



ERCC Data Analysis Workshop

**Use Case 1: Exogenous exRNA in plasma
of patients with Colorectal Cancer
and Ulcerative Colitis**

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

**Wednesday, Nov 5th, 2014
6:00 – 8:30 pm**

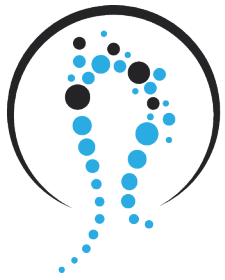
Data kindly provided by David Galas, Pacific Northwest Diabetes Research Institute
(PNDRI)



Use Case 1: Exogenous exRNA

Background: Comparison of human plasma small RNA profiles of patients with colorectal cancer to those with ulcerative colitis, indicated that a large fraction of reads were not mapping to the human genome. This raised the question as to what was the origin of those small RNAs?

Results: Mapping suggested that a significant fraction of small RNA reads were derived from bacterial, fungal, and plant sources.



Use Case 1: Exogenous exRNA

We will use the Genboree Workbench to check what fraction of reads do not map to the human genome.

We will also use the output of the small RNA-seq Pipeline to answer the following questions:

Do all plasma small RNAs map to the human genome (slide 17)?

Which miRNAs are normally present in human plasma (slide 18)?

What are the sources of small RNAs found in human plasma that do not map to the human genome (exercise)?



Use Case 1: Exogenous exRNA

Biological Samples to Be Analyzed

Patient Number	Sample	Input File Name	Biosample Metadata # in KB
#1	Plasma (Colorectal)	SM1_crc1_sequence.fastq.gz	EXR-022273PF-BS
#2	Plasma (Colorectal)	SM2_crc2_sequence.fastq.gz	EXR-022163PF-BS
#3	Plasma (Colorectal)	SM3_crc3_sequence.fastq.gz	EXR-022299PM-BS
#4	Plasma (Ulcerative)	SM6_uc1_sequence.fastq.gz	EXR-93163PMC-BS
#5	Plasma (Ulcerative)	SM7_uc2_sequence.fastq.gz	EXR-93164PMC-BS
#6	Plasma (Ulcerative)	SM8_uc3_sequence.fastq.gz	EXR-93166PFC-BS
#7	Plasma (Control)	SM11_norm1_sequence.fastq.gz	EXR-D3340PMN-BS
#8	Plasma (Control)	SM12_norm2_sequence.fastq.gz	EXR-D3176PFN-BS
#9	Plasma (Control)	SM3_norm3 _sequence.fastq.gz	EXR-D3142PFN-BS

Input files are located in the Data Selector in the following Group → Database → Folder:

Group: exRNA Metadata Standards

Database: Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis

Folder: 1. Inputs (FASTQ)



Genboree Workbench – Getting Started

- Getting Started
 - http://genboree.org/theCommons/projects/public-commons/wiki/Getting_started
- Genboree Workbench Icons Explanation
 - http://genboree.org/theCommons/projects/public-commons/wiki/genboree_icons
- FAQs
 - <http://genboree.org/theCommons/ezfaq/index/public-commons>



Genboree Workbench – Create Database

- Create a Genboree Workbench Database
 - http://genboree.org/theCommons/ezfaq/show/public-commons?faq_id=491

- hg19

Note:

- You will be using this newly created Genboree Workbench Database to hold the output of tool runs. This will be the database that we're referring to when we say 'your database'.

System/Network

Welcome to

Data Selector

Refresh

genboree.org

ARJ

Epigenome

Epigenome

Epigenomic

Examples ar

exRNA Meta

exRNA dem

First_Time_

Genboree Vi

New_Genb

ROI Reposit

Tool Settings

Create Database

Tool Overview

Target Group:

Group: First_Time_Genboree_User_group

Settings

Reference Sequence

Template: Human (Hg16)

Template: Human (Hg17)

Template: Human (Hg18)

Template: Human (hg19)

Template: Human 3/12 (Hg15)

Database Name: new_database_hg19

Description:

Species: Homo sapiens

Version: hg19

Submit Cancel



Running the Pipeline: **Select Input Files**

Welcome to the Genboree Workbench! [Watch Intro Video](#)

Data Selector

Refresh Data Filter: Select a filter...

