

How to Use IGV-sRNA

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This is a step-by-step user-guide of IGV-sRNA. IGV-sRNA is developed on the basis of IGV (Integrative Genomics Viewer, <https://software.broadinstitute.org/software/igv/>), and is specifically optimized for small RNA data visualization. Several new functions, designed specifically for exploring NGC sRNA data, have been integrated into IGV-sRNA. For the general usage of IGV, please refer to its User Guide (<https://software.broadinstitute.org/software/igv/UserGuide>). How to use the new functions of IGV-sRNA are described below.

Download

IGV-sRNA is available from [sRNAanno Database](http://www.plantsRNAs.org) (www.plantsRNAs.org)



Welcome to sRNAanno

Small RNAs (sRNAs) are essential regulatory molecules in plants. The sRNAanno database hosts a large collection of miRNA, phasiRNA- and hc-siRNA-generating loci annotated from ~140 plants using consistent and high-confident criteria. All the annotations are made freely available to the scientific community via various services and tools.

Search

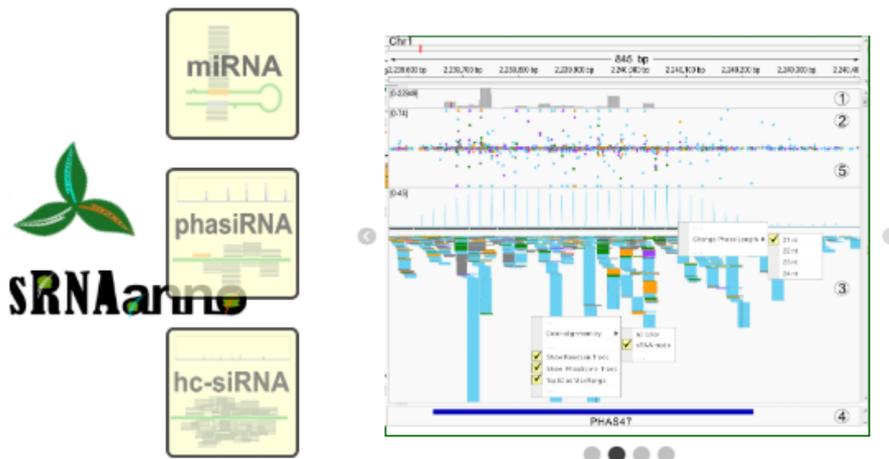
Blast your sequence against our annotated *MIRNA* and *PHAS* loci, or search for miRNA of interest by name, for example, "miR156".

Browse

Browse species of interest from a large phylogenetic tree of all plants studied and download corresponding sRNA annotation.

Resources

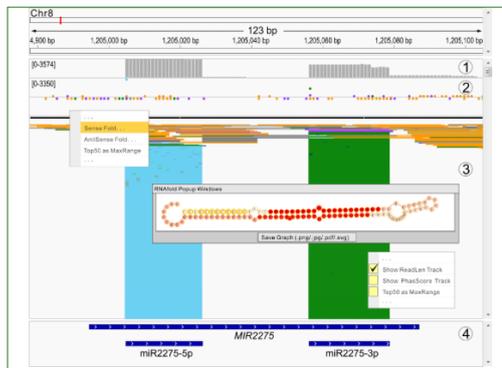
Download tools we developed or modified for plant small RNA analysis and explore our open data resources.



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Click Resources.

IGV-sRNA



IGV-sRNA is developed on the basis of IGV, and is specifically optimized for small RNA data visualization. Several useful features are introduced:

- **sRNA mode:** sRNA mode: display sRNA alignment with different color codes according to read length
- **ReadLen Track:** show sRNA abundance with color-coded dots
- **PhaseScore Track:** calculate phasing score of phasfRNAs instantly according their length
- **RNAfold invoker:** fold a sequence to show the secondary structure
- ...

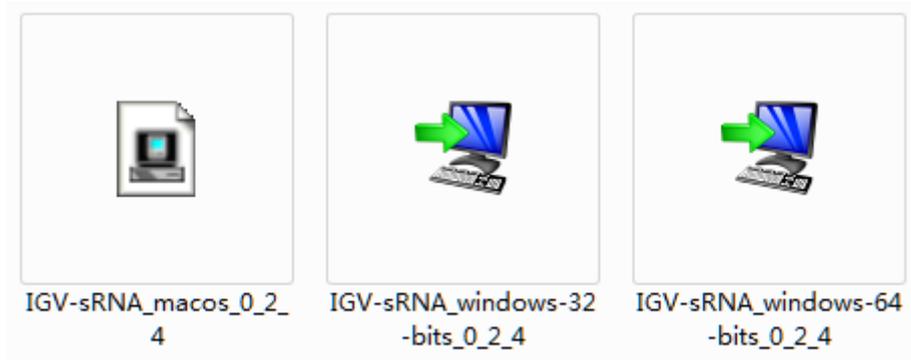
Download

- [windows-32-bits](#)
- [windows-64-bits](#)
- [macOS](#)
- [Linux](#)

At the bottom-right corner of the new page, you will find links to IGV-sRNA installers for different operation system. Choose your ideal version and download it.

Install IGV-sRNA

1. Windows users (32-bits and 64-bits) and Mac OS users



Double click the installer, and follow the instructions.

2. Linux users

Open the terminal and type,

```
sh IGV-sRNA_Linux-unix_0_2_4.sh
```

Press Enter.

Use IGV-sRNA



Double click the IGV-sRNA icon and wait.

Import Demo Data

Download the demo data.

