

Goal for this tutorial

- Perform comparative expression analysis to identify disease or tissue-specific loci
- Analyze user provided brain samples in hg19, provide regions of interest and identify highly expressed small noncoding RNAs that are limited to these regions
- Compare the results against brain and blood datasets in DASHR
- Note: refer to “SPAR_output_and_report_page.pdf” if you want to under the outputs more

SPAR

analysis, annotation, visualization of small RNA sequencing experiments
discover and characterize small RNAs from sequencing

[home](#) [analyze public datasets](#) [analyze your own data](#) [tutorial](#) [about](#)

Analyze your own data

Click here to
start

Genome

Human (Feb. 2009 hg19, GRCh37) ▾

Type of Input

Raw signal (BigWig) ▾

Provide URLs for signal tracks (BigWig format):

Positive (+) strand:

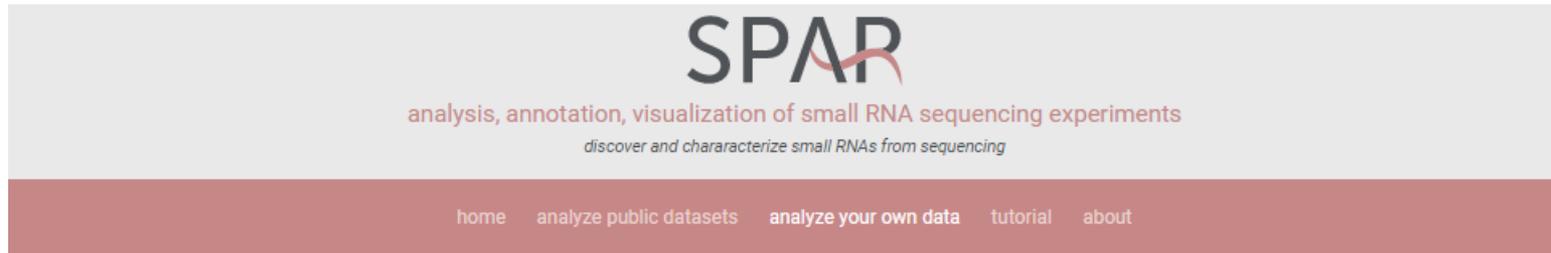
Negative (-) strand:

[Example data BigWig](#)

and click

Analyze your own BigWig

Select genome and upload data



Analyze your own data

Genome

Human (Feb. 2009 hg19, GRCh37) ▼

Step 1: Select hg19 as reference genome

Type of Input

Raw signal (BigWig) ▼

Step 2: Select "Raw signal (BigWig) as inputs

Provide URLs for signal tracks (BigWig format):

Positive (+) strand:

Negative (-) strand:

Step 3: Input URLs for the BigWig (one for each strand)

Example data BigWig

and click

Analyze your own BigWig

Step 4: Click "Analyze your own BigWig" to proceed

Optional parameters

SPAR
analysis, annotation, visualization of small RNA sequencing experiments
discover and characterize small RNAs from sequencing

home analyze public datasets **analyze your own data** tutorial about

Analyze your own data

Genome
Human (Feb. 2009 hg19, GRCh37) ▼

Type of input
Raw signal (BigWig) ▼

Provide URLs for signal tracks (BigWig format):

Positive (+) strand:

Negative (-) strand:

Example data BigWig
and click
Analyze your own BigWig

Analysis options:

Minimum read length (nt): Maximum read length (nt):

Minimum peak height (reads): Minimum peak fold change:

Specify regions of interest:

Custom region file (BED/GED/GRF/GTF): these regions will be overlapped with the peaks identified from the input data

Upload **Clear**

No errors

File testing.bed was successfully uploaded.

Optional (not included in current analyses): Change parameters for SPAR analyses:

- A) Range of length of peaks to be detected**
- B) how many reads are needed to be called a peak**

Step 1: Provide a BED file that contains regions of interest. SPAR analyses results will be limited to these regions if provided.

Landing results page (full view)

SPAR

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CUSTOM_ANNOTATION/peaks/testing_1.bed

Analysis results for job 05126cf

Input files:

http://hsa01.ncbi.nlm.nih.gov/FASTQ/aligned_out/filtered/aligned.sorted.bam.gz.bigwig
http://hsa01.ncbi.nlm.nih.gov/FASTQ/aligned_out/filtered/aligned.sorted.bam.gz.bigwig

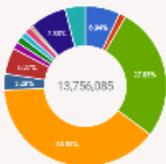
Link to results: https://www.broadinstitute.org/SPAR/SPAR_out/05126cf (will be kept for 2 weeks)

Link to results: Download results (ZIP) (will be kept for 2 weeks)

Link to report (PDF): Download report (PDF)

RUN SUMMARY

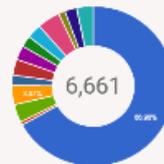
Reads vs RNA class



Unannotated miRNAprimary miR-2p miR-3p miR-3p3pna piRNA rRNA sRNA srRNA srp2-orf1b srp2-orf2 srRNA

