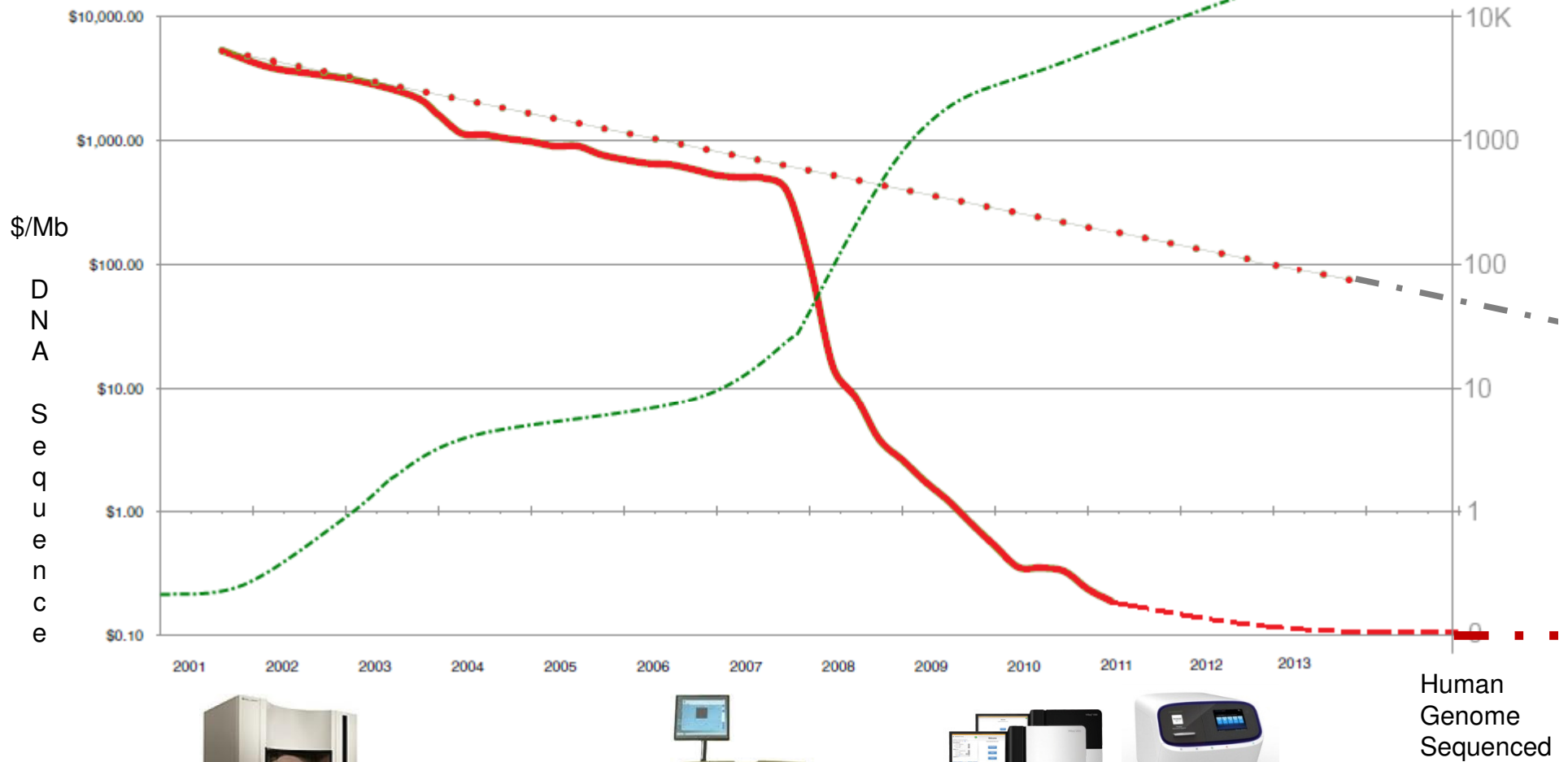
Senior Product Manager
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Contact Us

info@easygenomics.com



- Vision and Strategy
- Problems and Solutions
- Product Introduction
- LIVE Demo
- Future Roadmap
- Q&A

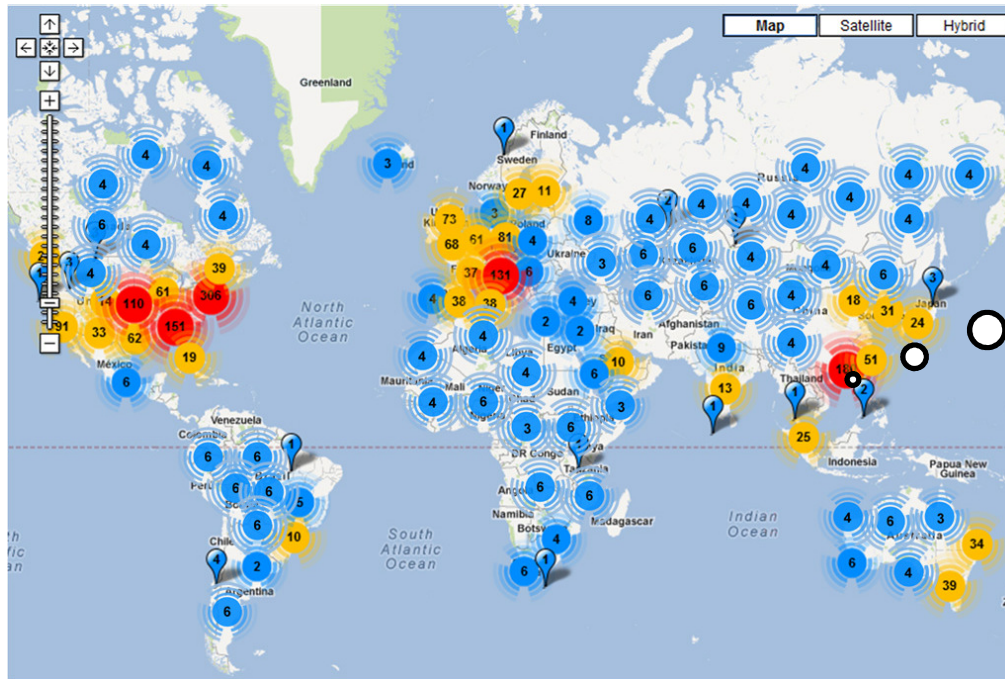


Human Genome Sequenced

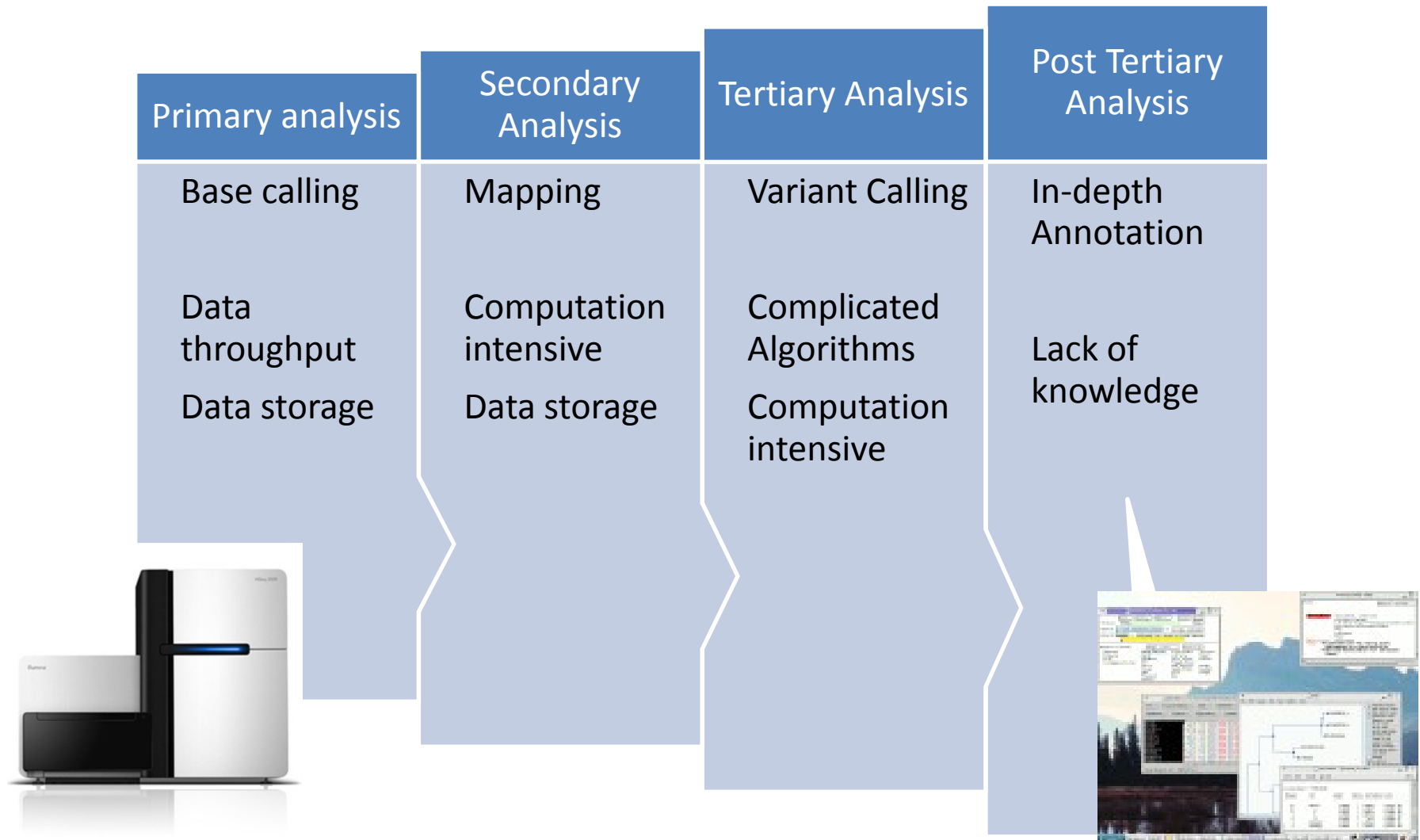
Figures adapted from Sboner A, *et al.*: The real cost of sequencing: higher than you think! *Genome Biology* 2011, 12:125
 Numbers and Images from private research and the open Internet



Sequencing is a **COMMODITY** and happens **EVERYWHERE.**



Images from omicsmaps.com



Solutions

Cloud

High Speed Data Exchange

Workflows

**+)
Resource Management**

EasyGenomics

Problems:

- ~~Big genomic data~~
- ~~Geological distribution~~
- ~~Algorithm integration~~
- ~~Computational demand~~



- **EasyGenomics is the bioinformatics platform for research and applications on the cloud**

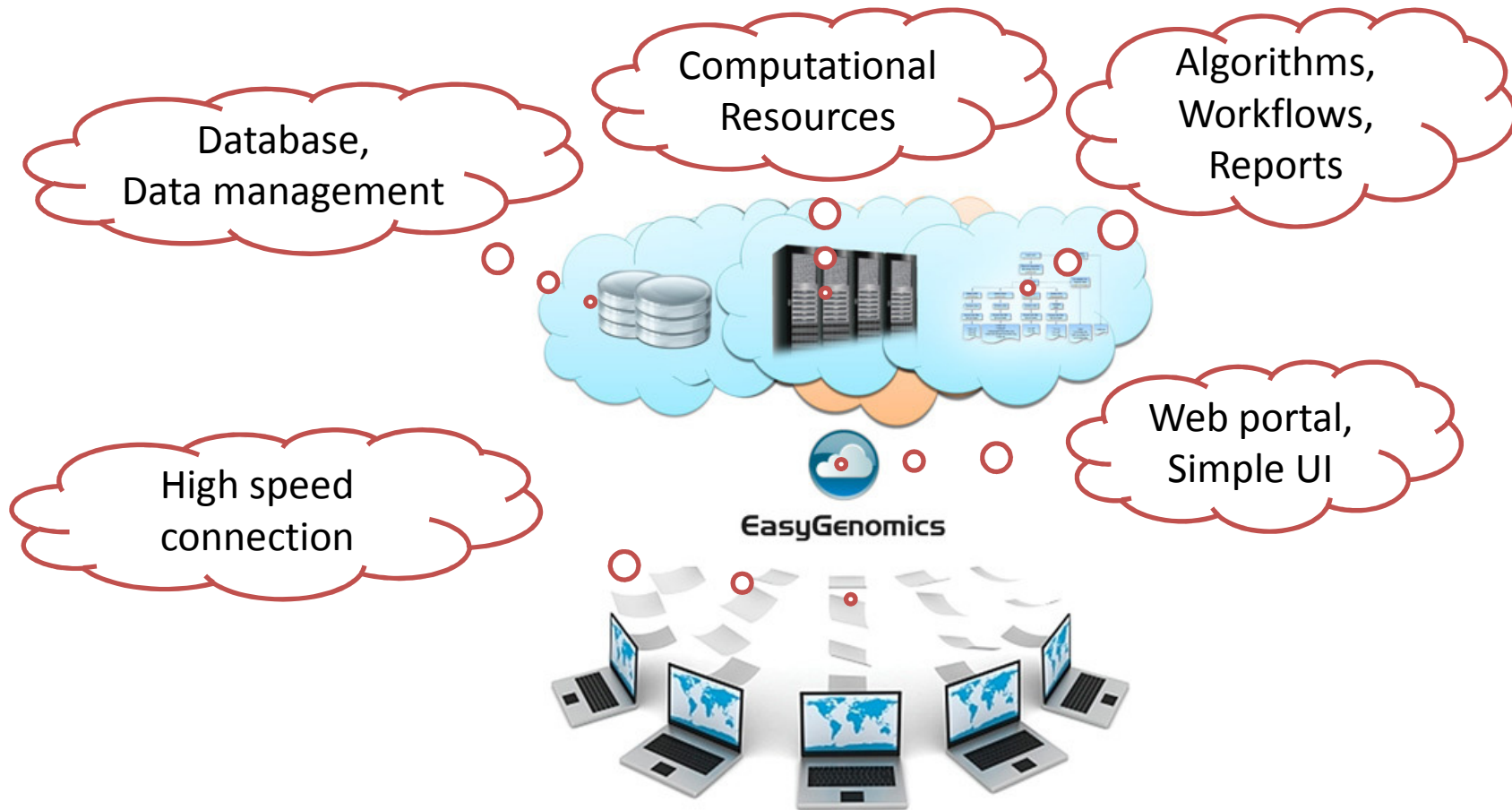


High speed data exchange

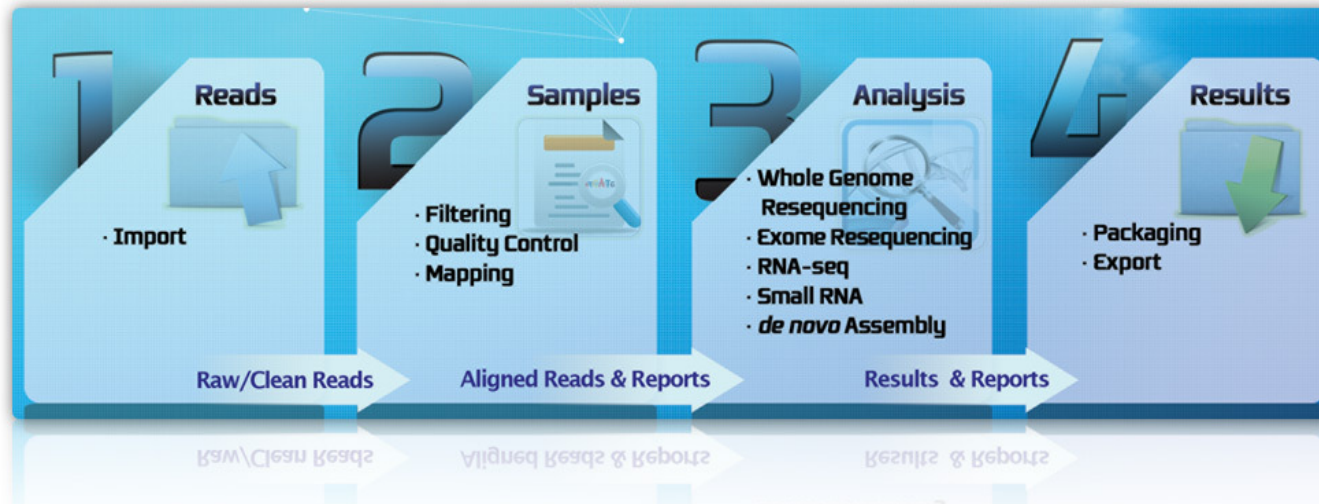
Fast and accurate pipelines

Easy and straightforward UI

Application integration



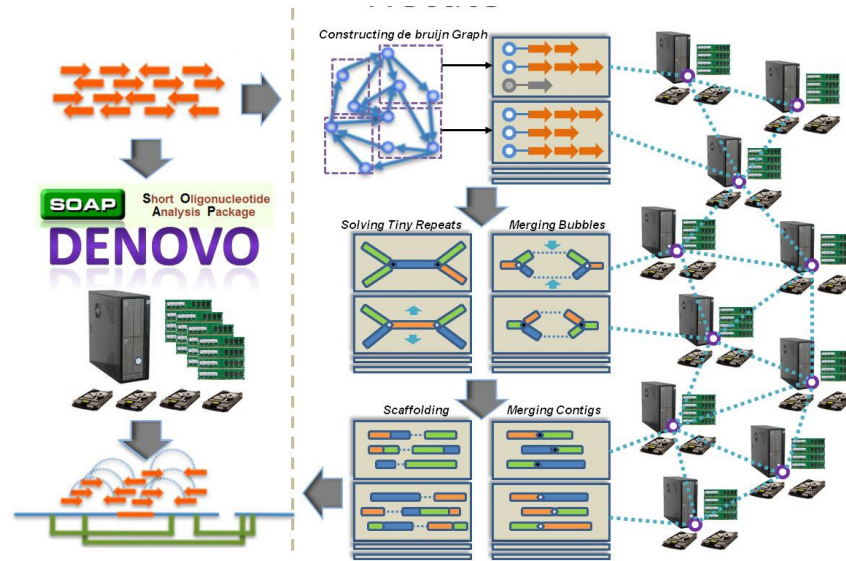
EasyGenomics is the bioinformatics platform for research and applications on the cloud



