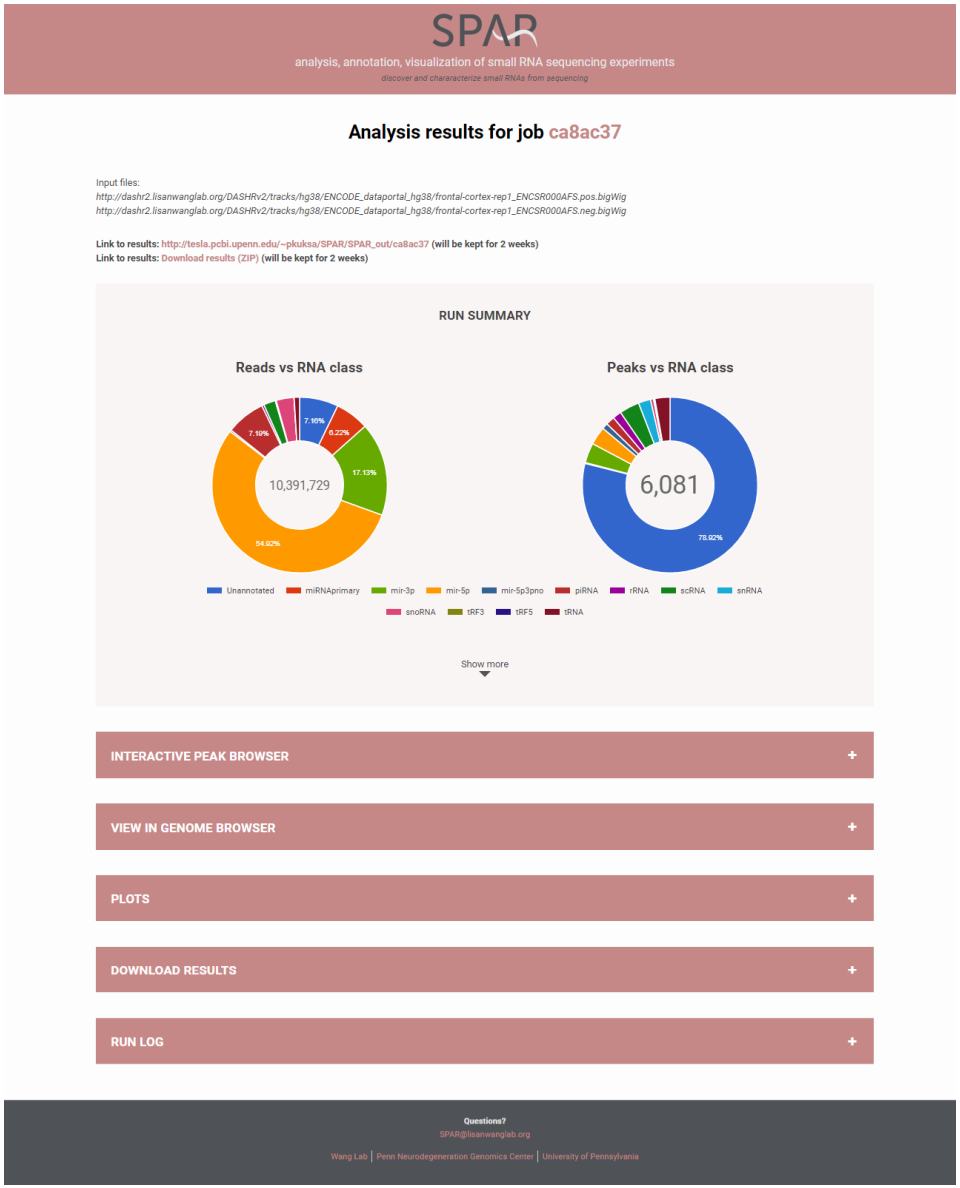
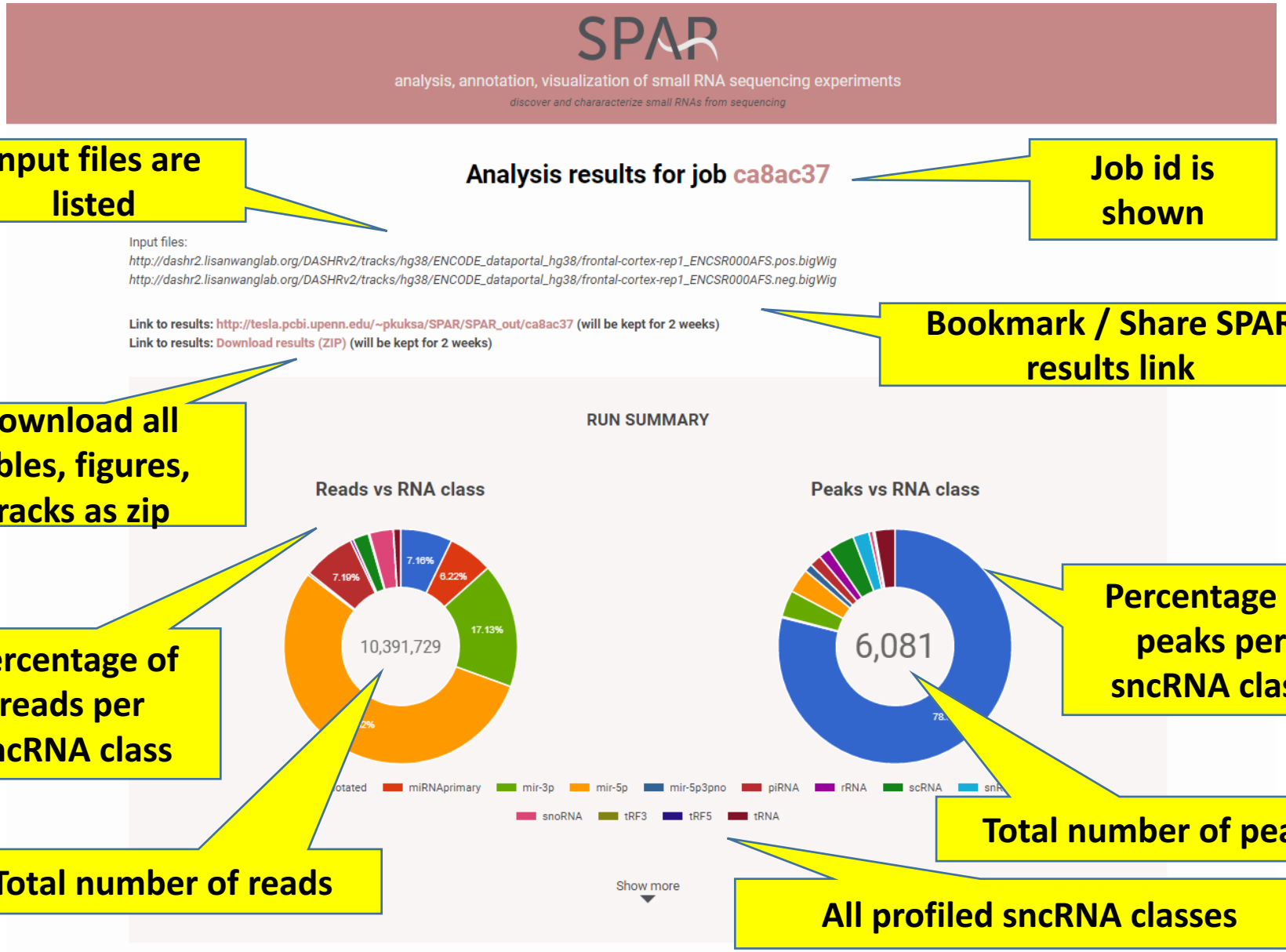
SPAR outputs and report page

Landing results page (full view)



Landing results / outputs page (top)



Landing results / outputs page (top)

SPAR

analysis, annotation, visualization of small RNA sequencing experiments

discover and chararacterize small RNAs from sequencing

Analysis results for job ca8ac37

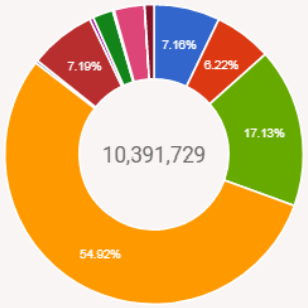
Input files:
http://dashr2.lisanwanglab.org/DASHRv2/tracks/hg38/ENCODE_dataportal_hg38/frontal-cortex-rep1_ENCSR000AFS.pos.bigWig
http://dashr2.lisanwanglab.org/DASHRv2/tracks/hg38/ENCODE_dataportal_hg38/frontal-cortex-rep1_ENCSR000A

Link to results: http://tesla.pcbi.upenn.edu/~pkuksa/SPAR/SPAR_out/ca8ac37 **(will be kept for 2 weeks)**
Link to results: Download results (ZIP) **(will be kept for 2 weeks)**

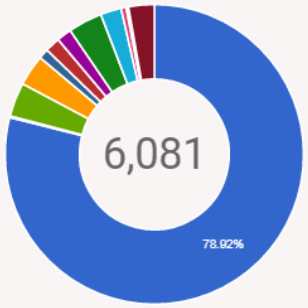
To view a report (in html / pdf): Click "Link to results: https://www.lisanwanglab.org/SPAR/SPAR_out/ca8ac37

RUN SUMMARY

Reads vs RNA class



Peaks vs RNA class



Unannotated miRNAprimary mir-3p mir-5p mir-5p3pno piRNA rRNA scRNA snRNA
snoRNA tRF3 tRF5 tRNA

Show more

Landing results → SPAR report page

Index of /~pkuksa/SPAR/SPAR_out/ca8ac37

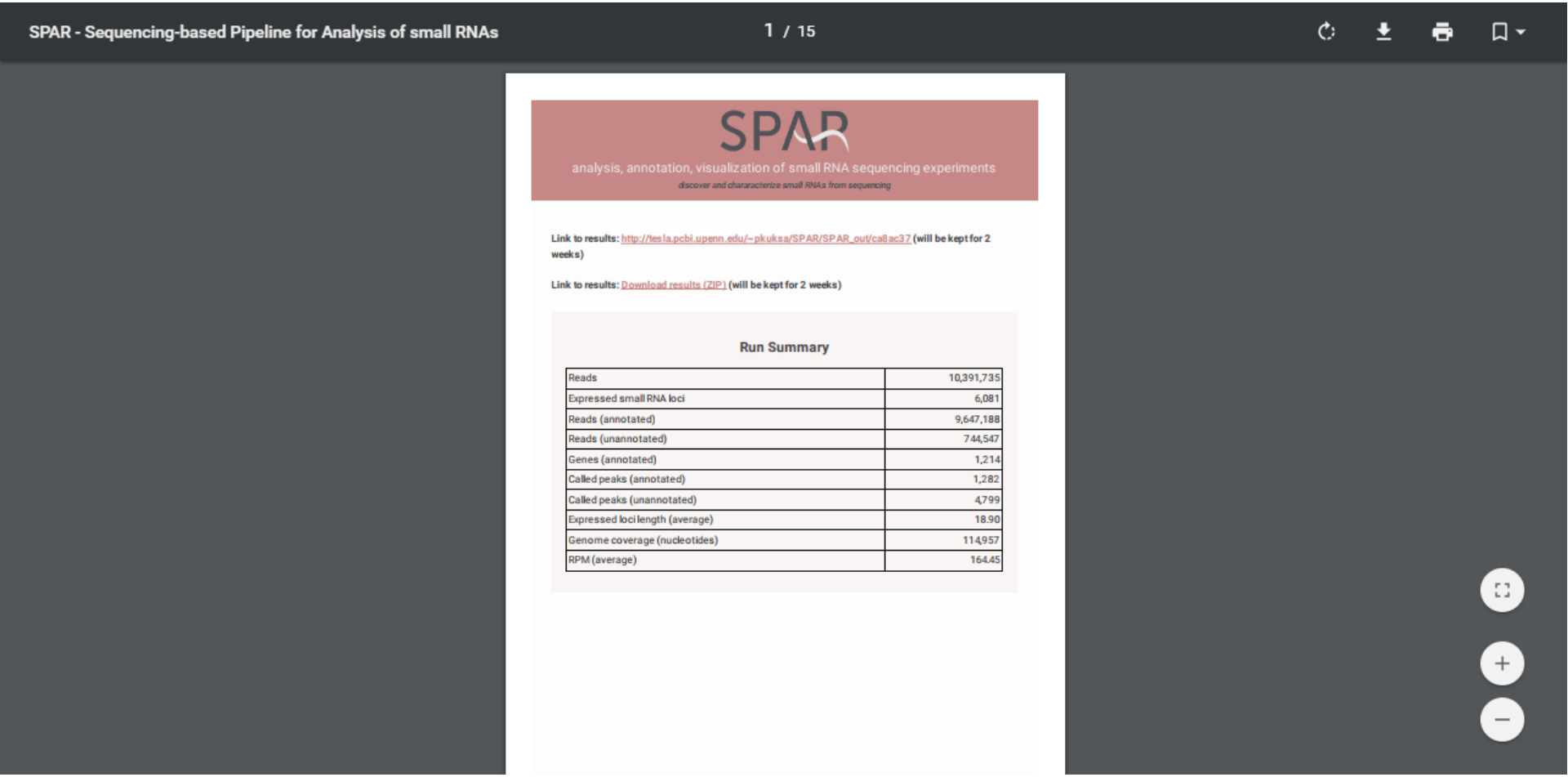
Name	Last modified	Size	Description
Parent Directory		-	
DASHR_comparison/	26-Jan-2018 15:38	-	
ENCODE_comparison/	26-Jan-2018 15:39	-	
figures/	26-Jan-2018 15:39	-	
inputs/	26-Jan-2018 15:37	-	
logs/	26-Jan-2018 15:39	-	
results/	26-Jan-2018 15:39	-	
tracks/	26-Jan-2018 15:[illegible]		
report.html	26-Jan-2018 15:39	40K	
report.pdf	26-Jan-2018 15:39	1.8M	
results.html	26-Jan-2018 15:39	2.4K	
run_summary.html	26-Jan-2018 15:39	584	
SPAR.hg38.config	26-Jan-2018 15:37	2.0K	

