

# Package ‘ELViS’

April 17, 2025

**Title** An R Package for Estimating Copy Number Levels of Viral Genome Segments Using Base-Resolution Read Depth Profile

**Version** 1.0.0

**Description** Base-resolution copy number analysis of viral genome. Utilizes base-resolution read depth data over viral genome to find copy number segments with two-dimensional segmentation approach. Provides publish-ready figures, including histograms of read depths, coverage line plots over viral genome annotated with copy number change events and viral genes, and heatmaps showing multiple types of data with integrative clustering of samples.

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**LazyData** false

**BugReports** <https://github.com/hyochoi/ELViS/issues>

**URL** <https://github.com/hyochoi/ELViS>

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**Depends** R (>= 4.5.0)

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Contents

|                                              |           |
|----------------------------------------------|-----------|
| coord_to_grng . . . . .                      | 2         |
| coord_to_lst . . . . .                       | 3         |
| depth_hist . . . . .                         | 4         |
| ELViS . . . . .                              | 4         |
| ELViS_toy_run_result . . . . .               | 5         |
| filt_samples . . . . .                       | 6         |
| gene_cn_heatmaps . . . . .                   | 6         |
| get_depth_matrix . . . . .                   | 8         |
| get_new_baseline . . . . .                   | 10        |
| integrative_heatmap . . . . .                | 11        |
| mtrx_samtools_reticulate . . . . .           | 13        |
| norm_fun . . . . .                           | 13        |
| plot_pileUp_multisample . . . . .            | 14        |
| run_ELViS . . . . .                          | 16        |
| total_aligned_base__host_and_virus . . . . . | 17        |
| toy_example . . . . .                        | 17        |
| <b>Index</b>                                 | <b>18</b> |

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|               |                                                 |
|---------------|-------------------------------------------------|
| coord_to_grng | <i>Convert coordinate string to grng object</i> |
|---------------|-------------------------------------------------|

---

Description

Convert coordinate string to grng object

**Usage**

```
coord_to_grng(coord)
```

**Arguments**

coord                      string in the form of "chr1:123-456" or "chr1:1,234-5,678,912"

**Value**

GRanges object corresponding to the input coordinate string

**Examples**

```
coord_to_grng("chr1:123-456")  
coord_to_grng("chr1:1,234-5,678,912")
```

---

|              |                                                               |
|--------------|---------------------------------------------------------------|
| coord_to_lst | <i>Convert coordinate string to list of chr,start and end</i> |
|--------------|---------------------------------------------------------------|

---

**Description**

Convert coordinate string to list of chr,start and end

**Usage**

```
coord_to_lst(coord)
```

**Arguments**

coord                      string in the form of "chr1:123-456" or "chr1:1,234-5,678,912"

**Value**

a list of 3 elements. Chromosome name, start position and end position.

**Examples**

```
coord_to_lst("chr1:123-456")  
coord_to_lst("chr1:1,234-5,678,912")
```

---

|            |                                                     |
|------------|-----------------------------------------------------|
| depth_hist | <i>Sample filtering threshold examination plot.</i> |
|------------|-----------------------------------------------------|

---

### Description

Sample filtering threshold examination plot.

### Usage

```
depth_hist(mtrx, th = 50, title_txt = NULL, smry_fun = max, ...)
```

### Arguments

|           |                                                                          |
|-----------|--------------------------------------------------------------------------|
| mtrx      | Matrix or data.frame. Rows are positions and columns are samples.        |
| th        | Numeric. Sample filtering threshold                                      |
| title_txt | figure title.                                                            |
| smry_fun  | function to calculate summary metric to apply sample filter threshold to |
| ...       | additional argument for smry_fun argument.                               |

### Value

ggplot2 object

### Examples

```
data(mtrx_samtools_reticulate)
th <- 50
depth_hist(mtrx_samtools_reticulate, th=th, smry_fun=max)
depth_hist(mtrx_samtools_reticulate, th=th, smry_fun = quantile, prob=0.95)
depth_hist(mtrx_samtools_reticulate, th=th, smry_fun = mean)
```

---

|       |                                                                                                                                  |
|-------|----------------------------------------------------------------------------------------------------------------------------------|
| ELViS | <i>ELViS : An R Package for Estimating Copy Number Levels of Viral Genome Segments Using Base-Resolution Read Depth Profile.</i> |
|-------|----------------------------------------------------------------------------------------------------------------------------------|

---

### Description

Base-resolution copy number analysis of viral genome. Utilizes base-resolution read depth data over viral genome to find copy number segments with two-dimensional segmentation approach. Provides publish-ready figures, including histograms of read depths, coverage line plots over viral genome annotated with copy number change events and viral genes, and heatmaps showing multiple types of data with integrative clustering of samples.

