



# ERCC Data Analysis Workshop

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## exRNA Data Analysis Tools in the Genboree Workbench

Organized and Hosted by the Data Management  
and Resource Repository (DMRR)

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Data Management and Resource Repository (DMRR) – ERCC  
Baylor College of Medicine  
Houston, TX, USA

**Thursday, 23<sup>rd</sup> April, 2015**  
**7:30 pm**



# Summary of Genboree Services

## DCC - Genboree Services for the ERCC ([www.genboree.org](http://www.genboree.org))

exRNA Data Analysis  
Tools - **Genboree**  
**Workbench**

[http://genboree.org/java-  
bin/workbench.jsp](http://genboree.org/java-bin/workbench.jsp)

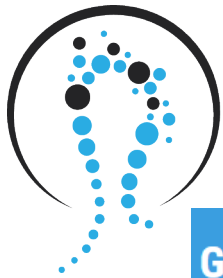
exRNA Document  
Sharing & Discussion  
Forums – **Genboree**  
**Commons**

[http://genboree.org/  
theCommons](http://genboree.org/<br/>theCommons)

exRNA Metadata  
Tracking System –  
**GenboreeKB**

[http://genboree.org/  
genboreeKB](http://genboree.org/<br/>genboreeKB)

Use the same user name and password for all of these Genboree Services



# Genboree Services at [genboree.org](http://genboree.org)

GENBOREE

WORKBENCH

COMMONS

KNOWLEDGEBASE

MORE ▾

LOGIN / REGISTER

Data Analysis Tools

## BRINGING DATA AND TOOLS TOGETHER

exRNA  
Metadata,  
exRNA  
Virtual  
Biorepository

New account  
in Genboree

Genboree is a web-based platform for multi-omic research and data analysis using the latest bioinformatics tools.

You can upload your data and perform various analyses using a “drag and drop” user interface. Keep it private or share with collaborators.

Bioinformatics tools and computational infrastructure are available for researchers who may not have programming expertise, or the time to pursue technical programming and/or scripting.





# Genboree Workbench

GENBOREE

Toolset Menus

System/Network ▾ Data ▾ Genome ▾ Transcriptome ▾ Cistrome ▾ Epigenome ▾ Metagenome ▾ Visualization ▾ **Help ▾**

Welcome to the Genboree Workbench! **Watch Intro Video**

**Data Selector**

Refresh Data Filter: Select a filter...

- Examples and Test Data
  - Databases
    - Atlas SNP2 - Example Data
    - Bowtie - Example Data
    - BWA hg19 - Example data
    - CreateHub hg19 - Example Data
    - FastQC - Example Data
    - Import Samples - Example Data
    - RSEQtools hg18 - Example Data
    - RSEQtools hg19 - Example Data
  - smallRNA-seq Pipeline - Example Data
    - Tracks
    - Lists & Selections
    - Sample Sets
    - Samples
    - Files
      - smallRNA\_4\_samples\_SRA.tar.gz
      - smallRNAseqPipeline
      - spikeInLibraries
      - SRR822433.fastq.gz
      - SRR822434.fastq.bz2
  - smallRNA-seq Pipeline Processing - Example Data

**Details**

Attribute	Value
-----------	-------

**Input Data**

↑ ↓ ✕ 📁

**Input Data Panel  
to drag & drop  
INPUT ENTITIES**

**Output Targets**

↑ ↓ ✕ 📁

**Output Targets  
Panel to drag &  
drop OUTPUT  
DESTINATIONS**



# Genboree Workbench – Getting Started

- Introduction to Genboree Workbench - Watch Video Tutorial

[https://docs.google.com/file/d/0Bz3\\_YiJBA\\_j3Tk1uOFllazdMbkk/](https://docs.google.com/file/d/0Bz3_YiJBA_j3Tk1uOFllazdMbkk/)

- Find Help within the Genboree Workbench

[http://genboree.org/theCommons/ezfaq/show/public-commons?faq\\_id=497](http://genboree.org/theCommons/ezfaq/show/public-commons?faq_id=497)

- Help » Getting Started
- Help » Tool Map
- Help » Tool Help Resources

Help: Tool Settings

Genboree

## Welcome to the Genboree Workbench!

 [Watch Intro Video](#)

- **Panels in the Genboree Workbench**
- **FAQs**
- **Detailed description of various panels**

### Panels in the Genboree Workbench

- **The Data Selector** tree on the left shows the data entities to which you have access. See [Help » Legend](#) for a description of various data entities appearing in this panel.
- Drag items to be used as tool *inputs* over to the **Input Data** area.
- Drag items to be used as *output destinations* for tool results over to the **Output Targets** area.
- Tools which can be run on your selections will be highlighted in **green**.
- Unsure about what kinds of items a particular tool needs in the **Input Data** and **Output Targets**?
  - Just click the tool button when it is *not highlighted* to see help information.
- The **Details** panel on the right contains information on any data entity, represented as an **Attribute-Value** Pair.

### FAQs

- 🔗 [How do I create a new Genboree !\[\]\(5d60fe8e38bc12bfb78103fc624e324c\_img.jpg\) Group?](#)
- 🔗 [How do I create a new Genboree !\[\]\(ffcc3930f6e82d7cb586237ada9d3332\_img.jpg\) Database?](#)
- 🔗 [How do I create a new Genboree !\[\]\(643201da8ca427135d452a5259d9e20e\_img.jpg\) Project?](#)
- 🔗 [How do I manage !\[\]\(4c625d6c32d16066b13eb52e34c8435a\_img.jpg\) Group permissions \(data access\)?](#)
- 🔗 [How do I run / complete tasks / perform an action?](#)
- 🔗 [How do I run / activate a tool?](#)
- 🔗 [How do I upload !\[\]\(25565195500fe89481742296ec0a66fe\_img.jpg\) files?](#)



## Tools in the Genboree Workbench

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### exRNA Data Analysis Tools available

