

PRIMR vignette

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This vignette explain how to use PRIMR

Overview

1. runPRIMR
2. Genreate Counts Matrix

Load PRIMR

```
library(PRIMR)
#>
#>  _ _ )  _ _ )  |  | \ / |  _ _ )
#>  |      |  \  |  |  |  |  \
#>

library(dplyr)
#> Warning: package 'dplyr' was built under R version 4.3.2
#>
#> Attaching package: 'dplyr'
#> The following objects are masked from 'package:stats':
#>
#>     filter, lag
#> The following objects are masked from 'package:base':
#>
#>     intersect, setdiff, setequal, union
library(reshape2)
#> Warning: package 'reshape2' was built under R version 4.3.2
library(ggplot2)
#> Warning: package 'ggplot2' was built under R version 4.3.2
#> Want to understand how all the pieces fit together? Read R for Data
#> Science: https://r4ds.had.co.nz/
```

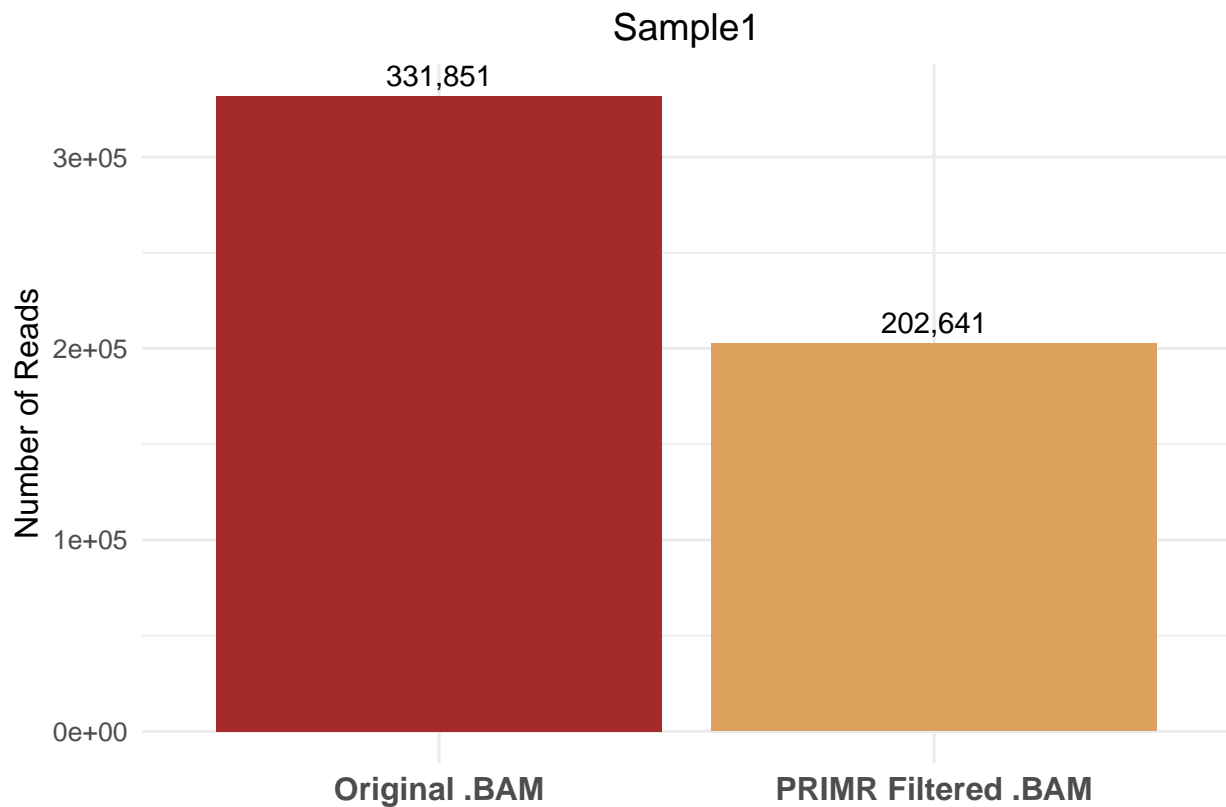
Inputs

```
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_all.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----"
```