Goal for this tutorial

- Annotate and visualize sncRNAs from small RNA sequencing experiment

- Analyze a publicly available **bipolar-spindle-neuron-rep1** sample from ENCODE in hg38

- Note: refer to SPAR output description ("SPAR_output_and_report_page.pdf") for detailed explanations of the SPAR outputs

SPAR

analysis, annotation, visualization of small RNA sequencing experiments

discover and chararacterize small RNAs from sequencing

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

Analyze public datasets

Click here to start

Genome

Step 1: Select hg38 as reference genome

Human (Dec. 2013 hg38, GRCh38) ▼

Select DASHR dataset (small RNA-seq) (Human hg38):

Select DASHR dataset ▼

Analyze DASHR

Select ENCODE data portal dataset (short total RNA-seq) (Human hg38):

bipolar-spindle-neuron-rep1_ENCSR603RPC ▼

Step 2: Select from dropdown: bipolar-spindle-neuron-rep1 to analyze

Analyze ENCODE

Step 3: Click "Analyze ENCODE" to proceed

Landing results page (full view)

Landing results / outputs page (top)

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

Analysis results for job **7c551fe**

Input files are listed

Input files:
http://dashr2.lisanwanglab.org/DASHRv2/tracks/hg38/ENCODE_dataportal_hg38/bipolar-spindle-neuron-rep1_ENCSR603RPC.pos.bigWig
http://dashr2.lisanwanglab.org/DASHRv2/tracks/hg38/ENCODE_dataportal_hg38/bipolar-spindle-neuron-rep1_ENCSR603RPC.neg.bigWig

Job id is shown

Results URL:
https://www.lisanwanglab.org/SPAR/SPAR_out/7c551fe

Bookmark / Share SPAR results link

Link to results: https://www.lisanwanglab.org/SPAR/SPAR_out/7c551fe (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)

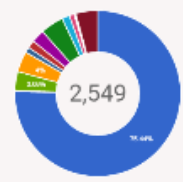**Download all tables, figures, tracks as zip**

Percentage of peaks per sncRNA class

Percentage of reads per sncRNA class

Reads vs RNA class

938,811

17.38%
22.21%
30.8%

Peaks vs RNA class

2,549

4%
3.00%
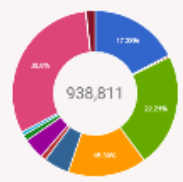
Unannotated   nary   mir-3p   mir-5p   mir-5p3pno   piRNA   rRNA   scRNA   snRNA

snoRNA   tRF3   tRF5   tRNA

Show more ▼

Total number of reads

Total number of peaks

All profiled sncRNA classes

Landing results / outputs page (top)

To view a report pdf: Click https://www.lisanwanglab.org/SPAR/SPAR_out/7c551fe/report.pdf
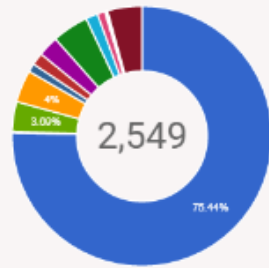
Landing results ➔ SPAR report page

Index of /SPAR/SPAR_out/7c551fe

Name	Last modified	Size	Description
Parent Directory		-	
DASHR_comparison/	04-Feb-2018 19:07	-	
ENCODE_comparison/	04-Feb-2018 19:07	-	
figures/	04-Feb-2018 19:07	-	
inputs/	04-Feb-2018 19:07	-	
logs/	04-Feb-2018 19:07	-	
results/	04-Feb-2018 19:08	-	
tracks/	04-Feb-2018 19:07	-	
report.html	04-Feb-2018 19:07	39K	
report.pdf	04-Feb-2018 19:08	1.7M	
results.html	04-Feb-2018 19:07	2.4K	
run_summary.html	04-Feb-2018 19:07	574	
SPAR.hg38.config	04-Feb-2018 19:07	2.0K	

Report is available in html / pdf

Apache/2.2.3 (CentOS) Server at www.lisanwanglab.org Port 443

SPAR report.pdf

A 14 page report containing tables and figures for download and sharing

Landing results / outputs page (bottom)

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

Reads	938,818
Expressed small RNA loci	2,549
Reads (annotated)	775,635
Reads (unannotated)	163,183
Genes (annotated)	595
Called peaks (annotated)	626
Called peaks (unannotated)	1,923
Expressed loci length (average)	20.00
Genome coverage (nucleotides)	50,980
RPM (average)	392.31

Show less

Summary information on reads

Summary information on peaks

Step 1: Expand this to view the interactive peak browser

INTERACTIVE PEAK BROWSER +

VIEW IN GENOME BROWSER +

PLOTS +

DOWNLOAD RESULTS +

RUN LOG +

Questions?
SPAR@lisanwanglab.org

Wang Lab | Penn Neurodegeneration Genomics Center | University of Pennsylvania

Interactive Peak Browser (Output)

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)

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

INTERACTIVE PEAK BROWSER

−

Browse peaks (expressed small RNAs)

