SPAR outputs and report page

Landing results page (full view)

SPAR Analysis results for job ca8ac37 Input files: http://dashr2.lisanwanalab.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_ENCSR000AFS.neg.bigWig 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) RUN SUMMARY Reads vs RNA class Peaks vs RNA class 6,081 10,391,729 💻 Unannotated 🗰 miRNAprimary 🚥 mir-3p 💻 mir-5p 📖 mir-5p3pno 💻 piRNA 📖 rRNA 🛤 scRNA 💶 snRNA snoRNA 🗰 tRF3 📩 tRF5 🛤 tRNA Show more INTERACTIVE PEAK BROWSER RUN LOG

Questions? SPAR@lisanwanglab.org

Wang Lab Penn Neurodegeneration Genomics Center University of Pennsylvania

Landing results / outputs page (top)



Landing results / outputs page (top)

SPAR

analysis, annotation, visualization of small RNA sequencing experiments

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_ENCSR0004

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)

RUN SUMMARY

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

Peaks vs RNA class

Reads vs RNA class



Show more

Landing results → SPAR report page

Index of /~pkuksa/SPAR/SPAR_out/ca8ac37

| | Name | Last modified | <u>Size</u> | Description |
|---|-----------------------------|-------------------|-------------|-----------------------------------|
| 2 | Parent Directory | | - | |
| | DASHR_comparison/ | 26-Jan-2018 15:38 | - | |
| | ENCODE_comparison/ | 26-Jan-2018 15:39 | - | |
| | figures/ | 26-Jan-2018 15:39 | - | |
| | <u>inputs/</u> | 26-Jan-2018 15:37 | - | |
| | logs/ | 26-Jan-2018 15:39 | - | |
| | <u>results/</u> | 26-Jan-2018 15:39 | - | Report is available in html / pdf |
| | <u>tracks/</u> | 26-Jan-2018 15-2 | | |
| ľ | <pre>report.html</pre> | 25 Jan-2018 15:39 | 40K | |
| | <u>report.pdf</u> | 26-Jan-2018 15:39 | 1.8M | |
| ľ | <u>results.html</u> | 26-Jan-2018 15:39 | 2.4K | |
| Ē | <pre>run_summary.html</pre> | 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

SPAR report.pdf

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



Landing results / outputs page (bottom)



DOWNLOAD RESULTS

RUN LOG



VIEW IN GENOME BROWSER

Total number of called peaks (annotated or unannotated)

-f 600

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

Browse peaks (expressed small RNA

INTERACTIVE PEAK BROWSER

Download Table

Loci 1-10 / 6001

| 1001.110 | 7 0001 | | | | 14 | Fage 1 | V 01 009 P | | Resul | us per page i | 0 * r | M COLUMNS |
|----------|--------|---------------------|---------|--------------------------|--|----------------------------|---|----------------|--------|---------------|----------------|----------------|
| chr | peakID | Expression (raw) | strand | Same 5' end read % | Expression Expression (PAN) (percentile Annotation definition definition (Percentile Annotation definition def | | 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 |
| | | | | | | | | | | | | |

Filter sncRNA loci with the top 5% of expression

| INTER# | ACTIVE P | EAK BROW | VSER | | | | Step 1: Typ | k and | - | | | | | |
|----------------------------|---------------------|---------------------|---------|--------------------------|------------------------|---------------------------------|---|--------------------|-------------|------------------|------------------|----------------|--|--|
| Browse peak Download Ta | s (expressed ble | l small RNAs) | l pa | Numbe assed t | er of loc his crite | <mark>i that</mark> eria: 60 | | | | | | | | |
| Loci: 1-10 | / 60 | | | | н | Paper | Iv of 6 ▶ ₩ | | Result | s per page 10 | ▼ ? } | 💥 Columnsv | | |
| 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 | | |

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



Hg38 reference genome



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

INTERACTIVE PEAK BROWSER

Step 1: click this to minimize this section

Browse peaks (expressed small RNAs)

Download Table Looit 1-4 / 4

| Loci: 1-4 / | 4 | | | | 14 4 | Page 1 🔻 | of 1 🕨 M | | Results p | er page 10 | • ? | 😿 Columnsv |
|-------------|--------|---------------------|--------|--------------------------|---------------------|----------------------------|---|--------------------|-------------|----------------|----------------|----------------|
| chr | peakID | Expression (raw) | strand | Same 5' end read % | Expression (RPM) | Expression (percentile) | Annotation | Annotated class | Conservatio | mRNA? | 1ncRNA? | repeat? |
| Clear V | | | Clea 🔻 | | | 95. | | 🔲 Clear | | m mDNA Even | 🗌 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 | 1736.59 | - | 0.358646 | 167.1132 | 95.76 | chr16:636735- 636806:-:tRNA-Gly- CCC-2-2 | tRNA | 0.9205 | Promoter | Non- lncRNA | Non- repeat |
| chr2 | P1479 | 1745.09 | - | 0.356899 | 167.9311 | 95.77 | chr2:70248990- 70249061:-:tRNA-Gly- CCC-2-1 | tRNA | 0.8976 | Promoter | Non- lncRNA | Non- repeat |

Step 2: click this to maximize this section

View in Genome Browser (Output)



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

Step 1: click this to minimize this

section

VIEW IN GENOME BROWSER

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

| Genome | Track View | Help | | | | | | | | | | | | Full-screen view |
|-------------|----------------------|--------------------------|---------------------------|------------|------------|--------------|------------|------------|-------------|-----------|------------|-------------|-------------|------------------|
| 0 | 10,000,000 | 20,000,000 | 30,000,000 | 40,000,000 | 50,000,000 | 60,000,000 | 70,000,000 | 80,000,000 | \$0,000,000 | | 00,000,000 | 110,000,000 | 120,000,000 | 130,000,000 |
| | ⇒ Q (| Q @ errs . | chr9:9417595794176090 (1) | 5 b) Go 🌙 | | | | | | | | | | |
| | | 24,175,275 | | 94,176, | 000 | | 94,176,0 | 25 | | \$4,176,0 | 30 | | 94,176,075 | |
| O DASHR | ennotation (hg38) | | | | | | | | • | | | | | |
| | rsa-let-7a-5p | | • | | | haa-let-7a-3 | 9 | · | | | | | | |
| () frontal- | contex-rep1_ENCSR00 | 0075.pos.bigWig FEAKS (+ | strend) | | | | 200,000 | | | | | | | |
| | | | | | | | 100,000 | | | | | | | |
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| | | | | | | | | | | | | | | |
| O frontel- | context-rep1_ENCSR00 | 03PS.pos.bigWig RAW sign | iel (+ strend) | | | | 200,000 | | | | | | | |
| | | | | | | | 100,000 | | | | | | | |
| | | | | | | | 0.1 | | | | | | | |
| O frontal- | contex-rep1_ENCSR00 | 03PS.pos.bigWig RAW sign | al (- strand) | | | | 7 | | | | | | | |
| | | | | | | | | | | | | | | |
| | | | | | | | | _ | | | | | | |

| PLOTS | Step 2: click this | + |
|-------|--------------------|---|
| | to maximize this | |
| | section | |

