BIOWULF

## Merge bam files in the same treatment group in BIOWULF (UNIX system in NIH)

(shammerge.bam = sham1 + sham2 + sham3, unxmerge.bam = unx1+unx2+unx3)

$ module load samtools

$ ls

1\_RMD.bam 2\_RMD.bam 3\_RMD.bam

$ samtools merge -o shammerge.bam 1\_RMD.bam 2\_RMD.bam 3\_RMD.bam

$ ls

1\_RMD.bam 2\_RMD.bam 3\_RMD.bam shammerge.bam shammerge.bam.bai

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## FLAG SIZE DISTRIBUTION

library(ATACseqQC)

library(MotifDb)

library(BSgenome.Mmusculus.UCSC.mm10)

bamQC("./BAM/FILE/LOCATION/shammerge.bam", outPath = NULL)

bamFiles.labels <- sub(".bam", "", basename("./BAM/FILE/LOCATION/shammerge.bam"))

fragSize\_sham <- fragSizeDist("./BAM/FILE/LOCATION/shammerge.bam", bamFiles.labels)

## FOOTPRINTING

PPARA <- query(MotifDb, c("PPARA"))

PPARA <- as.list(PPARA)

print(PPARA[[1]], digits=2)

 genome <- Mmusculus

 seqlev <- "chr1"

sigs <- factorFootprints(c ("./BAM/FILE/LOCATION/shammerge.bam","./BAM/FILE/LOCATIONunxmerge.bam"),

 pfm=PPARA[[1]],

 genome=genome,

 min.score="90%",

 seqlev = paste0("chr", c(1)),

 upstream=1000, downstream=1000,

 group= c("./BAM/FILE/LOCATION/shammerge.bam","./BAM/FILE/LOCATION/unxmerge.bam ") )

ctcf <- query(MotifDb, c("ctcf"))

ctcf <- as.list(ctcf)

print(ctcf[[1]], digits=2)

sigs\_ctcf <- factorFootprints(c ("./BAM/FILE/LOCATION/shammerge.bam","./BAM/FILE/LOCATION/unxmerge.bam"),

 pfm=ctcf[[1]],

 genome=genome,

 min.score="90%",

 seqlev = paste0("chr", c(1)),

 upstream=1000, downstream=1000,

 group= c("./BAM/FILE/LOCATION/shammerge.bam","./BAM/FILE/LOCATION/unxmerge.bam ") )