

# Visulization

## Contents

<b>1</b>	<b>Introduction</b>	<b>2</b>
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# 1 Introduction

As an example, let's visualize two neighboring genes of interest in asthma genomics.

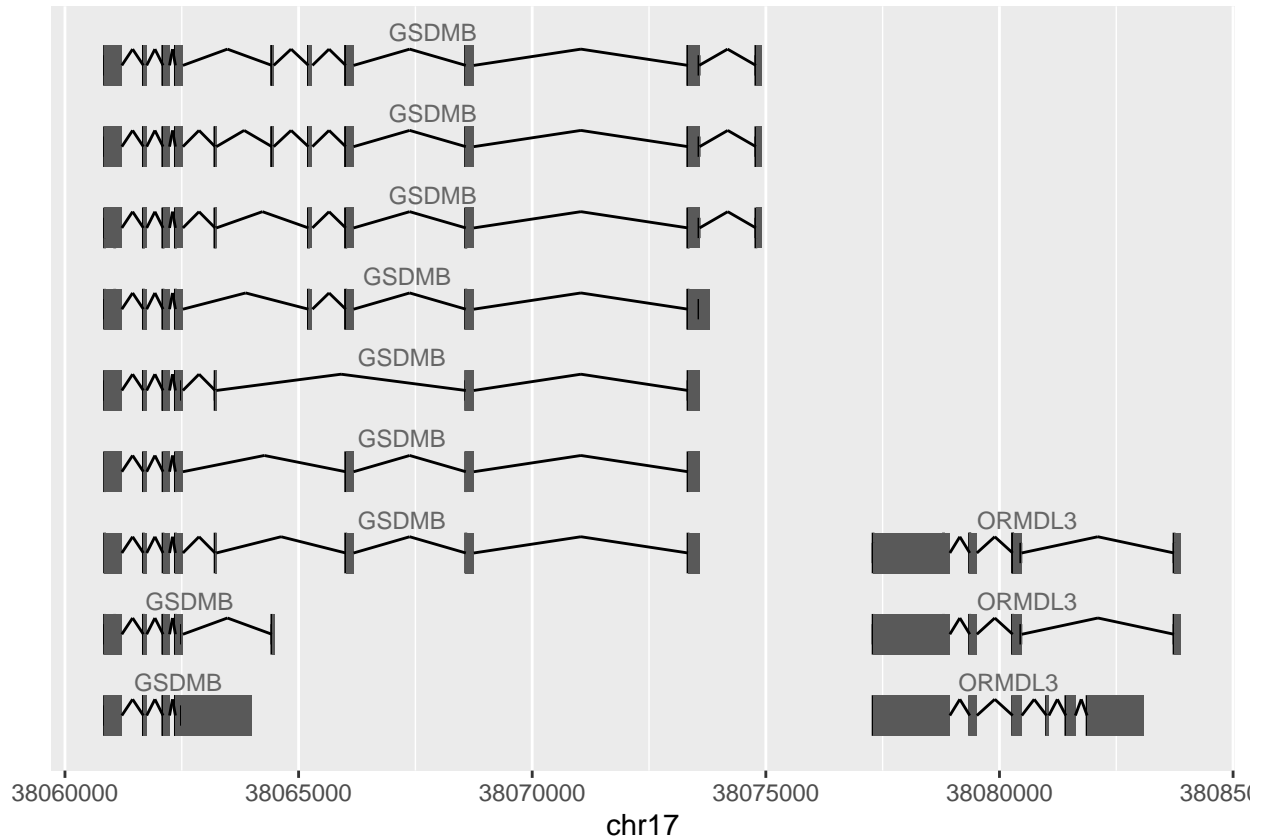
```
# Import packages
library(ggbio)
library(Homo.sapiens)
library(biovizBase)

# Import data and check it
data(genesymbol)
head(genesymbol)

## GRanges object with 6 ranges and 2 metadata columns:
##           seqnames           ranges strand |           symbol           ensembl_id
##           <Rle>             <IRanges> <Rle> | <character>         <character>
##   A1BG      chr19 58858174-58864865      - |      A1BG ENSG00000121410
##   A2M      chr12  9220304-9268558      - |      A2M ENSG00000175899
##   NAT1      chr8 18027971-18081197      + |      NAT1 ENSG00000171428
##   NAT1      chr8 18067618-18081197      + |      NAT1 ENSG00000171428
##   NAT1      chr8 18079177-18081197      + |      NAT1 ENSG00000171428
##   NAT2      chr8 18248755-18258723      + |      NAT2 ENSG00000156006
##   -----
##   seqinfo: 45 sequences from an unspecified genome; no seqlengths

# Obtain GRanges for two specific genes
oo = genesymbol[c("ORMDL3", "GSDMB")]

# Plot using the Homo.sapiens package as the reference
ap1 = autoplot(Homo.sapiens, which = oo, gap.geom = "chevron")
attr(ap1, "hasAxis") = TRUE
ap1 + xlab("chr17")
```



As another example, we obtain the GRanges for a different gene and use that to subset the ESRRA binding sites.

```
# Import packages
```

```
library(ERBS)
```

```
# Import data and check it
```

```
data(GM12878)
```

```
head(GM12878)
```

```
## GRanges object with 6 ranges and 7 metadata columns:
```

```
##      seqnames      ranges strand |      name      score      col
##      <Rle>        <IRanges> <Rle> | <numeric> <integer> <logical>
## [1]   chrX    1509355-1512462   * |         5         0      <NA>
## [2]   chrX    26801422-26802448   * |         6         0      <NA>
## [3]  chr19    11694102-11695359   * |         1         0      <NA>
## [4]  chr19     4076893-4079276   * |         4         0      <NA>
## [5]   chr3    53288568-53290767   * |         9         0      <NA>
## [6]  chr17    77894658-77895923   * |        11         0      <NA>
##      signalValue    pValue    qValue      peak
##      <numeric> <numeric> <numeric> <integer>
## [1]      157.92     310.000         32      1991
## [2]      147.38     310.000         32       387
## [3]       99.71     311.660         32       861
## [4]       84.74     310.000         32     1508
## [5]       78.20     299.505         32     1772
## [6]       76.10     280.409         32       752
## -----
```

```
## seqinfo: 93 sequences (1 circular) from hg19 genome
# Obtain GRanges for the specific gene
p1 = genesymbol["ATP5D"]

# Plot using the Homo.sapiens package as the reference
ap2 = autoplot(Homo.sapiens, which = p1 + 5000, gap.geom = "chevron")
ap3 = autoplot(subsetByOverlaps(GM12878, p1 + 5000))
ch = as.character(seqnames(p1)[1])
tracks(`ESRRA BS` = ap3,
       TX = ap2,
       heights = c(1, 3))
```

