

*This program uses a fastq sub sample of 500 reads. The original sequence file comes from Arabidopsis thaliana-Accession number SRR1971253. It contains DNA from leaf tissues sequenced on Illumina HiSeq 2000 which are single-read sequences with 50 base pairs length.*

```
> # load ShortRead
> library(ShortRead)
>
> # print fqsample
> fqsample
class: ShortReadQ
length: 500 reads; width: 50 cycles
>
> # class of fqsample
> class(fqsample)
[1] "ShortReadQ"
attr(,"package")
[1] "ShortRead"
>
> # class sread fqsample
> class(sread(fqsample))
[1] "DNASTringSet"
attr(,"package")
[1] "Biostrings"
>
> # id fqsample
> id(fqsample)
A BStringSet instance of length 500
width seq
[1] 63 SRR1971253.55828 HS2:546:C4DUWACXX:3:2310:19006:63818 length=50
[2] 63 SRR1971253.37947 HS2:546:C4DUWACXX:3:2113:13109:84610 length=50
[3] 62 SRR1971253.15442 HS2:546:C4DUWACXX:3:1210:6648:68689 length=50
[4] 62 SRR1971253.31075 HS2:546:C4DUWACXX:3:2102:9495:71119 length=50
[5] 62 SRR1971253.4534 HS2:546:C4DUWACXX:3:1109:10996:45700 length=50
... ..
[496] 63 SRR1971253.43593 HS2:546:C4DUWACXX:3:2207:12387:52082 length=50
[497] 63 SRR1971253.59528 HS2:546:C4DUWACXX:3:2315:19766:42624 length=50
[498] 62 SRR1971253.27308 HS2:546:C4DUWACXX:3:1313:3461:13904 length=50
[499] 62 SRR1971253.37657 HS2:546:C4DUWACXX:3:2113:7202:45293 length=50
[500] 62 SRR1971253.45211 HS2:546:C4DUWACXX:3:2210:7640:18421 length=50
>
```