Show more

Peaks vs RNA class



INTERACTIVE PEAK BROWSER

+

VIEW IN GENOME BROWSER

+

CUSTOM ANNOTATION SUMMARY

+

PLOTS

+

DOWNLOAD RESULTS

+

Landing results / outputs page (top)

CUSTOM_ANNOT=uploads/testing_1.bed

Region of interest file

Analysis results for job **05126cf**

Input files are listed

Job id is shown

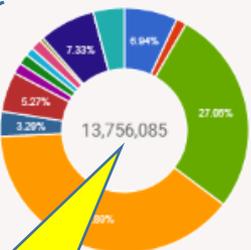
Input files:
<http://tesla.pcbi.upenn.edu/~yyee/Aligned.out.filtered.hardClipped.sorted.bam.pos.bigWig>
<http://tesla.pcbi.upenn.edu/~yyee/Aligned.out.filtered.hardClipped.sorted.bam.neg.bigWig>

Link to results: https://www.lisanwanglab.org/SPAR/SPAR_out/05126cf (will be kept for 2 weeks)
 Link to results: [Download results \(ZIP\)](#) (will be kept for 2 weeks)
 Link to report (PDF): [Download report \(PDF\)](#)

Bookmark / Share SPAR results link

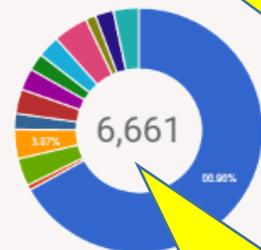
Download all tables, figures, tracks as zip

Reads vs RNA class



Percentage of reads per sncRNA class

Peaks vs RNA class



Percentage of peaks per sncRNA class

Total number of peaks

Total number of reads

- Unannotated
- lncRNA
- miR-5p
- miR-5p3pno
- piRNA
- rRNA
- scRNA
- snRNA
- snoRNA
- TRF-3-trf3b
- TRF-3-trf3b
- TRF3
- YRNA

Show more

All profiled sncRNA classes

Landing results / outputs page (top)



analysis, annotation, visualization of small RNA sequencing experiments
discover and characterize small RNAs from sequencing

CUSTOM_ANNOT=uploads/testing_1.bed

Analysis results for job 05126cf

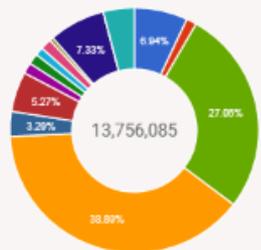
Input files:
<http://tesla.pcbi.upenn.edu/~yyee/Aligned.out.filtered.hardClipped.sorted.bam.pos.bigWig>
<http://tesla.pcbi.upenn.edu/~yyee/Aligned.out.filtered.hardClipped.sorted.bam.neg.bigWig>

Link to results: https://www.lisanwanglab.org/SPAR/SPAR_out/05126cf (will be kept for 2 weeks)
Link to results: [Download results \(ZIP\)](#) (will be kept for 2 weeks)
Link to report (PDF): [Download report \(PDF\)](#)

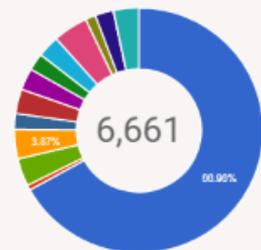
To view a report pdf: click
https://www.lisanwanglab.org/SPAR/SPAR_out/05126cf/report.pdf

RUN SUMMARY

Reads vs RNA class



Peaks vs RNA class



- Unannotated
- miRNAprimary
- miR-3p
- miR-5p
- miR-5p3pno
- piRNA
- irRNA
- scRNA
- snRNA
- snoRNA
- IRF-3-trfcb
- IRF-3-trfcb
- IRF3
- VRNA

Show more

Landing results → SPAR report page

Index of /SPAR/SPAR_out/05126cf

<u>Name</u>	<u>Last modified</u>	<u>Size</u>	<u>Description</u>
 Parent Directory		-	
 DASHR_comparison/	04-Feb-2018 19:53	-	
 ENCODE_comparison/	04-Feb-2018 19:53	-	
 figures/	04-Feb-2018 19:53	-	
 inputs/	04-Feb-2018 19:52	-	
 logs/	04-Feb-2018 19:53	-	
 results/	04-Feb-2018 19:53	-	
 tracks/	04-Feb-2018 19:53	-	
 report.html	04-Feb-2018 19:53	42K	
 report.pdf	04-Feb-2018 19:53	1.8M	
 results.html	04-Feb-2018 19:53	2.4K	
 run_summary.html	04-Feb-2018 19:53	585	
 SPAR.hg19.config	04-Feb-2018 19:52	2.1K	

Report is available in html / pdf

SPAR report.pdf

A 15 page report containing tables and figures for download and sharing

SPAR - Sequencing-based Pipeline for Analysis of small RNAs 1 / 15

SPAR
analysis, annotation, visualization of small RNA sequencing experiments
discover and characterize small RNAs from sequencing

Link to results: https://www.lisanwanglab.org/SPAR/SPAR_out/05126cf (will be kept for 2 weeks)

Link to results: [Download results \(ZIP\)](#) (will be kept for 2 weeks)

