

```
# Create zikv with one collated sequence using `zikaVirus`
> zikv <- unlist(zikaVirus)
>
> # Check the length of zikaVirus and zikv
> length(zikaVirus)
[1] 1
> length(zikv)
[1] 10794
>
> # Check the width of zikaVirus
> width(zikaVirus)
[1] 10794
>
> # Subset zikv to only the first 30 bases
> subZikv <- subseq(zikv, end = 30)
> subZikv
  30-letter "DNAStrng" instance
seq: AGTTGTTGATCTGTGTGAGTCAGACTGCGA
```