

ATCA-seq QC using R package ATACseqQC

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Abstract

ATCA-seq QC using R package ATACseqQC

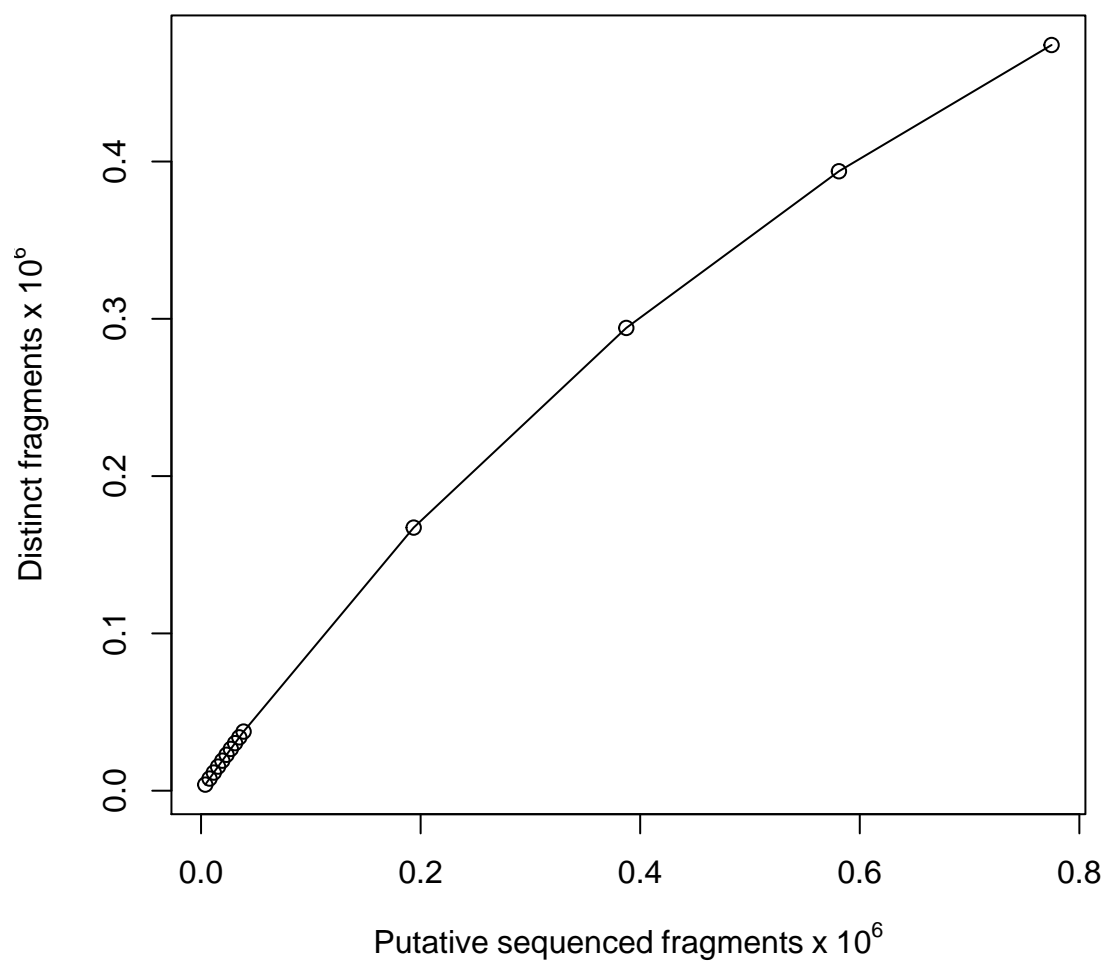
```
## test
bamfile <- system.file("extdata", "GL1.bam", package="ATACseqQC", mustWork=TRUE)
bamfile.labels <- gsub(".bam", "", basename(bamfile))
pdf("fragsize.pdf")
fragSizeDist(bamfile, bamfile.labels)
dev.off()
```

```
## pdf
## 2
```

Estimate the library complexity

```
#bamQC(bamfile, outPath=NULL)
estimateLibComplexity(readsDupFreq(bamfile))
```