**Functions**

- `get_depth_matrix` : Generate a read depth matrix of positions x samples from input BAM files list.
- `run_ELViS` : Run ELViS using input raw depth matrix.
- raw depth matrix.

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**See Also**

Useful links:

- <https://github.com/hyochoi/ELViS>
- Report bugs at <https://github.com/hyochoi/ELViS/issues>

---

ELViS\_toy\_run\_result    *ELViS Toy Example - Run Result*

---

**Description**

List containing ELViS run result

**Usage**

```
data(ELViS_toy_run_result)
```

**Format**

ELViS\_toy\_run\_result:

A list of

**is\_reduced\_output** Indicates whether this results is a reduced form

**final\_output** Final base-resolution segmentation output

**final\_call** Indices of samples in which copy number variants were detected

**new\_Y\_p2** Normalized read depth

---

|              |                                                     |
|--------------|-----------------------------------------------------|
| filt_samples | <i>Filtering samples based on summary statistic</i> |
|--------------|-----------------------------------------------------|

---

### Description

Filtering samples based on summary statistic

### Usage

```
filt_samples(mtrx, th = 50, smry_fun = max)
```

### Arguments

|          |                                                                                             |
|----------|---------------------------------------------------------------------------------------------|
| mtrx     | matrix or data.frame. Rows are positions and columns are samples.                           |
| th       | Sample filtering threshold (Default : 50)                                                   |
| smry_fun | function to generate summary value of samples, which is used for filtering. (Default : max) |

### Value

matrix or data.frame. data matrix with low depth samples filtered out.

### Examples

```
data(mtrx_samtools_reticulate)
th<-50
filtered_mtrx <- filt_samples(mtrx_samtools_reticulate,th=th,smry_fun=max)
```

---

|                  |                                 |
|------------------|---------------------------------|
| gene_cn_heatmaps | <i>Gene Copy Number Heatmap</i> |
|------------------|---------------------------------|

---

### Description

Gene Copy Number Heatmap

### Usage

```
gene_cn_heatmaps(
  X_raw,
  result,
  gff3_fn,
  gene_ref,
  baseline = 1,
  exclude_genes,
  col_cn = colorRamp2(c(0.5, 1, 1.5), c(muted("blue"), "white", muted("red"))),
  heatmap_height = unit(1.5, "in")
)
```

**Arguments**

|                |                                                                                                                                                         |
|----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|
| X_raw          | Raw depth matrix                                                                                                                                        |
| result         | Run result                                                                                                                                              |
| gff3_fn        | gene annotation file name                                                                                                                               |
| gene_ref       | The name of the gene to set as reference for relative gene dosage heatmap                                                                               |
| baseline       | Vector of state numbers to use as baseline for each sample. If it is single integer, then the given state number is used for all samples. (Default : 1) |
| exclude_genes  | name of genes to exclude from the annotation track (Default : NULL)                                                                                     |
| col_cn         | relative gene dosage color palette. (Default : colorRamp2(c(0.5,1,1.5),c(muted("blue"),"white"),1))                                                     |
| heatmap_height | heatmap height specified using unit function. (Default : unit(1.5,"in"))                                                                                |