Apache/2.2.3 (CentOS) Server at tesla.pcbi.upenn.edu Port 80

Report is available in html / pdf

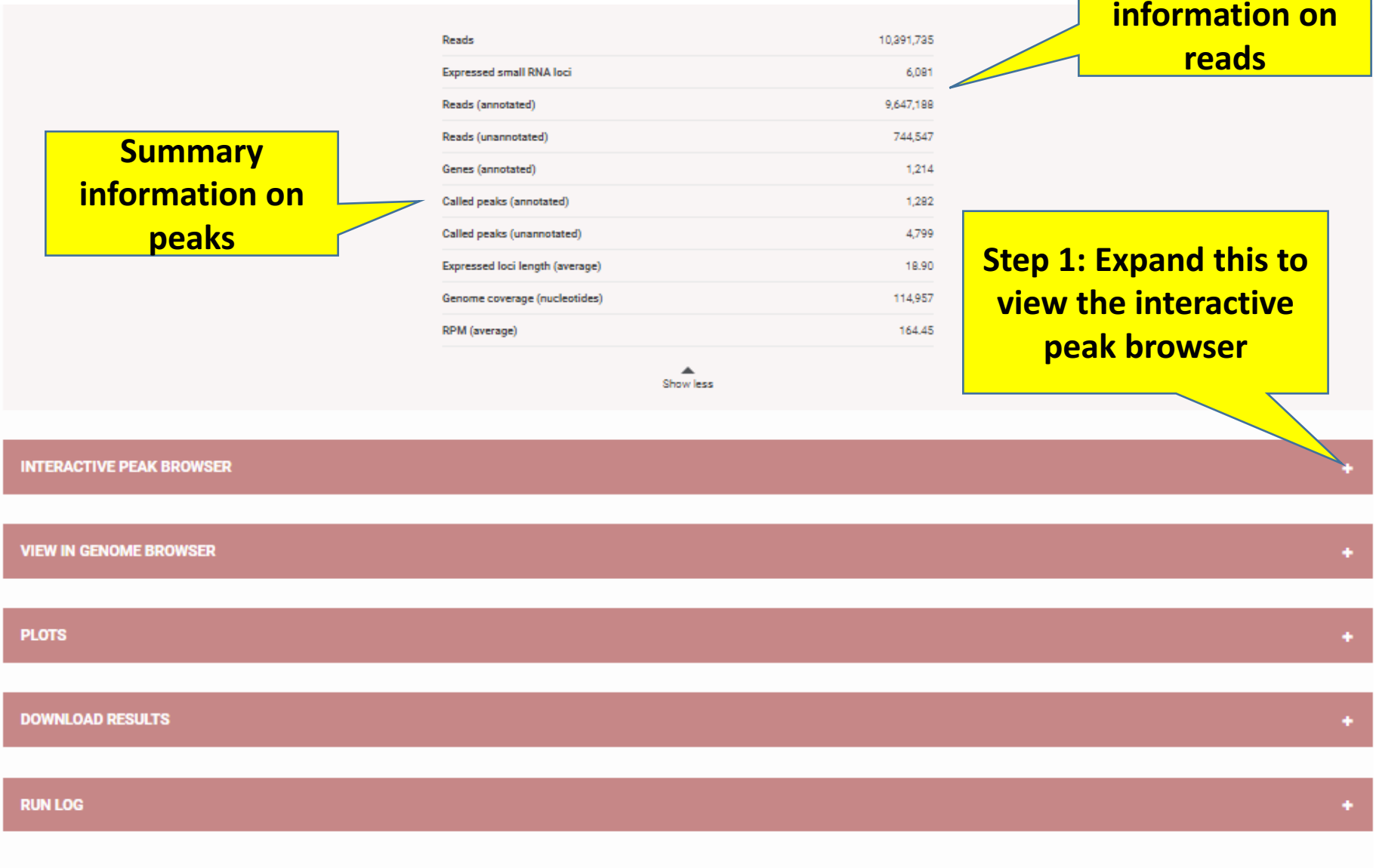
SPAR report.pdf

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

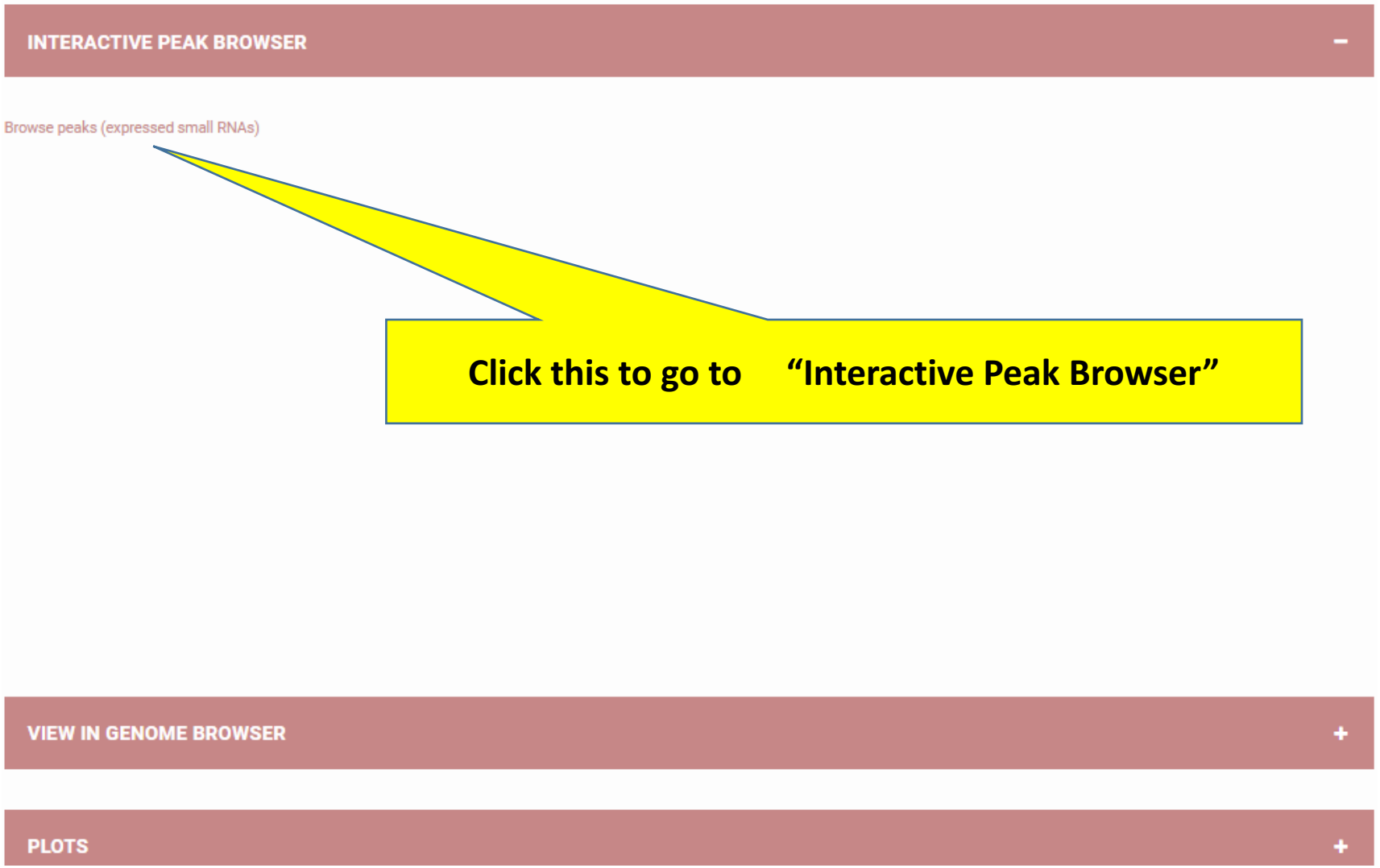


Landing results / outputs page (bottom)

After clicking show more at the bottom of the “Run Summary”



Interactive Peak Browser (Output)



Interactive Peak Browser (Output)

Total number of called peaks (annotated or unannotated)

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

INTERACTIVE PEAK BROWSER

Browse peaks (expressed small RNA

Download Table

Loci: 1-10 / 6081 Page 1 of 609 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	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 sncRNA loci with the top 5% of expression

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

Number of loci that passed this criteria: 60

INTERACTIVE PEAK BROWSER

Browse peaks (expressed small RNAs)

Download Table

Loci: 1-10 / 60 — Page 1 of 6 — 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			95.		Clear		Clear	Clear	Clear
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-	tRNA	0.8393	Intergenic	lncRNA Exon	Non-repeat

Interactive Peak Browser (Output)

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

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

INTERACTIVE PEAK BROWSER

Browse peaks (expressed small RNAs)

Download Table

Number of loci that fulfilled these criteria: 4

Loci: 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?
Clear			Clear			95.		Clear		mRNA	Clear	Clear
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	173 .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	-	0.3	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

Interactive Peak Browser (Output)

