```
##myStartFilter <- srFilter(function(x) substr(sread(x), 1, 5) ==
"ATGCA") This filter is being used to find reads that start with the
pattern "ATGCA" ######
```

> # Load package ShortRead
> library(ShortRead)
>
> # Check class of fqsample
> class(fqsample)
[1] "ShortReadQ"
attr(,"package")
[1] "ShortRead"
>
> # Filter reads into selectedReads using myStartFilter
> selectedReads <- fqsample[myStartFilter(fqsample)]
>
> # Check class of selectedReads
> class(selectedReads)
[1] "ShortReadQ"
attr(,"package")
[1] "ShortRead"
>
> # Check detail of selectedReads
> detail(selectedReads)
class: ShortReadQ

sread:
  A DNAStringSet instance of length 3
    width seq
[1]   50 ATGCAAGGCCAAGCCGCAGGGGTAATGGAATCTGCTAAGAAGATAGCTGA
[2]   50 ATGCAACTCTCATCCCTGACCGCAGGTGCTGATGATGACGCTGCTGTGGT
[3]   50 ATGCAGCTGGCCCAGGCACAAGCGCTCGAACGTTCGCGCCTGGATGCCGA

id:
  A BStringSet instance of length 3
    width seq
[1]   63 SRR1971253.18049 HS2:546:C4DUWACXX:3:1214:14671:38665 length=50
[2]   63 SRR1971253.43489 HS2:546:C4DUWACXX:3:2207:20237:31567 length=50
[3]   63 SRR1971253.43593 HS2:546:C4DUWACXX:3:2207:12387:52082 length=50
class: FastqQuality
quality:

A BStringSet instance of length 3

    width seq
[1]   50 @@CFFFFDFFDHFBHEGIHIBGCFHIIIIDIGHHGIEIIEGDHGEECFG9
[2]   50 CCCFFFFFHHHHHIJJJJJJJJJJIJFHIIJJJJJJJIGIJJIJJIIJJF
[3]   50 CCCFFFFFHHHHHJJJJJJJJGGHIIIIJJJJJJJJJJIJJJJJJJHHHF