**Long RNA-seq** - Transcriptome » Analyze RNA-Seq Data » Analyze RNA-Seq data by RSEQtools

**Small RNA-seq** - Transcriptome » Analyze Small RNA-Seq Data » smallRNA-seq Pipeline

### **Tutorials:**

<http://genboree.org/theCommons/projects/exrna-tools-may2014/wiki>



# exceRpt small RNA-seq tool in the Genboree Workbench

Help: Tool Settings

## Help: exceRpt small RNA-seq Pipeline for exRNA Profiling

Configure Tool

- Overview
- Inputs
- Settings
- Sources of small RNA Libraries
- Outputs
- Tutorials
- Addendum
- Workflow
- IMPORTANT NOTES

### Overview

The **exceRpt** small RNA-seq Pipeline is for the processing and analysis of RNA-seq data generated to profile small-exRNAs. The pipeline is highly modular, allowing the user to define the libraries containing small RNA sequences that are used during RNA-seq read-mapping, including an option to provide a library of spike-in sequences to allow absolute quantitation of small-RNA molecules. It also performs automatic detection and removal of 3' adapter sequences. The output data includes abundance estimates for each of the requested libraries, a variety of quality control metrics such as read-length distribution, summaries of reads mapped to each library, and detailed mapping information for each read mapped to each library.

Finally, after the pipeline finishes processing all submitted samples, a separate post-processing tool (processPipelineRuns) is run on all successful pipeline outputs. This tool generates useful summary plots and tables that can be used to compare and contrast different samples. You can find your post-processing results in the processedResults folder within your output folder.

The **workflow** and an example dataset to run the pipeline is provided in the **addendum** section below.

**Supported Reference Genomes: hg19, hg38, mm10**

**To create a Genboree database for reference genomes hg38 or mm10**  
Use Data » Databases » Create Database tool from the toolset menu.  
In the tool settings, select the **User Will Upload** option for **Reference Sequence** and provide appropriate values for the Species and Version text boxes as given below:

Your Genome of Interest	Species	Version
Human genome hg38	Homo sapiens	hg38





# exceRpt small RNA-seq tool in the Genboree Workbench

## Inputs

*Individual Input files* - One or more single-end sequencing read files in **FASTQ** or SRA formats. The input files can be compressed.

*Batches of Input file archives* - You can also upload one or more compressed archives of multiple FASTQ files, each FASTQ file can also be compressed inside these archives.

Please see **IMPORTANT NOTES** in the **addendum** section to prepare your input files.

**NOTE:** To upload input files to your database, use `Data » Files » Transfer File` from the toolset menu.

## Settings

### 3' Adapter Sequence

- If you know the 3' adapter sequence for this sample, it is highly recommended to provide that adapter sequence in the 3' `Adapter Sequence` text box.
- However, the pipeline has a step that finds the 3' adapter sequence in the input FASTQ file and removes it, so it is NOT required to provide an adapter-clipped input file. If the 3' adapter sequence is already clipped in your input FASTQ file, then check the box `Clipped Input FASTQ File` in the Tool Settings dialog while submitting the job.

**Custom Spike-in (oligo) sequences** You can upload a single file with all spike-in sequences in **FASTA** format.

### NOTE:

- Each FASTA sequence should have a description or define starting with ">" followed by a non-space character.
- Blank lines are not allowed in the middle of FASTA file.

### Sources of small RNA Libraries

- rRNAs from NCBI Sequence IDs **100861532** and **100169751**
- miRNAs from **miRBase** version 21
- tRNAs from **gtRNAdb**
- piRNAs from **RNAdb**
- Annotations from **Gencode** version 21 (hg38), version 18 (hg19), version M4 (mm10)

## Outputs

**NOTE:** To download any file from your database to your computer, click the file name in the `Data Selector` tree, then click on `Click to Download File` link from the `Details` panel.





# exRNA Tools in the Genboree Workbench

**GENBOREE** Baylor College of Medicine

**Toolset Menu**

System/Network | Data | Genome | **Transcriptome** | Cistrome | Epigenome | Metagenome | Visualization | **Help**

Welcome to the Genboree Workbench

**Data Selector**

Refresh | Data Filter: Select a filter...

- Examples and Test Data → **Group**
  - Databases
    - Atlas SNP2 - Example Data
    - Bowtie - Example Data
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    - FastQC - Example Data
    - Import Samples - Example Data
    - RSEQtools hg18 - Example Data
    - RSEQtools hg19 - Example Data
    - Database** → **smallRNA-seq Pipeline - Example Data**
      - Tracks
      - Lists & Selections
      - SampleSets
      - Samples
      - Files
        - Files** → smallRNA\_4\_samples\_SRA.tar.gz
        - smallRNaseqPipeline
        - spikeInLibraries
        - SRR822433.fastq.gz
        - SRR822434.fastq.bz2
      - smallRNA-seq Pipeline Processing - Example Data

**Toolset Menu (Transcriptome)**

- Analyze RNA-Seq Data
- Analyze Small RNA-Seq Data
  - exceRpt small RNA-seq Pipeline**
  - exceRpt small RNA-seq Post-processing
- Filter Reads
- Map Reads by Pash
- Profile Combined Coverage

Name	testHuman
Description	Testing bowtie Human hg19
Species	Homo sapiens

**Input Data Panel with your input FASTQ files**

- smallRNA\_4\_samples\_SRA.tar.gz
- SRR822433.fastq.gz
- SRR822434.fastq.bz2

**Output Targets Panel with your own database for results from analysis tools**

- testHuman



# exceRpt small RNA-seq Analysis Pipeline

Tool Settings

## exceRpt small RNA-seq Pipeline for exRNA Profiling

**Tool Overview**

**Input Files:**

<b>Database:</b>	<i>smallRNA-seq Pipeline - Example Data</i>	
<b>Group:</b>	<i>Examples and Test Data</i>	
<b>File:</b>	<i>smallRNA_4_samples_SRA.tar.gz</i>	
<b>Database:</b>	<i>smallRNA-seq Pipeline - Example Data</i>	
<b>Group:</b>	<i>Examples and Test Data</i>	
<b>File:</b>	<i>SRR822433.fastq.gz</i>	
<b>Database:</b>	<i>smallRNA-seq Pipeline - Example Data</i>	
<b>Group:</b>	<i>Examples and Test Data</i>	
<b>File:</b>	<i>SRR822434.fastq.bz2</i>	