Link to report (PDF): [Download report \(PDF\)](#)

Run Summary

Reads	13,756,091
Expressed small RNA loci	6,661
Reads (annotated)	12,801,044
Reads (unannotated)	955,047
Genes (annotated)	1,982
Genes (unannotated)	2,001

Landing results / outputs page (bottom)

After clicking show more at the bottom of the "Run Summary"

Reads	13,756,091
Expressed small RNA loci	6,661
Reads (annotated)	12,801,044
Reads (unannotated)	955,047
Genes (annotated)	1,982
Called peaks (annotated)	2,201
Called peaks (unannotated)	4,460
Expressed loci length (average)	21.10
Genome coverage (nucleotides)	140,575
RPM (average)	150.13

▲
Show less

Summary information on peaks

Summary information on reads

Step 1: Expand this to view the interactive peak browser

- INTERACTIVE PEAK BROWSER +
- VIEW IN GENOME BROWSER +
- CUSTOM ANNOTATION SUMMARY +
- PLOTS +
- DOWNLOAD RESULTS +
- RUN LOG +

Interactive Peak Browser (Output)

The image shows a screenshot of a web application interface. At the top, there is a dark red header bar with the text "INTERACTIVE PEAK BROWSER" on the left and a minus sign on the right. Below this header, the main content area is white. On the left side of this area, there is a link that says "Browse peaks (expressed small RNAs)". A yellow callout box with a black border points from this link to the right. Inside the callout box, the text reads "Click this to go to 'Interactive Peak Browser'". At the bottom of the interface, there are two more dark red header bars. The first one contains the text "VIEW IN GENOME BROWSER" on the left and a plus sign on the right. The second one contains the text "PLOTS" on the left and a plus sign on the right.

INTERACTIVE PEAK BROWSER -

Browse peaks (expressed small RNAs)

Click this to go to "Interactive Peak Browser"

VIEW IN GENOME BROWSER +

PLOTS +

Interactive Peak Browser (Output)

Total number of called peaks (annotated or unannotated)

INTERACTIVE PEAK BROWSER

Click "pointing down error" to select other features to display

Browse peaks (expressed small RNA)

Download Table

Loci: 1-10 / 6081 Page 1 of 609 Results per page 10

chr	peakID	Expression (raw)	strand	Same 5' end read %	Expression (RPM)	Expression (percentile)	Annotation	Annotated class	Conservatio	mRNA?	lncRNA?	repeat?
Clear			Clear					Clear		Clear	Clear	Clear
chr1	P116	305.5	+	0.973813	29.3985	87.7	chr1:109598939-109598961:+:hsa-miR-197-3p	mir-3p	0.2112	Intergenic	Non-lncRNA	Non-repeat
chr1	P253	121.426	-	0.986206	11.6849	76.6	chr1:10999855-10999945:-:HY1	scrNA	0.0197	Intergenic	Non-lncRNA	Non-repeat
chr1	P119	13.2556	+	0.933779	1.2756	12.33	chr1:111446797-111446916:+:HY1	scrNA	8e-04	Intergenic	Non-lncRNA	Non-repeat
chr1	P121	333.222	+	0.926571	32.0662	88.88	chr1:116671786-116671808:+:hsa-miR-320b	mir-5p3pno	5e-04	Intergenic	Non-lncRNA	Non-repeat
chr1	P7	38	+	0.947368	3.6568	52.05	chr1:1167159-1167181:+:hsa-miR-200b-3p	mir-3p	0.9188	Intergenic	lncRNA Exon	Non-repeat
chr1	P8	15.0556	+	1	1.4488	18.01	chr1:1169054-1169076:+:hsa-miR-429	mir-5p3pno	0.9834	Intergenic	lncRNA Exon	Non-repeat

Interactive Peak Browser (Output)

Filter snRNA loci with the top 5% of expression

INTERACTIVE PEAK BROWSER
—

Browse peaks (expressed small RNAs)

Download Table

Loci: 1-10 / 60 Results per page 10

chr	peakID	Expression (raw)	strand	Same 5' end read %	Expression (RPM)	Expression (percentile)	Annotation	Annotated class	Conservatio	mRNA?	lncRNA?	repeat?
chr1	P131	1358.61	+	0.587891	130.7399	95.13	chr1:145157156-145157229:+:tRNA-Val-CAC-chr1-16	tRNA	0.3593	Intergenic	Non-lncRNA	Non-repeat
chr1	P150	1400.25	+	0.656677	134.747	95.21	chr1:153671250-153671282:+:piR-35176	piRNA	0.8856	Intergenic	Non-lncRNA	Non-repeat
chr1	P109	1818.27	-	0.590711	174.9733	95.94	chr1:156420353-156420375:-:hsa-miR-9-3p	mir-3p	1	3' UTR Intron	lncRNA Intron	Non-repeat
chr1	P104	1709.2	-	0.809757	164.4774	95.71	chr1:159141610-159141684:-:tRNA-Arg-TCT-4-1	tRNA	1	Intergenic	Non-lncRNA	Non-repeat
chr1	P103	1303	-	0.590763	125.3885	95.02	chr1:159141610-159141684:-:tRNA-Arg-TCT-4-1	tRNA	1	Intergenic	Non-lncRNA	Non-repeat
chr1	P218	1779.94	+	0.574177	171.2848	95.84	chr1:204506526-204506599:+:tRNA-Lys-TTT-2-1	tRNA	0.8393	Intergenic	lncRNA Exon	Non-repeat

