# Step 1: Convert sam -> cpsOut -> znt4 files

cd sam\_file/

[qiuh@helix test]$ cd sam\_file

[qiuh@helix sam\_file]$ ./script.init\_sacCer2\_32

[qiuh@helix sam\_file]$ ln -s test.sam samLNS

[qiuh@helix sam\_file]$ ./script.cps\_all

[qiuh@helix sam\_file]$ ./script.mark\_cps32

# Step 2: Size-select the raw reads (e.g. 50-300bp, for ChIP-seq data). Create new znt4 files with the filtered reads

[qiuh@helix sam\_file]$ perl Unique\_cpsOut\_to\_znt4.pl 50 300 all > test\_50-300.znt4\_report.txt

# Step 3: Generate statistics of read counts (compute number of reads over coding regions, promoters, downstream regions, etc.)

[qiuh@helix sam\_file]$ cd ..

[qiuh@helix test]$ perl minetreatmentfeats\_mod.pl test\_statistics test