Download Table

Loci: 1-10 / 2549 　　　　　　　　|◄ ◄ Page 1 ▼ of 255 ► ►| 　　　 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?
Clear ▼			Clear ▼					☐ Clear		☐ Clear	☐ Clear	☐ Clear
chr1	P100	1327.29	−	0.725526	1413.7869	97.61	chr1:630995-631061:-:nm-tRNA-Tyr-GTA-chr1-142	tRNA	0.9916	Intergenic	lncRNA Intron	Non-repeat
chr1	P3	79	+	0.860759	84.1483	74.5	chr1:1167159-1167181:+:hsa-miR-200b-3p	mir-3p	0.9188	Intergenic	lncRNA Exon	Non-repeat
chr1	P90	17.5625	−	0.765125	18.707	27.7	chr1:7930321-7930348:-:piR-43768	piRNA	0.0057	mRNA Intron	Non-lncRNA	Non-repeat
chr1	P89	14	−	0.928571	14.9124	16.36	chr1:9151734-9151756:-:hsa-miR-34a-5p	mir-5p	1	Intergenic	lncRNA Exon	Non-repeat
chr1	P88	60.5885	−	0.943592	64.5369	68.73	chr1:10999855-10999945:-:HY1	scRNA	0.0217	Intergenic	Non-lncRNA	Non-repeat
chr1	P82	26.3618	−	0.510893	28.0797	44.33	chr1:16520584-16520658:-:tRNA-Asn-GTT-chr1-140-tRF5	tRF5	0.3596	Intergenic	Non-lncRNA	Non-repeat

View in Genome Browser (Output)
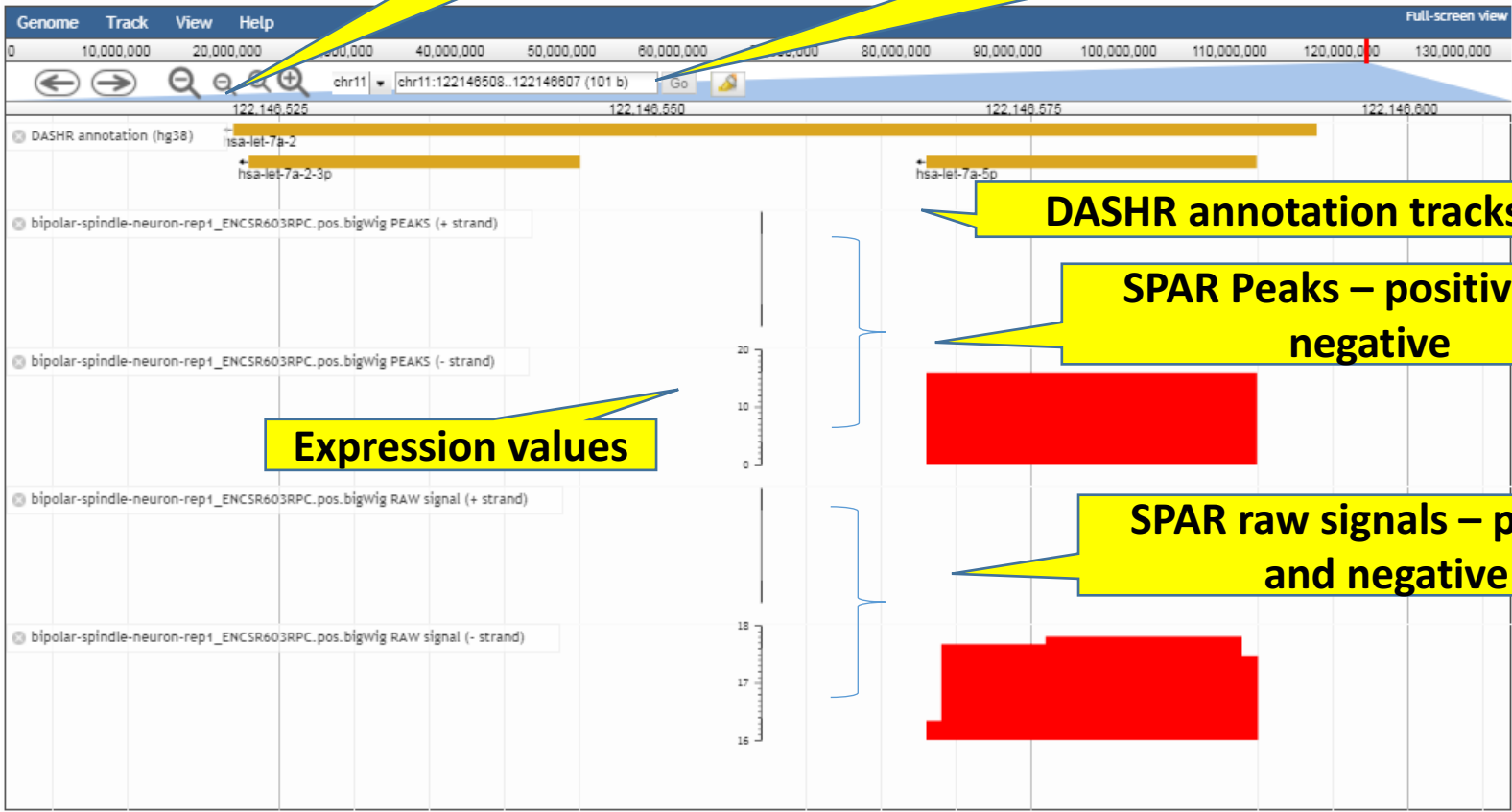
Plots (Output) – to navigate across all plots