Step 1: Type "95." in this text box and click enter

Number of loci that passed this criteria: 60

Interactive Peak Browser (Output)

Further filter sncRNA loci that only present in Promoter, 3' or 5' UTR exonic regions

INTERACTIVE PEAK BROWSER

Step 2: Select "Promoter", "3' UTR Exon", "5' UTR Exon"

Browse peaks (expressed small RNAs)

Download Table

Number of loci that fulfilled these criteria: 4

Loc: 1-4 / 4 Page 1 of 1 Results per page 10 Columns

chr	peakID	Expression (raw)	strand	Same 5' end read %	Expression (RPM)	Expression (percentile)	Annotation	Annotated class	Conservatio	mRNA?	lncRNA?	repeat?
chr16	P993	1512.66	+	0.965511	145.5642	95.44	chr16:15643300-15643322:+:hsa-miR-484	mir-5p3pno	0.9999	5' UTR Exon	Non-lncRNA	Non-repeat
chr16	P997	1355.09	+	0.466894	130.4012	95.12	chr16:19498609-19498750:+:U4	snRNA	0.0546	3' UTR Exon	Non-lncRNA	Non-repeat
chr16	P1032	1755.59	-	0.358646	167.1132	95.76	chr16:636735-636806:-:tRNA-Gly-CCC-2-2	tRNA	0.9205	Promoter	Non-lncRNA	Non-repeat
chr2	479	1745.09	-	0.358646	167.9311	95.77	chr2:70248990-70249061:-:tRNA-Gly-CCC-2-1	tRNA	0.8976	Promoter	Non-lncRNA	Non-repeat

Step 3: Export these 4 filtered sncRNAs

Optional: click this link to visualize this peak P993 in UCSC genome browser

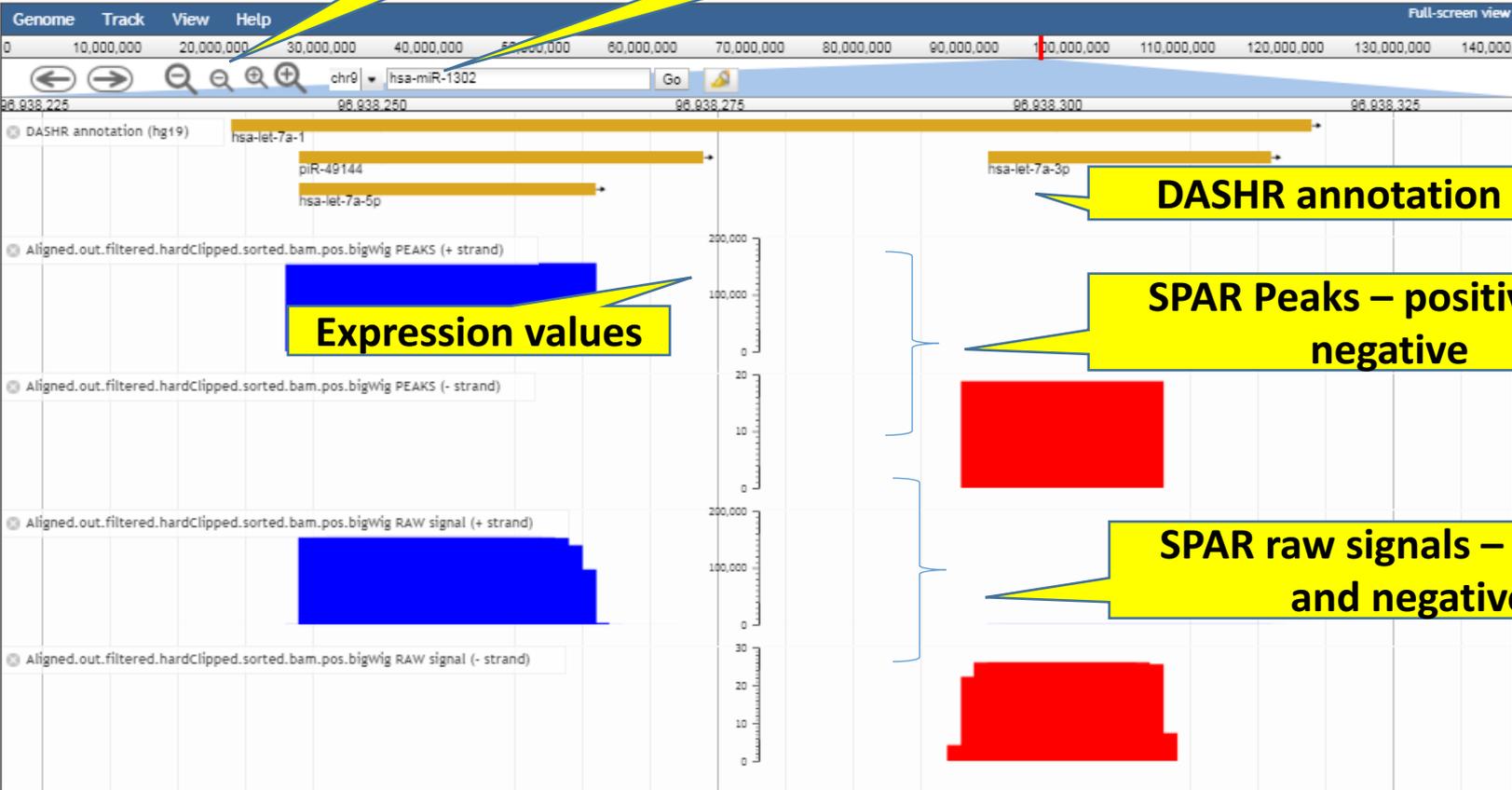
View in Genome Browser (Output)