**Output Location:**

<b>Database:</b>	<i>testHuman</i>	<b>Group:</b>	<i>genboreeuser11_group</i>
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**smallRNA-seq Pipeline Settings**

**Analysis Name**

**Genome Version**

- 3' Adapter Sequence Options**
- Oligo (Spike-in) Library Options**
- small RNA Libraries**
- Advanced Options - Mapping**



# exceRpt Analysis Pipeline – Tool settings

## 3' Adapter Sequence Options

Adapter Clipped   
Input FASTQ File

3' Adapter  
Sequence

## Oligo (Spike-in) Library Options

Select Library

## small RNA Libraries

Endogenous +   
Exogenous  
(miRNA)

Endogenous +   
Exogenous (miRNA  
+ genome)

Endogenous-only

tRNAs

piRNAs

Gencode   
Annotations

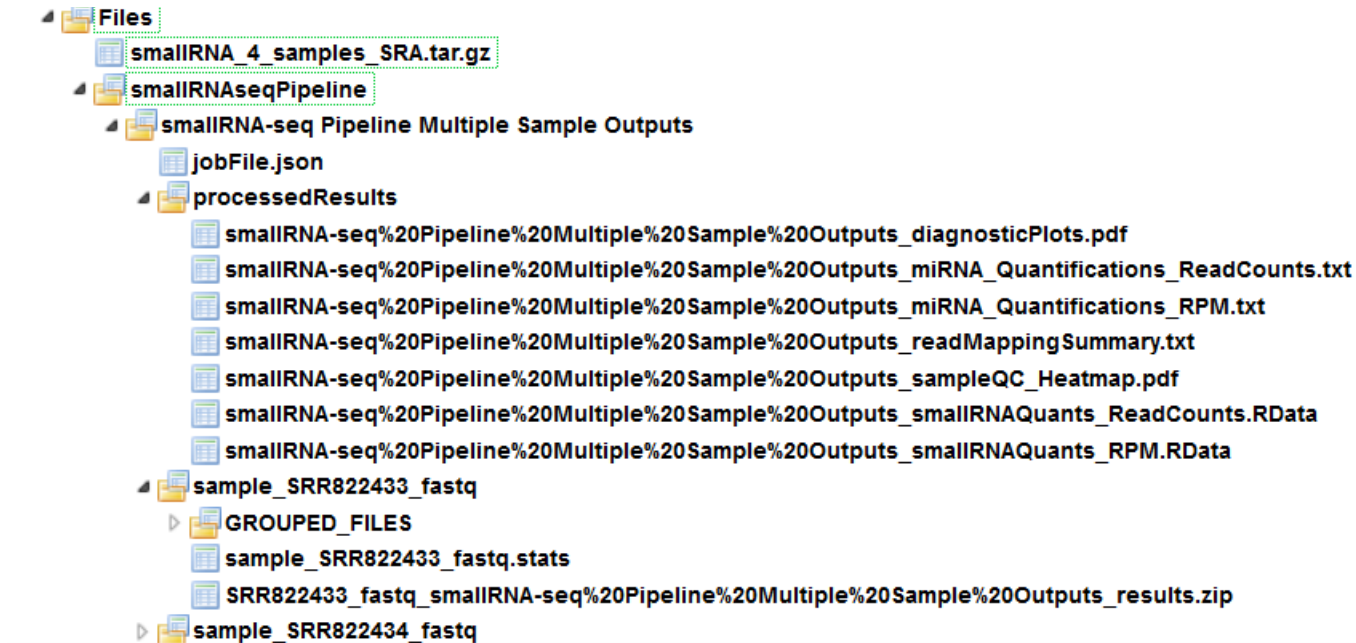
