

## Tools

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[hifive](#) manipulate, analyze, and plot HiC and 5C chromatin interaction data

[Workflows](#)

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## Select action to perform

## RE Cutsite BED File



## Data Format

## Mat file



## Maximum insert size

## Included chromosomes

If a subset of chromosomes are to be used, enter a comma-separated list of chromosome names.

## Minimum interactions per fend

## Minimum distance bin cutoff

## History



## Unnamed history

6 shown, 81 [deleted](#), 4 [hidden](#)

1.6 GB



[80: hifive on data 79: Hi C MR-heatmap](#)



[79: hifive on data 70 and data 69: HiC project express](#)



[78: hifive on data 70 and data 69: HiC data](#)



[77: hifive on data 70 and data 69: HiC fends](#)



[70: test\\_full.mat](#)



[69: test\\_fend.bed](#)