- **Algorithms:**
Carefully chosen, tested and optimized
- **Workflows:**
Whole genome resequencing, exome resequencing, RNA-Seq, small RNA, *de novo* Assembly

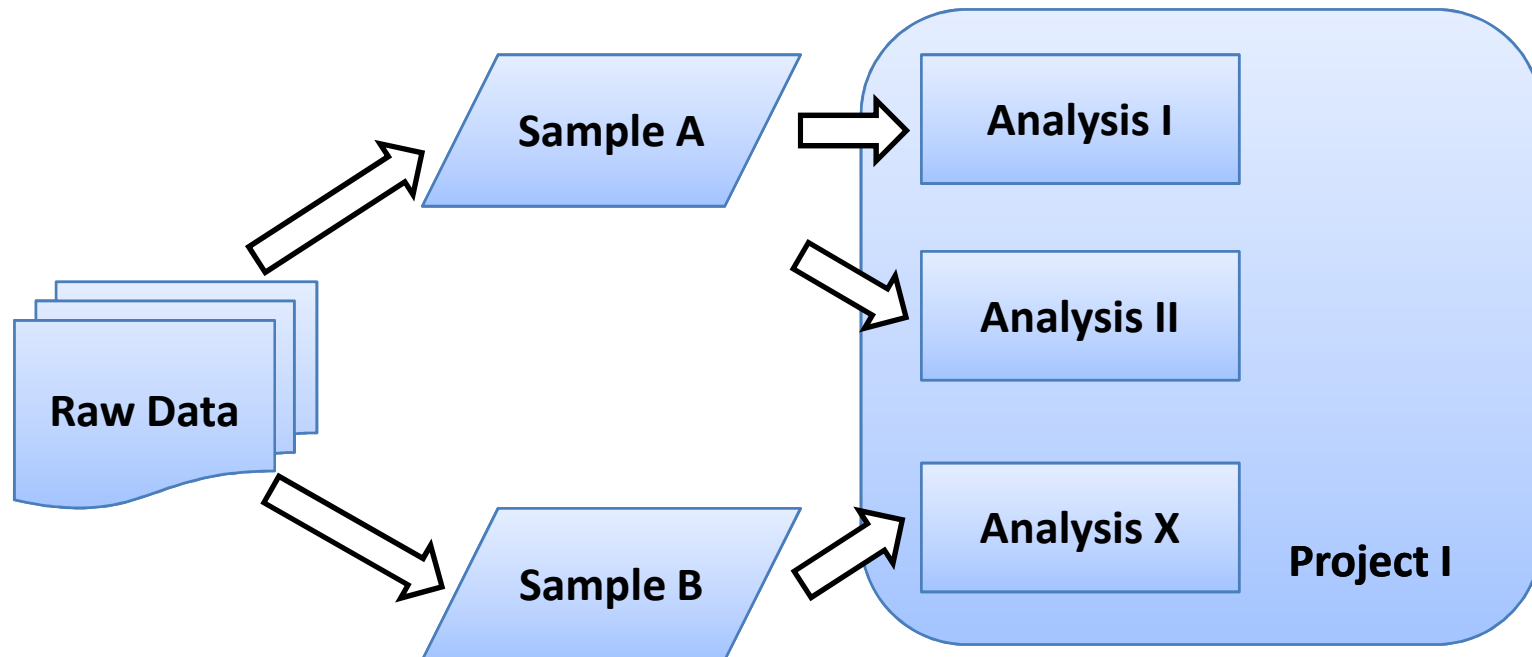


Best Practice Award for IT Infrastructure

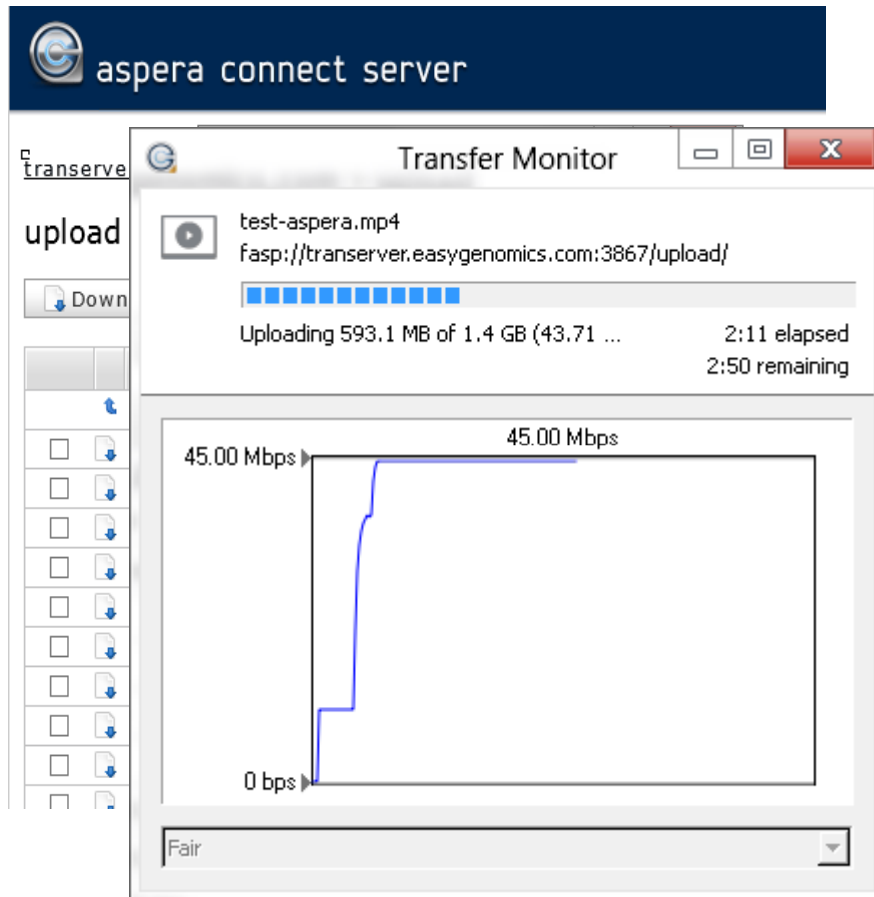


Hadoop-based Flexible Computing

Human Genome	SOAPdenovo	EasyGenomics™ (192 cores)
Genome Coverage	86%	86%
Assembly Time	70h	55h
No. of Servers	1	15
Memory Size	500GB x 1	24 GB x 15
Mode	Centralized	Distributed



- **“Sample”, “Analysis”, “Project”**
- **Mimicking real research procedure**
- **Automatic management of underlying data structure**



- Aspera's patented *fasp*TM high-speed file transferring technology
- **10~100X faster than FTP**



Multitenancy



Workspace



Managed
Data Structure



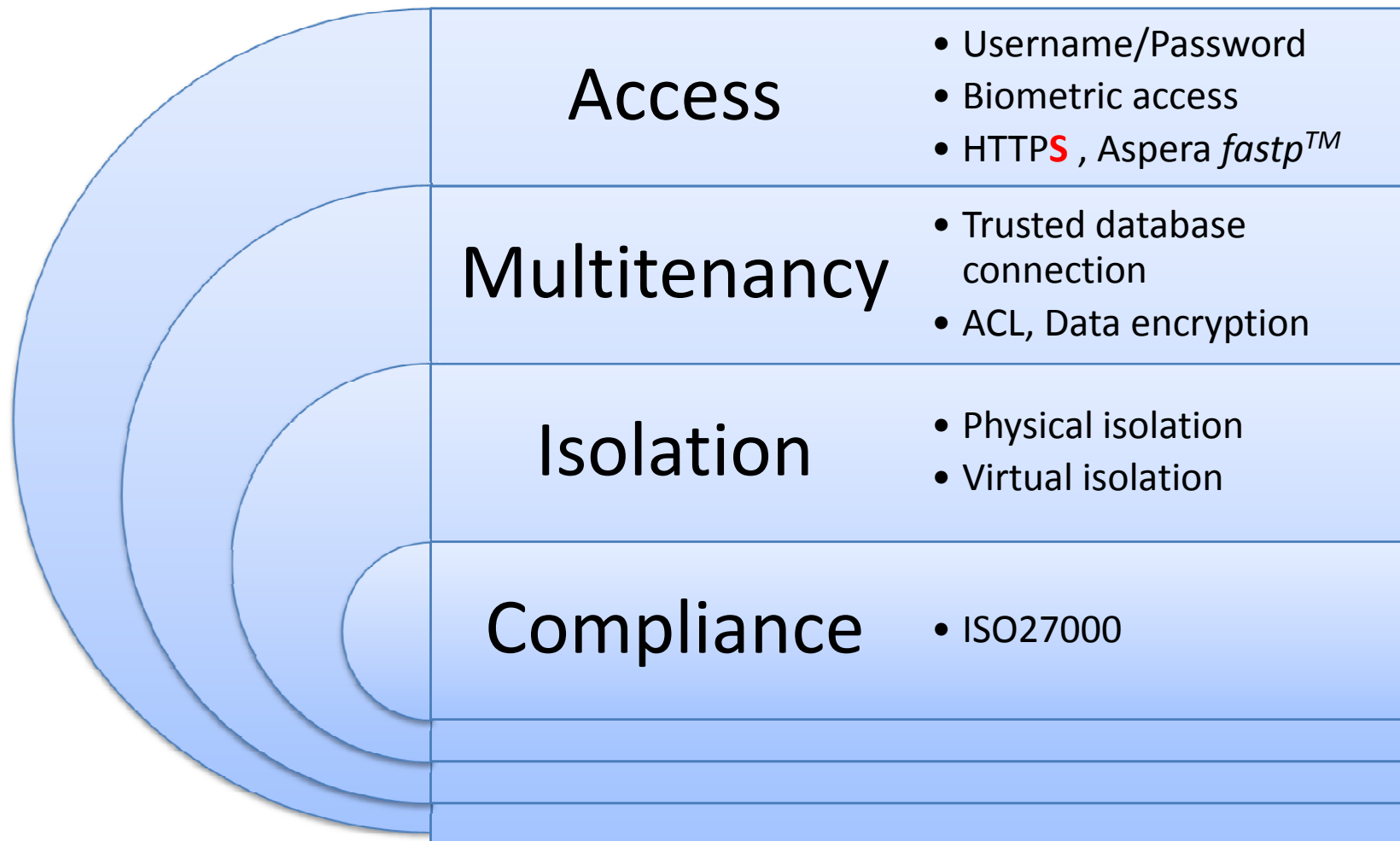
Managed
Task



Safe

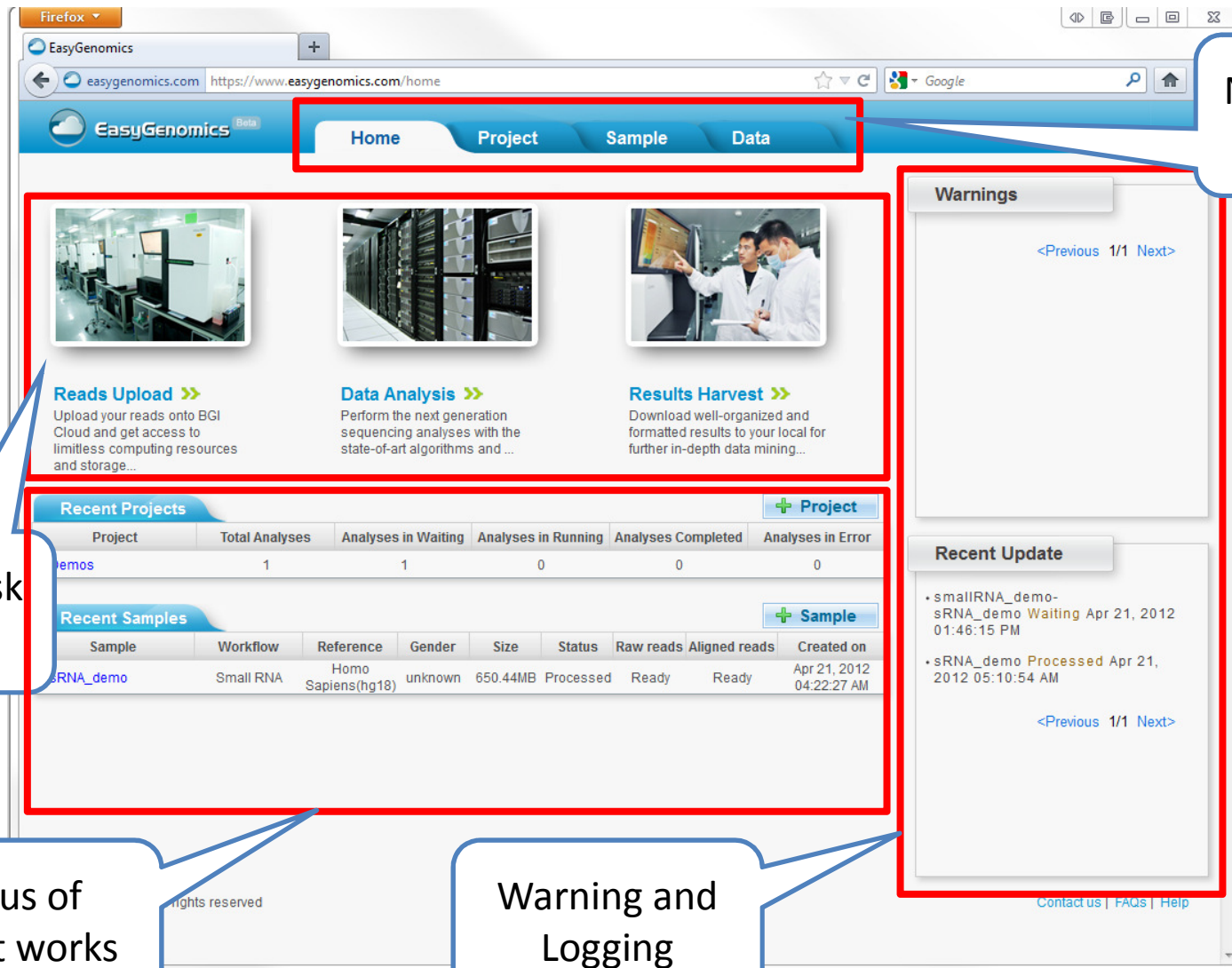


Backup



Introduction to EasyGenomics™

Xing Xu, Ph.D
Senior Product Manager



The screenshot shows the EasyGenomics homepage with several key sections highlighted by red boxes and callouts:

- Navigation Tabs:** A horizontal menu at the top with 'Home', 'Project', 'Sample', and 'Data' tabs.
- Three task portals:** Three main content areas: 'Reads Upload' (with a sub-image of a lab), 'Data Analysis' (with a sub-image of server racks), and 'Results Harvest' (with a sub-image of scientists).
- Status of recent works:** Two tables below the task portals: 'Recent Projects' and 'Recent Samples'.
- Warning and Logging:** A 'Warnings' section on the right side of the page, and a 'Recent Update' section below it.