## Advanced Options - Mapping

Number of  
Mismatches in  
miRNA Mapping

Number of  
Mismatches in  
Mapping to Other  
Libraries



# exceRpt Analysis Pipeline – Results

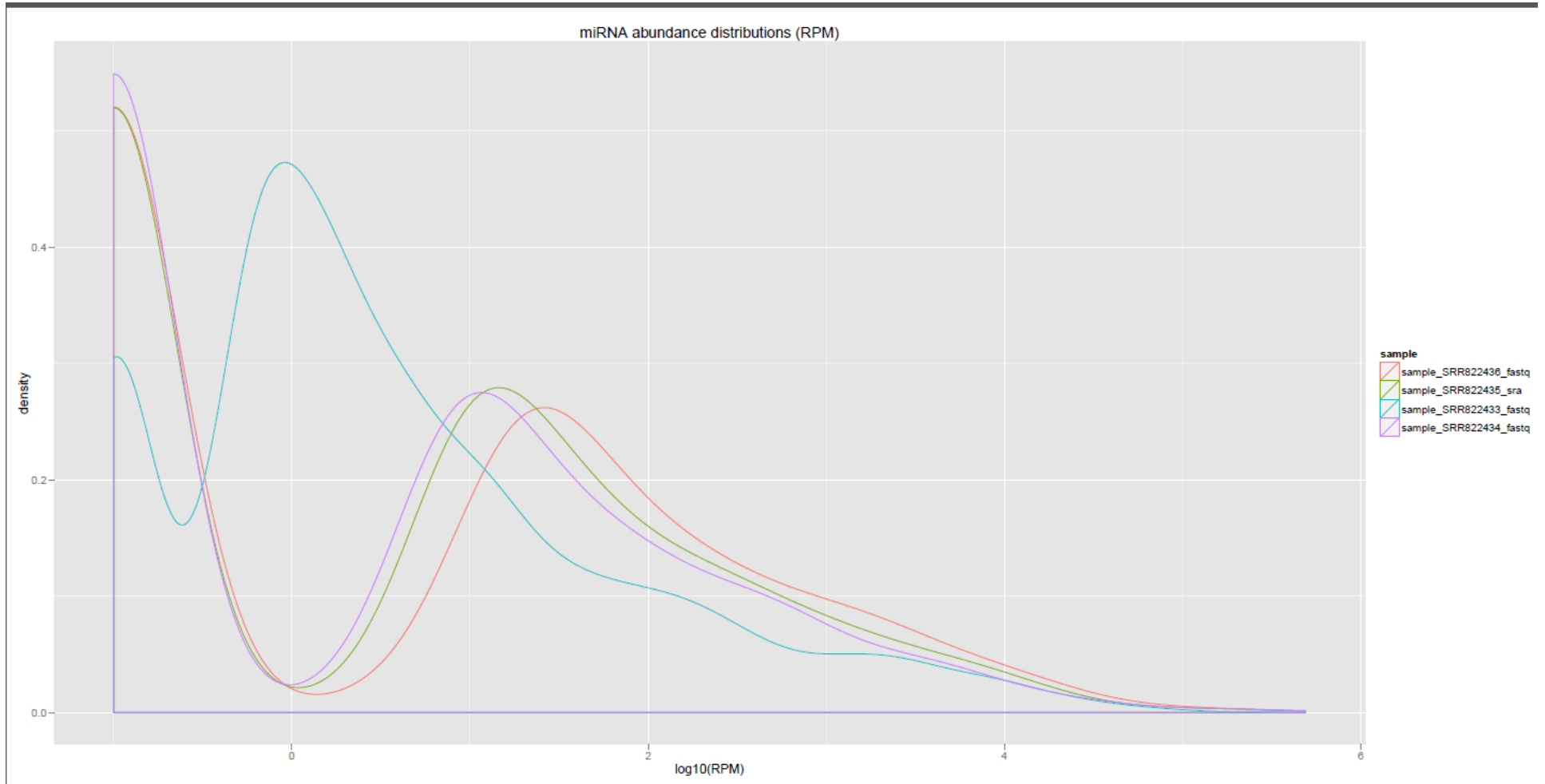


## OUTPUT FILES:

- Read length distribution, quantifications, read counts
- Endogenous Mapping results
- Exogenous Mapping results
- Files containing sequence reads following Adapter removal, rRNA/contaminant/repetitive sequence removal, Endogenous mapping & Exogenous mapping



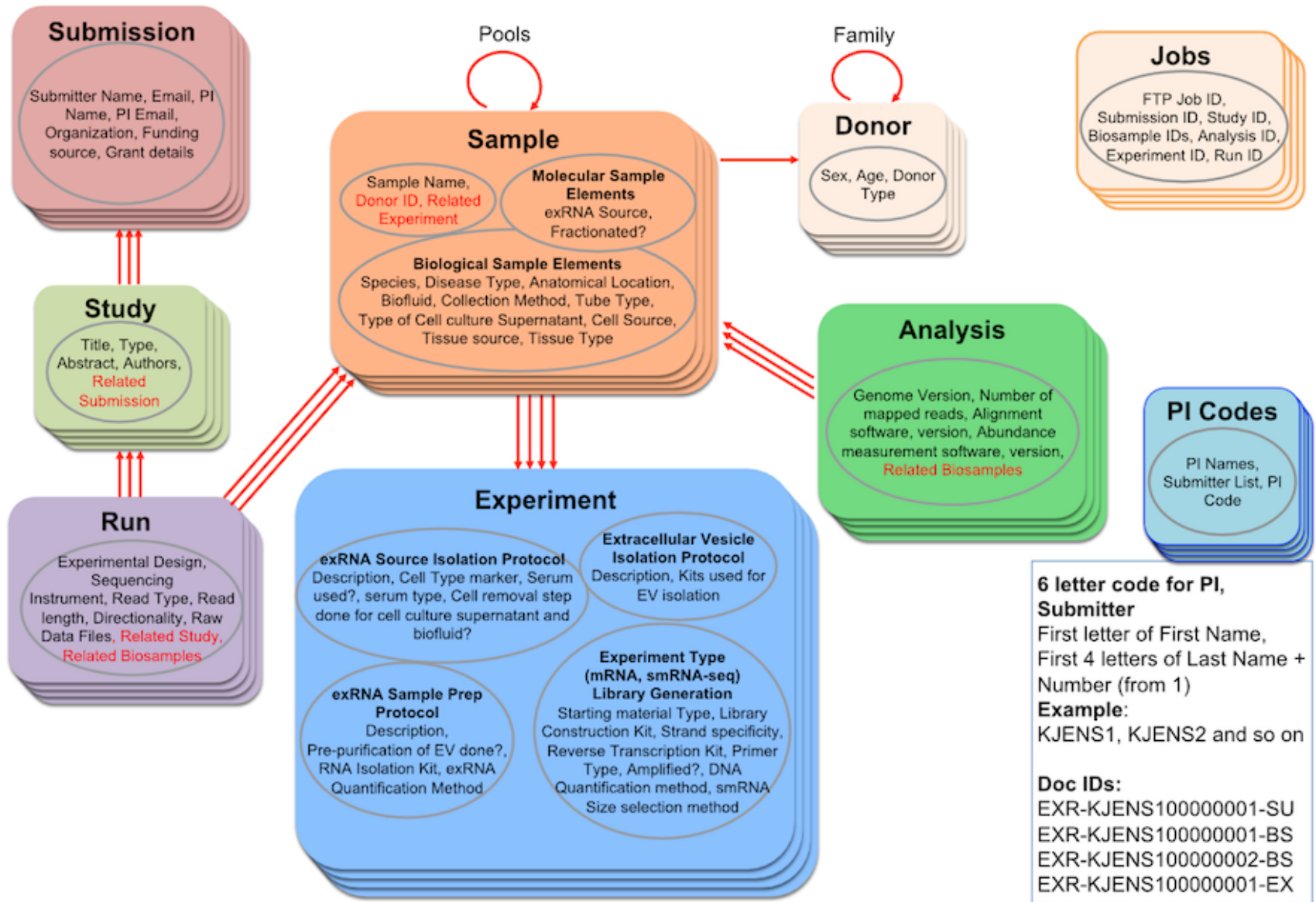
# exceRpt Analysis Pipeline – Plots





# exRNA Metadata Standards


## exRNA Metadata Standards





# exRNA Metadata Tracking - GenboreeKB

 Home

 [Genboree Home](#)

[Projects](#)

[Help](#)

[Sign in](#)

GenboreeKB

Search:

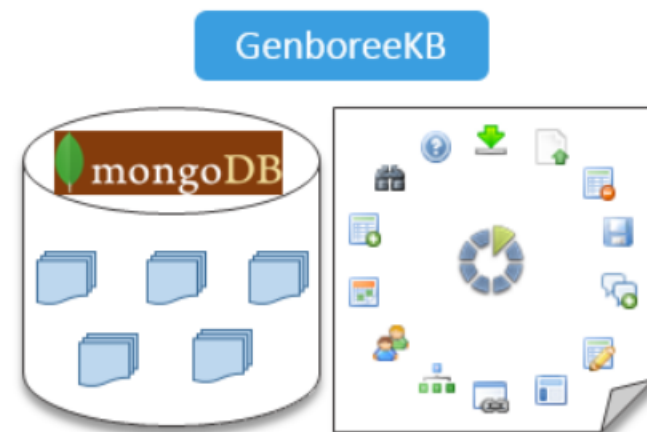
## Welcome to the GenboreeKB Redmine!

The **Genboree KnowledgeBase** (*GenboreeKB*) is an integrated software service developed at the [Bioinformatics Research Laboratory](#) (BRL) that allows storage of data in user defined collections in a document based Mongo database.

In addition to the usual Redmine functionality, this version has our custom developed "*Genboree KBs*" plugin, allowing Redmine Projects to display a [GenboreeKB](#) tab containing a GenboreeKB UI for visualization and management of the data stored in the Mongo database. This tab is enabled and configured by Project administrators, in cooperation with Genboree system administrators.

Click the buttons below to learn more about GenboreeKB or view the list of Redmine projects.

Note: This Redmine also has our "*Genboree Auth*" plugin, and in order to **Sign In** you will need a Genboree account at [genboree.org](#).



[Learn More About GenboreeKB](#)

[Redmine Project List](#)

For any questions or comments, please contact [genboree\\_admin@genboree.org](mailto:genboree_admin@genboree.org)





# exRNA Metadata Tracking - GenboreeKB

exRNA Metadata Standards Search:  exRNA Metadata Stan

Overview GenboreeKB Documents Wiki Forums Settings

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Collection: Biosamples

### Browse Biosamples

- As Dynamic tree
- Using a View

### Manage Biosamples

- Create Biosample
- Edit Biosample
- Delete Biosample
- Biosample History

### Manage Models

- View Biosample Model
- Biosample Model History
- Create Model

### Biosamples - Summary

#### Collection Stats

# Docs	421
# Doc creations	424
# Doc edits	128
# Doc version records	555
Last edited at	Mon, 13 Apr 2015 04:35:04 -00...
Last edited by	william_thistle
Avg doc storage size	1.7 KB
Total storage size	895.0 KB
# Doc deletions	3

#### # Docs Over Time (cumulative)

Month	# Docs
APR	421

#### Activity Over Time

Month	# Actions
APR	555

#### Doc Creations Over Time

Month	# Creations
APR	424

#### Doc Edits Over Time

Month	# Edits
APR	128

#### Doc Deletions Over Time

Month	# Deletions
APR	3



# exRNA Metadata Tracking - Biosamples

Collection: Biosamples

**Browse Biosamples**

- As Dynamic tree
- Using a View

**Manage Biosamples**

- Create Biosample
- Edit Biosample
- Delete Biosample
- Biosample History

**Manage Models**

- View Biosample Model
- Biosample Model History
- Create Model

**Query Results Grid (421 matches found)**

Biosample	Name	Biofluid Name	Disease Type	Anatomical Location	exRNA Source
EXR-KJENS10SER1032-...	1032 Healthy Control SER	Serum	Healthy Control	Entire brain	Total RNA
EXR-KJENS10CSF1036-...	1036 Alzheimer's disease C...	Cerebrospinal fl...	Alzheimer's disease	Entire brain	Total RNA
EXR-KJENS10SER1036-...	1036 Alzheimer's disease S...	Serum	Alzheimer's disease	Entire brain	Total RNA
EXR-KJENS10CSF1037-...	1037 Parkinson's Disease ...	Cerebrospinal fl...	Parkinson's Disease	Entire brain	Total RNA
EXR-KJENS10SER1037-...	1037 Parkinson's Disease S...	Serum	Parkinson's Disease	Entire brain	Total RNA
EXR-KJENS10CSF1039-...	1039 Healthy Control CSF	Cerebrospinal fl...	Healthy Control	Entire brain	Total RNA
EXR-KJENS10SER1039-...	1039 Healthy Control SER	Serum	Healthy Control	Entire brain	Total RNA
EXR-RCOFF1KCVSLE01-...	2572_KCV_1_25_VK	Plasma	Healthy Control	Entire colon	HDL
EXR-RCOFF1KCVSLE02-...	2572_KCV_1_26_CC	Plasma	Healthy Control	Entire colon	HDL
EXR-RCOFF1KCVSLE03-...	2572_KCV_1_27_AE	Plasma	Healthy Control	Entire colon	HDL
EXR-RCOFF1KCVSLE04-...	2572_KCV_1_28_CHL001	Plasma	systemic lupus erythem...	Entire colon	HDL
EXR-RCOFF1KCVSLE05-...	2572_KCV_1_29_CHL002	Plasma	systemic lupus erythem...	Entire colon	HDL
EXR-RCOFF1KCVSLE06-...	2572_KCV_1_30_CHL003	Plasma	systemic lupus erythem...	Entire colon	HDL
EXR-DGALA193163PMC...	93163P	Plasma	ulcerative colitis	Plasma cell	Plasma
EXR-DGALA193164PMC...	93164P	Plasma	ulcerative colitis	Plasma cell	Plasma
EXR-DGALA193166PFC...	93166P	Plasma	ulcerative colitis	Plasma cell	Plasma
EXR-KJENS10SER9431-...	9431 Parkinson's Disease S...	Serum	Parkinson's Disease	Entire brain	Total RNA
EXR-KJENS10SER9536-...	9536 Healthy Control SER	Serum	Healthy Control	Entire brain	Total RNA
EXR-KJENS10SER9539-...	9539 Healthy Control SER	Serum	Healthy Control	Entire brain	Total RNA
EXR-KJENS10CSF9540-...	9540 Healthy Control CSF	Cerebrospinal fl...	Healthy Control	Entire brain	Total RNA
EXR-KJENS10SER9540-...	9540 Healthy Control SER	Serum	Healthy Control	Entire brain	Total RNA
EXR-KJENS10SER9604-...	9604 Alzheimer's disease S...	Serum	Alzheimer's disease	Entire brain	Total RNA
EXR-KJENS10SER9609-...	9609 Alzheimer's disease S...	Serum	Alzheimer's disease	Entire brain	Total RNA
EXR-KJENS10CSF9611-...	9611 Alzheimer's disease C...	Cerebrospinal fl...	Alzheimer's disease	Entire brain	Total RNA
EXR-KJENS10SER9611-...	9611 Alzheimer's disease S...	Serum	Alzheimer's disease	Entire brain	Total RNA
EXR-KJENS10CSF9617-...	9617 Alzheimer's disease C...	Cerebrospinal fl...	Alzheimer's disease	Entire brain	Total RNA



