BamSnap

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BamSnap is a visualization tool for aligned BAM files that allows to generate high-quality snapshots of read level data in high-throughput, processing up to thousands of files. **BamSnap** is a command-line software based on python.

CHAPTER 1

Setting up BamSnap

In a command prompt or terminal window, run the following commands to install and test the software.

```
$ pip install bamsnap
$ bamsnap -bam test.bam -pos chr1:7364529 -out test.bam.png
```

More examples and commands are available in gallery. Use `-h` to list the options available for `bamsnap`.

```
$ bamsnap -h
```

Source code is available on github.

CHAPTER 2

Contents

2.1 Installation

2.1.1 Prerequisites

- python 3.4+
- Pillow (Python Imaging Library) (2.0.0+)
- pysam (0.11.2.2+)
- pyfaidx (0.5.3.1+)
- pytabix (0.0.2+)

2.1.2 Install with pypi

To install **BamSnap** with pip run:

```
$ pip install bamsnap
$ bamsnap
```

2.1.3 Install from source

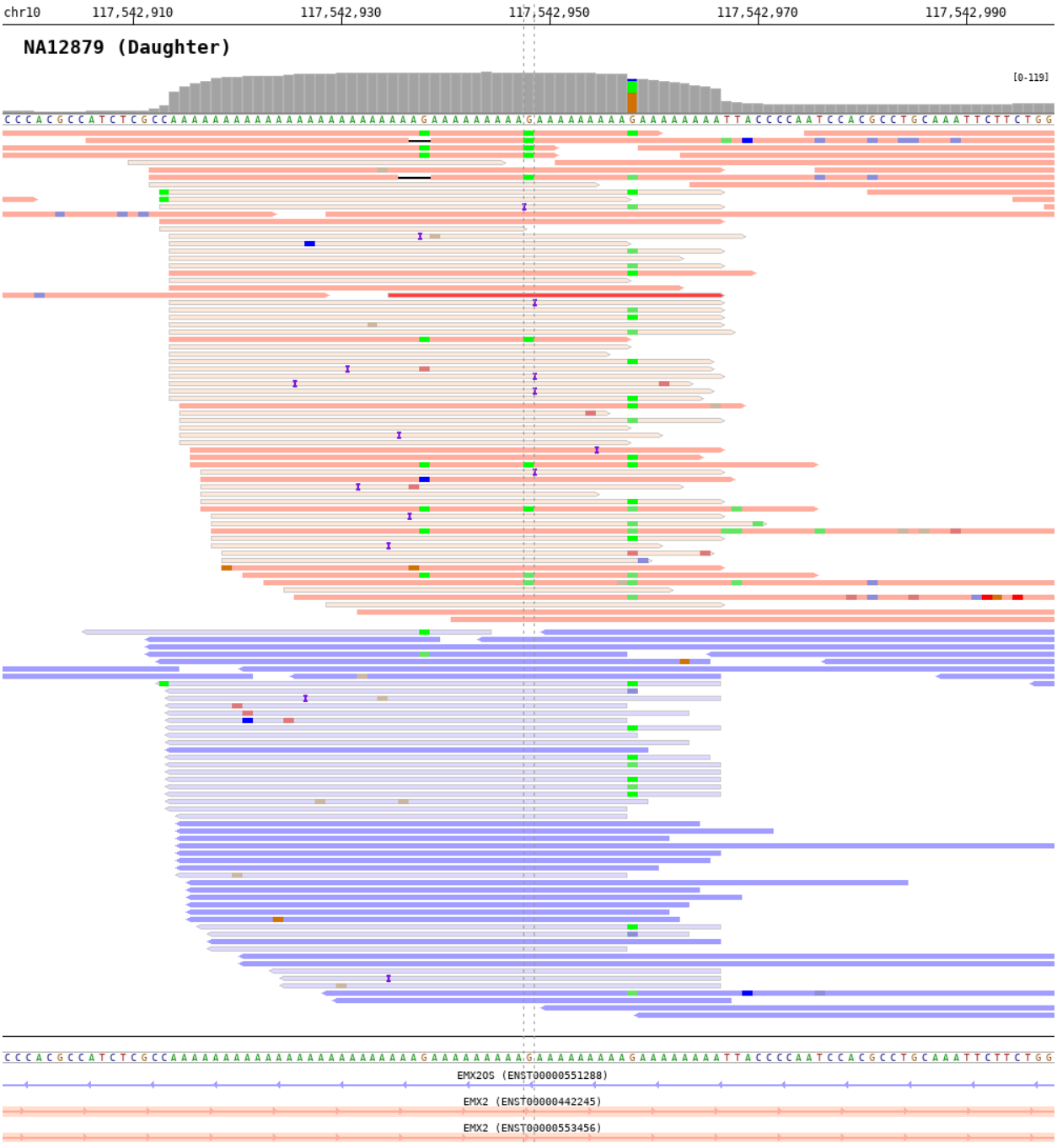
```
$ git clone https://github.com/parklab/bamsnap
$ cd bamsnap
$ python setup.py install
$ bamsnap
```

2.1.4 Install from docker hub

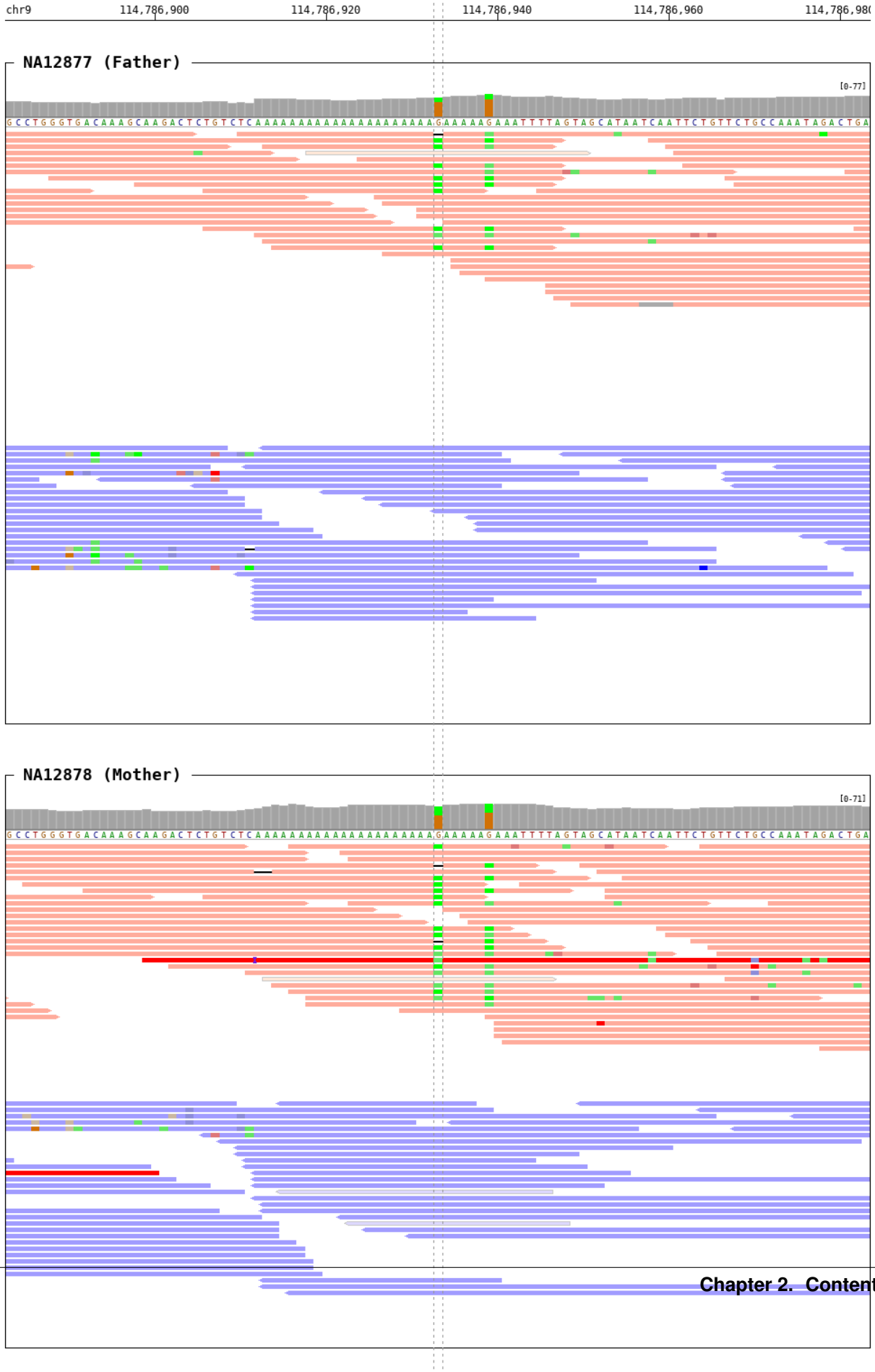
```
$ docker pull danielmsk/bamsnap
$ docker images

REPOSITORY          TAG                 IMAGE ID            CREATED             SIZE
danielmsk/bamsnap   latest              f9f6e61c7673        2 hours ago         997MB

$ docker run --rm -it -v /local_directory_path:/directory_path_in_image \
  danielmsk/bamsnap bamsnap \
    -bam /directory_path_in_image/test.bam \
    -pos 1:7364529 \
    -out /directory_path_in_image/test.png
```

The docker image can be pulled from the docker hub site (https://hub.docker.com/r/danielmsk/bamsnap). When you are using bamsnap from docker image, you should assign the local directory path (volume) and the image direcotry path (volume) using `-v` option.