Plots (Output) – to navigate across all plots



Length distribution of rpm of segmented loci

PLOTS

4 different plot sessions





Length distribution of rpm of segmented loci

PLOTS



Genomic length distribution of identified small rna loci

PLOTS



Rpm distribution of identified small rna loci

PLOTS



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

Percentile distribution of identified small ma loci across different lengths

0 10 20 30 40 50 60 70 80 90100

Small RNA class

PLOTS

SEGMENTAT Length distributio Genomic length d LENGTHEXP Rom distribution This shows the snoRNA loci called are lying in different parts of the snoRNA gene, inferring they may have different processing mechanisms

PROCESSING

Sp end positional offset between identified loci and small ma gen Processing specificity at Sp end of identified small ma loci Read pipeup at Sp end of identified small ma loci

GENOMEWIDE

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

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"

Normalized offset at 5' end, between annotated loci and sncRNA gene



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

PLOTS

SEGMENTATION

Length distribution of rpm of segmented loci

Genomic length distribution of identified small ma loci

LENGTHEXPRESSION

Rpm distribution of identified small ma loci

Percentile distribution of identified small malloci across different lengths

PROCESSING

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

Processing specificity at 5p end of identified small ma loci

Read pipeup at 5p end of identified small ma loci

GENOMEWIDE

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

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-1trfdb, unannot in this figure



PLOTS

SEGMENTATION

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

LENGTHEXPRESSION

Rpm distribution of identified small ma loci Percentile distribution of identified small ma loci across different lengths

PROCESSING

5p end positional offset between identified loci and small ma gene Processing specificity at 5p end of identified small ma loci

GENOMEWIDE

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

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



PLOTS

SEGMENTATION Length distribution of rpm of segmented loci Genomic length distribution of identified small ma loci

LENGTHEXPRESSION

Rpm distribution of identified small ma loci

Percentile distribution of identified small ma loci across different lengths

PROCESSING

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

GENOMEWIDE

Proportion of expressed annotated small ma genes

Genomewide distribution patterns of small ma loci

Genomewide distribution of expressed small ma loci

Proportion of mapped reads across all loci

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.



Genomewide distribution patterns of small ma loci

PLOTS

SEGMENTATION

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

LENGTHEXPRESSION

Rpm distribution of identified small ma loci Percentile distribution of identified small ma loci across different lengths

PROCESSING

Sp end positional offset between identified loci and small ma gene Processing specificity at Sp end of identified small ma loci Read pipeup at Sp end of identified small ma loci

GENOMEWIDE

Proportion of expressed annotated small rna genes Genomewide distribution patterns of small rna loci Genomewide distribution of expressed small rna loc

Proportion of mapped reads across all loci

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



Genomewide distribution of expressed small rna loci

PLOTS

SEGMENTATION

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

LENGTHEXPRESSION

Rpm distribution of identified small ma loci Percentile distribution of identified small ma loci across different lengths

PROCESSING

Sp end positional offset between identified loci and small ma gene Processing specificity at Sp end of identified small ma loci Read pipeup at Sp end of identified small ma loci

GENOMEWIDE

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

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



Proportion of mapped reads across all loci

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



INLOAD RESULTS

SEGMENTATION

LENGTHEXPRESSION

PROCESSING

GENOMEWIDE

Download results (Top) – sncRNA gene expression



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 | | | | | | |
|---|---------------------|---|-------------|--------|-----------|-------|----|
| Δ | name | | В | | С | D | |
| #Gene | | - | GeneClass | • | ReadCou 🖵 | RPM | • |
| chr6:151619978:151620068:-:HY4 | | | scRNA | | 66.7142 | 31.30 | 62 |
| chr3:48238061:48238078:+:hsa-miR-4443 | | | mir-5p3pno | | 105 | 49.27 | 22 |
| chr6_ssto_hap7:3077413:3077494:-:HY3 | | | scRNA | | 129.147 | 60.60 | 34 |
| chr1:17067010:17067174:+:U1 | | | snRNA | | 37.2714 | 17.48 | 99 |
| chr6_cox_hap2:97136:97167:+:DQ598188:piR-36254 | | | piRNA | | 174.713 | 81.98 | 56 |
| chrX:118780761:118780783:-:hsa-miR-766-5p | | | mir-5p | | 174.417 | 81.84 | 67 |
| chr10:38283790:38283901:+:HY1 | | | scRNA | | 14.5489 | 6.82 | 72 |
| chr17:80626156:80626177:-:hsa-miR-4525 | | | mir-5p3pno | | 60 | 28.15 | 55 |
| chr6:27248048:27248121:-:tRNA-Val-CAC-2-1 | | | tRNA | 41.799 | 19.61 | 46 | |
| chr3:125235822:125235927:+:HY1 | | | scRNA | | 30.4169 | 14.27 | 34 |
| chr10:103124606:103124792:-:U2 | | | snRNA | | 99.2588 | 46.57 | 81 |
| chr10:69524340:69524360:+:trfdb-1001_chr10.trna2-SerTGA_chr10-6 | 59524261-69524342 | | tRF-1-trfdb | | 18088.8 | 8488. | 33 |
| chr13:92003498:92003521:+:hsa-miR-19b-3p | | | mir-3p | | 22.5 | 10.55 | 83 |
| chr1:161493633:161493655:-:trfdb-3027b_chr1.trna68-GlyGCC_chr1- | 161493707-161493637 | | tRF-3-trfdb | | 16.2765 | 7.637 | 89 |
| chr16:3357711:3357744:-:DQ571003:piR-31115 | | | piRNA | | 84.5773 | 39.68 | 86 |
| chr19:24182635:24183468:-:LSU-rRNA_Hsa | | | rRNA | | 341.065 | 160.0 | 48 |
| chr6:86387011:86387086:-:U50 | | | snoRNA | | 13.2333 | 6.209 | 84 |
| chr12:109029624:109029646:+:hsa-miR-4496 | | | mir-5p3pno | | 63.4083 | 29.75 | 49 |
| chr7:128423560:128423578:+:trfdb-3002a_chr7.trna2-ProAGG_chr7- | 128423504-128423575 | | tRF-3-trfdb | | 47.6833 | 22.37 | 58 |
| chr11:79113120:79113143:-:hsa-miR-708-5p | | | mir-5p | | 11.3588 | 5.330 | 22 |
| chr16:22207031:22207113:-:tRNA-Leu-TAG-3-1 | | | tRNA | | 77.7613 | 36.49 | 02 |