# exRNA Metadata Tracking - Analysis

Edit Mode: OFF      Version: Current

Type document name...

Name	Value
Analysis	EXR-RCOFF1KCVSLE00-AN
Status	Add
Data Analysis Level	
Type	Reference Alignment
Level 1 Reference Alignment	
Alignment Method	exceRpt smallRNA-seq Pipeline
Genome Version	hg19
Biosamples	6
Biosample ID	EXR-RCOFF1KCVSLE06-BS
DocURL	<a href="coll/Biosamples/doc/EXR-RCOFF1KCVSLE06-BS">coll/Biosamples/doc/EXR-RCOFF1KCVSLE06-BS</a>
Read Counts at Various Stages	
Input Reads	17380921
After Clipping	14719915
Failed Quality Filter	176570
Failed Homopolymer Filter	11442
Calibrator	0
UniVec Contaminants	872375
rRNAs	1041103
Reads Used for Alignment	12618425
Genome	4780489
miRNAs Sense	12920
miRNAs Antisense	533
piRNAs Sense	5558
piRNAs Antisense	4357
tRNAs Sense	637
tRNAs Antisense	0
Gencode Annotations Sense	143785
Gencode Annotations Antisense	129303



# exRNA Atlas – Link from [exrna.org](http://exrna.org)



**exRNA**  
RESEARCH PORTAL

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## Resources



### Protocols

The consortium is working internally to compare Standard Operating Procedures (SOPs), i.e. protocols used by different labs for extracellular vesicle preparation and RNA analysis. Vetted results are here.



### Data

As consortium members begin to publish, datasets associated with their publications will be posted here. Please contact us if you have an extracellular RNA or EV dataset you would like to make available to the community.



**exRNA**  
RESEARCH PORTAL

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### Data

[exRNA Atlas](#)

The current version of the exRNA Atlas can only be accessed by ERCC members. If you are unable to login, please contact DCC ([sailakss@bcm.edu](mailto:sailakss@bcm.edu)) for assistance. A public version of the exRNA Atlas will be released very soon.



# exRNA Atlas – BETA version



Grid for exRNA Profiling Studies

Biofluids vs Experiment Types

Biofluids vs Diseases

Buttons to view 3 types of exRNA grids

**Click the buttons in the panel above to view the different types of exRNA Atlas Grids.**

The Extracellular RNA (exRNA) Atlas<sup>BETA</sup> includes reference exRNA Profiles and the results of their integrative and comparative analyses. The current release of the Atlas displays preliminary data generated by various Extracellular RNA Communications Consortium (ERCC) funded groups and analyzed using the exceRpt small RNA-seq pipeline. There are 3 grids available in this version of the exRNA Atlas, as described below.

#### Grid for exRNA Profiling Studies

This grid displays a summary of various "studies" deposited to the Data Coordination Center (DCC), along with details of submitters, their organization, their grant details and links to view RNA Profiles of biosamples submitted as part of the study. The RNA Profile grid summarizes the counts of reads mapped to various RNA libraries against which raw reads were mapped by the exceRpt small RNA-seq data analysis pipeline. This grid view also shows histograms of the read counts to enable quicker visualization of reads mapped to different RNA libraries.

#### Biofluids vs Experiment Types

This grid shows the number of biosamples from a biofluid-experiment type combination. Upon clicking each cell, users can view the list of biosamples, some metadata about each biosample and a histogram view of reads from each biosample mapped to various small RNA libraries.

#### Biofluids vs Diseases

This grid shows the number of biosamples obtained and profiled from a biofluid-disease combination. Upon clicking each cell, users can view the list of biosamples, some metadata about each biosample and a histogram view of reads from each biosample mapped to various small RNA libraries.

Description about exRNA grids

#### Links to various ERCC resources

[exRNA Portal](#)  
[Genboree Workbench](#)  
[ERCC Data and Metadata Standards](#)  
[exRNA Data Analysis Tools](#)  
[NIH Common Fund - ERCC](#)

ERCC resources – Useful links



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One Baylor Plaza, MS:BCM225 Suite 400D, Houston, TX, 77030

Funding Agency:



National Institutes of Health  
Office of Strategic Coordination - The Common Fund

[Questions or comments?](#)



# exRNA Atlas – Grid for Profiling Studies

Grid for exRNA Profiling Studies

Biofluids vs Experiment Types


Biofluids vs Diseases

**Grid for exRNA Profiling Studies**

Analysis Accession ID	Study Title	Experiment Type	PI Name	Funding Source
<a href="#">EXR-AKRIC1AKGBMexo-AN</a>	AK-exosome RNA	Small RNA-seq	Anna Krichevsky	NIH Common Fund
<a href="#">EXR-DGALA1GUTPLASM-AN</a>	The Complex Exogenous RNA Spectra in Huma...	Small RNA-seq	David Galas	NIH Common Fund
<a href="#">EXR-KJENS1ADPD0000-AN</a>	Profiles of Extracellular miRNA in Cerebrospinal...	Small RNA-seq	Kendall Jensen	Michael J Fox Foundation f...
<a href="#">EXR-LLAUR1M4TD4MUN-AN</a>	Sept2014_ExRNA	Small RNA-seq	Louise Laurent	NIH Common Fund
<a href="#">EXR-RCOFF1CRCDL00-AN</a>	RNAseq analysis of colorectal cancer cells: KRA...	Small RNA-seq	Robert Coffey	Common Fund/NIH: U19 ...
<a href="#">EXR-RCOFF1KCVSLE</a>				U19 ...