2.2 Gallery

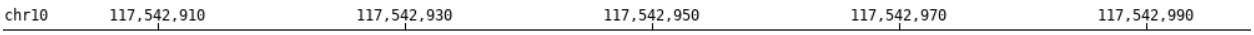



```
$ bamsnap \
  -bam ./data/NA12879.bam \
  -title "NA12879 (Daughter)" \
  -pos chr10:117542948 \
  -out ./out/NATRIO_chr10_117542948.png \
  -read_group strand
```


chr9
114,786,900
114,786,920
114,786,940
114,786,960
NA12877 (Father)
[0-77]
NA12878 (Mother)
[0-71]

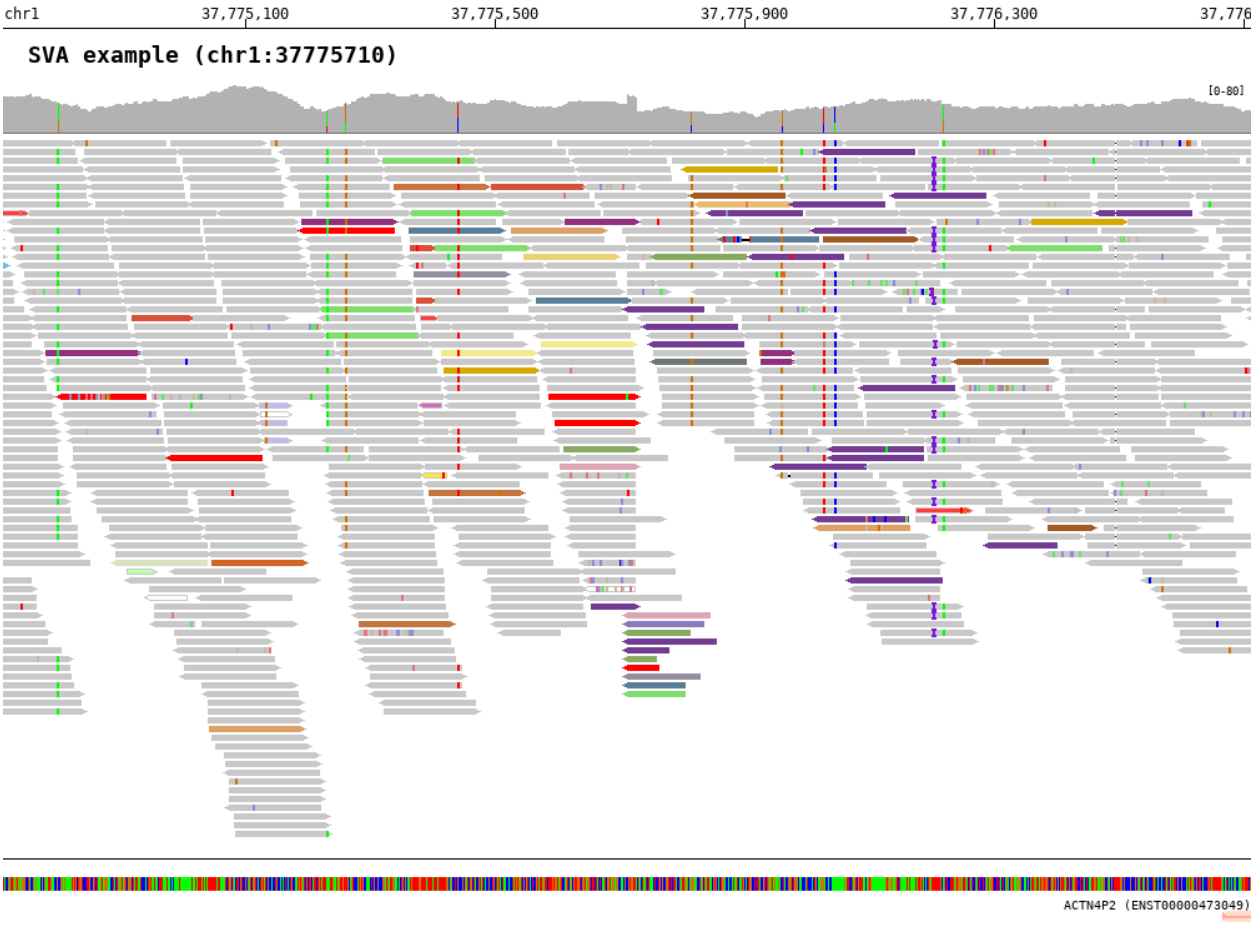
```
$ bamsnap \
  -bam ./data/NA12877.bam \
    ./data/NA12878.bam \
    ./data/NA12879.bam \
  -title "NA12877 (Father)" "NA12878 (Mother)" "NA12879 (Daughter)" \
  -pos chr9:114786933 \
  -out ./out/NATRIO_chr9:114786933.png \
  -draw coordinates bamplot base gene \
  -bamplot coverage base read \
  -margin 50 \
  -read_group strand \
  -plot_margin_left 20 \
  -plot_margin_right 20 \
  -border
```


```
$ bamsnap \
  -bam ./data/NA12879.bam \
  -pos chr10:117542948 \
  -no_title \
  -draw bamplot \
  -bamplot coverage \
  -out ./out/NATRIO_chr10_117542948_3.png \
  -separator_height 0
```



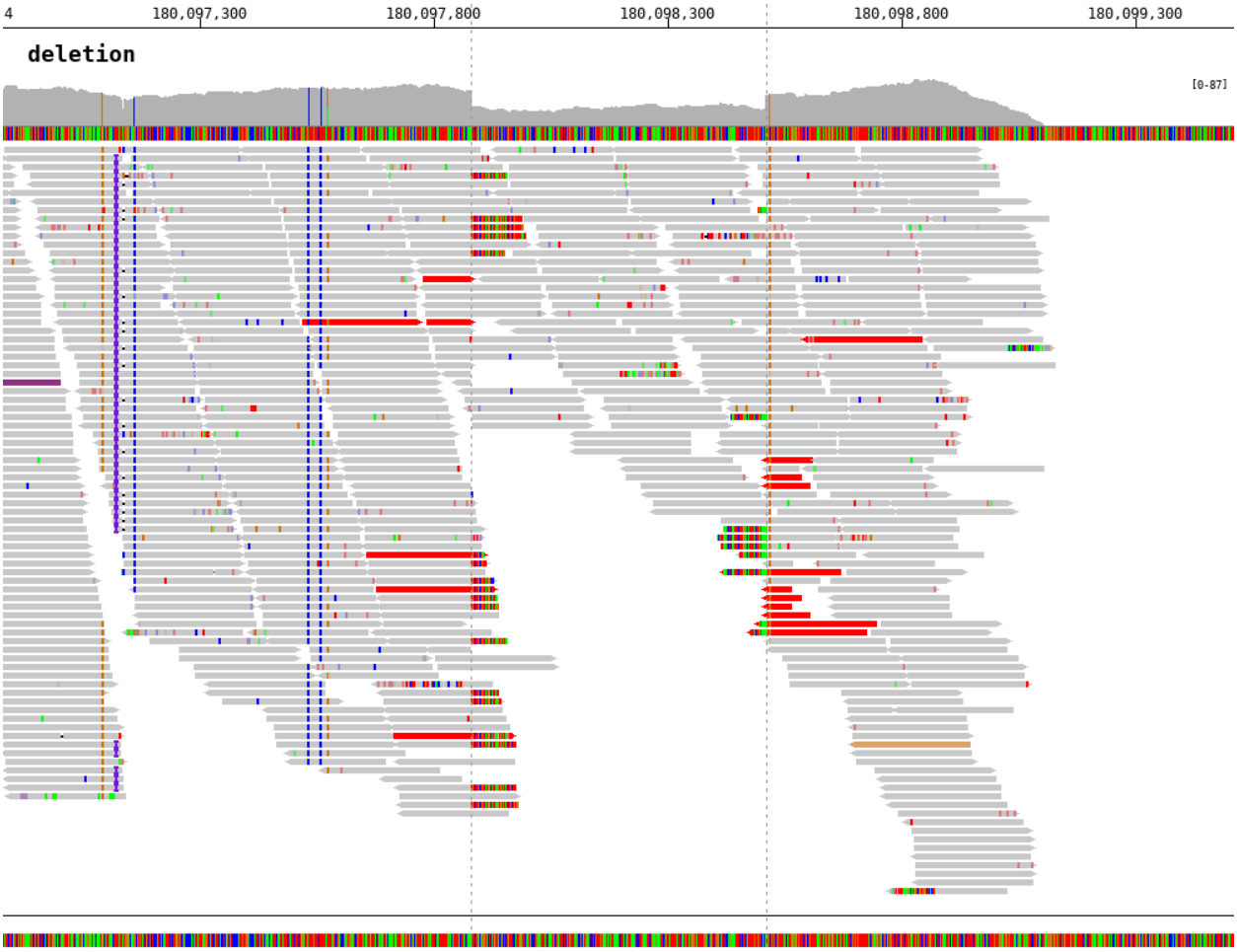

```
$ bamsnap \
  -bam ./data/NA12879.bam \
  -pos chr10:117542948 \
  -no_title \
  -draw coordinates \
  -out ./out/NATRIO_chr10_117542948_coordinates1.png \
  -no_target_line \
  -coordinates_axisloc bottom
```