**Value**

a ComplexHeatmap Heatmap List object

**Examples**

```
# gff3 gene model file
package_name <- "ELViS"
gff3_fn <- system.file("extdata", "HPV16REF_PaVE.gff", package = package_name)

# loading precalculated depth matrix
data(mtrx_samtools_reticulate)

# threshold
th <- 50

# filtered matrix
base_resol_depth <- filt_samples(mtrx_samtools_reticulate, th=th, smry_fun=max)

# viral load data
data(total_aligned_base__host_and_virus)
viral_load <- (10^6)*(apply(base_resol_depth, 2, \ (x) sum(x)) )/total_aligned_base__host_and_virus

# load ELViS run result
data(ELViS_toy_run_result)
result <- ELViS_toy_run_result

# genes to exclude from plotting
exclude_genes <- c("E6*", "E1^E4", "E8^E2")

# heatmap of gene dosage
gene_ref <- "E7"

gene_cn <-
  gene_cn_heatmaps(
    X_raw = base_resol_depth,
```

```
        result = result,
        gff3_fn = gff3_fn,
        baseline = 1,
        gene_ref = gene_ref,
        exclude_genes = exclude_genes
    )

gene_cn
```

---

|                  |                                                                                      |
|------------------|--------------------------------------------------------------------------------------|
| get_depth_matrix | <i>Generate a read depth matrix of positions x samples from input BAM files list</i> |
|------------------|--------------------------------------------------------------------------------------|

---

**Description**

Generate a read depth matrix of positions x samples from input BAM files list

**Usage**

```
get_depth_matrix(
  bam_files,
  mode = "samtools_basilisk",
  coord_or_target_virus_name,
  is_virus = TRUE,
  N_cores = detectCores(),
  min_mapq = 30,
  min_base_quality = 0,
  max_depth = 1e+05,
  modules = NULL,
  envs = NULL,
  tmpdir = tempdir(),
  samtools = NULL,
  condaenv = "env_samtools",
  condaenv_samtools_version = "1.21"
)
```

**Arguments**

|           |                                                                                                                                                                                                       |
|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| bam_files | Vector containing bam file names in character                                                                                                                                                         |
| mode      | Mode of read depth calculation. Either of c("samtools_basilisk", "samtools_custom", "Rsamtools") are acceptable. If run on Windows OS, it will coerced to "Rsamtools" (Default : "samtools_basilisk") |

|                            |                                                                                                                                                                                   |
|----------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| coord_or_target_virus_name | The name of the target virus. This should be equal to the name of the sequence in the FASTA file reads are aligned to.                                                            |
| is_virus                   | logical indicating if the coord_or_target_virus_name is for viral genome(TRUE) or non-viral genome(FALSE) (default : TRUE)                                                        |
| N_cores                    | Number of cores to use for parallel processing (Default : min(10,available cores))                                                                                                |
| min_mapq                   | Minimum MAPQ. (Default : 30)                                                                                                                                                      |
| min_base_quality           | Minimum basecall quality score (Default : 0)                                                                                                                                      |
| max_depth                  | (Rsamtools) Maximum read depth. (Default : 1e5)                                                                                                                                   |
| modules                    | (samtools) Environment modulefile name. (Default : NULL)                                                                                                                          |
| envs                       | (samtools) Environmental variables for samtools. (Default : NULL)                                                                                                                 |
| tmpdir                     | (samtools) Temporary file directory (Default : tmpdir())                                                                                                                          |
| samtools                   | (samtools) Absolute path to samtools executable (Default : NULL)                                                                                                                  |
| condaenv                   | (samtools_basilisk) Name of the conda environment in which samtools are installed. If no environment with this name is available, one will be created. (Default : "env_samtools") |
| condaenv_samtools_version  | (samtools_basilisk) The version of samtools to install in the conda environment using basilisk (Default : "1.21")                                                                 |

### Value

a matrix of positions x samples containing base-resolution raw read depth

### Examples

```
package_name <- "ELViS"

# The name of the target virus
# in the reference sequence FASTA file used for alignment.
# Can be check by samtools view -H input.bam
target_virus_name <- "gi|333031|lcl|HPV16REF.1|"

# get bam file pathes
ext_path <- system.file("extdata",package = package_name)
bam_files <- list.files(ext_path,full.names = TRUE,pattern = "bam$")

# number of threads to use
N_cores <- 1L

# get read depth matrix
tmpdir <- tmpdir()

mtrx_samtools_basilisk <-
  get_depth_matrix(
    bam_files = bam_files,coord_or_target_virus_name = target_virus_name,is_virus = TRUE
    ,mode = "samtools_basilisk"
```

```
,N_cores = N_cores  
,min_mapq = 30  
,tmpdir=tempdir()  
,condaenv = "env_samtools"  
)
```