Recent Projects Table:

Project	Total Analyses	Analyses in Waiting	Analyses in Running	Analyses Completed	Analyses in Error
emos	1	1	0	0	0

Recent Samples Table:

Sample	Workflow	Reference	Gender	Size	Status	Raw reads	Aligned reads	Created on
sRNA_demo	Small RNA	Homo Sapiens(hg18)	unknown	650.44MB	Processed	Ready	Ready	Apr 21, 2012 04:22:27 AM

Warnings Section:

<Previous 1/1 Next>

Recent Update Section:

- smallRNA_demo-sRNA_demo **Waiting** Apr 21, 2012 01:46:15 PM
- sRNA_demo **Processed** Apr 21, 2012 05:10:54 AM

<Previous 1/1 Next>

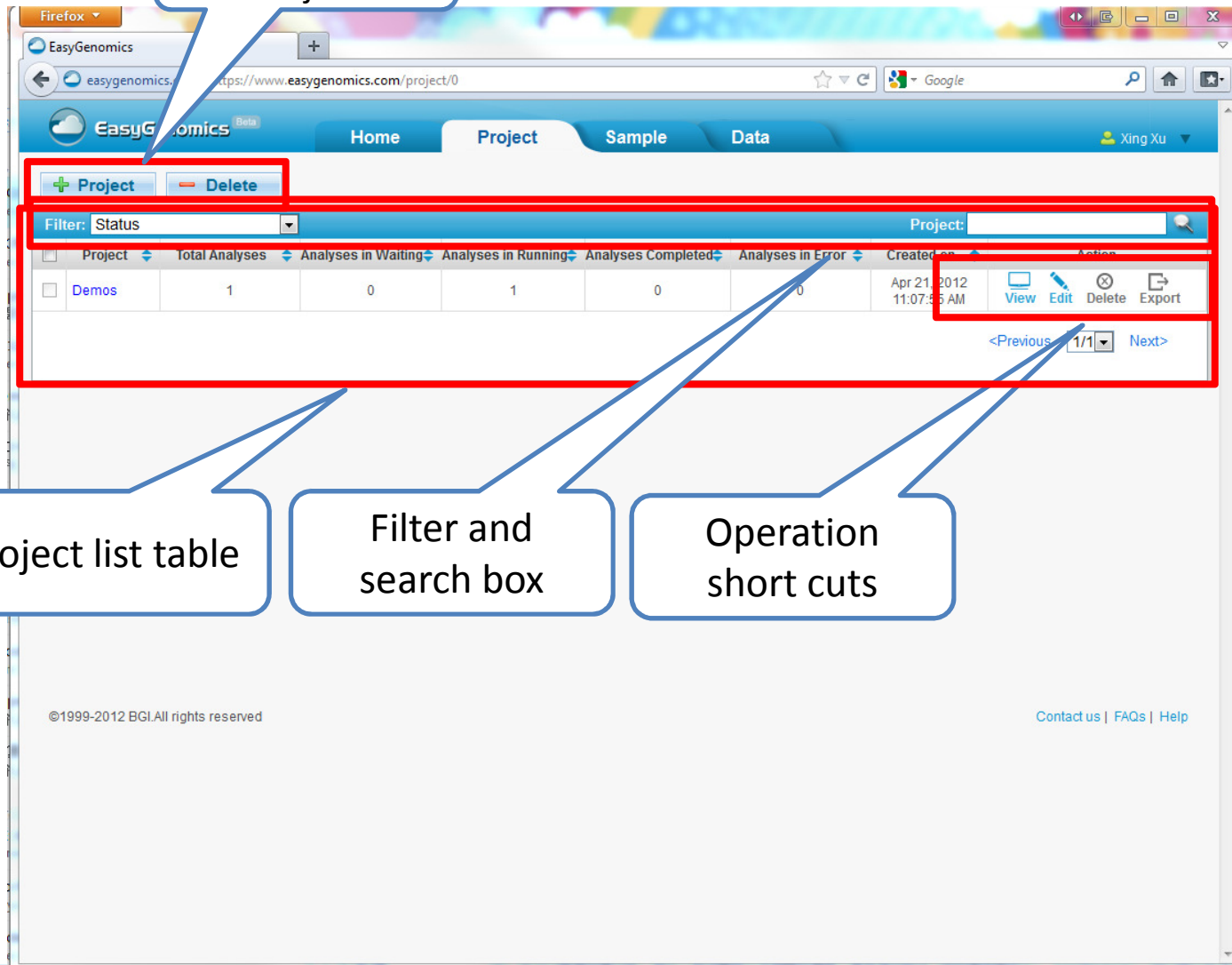
Navigation
Tabs

Three task
portals

Status of
recent works

Warning and
Logging

Add/Remove
Project



The screenshot shows the EasyGenomics web interface. At the top, there are navigation tabs for Home, Project, Sample, and Data. Below the navigation, there are buttons for '+ Project' and '- Delete'. A search bar labeled 'Filter: Status' and a 'Project:' search field are present. A table lists project details, including a 'Demos' project with 1 total analysis, 0 in waiting, 1 in running, 0 completed, and 0 in error. The table also shows a creation date of 'Apr 21, 2012 11:07:56 AM' and action buttons for 'View', 'Edit', 'Delete', and 'Export'. A pagination control shows '<Previous 1/1 Next>'. Callouts point to these elements: 'Add/Remove Project' points to the '+ Project' and '- Delete' buttons; 'Project list table' points to the table; 'Filter and search box' points to the 'Filter: Status' dropdown; and 'Operation short cuts' points to the 'View', 'Edit', 'Delete', and 'Export' buttons.

Project	Total Analyses	Analyses in Waiting	Analyses in Running	Analyses Completed	Analyses in Error	Created on	Action
<input type="checkbox"/> Demos	1	0	1	0	0	Apr 21, 2012 11:07:56 AM	View Edit Delete Export

Project list table

Filter and
search box

Operation
short cuts

Firefox | You may have already signed in to Outlook Web App on a different browser tab. If so, close this tab and ...

EasyGenomics | Home | **Project** | Sample | Data | Xing Xu

Project Details

Project Name: Demos
 Note: All Demo

Analysis List

+ Analysis | - Delete

Filter: Workflow | Status | Analysis:

<input type="checkbox"/>	Analysis	Workflow	Size	Status	Sample	Created on	Action
<input type="checkbox"/>	smallRNA_demo-sRNA_demo	Small RNA	0.00B	Running	sRNA_demo	Apr 21, 2012 01:46:14 PM	View Edit Delete Export

<Previous | 1/1 | Next>

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Firefox | You may have already signed in to Outlook Web App on a different browser tab. If so, close this tab and ...

EasyGenomics | Home | Project | **Sample** | Data | Richard Chan

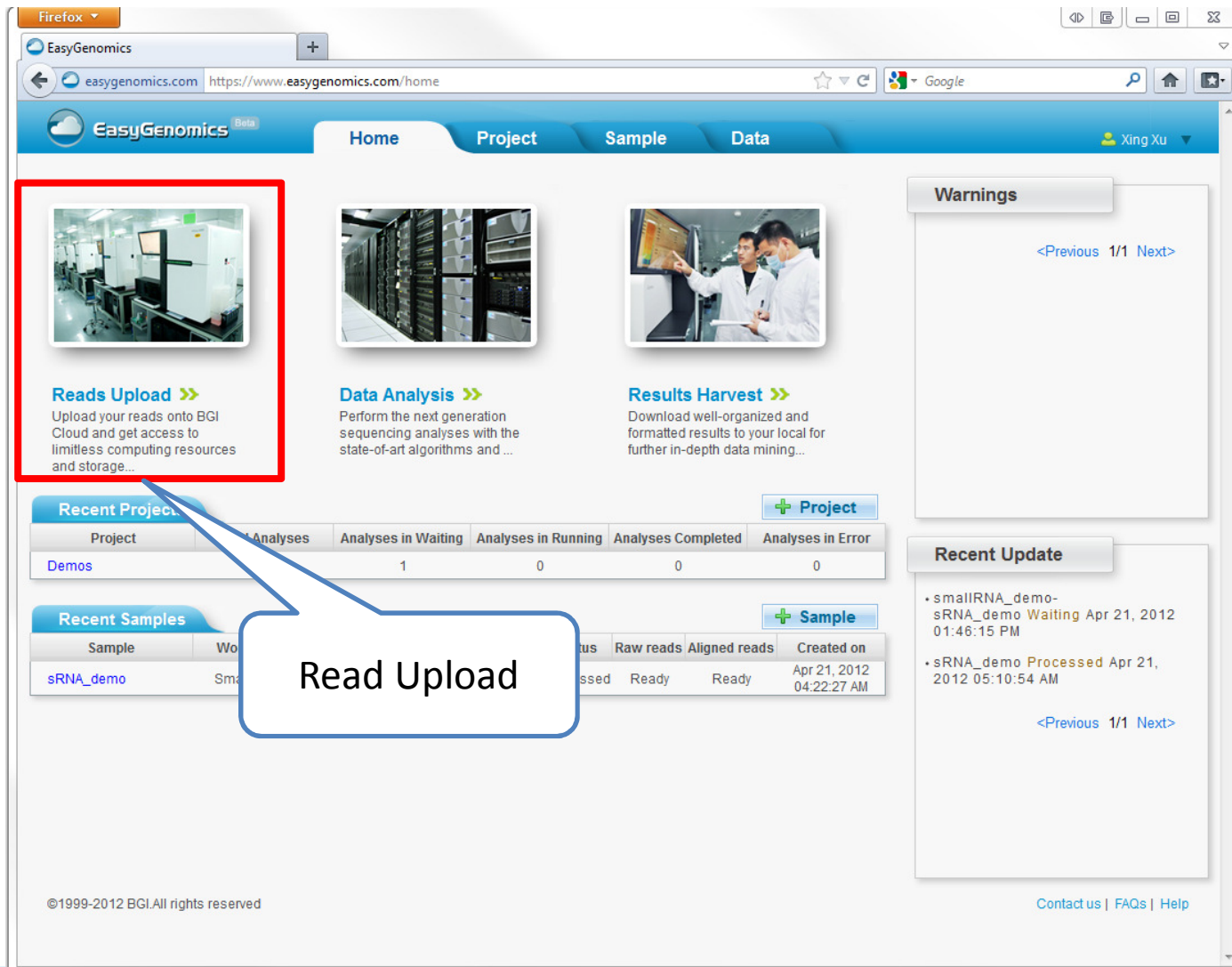
+ Sample | - Delete

Filter: Workflow | Reference | Status | Sample:

Sample	Workflow	Reference	Gender	Size	Status	Raw Reads	Aligned Reads	Created on	Action
<input type="checkbox"/> sample_wgrs_hg18_pe_f_1	Whole Genome Resequencing	Homo Sapiens(hg18)	female	100.65MB	Processed	Ready	Ready	Apr 21, 2012 10:09:47 AM	View Edit Delete Analysis Export

<Previous | 1/1 | Next>

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Firefox

EasyGenomics

easygenomics.com https://www.easygenomics.com/home

EasyGenomics **Home** Project Sample Data Xing Xu

Reads Upload >>
Upload your reads onto BGI Cloud and get access to limitless computing resources and storage...

Data Analysis >>
Perform the next generation sequencing analyses with the state-of-art algorithms and ...

Results Harvest >>
Download well-organized and formatted results to your local for further in-depth data mining...

Warnings

<Previous 1/1 Next>

Recent Projects + Project

Project	Analyses	Analyses in Waiting	Analyses in Running	Analyses Completed	Analyses in Error
Demos		1	0	0	0

Recent Samples + Sample

Sample	Workflows	Status	Raw reads	Aligned reads	Created on
sRNA_demo	Sma	Processed	Ready	Ready	Apr 21, 2012 04:22:27 AM

Read Upload

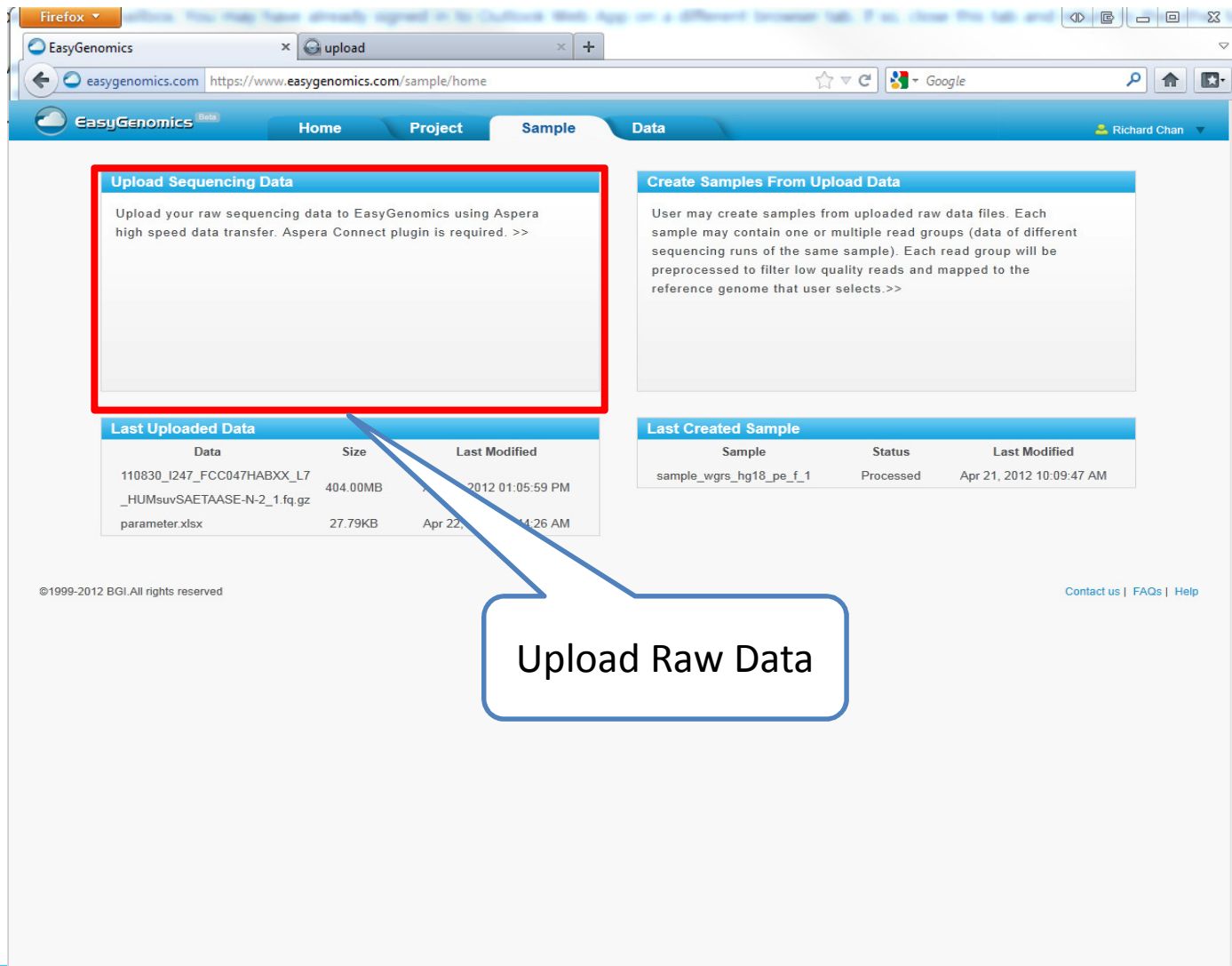
Recent Update

- smallRNA_demo-sRNA_demo **Waiting** Apr 21, 2012 01:46:15 PM
- sRNA_demo **Processed** Apr 21, 2012 05:10:54 AM

<Previous 1/1 Next>

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Upload Sequencing Data

Upload your raw sequencing data to EasyGenomics using Aspera high speed data transfer. Aspera Connect plugin is required. >>

Create Samples From Upload Data

User may create samples from uploaded raw data files. Each sample may contain one or multiple read groups (data of different sequencing runs of the same sample). Each read group will be preprocessed to filter low quality reads and mapped to the reference genome that user selects.>>