Color by inter-chromosomal rearrangements

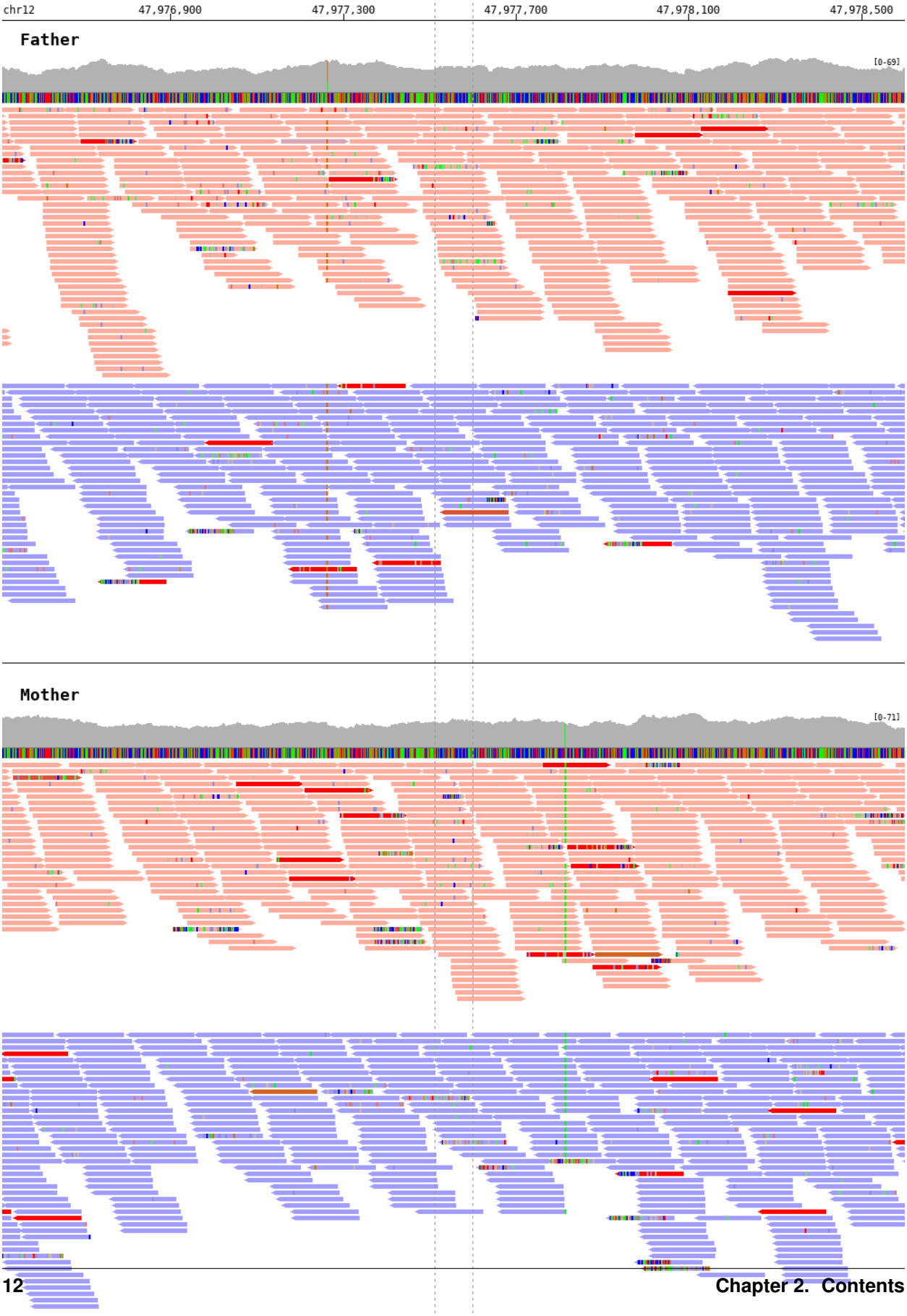



```
$ bamsnap \
  -bam ./data/test_SV1_chr1_37775710.bam \
  -title "SVA example (chr1:37775710)" \
  -pos chr1:37775710 \
  -out ./out/test_SV1-3.png \
  -bamplot coverage read \
  -margin 1000 \
  -no_target_line \
  -read_color_by interchrom \
  -save_image_only
```

Deletion




```
$ bamsnap \
    -bam ./data/test_DEL_4_180097876_180097877.bam \
    -pos 4:180097878-180098507 \
    -margin 1000 \
    -title deletion \
    -out ./out/test_DEL_1.png \
    -refversion hg19 \
    -show_soft_clipped \
    -read_color_by interchrom \
    -save_image_only
```


chr12
47,976,900
47,977,300
47,977,700
47,978,100
47,978,500
Father
[0-69]
Mother
[0-71]
Child

```
$ bamsnap \
   -bam ./data/test_DEL_chr12_47977510_F.bam ./data/test_DEL_chr12_47977510_M.bam ./
↪data/test_DEL_chr12_47977510_P.bam \
   -vcf ./data/test_DEL_chr12_47977510.vcf \
   -margin 1000 \
   -title "Father" "Mother" "Child" \
   -out ./out/test_DEL_chr12_2.png \
   -show_soft_clipped \
   -read_color_by interchrom \
   -read_group strand \
   -save_image_only
```

2.3 Optional arguments

-h, --help	show this help message and exit
-v, --version	show program's version number and exit
-silence	don't print any log.
-debug	turn on debugging mode
-process	number of process for multi-processing (default=1)

2.3.1 Input files

-bam	bam file(s) to use
-bamlist	file listing bam files to use
-title	label(s) to be used as title for bam file(s)
-no_title	(default: false) do not draw title
-title_fontsize	(default=18) font size of title
-pos	genomic position(s) to plot
-vcf	file listing genomic positions to plot in VCF format
-bed	file listing genomic positions to plot in BED format
-ref	reference sequence as fasta file
-ref_index_rebuild	(default=false) rebuild fasta index file (.fai)
-refversion	[hg38, hg19] (default=hg38) reference version
-conf	**'configuration file'_**

2.3.2 Output file

-out	output file name or title of output file
-imagetype	[png, jpg] (default=png) output file type
-save_image_only	(default=false) save image only
-image_dir_name	image directory name

-zipout (default=false) make a single zip file

-separated_bam (default=false) draw a plot for each bam

2.3.3 Plot layout

-draw (default=coordinates bamplot base gene) track composition

-bamplot (default=coverage base read) track composition in bamplot

-width (default=1000) image width (unit:px)

-height image height (unit:px)

-bgcolor (default=FFFFFF) background color

-plot_margin_top (default=20) top margin size of plot

-plot_margin_bottom (default=20) bottom margin size of plot

-plot_margin_left (default=0) left margin size of plot

-plot_margin_right (default=0) right margin size of plot

-border (default=false) draw border in plot

-separator_height (default=30) separator's height

2.3.4 Read alignment track

-read_thickness (default=5) read thickness (unit:px)

-read_gap_height (default=2) read gap height (unit:px)

-read_gap_width (default=2) read gap width (unit:px)

-read_bgcolor (default=FFFFFF) read background color

-read_color (default=C8C8C8) read color

-margin (default=50) genomic margin size

-center_line (default=false) draw center line

-no_target_line (default=false) do not draw target line

-read_group [‘’, strand] (default=”) read color

-read_pos_color (default=FFAC9C) positive strand read color

-read_neg_color (default=A19CFF) negative strand read color

-read_color_by [‘’, strand, intercom] (default=”) read color by

-read_color_interchrom_chr1 (default=64689b) paired read color located in chromosome 1

-read_color_interchrom_chr2 (default=D6503A) paired read color located in chromosome 2

-read_color_interchrom_chr3 (default=87AA62) paired read color located in chromosome 3

