

December 4th, 2014
Next Generation Sequencing Team
Analysis Department, Life Science Division
Hokkaido System Science Co., Ltd.

How to download your alignment data of SeqNova™CS (DNAnexus (Classic))

Dear customers,

Thank you for your usual order for our products and services.

We are regret to inform you that one of our next generation sequencing (NGS) data analysis service, “SeqNova™CS (DNAnexus (Classic))”, will be terminated.

We truly apologize for your inconvenience.

License term will be no more extended, and all data will be not available for analysis or browsing after March 31, 2015.

We ask all users who currently use our DNAnexus service to confirm the “EXPIRATION” of your data and make sure to follow all the procedures described below to download your data by the expiration date.

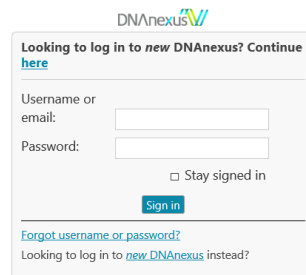
Sincerely yours,

<<How to download your data>>

1. Log in to DNAnexus (Classic) web site

Please go to the DNAnexus (Classic) web site from the below address and log in to the system.

<https://classic.dnanexus.com/login>



DNAnexus

Looking to log in to new DNAnexus? Continue [here](#)

Username or email:

Password:

Stay signed in

[Sign in](#)

[Forgot username or password?](#)

Looking to log in to [new DNAnexus](#) instead?

Fig 1. Log-in Screen of DNAnexus (Classic) site

2. List of “Samples”

After log-in, from the Home screen, please click “Samples” tab from tab menu on the upper part of the screen and go to the “Samples” screen.

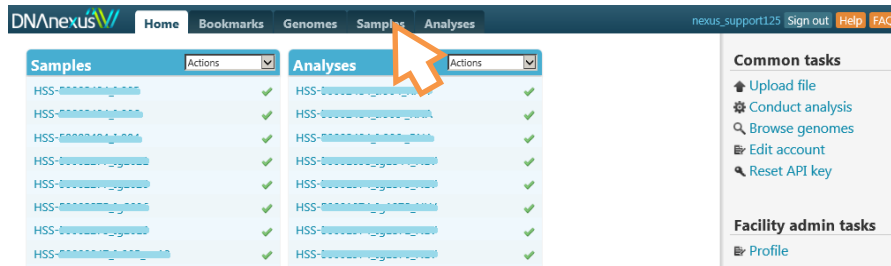


Fig 2. DNAnexus (Classic) Home screen

3. Select the download data

Please click the check box of the “NAME” for the data you want to download from the Sample list shown on the screen, and select “export mappings” from the pull down menu “more actions” on the upper right side of the screen.

*More than one data can be selected at one time.

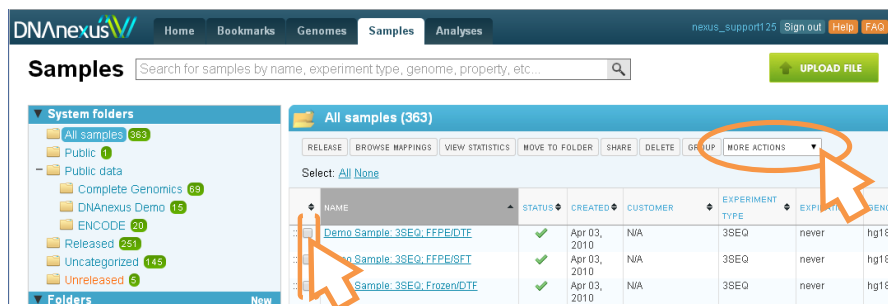


Fig 3-1. Check your data on the DNAnexus (Classic) Samples screen

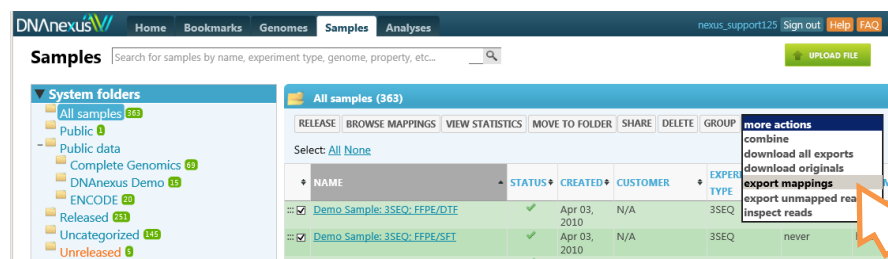


Fig 3-2. Select “export mappings” on the DNAnexus (Classic) Samples

4. Select the download file format

Please select the “export mappings” and the below screen will be shown. Please select the download file format from the “Standard file formats” list.