Hg38 reference genome

Peak coordinates and length

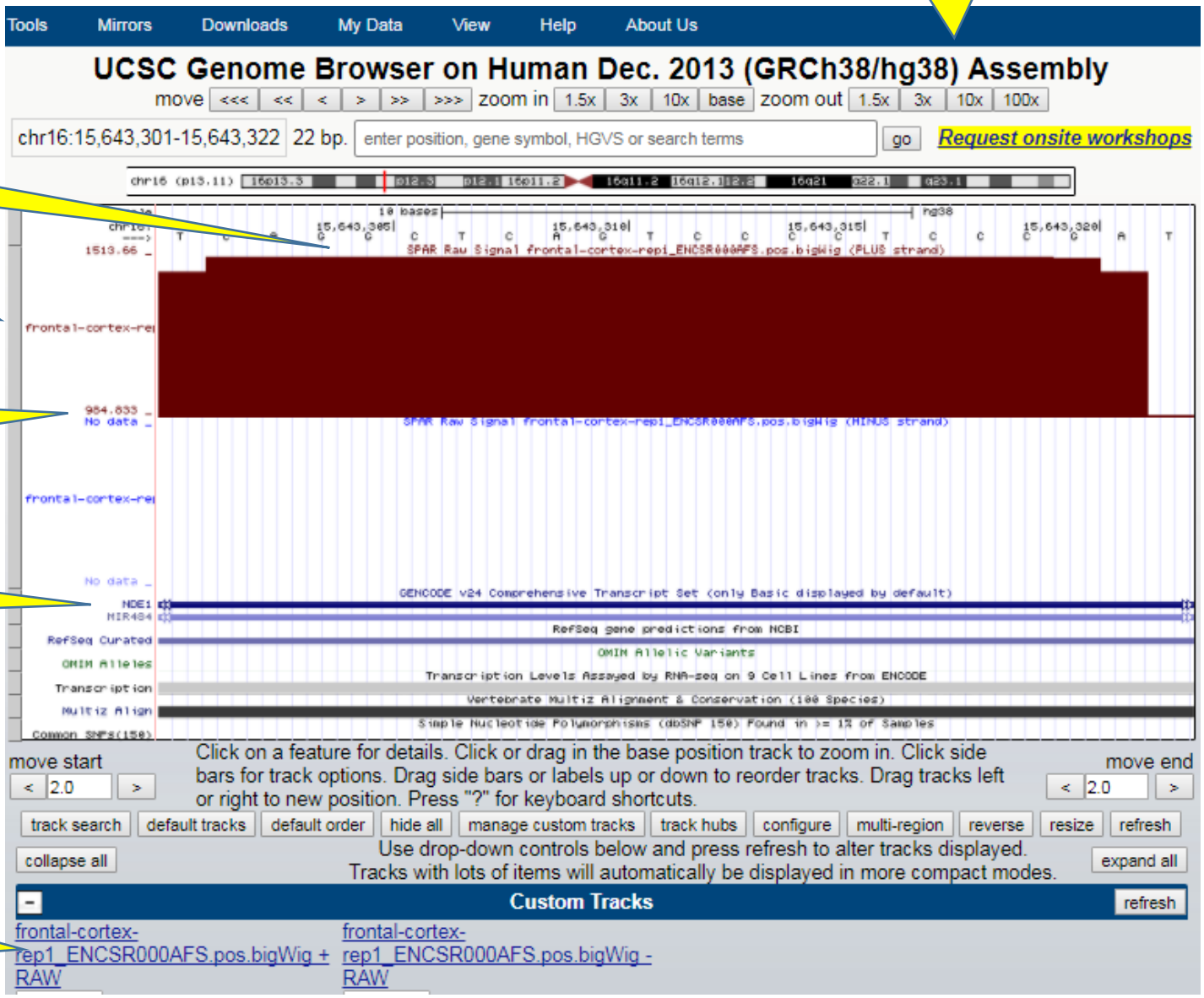
SPAR Peak profile on positive strand

Tissue: frontal cortex

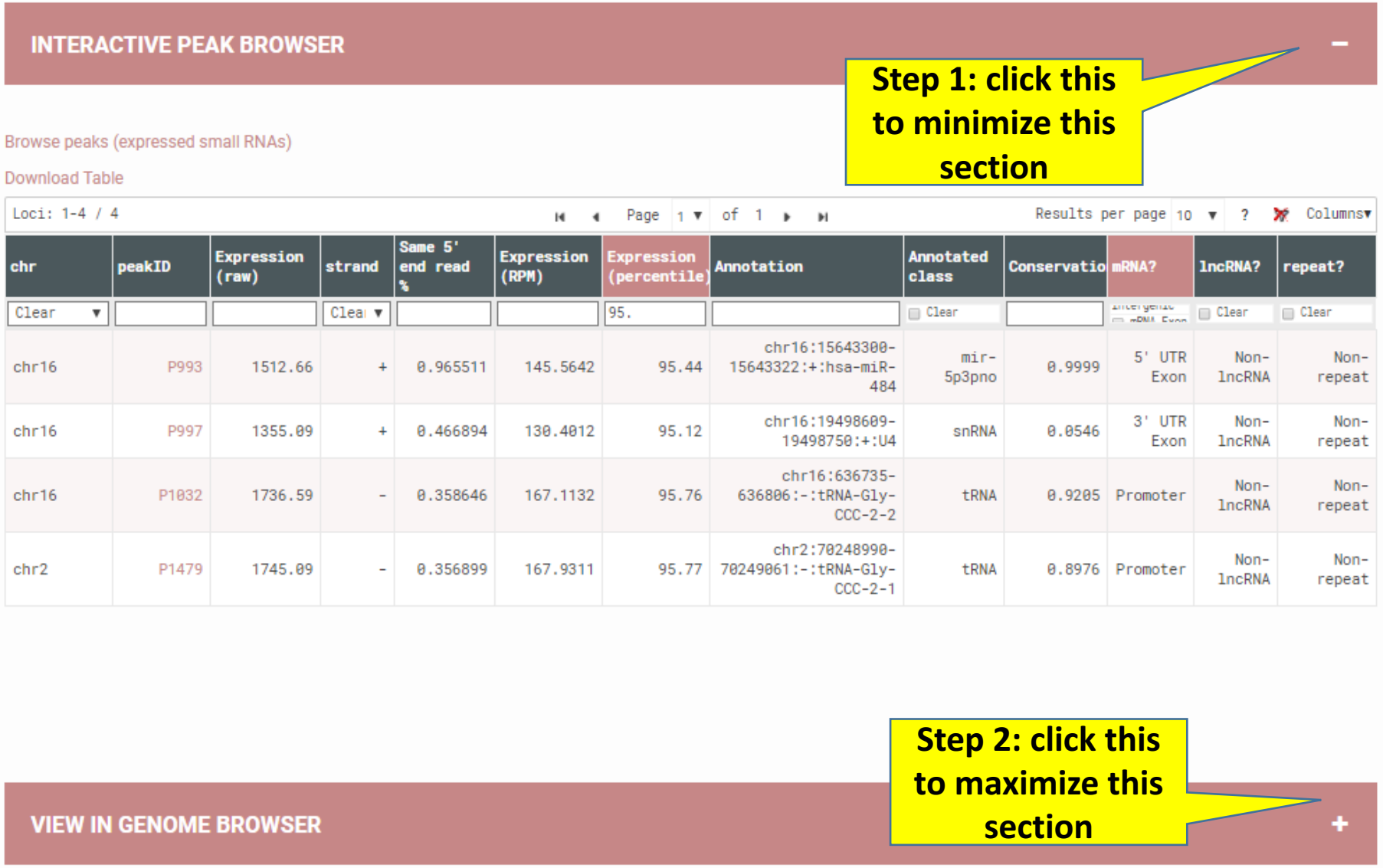
Peak expression value

Annotation: mir484

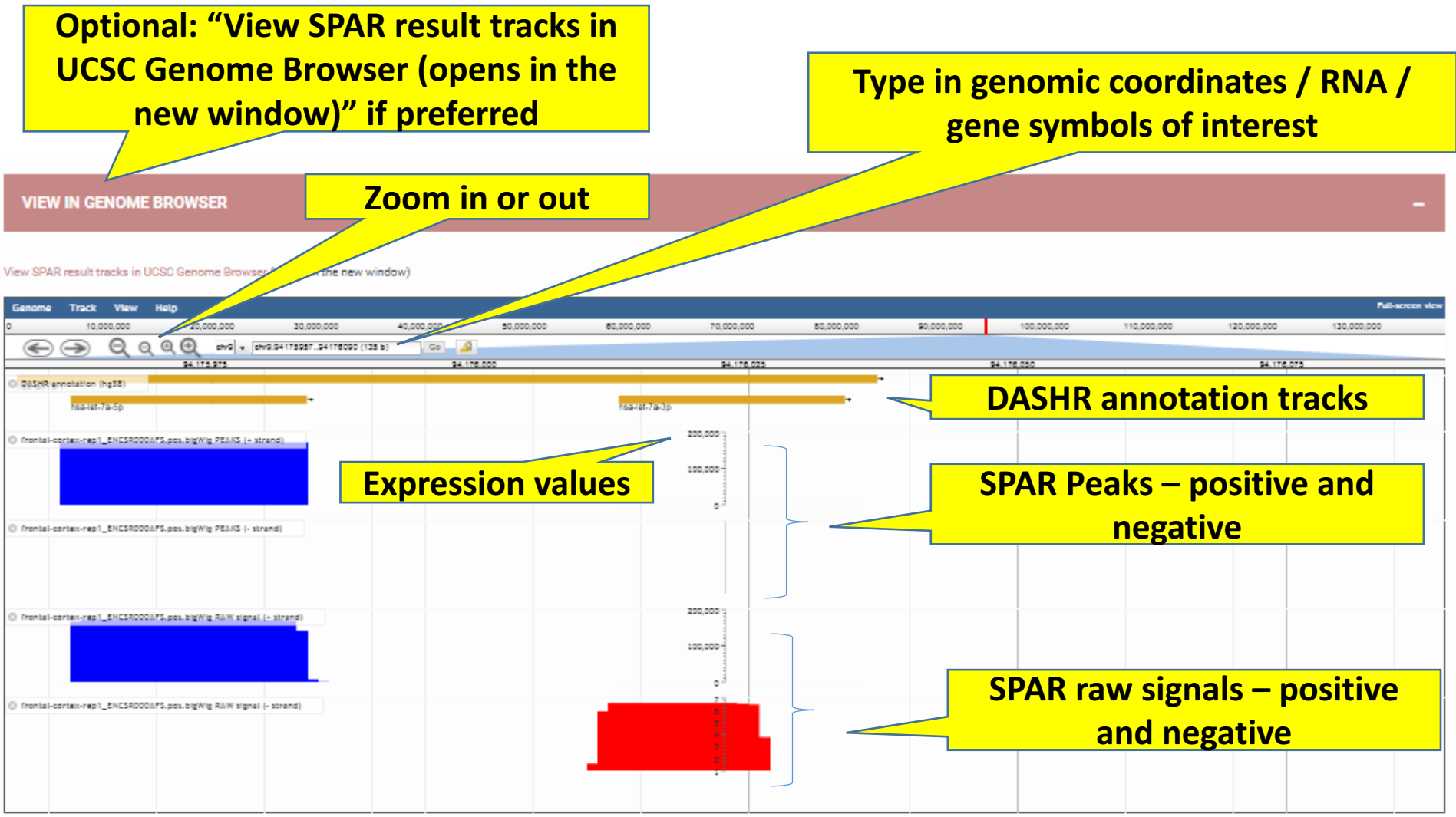
Configuration for SPAR tracks



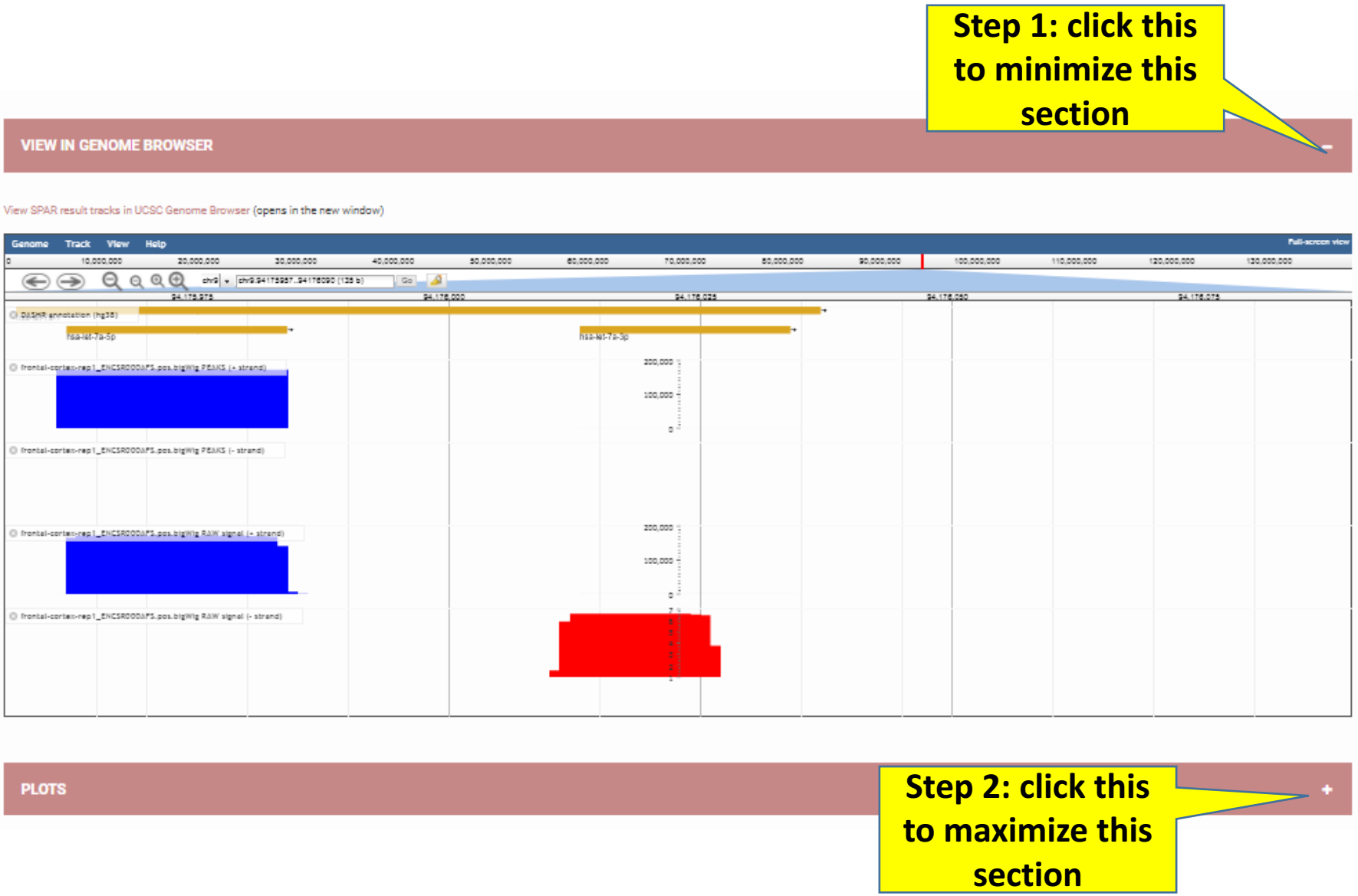
Finish exploring Interactive Peak Browser, next view peaks in genome browser



View in Genome Browser (Output)



Finish exploring Genome browser, quickly understand the data in a genomewide view



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

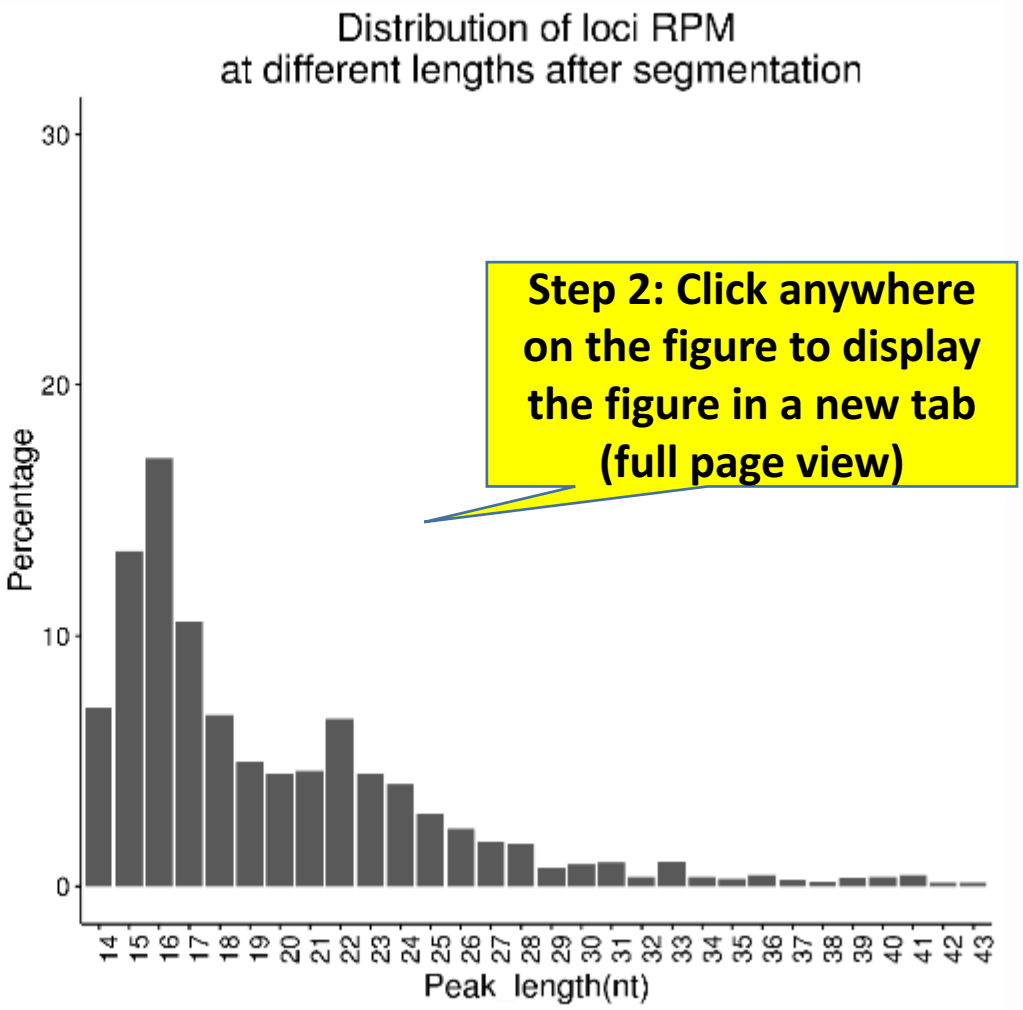
Proportion of expressed annotated small rna genes