-read_color_interchrom_chr4 (default=F2EB89) paired read color located in chromosome 4

-read_color_interchrom_chr5 (default=597E98) paired read color located in chromosome 5

-read_color_interchrom_chr6 (default=C5763E) paired read color located in chromosome 6

-read_color_interchrom_chr7 (default=70BFE7) paired read color located in chromosome 7

-read_color_interchrom_chr8 (default=91307F) paired read color located in chromosome 8

-read_color_interchrom_chr9 (default=80DE6E) paired read color located in chromosome 9

-read_color_interchrom_chr10 (default=DCA5B5) paired read color located in chromosome 10

-read_color_interchrom_chr11 (default=A35A24) paired read color located in chromosome 11

-read_color_interchrom_chr12 (default=978DA0) paired read color located in chromosome 12

-read_color_interchrom_chr13 (default=D16525) paired read color located in chromosome 13

-read_color_interchrom_chr14 (default=DCA167) paired read color located in chromosome 14

-read_color_interchrom_chr15 (default=8C79B9) paired read color located in chromosome 15

-read_color_interchrom_chr16 (default=E9BD71) paired read color located in chromosome 16

-read_color_interchrom_chr17 (default=4B2669) paired read color located in chromosome 17

-read_color_interchrom_chr18 (default=D7E4BF) paired read color located in chromosome 18

-read_color_interchrom_chr19 (default=733B91) paired read color located in chromosome 19

-read_color_interchrom_chr20 (default=BC2D7A) paired read color located in chromosome 20

-read_color_interchrom_chr21 (default=EBD176) paired read color located in chromosome 21

-read_color_interchrom_chr22 (default=6E786F) paired read color located in chromosome 22

-read_color_interchrom_chrX (default=D5AA00) paired read color located in chromosome X

-read_color_interchrom_chrY (default=A9D400) paired read color located in chromosome Y

-show_soft_clipped (default=False) show soft clipped part

2.3.5 Base track

-base_fontsize (default=9) font size of base

-base_height (default=30) base track height

-base_margin_top (default=0) top margin size of base track

-base_margin_bottom (default=0) bottom margin size of base track

2.3.6 Coverage track

-coverage_height (default=40) coverage track height

-coverage_fontsize (default=9) coverage font size

-coverage_vaf (default=0.2) coverage variant allele fraction threshold

-coverage_color (default=C8C8C8) coverage color

-coverage_bgcolor (default=FFFFFF) coverage track background color

2.3.7 Heatmap track

-heatmap_height (default=5) coverage heatmap height

-heatmap_bgcolor (default=FFFFFF) coverage heatmap track background color

2.3.8 Gene track

-gene_height (default=50) gene track height

-gene_fontsize (default=10) font size of gene track

-gene_pos_color (default=FFAC9C) positive strand color

-gene_neg_color (default=A19CFF) negative strand color

2.3.9 Coordinates track

-coordinates_height (default=20) coordinates height

-coordinates_fontsize (default=12) coordinates font size

-coordinates_axisloc [top, bottom, middle] (default=bottom) coordinates axis location

-coordinates_bgcolor (default=FFFFFF) coordinates background color

-coordinates_labelcolor (default=000000) coordinates label color

2.4 Input files

2.4.1 Alignment file

BamSnap requires sorted and indexed bam or cram files. For each alignment file, the index file (*.bam.bai*, *.bai*, *.cram.crai*, or *.crai*) should be located in the same directory.

2.4.1.1 Input files (`-bam` for BAM or CRAM format)

Input files to be used can be specified using the `-bam` argument. It is possible to specify a single file or list multiple files. Also, a cram file can be assigned with `-bam` argument.

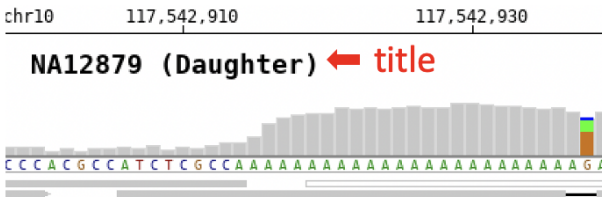
```
$ bamsnap -bam ./data/NA12878.bam
$ bamsnap -bam ./data/NA12878.bam ./data/NA12877.bam ./data/NA12879.bam
$ bamsnap -bam ./data/NA12878.cram
$ bamsnap -bam ./data/NA12878.cram ./data/NA12877.bam ./data/NA12879.bam
```

Note: BamSnap supports both the indexed BAM and the indexed CRAM format for the alignment files.

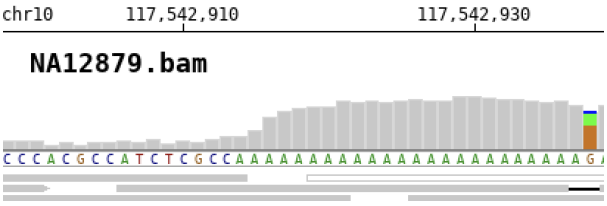
Title of alignment file(s) (`-title`)

A label can be assigned to each of the bam files using the `-title` argument. The label will be used as title for the corresponding plot.

```
$ bamsnap -bam ./data/NA12879.bam -title NA12879
$ bamsnap -bam ./data/NA12879.bam -title "NA12879  (Daughter)"
$ bamsnap -bam ./data/NA12878.bam ./data/NA12877.bam ./data/NA12879.bam \
  -title "NA12877 (Father)" "NA12878 (Mother)" "NA12879 (Daughter)"
```

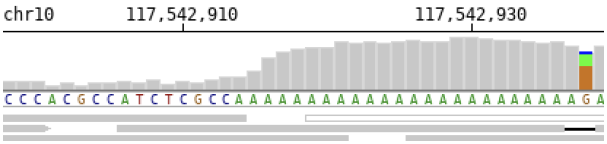


If no label is specified, the file name will be used as title by default.



To completely remove the title use the `-no_title` option.

```
$ bamsnap -bam ./data/NA12879.bam -no_title
```



Note: By default, the title font size is 18. It is possible to change the font size with `-title_fontsize` (e.g. `-title_fontsize 10`).

2.4.1.2 BAM list file (`-bamlist`)

```
$ bamsnap -bamlist ./data/NATRIO_bamlist.txt
```

It is possible to provide a single file listing all the input bam files to be used. The expected format is a tabular (tab-separated) file. The first column is mandatory and must contain the paths to files, the second column is optional and allows to associate labels to files. It also supports *.bam* and *.cram* file.

```
# example of bamlist file with lables
./data/NA12878.bam    NA12878 (F)
./data/NA12877.cram   NA12877 (M)
./data/NA12879.bam    NA12879 (D)
```

```
# example of bamlist file
./data/NA12878.bam
./data/NA12877.cram
./data/NA12879.bam
```

2.4.2 Genomic position

2.4.2.1 Genomic position (-pos)

Genomic positions to plot can be specified with the `-pos` option. It is possible to specify a single position or to list multiple regions.

```
$ bamsnap -bam ./data/NA12878.bam -pos chr1:7364529
$ bamsnap -bam ./data/NA12878.bam -pos chr1:7364529 chr3:7364529 chr1:7364529
$ bamsnap -bam ./data/NA12878.bam -pos chr1:7364509-7364559
```

Note: Chromosome names must match between the positions that are specified and the bam files. For example, 'chr' prefix should be omitted from regions if the bam files don't use 'chr' prefix in chromosome names (ex. 1:7364529).

2.4.2.2 VCF file (-vcf)

The program can read `.vcf` (raw) and `.vcf.gz` (gzip or bgzip compressed vcf) files.

```
$ bamsnap \
  -bam ./data/NA12878.bam \
  -vcf ./data/multiple_variants.vcf.gz \
  -out ./out/mutiple_variants_NA12878
```

2.4.2.3 BED file (-bed)

```
$ bamsnap \
  -bam ./data/NA12878.bam \
  -bed ./data/multiple_regions.bed \
  -out ./out/mutiple_regions_NA12878
```

2.4.3 Reference sequence file

User can provide a fasta file to be used as reference using the `-ref` option. Alternatively, it is possible to specify a reference version to be used with `-refversion`. The program will automatically obtain the corresponding sequence from UCSC database. The current default version for `-refversion` is `hg38`. `-refversion hg19` force the use of `hg19` release.

2.4.3.1 FASTA file (-ref)

```
$ bamsnap \
  -bam ./data/NA12879.bam_chr10_117542947.bam \
  -ref ./fasta/GRCh38_full_analysis_set_plus_decoy_hla.fa
```

Note: If a fasta file is specified, the program checks for its index file (.fai). If the index file does not exist it will be automatically created. If the index file exists but is older than the fasta file, the program can rebuild the index using the `-ref_index_rebuild` option.

2.5 Output files

`-out` option allows to specify the output directory or the name for the image file (if a single image file is the output).

