1. Peak to fasta (.fa)

bedtools getfasta -fi ./hg19/hg19.fa -bed ./peaks.bed -fo ./2\_peak.fa/peaks.bed.fa

1. Fimo scans the genome sequence to obtain the sequence position corresponding to motif

./meme-5.1.1/src/fimo --oc ./3\_scan --thresh 1e-5 --no-qvalue ./cisbp.human.motif.txt

./2\_peak.fa/peaks.bed.fa

1. tsv To txt

R run tsv\_to\_txt.R

1. Run perl d-motif\_combine-TFfamily.pl
2. Run perl e-tfpos\_combine.pl

1. Run perl f1-tf\_bed-new-c.pl

1. Run perl f2-delete-overlap.pl