Download

- [windows-32-bits](#)
- [windows-64-bits](#)
- [macOS](#)
- [Linux](#)
- [Demo Data](#)

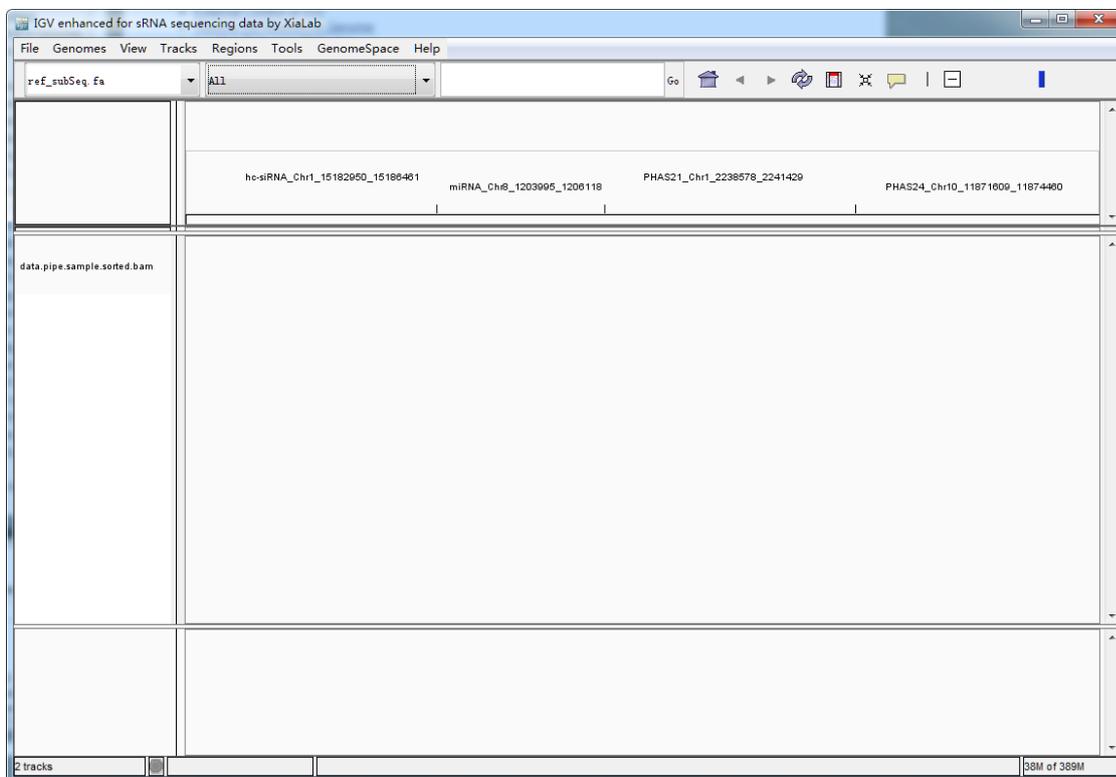
The demon data include four datasets:

<p>ref_subSeq.fa: sequence segments of the rice genome.</p> <p>ref_subSeq.fa.fai: fasta index of ref_subSeq.fa.</p> <p>data.pipe.sample.sorted.bam: alignmengt of sRNA sequencing reads in BAM format.</p> <p>data.pipe.sample.sorted.bam.bai: BAM index of data.pipe.sample.sorted.bam.</p> <p>repeat_score.bigWig: repeat score data of ref_subSeq.fa.</p>
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Load reference Genome file.

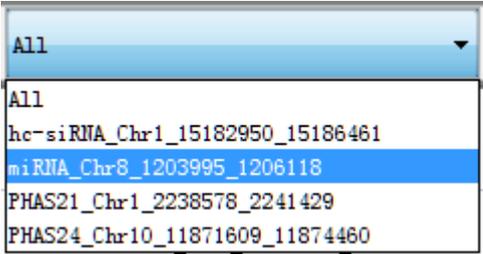
Load sample data file.

After demo data are loaded, you will get into the interface as follows.

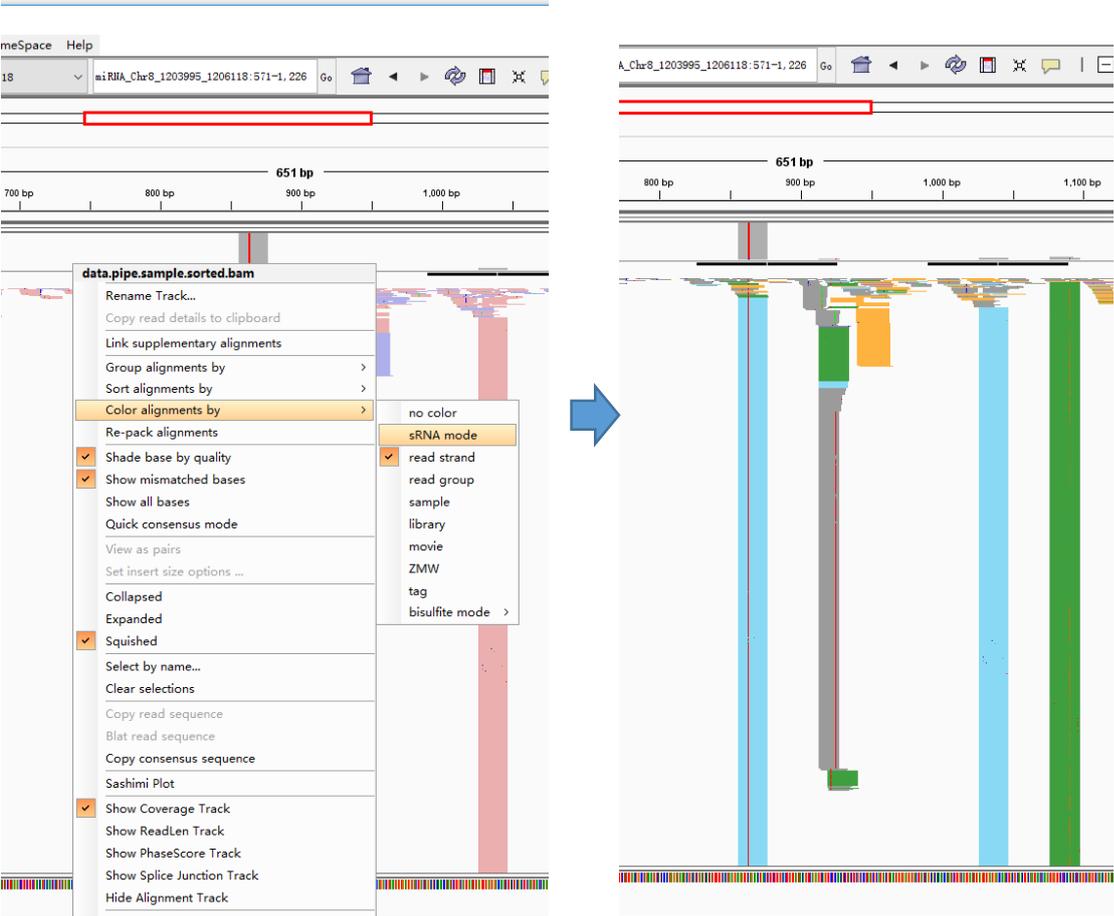


miRNA locus

Select the demo data for a miRNA locus.