Last Uploaded Data

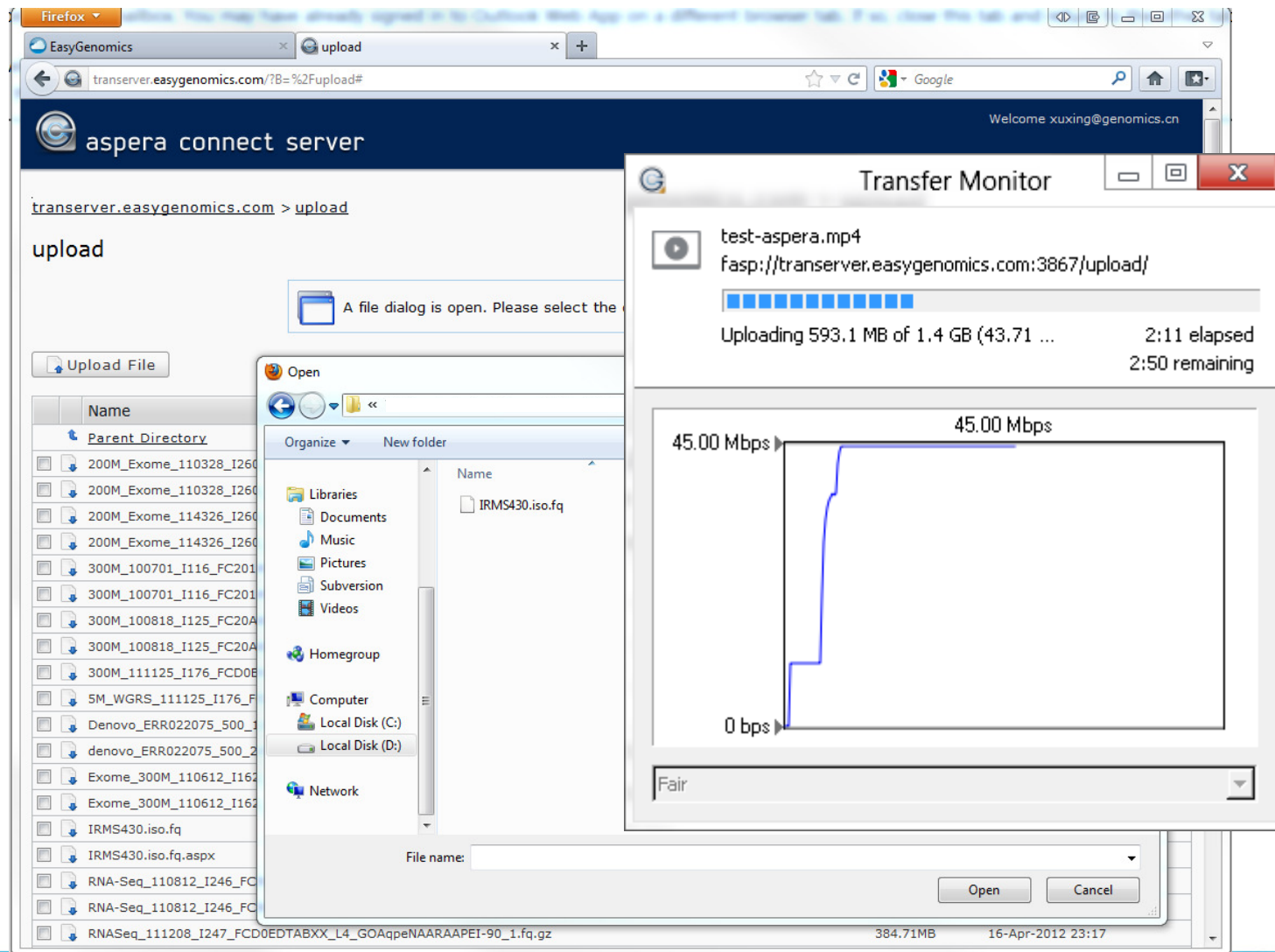
Data	Size	Last Modified
110830_I247_FCC047HABXX_L7_HUMsuvSAETAASE-N-2_1.fq.gz	404.00MB	2012 01:05:59 PM
parameter.xlsx	27.79KB	Apr 22, 2012 11:26 AM

Last Created Sample

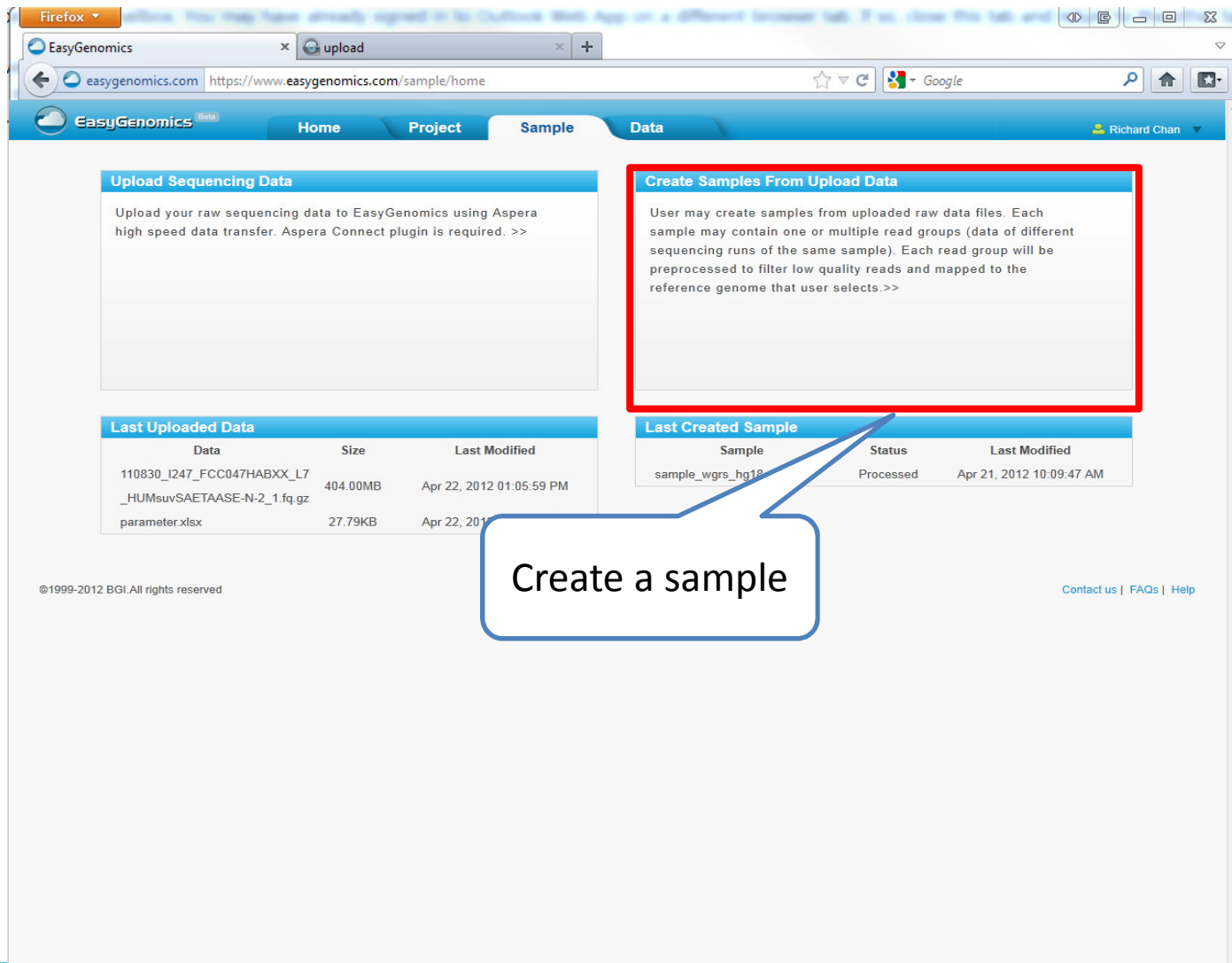
Sample	Status	Last Modified
sample_wgrs_hg18_pe_f_1	Processed	Apr 21, 2012 10:09:47 AM

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Upload Raw Reads (Aspera connect server)



The screenshot displays the Aspera Connect server interface in a Firefox browser window. The browser address bar shows the URL `transerver.easygenomics.com/?B=%2Fupload#`. The page title is "aspera connect server" and it includes a welcome message for "xuxing@genomics.cn". The main content area shows the path `transerver.easygenomics.com > upload` and a file list with columns for Name and file size. An "Open" file dialog is overlaid on the file list, showing the "Local Disk (D:)" with a file named "IRMS430.iso.fq". A "Transfer Monitor" window is also open, showing the upload progress for "test-aspera.mp4" to the destination `fasp://transerver.easygenomics.com:3867/upload/`. The progress bar indicates that 593.1 MB of 1.4 GB (43.71%) has been uploaded, with 2:11 elapsed and 2:50 remaining. The transfer speed is shown as 45.00 Mbps. A graph below the progress bar shows the transfer rate starting at 0 bps and reaching 45.00 Mbps. The "Fair" scheduling policy is selected.



Upload Sequencing Data

Upload your raw sequencing data to EasyGenomics using Aspera high speed data transfer. Aspera Connect plugin is required. >>

Last Uploaded Data

Data	Size	Last Modified
110830_I247_FCC047HABXX_L7_HUMsuvSAETAASE-N-2_1.fq.gz	404.00MB	Apr 22, 2012 01:05:59 PM
parameter.xlsx	27.79KB	Apr 22, 2012

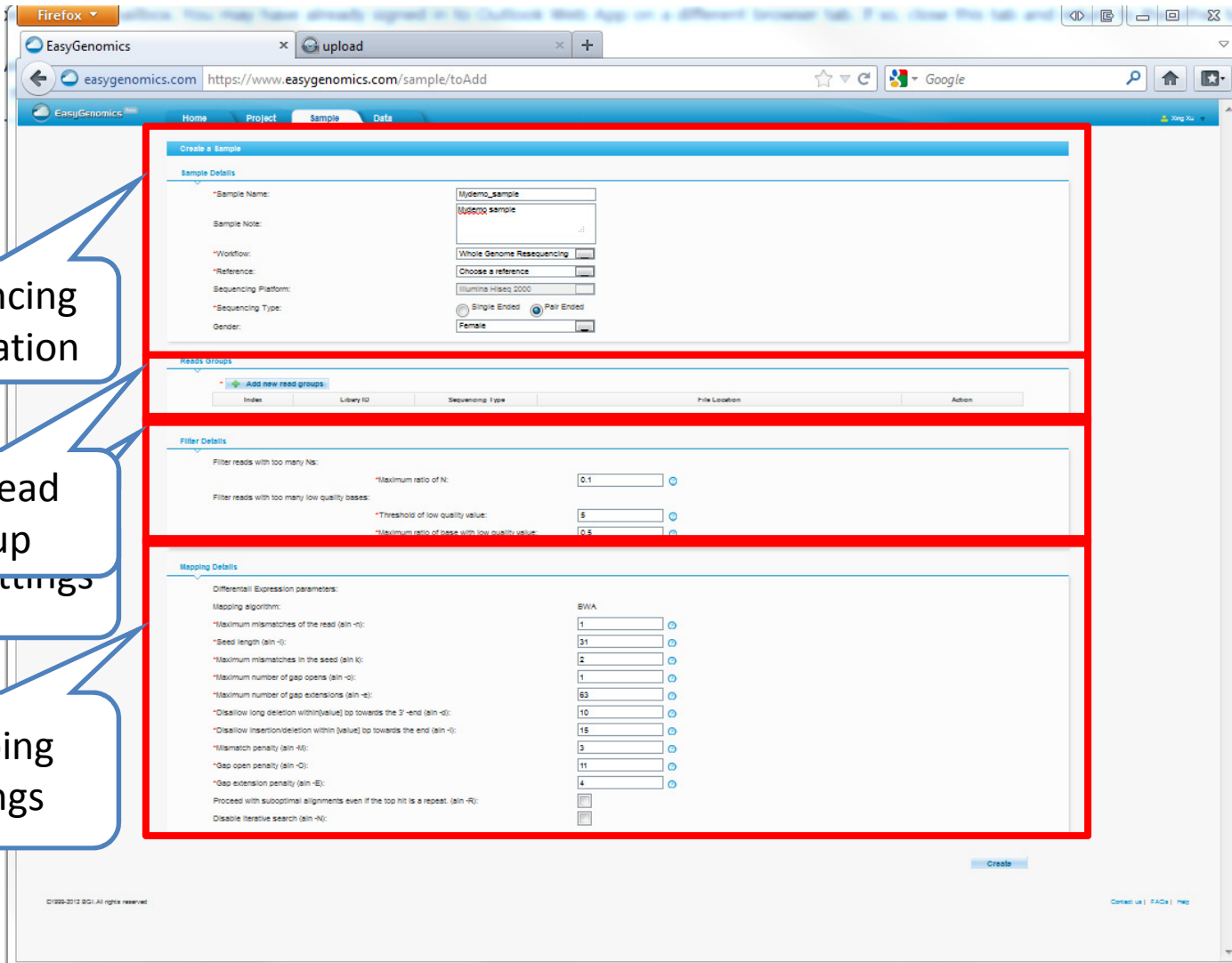
Create Samples From Upload Data

User may create samples from uploaded raw data files. Each sample may contain one or multiple read groups (data of different sequencing runs of the same sample). Each read group will be preprocessed to filter low quality reads and mapped to the reference genome that user selects.>>

Last Created Sample

Sample	Status	Last Modified
sample_wgrs_hg18	Processed	Apr 21, 2012 10:09:47 AM

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The screenshot shows the 'Create a Sample' form in a Firefox browser window. The form is divided into several sections, each highlighted with a red border and a callout box:

- Sequencing information:** This section includes fields for Sample Name (MyDemo_sample), Sample Note (Illumina sample), Workflow (Whole Genome Resequencing), Reference (Choose a reference), Sequencing Platform (Illumina HiSeq 2000), Sequencing Type (Pair Ended), and Gender (Female).
- Add Read Group:** This section features a table with columns for Index, Library ID, Sequencing Type, File Location, and Action. A button labeled 'Add new read groups' is positioned above the table.
- Filter settings:** This section contains filter parameters such as 'Filter reads with too many Ns' (Maximum ratio of N: 0.1), 'Filter reads with too many low quality bases' (Threshold of low quality value: 5, Maximum ratio of base with low quality value: 0.5).
- Mapping settings:** This section lists various mapping parameters for the BWA algorithm, including Maximum mismatches of the read (1), Seed length (31), Maximum mismatches in the seed (2), Maximum number of gap opens (1), Maximum number of gap extensions (63), and various penalties for mismatches and gaps.

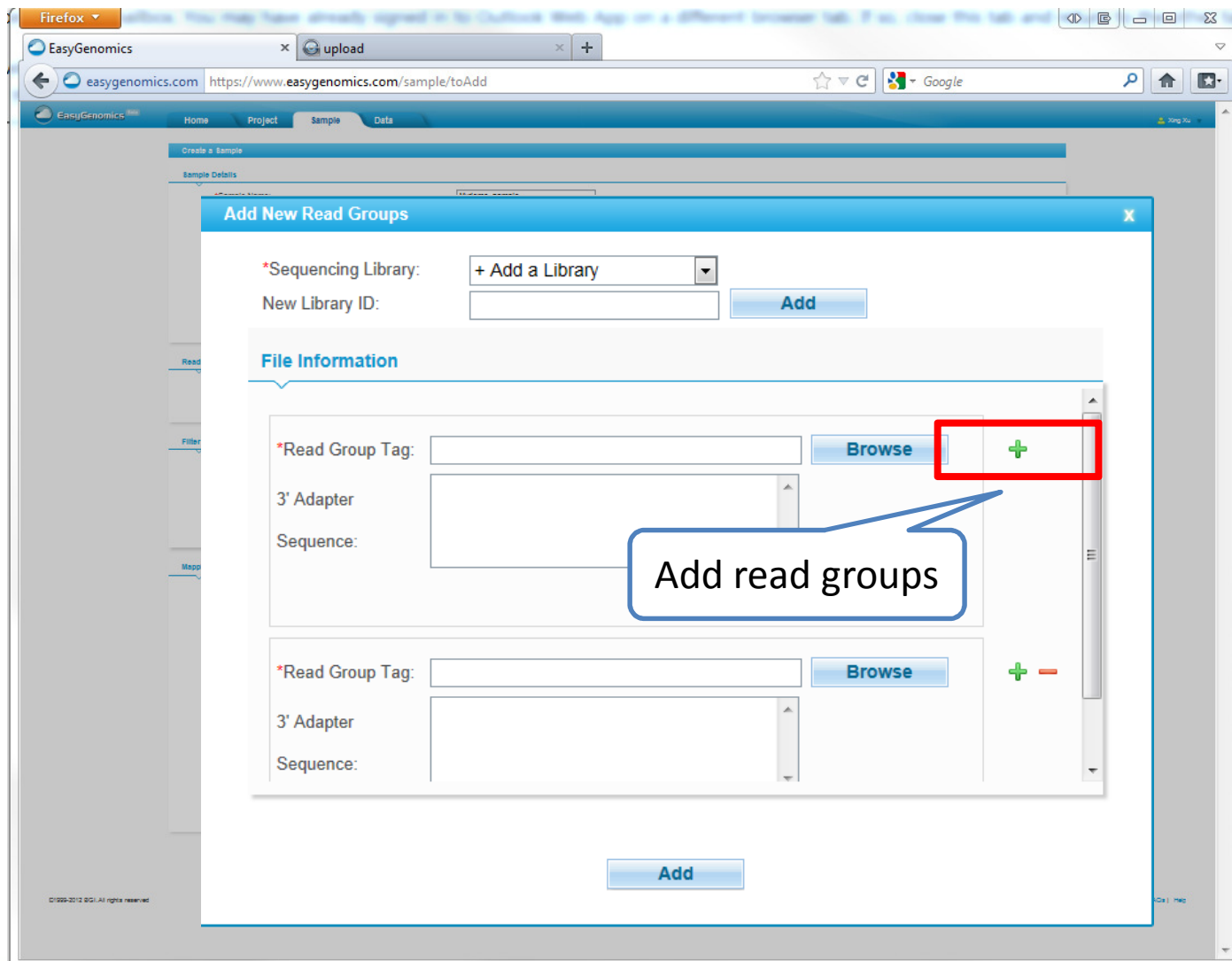
A 'Create' button is located at the bottom right of the form.