Genomewide distribution patterns of small rna loci

Genomewide distribution of expressed small rna loci

Proportion of mapped reads across all loci

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



Step 2: Click anywhere on the figure to display the figure in a new tab (full page view)

Plots (Output) – 1

PLOTS

4 different plot sessions

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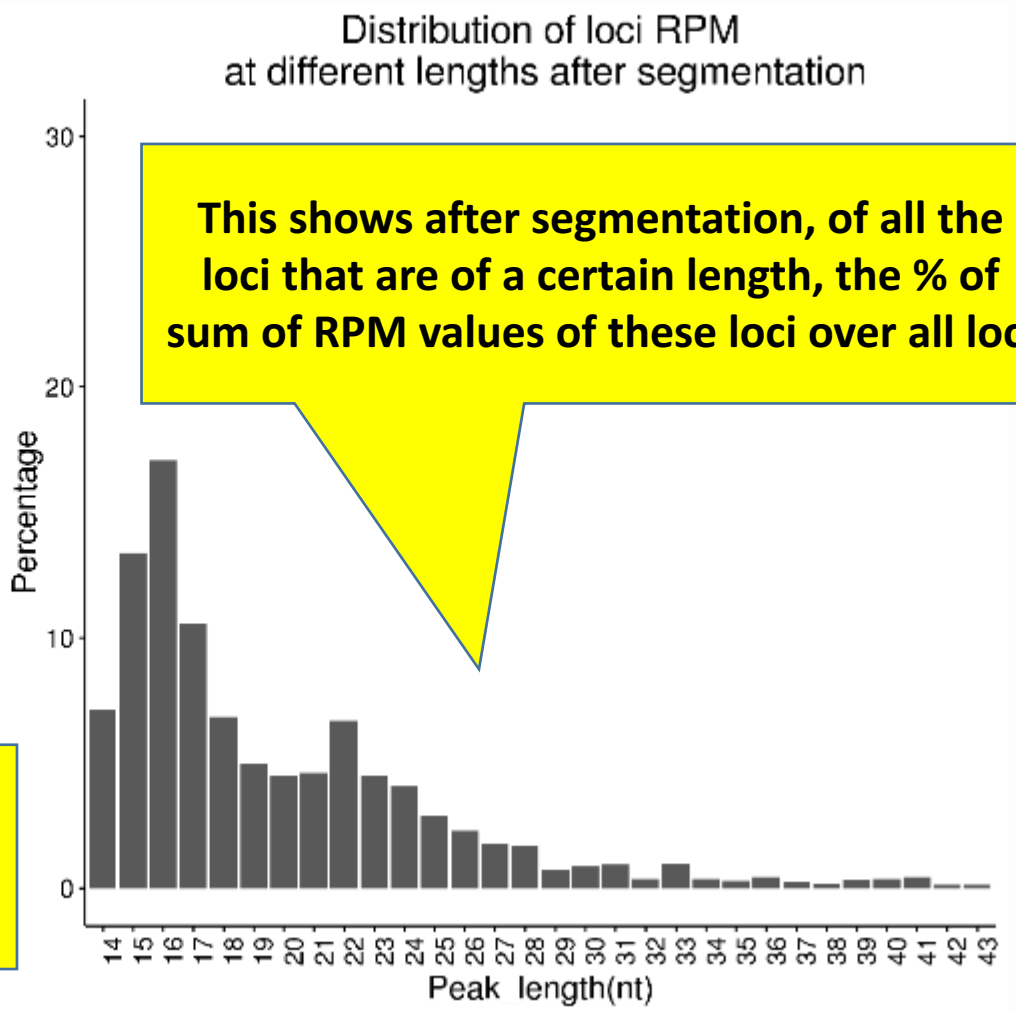

This shows after segmentation, of all the loci that are of a certain length, the % of sum of RPM values of these loci over all loci

Plots (Output) - 2

PLOTS –

SEGMENTATION

Length distribution of rpm of segmented loci

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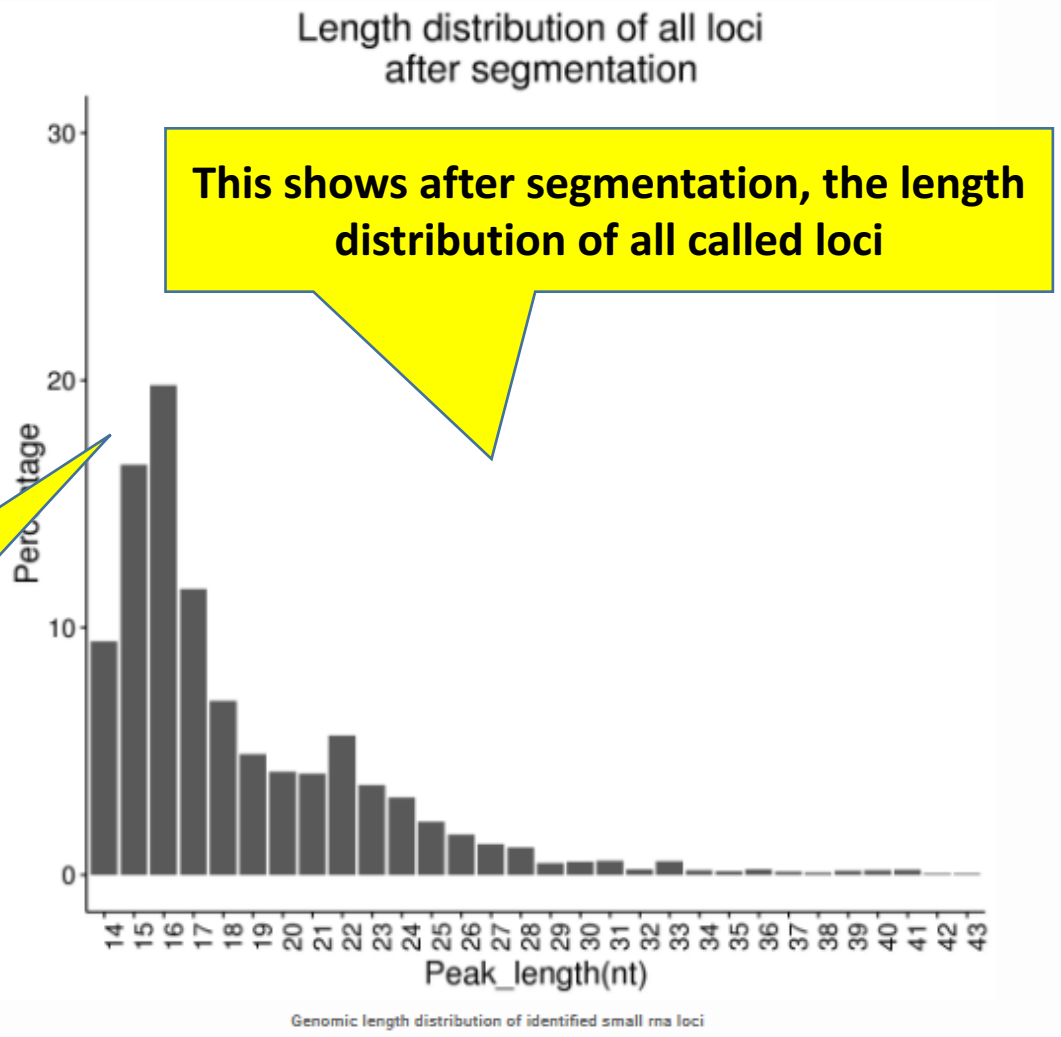

This shows after segmentation, the length distribution of all called loci

This shows most of the peaks are between 15-17 nt long

Plots (Output) - 3

PLOTS

SEGMENTATION

Length distribution of rpm of segmented loci

Genomic length distribution of identified small rna loci

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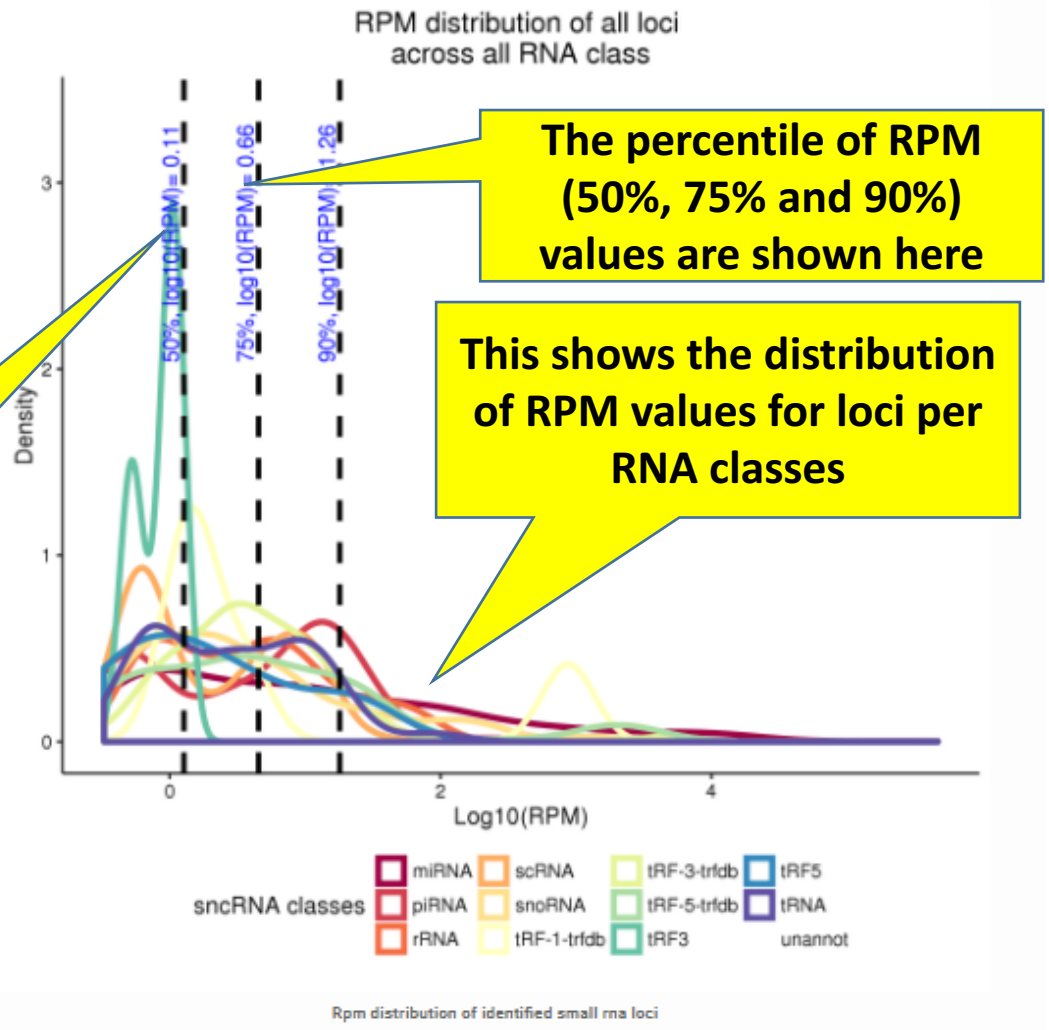