2.5.1 Image file (PNG, JPG)

By default, the program generates image files in `png` format. It is possible to select `jpg` format using the `-imagetype` option.

```
$ bamsnap \
  -bam ./data/NA12878.bam \
  -pos chr10:117542948 \
  -out ./out/NA12878_chr10_117542948.jpg \
  -imagetype jpg \
  -save_image_only
```

Note: To save only snap image files, use the `-save_image_only` option.

Inside the output directory, images are saved in a default sub-directory. It is possible to rename this folder using the the `-image_dir_name` option.

```
$ bamsnap \
  -bam ./data/NA12879.bam \
  -vcf ./data/NATRIO_test_3.vcf \
  -out ./out/NATRIO_test_3 \
  -image_dir_name test_images
```

This example creates `./out/NATRIO_test_3/test_images` folder that contains the generated snap image files.

By default, the program generates a single plot file for multiple bam files. `-separated_bam` option allows to generate a plot file for each of the bam files.

2.5.2 Compressed file (`-zipout`)

It is possible to save a compressed (`zip`) output file using the `-zipout` option.

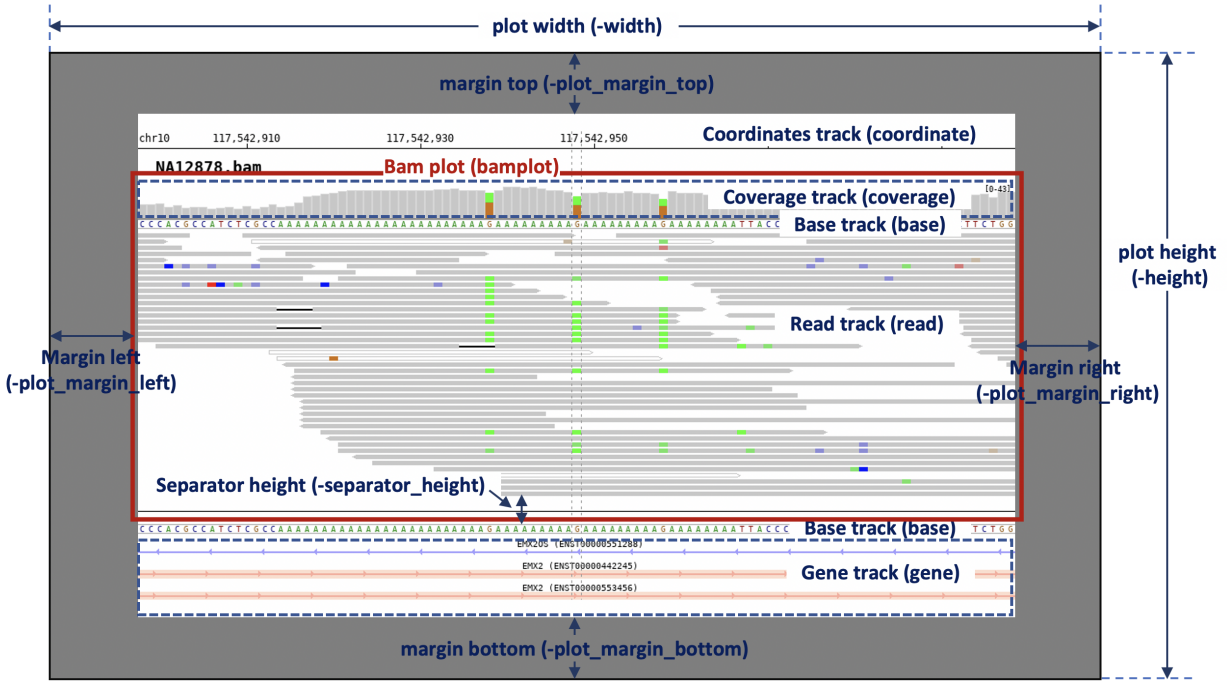
```
$ bamsnap \
  -bam ./data/NA12879.bam \
  -vcf ./data/NATRIO_test_3.vcf \
  -out ./out/NATRIO_test_3 \
  -save_image_only \
  -zipout
```

This example creates `./out/NATRIO_test_3.zip` file.

2.5.3 HTML file (index html)

If `-save_image_only` is not used, *index.html* is generated by default.

2.6 Plot options



2.6.1 Plot composition (`-draw`, `-bamplot`)

It is possible to add track list to a plot using the `-draw` option. The default tracks list is `coordinates bamplot base gene`. `bamplot` contains `coverage base read` tracks.

- `-draw` : track list (default: -draw coordinates bamplot base gene)
- **`-bamplot`** [plot (default: -bamplot coverage base read)]
  - `-bamplot read` : see more track options
  - `-bamplot coverage` : see more track options
  - `-bamplot base` : see more track options

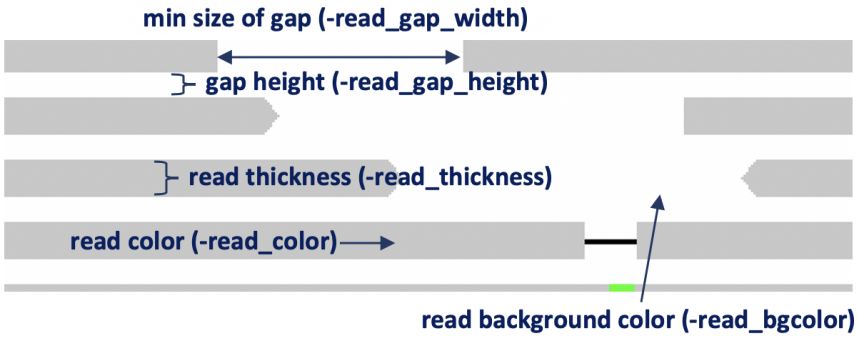
2.6.2 Plot layout options

- `-width` : image file size : width (unit:px, default:1000)
- `-height` : image file size : height (unit:px)
- `-bgcolor` : background color (default:FFFFFF)
- `-plot_margin_top` : top margin size of plot
- `-plot_margin_bottom` : bottom margin size of plot
- `-plot_margin_left` : left margin size of plot
- `-plot_margin_right` : right margin size of plot
- `-separator_height` : separator's height

- `-border` : draw border in plot

2.7 Read alignment track (`-bamplot read`)

2.7.1 Layout options

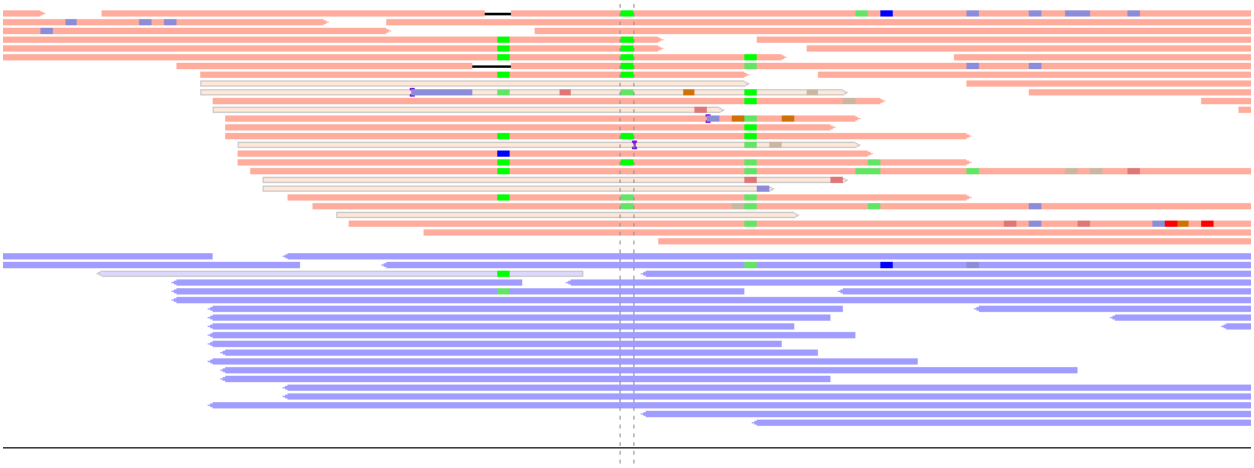


- `-read_thickness` (default=5) : read thickness (unit:px)
- `-read_gap_height` (default=2) : read gap height (unit:px)
- `-read_gap_width` (default=2) : min size of read gap width (unit:px)
- `-read_bgcolor` (default='FFFFFF') : read background color
- `-read_color` (default='C8C8C8') : read color
- `-center_line` (default=false): draw center line
- `-no_target_line` (default=false): do not draw target line

2.7.2 Read group (`-read_group`)

It is possible to plot the reads grouped by strand using the `-read_group strand` option.