Sequencing
information

Add Read
Group

Filter settings

Mapping
settings



Firefox

EasyGenomics

upload

easygenomics.com https://www.easygenomics.com/sample/toAdd

Home Project Sample Data

Create a Sample

Sample Details

Add New Read Groups

*Sequencing Library: + Add a Library

New Library ID: **Add**

File Information

*Read Group Tag: **Browse** **+**

3' Adapter

Sequence:

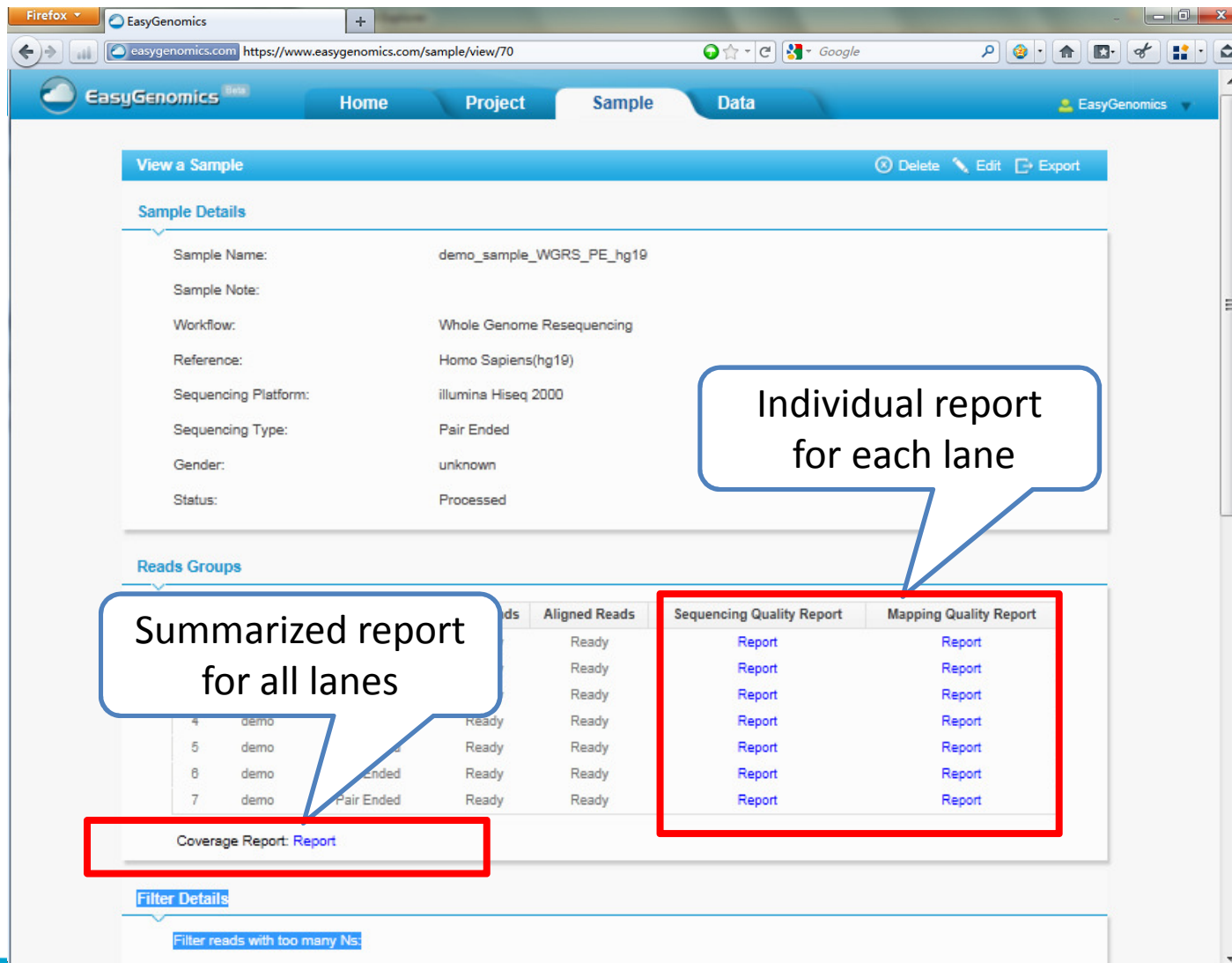
*Read Group Tag: **Browse** **+**

3' Adapter

Sequence:

Add

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The screenshot shows the 'View a Sample' page in the EasyGenomics web application. The page is titled 'View a Sample' and includes a navigation bar with 'Home', 'Project', 'Sample', and 'Data' tabs. The 'Sample Details' section displays the following information:

- Sample Name: demo_sample_WGRS_PE_hg19
- Sample Note:
- Workflow: Whole Genome Resequencing
- Reference: Homo Sapiens(hg19)
- Sequencing Platform: illumina Hiseq 2000
- Sequencing Type: Pair Ended
- Gender: unknown
- Status: Processed

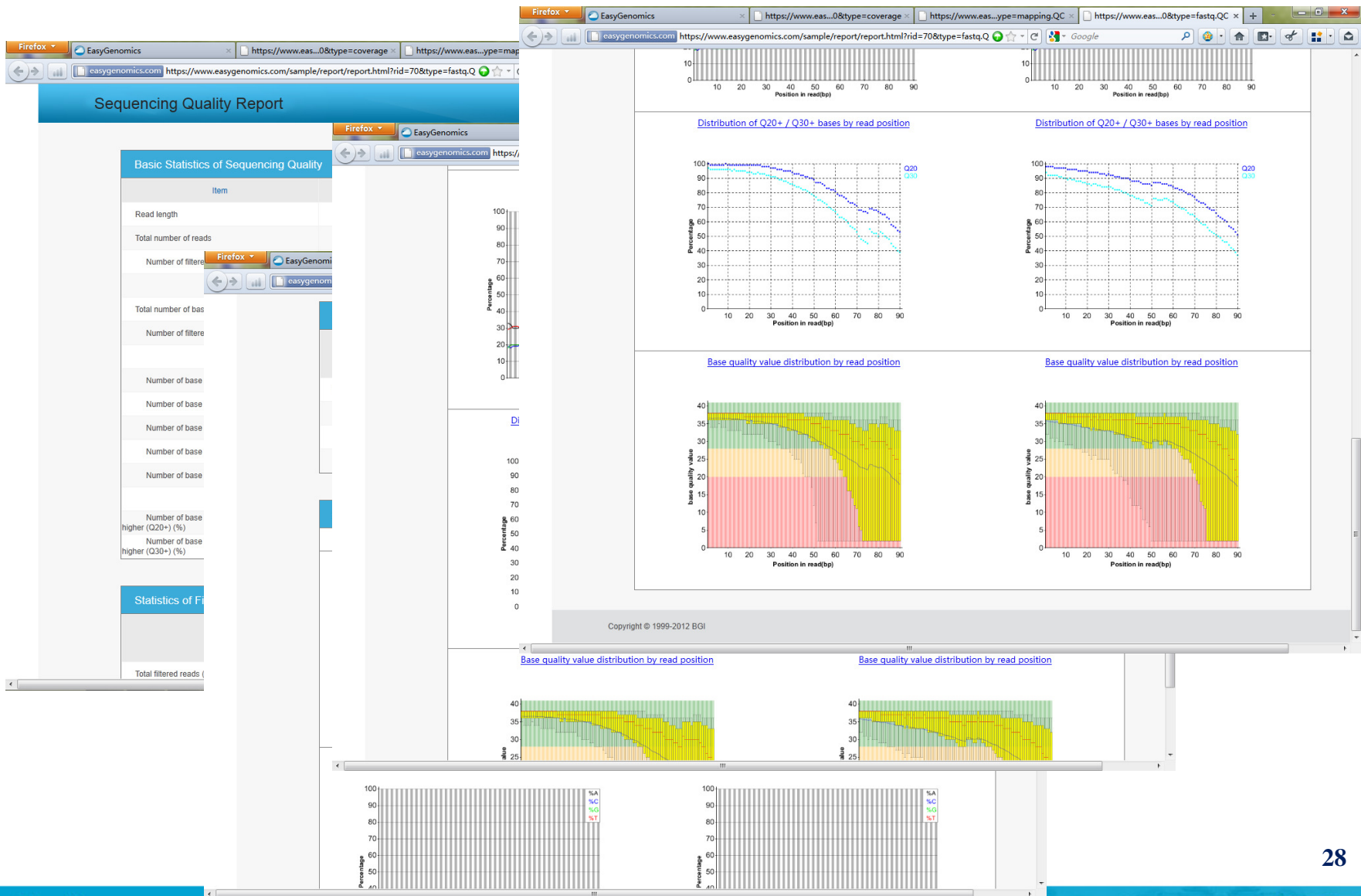
The 'Reads Groups' section contains a table with columns for 'Reads', 'Aligned Reads', 'Sequencing Quality Report', and 'Mapping Quality Report'. A red box highlights the 'Sequencing Quality Report' and 'Mapping Quality Report' columns, which contain links to individual reports for each lane. A blue callout bubble points to these reports with the text 'Individual report for each lane'. Another blue callout bubble points to the 'Reads' column with the text 'Summarized report for all lanes'. Below the table, a red box highlights the 'Coverage Report: Report' link.

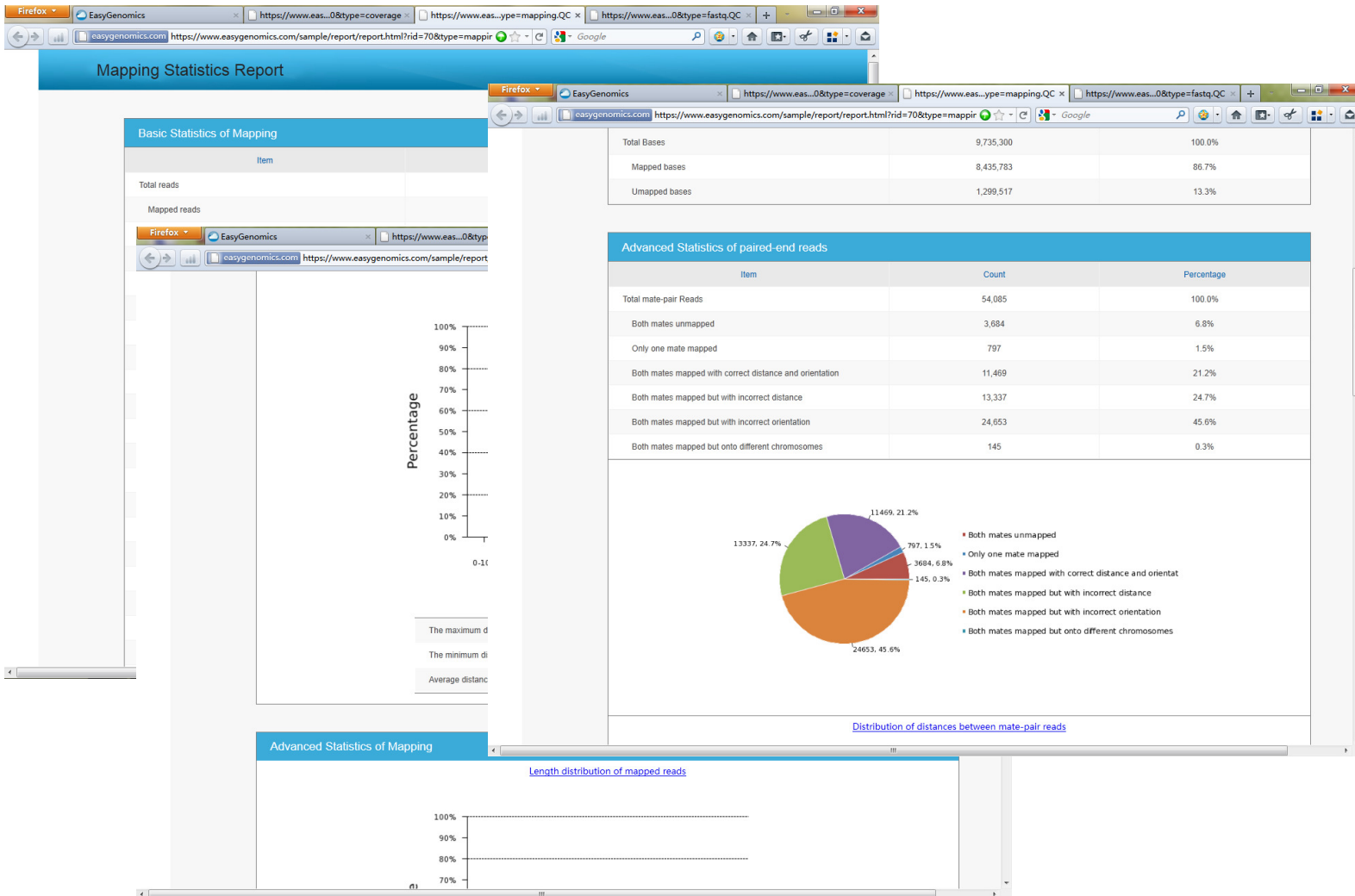
Reads	Aligned Reads	Sequencing Quality Report	Mapping Quality Report
	Ready	Report	Report
	Ready	Report	Report
	Ready	Report	Report
4 demo	Ready	Report	Report
5 demo	Ready	Report	Report
6 demo	Pair Ended	Report	Report
7 demo	Pair Ended	Report	Report

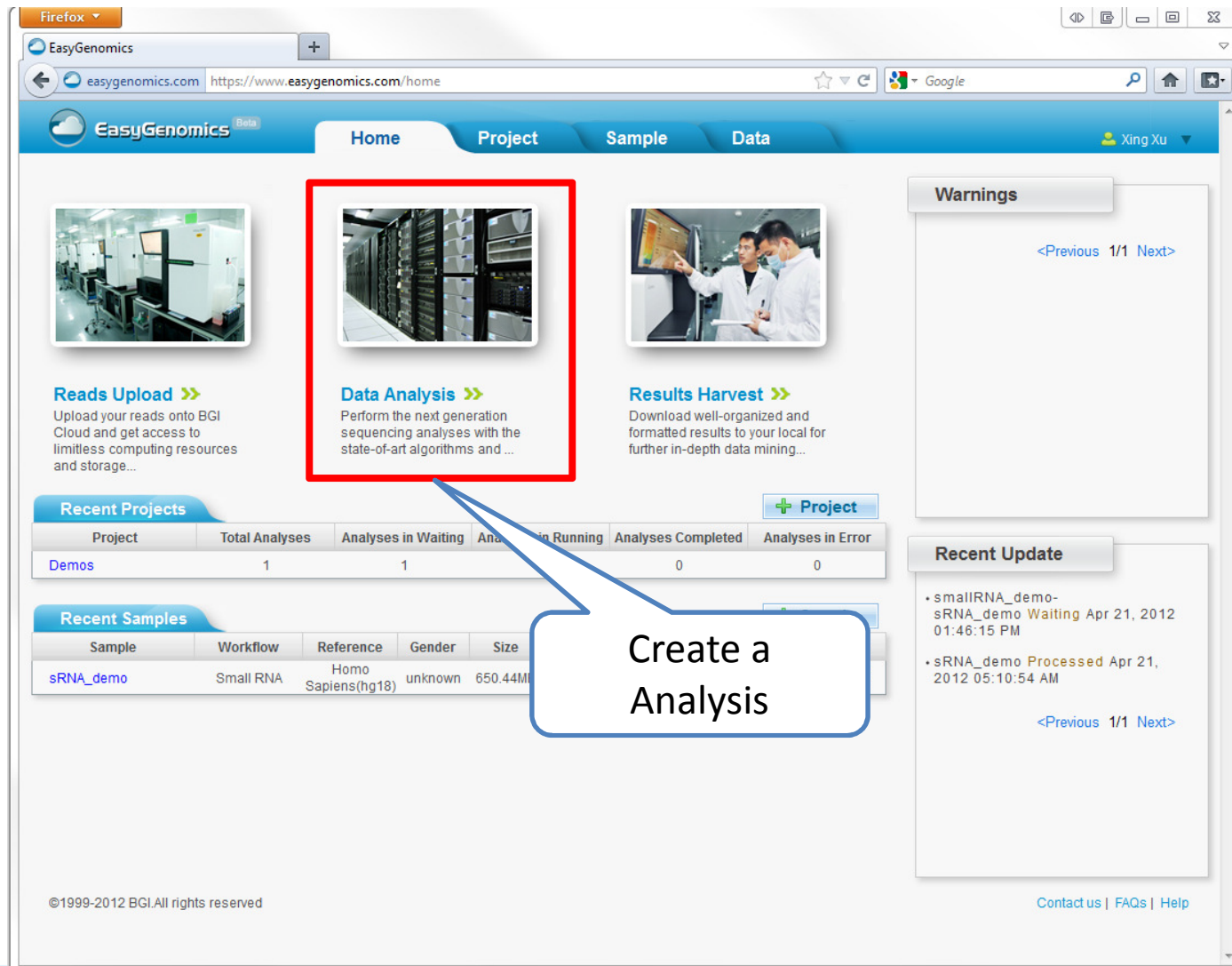
Coverage Report: [Report](#)

Filter Details

Filter reads with too many Ns.