View alignments in color scheme (sRNA mode).



Right-Click to show the **readLen** track

data.pipe.sample.sorted.bam

- Rename Track...
- Copy read details to clipboard
- Link supplementary alignments
- Group alignments by
- Sort alignments by
- Color alignments by
- Re-pack alignments
- Shade base by quality
- Show mismatched bases
- Show all bases
- Quick consensus mode
- View as pairs
- Set insert size options ...
- Collapsed
- Expanded
- Squished
- Select by name...
- Clear selections
- Copy read sequence
- Blat read sequence
- Copy consensus sequence
- Sashimi Plot
- Show Coverage Track
- Show ReadLen Track**
- Show Phasescore Track
- Show Splice Junction Track
- Hide Alignment Track
- Save image...
- Export Alignments...
- Export track names...
- Remove Track

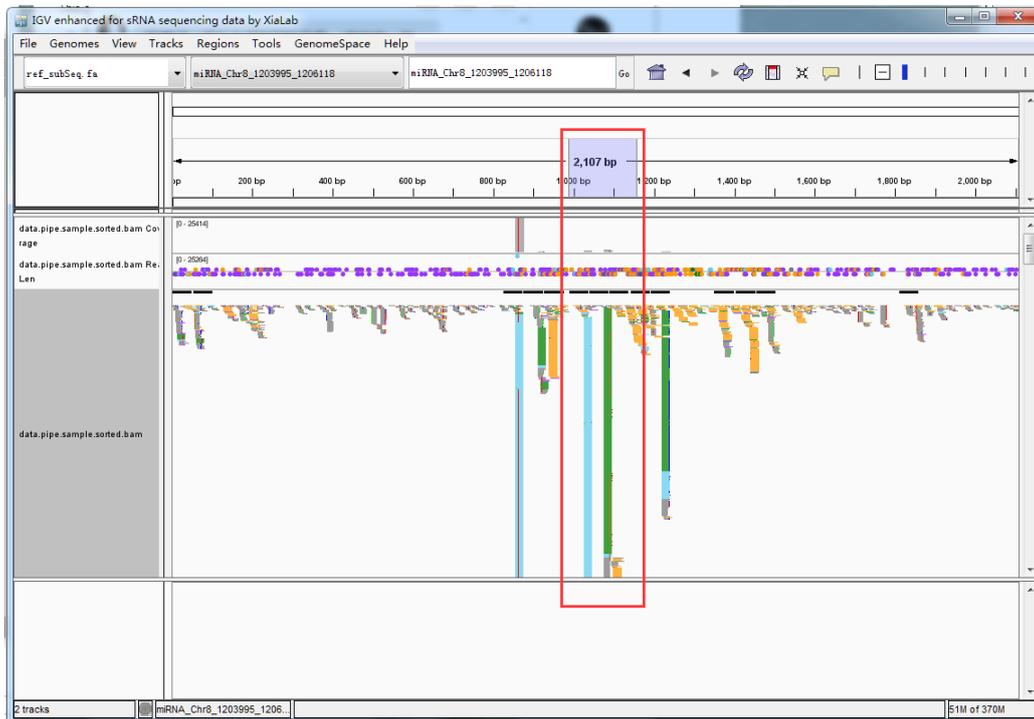


data.pipe.sample.sorted.bam Coverage [0 - 25414]

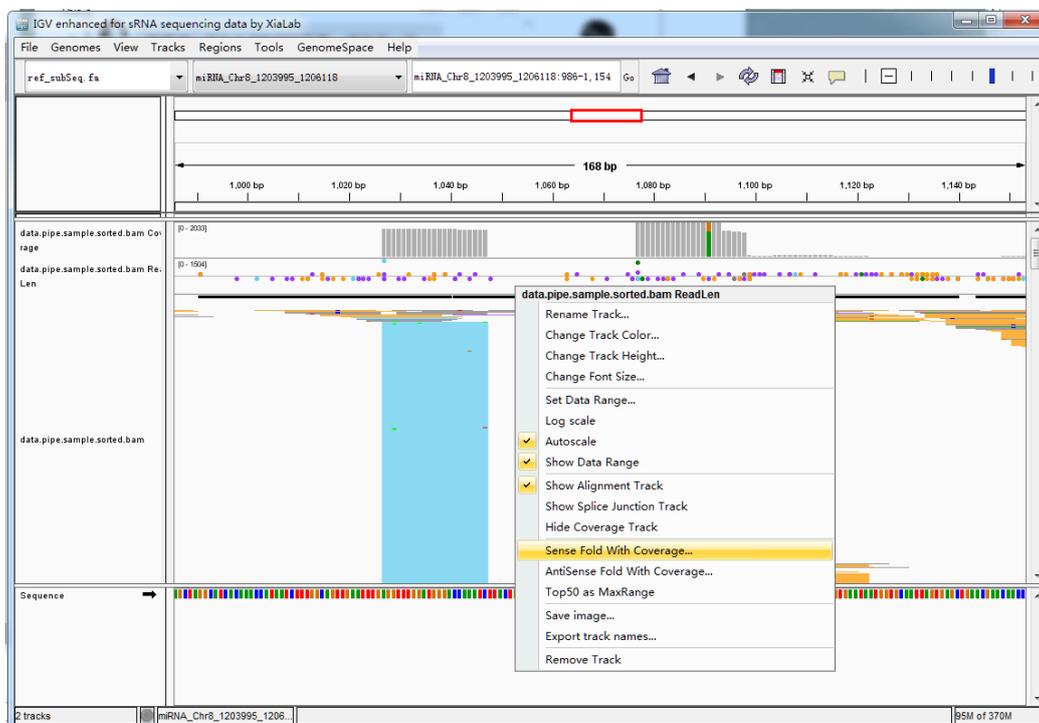
data.pipe.sample.sorted.bam ReadLen [0 - 25284]