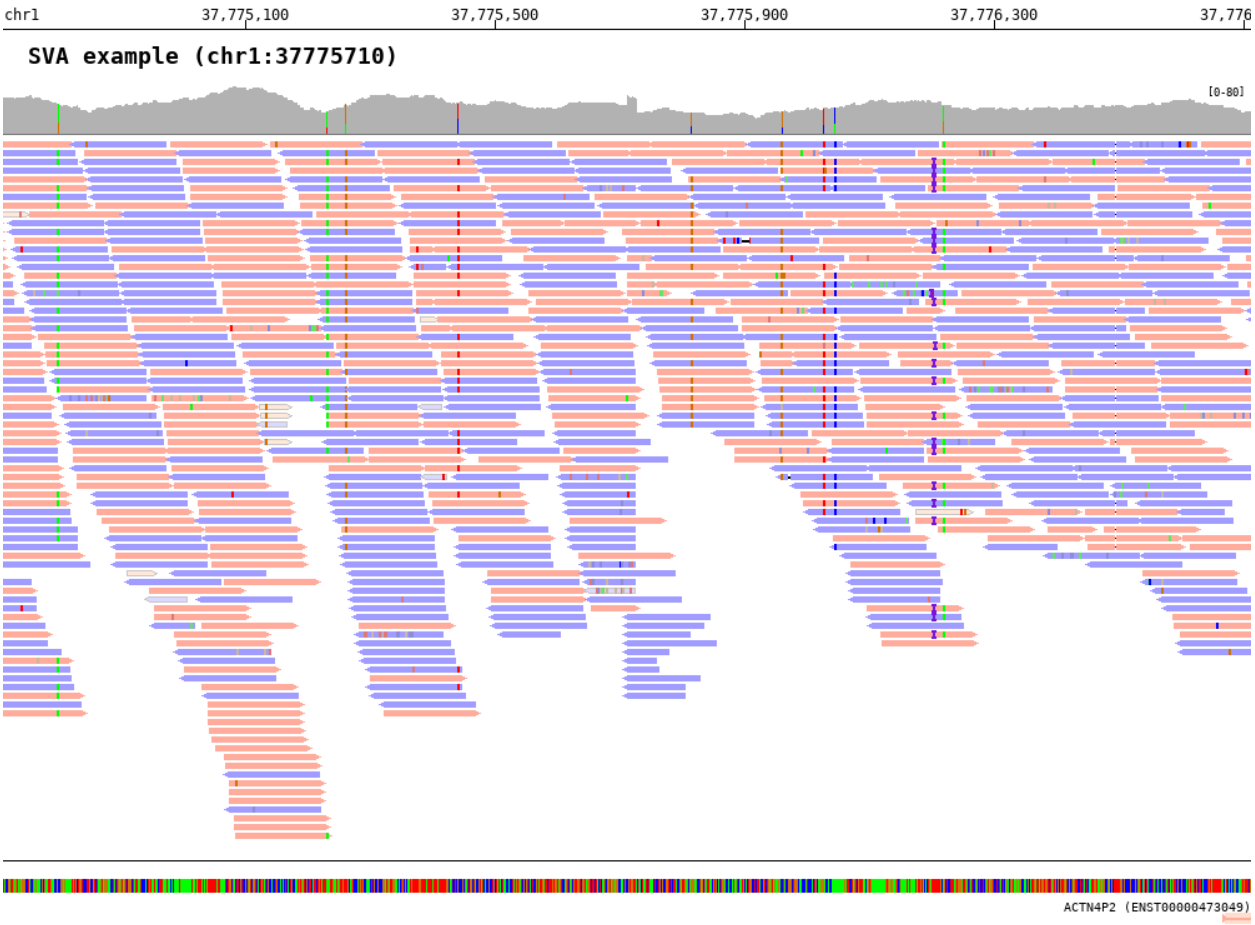
```
$ bamsnap \
  -bam ./data/NA12879.bam \
  -pos chr10:117542948 \
  -no_title \
  -draw bamplot \
  -bamplot read \
  -out ./out/NATRIO_chr10_117542948_6.png \
  -read_group strand
```



2.7.3 Read color (`-read_color_by`)

The program provides color sets for strand and chromosomes.

2.7.3.1 Color by strand (`-read_color_by strand`)

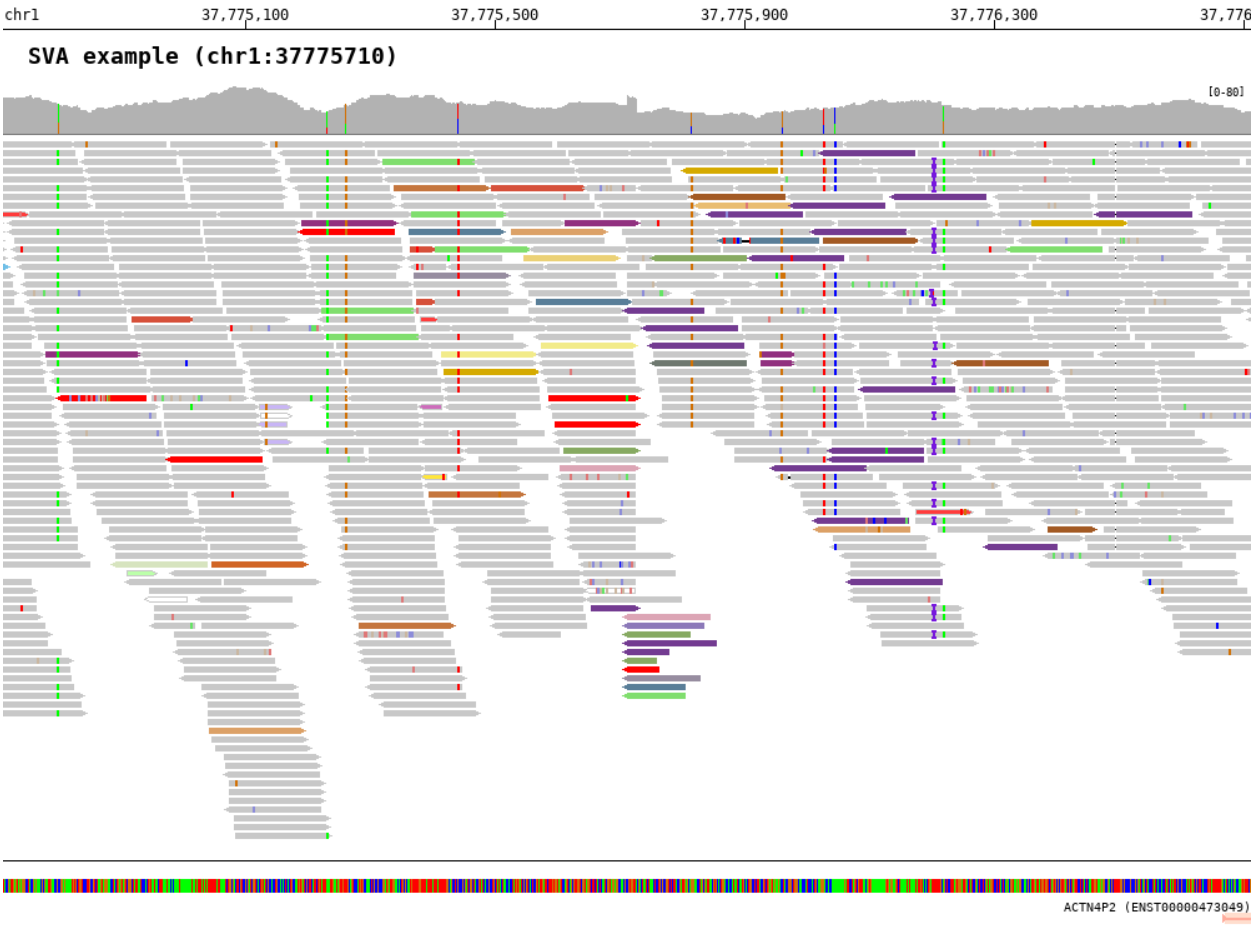



```
$ bamsnap \
    -bam ./data/test_SV1_chr1_37775710.bam \
    -title "SVA example (chr1:37775710)" \
    -pos chr1:37775710 \
    -out ./out/test_SV1-4.png \
    -bamplot coverage read \
    -margin 1000 \
    -no_target_line \
    -read_color_by strand \
    -save_image_only
```

The reads color by strand can be defined using `-read_pos_color` and `-read_neg_color` options.