- genboree.org
 - ARJ
 - Epigenome Informatics Demo Output Data
 - Epigenome ToolSet Demo Input Data
 - Epigenomics Roadmap Repository
 - Examples and Test Data
 - exRNA Metadata Standards
 - Databases
 - KB:exRNA Metadata
 - Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis
 - Tracks
 - Lists & Selections
 - SampleSets
 - Samples
 - Files
 - 1. Inputs (FASTQ)
 - SM11_norm1_sequence.fastq.gz
 - SM12_norm2_sequence.fastq.gz
 - SM13_norm3_sequence.fastq.gz
 - SM1_crc1_sequence.fastq.gz
 - SM2_crc2_sequence.fastq.gz

Details

Attribute	Value
Download	Click to Download File
Group	exRNA Metadata Standards
Database	Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis
Description	Plasma (Control)

Input Data

SM11_norm1_sequence.fastq.gz

Output Targets

Note:

You will input (1) fastq file per tool run. So, for each fastq file you wish to analyze, you will need to repeat the process shown on the next 3 slides.



Running the Pipeline: Select Output Database

Welcome to the Genboree Workbench! [Watch Intro Video](#)

Data Selector

Refresh Data Filter: Select a filter...

- genboree.org
 - ARJ
 - Epigenome Informatics Demo Output Data
 - Epigenome ToolSet Demo Input Data
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 - Examples and Test Data
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 - Samples
 - Files
 - 1. Inputs (FASTQ)
 - SM11_norm1_sequence.fastq.gz
 - SM12_norm2_sequence.fastq.gz
 - SM13_norm3_sequence.fastq.gz
 - SM1_crc1_sequence.fastq.gz
 - SM2_crc2_sequence.fastq.gz

Details

Attribute	Value
Group	exRNA Metadata Standards
Role	subscriber
Name	Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis
Description	Use Case 1

Input Data

SM11_norm1_sequence.fastq.gz

Output Targets

Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis

Note:
Drag Your newly created database to Output Targets.



Running the Pipeline: **Select Tool**

System/Network Data Genome Transcriptome Cistrome Epigenome Metagenome Visualization Help

Welcome to the Genboree V

Analyze RNA-Seq Data
Analyze Small RNA-Seq Data

smallRNA-seq Pipeline
smallRNA-seq Pipeline Processing
Filter Reads
Map Reads by Pash
Profile Combined Coverage

Data Selector

Refresh Data Filter: Select a filter...

genboree.org

- ARJ
- Epigenome Informatics Demo Output Data
- Epigenome ToolSet Demo Input Data
- Epigenomics Roadmap Repository
- Examples and Test Data
- exRNA Metadata Standards
 - Databases
 - KB:exRNA Metadata
 - Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis
 - Tracks
 - Lists & Selections
 - SampleSets
 - Samples
 - Files
 - 1. Inputs (FASTQ)
 - SM11_norm1_sequence.fastq.gz
 - SM12_norm2_sequence.fastq.gz
 - SM13_norm3_sequence.fastq.gz
 - SM1_crc1_sequence.fastq.gz
 - SM2_crc2_sequence.fastq.gz

Details

Attribute	
Group	
Role	
Name	Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis
Description	Use Case 1

Input Data

SM11_norm1_sequence.fastq.gz

Output Targets

Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis



Running the Pipeline: **Submit Job**

System/Network Data Genome Transcriptome Cistrome Epigenome Metagenome Visualization Help

Welcome

Data Select

Refresh

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Epi

Epi

Ex

exF

Tool Settings

smallRNA-seq Pipeline Settings

Analysis Name smallRNA-seq Pipeline-2014-11-3-16:31:45

Genome Version hg19

3' Adapter Sequence Options

Adapter Clipped ☐

Input FASTQ file

3' Adapter Sequence

small RNA Libraries

Human tRNAs ☒

Human snoRNAs ☒

Human piRNAs ☒

Human Rfam families of RNAs ☒

miRNAs in Plants and Viruses ☒

Submit **Cancel**



Post-processing: Select Input Files

Welcome to the Genboree Workbench! [Watch Intro Video](#)

Data Selector

Refresh Data Filter: Select a filter...

