

Visualization

Contents

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
```

```
## -----
```

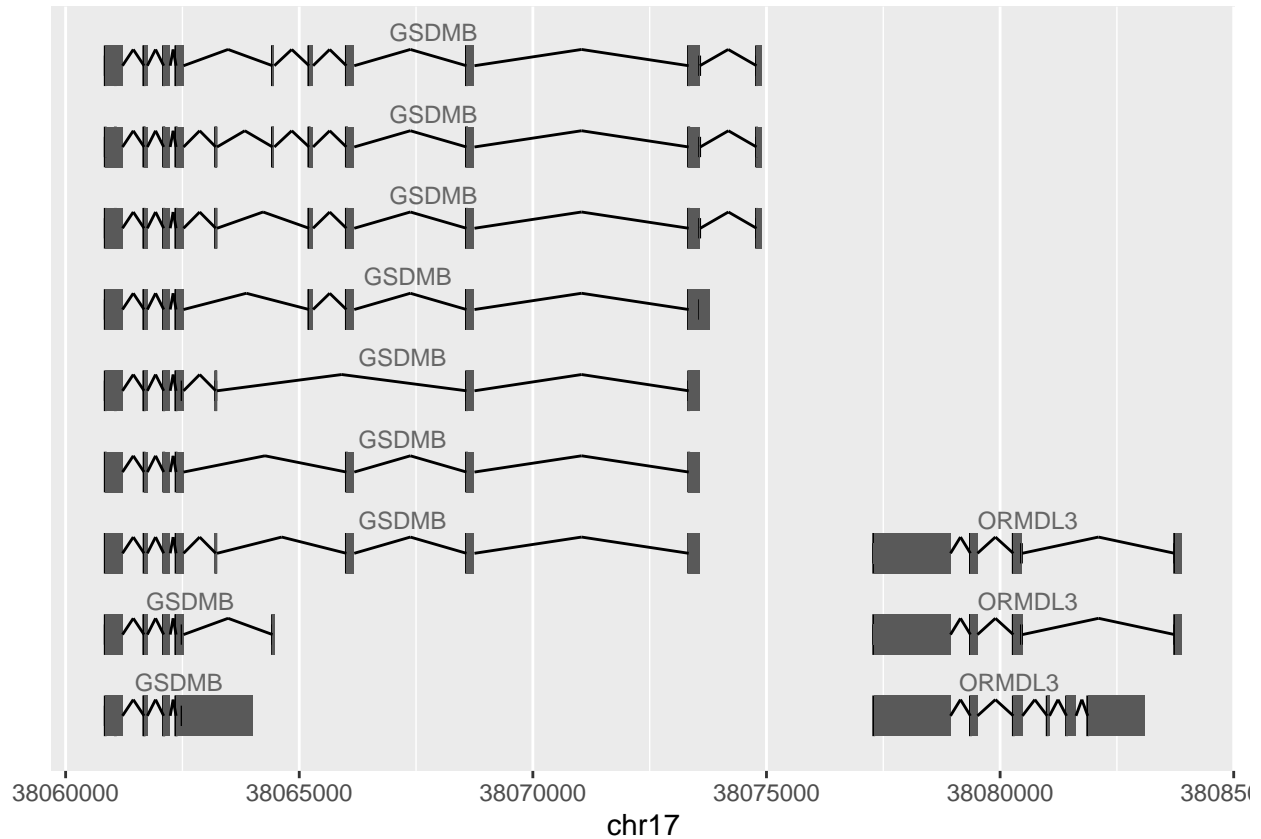
```
## seqinfo: 45 sequences from an unspecified genome; no seqlengths
```

```
# 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))
```