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

DOWNLOAD RESULTS

| Content | De | escription | | Download |
|------------------------|---|--|---|--|
| Peak tracks | Genome-wide tracks | | • plus • minu | Step 2: Click to download |
| Raw signal tracks | Genome-wide tracks | | • plus • minu | peaks present in both the |
| Peak tables | Tables with detailed in 1. Annotated peaks: pe or mature products | expression tables | AnnoUnan | expressed in DASHR |
| | 2. Unannotated peaks: annotated sncRNA ge | peaks on one overlap with nes or the products. | • All | called peaks [xls] [bed] |
| Gene expression | Small RNA gene expressio | on | • Gene | expression table (xls) [3.31 N |
| Comparison with DASHR | Integrated expression ta | ables | Anno Unan All Peak | tated peaks [xls] notated peaks [xls] (Annotated + Unannotated) peaks [xls] [bed] s not in DASHR [xls] |
| Comparison with ENCODE | Integrated expression ta | ables | Anno Unan All Peak | tated peaks [xls] notated peaks [xls] (Annotated + Unannotated) peaks [xls] [bed] s not in ENCODE [xls] |

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

Under "Comparison with DASHR", download "DASHR comparison all.xls"

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

Called peak annotation and features

| 1 | \$ p⊳akC | poakChr: | ooakChrl poakID | poakExp: poakStre | poakEntr | poakNori | poakMax | poakEntr | poakNori | poakMax | poakProj | poakPraj poakMi | r poakMe | u bofaroP | e poakFal- | d poakRPN | poakExpi annotCh | hi annatChi | annotChi annotID ani | notRN annotS | tr annotOv. | pøakOvø chr | chrStart ch | rEnd ancharlD | score strand | prozontir rnaClarz | rnalD ad | parol beelly | orr beo |
|----|-----------------|----------|-----------------|-------------------|----------|----------|----------|----------|----------|------------|----------|-----------------|----------|--------------------------|-----------------------|--------------------|-------------------------|-------------|-----------------------|--------------|-------------|--------------|-------------|---------------|--------------|--------------------|----------------|--------------|-------------|
| 2 | chr1 | 1102503 | 1102525 P10 | 429.7 + | 0.66023 | 0.33012 | 2 | 1.44567 | 0.62262 | 2.32193 | 0.84873 | 0.49561 | 1 2 | 2 | 1 365.7 | 14.1301 | 87.32 chr1 | 1102503 | 1102525 chr1:1102 mi | r-5p + | 1 | 1 chr1 | 1102503 11 | 102525 C9 | 3704.04 + | 23 mir-5p | chr1:1102 NA | NA | NA |
| 3 | chr1 | 1102539 | 1102562 P11 | 2094.62 + | 1.08303 | 0.54152 | 2 | 0.8464 | 0.32743 | 2.58496 | 0.73713 | 0.85744 | 1 2 | 3 | 4 387 | 68,8786 | 95.91 chr1 | 1102539 | 1102561 chr1:1102 mi | r-3p + | 1 | 0.95652 chr1 | 1102539 11 | 102562 C10 | 47735.6 + | 31 mir-3p | chr1:1102 1 | 18.833 15. | 25 NA |
| 4 | chr1 | 1103295 | 1103318 P12 | 1682.25 + | 0.38254 | 0.24136 | 1.58496 | 1.55712 | 0.55466 | 2.80735 | 0.92788 | 0.62506 | 1 2 | 3 1 | 6 261.153 | 55.3184 | 95.34 chr1 | 1103295 | 1103317 chr1:1103 mi | r-3p + | 1 | 0.95652 chr1 | 1103295 11 | 103318 C12 | 32262.1 + | 32 mir-3p | chr1:1103 NA | NA | NA |
| 5 | chr1 | 1104434 | 1104456 P13 | 273.25 + | 0.19075 | 0.19075 | 1 | 0.94124 | 0.36412 | 2.58496 | 0.97072 | 0.83012 | 1 2 | 2 | 1 266.25 | 8.9854 | 83.3 chr1 | 1104434 | 1104456 chr1:1104 mi | r-5p3p + | 1 | 1 chr1 | 1104434 11 | 104456 C14 | 17403.8 + | 22 mir-5p3p | chr1:1104 1 | 1.0588 NA | NA |
| 6 | chr1 | 9211750 | 9211773 P301 | 116.5 - | 0.83403 | 0.52622 | 1.58496 | 0.6124 | 0.3062 | 2 | 0.76824 | 0.89157 | 2 2 | 3 : | 8 4.25 | 3.8309 | 72.8 chr1 | 9211751 | 9211773 chr1:9211 mi | -3p - | 1 | 0.95652 chr1 | 9211751 92 | 211773 011442 | 191.609 - | 19 mir-3p | chr1:9211 NA | NA | NA |
| 7 | chr1 | 9211793 | 9211815 P300 | 44.1 - | 1.44967 | 0.62434 | 2.32193 | 1.77131 | 0.68524 | 2.58496 | 0.70522 | 0.63123 | 1 2 | 2 | 1 32.1 | 1.4502 | 53.31 chr1 | 9211793 | 9211815 chr1:9211 mit | -50 - | 1 | 1 shr1 | 9211795 9 | 211817 011443 | 3999.84 - | 34 mir-5e | chr1:9211 8 | 2.463 NA | NA |