- genboree.org
 - ARJ
 - Epigenome Informatics Demo Output Data
 - Epigenome ToolSet Demo Input Data
 - Epigenomics Roadmap Repository
 - Examples and Test Data
 - exRNA Metadata Standards
 - Databases
 - KB:exRNA Metadata
 - Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis
 - Tracks
 - Lists & Selections
 - SampleSets
 - Samples
 - Files
 - 1. Inputs (FASTQ)
 - 2. smallRNA-seq Pipeline Results (Raw)
 - SM11_norm1_sequence_results.zip
 - SM12_norm2_sequence_results.zip
 - SM13_norm3_sequence_results.zip
 - SM1_crc1_sequence_results.zip

Details

Attribute	Value
Download	Click to Download File
Group	exRNA Metadata Standards
Database	Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis
Description	Results from

Input Data

SM11_norm1_sequence_results.zip
SM12_norm2_sequence_results.zip
SM13_norm3_sequence_results.zip
SM1_crc1_sequence_results.zip
SM8_uc3_sequence_results.zip

Output Targets

Note:

These zip files will be in *your database*, in the folder that you named: Files/smallRNAseqPipeline/[**your analysis name**]/



Post-processing: Select Output Database

Welcome to the Genboree Workbench! [Watch Intro Video](#)

Data Selector

Refresh Data Filter: Select a filter...

- genboree.org
 - ARJ
 - Epigenome Informatics Demo Output Data
 - Epigenome ToolSet Demo Input Data
 - Epigenomics Roadmap Repository
 - Examples and Test Data
 - exRNA Metadata Standards
 - Databases
 - KB:exRNA Metadata
 - Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis**
 - Tracks
 - Lists & Selections
 - SampleSets
 - Samples
 - Files
 - 1. Inputs (FASTQ)
 - 2. smallRNA-seq Pipeline Results (Raw)
 - SM11_norm1_sequence_results.zip
 - SM12_norm2_sequence_results.zip
 - SM13_norm3_sequence_results.zip
 - SM1_crc1_sequence_results.zip

Details

Attribute	Value
Group	exRNA Metadata Standards
Role	author
Name	Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis
Description	Use Case 1

Input Data

- SM11_norm1_sequence_results.zip
- SM12_norm2_sequence_results.zip
- SM13_norm3_sequence_results.zip
- SM1_crc1_sequence_results.zip
- SM8_uc3_sequence_results.zip

Output Targets

- Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis

Note:
Drag Your newly created database to Output Targets.



Post-processing: Select Tool

System/Network Data Genome Transcriptome Cistrome Epigenome Metagenome Visualization Help

Welcome to the Genboree V

Analyze RNA-Seq Data
Analyze Small RNA-Seq Data

smallRNA-seq Pipeline
smallRNA-seq Pipeline Processing
Filter Reads
Map Reads by Pash
Profile Combined Coverage

Data Selector

Refresh Data Filter: Select a filter...

genboree.org

- ARJ
- Epigenome Informatics Demo Output Data
- Epigenome ToolSet Demo Input Data
- Epigenomics Roadmap Repository
- Examples and Test Data
- exRNA Metadata Standards
 - Databases
 - KB:exRNA Metadata
 - Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis
 - Tracks
 - Lists & Selections
 - SampleSets
 - Samples
 - Files
 - 1. Inputs (FASTQ)
 - 2. smallRNA-seq Pipeline Results (Raw)
 - SM11_norm1_sequence_results.zip
 - SM12_norm2_sequence_results.zip
 - SM13_norm3_sequence_results.zip
 - SM1_crc1_sequence_results.zip

Details

Attribute Group Role Name Description

Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis

Use Case 1

Input Data

SM11_norm1_sequence_results.zip
SM12_norm2_sequence_results.zip
SM13_norm3_sequence_results.zip
SM1_crc1_sequence_results.zip
SM8_uc3_sequence_results.zip

Output Targets

Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis



Post-processing: Submit Job

System/Network

Welcome to

Data Selector

Refresh

genboree.org

- ARJ
- Epigenom
- Epigenom
- Epigenom
- Examples
- exRNA Me

Database

- KB: e
- Use
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- F

Tool Settings

File: 2. smallRNA-seq Pipeline Results (Raw)/SM6_uc1_sequence_results.zip

Database: Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis

Group: exRNA Metadata Standards

File: 2. smallRNA-seq Pipeline Results (Raw)/SM3_crc3_sequence_results.zip

Database: Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis

Group: exRNA Metadata Standards

File: 2. smallRNA-seq Pipeline Results (Raw)/SM2_crc2_sequence_results.zip

Output Location:

Database: Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis

Group: exRNA Metadata Standards

Process Pipeline Runs Settings

Analysis Name PPR-2014-11-3-16:43:29

Submit Cancel



Post-processing: Begin Analysis (Excel)

Welcome to the Genboree Workbench! [Watch Intro Video](#)

Data Selector

Refresh Data Filter: Select a filter...