*For use of analysis program made by any third party, “SAM file, gzipped” or “BAM file” is generally used.

For “SAM file, gzipped” format, please download it as a compressed tab-delimited text file, then decompress it to browse it by text viewer etc.

“BAM file” is a binary compressed data of the above “SAM file”. A dedicated program is required to browse this data.

Data format available for import is different depend on analysis programs, so unless otherwise specified, it is recommended to download data as both format type.

*Only one download file format can be selected per one download operation. To change the file format, please repeat the operations from the step 3, “Select the download data”.

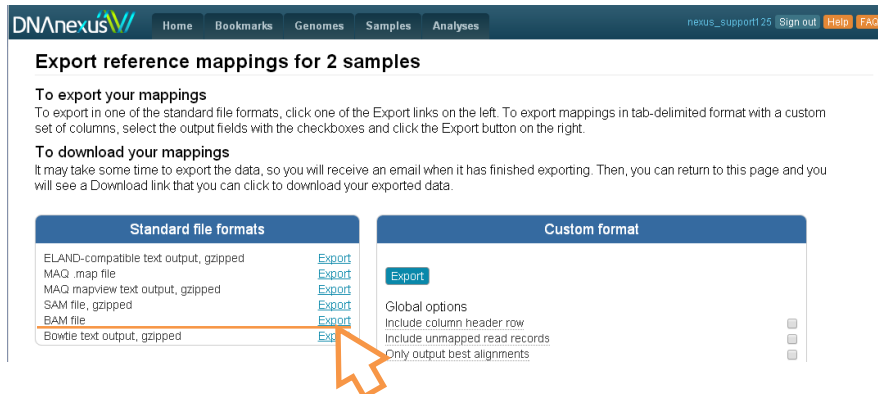


Fig 4-1. Screen to select a file format

When you click “Export” on the screen, “Exporting...” message will appear and the data will be prepared to be downloaded on DNAnexus server. It will take approx. couple of hours to be ready for download.

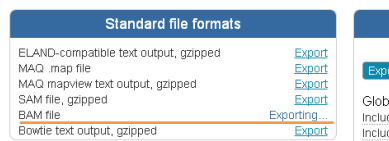


Fig 4-2. Screen to select file format (after clicking “Export”)

*When the data becomes ready for download, an e-mail titled “Sample mappings export ready” will be sent to your registered e-mail address from DNAnexus.

After the above operation, you can close your browser till data is ready for download.

5. Data Download

When the data is ready for download on the DNAnexus server, an announcement mail will be sent to you from DNAnexus. Please click the URL described in this e-mail, then the list of data available for download will be shown. Please click “[Download](#)”, select where to be saved and save the file(s).

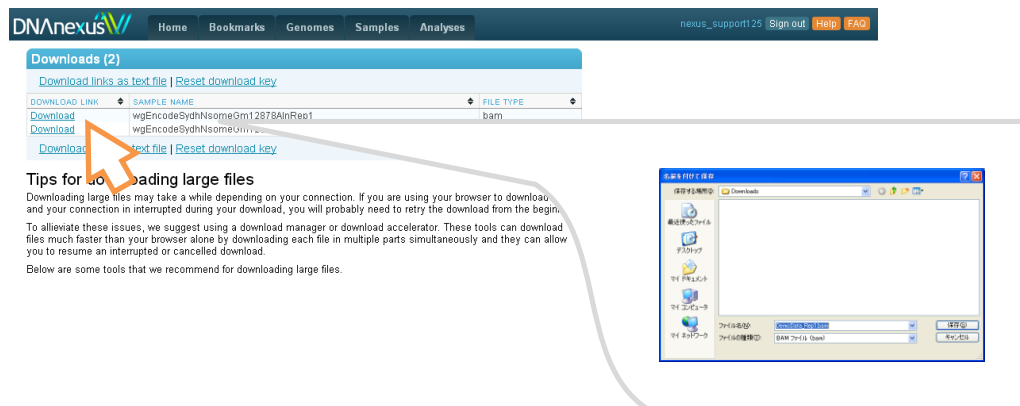


Fig 5. Download and save the data

*** In the above step 3, if you select “export unmapped reads” from the pull down menu of “more actions”, you can also download the reads which were not mapped to a reference genome.**
It is recommended to download such reads as appropriate.