

PRIMR vignette

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2023-12-15

This vignette explain how to use PRIMR

Overview

1. runPRIMR
2. Genreate Counts Matrix

Load PRIMR

```
library(PRIMR)

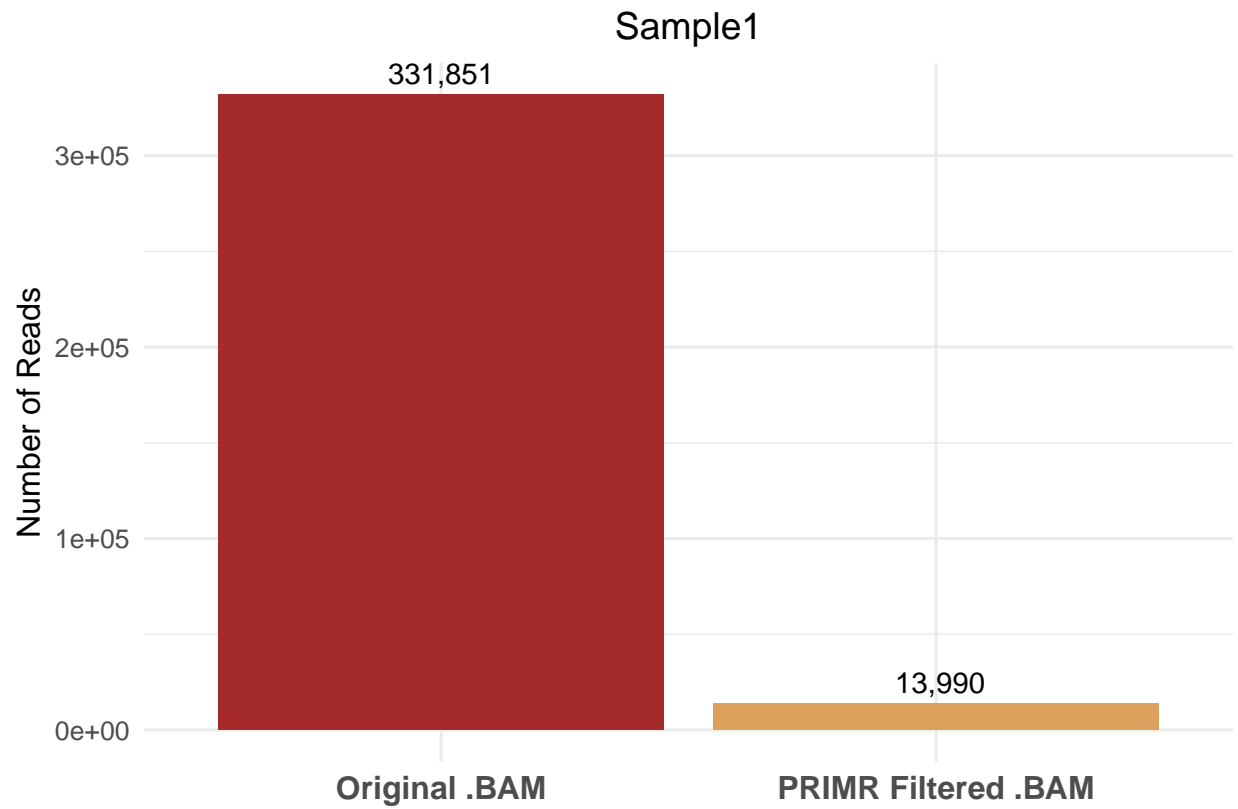
library(dplyr)
library(reshape2)
library(ggplot2)
```

Inputs

```
out='/gpfs/commons/home/tbotella/missionbio/primr_package/data'
bamfile='/gpfs/commons/home/tbotella/missionbio/primr_package/data/datatest.bam'
ampfile='/gpfs/commons/home/tbotella/missionbio/primr_package/data/ampliconsPanel.txt'
sample.id='Sample1'
nthreads=40
```

runPRIMR

```
runPRIMR(out=out, bamfile=bamfile, ampfile=ampfile,sample.id=sample.id,nthreads=nthreads)
#> Saving 6.5 x 4.5 in image
```



countReads

```
qnames.path=paste0(out,'/',sample.id,'/filtered_qnames/qnames_',sample.id,'.txt')
format='seurat'

countReads(out=out, qnames.path=qnames.path, sample.id=sample.id, format=format)
#> [1] "----SAVING COUNTS MATRIX----
```