- `-read_pos_color` (default='FFAC9C') : positive strand read color
- `-read_neg_color` (default='A19CFF') : negative strand read color

2.7.3.2 Color by inter-chromosomal rearrangements (`-read_color_by interchrom`)



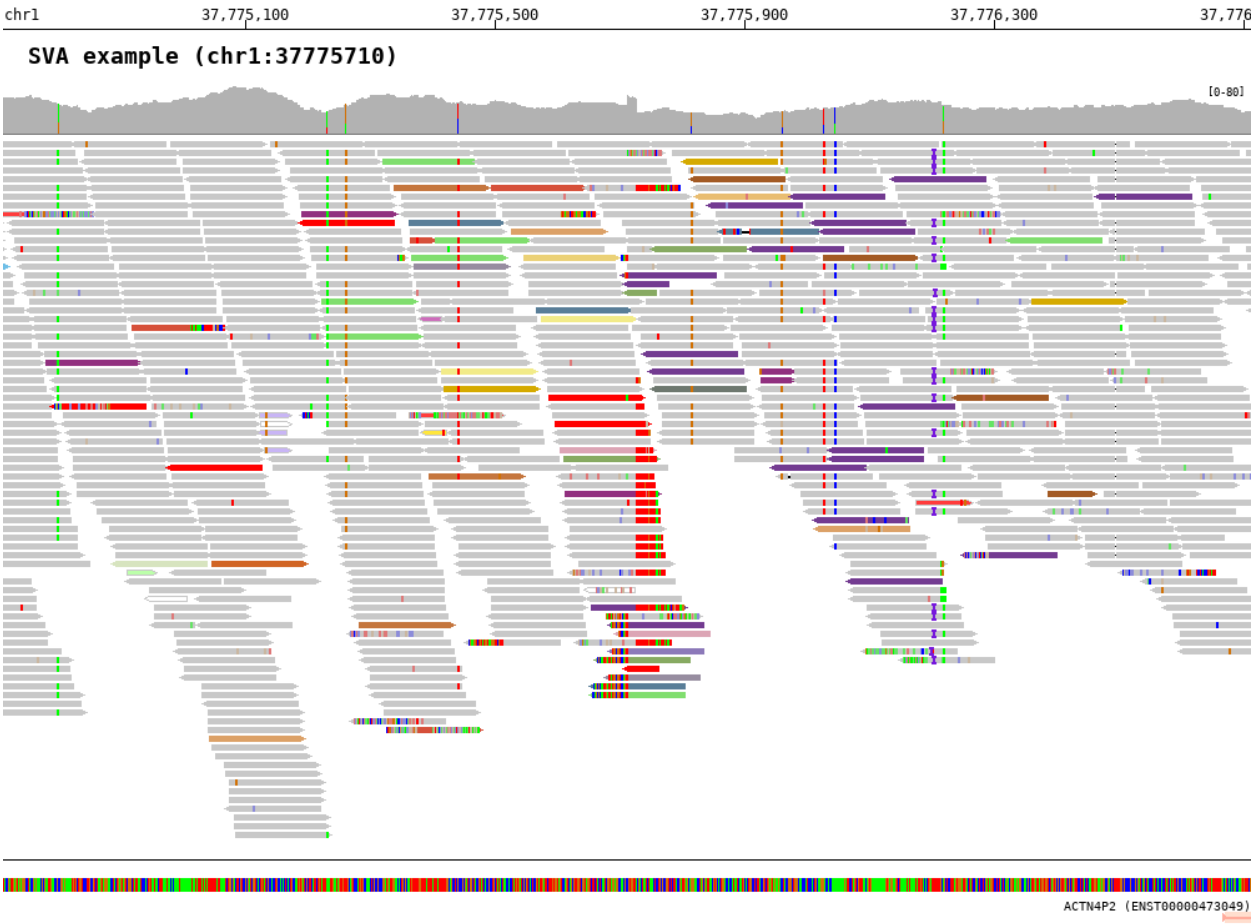

```
$ bamsnap \
    -bam ./data/test_SV1_chr1_37775710.bam \
    -title "SVA example (chr1:37775710)" \
    -pos chr1:37775710 \
    -out ./out/test_SV1-3.png \
    -bamplot coverage read \
    -margin 1000 \
    -no_target_line \
    -read_color_by interchrom \
    -save_image_only
```

The reads color by chromosome can be defined using `-read_color_interchrom_chr1`, `-read_color_interchrom_chr2`, .., and `-read_color_interchrom_chrY` options.

- **Default color codes**
  - chr1: #64689b
  - chr2: #D6503A
  - chr3: #87AA62
  - chr4: #F2EB89

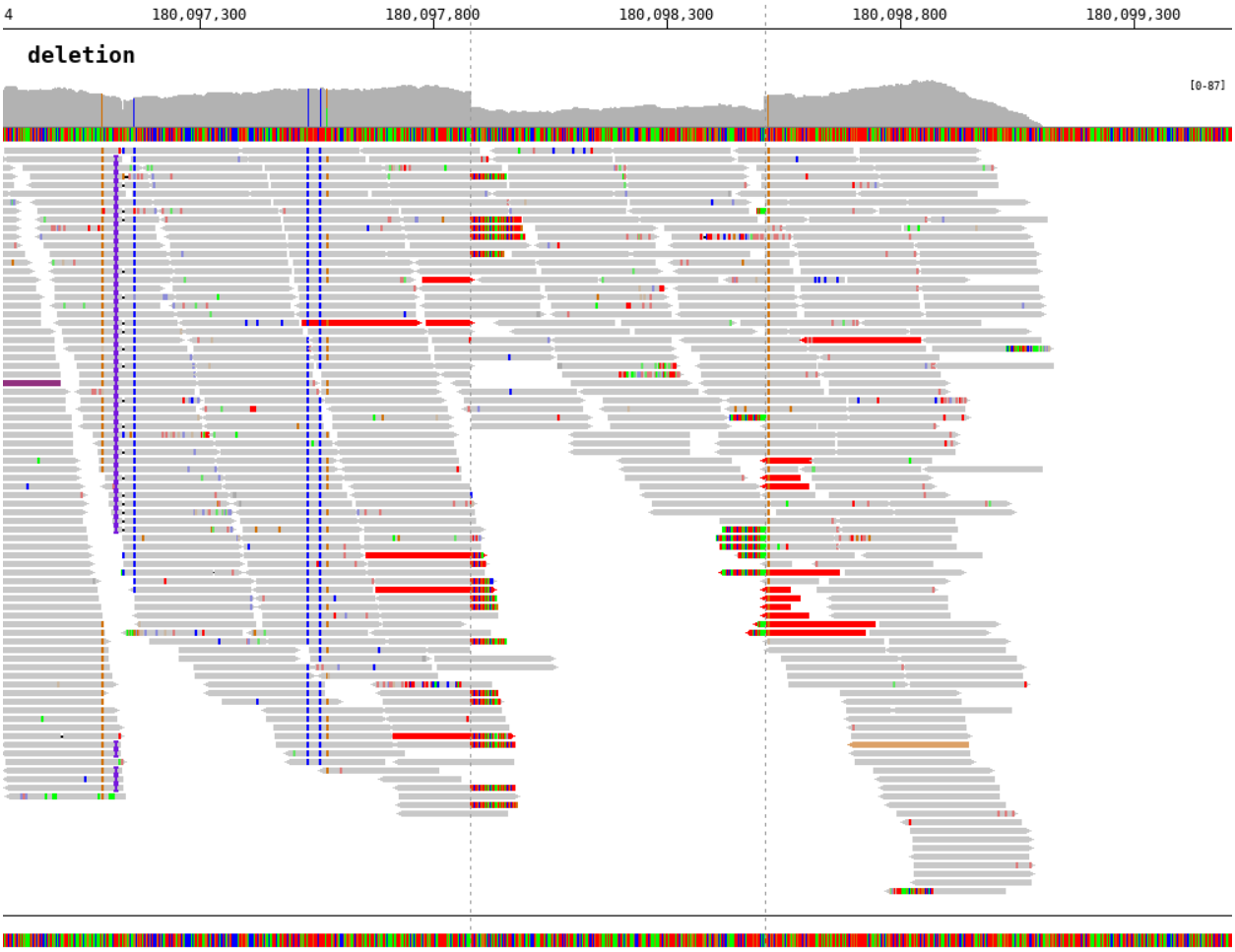
- chr5: #597E98
- chr6: #C5763E
- chr7: #70BFE7
- chr8: #91307F
- chr9: #80DE6E
- chr10: #DCA5B5
- chr11: #A35A24
- chr12: #978DA0
- chr13: #D16525
- chr14: #DCA167
- chr15: #8C79B9
- chr16: #E9BD71
- chr17: #4B2669
- chr18: #D7E4BF
- chr19: #733B91
- chr20: #BC2D7A
- chr21: #EBD176
- chr22: #6E786F
- chrX: #D5AA00
- chrY: #A9D400
- other chromosome: #555555

2.7.4 Show soft clipped part (`-show_soft_clipped`)




```
$ bamsnap \
    -bam ./data/test_SV1_chr1_37775710.bam \
    -title "SVA example (chr1:37775710)" \
    -pos chr1:37775710 \
    -out ./out/test_SV1-3_1.png \
    -bamplot coverage read \
    -margin 1000 \
    -no_target_line \
    -show_soft_clipped \
    -read_color_by interchrom \
    -save_image_only
```

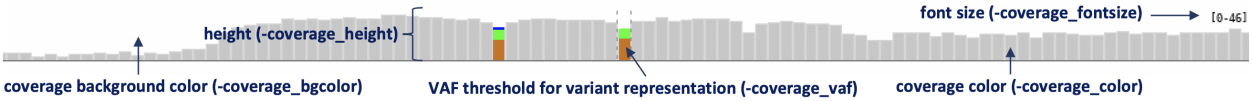
2.7.5 Deletion




```
$ bamsnap \
    -bam ./data/test_DEL_4_180097876_180097877.bam \
    -pos 4:180097878-180098507 \
    -margin 1000 \
    -title deletion \
    -out ./out/test_DEL_1.png \
    -refversion hg19 \
    -show_soft_clipped \
    -read_color_by interchrom \
    -save_image_only
```

The insert size threshold between read mates to detect deletions is set by `-insert_size_del_threshold` (default is 1000). The color of reads for deletion is #FF0000 by default. You can change the color using `-read_color_deletion` option.