data.pipe.sample.sorted.bam

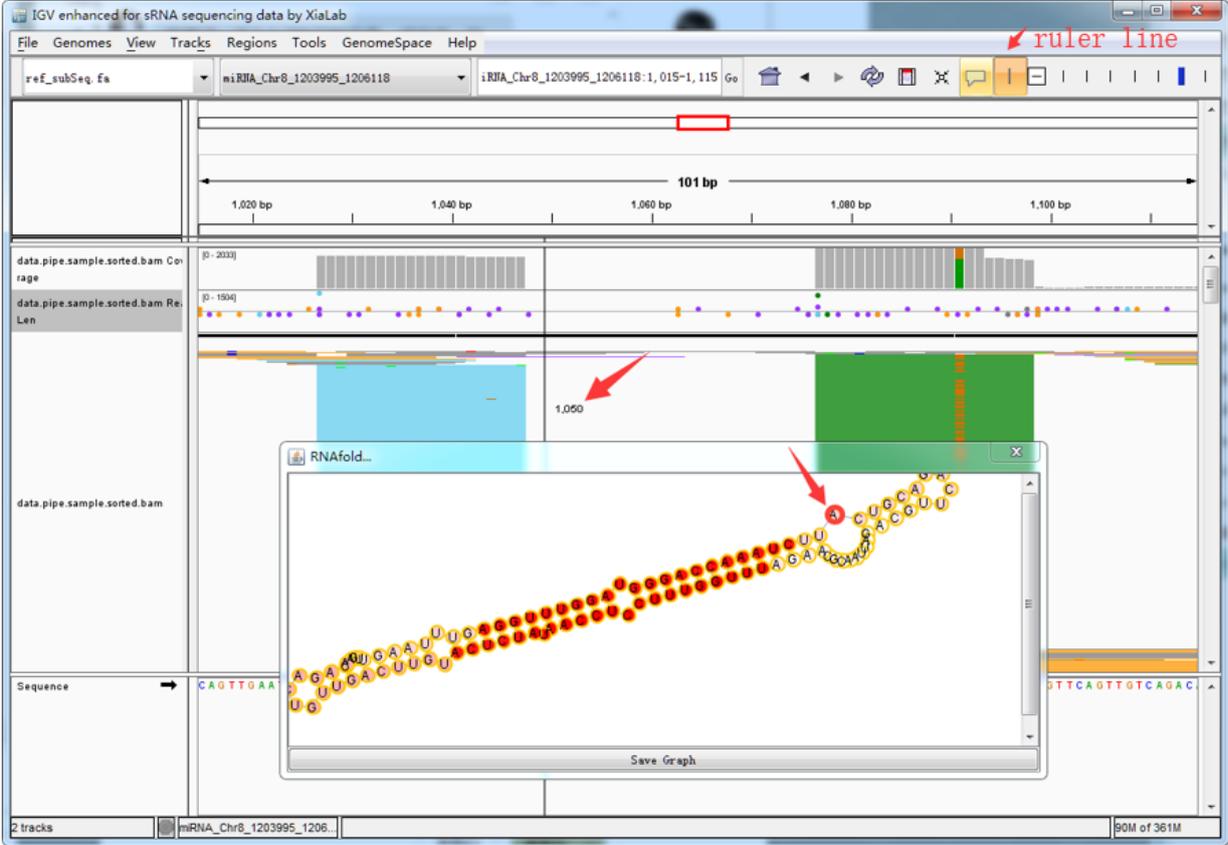
Zoom in to a smaller part of the window.



Right-Click on the track of **ReadLen** and select the **Sense Fold With Coverage** function.
[If the miRNA locus was located in the minus strand, select the **AntiSense Fold with Coverage** function.]

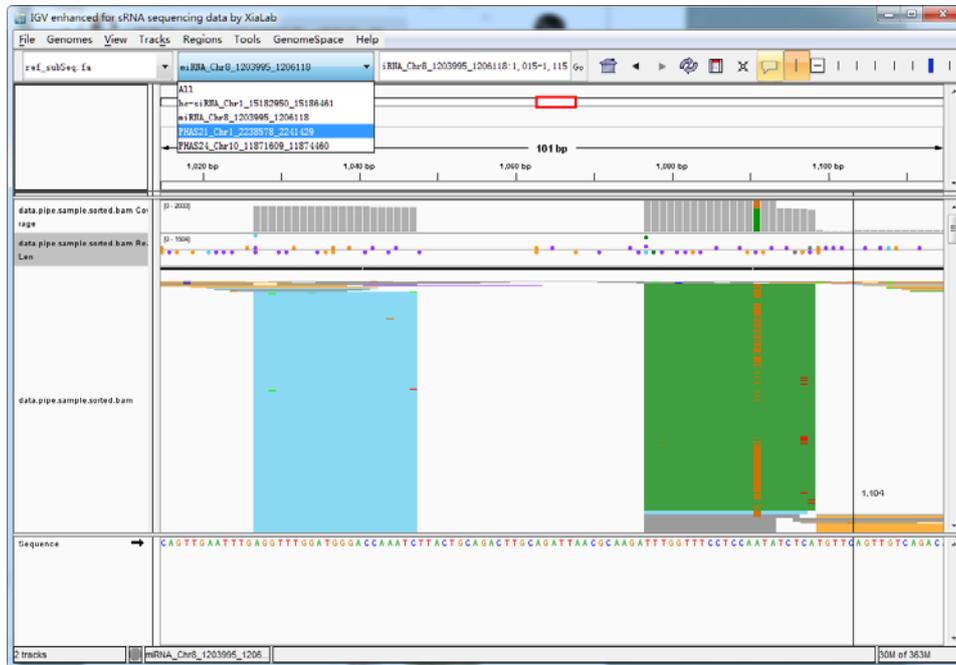


You are able to inspect each base on the context of secondary structure by moving the mouse in IGV main panel (You need to enable the “ruler line”). Color density of each base on secondary structure corresponds to its data coverage.