Optional: "View SPAR result tracks in UCSC Genome Browser (opens in the new window)" if preferred

Type in genomic coordinates / RNA / gene symbols of interest

Zoom in or out

View SPAR result tracks in UCSC Genome Browser (opens in the new window)



DASHR annotation tracks

SPAR Peaks – positive and negative

Expression values

SPAR raw signals – positive and negative

View in Genome Browser (Output)

CUSTOM ANNOTATION SUMMARY

Shows the specific region bed file used as input

Custom annotation file used: uploads/testing_1.bed

Annotated SPAR peaks

Peaks with annotation

- Peaks overlapping custom intervals
- Custom intervals with peaks

Table showing annotated peaks that are residing in the target region file

Summary of results

#Custom intervals:	1
#Peaks within the custom intervals:	2201
#Peaks outside the custom intervals:	0
#Custom intervals with at least one peak:	1101

Un-annotated SPAR peaks

Peaks without annotation

- Peaks overlapping custom intervals
- Intervals with peaks

#Custom intervals:	1
#Peaks within the custom intervals:	4460
#Peaks outside the custom intervals:	0
#Custom intervals with at least one peak:	2230

Plots (Output)

PLOTS

4 different plot sessions

SEGMENTATION

Length distribution of rpm of segmented loci
Genomic length distribution of identified small rna loci