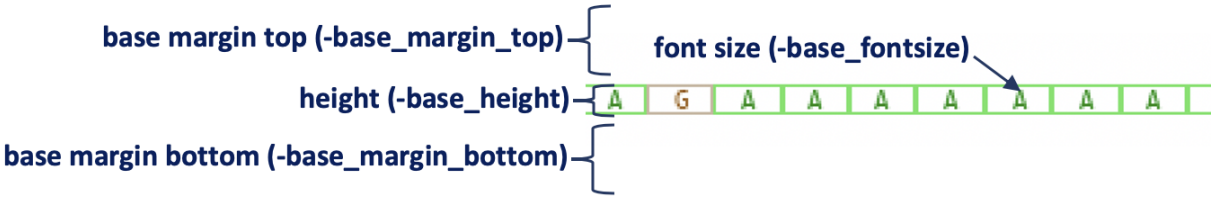
2.8 Coverage track (`-bamplot coverage`)



- `-coverage_height` (default=40) : coverage plot height
- `-coverage_fontsize` (default=9) : coverage font size
- `-coverage_vaf` (default=0.2) : coverage variant allele fraction threshold
- `-coverage_color` (default=C8C8C8) : coverage color
- `-coverage_bgcolor` (default=FFFFFFF) : coverage plot background color

2.9 Base track (`-draw base`, `-bamplot base`)

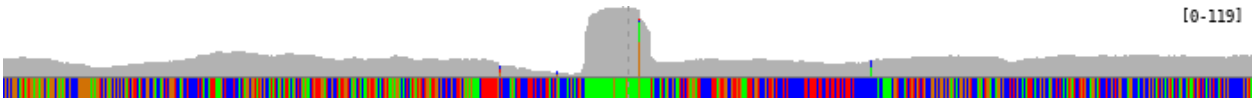
2.9.1 Layout options



- `-base_fontsize` (default=9) : font size of base
- `-base_height` (default=30) : base track height
- `-base_margin_top` (default=0) : top margin size of base track
- `-base_margin_bottom` (default=0) : bottom margin size of base track

2.9.2 Base track types

The base track has three formats which are automatically defined based on the width-span of the base.




```
$ bamsnap \
  -bam ./data/NA12879.bam \
  -draw bamplot \
  -bamplot coverage base \
  -pos chr10:117542948 \
  -separator_height 0 \
  -margin 500 \
  -no_title \
```

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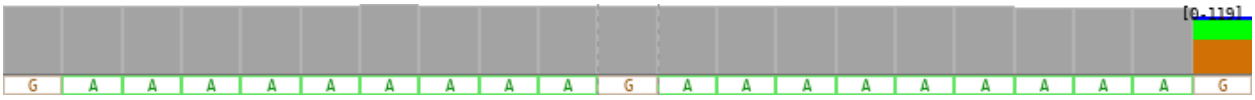
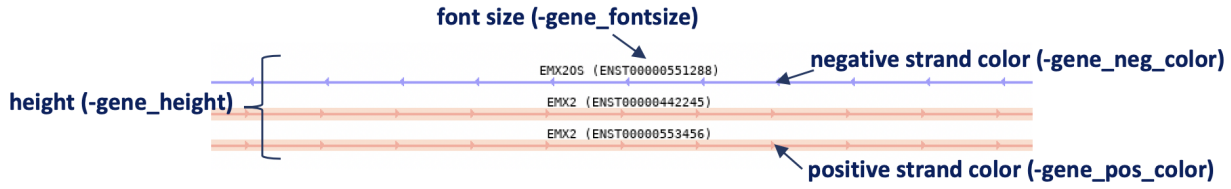
```
  -width 700 \
  -plot_margin_top 0 \
  -plot_margin_bottom 0 \
  -out ./out/NATRIO_chr10_117542948_baseplot_ex1.png
```


```
$ bamsnap \
  -bam ./data/NA12879.bam \
  -draw bamplot \
  -bamplot coverage base \
  -pos chr10:117542948 \
  -separator_height 0 \
  -margin 50 \
  -no_title \
  -width 700 \
  -plot_margin_top 0 \
  -plot_margin_bottom 0 \
  -out ./out/NATRIO_chr10_117542948_baseplot_ex2.png
```




```
$ bamsnap \
  -bam ./data/NA12879.bam \
  -draw bamplot \
  -bamplot coverage base \
  -pos chr10:117542948 \
  -separator_height 0 \
  -margin 10 \
  -no_title \
  -width 700 \
  -plot_margin_top 0 \
  -plot_margin_bottom 0 \
  -out ./out/NATRIO_chr10_117542948_baseplot_ex3.png
```

2.10 Gene track (`-draw gene`)



- `-gene_height` (default=50) : gene track height
- `-gene_fontsize` (default=10) : font size of gene track
- `-gene_pos_color` (default=FFAC9C) : positive strand color

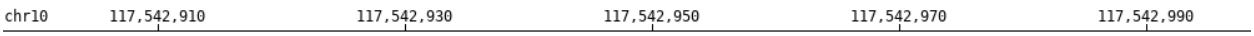
- `-gene_neg_color` (default=A19CFF) : negative strand color

2.11 Coordinates track (`-draw coordinates`)

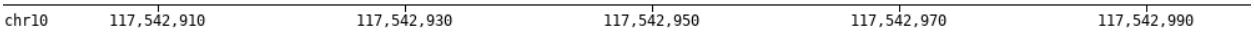
- `-coordinates_height` (default=20) : coordinates height
- `-coordinates_fontsize` (default=12) : coordinates font size
- `-coordinates_axisloc [top, bottom, middle]` (default=bottom) : coordinates axis location
- `-coordinates_bgcolor` (default=FFFFFF) : coordinates background color
- `-coordinates_labelcolor` (default=000000) : coordinates label color

2.11.1 Axis location (`-coordinates_axisloc`)

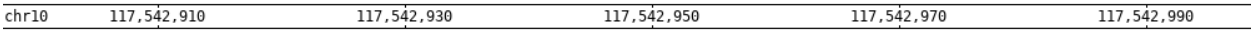
- bottom location: `-coordinates_axisloc bottom`



- top location: `-coordinates_axisloc top`



- middle location: `-coordinates_axisloc middle`



2.12 Heatmap track (`-bamplot heatmap`)

- `-heatmap_height` (default=5) : coverage heatmap height
- `-heatmap_bgcolor` (default=FFFFFF) : coverage heatmap background color

2.13 Version History

2.13.1 v0.2.x release series

0.2.13 (2020.09.13):

- adjust target line for deletion in VCF

0.2.12 (2020.09.15):

- adjust target line for deletion in VCF

0.2.11 (2020.09.08):

- adjust target line

0.2.10 (2020.09.08):

- debug ValueError when MD tag of read is missing (**‘issue #5<https://github.com/parklab/bamsnap/issues/5>‘_**)

0.2.9 (2020.09.03):

- add `insert_size_del_threshold` for deletion, `insert_size_ins_threshold` for insertsion
- add `read_color_deletion` for deletion, `read_color_insersion` for insertion

0.2.8 (2020.08.25):

- add `show_soft_clipped` option to show soft clipped part of reads. (=> manual and **‘issue #4<https://github.com/parklab/bamsnap/issues/4>‘_**)

0.2.7 (2020.08.24):

- add `-read_color_by` option for strand and inter-chromosomal rearrangement (=> manual)
- convert pileup-based to fetch-based for read retrieval in drawreadset.py

0.2.6 (2020.07.22):

- debug in saving JPG file.
- debug in coodinates axis location (middle)
- debug in base font size.
- update document.

0.2.5 (2020.07.17):

- add multiprocessing option(`-process`)

0.2.4 (2020.07.15):

- fix bug in version number
- add separator height option
- add -ref_index_rebuild option (to prevent to rebuild a fasta index file, when the fasta index file is older than the fasta file.)
- update documentation

0.2.2 (2020.07.09):

- debug typos

0.2.0 (2020.06.09):

- add gene plot
- add base plot
- improve layout
- add coordinates
- add read group

2.13.2 v0.1.x release series

0.1 :

- basic read alignment view

2.13.3 Todo

- add SVG output
- add PDF output
- add bamviewer