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 pileup at 5p end of identified small rna loci

GENOMEWIDE
Proportion of expressed annotated small rna genes
Genomewide distribution patterns of small rna loci
Genomewide distribution of expressed small rna loci
Proportion of mapped reads across all loci

Distribution of loci RPM
at different lengths after segmentation
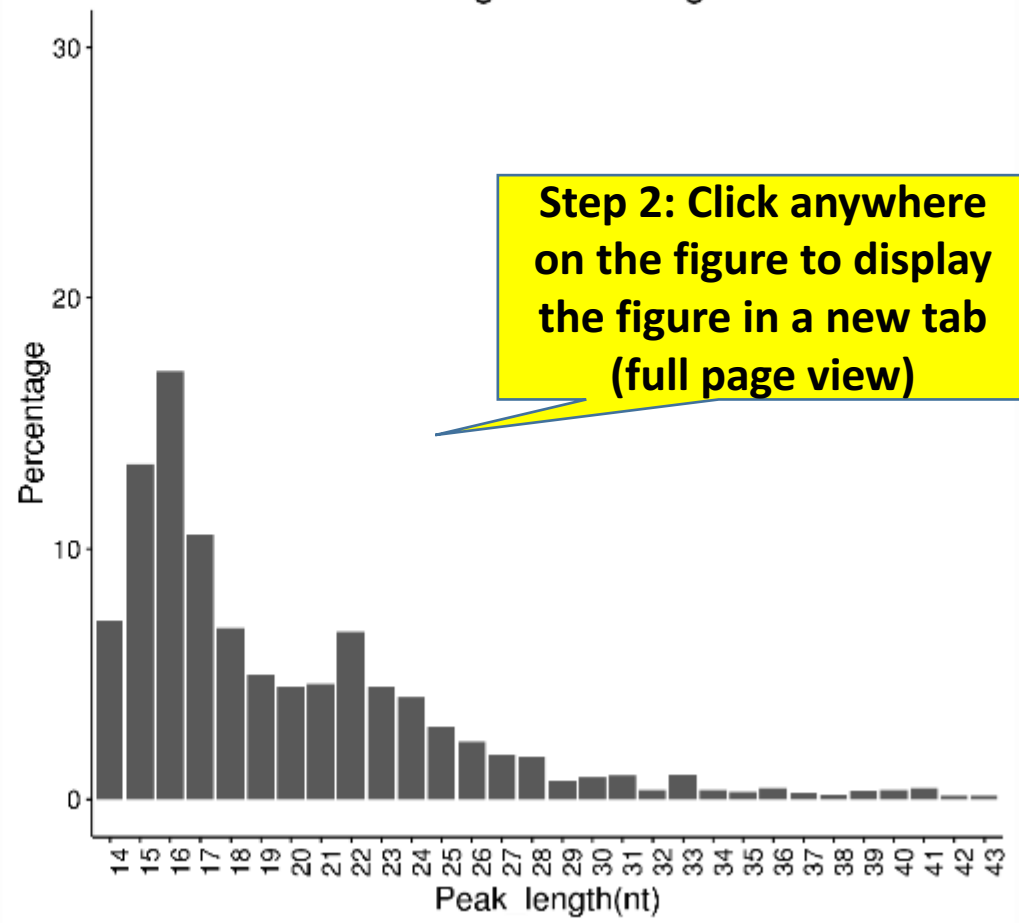
Step 2: Click anywhere on the figure to display the figure in a new tab (full page view)

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

Length distribution of rpm of segmented loci

Download results (Top) – sncRNA gene expression

Tracks for browsing

DOWNLOAD RESULTS —

Step 1: Click to download sncRNA gene expression data (instead of individual loci' RPM will be shown)

Content	Description	Download
Peak tracks	Genome-wide tracks	• plus ... [bigWig RPM] [... KB] • minus ...
Raw signal tracks	Genome-wide tracks	• plus ... • minus ...
Peak tables	Tables with detailed information: 1. Annotated peaks: peaks overlapping sncRNA genes or mature products with annotations. 2. Unannotated peaks: peaks that do not overlap with annotated sncRNA genes or mature products.	• Anno... • Unan... • All called peaks ... [bed]
Gene expression	Small RNA gene expression	• Gene expression table (xls) [3.31 MB]
Comparison with DASHR	Integrated expression tables	• Annotated peaks [xls] • Unannotated peaks [xls] • All (Annotated + Unannotated) peaks [xls] [bed] • Peaks not in DASHR [xls]
Comparison with ENCODE	Integrated expression tables	• Annotated peaks [xls] • Unannotated peaks [xls] • All (Annotated + Unannotated) peaks [xls] [bed] • Peaks not in ENCODE [xls]

Download results (Output)- sncRNA gene expression

Under "Gene Expression" section "smRNA_gene_expression.xls":