| * | chr1 | 2.4E+07 | 2.4E+07 P56 | 133,186 + | 0.65496 | 0.2333 | 2.80735 | 2.28896 | 0.68905 | 3.32193 | 0.89335 | 0.55538 | 1 2 | 4 | 1 119.98 | 4.3796 | 74.66 chr1 | 2.4E+07 | 2.4E+07 chr1:2361zcf | SNA + | 0.28571 | 1 shr1 | 2.4E+07 2. | 4E+07 C94 | 1553.23 + | 40 zeBNA | chr1:2361 1 | 48.44 45.19 | 52 62 |
| 9 | chr1 | 2.9E+07 | 2.9E+07 P59 | 18,1667 + | 1.00691 | 0.50346 | 2 | 1.56064 | 0.78032 | 2 | 0.80734 | 0.53731 | 1 2 | 6 | 1 15.6667 | 0.5974 | 24.84 chr1 | 2.9E+07 | 2.9E+07 chr1:288; and | BNA + | 0.1256 | 1 chr1 | 2.9E+07 2 | 9E+07 C119 | 168,998 + | 13 zogBNA | chr1:288; N4 | NA | NA |
| 10 | chr1 | 2.9E+07 | 2.9E+07 P60 | 159.05 + | 0.28552 | 0.18014 | 1.58496 | 1.84452 | 0.61484 | 3 | 0.95934 | 0.486 | 1 1 | 7 | 5 31.5166 | 5.2301 | 77.12 chr1 | 2.9E+07 | 2.9E+07 chr1:288; and | SNA + | 0,10891 | 1 shr1 | 2.9E+07 2. | 9E+07 C121 | 725.583 + | 24 zoBNA | chr1:288 | 16 NA | |
| 11 | che1 | 2.9E+07 | 2.9E+07 P61 | 98.167 + | 1.14358 | 0.57179 | 2 | 0.99273 | 0.29224 | 3.32193 | 0.73005 | 0.25972 | 1 2 | 7 1 | 0 8.16667 | 3.2281 | 70.06 chr1 | 2.9E+07 | 2.9E+07 chr1:2881 ene | BNA + | 0.13171 | 1 chr1 | 2.9E+07 2 | 9E+07 C124 | 238.148 + | 11 conBNA | chr1-2881 Nd | NA | NA |
| 12 | chr1 | 3.1E+07 | 3.1E+07 P270 | 47 - | 1.37337 | 0.2665 | 1.58496 | 1.7666 | 0.76084 | 2.32193 | 0.5 | 0.5 | 2 2 | 0 | 1 19.5 | 1.5455 | 54.73 chr1 | 3.1E+07 | 3.1E+07 chr1:3146 ene | BNA - | 0.29333 | 1 chr1 | 3.1E+07 3 | 1E+07 C11619 | 160.544 - | 22 zogBNA | chr1:3146 1 | 4.209 NA | 53 |
| 13 | che1 | 3 55+07 | 3 5E+07 P70 | 33 9959 + | 2.69614 | 0 77936 | 3 45943 | 1 872 | 0.56353 | 3 32193 | 0.396.99 | 0.57232 | 1 2 | • 5 17023: | 8 8 92762 | 1 1179 | 46.25 chr1 | 3.55+07 | 3 5E+07 chr1:3451 rB | NA + | 0.2809 | 1 chr1 | 3.55+07 3 | 5E+07 C131 | 461 751 + | A rBNA | che1:3451 N | NA | NA |
| 14 | ahat . | 4 15+07 | 4 1E+07 P79 | 20206.1 + | 0.43044 | 0.12959 | 2 22492 | 0.76646 | 0 2417 | 2 16 992 | 0.92921 | 0.256.52 | , , | 5 | 2 69 6665 | 664 449 | 92.22 cha1 | 4 15+07 | d 1E+07 ab-1-0122 mil | 5 + | 1 | 0.88 chat | 4 15+07 4 | 15+07 0142 | 100093 + | 40 mir-5n | aka1:4122 | 75274 2059 | 55 93 |
| 15 | aket . | d 1E+07 | 4.1E+07 P79 | 1292.22 + | 0.30016 | 0.116.12 | 2 52496 | 0 71146 | 0.23745 | 3.10775 | 0.9557 | 0.89049 | 1 2 | 2 | 7 260 13 | 62 4223 | 95.74 che1 | d 1E+07 | d 1E+07 ch-1:4122 mit | -3. + | | 1 che1 | 4.12+07 4 | 15+07 0142 | 15731.1 + | 40 mir 3p | chi1.4122 9 | 780 15 7701 | 21 58 |
| 16 | shri .L.1 | 4.15+07 | 4.16+01 P17 | 1657.14 4 | 0.30010 | 0.0674 | 2.30470 | 1.00455 | 0.24562 | 2 16 0 0 2 | 0.9991 | 0.07047 | 1 2 | 4 | 2 642 643 | 62.4223 E4 2602 | 45.74 chr1 | 4.15+07 | 4.1E+01 Chris4122 mil | | | 0.05022 -1-1 | 4.15+07 4 | 15+07 0144 | 20642.2 4 | 27 - : PNA | -L-1.4122 3 | 4640 6 376 6 | 67 AA |
| 42 | shr1 | 4.15+07 | 4.16407 0.04 | 024.467.4 | 0.60520 | 0.20404 | 4 50.404 | 0.22740 | 0.44274 | 2.10772 | 0.90699 | 0.00124 | | 0 4 2222 | 2 40E 4E4 | 20 7296 | 42.4 -1-4 | 4.15+07 | 4 4E+07 | - 20 - 4 | 0 00000 | 0.99099 chr1 | 4.15+07 4 | 45407 0445 | 240 425 4 | 20 - 12- | -1-4422 4 | 0 467 MA | 76 44 NA |
| 40 | | 4.12401 | 4.16701 POT | 40 3306 - | 0.60335 | 0.30190 | 1.30490 | 0.456.49 | 0.11314 | | 0.03555 | 0.96134 | | 0 4.33333. 6 3.6.4001 | 5 103.434 | 0 5000 | 75.4 chri 25.09 -1-4 | 4.16701 | 4.1E+01 chr1:4122 mi | гор т | 0.90909 | 1 chr1 | 4.12+01 4. | EE+07 C145 | 317.435 T | 20 PNA | chr1:4122 | 0 004 NA | NA NA |
| 40 | chri | 4.56+01 | 4.56+01 F252 | 10.6300 - | 0.52705 | 0.26473 | 2 22402 | 4.04750 | 0.01024 | | 0.91964 | 0.70104 | | 6 6.0400; | 4 447 | 0.3770 | 29.00 chr1 | 4.52+01 | 4.5E+01 Chr1:446 Jer | DHA - | 0.11204 | 0.05(52 -1-4 | 4.55+01 4. | 55+07 0453 | 644.03 | 20 John | chr1:446 3 | 5.004 IIH | 11H |
| 17 | chri chri | 4.56+07 | 4.56407 000 | 457.655 4 | 0.22211 | 0.07574 | 2.32193 | 1.01190 | 0.33919 | 2 50404 | 0.91120 | 0.03919 | | 2 14 - 21 | 1 14.5 | 4 5333 | 70.71 chr1 | 4.55+07 | 4.5E+01 chr1:452-5ht | | 0.2913 | 0.99692 chri | 4.55+07 4. | 55+07 0463 | 541.74 T | 33 MONIN | chr1:452, 2 | .9160 00 | 20 |