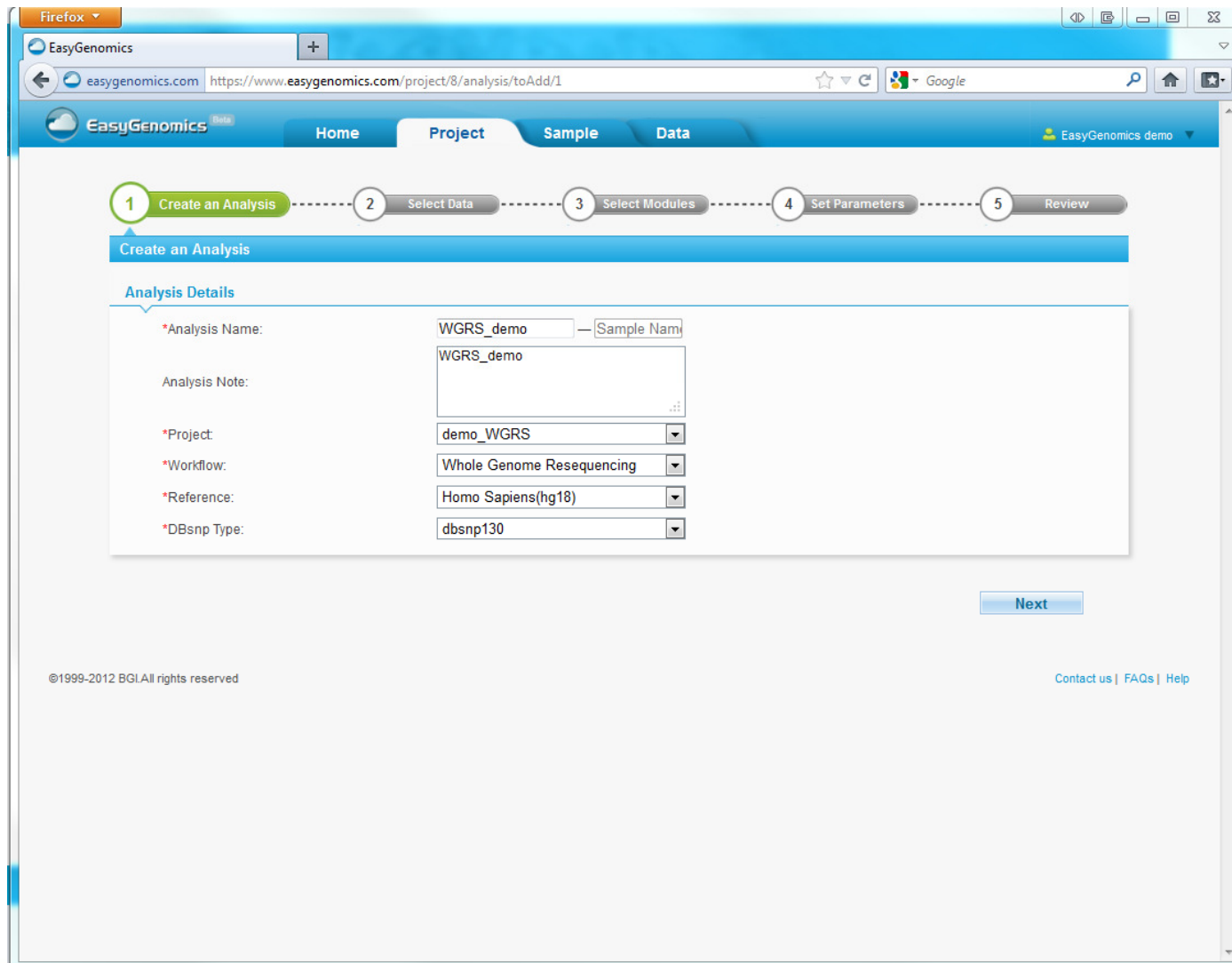




The screenshot shows the EasyGenomics Data Analysis Portal interface. The main navigation bar includes 'Home', 'Project', 'Sample', and 'Data'. The user is logged in as 'Xing Xu'. The 'Data Analysis' section is highlighted with a red box and a callout bubble that says 'Create a Analysis'. Below this, there are sections for 'Recent Projects' and 'Recent Samples'. The 'Recent Projects' table shows one project named 'Demos' with 1 total analysis, 1 in waiting, 0 in running, 0 completed, and 0 in error. The 'Recent Samples' table shows one sample named 'sRNA_demo' with a workflow of 'Small RNA', reference 'Homo Sapiens(hg18)', gender 'unknown', and size '650.44M'. There are also sections for 'Warnings' and 'Recent Update'.

Project	Total Analyses	Analyses in Waiting	Analyses in Running	Analyses Completed	Analyses in Error
Demos	1	1	0	0	0

Sample	Workflow	Reference	Gender	Size
sRNA_demo	Small RNA	Homo Sapiens(hg18)	unknown	650.44M



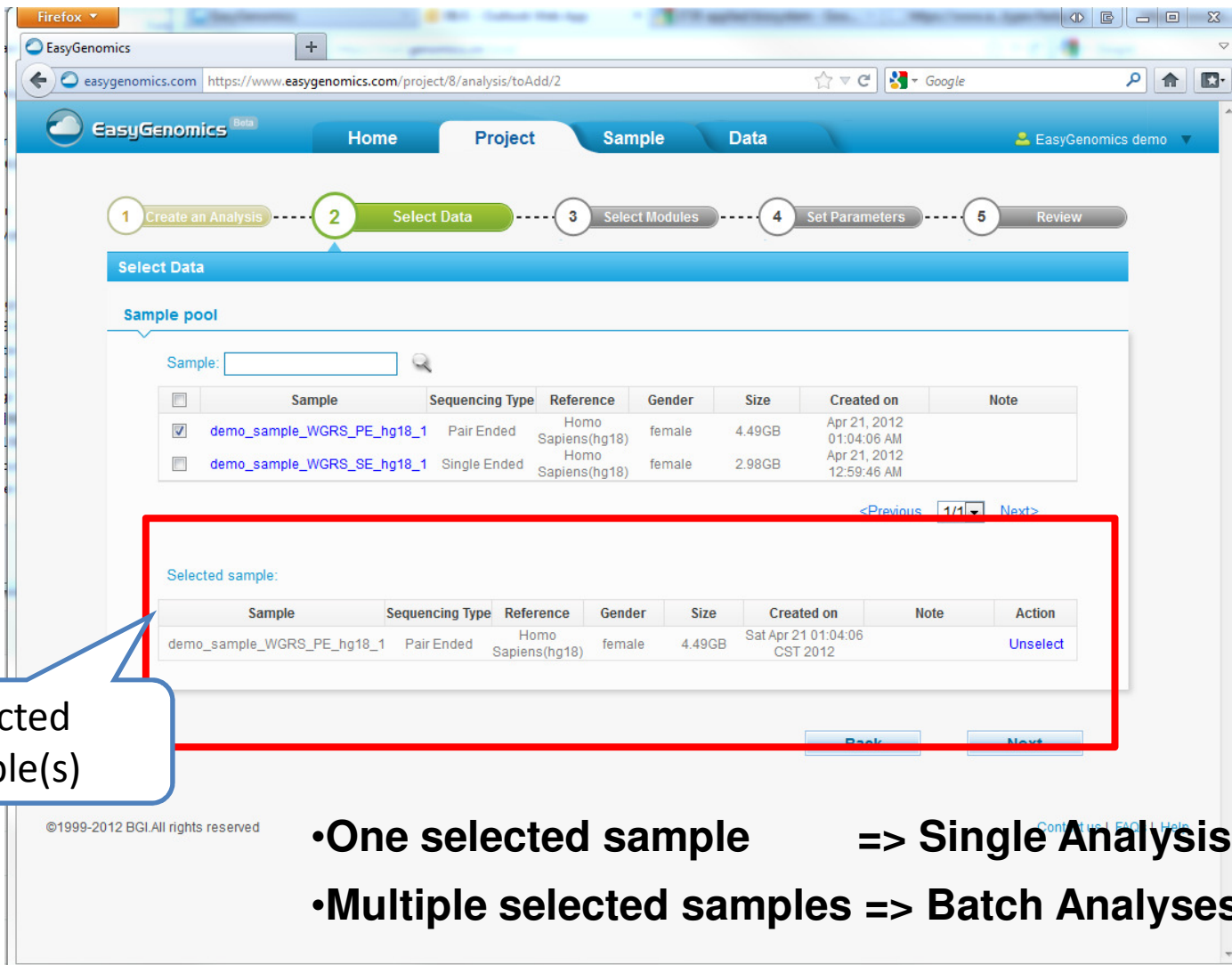
The screenshot shows a web browser window with the URL <https://www.easygenomics.com/project/8/analysis/toAdd/1>. The page features a navigation bar with 'Home', 'Project', 'Sample', and 'Data' tabs. A progress indicator at the top shows five steps: 1. Create an Analysis (highlighted), 2. Select Data, 3. Select Modules, 4. Set Parameters, and 5. Review.

The main content area is titled 'Create an Analysis' and contains a form with the following fields:

- *Analysis Name:** A text input field containing 'WGRS_demo' and a dropdown menu labeled 'Sample Name'.
- Analysis Note:** A large text area with a vertical scrollbar.
- *Project:** A dropdown menu with 'demo_WGRS' selected.
- *Workflow:** A dropdown menu with 'Whole Genome Resequencing' selected.
- *Reference:** A dropdown menu with 'Homo Sapiens(hg18)' selected.
- *DBsnp Type:** A dropdown menu with 'dbsnp130' selected.

A 'Next' button is located at the bottom right of the form area.

At the bottom of the page, there is a copyright notice: ©1999-2012 BGI. All rights reserved. and a link for [Contact us | FAQs | Help](#).



1 Create an Analysis — 2 **Select Data** — 3 Select Modules — 4 Set Parameters — 5 Review

Select Data

Sample pool

Sample:

<input type="checkbox"/>	Sample	Sequencing Type	Reference	Gender	Size	Created on	Note
<input checked="" type="checkbox"/>	demo_sample_WGRS_PE_hg18_1	Pair Ended	Homo Sapiens(hg18)	female	4.49GB	Apr 21, 2012 01:04:06 AM	
<input type="checkbox"/>	demo_sample_WGRS_SE_hg18_1	Single Ended	Homo Sapiens(hg18)	female	2.98GB	Apr 21, 2012 12:59:46 AM	

<Previous 1/1 Next>

Selected sample:

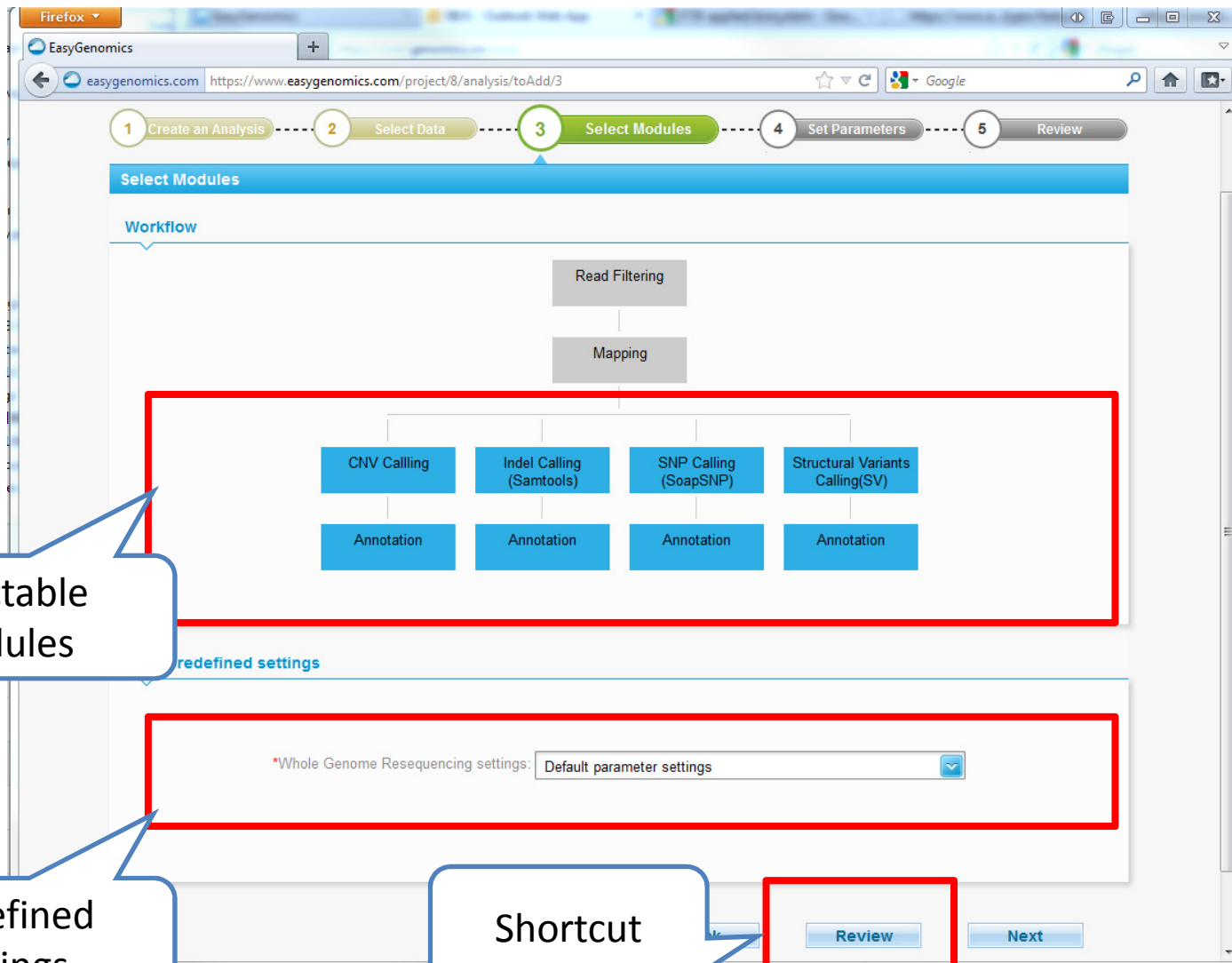
Sample	Sequencing Type	Reference	Gender	Size	Created on	Note	Action
demo_sample_WGRS_PE_hg18_1	Pair Ended	Homo Sapiens(hg18)	female	4.49GB	Sat Apr 21 01:04:06 CST 2012		Unselect

Back Next

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Selected sample(s)

- One selected sample ==> Single Analysis
- Multiple selected samples ==> Batch Analyses