This table displays the read counts, as well as RPM expression values for the sncRNA genes identified

sncRNA gene name

#Gene	GeneClass	ReadCou	RPM
chr6:151619978:151620068:-:HY4	scRNA	66.7142	31.3062
chr3:48238061:48238078:+:hsa-miR-4443	mir-5p3pno	105	49.2722
chr6_ssto_hap7:3077413:3077494:-:HY3	scRNA	129.147	60.6034
chr1:17067010:17067174:+:U1	snRNA	37.2714	17.4899
chr6_cox_hap2:97136:97167:+:DQ598188:piR-36254	piRNA	174.713	81.9856
chrX:118780761:118780783:-:hsa-miR-766-5p	mir-5p	174.417	81.8467
chr10:38283790:38283901:+:HY1	scRNA	14.5489	6.8272
chr17:80626156:80626177:-:hsa-miR-4525	mir-5p3pno	60	28.1555
chr6:27248048:27248121:-:tRNA-Val-CAC-2-1	tRNA	41.799	19.6146
chr3:125235822:125235927:+:HY1	scRNA	30.4169	14.2734
chr10:103124606:103124792:-:U2	snRNA	99.2588	46.5781
chr10:69524340:69524360:+:trfdb-1001_chr10.trna2-SerTGA_chr10-69524261-69524342	tRF-1-trfdb	18088.8	8488.33
chr13:92003498:92003521:+:hsa-miR-19b-3p	mir-3p	22.5	10.5583
chr1:161493633:161493655:-:trfdb-3027b_chr1.trna68-GlyGCC_chr1-161493707-161493637	tRF-3-trfdb	16.2765	7.63789
chr16:3357711:3357744:-:DQ571003:piR-31115	piRNA	84.5773	39.6886
chr19:24182635:24183468:-:LSU-rRNA_Hsa	rRNA	341.065	160.048
chr6:86387011:86387086:-:U50	snoRNA	13.2333	6.20984
chr12:109029624:109029646:+:hsa-miR-4496	mir-5p3pno	63.4083	29.7549
chr7:128423560:128423578:+:trfdb-3002a_chr7.trna2-ProAGG_chr7-128423504-128423575	tRF-3-trfdb	47.6833	22.3758
chr11:79113120:79113143:-:hsa-miR-708-5p	mir-5p	11.3588	5.33022
chr16:22207031:22207113:-:tRNA-Leu-TAG-3-1	tRNA	77.7613	36.4902

Download results (Top) – comparison expression results with DASHR/ENCODE (1)

DOWNLOAD RESULTS   —

Content	Description	Download
Peak tracks	Genome-wide tracks	• plus ...track [...bed] [...] • minus...
Raw signal tracks	Genome-wide tracks	• plus... • minus...

Peak tables	Tables with detailed in...
	
	1. Annotated peaks: pe...
	   or mature products
	2. Unannotated peaks: peaks ...o not overlap with
	   annotated sncRNA genes or ...re products.
		• Anno...
		• Unan...
		• All called peaks [xls] [bed]

Gene expression	Small RNA gene expression	• Gene expression table (xls) [3.31 M...
Comparison with DASHR	Integrated expression tables	• Annotated peaks [xls] • Unannotated peaks [xls] • All (Annotated + Unannotated) peaks [xls] [bed] • Peaks not in DASHR [xls]
Comparison with ENCODE	Integrated expression tables	• Annotated peaks [xls] • Unannotated peaks [xls] • All (Annotated + Unannotated) peaks [xls] [bed] • Peaks not in ENCODE [xls]

Comparison expression tables

Step 2: Click to download peaks present in both the analysed data and also expressed in DASHR

Download results – comparison expression tables (using DASHR as example)

Under "Comparison with DASHR", download "DASHR_comparison_all.xls"

Called peak annotation and features

Comparison columns with all DASHR tissues (a total of 54 columns)

······

Download results (Top) – comparison expression results with DASHR/ENCODE (2)

DOWNLOAD RESULTS −

Content	Description	Download
Peak tracks	Genome-wide tracks	• plus strand [bigBED] [382.36 KB] • minus strand [bigBED] [384.94 KB]
Raw signal tracks	Genome-wide tracks	• plus strand [bigWig] [5.06 MB] • minus strand [bigWig] [3.60 MB]

Peak tables	Tables with detailed in
	1. Annotated peaks: pe
	   or mature products
	2. Unannotated peaks: peaks o not overlap with
	   annotated sncRNA genes o re products.
		• 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	• Annotated peaks [xls] • Unannotated peaks [xls] • All (Annotated + Unannotated) peaks [xls] [bed] • Peaks not in DASHR [xls]
Comparison with ENCODE	Integrated expression tables	• A ed peaks [xls] • Unannotated peaks [xls] • All (Annotated + Unannotated) peaks [xls] [bed] • Peaks not in ENCODE [xls]

Comparison expression tables

Step 3: Click to download peaks only in analysed data but not in DASHR

Download results – comparison expression tables (using DASHR as example)

Under "Comparison with DASHR", download "not_in_DASHR.xls"

Called peak annotation and features

Comparison columns with all DASHR tissues (a total of 54 columns)

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Since this loci are characterized in the analyzed data, but not in DASHR, therefore these columns do not contain and information from DASHR