LENGTHEXPRESSION

Rpm distribution of identified small rna loci

Percentile distribution of identified small rna loci across different lengths

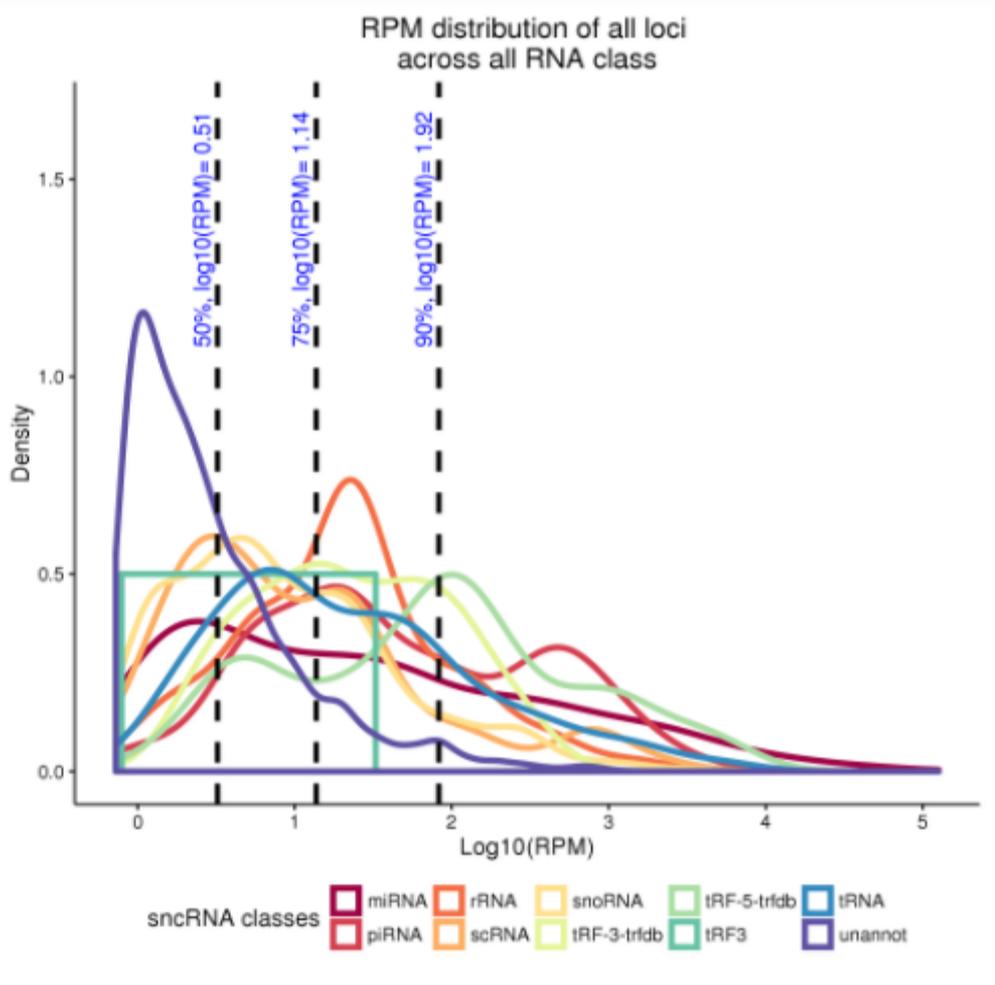
PROCESSING

5p end positional offset between identified loci and small rna gene
Processing specificity at 5p end of identified small rna loci
Read pipeup at 5p end of identified small rna loci

GENOMEWIDE

Proportion of expressed annotated loci
Genomewide distribution pattern of identified small rna loci
Genomewide distribution of expression of identified small rna loci
Proportion of mapped reads

Click to display, corresponding plot will be shown in the right



Rpm distribution of identified small rna loci

Plots (Output)

PLOTS

4 different plot sessions

SEGMENTATION

- Length distribution of rpm of segmented loci
- Genomic length distribution of identified small rna loci

LENGTHEXPRESSION

- Rpm distribution of identified small rna loci
- Percentile distribution of identified small rna loci across different lengths

PROCESSING

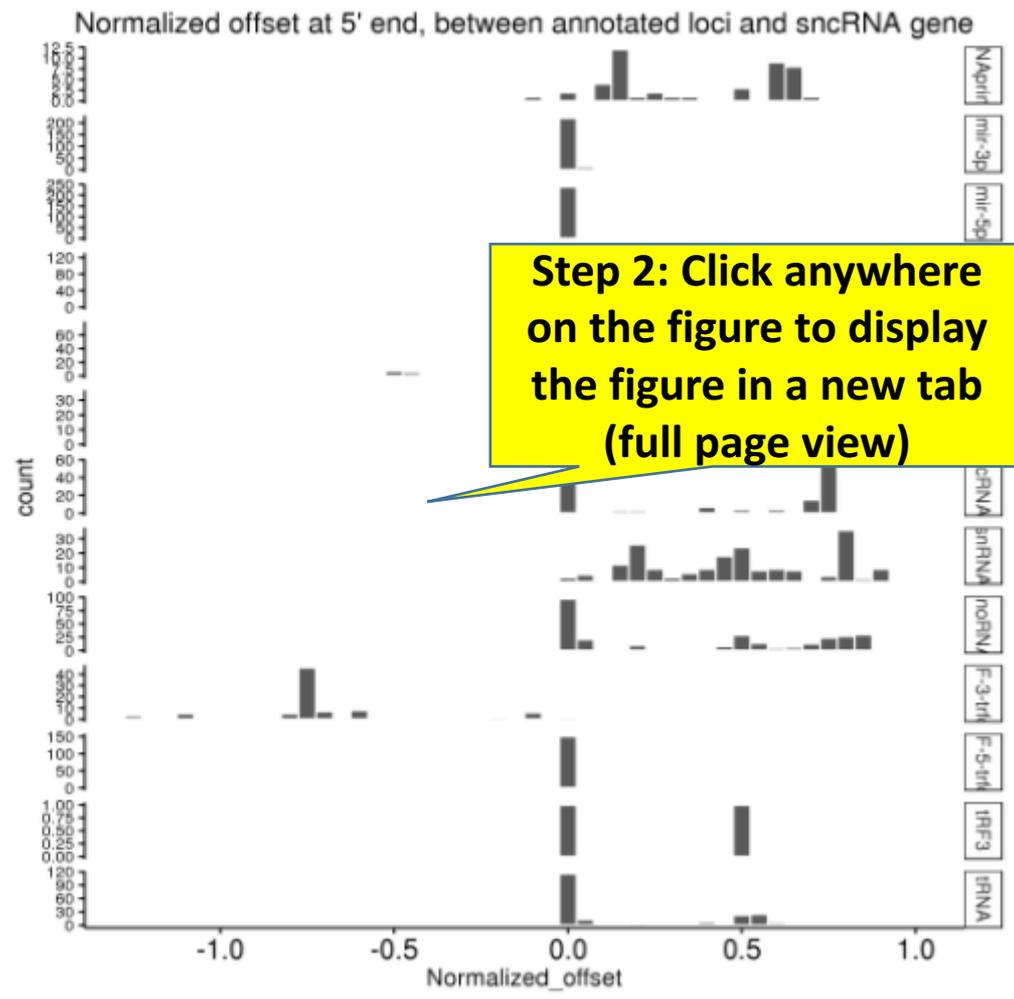
5p end positional offset between identified loci and small rna gene

- Processing specificity at 5p end of identified small rna loci
- Read pipeup at 5p end of identified small rna loci

GENOMEWIDE

- Proportion of expression
- Genomewide distribution
- Genomewide distribution
- Proportion of mapping