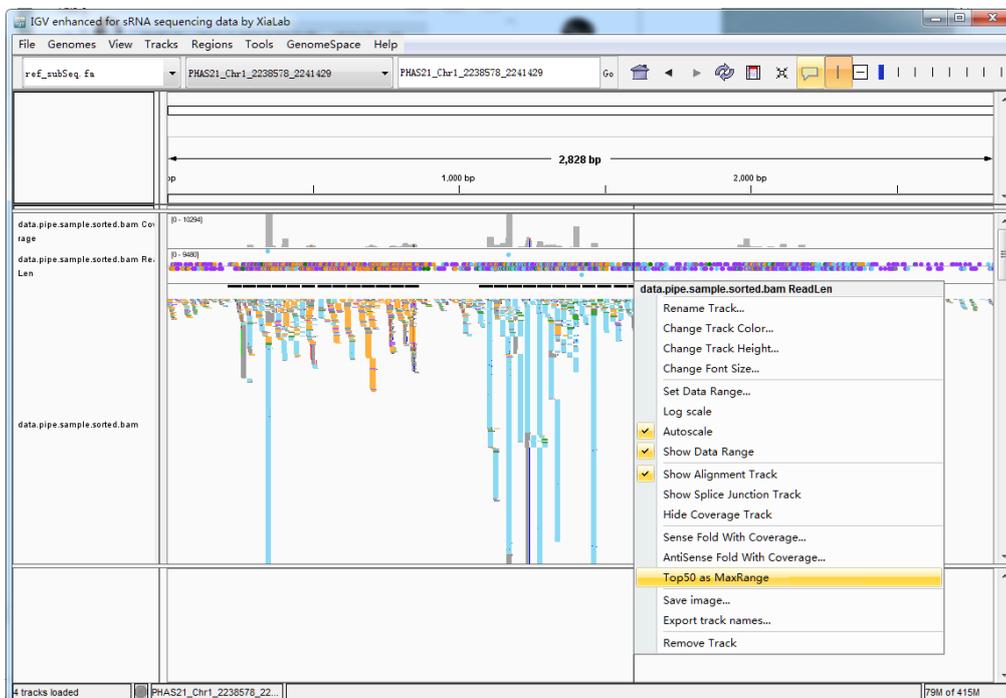


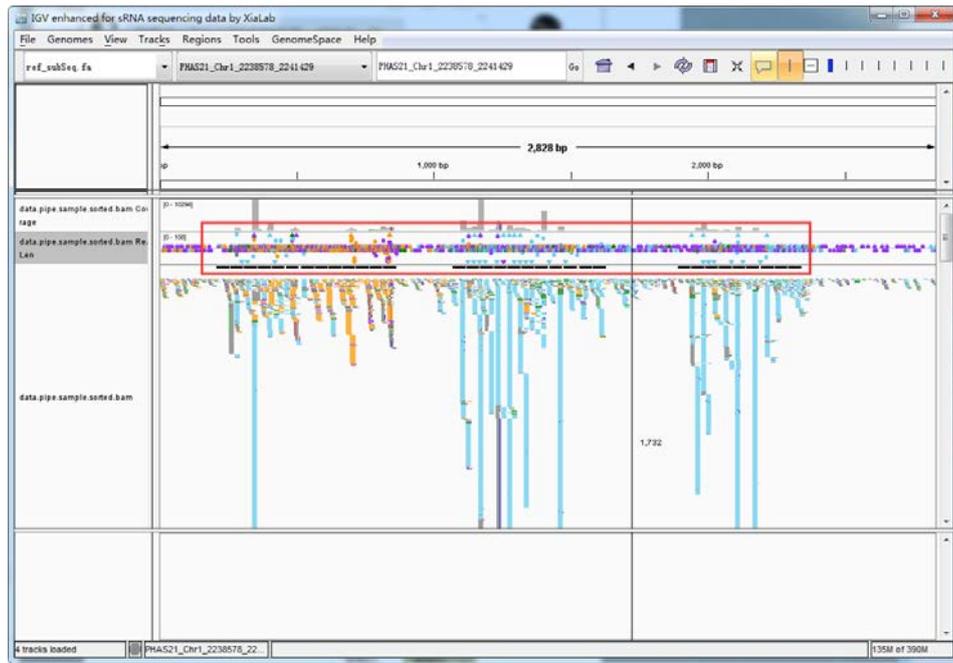
21-nt PHAS locus

Select the demo data for a 21-nt PHAS locus

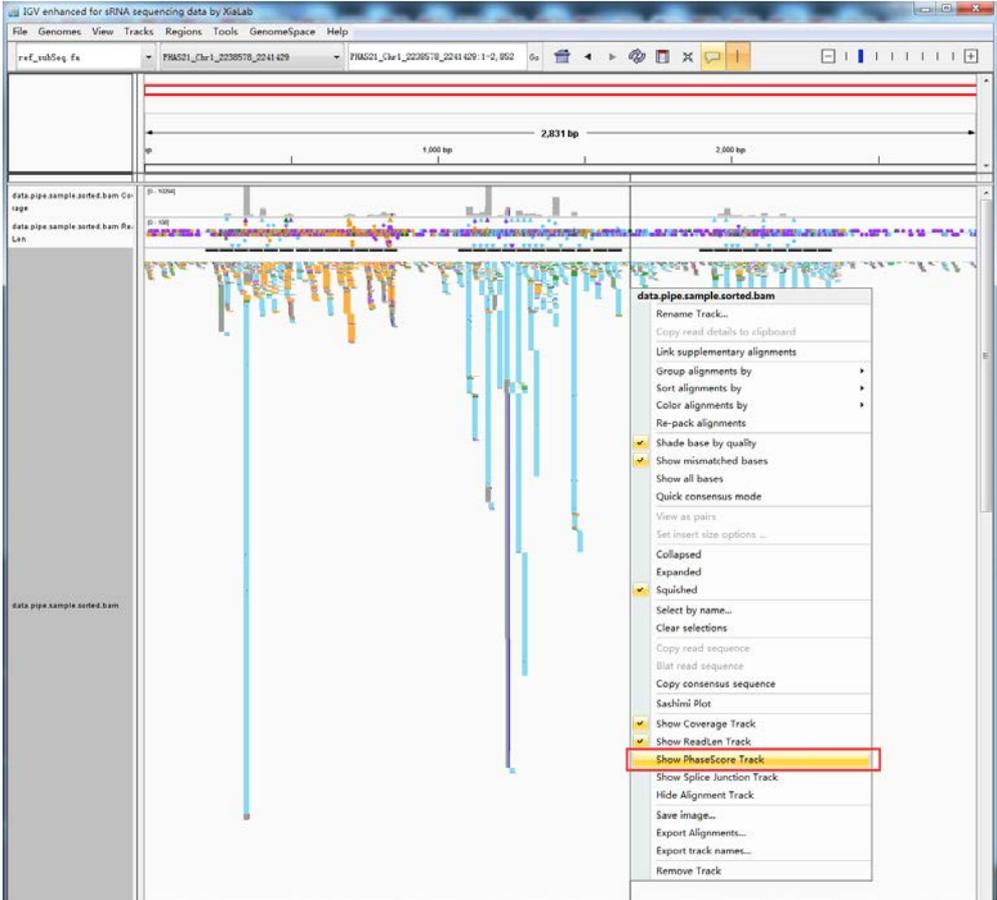


Use the **Top50 as MaxRange** mode in the **ReadLen** track (Right-Click on the **ReadLen** track).