The percentile of RPM (50%, 75% and 90%) values are shown here

This shows the distribution of RPM values for loci per RNA classes

This shows tRF3 are lowly expressed, compared to other classes

Rpm distribution of identified small rna loci

Plots (Output) – 4

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

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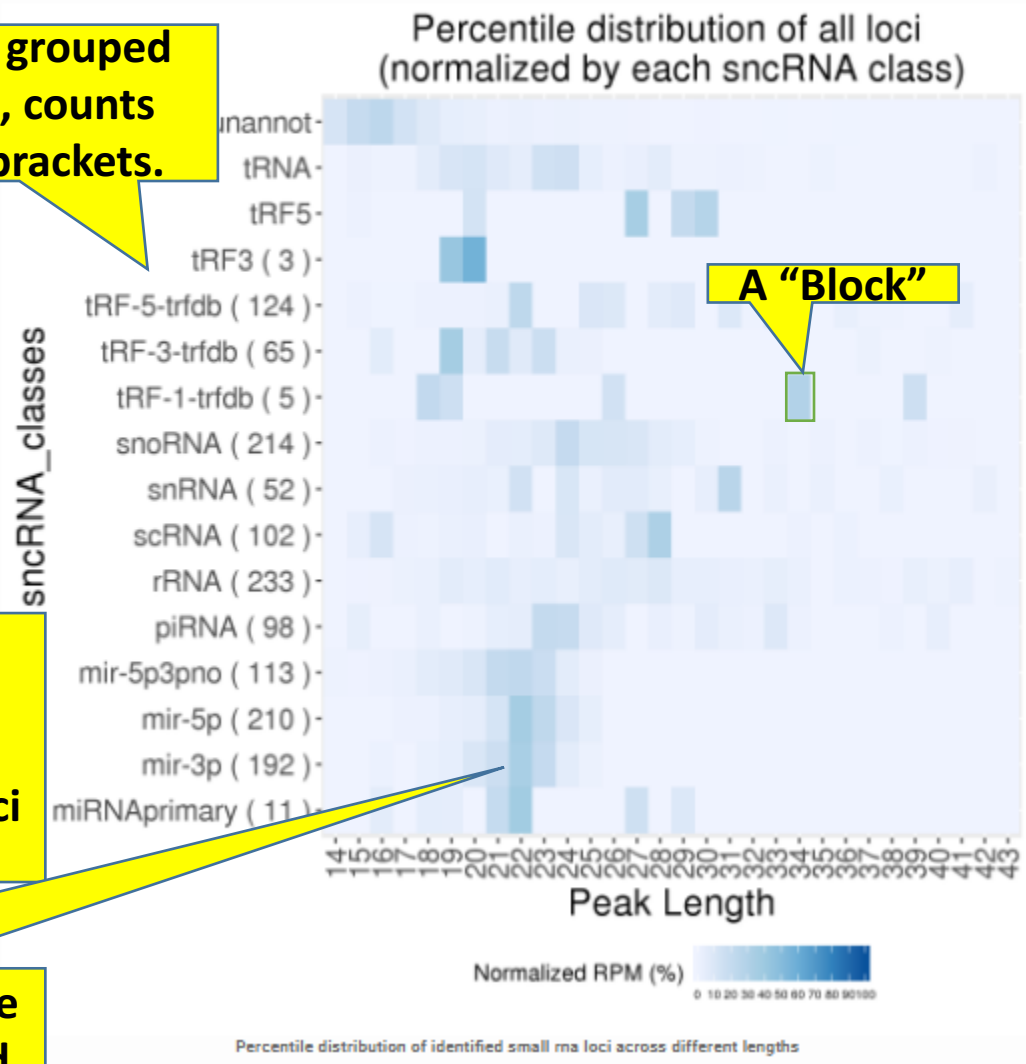
Proportion of expressed annotated small rna genes

Genomewide distribution patterns of small rna loci

Genomewide distribution of expressed small rna loci

Proportion of mapped reads across all loci

All loci are grouped by classes, counts shown in brackets.



For loci in each class, we divided them into groups of specific length (x axis). Each small "block" in this heatmap shows the normalized RPM values of loci of specific length for each RNA class.

This shows there are 192 mir-3p loci, the 22nt ones are the most highly expressed.

Plots (Output) - 5

Small RNA class

PLOTS

SEGMENTAT
Length distributio
Genomic length d
LENGTHEXP
Rpm distribution
Percentile distribution of identified small rna loci across different length

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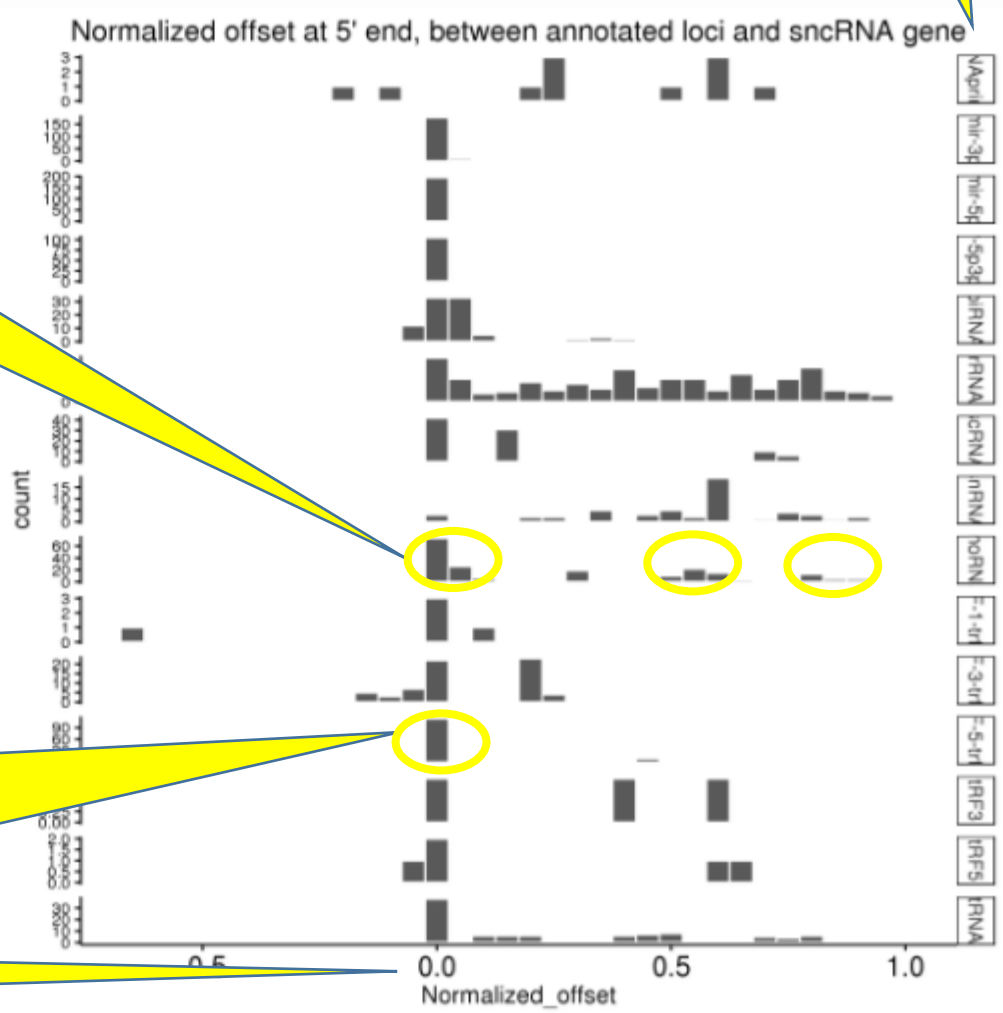
Genomewide distribution of expressed small rna loci
Proportion of mapped reads across all loci

This shows the snoRNA loci called are lying in different parts of the snoRNA gene, inferring they may have different processing mechanisms



With respect to the sncRNA gene annotation, the genome wide location of where the sncRNA loci are called. E.g. 90 sncRNAs of tRF-5-trfdb starts at the 1st position of the annotation, meaning the "processing patterns" of these loci are very specific for this class

sncRNA gene annotations start at "0.0"

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

Plots (Output) - 6

PLOTS

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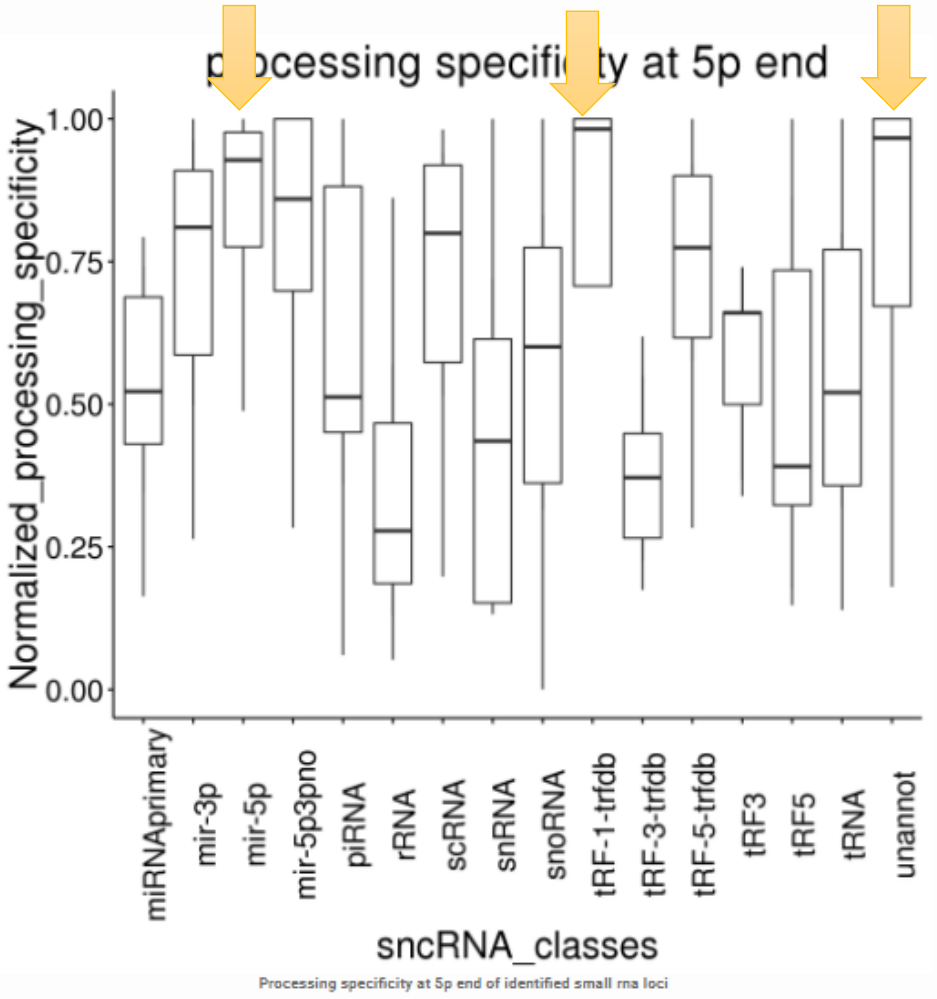

The plot shows the distribution of % of reads that are with the same 5' end. The higher the values, meaning that most reads have the same 5' end, e.g. mir-5p, tRF-1-trfdb, unannot in this figure

Plots (Output) - 7

PLOTS

SEGMENTATION

Length distribution of rpm of segmented loci

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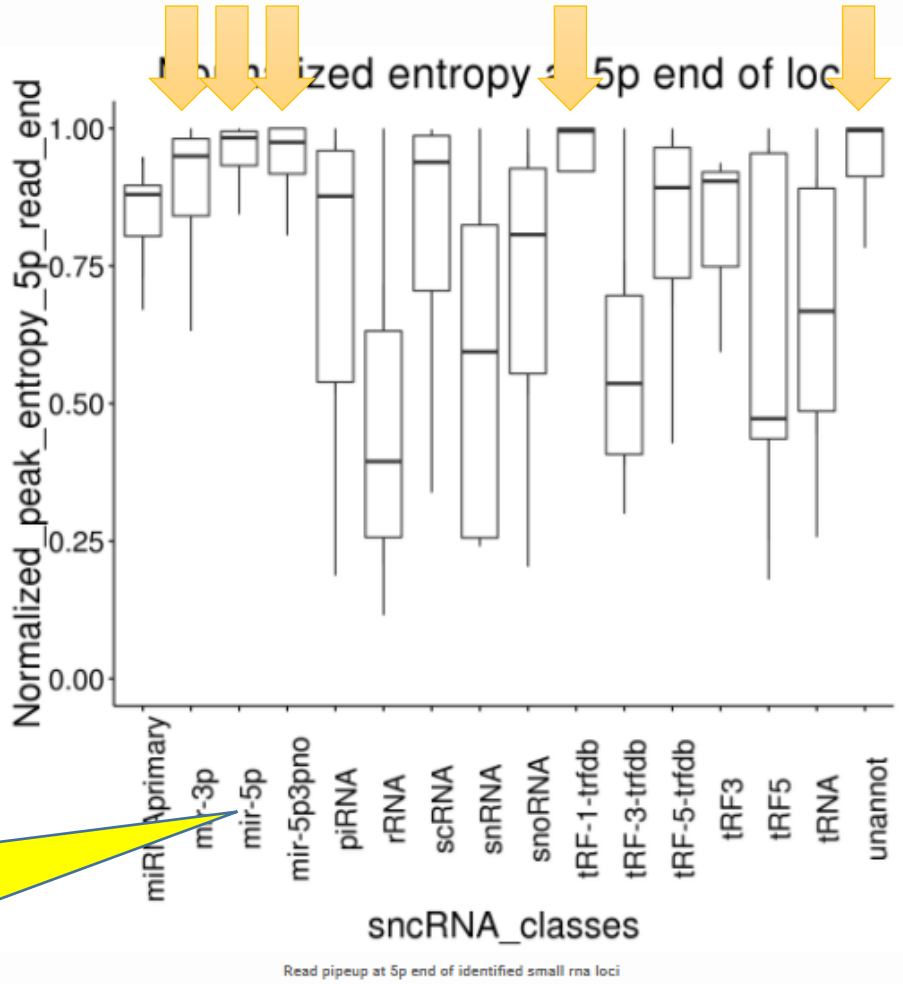

The closer the values to 1, the more specific the processing patterns are, e.g. mir-3p, mir-5p, mir-5p3pno, tRF-1-trfdb, unanno

This shows the distribution of the score "processing specificity at the 5' end" across loci for each sncRNA classes