Download results (Bottom) – download by sncRNA class

Total number of reads falling onto this RNA class

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	10	10	646,698	6.22
mir-3p	224	224	1,779,736	17.13
mir-5p	205	205	5,706,729	54.92
mir-5p3pno	66	66	30,553	0.29
piRNA	99	99	747,600	7.19
rRNA	98	81	42,675	0.41
scRNA	225	215	227,677	2.19
snRNA	137	132	17,896	0.17
snoRNA	34	29	341,572	3.29
tRF3	6	6	1,323	0.01
tRF5	9	9	998	0.01
tRNA	169	138	103,725	1.00

Step 1: Click to download, e.g. tRNA only loci results from SPAR

Download results (Output)

"peaks.byClass.tRNA.xls" shows all the tRNAs only loci results from SPAR

tRNA
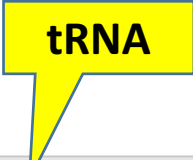
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
	#peakCl	peakChr	peakChr	peakID	peakExp	peakStra	peakEnt	peakNoi	peakMa	peakEnt	peakNoi	peakMa	peakPrc	peakPrc	peakMo	peakMo	beforeP	peakFol	peakRP	peakExp	annotCl	annotCl	annotCl	annotID	annotRM	annotSt	annotOv	peakOverlap
chr1	566409	566441	P208	165.52	-	1.5066	0.3686	4.0875	1.814	0.4765	3.8074	0.764	0.5786	1	32	1	127.46	77.673	83.84	chr1	566375	566375	chr1:566:	tRNA	-	0.4848	1
chr1	2E+07	2E+07	P182	14.343	-	0.5828	0.5828	1	1.3059	0.6529	2	0.8606	0.481	1	20	1	13.343	6.7305	17.28	chr1	2E+07	2E+07	chr1:1700	tRNA	-	0.2113	0.7143
chr1	6E+07	6E+07	P150	99.897	-	2.4114	0.6971	3.4594	2.117	0.6119	3.4594	0.3977	0.4232	2	21	14.32	2.2292	46.878	76	chr1	6E+07	6E+07	chr1:554:	tRNA	-	0.3014	1
chr1	9E+07	9E+07	P133	60.214	-	2.549	0.6113	4.1699	2.6187	0.5789	4.5236	0.4212	0.5349	16	42	6.4	3.3179	28.256	65.29	chr1	9E+07	9E+07	chr1:939:	tRNA	-	0.5753	1
chr1	9E+07	9E+07	P73	61.063	+	1.3674	0.4558	3	0.3504	0.2211	1.585	0.7566	0.944	1	19	2	24.1	28.654	65.48	chr1	9E+07	9E+07	chr1:943:	tRNA	+	0.2235	1
chr1	1E+08	1E+08	P90	35.067	+	2.1212	0.5732	3.7004	3.2388	0.8752	3.7004	0.585	0.2006	1	19	1	21.515	16.455	50.18	chr1	1E+08	1E+08	chr1:1465	tRNA	+	0.375	1
chr1	1E+08	1E+08	P109	28.893	-	1.2404	0.6202	2	0	0	0	0.7231	1	1	14	10.333	3.0219	13.558	43.39	chr1	1E+08	1E+08	chr1:1492	tRNA	-	0.1918	1
chr1	2E+08	2E+08	P116	12.143	+	0.0923	0.0923	1	1.6628	0.8314	2	0.9882	0.3889	1	22	1	13	5.6982	8.34	chr1	2E+08	2E+08	chr1:1615	tRNA	+	0.2222	0.7273
chr1	2E+08	2E+08	P117	13.813	+	1.1905	0.5953	2	0.4819	0.2075	2.3219	0.7538	0.9341	1	16	6.5028	2.6013	6.4817	15.05	chr1	2E+08	2E+08	chr1:1615	tRNA	+	0.2162	1
chr1	2E+08	2E+08	P177	68.028	+	0.715	0.2547	2.8074	2.8814	0.8329	3.4594	0.8802	0.1998	1	22	1	60.875	31.923	68.13	chr1	2E+08	2E+08	chr1:249:	tRNA	+	0.1981	0.84
chr1	2E+08	2E+08	P178	416.03	+	2.2091	0.6386	3.4594	0.9106	0.2872	3.1699	0.3551	0.8561	5	22	8.6167	3.6693	195.23	92.45	chr1	2E+08	2E+08	chr1:249:	tRNA	+	0.2075	1
chr10	7E+07	7E+07	P211	64.232	+	0.6255	0.169	3.7004	2.6592	0.8389	3.1699	0.9181	0.3211	1	19	1	60.2	30.141	66.76	chr10	7E+07	7E+07	chr10:69:	tRNA	-	0.3049	1
chr11	7E+07	7E+07	P285	33.504	+	1.8653	0.5041	3.7004	2.9986	0.8668	3.4594	0.5046	0.2813	5	23	5	3.0667	15.722	48.42	chr11	7E+07	7E+07	chr11:661	tRNA	+	0.2927	0.8571
chr13	3E+07	3E+07	P520	29.389	-	1.1193	0.7062	1.585	1.9064	0.6355	3	0.6805	0.5711	1	28	3	7.6667	13.791	43.93	chr13	3E+07	3E+07	chr13:312	tRNA	-	0.2973	0.7857
chr13	4E+07	4E+07	P515	93.093	-	2.3879	0.796	3	0.5992	0.189	3.1699	0.3343	0.9241	1	22	10.467	3.9754	43.685	74.68	chr13	4E+07	4E+07	chr13:416	tRNA	-	0.2917	0.9545