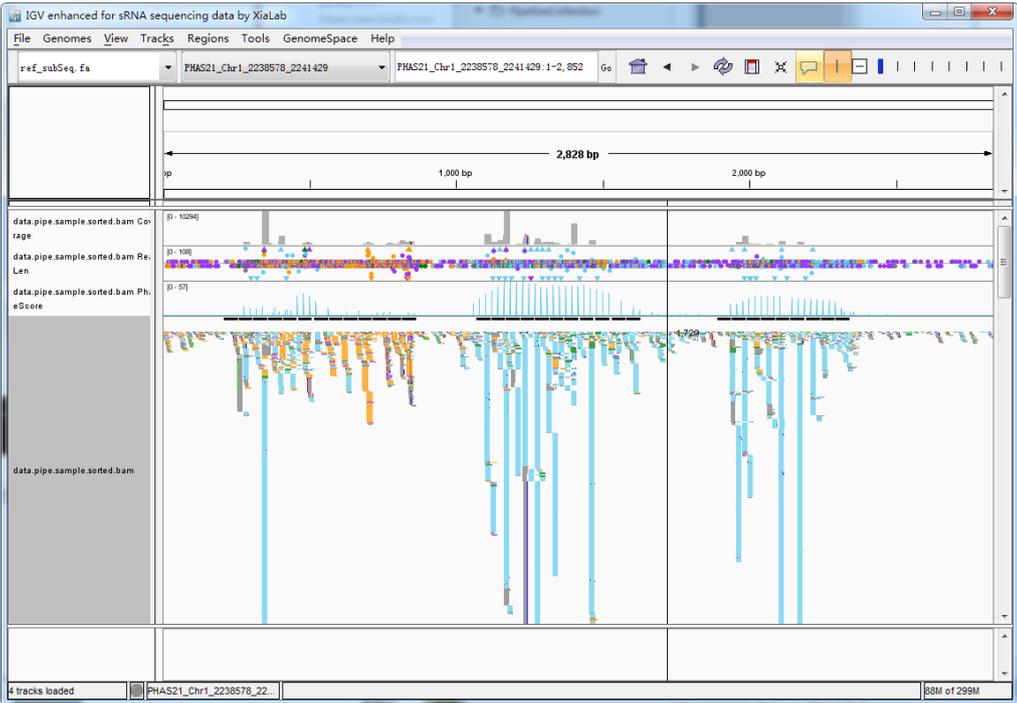




Show the **Phasing Score** Track

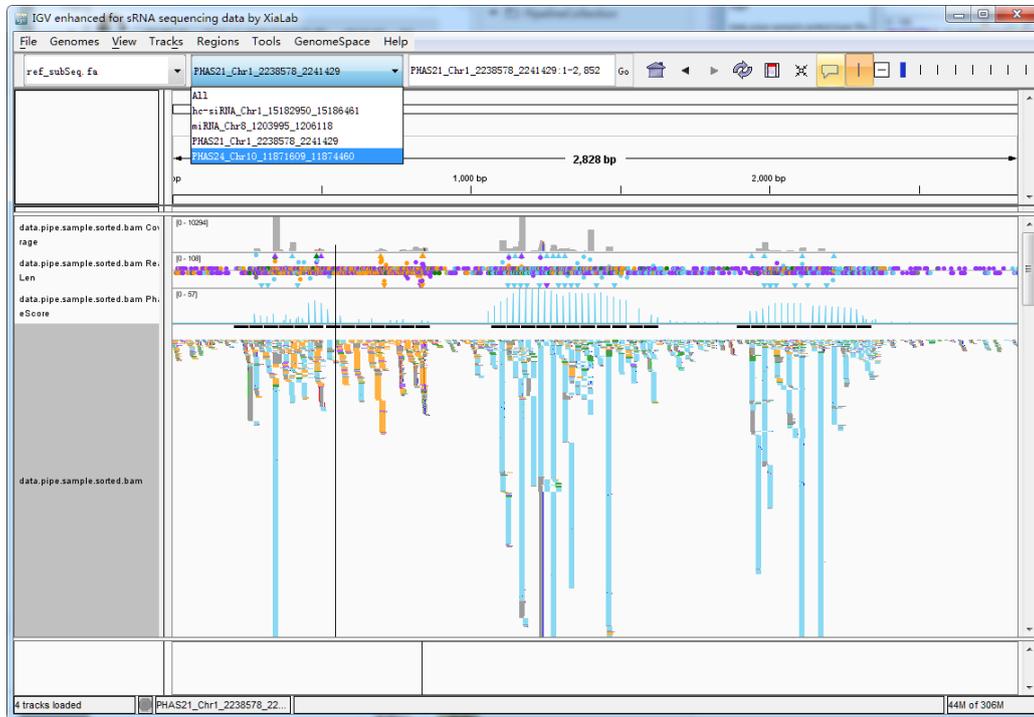


Phase score is calculated and shown instantly in a separate data track (phasing score track).