Plots (Output) - 8

PLOTS

SEGMENTATION

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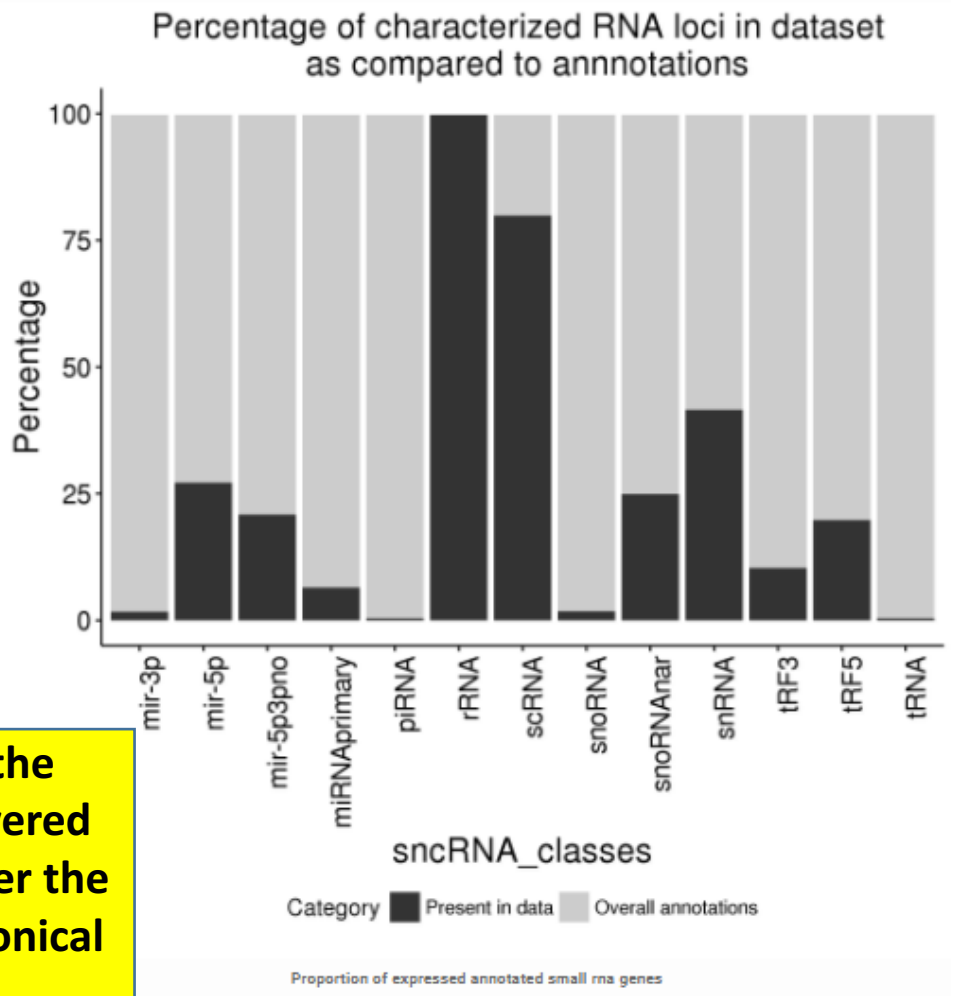

The plot compares per sncRNA class, the count of RNA loci characterized / discovered to that of the full annotations. The higher the percentage, meaning that the more canonical loci are present in the data.

Plots (Output) - 9

PLOTS

SEGMENTATION

Length distribution of rpm of segmented loci

Genomic length distribution of identified small rna loci

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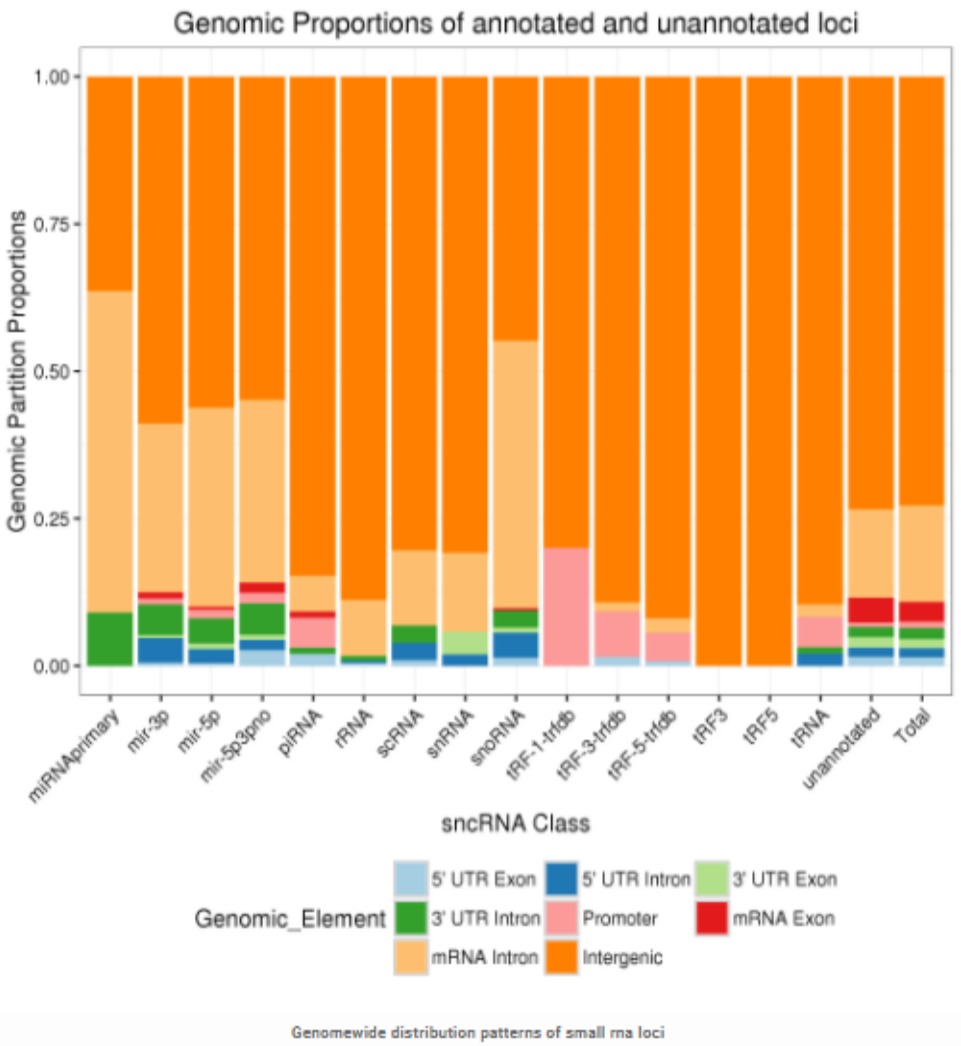
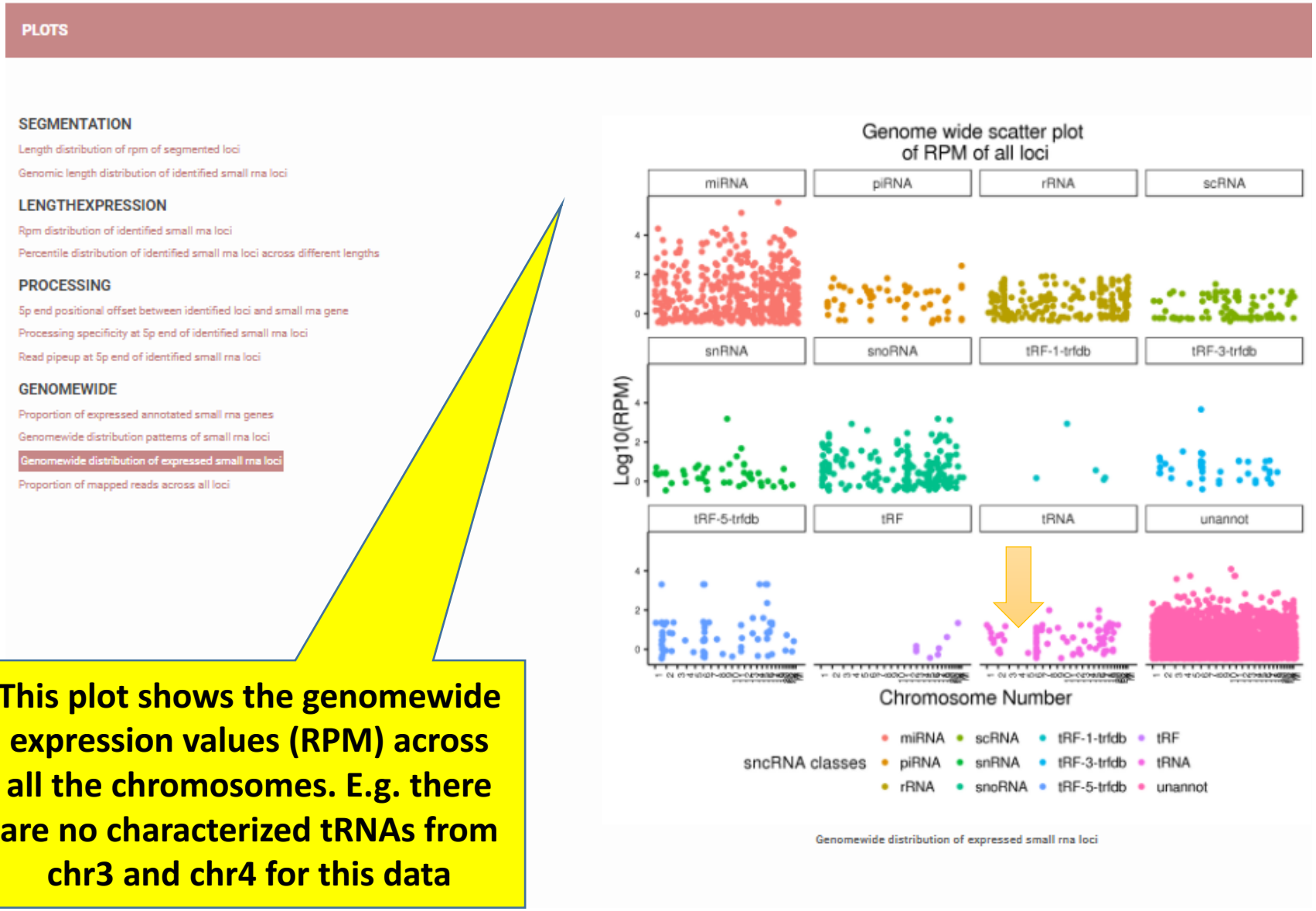


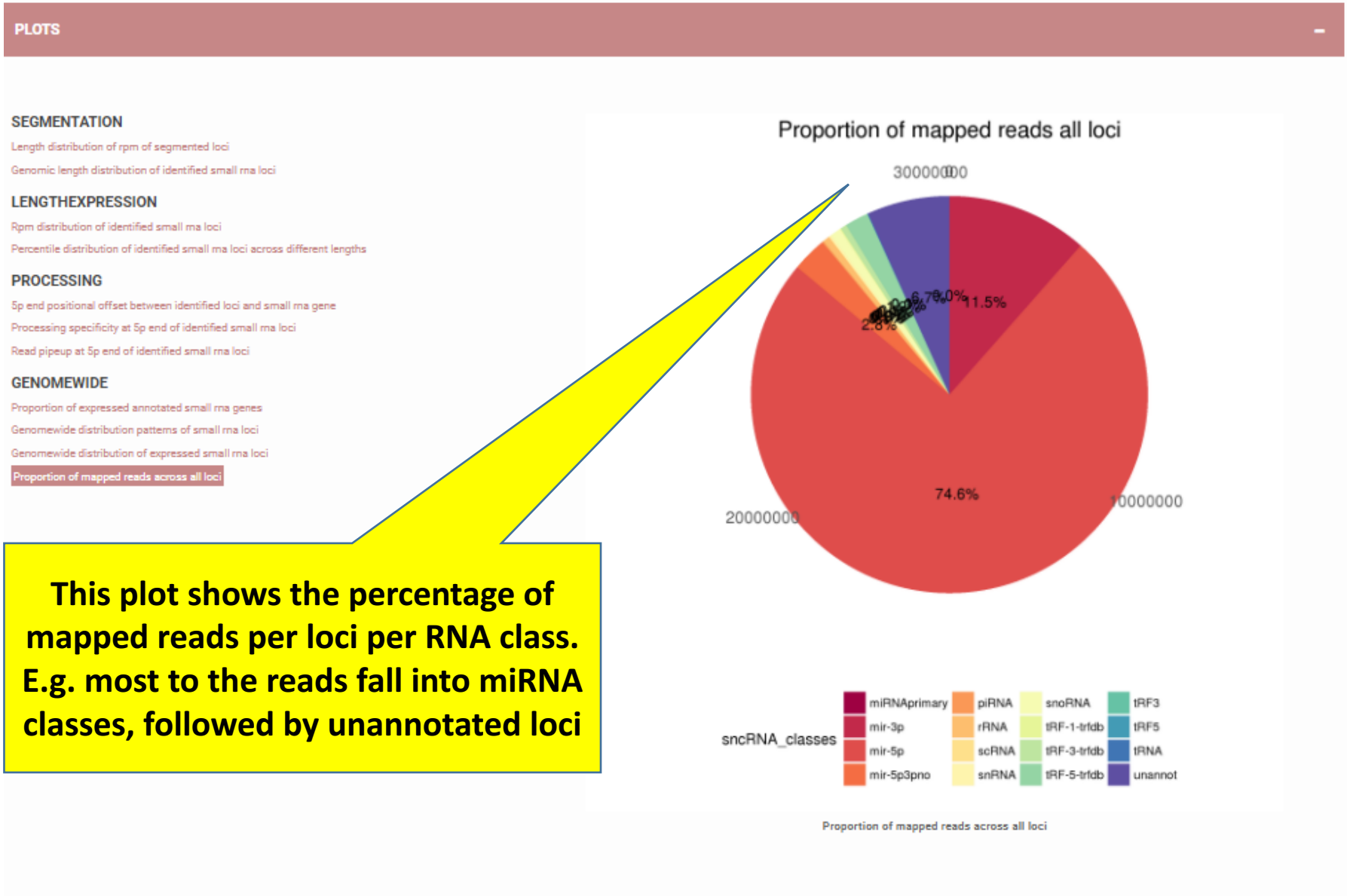
This plot shows per sncRNA class, which genomic elements they reside in. Take mir-3p as an example, most mir-3p resides in intergenic region, followed by mRNA introns, 3'UTR introns and 5' introns regions (i.e. intronic regions). A tiny amount falls into mRNA exon regions.