chr14	3E+07	3E+07	P469	164.52	+	1.5134	0.3703	4.0875	1.814	0.4765	3.8074	0.7626	0.5786	1	32	2	63.732	77.203	83.65	chr14	3E+07	3E+07	chr14:32:	tRNA	+	0.4848	1
chr14	7E+07	7E+07	P495	32.907	+	0.9171	0.3548	2.585	1.2323	0.2901	4.2479	0.8199	0.8394	1	27	10.185	3.649	15.442	47.63	chr14	7E+07	7E+07	chr14:73:	tRNA	+	0.375	1
chr15	4E+07	4E+07	P686	32.838	-	1.3028	0.3766	3.4594	2.6176	0.8725	3	0.5148	0.3322	3	21	1	15.667	15.409	47.59	chr15	4E+07	4E+07	chr15:40:	tRNA	-	0.2683	0.9167
chr15	8E+07	8E+07	P552	25.506	+	0.2239	0.1413	1.585	1.8486	0.4145	4.4594	0.9701	0.725	1	27	23.774	2.057	11.969	39.37	chr15	8E+07	8E+07	chr15:800	tRNA	+	0.3699	1
chr15	9E+07	9E+07	P560	591.57	+	3.5177	0.7575	4.6439	1.7207	0.4519	3.8074	0.2132	0.6654	26	43	4.4995	10.375	277.6	94.39	chr15	9E+07	9E+07	chr15:89:	tRNA	+	0.589	1
chr16	686734	686754	P763	911.02	-	2.0836	0.6573	3.1699	0.1019	0.0363	2.8074	0.538	0.9899	5	20	62.102	3.6824	427.51	95.81	chr16	686735	686806	chr16:68!	tRNA	-	0.2676	0.95
chr16	3E+06	3E+06	P571	116.42	+	2.0454	0.6818	3	0.2589	0.1115	2.3219	0.5146	0.9643	4	20	2.037	8.1318	54.632	79.09	chr16	3E+06	3E+06	chr16:32(	tRNA	+	0.274	1
chr16	3E+06	3E+06	P572	294.87	+	1.8991	0.549	3.4594	0.1858	0.08	2.3219	0.663	0.9781	3	22	3.85	4.303	138.37	90.29	chr16	3E+06	3E+06	chr16:32(	tRNA	+	0.3014	1
chr16	3E+06	3E+06	P582	294.67	+	1.8991	0.5461	3.4594	0.1985	0.0855	2.3219	0.6635	0.9763	3	22	3.6	4.6019	138.27	90.27	chr16	3E+06	3E+06	chr16:32(	tRNA	+	0.3014	1
chr16	1E+07	1E+07	P588	36.374	+	0	0	0	0	0	0	1	1	1	15	2	19.187	17.069	51.34	chr16	1E+07	1E+07	chr16:143	tRNA	+	0.2083	1
chr16	2E+07	2E+07	P740	50.523	-	2.1219	0.7073	3	1.8152	0.7818	2.3219	0.5542	0.4519	1	20	8.5	4.2941	23.709	61.36	chr16	2E+07	2E+07	chr16:22:	tRNA	-	0.2439	1
chr16	2E+07	2E+07	P739	27.238	-	2.4514	0.6838	3.585	3.2661	0.836	3.9069	0.4001	0.213	1	23	1	13	12.782	41.55	chr16	2E+07	2E+07	chr16:22:	tRNA	-	0.3902	0.8
chr17	8E+06	8E+06	P643	13.5	+	0	0	0	0	0	0	1	1	1	15	1	14.5	6.335	13.56	chr17	8E+06	8E+06	chr17:80:	tRNA	+	0.1705	1
chr17	8E+06	8E+06	P645	57.349	+	2.2389	0.7063	3.1699	0.5244	0.2259	2.3219	0.5014	0.923	1	19	19.297	2.4901	26.911	64.21	chr17	8E+06	8E+06	chr17:80:	tRNA	-	0.2639	1
chr17	8E+06	8E+06	P646	13.682	+	0.4877	0.1737	2.8074	2.0583	0.7332	2.8074	0.936	0.5388	1	18	7.7333	2.7292	6.4203	14.1	chr17	8E+06	8E+06	chr17:80:	tRNA	+	0.2195	1
chr17	8E+06	8E+06	P833	50.482	-	1.7882	0.7701	2.3219	0.6439	0.2294	2.8074	0.5611	0.9091	1	19	19.297	2.4901	23.689	61.27	chr17	8E+06	8E+06	chr17:812	tRNA	-	0.2639	1
chr17	2E+07	2E+07	P664	41.5	+	0.8671	0.3735	2.3219	0.2233	0.2233	1	0.8514	0.9641	1	18	1	36.333	19.474	55.63	chr17	2E+07	2E+07	chr17:194	tRNA	+	0.25	1
chr17	2E+07	2E+07	P665	556.58	+	2.0738	0.6542	3.1699	0.389	0.1675	2.3219	0.564	0.9474	3	21	40.073	2.2712	261.18	94.07	chr17	2E+07	2E+07	chr17:194	tRNA	+	0.2917	1
chr17	3E+07	3E+07	P674	32.374	+	0	0	0	0	0	0	1	1	1	15	6	6.3957	15.192	47.24	chr17	3E+07	3E+07	chr17:29:	tRNA	+	0.2083	1
chr17	4E+07	4E+07	P810	23.223	-	1.4475	0.7237	2	1.7436	0.5812	3	0.5598	0.4829	1	28	1	14	10.898	36.16	chr17	4E+07	4E+07	chr17:36:	tRNA	-	0.2973	0.7857
chr17	4E+07	4E+07	P809	33.292	-	0.9682	0.3449	2.8074	1.3061	0.3195	4.0875	0.8135	0.8204	1	27	10.303	3.6285	15.622	48.05	chr17	4E+07	4E+07	chr17:36:	tRNA	+	0.375	1
chr17	7E+07	7E+07	P775	2690.3	-	1.5571	0.381	4.0875	0.2108	0.0703	3	0.499	0.9761	8	28	11.313	2.1491	1262.5	98.11	chr17	7E+07	7E+07	chr17:66(	tRNA	-	0.3836	1