---

|                  |                                                                |
|------------------|----------------------------------------------------------------|
| get_new_baseline | <i>Get new baselines according to criteria user designates</i> |
|------------------|----------------------------------------------------------------|

---

### Description

Get new baselines according to criteria user designates

### Usage

```
get_new_baseline(result, mode = "longest")
```

### Arguments

|        |                                                                |
|--------|----------------------------------------------------------------|
| result | Run result                                                     |
| mode   | Indicate how new baseline should be set ("longest","shortest") |

### Value

a integer vector indicating new baseline index for each sample

### Examples

```
# its usage example is given in vignette in detail  
  
data(ELViS_toy_run_result)  
result <- ELViS_toy_run_result  
  
get_new_baseline(result,mode="longest")
```

---

|                     |                                                                                  |
|---------------------|----------------------------------------------------------------------------------|
| integrative_heatmap | <i>Plot heatmaps based on simple integrative clustering of multiple matrices</i> |
|---------------------|----------------------------------------------------------------------------------|

---

## Description

Plot heatmaps based on simple integrative clustering of multiple matrices

## Usage

```
integrative_heatmap(
  X_raw,
  result,
  gff3_fn,
  exclude_genes,
  col_pal_gene = col_yarrr_info2,
  col_cn = colorRamp2(c(0.5, 1, 1.5), c(muted("blue"), "white", muted("red"))),
  col_y = colorRamp2(c(0.5, 1, 2), c(muted("blue"), "white", muted("red"))),
  col_z = colorRamp2(c(-4, 0, 4), c(muted("blue"), "white", muted("red"))),
  col_x_scaled = "auto",
  col_vl = "auto",
  baseline = 1,
  matrices_to_plot = "all",
  matrices_integ_cluster = "all",
  total_aligned_base__host_and_virus = NULL,
  return_data_matrices = FALSE
)
```

## Arguments

|               |                                                                                                                                                         |
|---------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|
| X_raw         | Raw depth matrix                                                                                                                                        |
| result        | Run result                                                                                                                                              |
| gff3_fn       | gene annotation file name                                                                                                                               |
| exclude_genes | name of genes to exclude from the annotation track (Default : NULL)                                                                                     |
| col_pal_gene  | color palette for gene colors                                                                                                                           |
| col_cn        | Color scheme for copy number heatmap (Default : colorRamp2(c(0.5, 1, 1.5), c(muted("blue"), "white", muted("red"))))                                    |
| col_y         | Color scheme for normalized read depth(Y) heatmap (Default : colorRamp2(c(0.5, 1, 2), c(muted("blue"), "white", muted("red"))))                         |
| col_z         | Color scheme for Z-score heatmap (Default : colorRamp2(c(-4, 0, 4), c(muted("blue"), "white", muted("red"))))                                           |
| col_x_scaled  | Color scheme for scaled raw depth(X) heatmap (Default : "auto")                                                                                         |
| col_vl        | Color scheme for positional viral load heatmap (Default : "auto")                                                                                       |
| baseline      | Vector of state numbers to use as baseline for each sample. If it is single integer, then the given state number is used for all samples. (Default : 1) |

**matrices\_to\_plot**  
Names and orders of the matrices to show as heatmap. Any permutation of `c("CN", "Y", "Z", "X_Scaled", "Viral_Load")` of any length is allowed. The vertical orders of stacked heatmaps follows the order of this vector. If set to "all", `c("CN", "Y", "Z", "X_Scaled", "Viral_Load")` is used. (Default : "all")

**matrices\_integ\_cluster**  
Names of the matrices to be used for integrative clustering for column orders. Any combination of `c("CN", "Y", "Z", "X_Scaled", "Viral_Load")` of length > 1 is allowed. If the length is less than 2, then it is ignored and the first matrix specified in `matrices_to_plot` argument is used for column ordering. The vertical orders of stacked heatmaps follows the order of this vector. If set to "all", `c("CN", "Y", "Z", "X_Scaled", "Viral_Load")` is used. (Default : "all")

**total\_aligned\_base\_\_host\_and\_virus**  
Total aligned bases for each sample(i.e. from picard,gatk,qualimap). Used to calculate positional load of viral DNA. Makes sense if regions in host genome are also included in the target panel. Ignored if set to NULL. (Default : NULL)