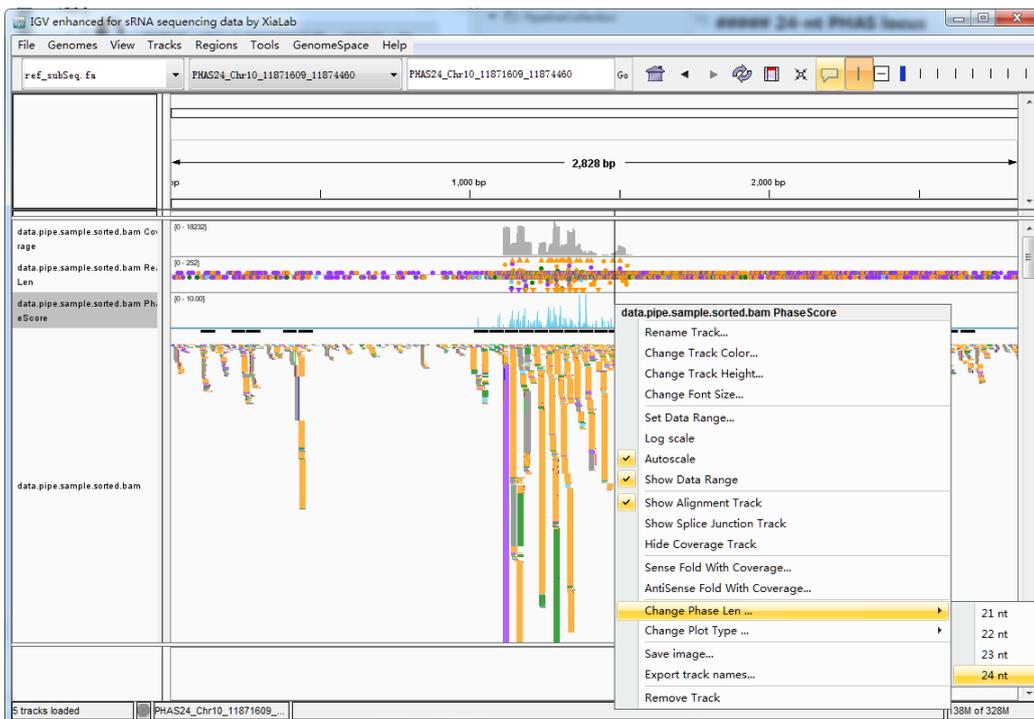


24-nt PHAS locus

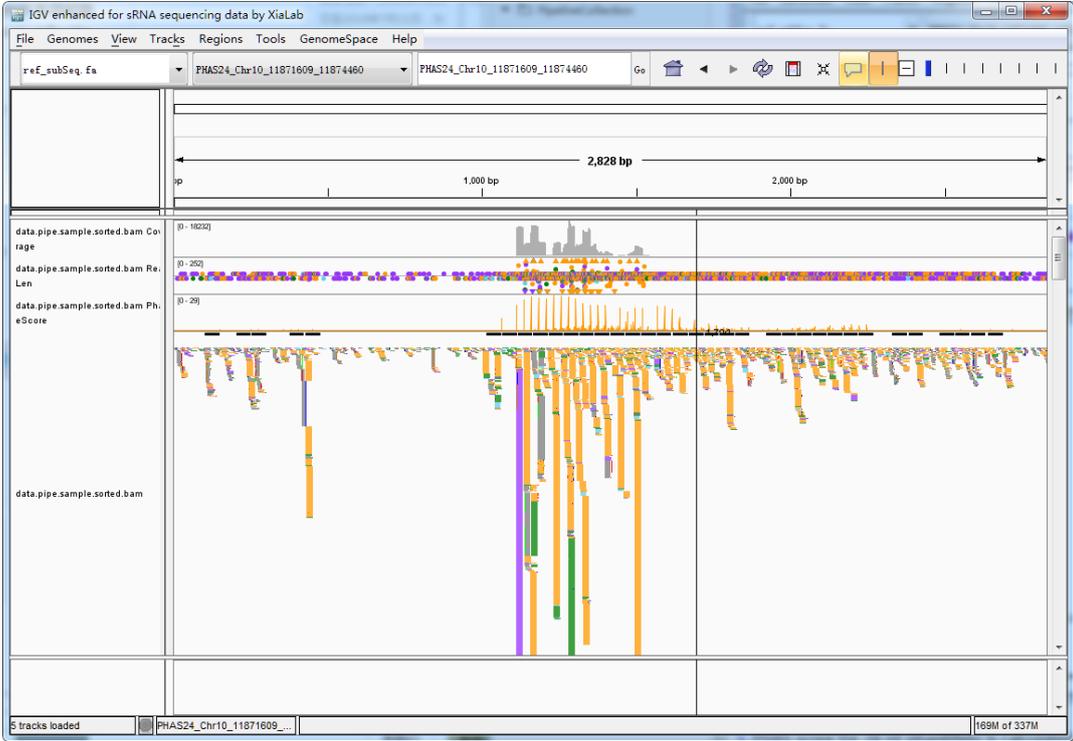
Select the demo data for a 24-nt PHAS locus.



Switch **Phase Length** to 24-nt by Right-Click on the phasing score track.