1 Create an Analysis — 2 Select Data — 3 Select Modules — 4 Set Parameters — 5 Review

Select Modules

Workflow

```
graph TD; RF[Read Filtering] --> M[Mapping]; M --> CNV[CNV Calling]; M --> Indel[Indel Calling (Samtools)]; M --> SNP[SNP Calling (SoapSNP)]; M --> SV[Structural Variants Calling (SV)]; CNV --> AN1[Annotation]; Indel --> AN2[Annotation]; SNP --> AN3[Annotation]; SV --> AN4[Annotation];
```

redefined settings

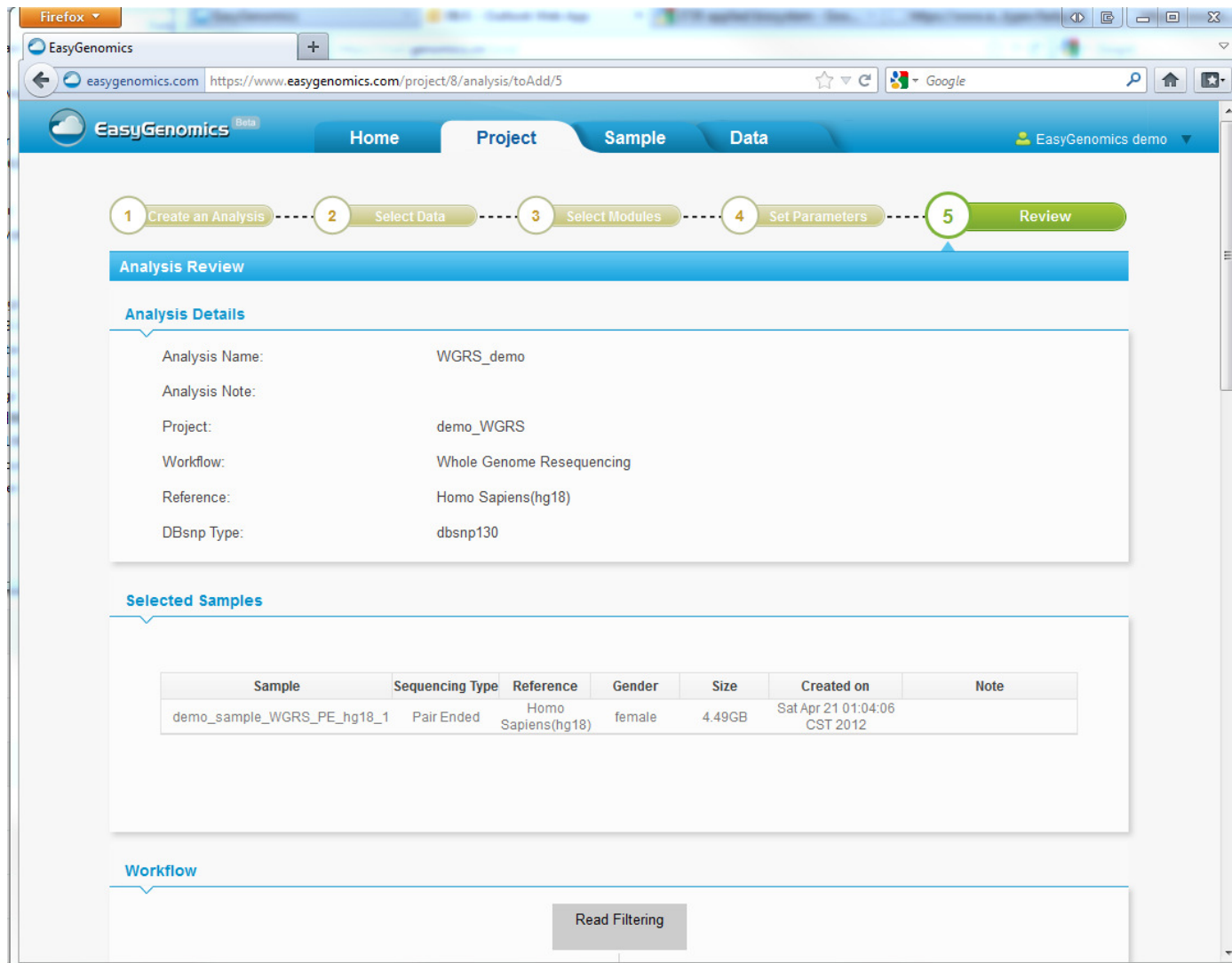
*Whole Genome Resequencing settings: Default parameter settings

Review Next

Selectable modules

Predefined Settings

Shortcut



The screenshot shows the 'Review' step (5) of a 5-step process to create an analysis. The steps are: 1. Create an Analysis, 2. Select Data, 3. Select Modules, 4. Set Parameters, and 5. Review. The 'Review' step is highlighted in green.

Analysis Review

Analysis Details

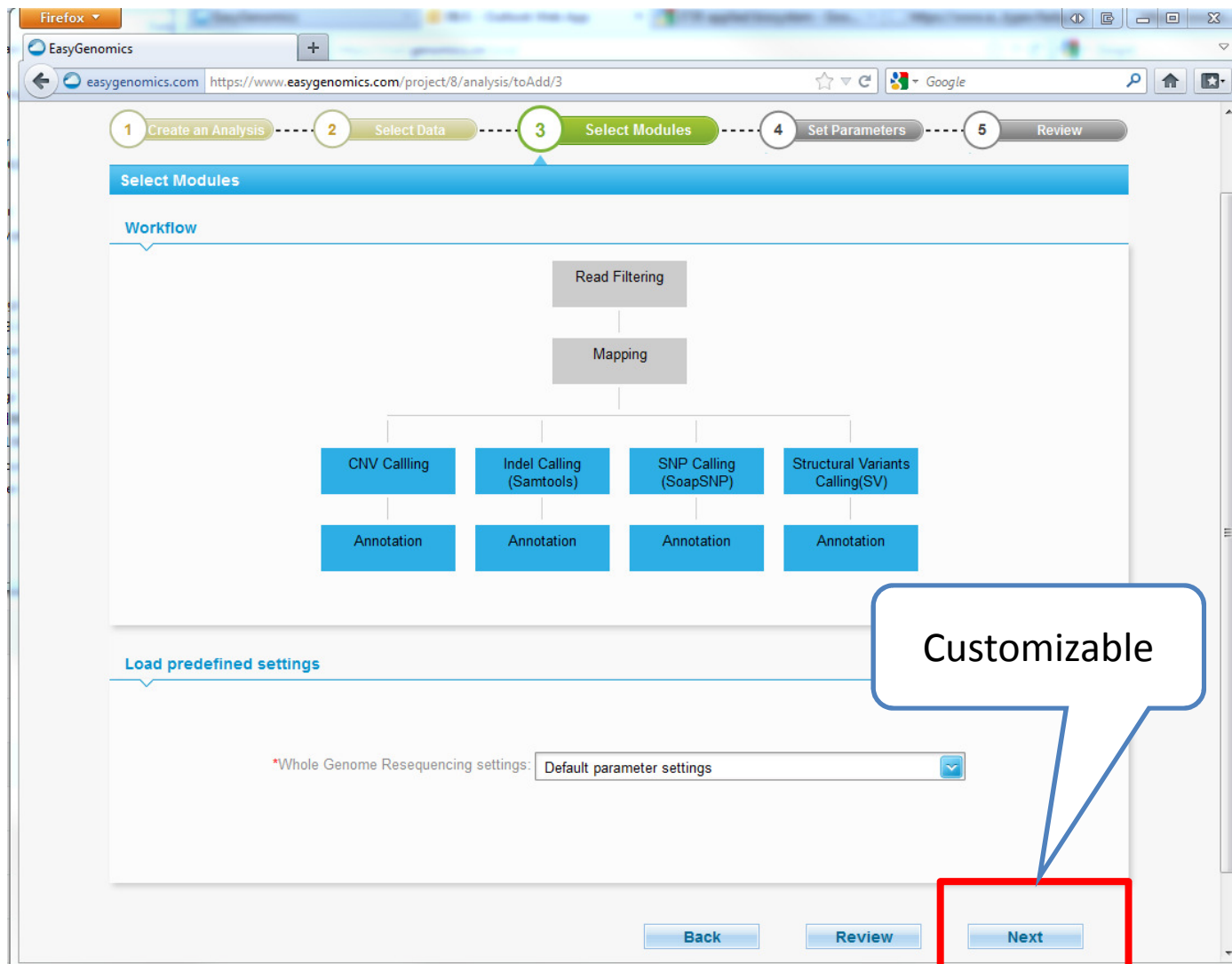
Analysis Name: WGRS_demo
 Analysis Note:
 Project: demo_WGRS
 Workflow: Whole Genome Resequencing
 Reference: Homo Sapiens(hg18)
 DBsnp Type: dbsnp130

Selected Samples

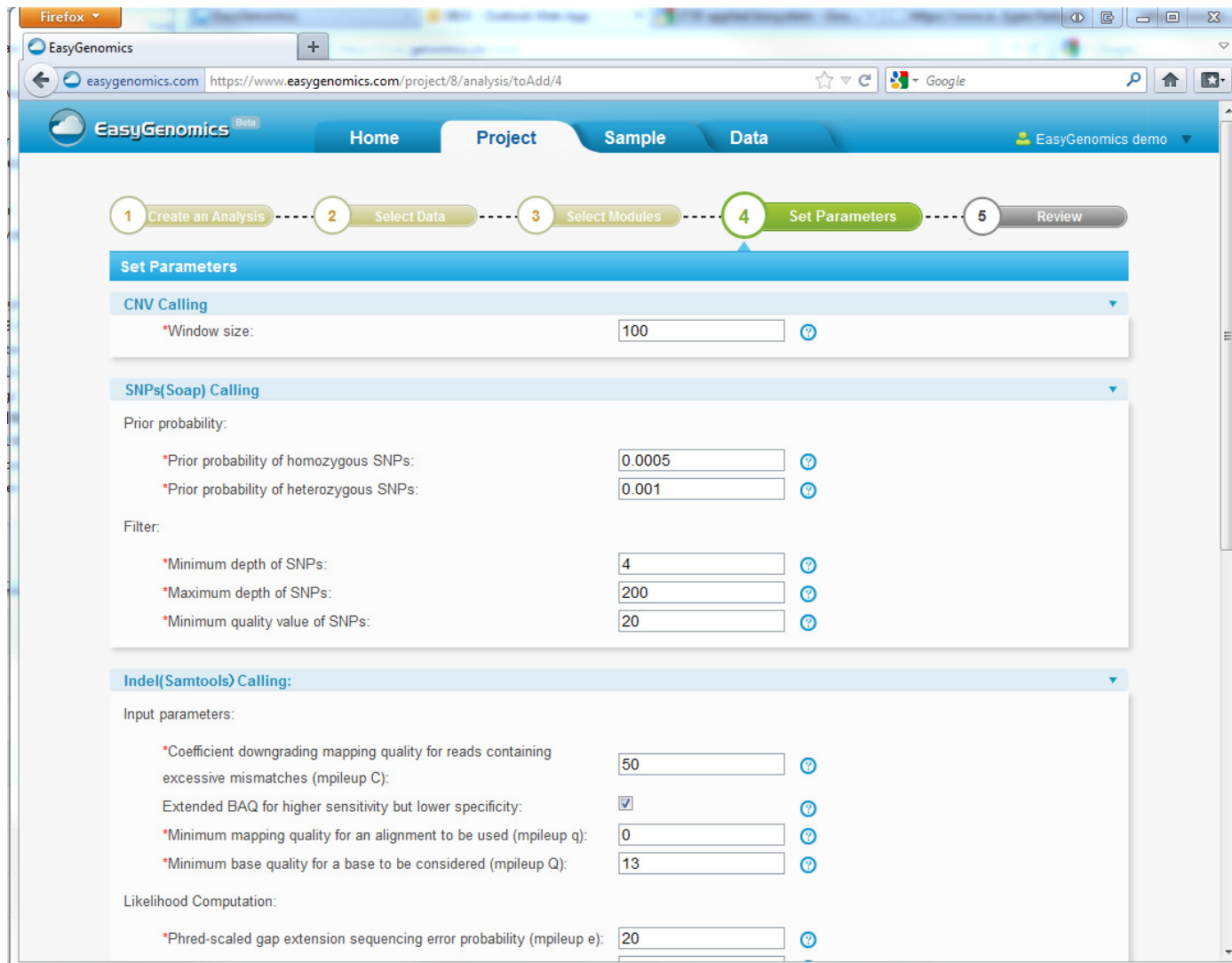
Sample	Sequencing Type	Reference	Gender	Size	Created on	Note
demo_sample_WGRS_PE_hg18_1	Pair Ended	Homo Sapiens(hg18)	female	4.49GB	Sat Apr 21 01:04:06 CST 2012	

Workflow

Read Filtering



The screenshot shows a web browser window with the URL <https://www.easygenomics.com/project/8/analysis/toAdd/3>. The page features a progress bar at the top with five steps: 1. Create an Analysis, 2. Select Data, 3. Select Modules (highlighted), 4. Set Parameters, and 5. Review. Below the progress bar is a 'Select Modules' section with a 'Workflow' diagram. The diagram shows a sequence of steps: Read Filtering, Mapping, and then four parallel paths: CNV Calling, Indel Calling (Samtools), SNP Calling (SoapSNP), and Structural Variants Calling (SV). Each of these four paths leads to an 'Annotation' step. Below the workflow is a 'Load predefined settings' section with a dropdown menu for 'Whole Genome Resequencing settings' currently set to 'Default parameter settings'. At the bottom of the page are three buttons: 'Back', 'Review', and 'Next'. The 'Next' button is highlighted with a red box. A blue callout bubble with the text 'Customizable' points to the 'Next' button.



Firefox

EasyGenomics

easygenomics.com https://www.easygenomics.com/project/8/analysis/toAdd/4

EasyGenomics **Home** Project Sample Data EasyGenomics demo

1 Create an Analysis 2 Select Data 3 Select Modules 4 Set Parameters 5 Review

Set Parameters

CNV Calling

*Window size:

SNPs(Soap) Calling

Prior probability:

*Prior probability of homozygous SNPs:

*Prior probability of heterozygous SNPs:

Filter:

*Minimum depth of SNPs:

*Maximum depth of SNPs:

*Minimum quality value of SNPs:

Indel(Samtools) Calling:

Input parameters:

*Coefficient downgrading mapping quality for reads containing excessive mismatches (mpileup C):

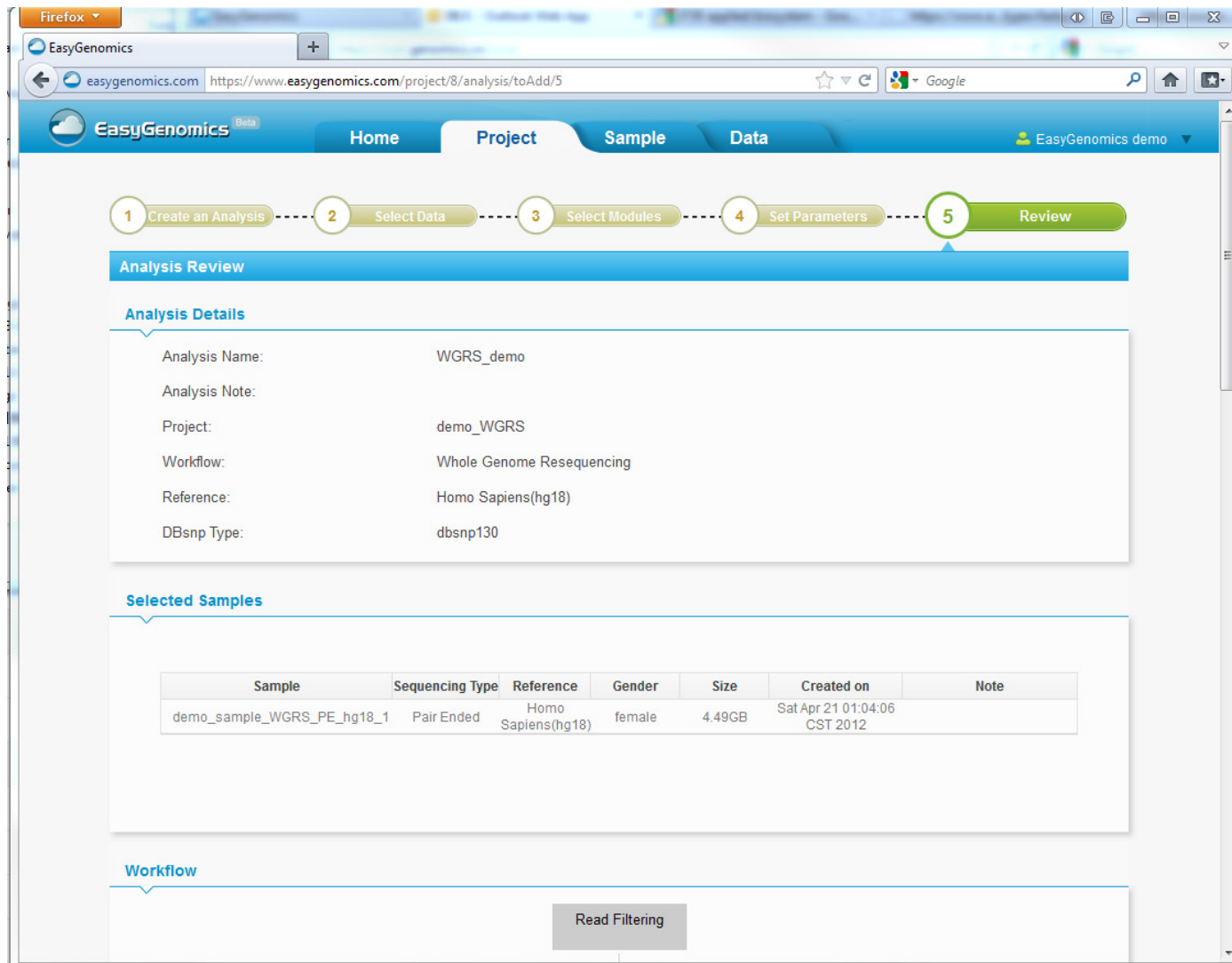
Extended BAQ for higher sensitivity but lower specificity:

*Minimum mapping quality for an alignment to be used (mpileup q):

*Minimum base quality for a base to be considered (mpileup Q):

Likelihood Computation:

*Phred-scaled gap extension sequencing error probability (mpileup e):



The screenshot shows a web browser window with the URL <https://www.easygenomics.com/project/8/analysis/toAdd/5>. The navigation bar includes 'Home', 'Project', 'Sample', and 'Data'. A progress indicator at the top shows five steps: 1. Create an Analysis, 2. Select Data, 3. Select Modules, 4. Set Parameters, and 5. Review (highlighted in green).