**return\_data\_matrices**  
boolean whether to return the data matrices used. (Default : FALSE)

## Value

A ComplexHeatmap Heatmap List object vertically stacked

## Examples

```
# gff3 gene model file
package_name <- "ELViS"
gff3_fn <- system.file("extdata", "HPV16REF_PaVE.gff", package = package_name)

# loading precalculated depth matrix
data(mtrx_samtools_reticulate)

# threshold
th <- 50

# filtered matrix
base_resol_depth <- filt_samples(mtrx_samtools_reticulate, th=th, smry_fun=max)

# viral load data
data(total_aligned_base__host_and_virus)
viral_load <- (10^6)*(apply(base_resol_depth, 2, \ (x) sum(x)) )/total_aligned_base__host_and_virus

# load ELViS run result
data(ELViS_toy_run_result)
result <- ELViS_toy_run_result

# genes to exclude from plotting
exclude_genes <- c("E6*", "E1^E4", "E8^E2")
```

```
# heatmap based on integrative clustering
integ_ht_result <- integrative_heatmap(
  X_raw = base_resol_depth,
  result = result,
  gff3_fn = gff3_fn,
  exclude_genes = exclude_genes,
  baseline=1,
  total_aligned_base__host_and_virus = total_aligned_base__host_and_virus
)

integ_ht_result
```

---

|                          |                                                           |
|--------------------------|-----------------------------------------------------------|
| mtrx_samtools_reticulate | <i>ELViS Toy Example - Base-Resolution Raw Read Depth</i> |
|--------------------------|-----------------------------------------------------------|

---

**Description**

Base-resolution raw read depth profile over viral genome

**Usage**

```
data(mtrx_samtools_reticulate)
```

**Format**

mtrx\_samtools\_reticulate:  
A matrix with 7906 rows and 120 columns

---

|          |                                                    |
|----------|----------------------------------------------------|
| norm_fun | <i>Normalization - scaling by certain quantile</i> |
|----------|----------------------------------------------------|

---

**Description**

Normalization - scaling by certain quantile

**Usage**

```
norm_fun(x, probs = 0.75)
```

**Arguments**

- x                    numeric vector to normalize.
- probs                a single numeric value of probabilities in [0, 1] used for normalization.(Default = 0.75)

**Value**

numeric vector of normalized values

**Examples**

```
norm_fun(seq_len(5))
# [1] 0.25 0.50 0.75 1.00 1.25
```

---

```
plot_pileUp_multisample
```

*Get a list of pile-up plots over multiple samples*

---

**Description**

Get a list of pile-up plots over multiple samples

**Usage**

```
plot_pileUp_multisample(
  result,
  X_raw,
  target_indices = NULL,
  plot_target = "x",
  gff3_fn,
  baseline = 1,
  annot_margin = 0.01,
  arrow_spacing = 0.05,
  gene_name_space = 0.5,
  col_pal = col_yarr_info2,
  col_cn_baseline = "#708C98",
  col_pal_cn = col_yarr_info2[-5],
  exclude_genes = NULL,
  annot_plot_ratio = 0.3
)
```

**Arguments**

|                |                                                  |
|----------------|--------------------------------------------------|
| result         | analysis result                                  |
| X_raw          | input raw depth matrix                           |
| target_indices | sample indices to plot                           |
| plot_target    | target data type to plot (Default : "x")         |
| gff3_fn        | gene annotation file name                        |
| baseline       | the state index to set as baseline (Default : 1) |

annot\_margin     minimum of margin between gene annotations allowed. As a fraction of plotting area. (Default : 0.01)  
 arrow\_spacing     gene annotation arrow spacing. As a fraction of plotting area. (Default : 0.05)  
 gene\_name\_space     the height of white space reserved for gene names in the annotation. (Default : 0.5)  
 col\_pal     gene color palette  
 col\_cn\_baseline     color for baseline (Default : "#708C98")  
 col\_pal\_cn     color palette for non-baseline copy number states  
 exclude\_genes     name of genes to exclude from the annotation track (Default : NULL)  
 annot\_plot\_ratio     ratio of the annotation plot under the pileup plot