**RNA PROFILE GRID**

Property	Value
<b>Analysis</b>	<a href="#">EXR-KJENS1ADPD0000-AN</a>
<b>Genome Version</b>	hg19
<b>Type</b>	Reference Alignment
<b>Alignment Method</b>	exceRpt smallRNA-seq Pipeline
<b>Grid View</b>	

Click to view grid view of read counts mapped to various RNA libraries



# exRNA Atlas – RNA Profiling Grid View

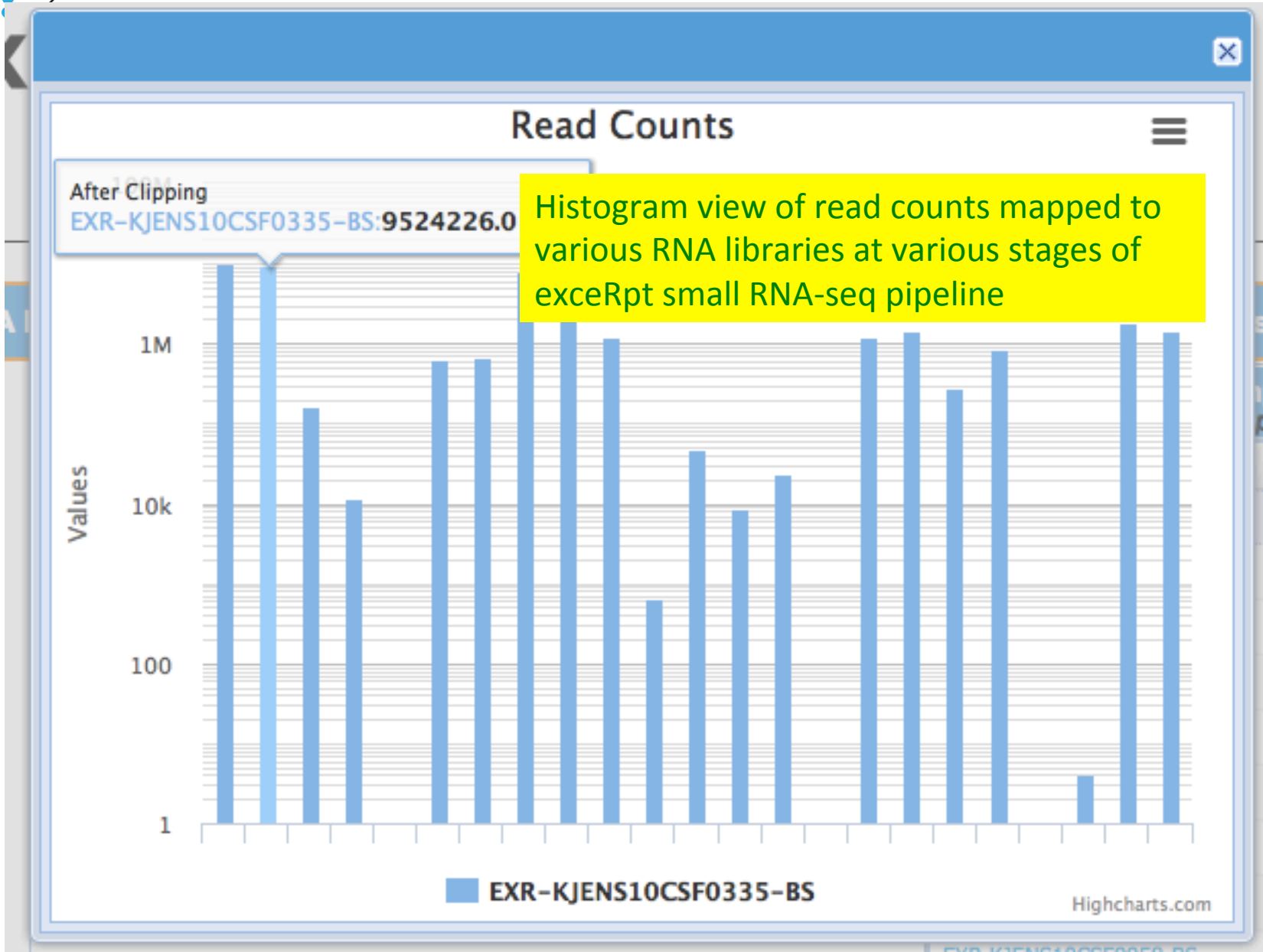
Grid with RNA Profile of Biosamples											
<b>Analysis:</b> <b>EXR-KJENS1ADPD0000-AN</b> <b>Genome Version: hg19</b> <small>Type: Reference Alignment</small>	Total Mapped Reads	Circular RNAs Antisense	Circular RNAs Sense	tRNAs Sense	After Clipping	Reads Used for Exogenous Alignments	Failed Homopolymer Filter	Exogenous miRNAs	tRNAs Antisense	Input Reads	Repetitive Elements Sense
EXR-KJENS10SER0757-BS  <small>BiosampleFluids: Serum</small> <small>ExperimentType: smRNA-Seq</small>	2214341	0.0	0.0	0.0	21.06	0.41	0.11	0.29	0.0	23.39	0.06
EXR-KJENS10SER9925-BS  <small>BiosampleFluids: Serum</small> <small>ExperimentType: smRNA-Seq</small>	9743266	0.0	0.0	0.0	21.89	4.2	0.03	3.37	0.0	23.5	0.63
EXR-KJENS10CSF0335-BS  <small>BiosampleFluids: Cerebrospinal fluid</small> <small>ExperimentType: smRNA-Seq</small>	10220887	0.0	0.0	0.05	21.39	0.74	0.02	0.03	0.0	22.91	0.08
EXR-KJENS10SER9604-BS  <small>BiosampleFluids: Serum</small> <small>ExperimentType: smRNA-Seq</small>	96237	0.0	0.0	0.0	22.14	1.77	0.01	1.47	0.0	25.21	0.35
EXR-KJENS10CSF0702-BS  <small>BiosampleFluids: Cerebrospinal fluid</small> <small>ExperimentType: smRNA-Seq</small>	11471844	0.0	0.0	0.01	22.14	1.77	0.01	1.47	0.0	25.21	0.35

