

```

> library(GenomicRanges)
>
> # print df
> seq_intervals
  seqnames start end
1  chrI   11  36
2  chrI   12  37
3  chrII  13  38
4  chrII  14  39
>
> # create myGR
> myGR <- as(seq_intervals, "GRanges")
>
> # print myGR
> myGR
GRanges object with 4 ranges and 0 metadata columns:
  seqnames  ranges strand
   <Rle> <IRanges> <Rle>
[1]  chrI  [11, 36]  *
[2]  chrI  [12, 37]  *
[3] chrII [13, 38]  *
[4] chrII [14, 39]  *
-----
seqinfo: 2 sequences from an unspecified genome; no seqlengths

```