- exRNA Metadata Standards
 - Databases
 - KB:exRNA Metadata
 - Use Case 1: Exogenous exRNA in Colorectal Cancer
 - Tracks
 - Lists & Selections
 - Sample Sets
 - Samples
 - Files
 - 1. Inputs (FASTQ)
 - 2. smallRNA-seq Pipeline Results (Raw)
 - 3. smallRNA-seq Pipeline Results (Processed)
 - DG_diagnosticPlots.pdf
 - DG_miRNA_Quantifications_ReadCounts.txt
 - DG_miRNA_Quantifications_RPM.txt
 - DG_readMappingSummary.txt**
 - DG_sampleQC_Heatmap.pdf
 - DG_smallRNAQuants_ReadCounts.RData
 - DG_smallRNAQuants_RPM.RData
- Use Case 2: Small RNA Profiles in Lupus

Details

Attribute	Value
Download	Click to Download File
Group	exRNA Metadata Standards
Database	Use Case 1: Exogenous exRNA in Colorectal Cancer and Ulcerative Colitis
Description	Read Mapping Summary for

Input Data

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Note:

The processed files to the left will be in *your database*, but will be in the folder that you named: Files/processPipelineRuns/[your analysis name]/



Use Case 1: Pipeline Results - Number of Input Reads

Table S1. Wang et al (2012)

Sample ID	Gender	Age	Ethnic background	Classification	Disease stage	Number of reads	Processed reads
D3340P	M	58	Caucasian	Normal		27,002,901	5,085,400
D3176P	F	52	Caucasian	Normal		27,957,185	4,933,712
D3142P	F	54	Caucasian	Normal		28,214,261	4,826,682
022273P	F	52	Caucasian	Colorectal cancer	I	21,132,674	2,183,460
022163P	F	56	Caucasian	Colorectal cancer	III	23,547,368	2,879,950
022299P	M	46	Caucasian	Colorectal cancer	III	22,729,858	1,351,471
93163P	M	67	Caucasian	Ulcerative colitis	10 ^(a)	20,626,993	2,638,989
93164P	M	58	Caucasian	Ulcerative colitis	11 ^(a)	18,186,259	2,807,184
93166P	F	48	Caucasian	Ulcerative colitis	11 ^(a)	28,426,819	3,378,222

(a): Based on Mayo Scoring System for Assessment of Ulcerative Colitis Activity

Summary Table from small RNAseq Pipeline

Sample ID	input	clipped	calibrator rRNA	not_rRNA	genome	miRNA sense	miRNA antisense	tRNA sense	tRNA antisense	piRNA sense	piRNA antisense	snoRNA sense	snoRNA antisense	Rfam sense	Rfam antisense	miRNA plantVirus sense
norm1	27,002,901	30,349,566 NA	3,483,706	6,865,860	3,154,174	156,670	12	14,751	44	730	162	111	22	0	0	12,323
norm2	27,957,185	9,872,947 NA	3,253,551	6,619,396	2,969,730	72,638	12	11,756	51	609	264	118	176	0	0	9,776
norm3	28,214,261	9,316,527 NA	2,929,074	6,387,453	2,901,247	91,661	15	12,492	38	732	197	130	23	0	0	8,048
crc2	21,132,674	4,455,562 NA	1,508,605	2,946,957	1,307,657	47,204	8	5,494	18	504	198	85	168	0	0	3,266
crc3	23,547,368	5,737,688 NA	1,901,356	3,836,332	1,721,248	55,287	10	7,950	18	667	171	77	282	0	0	4,076
crc1	22,729,858	2,431,702 NA	704,887	1,726,815	767,523	13,768	4	1,779	6	243	62	24	4	0	0	1,817
uc1	20,626,993	5,265,060 NA	1,714,180	3,550,880	1,553,158	21,834	6	11,400	25	662	229	184	180	0	0	2,915
uc2	18,186,259	5,742,022 NA	1,937,719	3,804,303	1,642,329	21,307	4	7,066	17	666	148	58	168	0	0	4,510
uc3	28,426,819	7,095,086 NA	2,447,302	4,647,784	2,099,770	155,573	8	10,296	33	720	239	133	171	0	0	5,218



Use Case 1: Pipeline Results -

Do all plasma small RNAs map to the human genome?

