

```
# Load Package Genomic Ranges
> library(GenomicRanges)
>
> # Print the GRanges object myGR
> myGR
```

An object of class "GRanges"

Slot "seqnames":

factor-Rle of length 8 with 3 runs

Lengths: 3 3 2

Values : chr1 chr2 chr3

Levels(3): chr1 chr2 chr3

Slot "ranges":

IRanges object with 8 ranges and 0 metadata columns:

	start	end	width
	<integer>	<integer>	<integer>
a	10	19	10
b	20	29	10
c	30	39	10
d	40	49	10
e	50	59	10
f	60	69	10
g	70	79	10
h	80	89	10

Slot "strand":

factor-Rle of length 8 with 4 runs

Lengths: 1 2 2 3

Values : - + \* +

Levels(3): + - \*

Slot "elementMetadata":

DataFrame with 8 rows and 2 columns

	score	GC
	<numeric>	<numeric>
1	1	1.000
2	15	0.857
3	29	0.714
4	43	0.571
5	58	0.429
6	72	0.286
7	86	0.143
8	100	0.000

Slot "seqinfo":

Seqinfo object with 3 sequences from an unspecified genome:

```
seqnames seqlengths isCircular genome
```

```
chr1      100      NA <NA>
```

```
chr2      150      NA <NA>
```

```
chr3      300      NA <NA>
```

Slot "metadata":

```
list()
```

```
>
```

```
> # Check the metadata, if any
```

```
> mcols(myGR)
```

DataFrame with 8 rows and 2 columns

```
score    GC
```

```
<numeric> <numeric>
```

```
1      1  1.000
```

```
2     15  0.857
```

```
3     29  0.714
```

```
4     43  0.571
```

```
5     58  0.429
```

```
6     72  0.286
```

```
7     86  0.143
```

```
8    100  0.000
```