### Value

a list of pile-up ggplot object

### Examples

```

# gff3 gene model file
package_name <- "ELViS"
gff3_fn <- system.file("extdata", "HPV16REF_PaVE.gff", package = package_name)

# loading precalculated depth matrix
data(mtrx_samtools_reticulate)

# threshold
th <- 50

# filtered matrix
base_resol_depth <- filt_samples(mtrx_samtools_reticulate, th=th, smry_fun=max)

data(ELViS_toy_run_result)
result <- ELViS_toy_run_result

# get line plots for shape-change samples
gg_lst_x <-
plot_pileUp_multisample(
  result = result,
  X_raw = base_resol_depth,
  plot_target = "x",
  gff3 = gff3_fn,
  baseline=1,
  exclude_genes = c("E6*", "E1^E4", "E8^E2"),
  target_indices = result$final_call$cnv_samples[seq_len(3)]
)

gg_lst_x[[1]]

```

run\_ELViS

*Run ELViS using input raw depth matrix***Description**

Run ELViS using input raw depth matrix

**Usage**

```
run_ELViS(
  X,
  N_cores = min(10L, detectCores()),
  reduced_output = TRUE,
  verbose = FALSE,
  save_intermediate_data = FALSE,
  save_dir = "save_dir",
  overwrite = FALSE
)
```

**Arguments**

|                        |                                                                                     |
|------------------------|-------------------------------------------------------------------------------------|
| X                      | Raw depth matrix of position x samples                                              |
| N_cores                | The number of cores to use (Default : min(10L,detectCores()))                       |
| reduced_output         | logical indicating whether to return only reduced output                            |
| verbose                | logical whether to print out information for debugging                              |
| save_intermediate_data | logical indicating whether to save intermediate data as rds file. (default : FALSE) |
| save_dir               | Name of the directory to save intermediate files in. (default : "save_dir")         |
| overwrite              | logical indicating whether to overwrite intermediate files. (default : FALSE)       |

**Value**

list containing ELViS run results

**Examples**

```
data(mtrx_samtools_reticulate)
th<-50
filtered_mtrx <- filt_samples(mtrx_samtools_reticulate,th=th,smry_fun=max)

result <- run_ELViS(filtered_mtrx[,seq_len(5)],N_cores=1L)
```

---

|                                    |                                               |
|------------------------------------|-----------------------------------------------|
| total_aligned_base__host_and_virus | <i>ELViS Toy Example - Total Aligned Base</i> |
|------------------------------------|-----------------------------------------------|

---

**Description**

Total aligned base both to host and viral genome.

**Usage**

data(total\_aligned\_base\_\_host\_and\_virus)

**Format**

total\_aligned\_base\_\_host\_and\_virus:  
A vector of length 120

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|             |                                     |
|-------------|-------------------------------------|
| toy_example | <i>ELViS Toy Example - Metadata</i> |
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**Description**

Metadata of samples in the toy examples

**Usage**

data(toy\_example)

**Format**

toy\_example:  
A data frame with 120 rows and 6 columns:  
**VarType** Variant type. Set to control if there is no variant  
**Copies\_Altered** The number of copies duplicated or deleted  
**Event\_Size** Variant size  
**Mean\_Depth** Mean read depth

# Index

## \* datasets

- ELViS\_toy\_run\_result, [5](#)
- mtrx\_samtools\_reticulate, [13](#)
- total\_aligned\_base\_\_host\_and\_virus,  
[17](#)
- toy\_example, [17](#)

coord\_to\_grng, [2](#)  
coord\_to\_lst, [3](#)

depth\_hist, [4](#)

ELViS, [4](#)  
ELViS-package (ELViS), [4](#)  
ELViS\_toy\_run\_result, [5](#)

filt\_samples, [6](#)

gene\_cn\_heatmaps, [6](#)  
get\_depth\_matrix, [8](#)  
get\_new\_baseline, [10](#)

integrative\_heatmap, [11](#)

mtrx\_samtools\_reticulate, [13](#)

norm\_fun, [13](#)

plot\_pileUp\_multisample, [14](#)

run\_ELViS, [16](#)

total\_aligned\_base\_\_host\_and\_virus, [17](#)  
toy\_example, [17](#)