| 20 | enri | 4.56+01 | 4.55+01 F 00 | 452,722 4 | 0.03216 | 0.41600 | 4 50 404 | 1.00134 | 0.13012 | 2.50476 | 0.01979 | 0.91307 | | 4 4 2 2 2 2 | 5 7.40000 D DE DAE | 4.9322 | 14.70 chri | 4.52+01 | 4.5E+01 Chr1:452-5ht | | 0.29910 | I Chri | 4.55+07 4. | 55-07 0470 | 200.007 | 23 MBNIN | Chr (:452) 116 | | 20 |
| 21 | chr1 | 4.56+07 | 4.5E+07 P89 | 192.722 + | 0.9014 | 0.96872 | 1.58496 | 1.40055 | 0.54181 | 2.98496 | 0.69772 | 0.60213 | 4 4 | 1 1.3333 | 3 39.395 | 9.022 | 16.31 chr1 | 4.55+07 | 4.5E+07 chr1:452 she | | 0.30439 | 1 chr1 | 4.56+07 4. | 55+07 0170 | 290.807 + | 23 JABRINA | Chr1:452 MP | | 14 |
| 22 | chr1 | 4.56707 | 4.52407 P90 | 1910.12 * | 1.32110 | 0.39112 | 3.32193 | 0.16619 | 0.21303 | 2.00139 | 0.72266 | 0.01919 | 1 4 | | 2 691.105 | 62.0116 | 99.11 chr1 | 4.52+07 | 4.5E+01 Chr1:452 Int | | 0.333333 | 1 chr1 | 4.52707 4. | SETOT C113 | 1910.12 * | 1 2000000 | Chr1:4521 11 | | ne N/ AA |
| 23 | chr1 | 6.6E+07 | 6.6E+07 P236 | 644025 - | 0.9652 | 0.34381 | 2.80735 | 0.89465 | 0.31868 | 2.80735 | 0.61158 | 0.78182 | | 2 | 5 40544.4 | 211((.9 | 99.95 chr1 | 6.6E+07 | 6.6E+01 chr1:655, mi | r-3p - | | 0.95455 chr1 | 6.6E+07 6. | 6E+07 C11693 | 136072 - | 39 mir-3p | chr1:655, 2 | 66914 3542. | 26 89 |
| 24 | chr1 | 6.6E+07 | 6.6E+07 P103 | 67.3774 + | 1.72807 | 0.66851 | 2.58496 | 1.13941 | 0.44078 | 2.58496 | 0.5018 | 0.7605 | 3 Z | 0 13.369 | 8 Z.0496 | 2.2156 | 62.65 chr1 | 6.6E+07 | 6.6E+07 chr1:658: snl | sna + | 0.10695 | 1 chr1 | 6.6E+07 6. | 6E+07 C191 | 103.605 + | 4 snBNA | chr1:658: NF | NA | NA |
| 25 | chr1 | 6.9E+07 | 6.9E+07 P234 | 11 - | 0 | 0 | 0 | 0.41382 | 0.41382 | 1 | 1 | 0.91667 | 1 2 | 2 | 1 12 | 0.3617 | 3.62 chr1 | 6.9E+07 | 6.9E+07 chr1:686(mi | r-5p3p - | 1 | 1 chr1 | 6.9E+07 6. | 9E+07 C11702 | 121.402 - | 25 mir-5p3p | chr1:686(N# | NA | NA |
| 26 | chr1 | 7.2E+07 | 7.2E+07 P230 | 4069.42 - | 0.46208 | 0.29154 | 1.58496 | 1.21415 | 0.40472 | 3 | 0.91379 | 0.69771 | 2 2 | 4 | 1 33.5 | 133.817 | 97.64 chr1 | 7.2E+07 | 7.2E+07 chr1:7153 mi | -5p - | 1 | 0.91667 chr1 | 7.2E+07 7. | 2E+07 C11705 | 37228.1 - | 41 mir-5p | chr1:7153 2 | 54783 753.5 | 83 |
| 27 | chr1 | 7.6E+07 | 7.6E+07 P111 | 1549.44 + | 0.88333 | 0.38043 | 2.32193 | 0.34769 | 0.10467 | 3.32193 | 0.79675 | 0.95818 | 2 2 | 5 7.1989 | 2 38.8182 | 50.9512 | 95.08 chr1 | 7.6E+07 | 7.6E+07 chr1:762!sna | RNA + | 0.32051 | 1 chr1 | 7.6E+07 7. | .6E+07 C194 | 363.859 + | 18 snaRNA | chr1:762! 8 | 8.1699 NA | NA |
| 28 | chr1 | 9.2E+07 | 9.2E+07 P215 | 262.62 - | 3.61553 | 0.88454 | 4.08746 | 4.06655 | 0.94091 | 4.32193 | 0.22066 | 0.14362 | 3 2 | 1 15.416 | 7 2.02702 | 8.6359 | 82.95 chr1 | 9.2E+07 | 9.2E+07 chr1:9185 rR | NA - | 0.09945 | 0.97297 chr1 | 9.2E+07 9. | 2E+07 C11743 | 2818.84 - | 9 rBNA | chr1:9185 N# | 71.07 | 45 NA |
| 29 | chr1 | 9.3E+07 | 9.3E+07 P127 | 294.417 + | 0.21159 | 0.09113 | 2.32193 | 1.27176 | 0.4012 | 3.16993 | 0.97263 | 0.78717 | 1 2 | 4 | 1 287.358 | 9.6815 | 83.99 chr1 | 9.3E+07 | 9.3E+07 chr1:9331 sna | RNA + | 0.25263 | 1 chr1 | 9.3E+07 9. | .3E+07 C222 | 120.129 + | 3 snaRNA | chr1:933(N# | NA | NA |
| 30 | chr1 | 9.3E+07 | 9.3E+07 P128 | 127.9 + | 2.95044 | 0.85287 | 3.45943 | 0.43553 | 0.18757 | 2.32193 | 0.20328 | 0.9409 | 8 2 | 4 : | 8 3.5 | 4.2058 | 74.12 chr1 | 9.3E+07 | 9.3E+07 chr1:9331 sna | RNA + | 0.25263 | 1 chr1 | 9.3E+07 9. | .3E+07 C224 | 7406.45 + | 22 snaRNA | chr1:933(N# | 48.83 | 33 75 |
| 31 | chr1 | 9.4E+07 | 9.4E+07 P131 | 206.301 + | 1.80185 | 0.54241 | 3.32193 | 2.21568 | 0.59876 | 3.70044 | 0.39948 | 0.52572 | 1 3 | 1 1 | 6 14.8333 | 6.7839 | 80.37 chr1 | 9.4E+07 | 9.4E+07 chr1:9431 tR | NA + | 0.36471 | 1 chr1 | 9.4E+07 9. | 4E+07 C237 | 494.387 + | 10 KBNA | chr1:9431 4 | 6.297 NA | NA |
| 32 | chr1 | 9.4E+07 | 9.4E+07 P132 | 109.9 + | 0.67651 | 0.26171 | 2.58496 | 2.79969 | 0.78096 | 3.58496 | 0.90081 | 0.3298 | 1 2 | 2 15.416 | 7 7.4800 | 3.6139 | 71.94 chr1 | 9.4E+07 | 9.4E+07 chr1:943* tR | NA + | 0.25882 | 1 chr1 | 9.4E+07 9. | 4E+07 C242 | 346.88 + | 6 piBNA | chr1:9431 N# | NA | NA |
| 33 | chr1 | 9.5E+07 | 9.5E+07 P213 | 106.426 - | 0.28459 | 0.28459 | 1 | 0.00916 | 0.00916 | 1 | 0.95043 | 0.99922 | 1 2 | 0 2.2 | 5 45.9556 | 3.4997 | 71.29 chr1 | 9.5E+07 | 9.5E+07 chr1:952' mi | r-5p3p - | 1 | 1 chr1 | 9.5E+07 9. | 5E+07 C11759 | 190.955 - | 22 mir-5p3p | chr1:9521 3 | 9.6167 NA | NA |
