A

```
#! /usr/local/perl –w
@filenames=("H3K27ac_rep1","H3K27ac_rep2","H3K4me1_rep1","H3K4me1_rep2");
@chromo=("chr1","chr2","chr3","chr4","chr5","chr6","chr7","chr8","chr9","chr10","chr11","chr12","chr13","chr14","chr15","chr16","chr17","chr18","chr19","chrX","chrY");
foreach $sam (@filenames)
{
open(OUT,">$sam\_ChIP_whole_gene_Jerry.txt")||die("Can't write OUT:$!\n");
my $total_reads=$overlap=$others=0;
foreach $chromosome (@chromo)
{
 open(INA,"Mus_musculus.GRCm38.75.gtf.gene")||die("Can't open INA:$!\n");
 open(INC,"$sam\.sam.$chromosome")||die("Can't open INC:$!\n");
 while(<INA>)
 {
  chomp;
  if(/^(\w\w?)\t(\w+)\tgene\t(\d+)\t(\d+)\t([+|-])\t(ENSMUSG\d+)\t([\w\.\-\(\)]+)$/)
  {
   $chromosome_gene="chr$1";
   if($chromosome_gene eq $chromosome)
   {
    $total_gene_id++;  $TSS_id="$chromosome_gene:$3-$4:$6_$7:$2:$5"; $count{$TSS_id}=0;
    for($i=$3;$i<=$4;$i++)
    {
     if(exists $gene{$i}){$gene{$i}.=";;$TSS_id";} ## overlaped regions, more TSS IDs
     else{$gene{$i}=$TSS_id;} }}
  }  else{print "error1\t$_\n";}
 }
 while(<INC>)
 {
  chomp;
  if(/^([\w\.\:\-]+)\t(\d+)\t(chr\w\w?)\t(\d+)\t\d+\t(\d+)M\t/)
  {
   if($2 == 0){$str="plus"; $left=$4; $right=$4+250-1;} ## entend to 250 bp for each fragment
   elsif($2 == 16){$str="minus"; $right=$4+$5-1; $left=$right-250+1; }
   else{print "error Strand-FLAG: $_\n";}
   $read_id=$1;  $chr=$3;  if($chr ne $chromosome){print "error wrong sam-chr: $_\n";}
   $label=0; ##
   for ($j=$left; $j<=$right; $j++)
   {
    if(exists $gene{$j}) ## read overlap with gene
    {
     $label=1;
     if(exists $name{$read_id}) ## this read already overlap with gene
     {
      if($name{$read_id} =~ /$gene{$j}/){} ## already this gene ID
      else{$name{$read_id}.=";;$gene{$j}";} ## add this gene ID to this reads
     }
     else{$name{$read_id}=$gene{$j};} ## First intron overlap with this read
    }
   }
   if($label==0){$non_overlap++;}
   elsif($label==1) ## fragment mapped to gene
   {
    $overlap++; @arraylist=split(/;;/,$name{$read_id});  foreach (@arraylist){$tmphash{$_}=0;}    @newlist=keys %tmphash;     foreach (@newlist){$count{$_}++;};
   }
   else{$others++;}
   delete $name{$read_id};   foreach (keys %tmphash){delete $tmphash{$_};}
  }  else{print "error2\t$_\n";}
 }
 foreach (keys %count){print OUT "$_\t$count{$_}\n"; $result++; delete $count{$_};}  foreach (keys %gene){delete $gene{$_};}
 close INA; close INC;}close INA; close OUT;}
```

B

```
library("edgeR")
data <- read.table("Total_merge_Kdm5c_exonic_gene_Jerry.txt",sep="\t",header=T,row.names=1)
data_y <- DGEList(counts=data, group=c("WT","WT","WT","KO","KO","KO"))
keep <- rowSums(cpm(data_y)) >= 2
y <- data_y[keep,]
y$samples$lib.size <- colSums(y$counts)
y <- calcNormFactors(y)
y <- estimateCommonDisp(y,verbose=TRUE)
y <- estimateTagwiseDisp(y)
test_result  <- exactTest(y, pair=c("WT","KO"))
diff_total <- data.frame(topTags(test_result, n=length(y$AveLogCPM)))
length_gene <- read.table("Gene_length.txt",header=T,row.names=1,sep="\t")
total <- cbind(diff_total,Length=length_gene[row.names(diff_total),])
write.table(total,file="results_edgeR_Kdm5c_WT_KO_exonic_gene.xls",quote=FALSE,sep="\t")
```

Supplemental Figure S8. Scripts used for gene based counting and comparison. (A) Perl script used to count sequencing signals in gene bodies for ChIP-seq, ATAC-seq, GRO-seq, and RNA-seq data sets. Counting ChIP-seq signals of H3K27ac and H3K4me1 was used as an example. (B) R script used to compare gene expression changes. Comparison of RNAseq counts between WT and *Kdm5c* mutant was used as an example.