Step 1: Click to display, corresponding plot will be shown in the right



5p end positional offset between identified loci and small rna gene

Finish viewing the plots, want to perform own analyses with SPAR results – visit download

PLOTS

- SEGMENTATION**
 - Length distribution of rpm of segmented loci
 - Genomic length distribution of identified small rna loci
- LENGTHEXPRESSION**
 - Rpm distribution of identified small rna loci
 - Percentile distribution of identified small rna loci across different lengths**
- PROCESSING**
 - 5p end positional offset between identified loci and small rna genes
 - Processing specificity at 5p end of identified small rna loci
 - Read group at 5p end of identified small rna loci
- GENOMEWIDE**
 - Proportion of expressed annotated small rna genes
 - Genome-wide distribution patterns of small rna loci
 - Circular genome data visualization
 - Genome-wide distribution of expressed small rna loci
 - Proportion of mapped reads across all loci

Step 1: click this to minimize this section

Step 2: click this to maximize this section

DOWNLOAD RESULTS

Download results (Top) – bulk download

DOWNLOAD RESULTS		
Content	Description	Download
Peak tracks	Genome-wide tracks	<ul style="list-style-type: none"> • plus • minus
Raw signal tracks	Genome-wide tracks	<ul style="list-style-type: none"> • plus • minus
Peak tables	Tables with detailed information 1. Annotated peaks: peaks overlapping with annotated genes or mature products 2. Unannotated peaks: peaks that do not overlap with annotated snRNA genes or mature products.	<ul style="list-style-type: none"> • Annotated peaks [xls] • Unannotated peaks [xls] • All called peaks [xls] [bed]
Gene expression	Small RNA gene expression	<ul style="list-style-type: none"> • Gene expression table (xls) [3.31 M]
Comparison with DASHR	Integrated expression tables	<ul style="list-style-type: none"> • Annotated peaks [xls] • Unannotated peaks [xls] • All (Annotated + Unannotated) peaks [xls] [bed] • Peaks not in DASHR [xls]
Comparison with ENCODE	Integrated expression tables	<ul style="list-style-type: none"> • Annotated peaks [xls] • Unannotated peaks [xls] • All (Annotated + Unannotated) peaks [xls] [bed] • Peaks not in ENCODE [xls]

Tracks for browsing

Comparison expression tables

Step 1: Click to download peaks present in both the analysed data and also expressed in DASHR

Step 2: Click to download peaks only in analysed data but not in DASHR

Download results (Bottom) – download by sncRNA class

Step 1: Click to download, e.g. all annotated loci by SPAR that falls within custom annotation region

Step 2: Click to download, e.g. all genomewide unannotated loci from SPAR

Total number of reads falling onto this RNA class

bash annotate_custom.sh SPAR_out/05126cf/results/peaks_annot.xls uploads/
Annotated SPAR peaks (Custom annotation)
Un-annotated SPAR peaks (Custom annotation)

DOWNLOAD PEAK TABLES BY RNA CLASS

RNA class	Peaks	Genes	Reads	Percentage of reads
Annotated	2,201	1,982	12,801,044	93.06
Unannotated	4,460	4,460	955,047	6.94
miRNAprimary	45	45	182,566	1.33
mir-3p	242	242	3,721,158	27.05
mir-5p	258	258	5,349,913	38.89
mir-5p3pno	139	139	452,096	3.29
piRNA	215	203	724,936	5.27
rRNA	190	126	196,397	1.43
scRNA	151	146	193,519	1.41
snRNA	192	167	151,364	1.10
snoRNA	302	223	198,124	1.44
tRF-3-trfdb	89	89	67,183	0.49
tRF-5-trfdb	158	158	1,007,724	7.33
tRF3	2	2	461	0.00
tRNA	218	184	555,597	4.04

Step 3: Click to download, e.g. tRNA only loci results from SPAR

Download results (Output)

We found earlier that P1032, P993, P997, P1479 are of interest, not sure if these peaks are found in any of the DASHR brain tissues.

First excel file downloaded:

- 1) DASHR_comparison_all.xls – if any of the above peaks are found in this file, meaning they can be present in any DASHR tissue; not necessarily expressed in brain.

The screenshot shows the Microsoft Excel interface with the 'Data' tab selected. The data table is as follows:

	A	B	C	D	E	F	G	H	I	J	K	L
1	#peakChr	peakChrS	peakChrE	peakID	peakExpri	peakExpri	annotID	annotRNAclass	brainog1_SRA012516	brainpfc1_GSE43335	brainpfc2_GSE48552	braintgm1_GSE46131
2	chr16	15643300	15643322	P993	1512.66	95.44	chr16:15643300:15643322:+:hsa-miR-484	mir-5p3pno	NA	1083.58	2661.43	594.515
3	chr16	19498716	19498750	P997	1355.09	95.12	chr16:19498609:19498750:+:U4	snRNA	NA	3997.57	NA	NA

P993 and P997 were found in this table. We extracting the four brain related DASHR tissues (now in column I to L). Only column J (a prefrontal cortex brain data) have both peaks expressed.