| 34 | chr1 | 1.1E+08 | 1.1E+08 P197 | 116.188 - | 3.23144 | 0.82711 | 3.90689 | 4.15932 | 0.89566 | 4.64386 | 0.29476 | 0.12906 | 1 2 | 3 2.08333 | 3 17.4385 | 3.8207 | 72.77 chr1 | 1.1E+08 | 1.1E+08 chr1:1081 rR | NA - | 0.07117 | 1 chr1 | 1.1E+08 1. | .1E+08 C11790 | 245.089 - | 2 rBNA | chr1:1081 N# | NA | NA |
| 35 | chr1 | 1.1E+08 | 1.1E+08 P144 | 45.4444 + | 0.15255 | 0.15255 | 1 | 0.65218 | 0.28088 | 2.32193 | 0.978 | 0.88733 | 1 2 | 2 | 1 45.4444 | 1.4944 | 54.07 chr1 | 1.1E+08 | 1.1E+08 chr1:1101 mi | r-3p + | 1 | 1 chr1 | 1.1E+08 1. | .1E+08 C261 | 3216.22 + | 34 miRNApr | chr1:1101 6 | 66.48 NA | NA |
| 36 | chr1 | 1.2E+08 | 1.2E+08 P149 | 2921.5 + | 0.38374 | 0.13669 | 2.80735 | 0.88343 | 0.38047 | 2.32193 | 0.93986 | 0.83761 | 2 2 | 1 1 | 4 8.09773 | 96.0694 | 96.91 chr1 | 1.2E+08 | 1.2E+08 chr1:1172 mi | r-5p3p + | 0.90909 | 0.95238 chr1 | 1.2E+08 1. | .2E+08 C275 | 2197.64 + | 42 mir-5p3p | chr1:1172 | 366.16 87.51 | 04 19 |
| 37 | chr1 | 1.2E+08 | 1.2E+08 P187 | 33.2157 - | 0.60545 | 0.21567 | 2.80735 | 0.77641 | 0.33438 | 2.32193 | 0.91866 | 0.86662 | 1 1 | 7 8.75 | 5 4.4873 | 1.0923 | 45.68 chr1 | 1.2E+08 | 1.2E+08 chr1:1205 rR | NA - | 0.07025 | 1 chr1 | 1.2E+08 1. | 2E+08 C11806 | 426.412 - | 22 rRNA | chr1:1205 N# | 21.50 | 76 1 |
| 38 | chr1 | 1.4E+08 | 1.4E+08 P183 | 10.657 - | 0.1525 | 0.06568 | 2.32193 | 0.06239 | 0.06239 | 1 | 0.9835 | 0.99269 | 1 1 | 7 | 1 11.4812 | 0.3504 | 2.64 chr1 | 1.4E+08 | 1.4E+08 chr1:1448 tR | F-5-trl - | 1 | 0.82353 chr1 | 1.4E+08 1. | 4E+08 C11836 | 106.659 - | 11 tBF-5-tri | chr1:1445 N# | NA | NA |
| 39 | chr1 | 1.5E+08 | 1.5E+08 P155 | 33.2157 + | 0.60545 | 0.21567 | 2.80735 | 0.77641 | 0.33438 | 2.32193 | 0.91866 | 0.86662 | 1 1 | 7 8.75 | 5 4.4873 | 1.0923 | 45.69 chr1 | 1.5E+08 | 1.5E+08 chr1:1452 rR | NA + | 0.07025 | 1 chr1 | 1.5E+08 1. | 5E+08 C290 | 426.412 + | 22 rBNA | chr1:1452 NA | 21.50 | 76 1 |
| 40 | chr1 | 1.5E+08 | 1.5E+08 P182 | 10.657 - | 0.1525 | 0.06568 | 2.32193 | 0.06239 | 0.06239 | 1 | 0.9835 | 0.99269 | 1 1 | 7 | 1 11.4812 | 0.3504 | 2.65 chr1 | 1.5E+08 | 1.5E+08 chr1:1453 tR | F-5-trl - | 1 | 0.82353 chr1 | 1.5E+08 1. | .5E+08 C11838 | 106.653 - | 11 tRF-5-tri | chr1:1453 N/ | NA | NA |
| 41 | chr1 | 1.5E+08 | 1.5E+08 P181 | 61401.7 - | 0.10055 | 0.02574 | 3.90689 | 1.44378 | 0.39016 | 3.70044 | 0.99075 | 0.72617 | 1 2 | 8 5.1666 | 7 11775.2 | 2019.11 | 99.33 chr1 | 1.5E+08 | 1.5E+08 chr1:1453 tR | F-5-trl - | 1 | 0.89286 chr1 | 1.5E+08 1. | 5E+08 C11844 | 4625.81 - | 31 piBNA | chr1:1453 2 | 869.8 195.1 | 34 10 |
| 42 | chr1 | 1.5E+08 | 1.5E+08 P178 | 52.7221 - | 1.61239 | 0.4127 | 3.90689 | 2.36527 | 0.71202 | 3.32193 | 0.61581 | 0.51333 | 7 2 | :1 | 1 16 | 1.7337 | 57.53 chr1 | 1.5E+08 | 1.5E+08 chr1:1453 kR | F-5-trl - | 0.95652 | 0.78571 chr1 | 1.5E+08 1. | 5E+08 C11870 | 3718.33 - | 1 tRF-5-tri | chr1:1453 N# | NA | NA |
| 43 | chr1 | 1.5E+08 | 1.5E+08 P177 | 706.01 - | 2.10531 | 0.48712 | 4.32193 | 2.66242 | 0.71949 | 3.70044 | 0.56022 | 0.29565 | 1 3 | 3 | 1 398.641 | 23.2161 | 91.97 chr1 | 1.5E+08 | 1.5E+08 chr1:1453 tR | F-5-trl - | 1 | 0.93939 chr1 | 1.5E+08 1. | 5E+08 C11875 | 13059.6 - | 24 tRF-5-trl | chr1:1453 5 | 27.42 NA | NA |
| 44 | chr1 | 1.5E+08 | 1.5E+08 P157 | 116.5 + | 0.24137 | 0.12069 | 2 | 0 | 0 | 0 | 0.96996 | 1 | 1 1 | * : | 3 38.6667 | 3.8309 | 72.79 chr1 | 1.5E+08 | 1.5E+08 chr1:1454 piF | NA + | 0.64286 | 1 chr1 | 1.5E+08 1. | 5E+08 C300 | 112.91 + | 8 piBNA | chr1:1454 N# | | 17 NA |
| 45 | chr1 | 1.5E+08 | 1.5E+08 P159 | 10.6055 + | 0.19781 | 0.08519 | 2.32193 | 0.06261 | 0.06261 | 1 | 0.97668 | 0.99266 | 1 1 | 7 1.1229 | 6 10.224 | 0.3487 | 2.41 chr1 | 1.5E+08 | 1.5E+08 chr1:1459 tR | F-5-trl + | 1 | 0.82353 chr1 | 1.5E+08 1. | 5E+08 C302 | 106.884 + | 8 tRF-5-tri | chr1:1459 N# | NA | NA |
| | 4 |). | DASH | IR comparie | son a | | G |) | | | | | | | | | | | | 4 | | | | | | | | | |
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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 AH AI AJ AK