peaks.byClass.tRNA

Download results (Bottom) – download by sncRNA class

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

Total number of reads falling onto this RNA class

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
iRNAprimary	10	10	646,698	6.22
r-3p	224	224	1,779,736	17.13
-5p	205	205	5,706,729	54.92
5p3pno	66	66	30,553	0.29
	99	99	747,600	7.19
	98	81	42,675	0.41
s	225	215	227,677	2.19
s	137	132	17,896	0.17
s	34	29	341,572	3.29
tR	6	6	1,323	0.01
tR	9	9	998	0.01
tR	169	138	103,725	1.00

Optional: Click to download all annotated loci from SPAR

Download results (Output)

"peaks_unannot.xls" under "Peak Tables" show all the unannotated peaks found by running SPAR

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	#peakChr	peakChrS	peakChrE	peakID	peakExpr	peakStra	peakEntr	peakNorr	peakMax	peakEntr	peakNorr	peakMax	peakProp	peakProp	peakMos	peakMos	beforePe	peakFolc	peakRPN	peakExpr	annotChr	annotChr	annotChr	annotID	annotRN
2	chr1	564929	564950	P209	1061.8	-	0.1062	0.0378	2.8074	1.0059	0.3891	2.585	0.9888	0.8137	1	21	1.5	700.96	498.27	96.37	.	-1	-1	.	OTHER
3	chr1	568037	568065	P207	18.806	-	0.4746	0.2994	1.585	1.8945	0.5976	3.1699	0.9202	0.6489	1	28	2	9.6528	8.8247	27.87	.	-1	-1	.	OTHER
4	chr1	568136	568160	P1	12.608	+	0	0	0	2.3345	0.9031	2.585	1	0.3082	1	18	6.125	3.0585	5.9166	9.81	.	-1	-1	.	OTHER
5	chr1	568203	568220	P206	11.535	-	0	0	0	0.4914	0.31	1.585	1	0.9034	1	17	1	12.535	5.4127	5.66	.	-1	-1	.	OTHER
6	chr1	568843	568873	P2	37.682	+	0.0731	0.0731	1	2.712	0.7839	3.4594	0.9912	0.3864	1	27	1	38.349	17.683	52.73	.	-1	-1	.	OTHER
7	chr1	1E+06	1E+06	P205	369.53	-	0.0191	0.0191	1	0.0347	0.0347	1	0.9982	0.9964	1	16	6	62.477	173.4	91.69	.	-1	-1	.	OTHER
8	chr1	1E+06	1E+06	P3	13.052	+	0.087	0.087	1	0	0	0	0.9891	1	1	15	3	5.3032	6.125	11.82	.	-1	-1	.	OTHER
9	chr1	1E+06	1E+06	P4	219.81	+	0.9901	0.6247	1.585	0	0	0	0.5917	1	1	15	3	44.353	103.15	87.28	.	-1	-1	.	OTHER
10	chr1	1E+06	1E+06	P204	236.5	-	1.5563	0.9819	1.585	0.3038	0.3038	1	0.4253	0.9458	2	16	2	37.458	110.98	87.91	.	-1	-1	.	OTHER
11	chr1	2E+06	2E+06	P203	39.912	-	0.9965	0.6287	1.585	0	0	0	0.6655	1	2	15	2	7.4249	18.729	54.72	.	-1	-1	.	OTHER
12	chr1	3E+06	3E+06	P202	22.048	-	0.8166	0.8166	1	0	0	0	0.7466	1	1	15	1.3333	13.346	10.346	34.15	.	-1	-1	.	OTHER
13	chr1	3E+06	3E+06	P201	178.76	-	0	0	0	0	0	0	1	1	1	14	1	179.76	83.885	85.19	.	-1	-1	.	OTHER
14	chr1	4E+06	4E+06	P200	63.217	-	0	0	0	0	0	0	1	1	1	14	4.95	13.771	29.665	66.24	.	-1	-1	.	OTHER
15	chr1	4E+06	4E+06	P199	23.086	-	0.2843	0.2843	1	0	0	0	0.9505	1	1	14	1.5	15.629	10.833	35.84	.	-1	-1	.	OTHER
16	chr1	5E+06	5E+06	P5	15.336	+	0.8645	0.5455	1.585	0.1435	0.1435	1	0.802	0.9796	1	16	1.0333	12.903	7.1967	19.86	.	-1	-1	.	OTHER
17	chr1	5E+06	5E+06	P198	12.07	-	0.1286	0.1286	1	0	0	0	0.9822	1	1	15	1	12.855	5.6637	7.99	.	-1	-1	.	OTHER
18	chr1	6E+06	6E+06	P197	12.032	-	0.0424	0.0424	1	0	0	0	0.9954	1	1	15	1	12.976	5.646	7.97	.	-1	-1	.	OTHER