Download results (Output)

Second excel files downloaded:
2) not_in_DASHR.xls (for sanity check only)

The screenshot shows an Excel spreadsheet titled 'not_in_DASHR - Excel'. The ribbon is set to 'Data'. The active cell is A1, containing the text '#peakChr'. The table below has the following data:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	#peakChr	peakChrS	peakChrE	peakID	peakExpress	peakExprPe	annotID	annotRNAclass	brainog1	brainpfc1	brainpfc2	braintgm	overlap	peakOver	DASHRpeakOverlapPct	
2	chr16	636771	636809	P1032	1736.59	95.76	chr16:636735:636806:-:tRNA-Gly-CCC-2-2	tRNA	0	0	0	
3	chr2	70249026	70249065	P1479	1745.09	95.77	chr2:70248990:70249061:-:tRNA-Gly-CCC-2	tRNA	0	0	0	

P1032 and P1479 were found in this table, i.e. not expressed in any of the DASHR tissues, but present in the ENCODE prefrontal cortex data.

Conclusion – out of the 4 sncRNAs we identified, two were in silico confirmed to be highly expressed across different brain datasets in both DASHR and ENCODE.

Run log (Output)

Step 1: click this to minimize "Download results"

DOWNLOAD RESULTS -

Content	Description	Download
Peak tracks	Genome-wide tracks	<ul style="list-style-type: none"> plus strand [bigBED] [382.36 KB] minus strand [bigBED] [384.94 KB]
Raw signal tracks	Genome-wide tracks	<ul style="list-style-type: none"> plus strand [bigWig] [3.66 MB] minus strand [bigWig] [3.66 MB]
Peak tables	Tables with detailed information: 1. Annotated peaks: peaks overlapping snRNA genes or mature products with annotations. 2. Unannotated peaks: peaks that do not overlap with annotated snRNA genes or mature products.	<ul style="list-style-type: none"> Annotated peaks [xls] Unannotated peaks [xls] All called peaks [xls] [bed]
Gene expression	Small RNA gene expression	Gene expression table (xls) [3.31 MB]
Comparison with DASHR	Integrated expression tables	<ul style="list-style-type: none"> Annotated peaks [xls] Unannotated peaks [xls] All (Annotated + Unannotated) peaks [xls] [bed] Peaks not in DASHR [xls]
Comparison with ENCODE	Integrated expression tables	<ul style="list-style-type: none"> Annotated peaks [xls] Unannotated peaks [xls] All (Annotated + Unannotated) peaks [xls] [bed] Peaks not in ENCODE [xls]

DOWNLOAD PEAK TABLES BY RNA CLASS

RNA class	Peaks	Genes	Reads	Percentage of reads
Annotated	1,282	1,214	9,647,188	92.84
Unannotated	4,799	4,799	744,547	7.16
miRNAprimary	18	18	646,698	6.22
mir-3p	224	224	1,779,736	17.13
mir-5p	265	265	5,786,729	54.92
mir-3p&pno	66	66	38,553	0.29
piRNA	99	99	747,688	7.19
rRNA	98	81	42,675	0.41
scRNA	225	215	227,677	2.19
snRNA	137	132	17,896	0.17
snRNA	34	29	341,572	3.29
trf3	6	6	1,323	0.01
trf3	9	9	998	0.01
tRNA	169	138	183,725	1.88

RUN LOG +

Step 2: click this to maximize "Run log"

Questions?
SPAR@tsanwanglab.org

Wang Lab | Stem Neurodevelopmental Genomics Center | UC Berkeley

Run log (Output)

Run log displayed again

RUN LOG

```
Genome: hg38
Fri, 26 Jan 2018 15:37:49 -0500 ..... Loading PLUS strand: http://dashr2.lisanwanglab.org/DASHRv2/tracks/hg38/ENCODE_dataportal_hg38/fron
Fri, 26 Jan 2018 15:37:49 -0500 ..... Loading MINUS strand: http://dashr2.lisanwanglab.org/DASHRv2/tracks/hg38/ENCODE_dataportal_hg38/fro
Fri, 26 Jan 2018 15:37:49 -0500 ..... Starting SPAR run
Fri, 26 Jan 2018 15:37:49 -0500 ..... Analysis parameters: min. fold change=2; min. coverage=10; min. size=14; max. size=44
bash run_SPAR.sh SPAR_out/ca8ac37/tracks/raw.pos.bigWig SPAR_out/ca8ac37 pos SPAR_out/ca8ac37/config.hg38.sh 2>&1
Fri, 26 Jan 2018 15:37:49 -0500 ..... Processing job ca8ac37.....
Fri, 26 Jan 2018 15:37:55 -0500 ..... DONE.

Fri, 26 Jan 2018 15:37:55 -0500 ..... Sending results to the web server.....
Fri, 26 Jan 2018 15:39:38 -0500 ..... Processed 10,391,735 reads in 109 seconds (95,337 reads / second)

Fri, 26 Jan 2018 15:39:38 -0500 ..... Creating plots
Fri, 26 Jan 2018 15:39:46 -0500 ..... DONE creating plots
```

SPAR run log

Send questions to this email:
SPAR@lisanwanglab.org

END