

Compute coverage

```
bedtools genomecov -i a.bam  
-bga
```

Select zero runs

```
awk '$4 == 0'
```

Find intersection with regions

```
bedtools intersect -a b.bed -a  
-
```

```
coverage("a.bam") %>% GRanges()
```

```
subset(score > 0)
```

```
intersect(import("b.bed"))
```