Analysis Review

Analysis Details

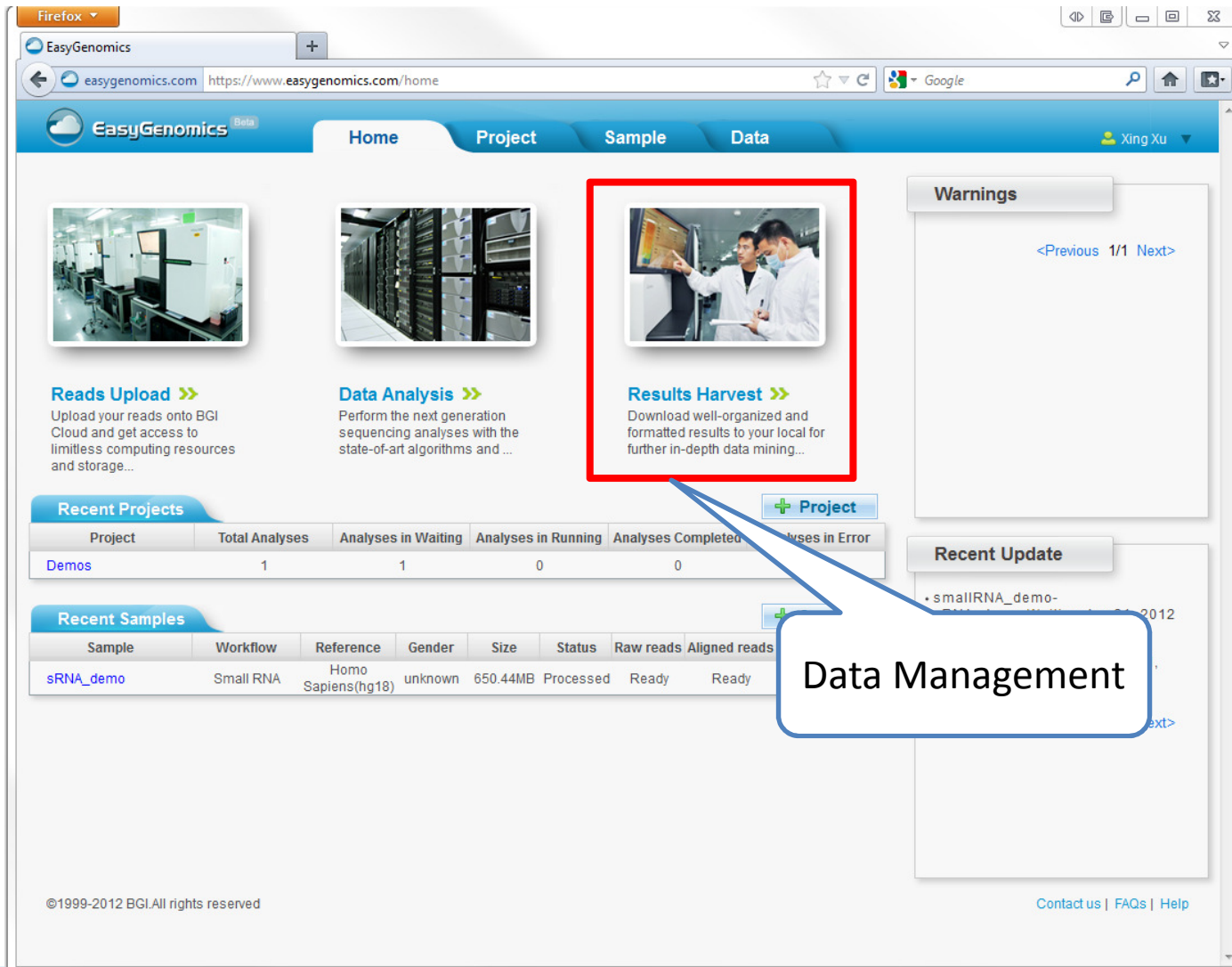
Analysis Name: WGRS_demo
 Analysis Note:
 Project: demo_WGRS
 Workflow: Whole Genome Resequencing
 Reference: Homo Sapiens(hg18)
 DBsnp Type: dbsnp130

Selected Samples

Sample	Sequencing Type	Reference	Gender	Size	Created on	Note
demo_sample_WGRS_PE_hg18_1	Pair Ended	Homo Sapiens(hg18)	female	4.49GB	Sat Apr 21 01:04:06 CST 2012	

Workflow

Read Filtering



Firefox

EasyGenomics

easygenomics.com https://www.easygenomics.com/home

EasyGenomics **Home** Project Sample Data Xing Xu

Reads Upload >>
Upload your reads onto BGI Cloud and get access to limitless computing resources and storage...

Data Analysis >>
Perform the next generation sequencing analyses with the state-of-art algorithms and ...

Results Harvest >>
Download well-organized and formatted results to your local for further in-depth data mining...

Warnings
<Previous 1/1 Next>

Recent Projects

Project	Total Analyses	Analyses in Waiting	Analyses in Running	Analyses Completed	Analyses in Error
Demos	1	1	0	0	

Recent Samples

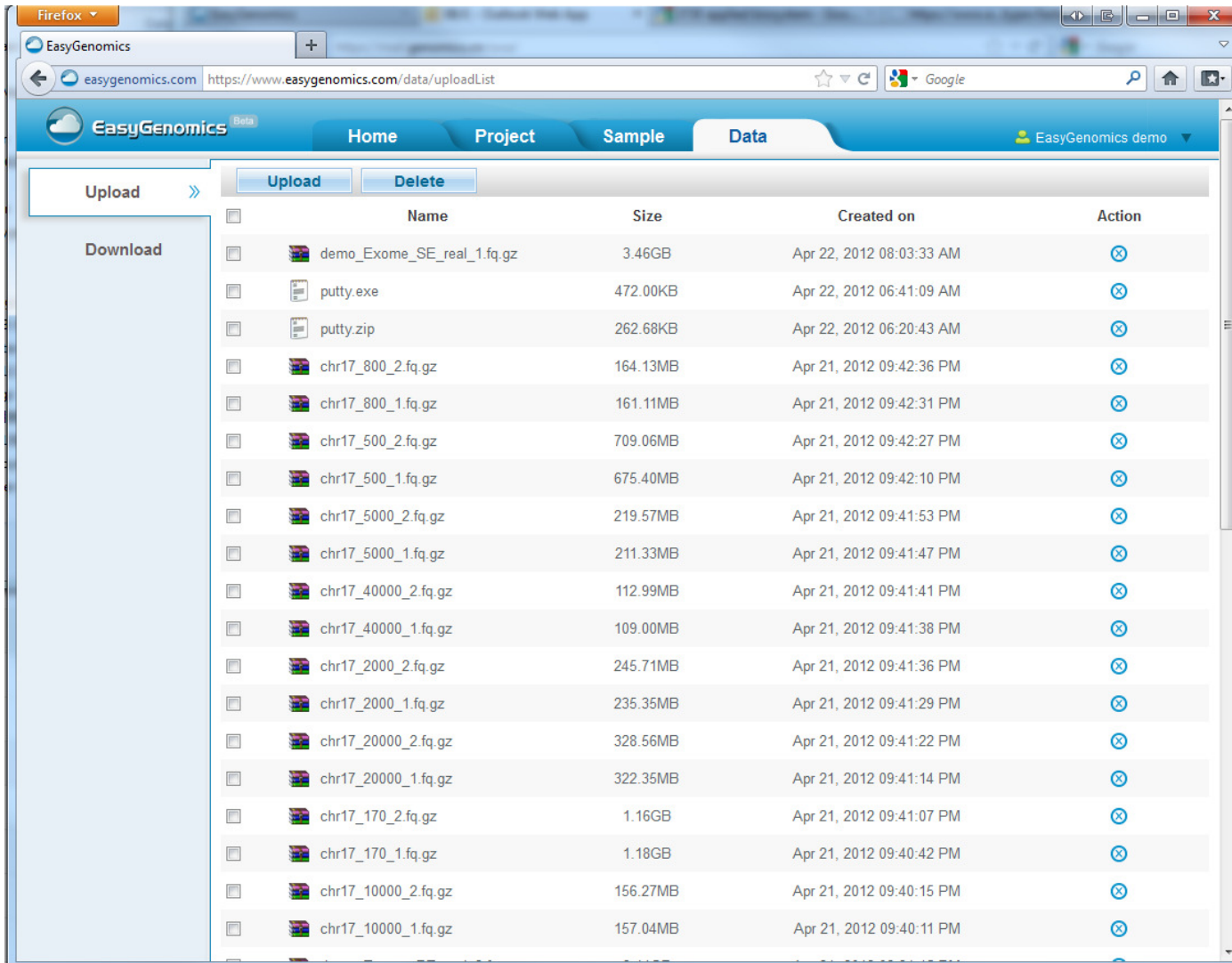
Sample	Workflow	Reference	Gender	Size	Status	Raw reads	Aligned reads
sRNA_demo	Small RNA	Homo Sapiens(hg18)	unknown	650.44MB	Processed	Ready	Ready

Data Management

Recent Update
smallRNA_demo- 2012

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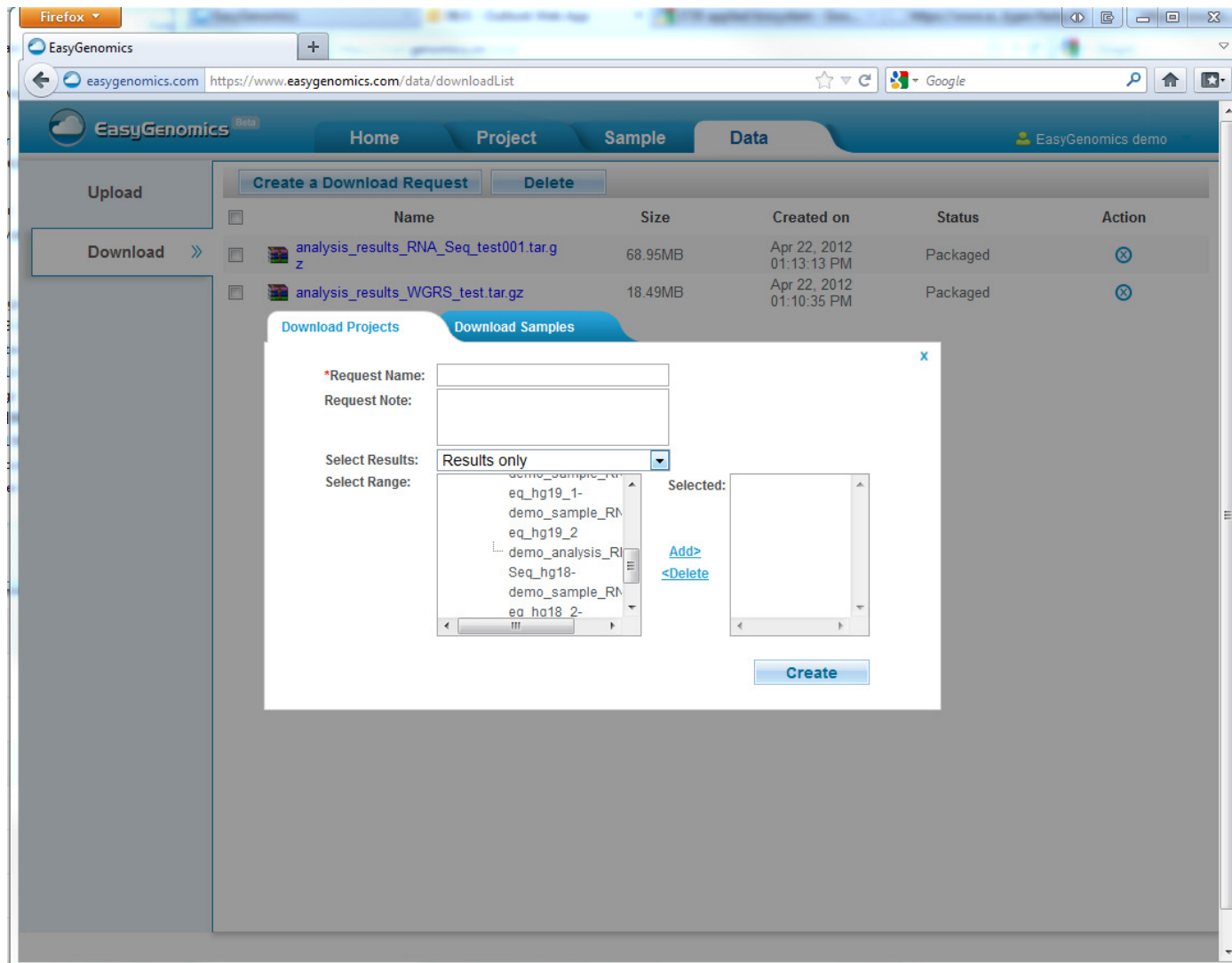
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EasyGenomics **Home** Project Sample **Data** EasyGenomics demo

Upload >>

Name	Size	Created on	Action
demo_Exome_SE_real_1.fq.gz	3.46GB	Apr 22, 2012 08:03:33 AM	<input type="button" value="X"/>
putty.exe	472.00KB	Apr 22, 2012 06:41:09 AM	<input type="button" value="X"/>
putty.zip	262.68KB	Apr 22, 2012 06:20:43 AM	<input type="button" value="X"/>
chr17_800_2.fq.gz	164.13MB	Apr 21, 2012 09:42:36 PM	<input type="button" value="X"/>
chr17_800_1.fq.gz	161.11MB	Apr 21, 2012 09:42:31 PM	<input type="button" value="X"/>
chr17_500_2.fq.gz	709.06MB	Apr 21, 2012 09:42:27 PM	<input type="button" value="X"/>
chr17_500_1.fq.gz	675.40MB	Apr 21, 2012 09:42:10 PM	<input type="button" value="X"/>
chr17_5000_2.fq.gz	219.57MB	Apr 21, 2012 09:41:53 PM	<input type="button" value="X"/>
chr17_5000_1.fq.gz	211.33MB	Apr 21, 2012 09:41:47 PM	<input type="button" value="X"/>
chr17_40000_2.fq.gz	112.99MB	Apr 21, 2012 09:41:41 PM	<input type="button" value="X"/>
chr17_40000_1.fq.gz	109.00MB	Apr 21, 2012 09:41:38 PM	<input type="button" value="X"/>
chr17_2000_2.fq.gz	245.71MB	Apr 21, 2012 09:41:36 PM	<input type="button" value="X"/>
chr17_2000_1.fq.gz	235.35MB	Apr 21, 2012 09:41:29 PM	<input type="button" value="X"/>
chr17_20000_2.fq.gz	328.56MB	Apr 21, 2012 09:41:22 PM	<input type="button" value="X"/>
chr17_20000_1.fq.gz	322.35MB	Apr 21, 2012 09:41:14 PM	<input type="button" value="X"/>
chr17_170_2.fq.gz	1.16GB	Apr 21, 2012 09:41:07 PM	<input type="button" value="X"/>
chr17_170_1.fq.gz	1.18GB	Apr 21, 2012 09:40:42 PM	<input type="button" value="X"/>
chr17_10000_2.fq.gz	156.27MB	Apr 21, 2012 09:40:15 PM	<input type="button" value="X"/>
chr17_10000_1.fq.gz	157.04MB	Apr 21, 2012 09:40:11 PM	<input type="button" value="X"/>

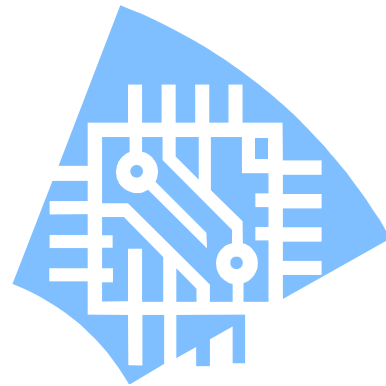


The screenshot shows the EasyGenomics web interface in a Firefox browser window. The URL is <https://www.easygenomics.com/data/downloadList>. The navigation menu includes Home, Project, Sample, and Data. The main content area has a sidebar with 'Upload' and 'Download' options. A table lists download requests:

Name	Size	Created on	Status	Action
analysis_results_RNA_Seq_test001.tar.gz	68.95MB	Apr 22, 2012 01:13:13 PM	Packaged	
analysis_results_WGRS_test.tar.gz	18.49MB	Apr 22, 2012 01:10:35 PM	Packaged	

A modal dialog titled 'Download Projects' is open, showing a form to create a new request. The form includes:

- *Request Name:**
- Request Note:**
- Select Results:** Results only (dropdown menu)
- Select Range:** A list of items including 'demo_sample_RN', 'eq_hg19_1-', 'demo_sample_RN', 'eq_hg19_2', 'demo_analysis_RI', 'Seq_hg18-', 'demo_sample_RN', and 'eq_ho18_2-'. There are 'Add>' and '<Delete' buttons between the list and a 'Selected:' list.
- Selected:**
- Create** button



Sifei He

Director of BGI Cloud

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