Estimation of ATAC-seq library complexity



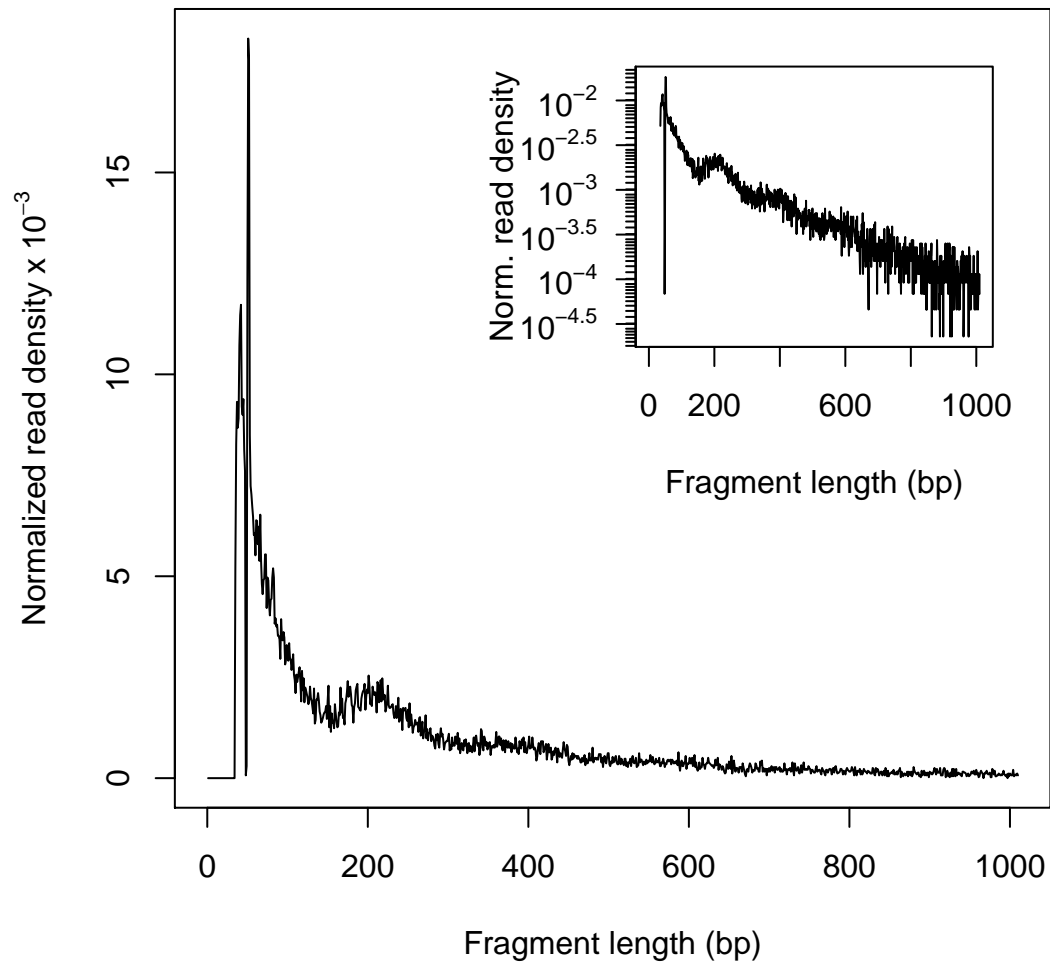
fragment size/insert length

```
# setwd("/home/dic/bassing_lab/users/dic/ATAC-seq/workflow/")
## input is bamFile
#bamfile <- list.files(path="./STAR_align_filter", pattern=glob2rx("ctrlA.rmBList.bam$"), full.names=TRUE)
# bamfile <- snakemake@input[["rmBList"]]
# bamfile.labels <- sub(".rmBList.bam", "", basename(bamfile))
#
# ## generate fragment size distribution
# pdf(snakemake@output[["fragsize"]])
# fragSizeDist(bamfile, bamfile.labels)
# dev.off()

## test
bamfile <- system.file("extdata", "GL1.bam", package="ATACseqQC", mustWork=TRUE)
```

```
bamfile.labels <- gsub(".bam", "", basename(bamfile))  
# pdf("fragsize.pdf")  
fragSizeDist(bamfile, bamfile.labels)
```

GL1 fragment sizes



```
# dev.off()
```