Table S3. Wang et al (2012)

Category	0 mismatch			1 mismatch			2 mismatch		
	Normal (3) ^b	Colorectal Cancer (3) ^b	Ulcerative colitis (3) ^b	Normal (3) ^b	Colorectal Cancer (3) ^b	Ulcerative colitis (3) ^b	Normal (3) ^b	Colorectal Cancer (3) ^b	Ulcerative colitis (3) ^b
Human microRNA ^a	1.43%	1.25%	1.63%	1.43%	1.25%	1.63%	1.43%	1.25%	1.63%
Human transcript	2.78%	2.51%	2.55%	19.27%	18.09%	19.32%	42.30%	40.33%	43.43%
Human genome	8.41%	7.86%	8.41%	19.24%	18.41%	19.55%	14.98%	14.87%	15.10%
Unmapped sequence	87.38%	88.38%	87.42%	60.06%	62.25%	59.51%	41.29%	43.55%	39.85%

a. Due to high sequence similarity for various miRNA species, we did not allow any sequence mismatch in miRNA alignment.

b. Numbers in parentheses represents number of samples in each group.

Summary Table from small RNA-Seq Pipeline

Sample	not_rRNA	genome	Mapped Fraction	Unmapped Fraction
norm1	6865860	3154174	46%	54%
norm2	6619396	2969730	45%	55%
norm3	6387453	2901247	45%	55%
crc2	2946957	1307657	44%	56%
crc3	3836332	1721248	45%	55%
crc1	1726815	767523	44%	56%
uc1	3550880	1553158	44%	56%
uc2	3804303	1642329	43%	57%
uc3	4647784	2099770	45%	55%

Fraction mapping to the human genome = genome / not_rRNA



Use Case 1: Pipeline Results – Reads Mapping to miRNA

Table S3. Wang et al (2012)

Category	0 mismatch			1 mismatch			2 mismatch		
	Normal (3) ^b	Colorectal Cancer (3) ^b	Ulcerative colitis (3) ^b	Normal (3) ^b	Colorectal Cancer (3) ^b	Ulcerative colitis (3) ^b	Normal (3) ^b	Colorectal Cancer (3) ^b	Ulcerative colitis (3) ^b
Human microRNA ^a	1.43%	1.25%	1.63%	1.43%	1.25%	1.63%	1.43%	1.25%	1.63%
Human transcript	2.78%	2.51%	2.55%	19.27%	18.09%	19.32%	42.30%	40.33%	43.43%
Human genome	8.41%	7.86%	8.41%	19.24%	18.41%	19.55%	14.98%	14.87%	15.10%
Unmapped sequence	87.38%	88.38%	87.42%	60.06%	62.25%	59.51%	41.29%	43.55%	39.85%

a. Due to high sequence similarity for various miRNA species, we did not allow any sequence mismatch in miRNA alignment.

b. Numbers in parentheses represents number of samples in each group.

Summary Table from Pipeline

Fraction of reads mapping to miRNA =
miRNA_sense / not_rRNA

sample	input	clipped	rRNA	not rRNA	genome	miRNA sense	miRNA antisense	tRNA sense	tRNA antisense	piRNA sense	piRNA antisense	snoRNA sense	snoRNA antisense	miRNA plantVirus sense	miRNA sense average
norm1	393%	151%	51%	100%	46%	2.28%	0.0002%	0.2148%	0.0006%	0.0106%	0.0024%	0.0016%	0.0003%	0.1795%	1.60%
norm2	422%	149%	49%	100%	45%	1.10%	0.0002%	0.1776%	0.0008%	0.0092%	0.0040%	0.0018%	0.0027%	0.1477%	
norm3	442%	146%	46%	100%	45%	1.44%	0.0002%	0.1956%	0.0006%	0.0115%	0.0031%	0.0020%	0.0004%	0.1260%	
crc2	717%	151%	51%	100%	44%	1.60%	0.0003%	0.1864%	0.0006%	0.0171%	0.0067%	0.0029%	0.0057%	0.1108%	1.28%
crc3	614%	150%	50%	100%	45%	1.44%	0.0003%	0.2072%	0.0005%	0.0174%	0.0045%	0.0020%	0.0074%	0.1062%	
crc1	1316%	141%	41%	100%	44%	0.80%	0.0002%	0.1030%	0.0003%	0.0141%	0.0036%	0.0014%	0.0002%	0.1052%	
uc1	581%	148%	48%	100%	44%	0.61%	0.0002%	0.3210%	0.0007%	0.0186%	0.0064%	0.0052%	0.0051%	0.0821%	1.51%
uc2	478%	151%	51%	100%	43%	0.56%	0.0001%	0.1857%	0.0004%	0.0175%	0.0039%	0.0015%	0.0044%	0.1185%	
uc3	612%	153%	53%	100%	45%	3.35%	0.0002%	0.2215%	0.0007%	0.0155%	0.0051%	0.0029%	0.0037%	0.1123%	



Use Case 1: Which miRNAs are normally present in human plasma?