AL AM I

17 NA NA 🚽

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: peopression tables or mature products 2. Unannotated peaks: peaks 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 Step 3: Click to download | Arr ced peaks [xls] onannotated peaks [xls] All (Annotated + Unannotated) peaks [xls] [bed] Peaks not in ENCODE [xls] |
| | 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 | в | С | D | E | F | G | н | I. | J | к | L | M | N | 0 | Р | Q | B | s | т | U | V | w x | Y | z | AA | AF AC | AD | AE AF | F AG |
|----|--------|---------|---------|--------|---------|------|--------------|--------|--------|---------|---------|--------|---------|---------|--------|--------|---------|---------|----------|---------|--------|-----------|---------------|--------------|----------|---------|------------|-------------|------------|-------------|
| 1 | #peakC | peakChr | peakChr | peakID | peakExp | peak | (StrapeakEnt | peakNo | peakMa | peakEnt | peakNot | peakMa | peakPrd | peakPro | peakMo | peakMo | beforeP | peakFol | peakRP p | peakExp | annotC | ł annotCł | annotCF annot | ID annotRi | annotSti | annotOv | pe Øve chr | chrStart cł | nrEnd anch | norIE 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 chr1:5 | 66 tRNA | - | 0.3636 | 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 chr1:1 | 84 snRNA | - | 0.18 | 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 chr1:10 | 87 tRF-5-tr | (- | | 0.88 | -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 chr1:10 | 395 snRNA | • | | 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 chr1:1 | 706 snRNA | + | | 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 chr1:1 | 718 tRF-5-tr | (+ 🖊 | | 0.88 . | -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 chr1:1 | 22 snRNA | • | 9 | 1. | -1 | -1 . | |
| э | 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 chr1:2 | 88: snoRN/ | • | 63 | 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 chr1:2 | 89) snoRN/ | :/ | 154 | 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 chr1:2 | 89 snoRM | | 1364 | 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 chr1:3 | 144 sno | | .3333 | 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 chr1:3 | 37: m | | 1 | 0.92 . | -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 chr1:3 | 68: | | 0.1985 | 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 chr1:4 | F | | 0.2973 | 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 . | |
| 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 c | | | 0.253 | 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 . | |
| 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+9 | | | 0.0445 | 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 | 15 | | | 0.0391 | 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 . | |
| 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 . | |
| 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 . | |
| 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 | 15 | | / | • | 0.1074 | 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 | | | A | | 0.9375 | 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-tr | · | 0.8636 | 0.9048 | -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 | | | NA. | | 0,189 | 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 . | |
| 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 | 1 | | | BNA | | 0.189 | 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 | | | | biBNA | • | 0.9063 | 0.9667 | -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 | | | | DIBNA | | 0.9375 | 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 | 1 | | | | 8 snBNA | | 0.189 | 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 | / | | | | 91 tBF-5-tr | + | 1 | 0.8235 | -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 | 2.6132 | | | | h. | 92 snRNA | | 0.189 | 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 | | | | 1 | 92 tBE-5-tr | | 1 | 0.8182 | -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 | | | | | r1:1 | 96 tBE-3-tr | | 0.9545 | 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 | 12667 | 60.841 | | | | | hr1:1 | 96 tBE-5-tr | | 1 | 0.8182 | -1 | -1 | |
| 38 | chr1 | 2E+08 | 2E+08 | P166 | 17 739 | | 0.3584 | 0.2261 | 1585 | | 0 | ů. | 0.9456 | 1 | 1 | 15 | 2 4872 | 7 7439 | | | | | chri-1 | 14 scBMA | • | 0 1596 | 1 | | -1 | |
| | - | | not | in DA | SHR | | (\pm) | | | | | | | | | | | | | | | | | | | | | | | |

