

```
A library(plyranges)
gwas <- read_bed('snps.bed')
exons <- read_bed('exons.bed')
res <- exons %>%
  join_overlap_inner(snps) %>%
  group_by(rsID) %>%
  summarise(n = n_distinct(exonID))
```

```
B library(GenomicRanges)
library(rtracklayer)
gwas <- import('snps.bed')
exons <- import('exons.bed')
hits <- findOverlaps(exons, gwas,
  ignore.strand = FALSE)
olap <- splitAsList(exons$name[queryHits(hits)],
  gwas$name[subjectHits(hits)])
n <- lengths(unique(olap))
res <- DataFrame(rsID = names(n),
  n = as.integer(n))
```