We can look for the answer to this question in the processed pipeline output file DG_miRNA_Quantifications_RPM.txt.

DG_miRNA_Quantifications_RPM.txt.										Averages			Diff. Expr.	
miRNA	norm1	norm2	norm3	crc1	crc2	crc3	uc1	uc2	uc3	norm	crc	uc	crc/norm	uc/norm
hsa-let-7b-5p	1984.6	1502.2	1442.2	363.6	1670.5	1659.6	614.0	674.8	4728.0	1643.0	1231.2	2005.6	0.7494	1.2207
hsa-miR-451a	864.2	996.1	2765.0	1610.3	2740.2	3287.0	994.1	294.3	8648.2	1541.8	2545.8	3312.2	1.6512	2.1483
hsa-let-7a-5p	1553.6	871.3	1151.9	320.2	906.2	1069.6	410.7	341.2	2000.5	1192.3	765.3	917.5	0.6419	0.7695
hsa-miR-378a-3p	904.5	1330.3	938.4	516.2	1462.7	478.7	162.4	286.5	865.1	1057.8	819.2	438.0	0.7745	0.4141
hsa-miR-143-3p	1471.7	714.1	935.4	1326.8	1050.5	508.2	198.5	101.8	179.7	1040.4	961.8	160.0	0.9245	0.1538
hsa-let-7f-5p	1547.2	490.0	765.8	602.3	540.2	517.3	215.3	262.0	1125.8	934.3	553.3	534.3	0.5922	0.5719
hsa-miR-486-5p	1047.0	612.5	708.8	472.8	634.5	1246.0	246.2	207.6	4135.3	789.4	784.4	1529.7	0.9937	1.9376
hsa-miR-1	2071.1	22.1	31.9	14.2	25.5	34.5	332.7	202.0	73.4	708.4	24.7	202.7	0.0349	0.2861
hsa-miR-184	1864.8	11.1	14.0	21.0	7.8	7.7	134.9	22.6	13.8	630.0	12.2	57.1	0.0193	0.0906
hsa-miR-1246	854.3	296.5	226.1	306.6	161.7	80.0	369.7	221.2	577.3	458.9	182.8	389.4	0.3982	0.8485
hsa-miR-423-5p	817.4	242.4	141.6	1147.0	323.5	274.6	52.9	115.8	715.2	400.5	581.7	294.6	1.4525	0.7357
hsa-miR-24-3p	531.6	279.3	318.8	130.9	356.8	291.7	122.3	158.7	190.9	376.5	259.8	157.3	0.6900	0.4178
hsa-miR-3168	318.9	324.2	276.6	11.5	626.0	390.4	527.2	299.1	592.4	306.6	342.7	472.9	1.1176	1.5424
hsa-miR-146a-5p	418.8	220.8	257.8	35.3	250.0	231.1	82.3	133.9	160.4	299.1	172.1	125.5	0.5755	0.4196
hsa-miR-21-5p	304.1	210.8	372.5	84.1	313.2	268.8	162.7	195.6	477.3	295.8	222.0	278.5	0.7507	0.9416
hsa-miR-140-3p	260.4	242.1	381.3	214.3	417.8	379.7	117.7	67.5	1215.9	294.6	337.3	467.0	1.1449	1.5853
hsa-miR-122-5p	480.7	83.7	301.6	13.6	285.2	116.9	62.1	457.0	768.4	288.7	138.5	429.1	0.4799	1.4865
hsa-miR-148a-3p	445.7	112.6	287.9	72.6	304.0	238.5	71.2	149.0	283.2	282.1	205.0	167.8	0.7268	0.5948
hsa-let-7g-5p	374.1	183.9	221.1	42.7	212.1	209.8	78.9	84.8	284.3	259.7	154.9	149.3	0.5964	0.5750

We added columns for averages and differential expression, and then sorted by the average expression level in normal plasma.



Use Case 1: Summary

- 55-60% of miRNA reads do not map to the human genome.
- ~1.5% of reads map to human miRNA.
- A fraction of a percent of reads map to plant or viral miRNA.