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

| 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

| A | в | с | D | E | F | G | н | 1.1 | J | к | L | M | N | 0 | P | Q | в | s | т | υ | V I | v I | x | ⊥ / _Y − | z | AA I | AB | AC |
|--------|---------|--------------------|----------|---------|----------|---------|---------|--------|---------|---------|--------|---------|---------|----------|-------|---------|---------|--------|---------|---------|---------|---------|-----------|--------------------|----------|---------|----------|-----|
| #peakC | peakChr | peakCh | r peakID | peakExp | peakStr. | peakEnt | peakNor | peakMa | peakEnt | peakNor | peakMa | peakPro | peakPro | peakMo p | eakMo | beforeP | peakFol | peakRP | peakExp | annotCł | annotCł | annotCł | annoti⊡ |) annotRi | annotSti | annotOv | peakOver | lap |
| 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 | ohr1 | 566375 | 566441 | chr1:566 | : tBNA | | 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 | ohr1 | 2E+07 | 2E+07 | chr1:170 | d 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 | ohr1 | 6E+07 | 6E+07 | chr1:554 | R 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 | ohr1 | 9E+07 | 9E+07 | chr1:939 | RNA | | 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 | ohr1 | 9E+07 | 9E+07 | chr1:943 | RNA | • | 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 | chr1:146 | 5 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 | chr1:149 | 2 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 | 5 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 | 5 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 | t BNA | + | 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 | t BNA | + | 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 | RNA | + | 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 | chr11:66 | 1 tBNA | + | 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 | chr13:31 | 2 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 | chr13:41 | 6 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 | BNA | + | 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 | RNA | + | 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 | RNA | | 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 | I tBNA | • | 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 | RNA | • | 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 | RNA | | 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 | RNA | • | 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 | RNA | • | 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 | t BNA | • | 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 | chr16:14 | 3 tBNA | • | 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 | RNA | | 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 | RNA | | 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 | ohr17 | 8E+06 | 8E+06 | chr17:80 | RNA | + | 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 | RNA | + | 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 | t BNA | + | 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 | chr17:81 | 2 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 | chr17:19 | 4 tBNA | • | 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 | chr17:19 | 4 tBNA | • | 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 | RNA | • | 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 | BNA | | 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 | BNA | - | 0.375 | 1 | |
| chr17 | 7E+07 | 7E+07 | P775 | 2690.3 | | 15571 | 0.381 | 4 0875 | 0.2108 | 0.0703 | 3 | 0 4 9 9 | 0.9761 | 8 | 28 | 11.313 | 2 14 91 | 1262.5 | 98 11 | ohr17 | 7E+07 | 7E+07 | chr17-66 | BMA | | 0.3836 | 1 | |
| | | peaks.byClass.tRN/ | | NA | (+ |) | | | | | | | | | | | | | 4 | | | | | | | | | |

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

| RN/ .ss | 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 |
| s | 137 | 132 | 17,896 | 0.17 |
| s | 34 | 29 | 341,572 | 3.29 |
| tř | 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 | A | в | С | D | E | F | G | н | I | J | к | L | м | N | Ο | Р | Q | В | s | т | U | V | W | х | Y |
|----|---------|---------|----------|--------|---------|------------|------------|----------|---------|----------|----------|---------|----------|----------|---------|-----------|----------|----------|---------|----------|---------|------------|----------|---------|---------|
| 1 | #peakCh | peakChr | peakChrf | peakID | peakExp | i peakStra | a peakEntr | peakNorr | peakMax | peakEntr | peakNorr | peakMax | peakProp | peakProp | peakMos | ; peakMos | beforePe | peakFolc | peakRPN | peakExpi | annotCh | i annotChi | annotChi | 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 |
| 0 | 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| - | | | | | | - | - | | | | | | | | | | | | | | | | | | |

No

annotation

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] [5.00 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] Umannotated peaks [xls] All (Annotated + Umannotated) peaks [xls] [bed] Peaks not in DASHR [xls] |
| Comparison with ENCODE | Integrated expression tables | Annotated peaks [x1s] Umannotated peaks [x1s] All (Annotated + Unannotated) peaks [x1s] [bed] Peaks not in ENCODE [x1s] |

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 | 040,098 | 6.22 |
| mir-3p | 224 | 224 | 1,779,736 | 17.13 |
| mir-5p | 285 | 285 | 5,786,729 | 54.92 |
| mir-5p3pno | 00 | 00 | 39,553 | 8.29 |
| piRNA | 99 | 99 | 747,688 | 7.19 |
| rRNA | 98 | 81 | 42,675 | 8.41 |
| scRNA | 225 | 215 | 227,677 | 2.19 |
| snRNA | 137 | 132 | 17,896 | 8.17 |
| SNORNA | 34 | 29 | 341, 572 | 3.29 |
| tRF3 | 6 | 6 | 1,323 | 0.01 |
| tRF5 | 9 | 9 | 998 | 0.01 |
| trna | 109 | 138 | 183,725 | 1.88 |

Step 2: click this to maximize "Run log"

Run log (Output)

Run log displayed agin

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?

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 Penn Neurodegeneration inomics Center
 University of Pennsylvania

 Send questions to this email: SPAR@lisanwanglab.org

END