

steps

```
test@bioinfo_docker:~/mapping$ bowtie -v 2 -m 10 --best --strata BowtieIndex/YeastGenome -f THA2.fa -S THA2.sam
# reads processed: 1250
# reads with at least one reported alignment: 1158 (92.64%)
# reads that failed to align: 77 (6.16%)
# reads with alignments suppressed due to -m: 15 (1.20%)
Reported 1158 alignments to 1 output stream(s)
```

```
test@bioinfo_docker:~/mapping$ bowtie -v 1 -m 10 --best --strata bowtie-src/indexes/e_coli -q e_coli_500.fq -S e_coli_500.sam
# reads processed: 500
# reads with at least one reported alignment: 499 (99.80%)
# reads that failed to align: 0 (0.00%)
# reads with alignments suppressed due to -m: 1 (0.20%)
Reported 499 alignments to 1 output stream(s)
```

```
test@bioinfo_docker:~/mapping$ perl sam2bed.pl THA2.sam > THA2.bed
test@bioinfo_docker:~/mapping$ perl sam2bed.pl e_coli_500.sam > e_coli_500.bed
```

```
test@bioinfo_docker:~/mapping$ grep -v chrV THA2.bed > THA2_noV.bed
```

```
test@bioinfo_docker:~/mapping$ grep '$chrXII\t' THA2.bed > THA2_XII.bed
```

```
test@bioinfo_docker:~/mapping$ wc -l THA2_noV.bed
1125 THA2_noV.bed
test@bioinfo_docker:~/mapping$ wc -l THA2_XII.bed
169 THA2_XII.bed
```

结果是第一个文件有1125行，第二个位169行