Plots (Output) - 10



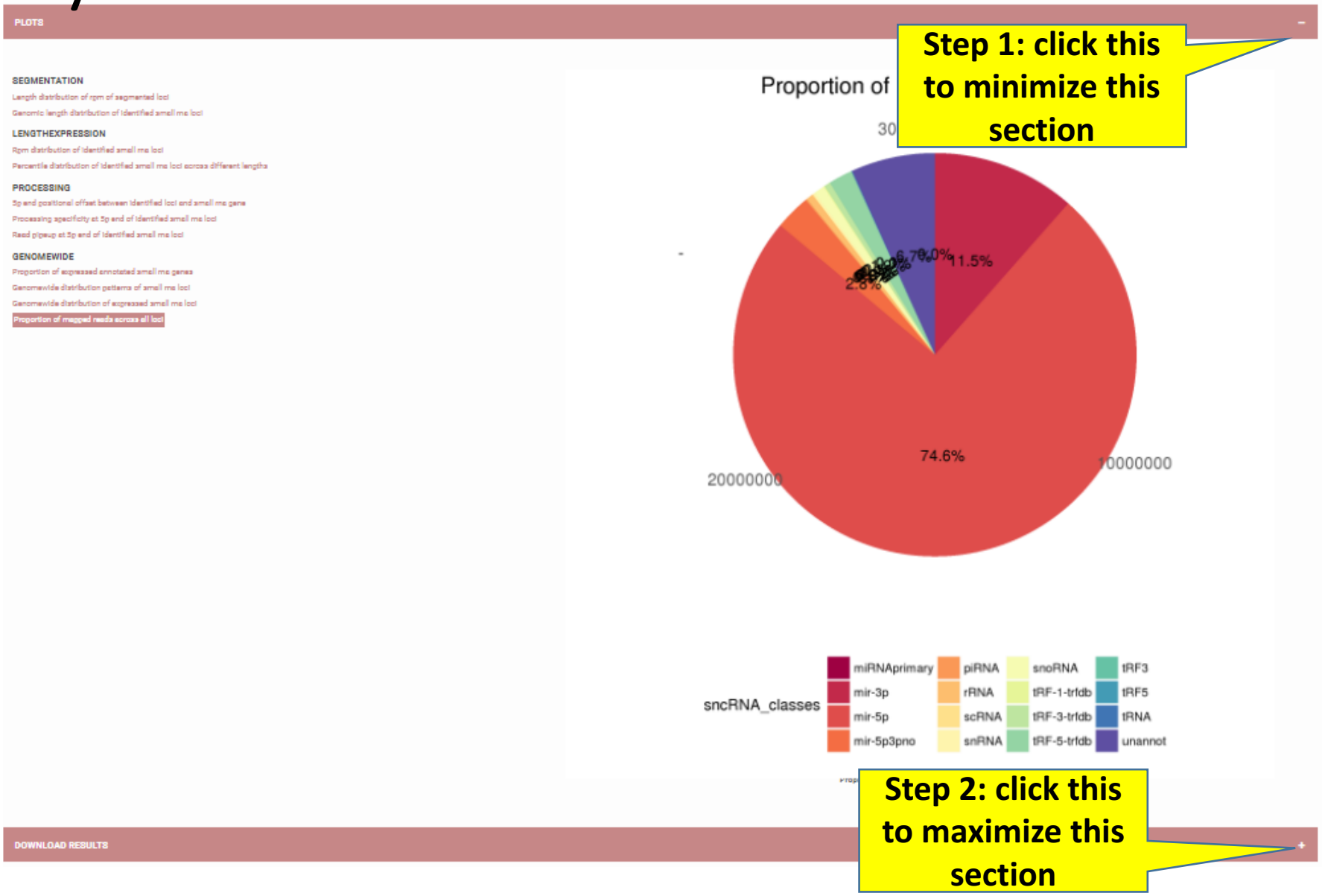
This plot shows the genomewide expression values (RPM) across all the chromosomes. E.g. there are no characterized tRNAs from chr3 and chr4 for this data

Plots (Output) - 11



This plot shows the percentage of mapped reads per loci per RNA class. E.g. most to the reads fall into miRNA classes, followed by unannotated loci

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



Download results (Top) – sncRNA gene expression

DOWNLOAD RESULTS −

Tracks for browsing

Content	Description	Download
Peak tracks	Genome-wide tracks	• plus • 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]

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

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 • 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

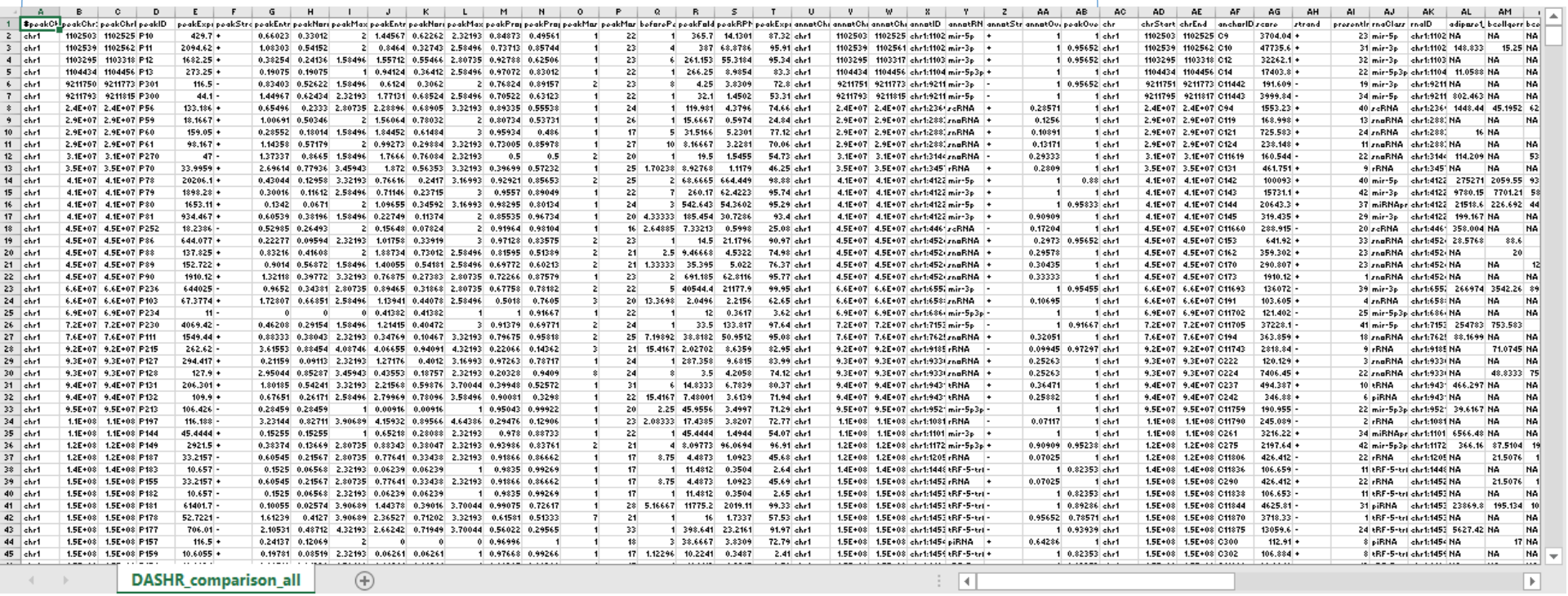
Download results – comparison expression tables (using DASHR as example)

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)

……



DASHR_comparison_all

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 or 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	• Annotated 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

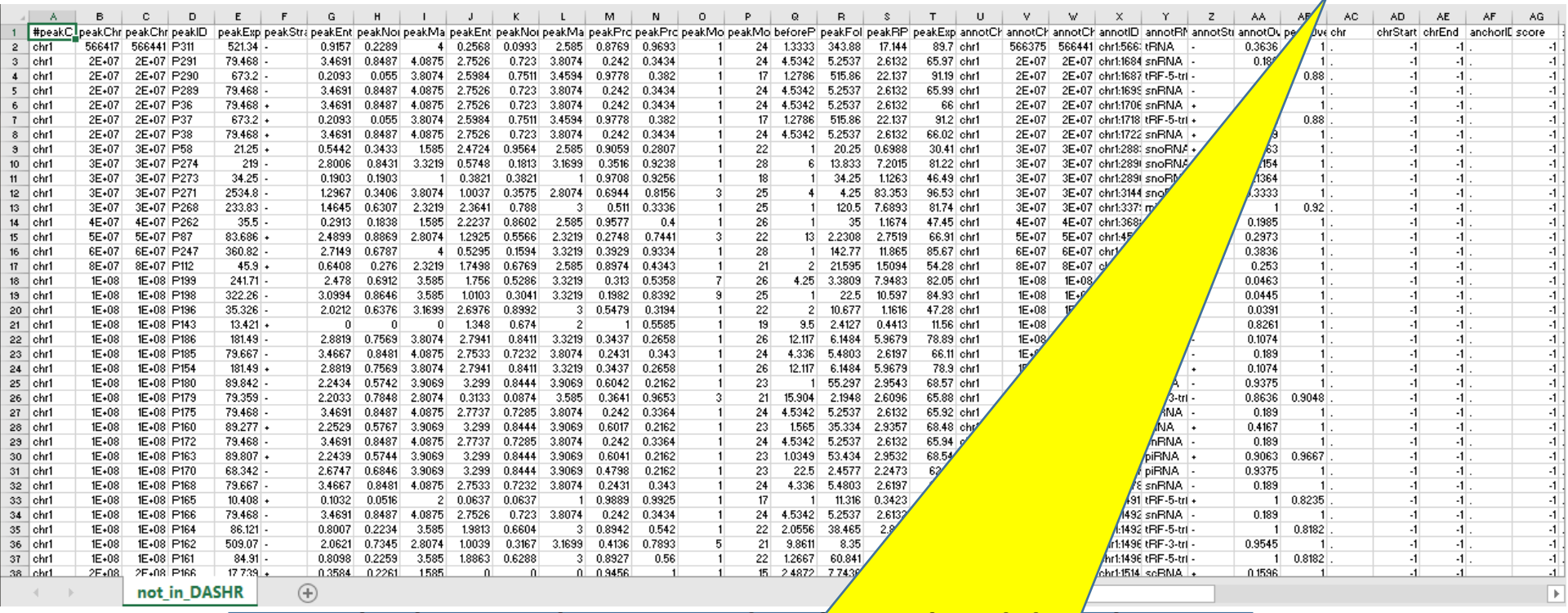
Download results – comparison expression tables (using DASHR as example)

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)

.....