Click to view histogram view of read counts mapped to various RNA libraries





# exRNA Atlas – RNA Profiling Histogram View





# exRNA Atlas – Biofluids vs Experiment Types

Grid for exRNA Profiling Studies

Biofluids vs Experiment Types

Biofluids vs Diseases

BioFluids vs Experiment Types	
BioFluid:	Experiment Type:
PLASMA	smRNA-Seq 15
SERUM	212
CEREBROSPINAL FLUID	181

Metadata about Biosamples:  
*smRNA-Seq » Cerebrospinal fluid*

Biosample	Histogram View
<a href="#">EXR-KJENS10CSF0335-BS</a>	
<a href="#">EXR-KJENS10CSF0702-BS</a>	
<a href="#">EXR-KJENS10CSF9927-BS</a>	
<a href="#">EXR-KJENS10CSF9829-BS</a>	
<a href="#">EXR-KJENS10CSF9963-BS</a>	
<a href="#">EXR-KJENS10CSF0915-BS</a>	
<a href="#">EXR-KJENS10CSF0129-BS</a>	
<a href="#">EXR-KJENS10CSF9834-BS</a>	
<a href="#">EXR-KJENS10CSF9958-BS</a>	
<a href="#">EXR-KJENS10CSF0422-BS</a>	

Click each cell to view names of Biosamples from the selected biofluid-experiment type combination and links to view each biosample in GenboreeKB



# exRNA Atlas – Biofluids vs Diseases

BioFluids vs Diseases					
BioFluid:	Disease: Alzheimer's disease	Chronic Maternal Hypertension with Superimposed Preeclampsia	Fetus Small for Gestational Age	HELLP syndrome	Health Control
PLASMA					6
SERUM	52	2	4	1	62
CEREBROSPINAL FLUID	62				62

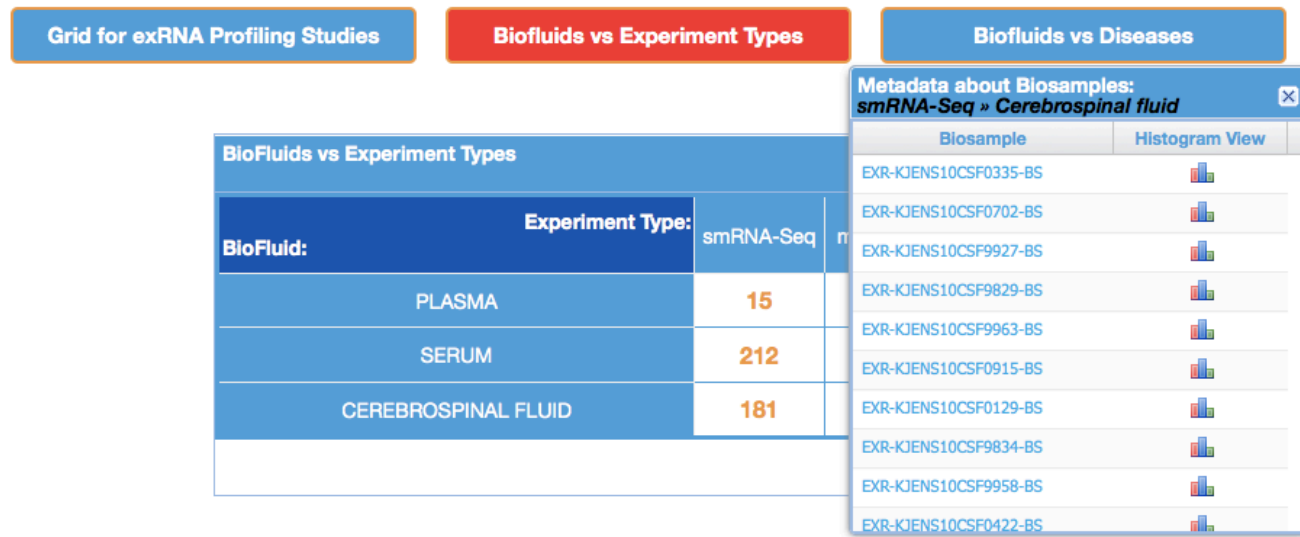
  

Metadata about Biosamples: Alzheimer's disease » Cerebrospinal fluid	
Biosample	Histogram View
EXR-KJENS10CSF0702-BS	
EXR-KJENS10CSF0422-BS	
EXR-KJENS10CSF0757-BS	
EXR-KJENS10CSF0652-BS	
EXR-KJENS10CSF9617-BS	
EXR-KJENS10CSF0118-BS	
EXR-KJENS10CSF9910-BS	
EXR-KJENS10CSF0829-BS	
EXR-KJENS10CSF0764-BS	
EXR-KJENS10CSF9960-BS	
EXR-KJENS10CSF9928-BS	

Click each cell to view names of Biosamples from the selected biofluid-disease combination and links to view each biosample in GenboreeKB.



# exRNA Atlas – Features Coming Soon



- Filter samples based on metadata
- Select samples of interest -
  - Analyze using downstream analysis tools in the Genboree Workbench
  - Download processed results
- Generate other types of grids using metadata for sub-selecting samples of interest



# Useful Links

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**Genboree  
Workbench**

- <http://genboree.org/java-bin/workbench.jsp>

**ERCC Data  
Coordination  
Center Wiki**

- <http://genboree.org/theCommons/projects/exrna-mads/wiki>

**exRNA Data  
Analysis Tools  
Wiki**

- <http://genboree.org/theCommons/projects/exrna-tools-may2014/wiki>

**GenboreeKB**

- <http://genboree.org/genboreeKB>

**exRNA Atlas**

- <http://genboree.org/java-bin/exRNAAtlas.jsp>

**exRNA Portal  
Resources**

- <http://exrna.org/resources/>



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# Questions?