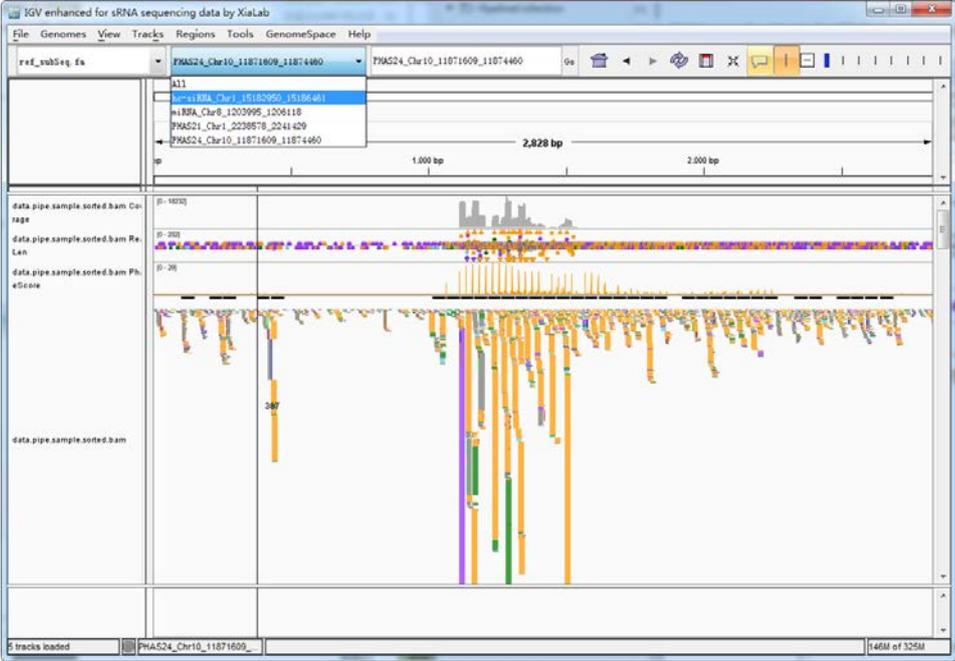


Phasing score for 24-nt phasiRNAs is calculated and shown instantly.

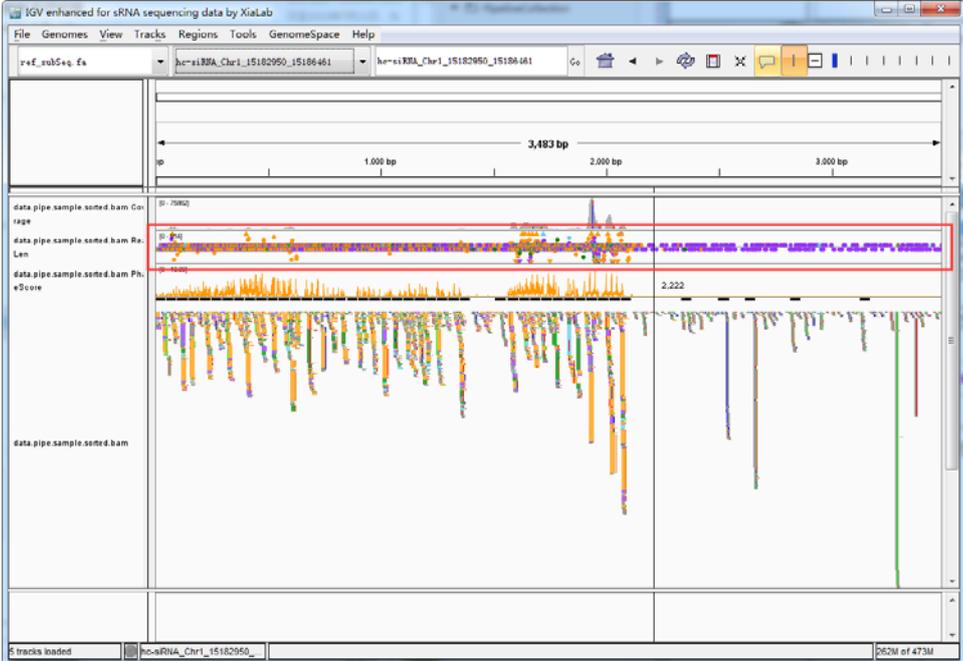


hc-siRNA locus

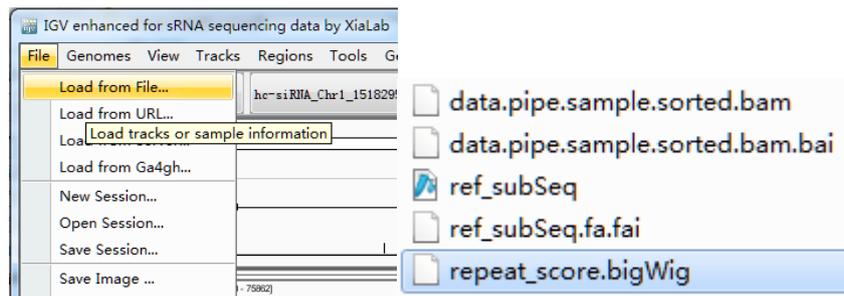
Select the demo data for a hc-siRNA locus.



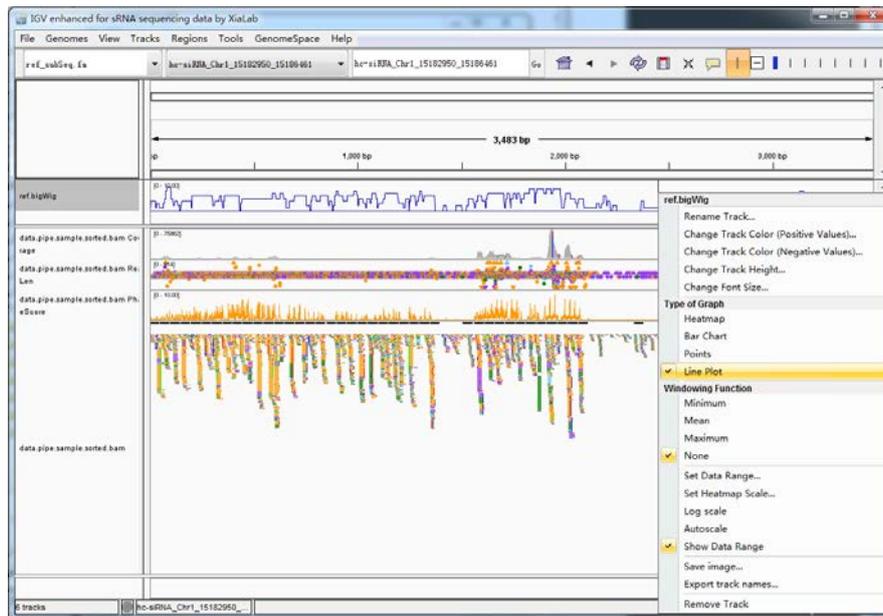
hc-siRNA loci are dominated by 23-24-nt small RNAs. In addition, no significant phase pattern exists.



Load the repeat score data



Repeat score is high across the hc-siRNA locus.



In contrast, repeat score remains low for the 24-nt PHAS locus.

