**Guide RNA Utail length**

1 Prepare the following files:

gRNA.list *a list of containing the selected gRNA*

example.bam *the alignment of mapping to minicircle gRNA*

gRNA\_Utail\_length.py *the script of calculate gRNA average Utail length*

2 run the bash script:

Bash gRNA\_Utail\_length.sh

**Violinplot lot of the average Utail length**

1. prepare the input file: there are 2 columns (Utail\_length and sample) in the input file

Utail\_length sample

11 RESC1

9 RESC1

9 RESC1

……

11 RESC2

10 RESC2

10 RESC2

……

1. usage:

python average\_utail\_length\_violinplot –i1 input

**Violinplot of the gRNA fragment length**

1. prepare the input file: there are 2 columns (Utail\_length and sample) in the input file

read\_length sample

57 RESC1

59 RESC1

59 RESC1

……

63 RESC2

34 RESC2

34 RESC2

……

2 usage:

python average\_utail\_length\_violinplot –i1 input