	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	AD	AE	AF	AG
1	#peakC	peakChr	peakChr	peakID	peakExp	peakStra	peakEnt	peakNoi	peakMa	peakEnt	peakNoi	peakMa	peakPrc	peakPrc	peakMo	peakMo	beforeP	peakFol	peakRP	peakExp	annotCh	annotCh	annotCh	annotID	annotRN	annotStr	annotOv	pe	ove	chr	chrStart	chrEnd	anchorID	score
2	chr1	566417	566441	P311	521.34	-	0.9157	0.2289	4	0.2568	0.0993	2.585	0.8769	0.9693	1	24	1.3333	343.88	17.144	89.7	chr1	566375	566441	chr1:566	tRNA	-	0.3636		1	.	-1	-1	.	-1
3	chr1	2E+07	2E+07	P291	79.468	-	3.4691	0.8487	4.0875	2.7526	0.723	3.8074	0.242	0.3434	1	24	4.5342	5.2537	2.6132	65.97	chr1	2E+07	2E+07	chr1:1684	snRNA	-	0.18		1	.	-1	-1	.	-1
4	chr1	2E+07	2E+07	P290	673.2	-	0.2093	0.055	3.8074	2.5984	0.7511	3.4594	0.9778	0.382	1	17	1.2786	515.86	22.137	91.19	chr1	2E+07	2E+07	chr1:1687	tRF-5-trl	-		0.88		.	-1	-1	.	-1
5	chr1	2E+07	2E+07	P289	79.468	-	3.4691	0.8487	4.0875	2.7526	0.723	3.8074	0.242	0.3434	1	24	4.5342	5.2537	2.6132	65.99	chr1	2E+07	2E+07	chr1:1695	snRNA	-		1		.	-1	-1	.	-1
6	chr1	2E+07	2E+07	P36	79.468	+	3.4691	0.8487	4.0875	2.7526	0.723	3.8074	0.242	0.3434	1	24	4.5342	5.2537	2.6132	66	chr1	2E+07	2E+07	chr1:1706	snRNA	+		1		.	-1	-1	.	-1
7	chr1	2E+07	2E+07	P37	673.2	+	0.2093	0.055	3.8074	2.5984	0.7511	3.4594	0.9778	0.382	1	17	1.2786	515.86	22.137	91.2	chr1	2E+07	2E+07	chr1:1718	tRF-5-trl	+		0.88		.	-1	-1	.	-1
8	chr1	2E+07	2E+07	P38	79.468	+	3.4691	0.8487	4.0875	2.7526	0.723	3.8074	0.242	0.3434	1	24	4.5342	5.2537	2.6132	66.02	chr1	2E+07	2E+07	chr1:1722	snRNA	+		1		.	-1	-1	.	-1
9	chr1	3E+07	3E+07	P58	21.25	+	0.5442	0.3433	1.585	2.4724	0.9564	2.585	0.9059	0.2807	1	22	1	20.25	0.6988	30.41	chr1	3E+07	3E+07	chr1:288	snoRNA	+		1		.	-1	-1	.	-1
10	chr1	3E+07	3E+07	P274	219	-	2.8006	0.8431	3.3219	0.5748	0.1813	3.1699	0.3516	0.9238	1	28	6	13.833	7.2015	81.22	chr1	3E+07	3E+07	chr1:2891	snoRNA			1		.	-1	-1	.	-1
11	chr1	3E+07	3E+07	P273	34.25	-	0.1903	0.1903	1	0.3821	0.3821	1	0.9708	0.9256	1	18	1	34.25	1.1263	46.49	chr1	3E+07	3E+07	chr1:2891	snoRN			1		.	-1	-1	.	-1
12	chr1	3E+07	3E+07	P271	2534.8	-	1.2967	0.3406	3.8074	1.0037	0.3575	2.8074	0.6944	0.8156	3	25	4	4.25	83.353	96.53	chr1	3E+07	3E+07	chr1:3144	snoR			1		.	-1	-1	.	-1
13	chr1	3E+07	3E+07	P268	233.83	-	1.4645	0.6307	2.3219	2.3641	0.788	3	0.511	0.3336	1	25	1	120.5	7.6893	81.74	chr1	3E+07	3E+07	chr1:3375	m			1	0.92	.	-1	-1	.	-1
14	chr1	4E+07	4E+07	P262	35.5	-	0.2913	0.1838	1.585	2.2237	0.8602	2.585	0.9577	0.4	1	26	1	35	1.1674	47.45	chr1	4E+07	4E+07	chr1:368			0.1985	1		.	-1	-1	.	-1
15	chr1	5E+07	5E+07	P87	83.686	+	2.4899	0.8869	2.8074	1.2925	0.5566	2.3219	0.2748	0.7441	3	22	13	2.2308	2.7519	66.91	chr1	5E+07	5E+07	chr1:45			0.2973	1		.	-1	-1	.	-1
16	chr1	6E+07	6E+07	P247	360.82	-	2.7149	0.6787	4	0.5295	0.1594	3.3219	0.3929	0.9334	1	28	1	142.77	11.865	85.67	chr1	6E+07	6E+07	chr1			0.3836	1		.	-1	-1	.	-1
17	chr1	8E+07	8E+07	P112	45.9	+	0.6408	0.276	2.3219	1.7498	0.6769	2.585	0.8974	0.4343	1	21	2	21.595	1.5094	54.28	chr1	8E+07	8E+07	ch			0.253	1		.	-1	-1	.	-1
18	chr1	1E+08	1E+08	P199	241.71	-	2.478	0.6912	3.585	1.756	0.5286	3.3219	0.313	0.5358	7	26	4.25	3.3809	7.9483	82.05	chr1	1E+08	1E+08				0.0463	1		.	-1	-1	.	-1
19	chr1	1E+08	1E+08	P198	322.26	-	3.0994	0.8646	3.585	1.0103	0.3041	3.3219	0.1982	0.8392	9	25	1	22.5	10.597	84.93	chr1	1E+08	1E+08				0.0445	1		.	-1	-1	.	-1
20	chr1	1E+08	1E+08	P196	35.326	-	2.0212	0.6376	3.1699	2.6976	0.8992	3	0.5479	0.3194	1	22	2	10.677	1.1616	47.28	chr1	1E+08	1E+08				0.0391	1		.	-1	-1	.	-1
21	chr1	1E+08	1E+08	P143	13.421	+	0	0	0	1.348	0.674	2	1	0.5585	1	19	9.5	2.4127	0.4413	11.56	chr1	1E+08					0.8261	1		.	-1	-1	.	-1
22	chr1	1E+08	1E+08	P186	181.49	-	2.8819	0.7569	3.8074	2.7941	0.8411	3.3219	0.3437	0.2658	1	26	12.117	6.1484	5.9679	78.89	chr1	1E+08				-	0.1074	1		.	-1	-1	.	-1
23	chr1	1E+08	1E+08	P185	79.667	-	3.4667	0.8481	4.0875	2.7533	0.7232	3.8074	0.2431	0.343	1	24	4.336	5.4803	2.6197	66.11	chr1	1E+					0.189	1		.	-1	-1	.	-1
24	chr1	1E+08	1E+08	P154	181.49	+	2.8819	0.7569	3.8074	2.7941	0.8411	3.3219	0.3437	0.2658	1	26	12.117	6.1484	5.9679	78.9	chr1	1E				+	0.1074	1		.	-1	-1	.	-1
25	chr1	1E+08	1E+08	P180	89.842	-	2.2434	0.5742	3.9069	3.299	0.8444	3.9069	0.6042	0.2162	1	23	1	55.297	2.9543	68.57	chr1					-	0.9375	1		.	-1	-1	.	-1
26	chr1	1E+08	1E+08	P179	79.359	-	2.2033	0.7848	2.8074	0.3133	0.0874	3.585	0.3641	0.9653	3	21	15.904	2.1948	2.6096	65.88	chr1					3-trl	0.8636	0.9048		.	-1	-1	.	-1
27	chr1	1E+08	1E+08	P175	79.468	-	3.4691	0.8487	4.0875	2.7737	0.7285	3.8074	0.242	0.3364	1	24	4.5342	5.2537	2.6132	65.92	chr1					RNA	0.189	1		.	-1	-1	.	-1
28	chr1	1E+08	1E+08	P160	89.277	+	2.2529	0.5767	3.9069	3.299	0.8444	3.9069	0.6017	0.2162	1	23	1.565	35.334	2.9357	68.48	chr					NA	0.4167	1		.	-1	-1	.	-1
29	chr1	1E+08	1E+08	P172	79.468	-	3.4691	0.8487	4.0875	2.7737	0.7285	3.8074	0.242	0.3364	1	24	4.5342	5.2537	2.6132	65.94	c					nRNA	0.189	1		.	-1	-1	.	-1
30	chr1	1E+08	1E+08	P163	89.807	+	2.2439	0.5744	3.9069	3.299	0.8444	3.9069	0.6041	0.2162	1	23	1.0349	53.434	2.9532	68.54					piRNA	+	0.9063	0.9667		.	-1	-1	.	-1
31	chr1	1E+08	1E+08	P170	68.342	-	2.6747	0.6846	3.9069	3.299	0.8444	3.9069	0.4798	0.2162	1	23	22.5	2.4577	2.2473	62					piRNA	-	0.9375	1		.	-1	-1	.	-1
32	chr1	1E+08	1E+08	P168	79.667	-	3.4667	0.8481	4.0875	2.7533	0.7232	3.8074	0.2431	0.343	1	24	4.336	5.4803	2.6197					8	snRNA	-	0.189	1		.	-1	-1	.	-1
33	chr1	1E+08	1E+08	P165	10.408	+	0.1032	0.0516	2	0.0637	0.0637	1	0.9889	0.9925	1	17	1	11.316	0.3423					491	tRF-5-trl	+	1	0.8235		.	-1	-1	.	-1
34	chr1	1E+08	1E+08	P166	79.468	-	3.4691	0.8487	4.0875	2.7526	0.723	3.8074	0.242	0.3434	1	24	4.5342	5.2537	2.613					492	snRNA	-	0.189	1		.	-1	-1	.	-1
35	chr1	1E+08	1E+08	P164	86.121	-	0.8007	0.2234	3.585	1.9813	0.6604	3	0.8942	0.542	1	22	2.0556	38.465	2.8					1492	tRF-5-trl	-	1	0.8182		.	-1	-1	.	-1
36	chr1	1E+08	1E+08	P162	509.07	-	2.0621	0.7345	2.8074	1.0039	0.3167	3.1699	0.4136	0.7893	5	21	9.8611	8.35						1496	tRF-3-trl	-	0.9545	1		.	-1	-1	.	-1
37	chr1	1E+08	1E+08	P161	84.91	-	0.8098	0.2259	3.585	1.8863	0.6288	3	0.8927	0.56	1	22	1.2667	60.841						hr1:1496	tRF-5-trl	-	1	0.8182		.	-1	-1	.	-1
38	chr1	2E+08	2E+08	P166	17.739	+	0.3584	0.2261	1.585	0	0	0	0.9456	1	1	15	2.4872	7.7436						chr1:1514	scRNA	+	0.1596	1		.	-1	-1	.	-1

not_in_DASHR

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	peakNor	peakMa	peakEnt	peakNor	peakMa	peakPrc	peakPrc	peakMo	peakMo	beforeP	peakFol	peakRP	peakExp	annotCh	annotCh	annotCh	annotID	annotRN	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	566441	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	chr1:2491	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	chr1:2491	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	chr15:80	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	+	1.8891	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
	225	215	227,677	2.19
	137	132	17,896	0.17
	34	29	341,572	3.29
	6	6	1,323	0.01
	9	9	998	0.01
	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

No annotation

	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	#peakCh	peakChr	peakChr	peakID	peakExp	peakStra	peakEntr	peakNorr	peakMax	peakEntr	peakNorr	peakMax	peakProp	peakProp	peakMos	peakMos	beforePe	peakFolc	peakRPM	peakExp	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	0.9949	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)

Step 1: click this to minimize "Download results"

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

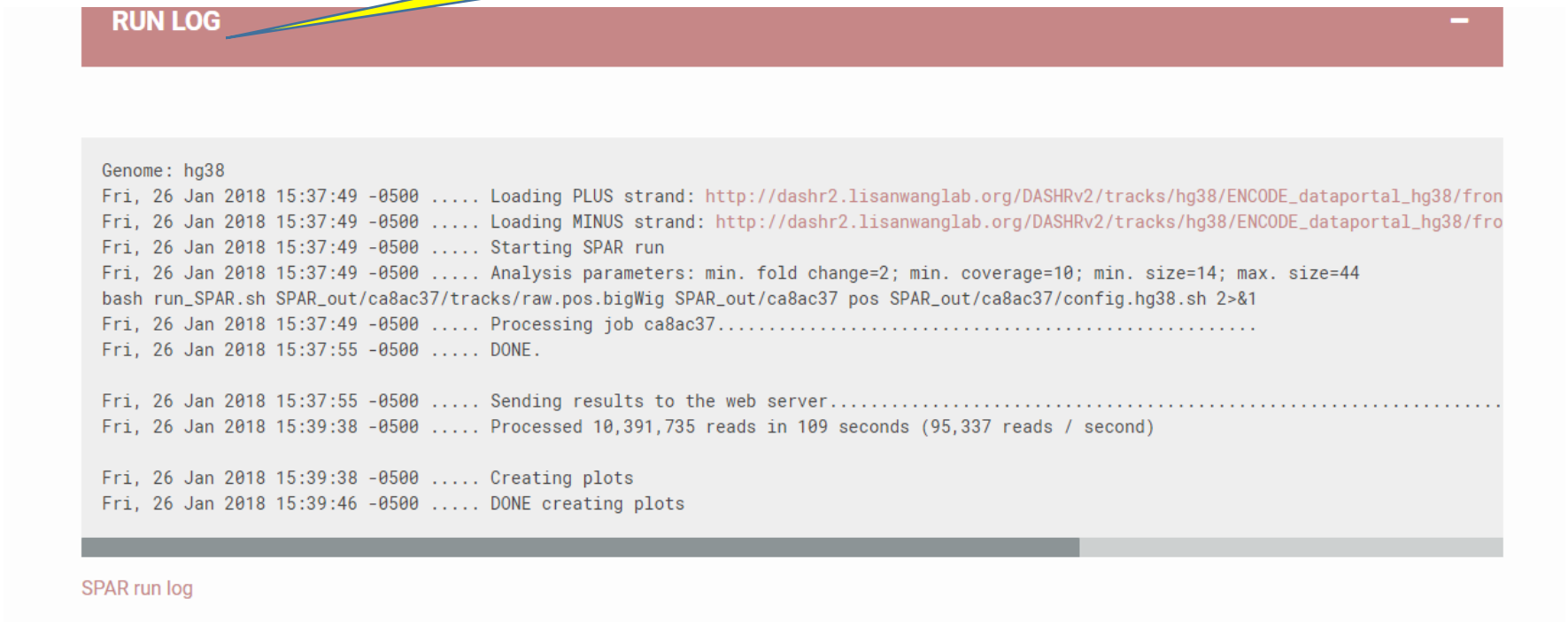
RNA class	Peaks	Genes	Reads	Percentage of reads
Annotated	1,282	1,214	9,647,188	92.84
Unannotated	4,799	4,799	744,547	7.16
miRNAprimary	10	10	646,698	6.22
mir-3p	224	224	1,779,736	17.13
mir-5p	285	285	5,706,729	54.92
mir-5p3pno	66	66	38,553	0.29
piRNA	99	99	747,688	7.19
rRNA	98	81	42,675	0.41
scRNA	225	215	227,677	2.19
snRNA	137	132	17,896	0.17
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 +

Step 2: click this to maximize "Run log"

Run log (Output)

Run log displayed agin



Send questions to this email: SPAR@lisanwanglab.org

END