

```

> # Load the yeast genome
> library(BSgenome.Scerevisiae.UCSC.sacCer3)
>
> # Assign data to the yeastGenome object
> yeastGenome <- BSgenome.Scerevisiae.UCSC.sacCer3
>
> # Get the first 30 bases of each chromosome
> getSeq(yeastGenome, end = 30)
A DNAStringSet instance of length 17
  width seq                      names
[1] 30 CCACACCACACCCACACACCCACACACCAC        chrI
[2] 30 AAATAGCCCTCATGTACGTCTCCTCCAAGC        chrII
[3] 30 CCCACACACCACACCCACACCACACCCACA        chrIII
[4] 30 ACACCACACCCACACCACACCCACACACAC        chrIV
[5] 30 CGTCTCCTCCAAGCCCTGTTGTCTCTTACC        chrV
... ..
[13] 30 CCACACACACACCACACCCACACCACACCC        chrXIII
[14] 30 CCGGCTTTCTGACCGAAATTAATAAAAAAAAAA        chrXIV
[15] 30 ACACCACACCCACACCACACCCACACCCAC        chrXV
[16] 30 AAATAGCCCTCATGTACGTCTCCTCCAAGC        chrXVI
[17] 30 TTCATAATTAATTTTTTATATATATATTAT        chrM

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