19	chr1	6E+06	6E+06	P196	61	-	0.967	0.967	1	0	0	0	0.6066	1	1	15	1	38	28.625	65.46	.	-1	-1	.	OTHER
20	chr1	7E+06	7E+06	P195	35.1	-	0.1868	0.1868	1	0.5412	0.5412	1	0.9715	0.8759	1	15	4.8333	8.0552	16.471	50.23	.	-1	-1	.	OTHER
21	chr1	7E+06	7E+06	P6	14.926	+	0.4463	0.2231	2	1.4408	0.6205	2.3219	0.9337	0.6707	1	17	10.659	2.3074	7.0039	18.73	.	-1	-1	.	OTHER
22	chr1	7E+06	7E+06	P194	16.016	-	0.9698	0.6119	1.585	0	0	0	0.7766	1	1	15	2.5	5.9752	7.5155	21.62	.	-1	-1	.	OTHER
23	chr1	8E+06	8E+06	P193	33.786	-	1.1748	0.7412	1.585	0.1668	0.1668	1	0.68	0.9754	1	16	1	23.974	15.854	48.64	.	-1	-1	.	OTHER
24	chr1	9E+06	9E+06	P192	12.962	-	0.5719	0.3608	1.585	0.6173	0.6173	1	0.8942	0.847	1	16	1.616	8.1724	6.0827	11.13	.	-1	-1	.	OTHER
25	chr1	1E+07	1E+07	P191	15.083	-	0	0	0	0	0	0	1	1	1	15	1	16.083	7.078	19.29	.	-1	-1	.	OTHER
26	chr1	1E+07	1E+07	P190	16.7	-	0	0	0	0	0	0	1	1	1	14	3.1333	6.3298	7.8366	23.07	.	-1	-1	.	OTHER
27	chr1	1E+07	1E+07	P7	28.167	+	0	0	0	0	0	0	1	1	1	16	6	5.6945	13.218	42.44	.	-1	-1	.	OTHER
28	chr1	1E+07	1E+07	P189	91.208	-	1.4214	0.8968	1.585	0.0466	0.0466	1	0.546	0.9943	1	16	3.7833	14.162	42.8	74.48	.	-1	-1	.	OTHER
29	chr1	1E+07	1E+07	P8	201.88	+	0.0166	0.0166	1	0	0	0	0.9985	1	1	14	4.0846	50.35	94.736	86.32	.	-1	-1	.	OTHER
30	chr1	1E+07	1E+07	P9	33.125	+	0.3437	0.3437	1	0	0	0	0.9358	1	1	16	1	32	15.544	47.95	.	-1	-1	.	OTHER
31	chr1	2E+07	2E+07	P188	65.392	-	0.1309	0.0826	1.585	0.0059	0.0059	1	0.9839	0.9995	1	16	1	65.341	30.686	67.3	.	-1	-1	.	OTHER
32	chr1	2E+07	2E+07	P10	26.967	+	0	0	0	0	0	0	1	1	1	14	2.7	10.988	12.654	41.19	.	-1	-1	.	OTHER

Run log (Output)

DOWNLOAD RESULTS −

Content	Description	Download
Peak tracks	Genome-wide tracks	plus strand [bigBED] [382.36 KB] minus strand [bigBED] [384.94 KB]
Raw signal tracks	Genome-wide tracks	plus strand [bigWig] [5.86 MB] minus strand [bigWig] [3.60 MB]
Peak tables	Tables with detailed information: 1. Annotated peaks: peaks overlapping sncRNA genes or mature products with annotations. 2. Unannotated peaks: peaks that do not overlap with annotated sncRNA genes or mature products.	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	Annotated peaks [xls] Unannotated peaks [xls] All (Annotated + Unannotated) peaks [xls] [bed] Peaks not in DASHR [xls]
Comparison with ENCODE	Integrated expression tables	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	285	285	5,706,729	54.92
mir-5p3pno	66	66	30,553	0.29
piRNA	99	99	747,608	7.19
rRNA	98	81	42,675	0.41
scRNA	225	215	227,677	2.19
snRNA	137	132	17,896	0.17
snoRNA	34	29	341,572	3.29
tRF3	6	6	1,323	0.01
tRF5	9	9	998	0.01
tRNA	169	138	103,725	1.00

RUN LOG +

Questions?
SPAR@tsenwenglab.org

Run log (Output)

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

Questions?
SPAR@lisanwanglab.org

Wang Lab | Penn Neurodegeneration ... nomics Center | University of Pennsylvania

**Send questions to this email:
SPAR@lisanwanglab.org**

END