Visualisation of alignment results

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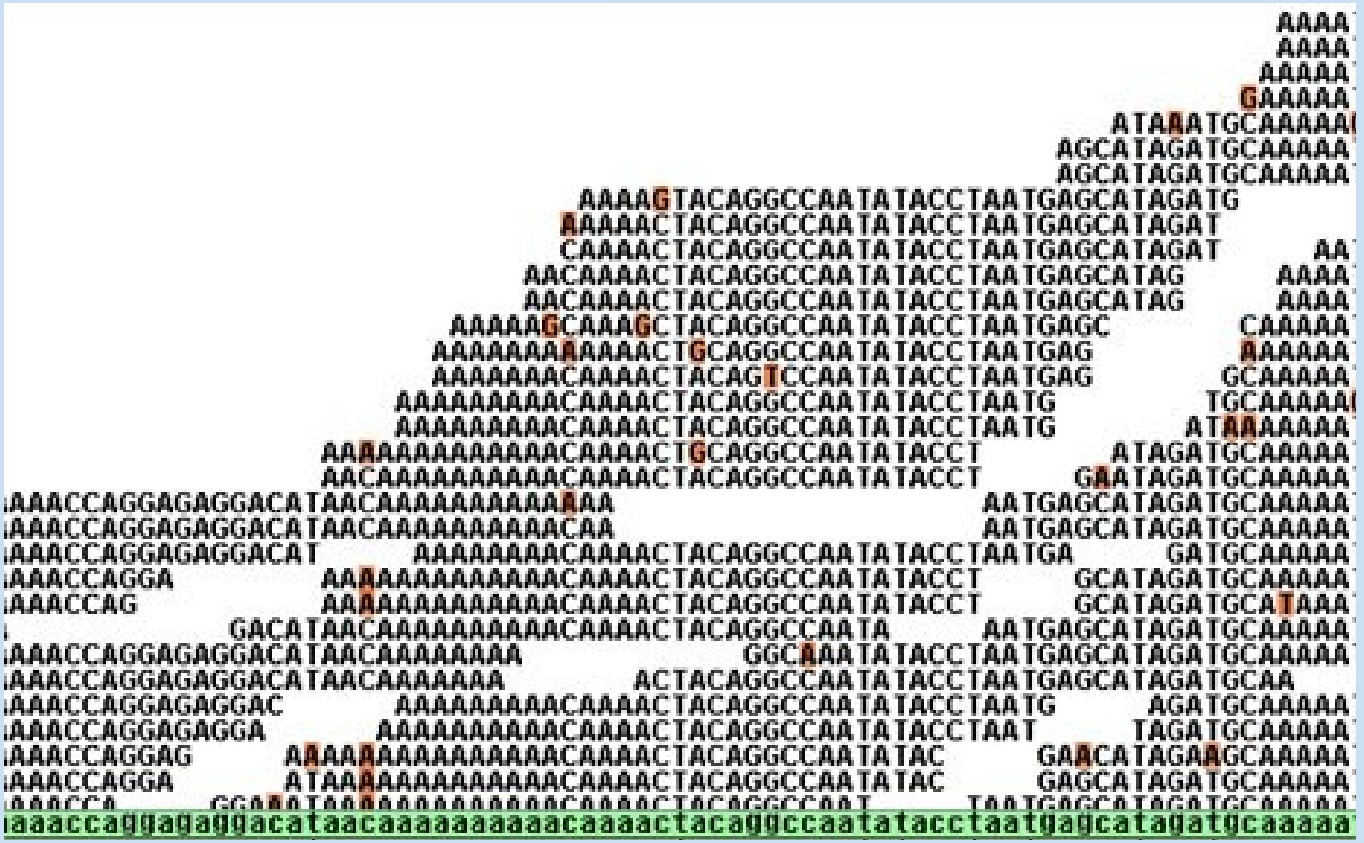
Alignment (1)

Alignment (2)

```
...ACTTTTACCGAACGTACGTACGTAGCTAGTCGATGCTAGCCGCA...
     TTTT  CGAA GTAC  ACGT GCTAG   GATG TAGC
      TTTA          CGTA GTAG       ATGC  GCCG
    CTTT                  TAGC        TGCT  CCGC
```

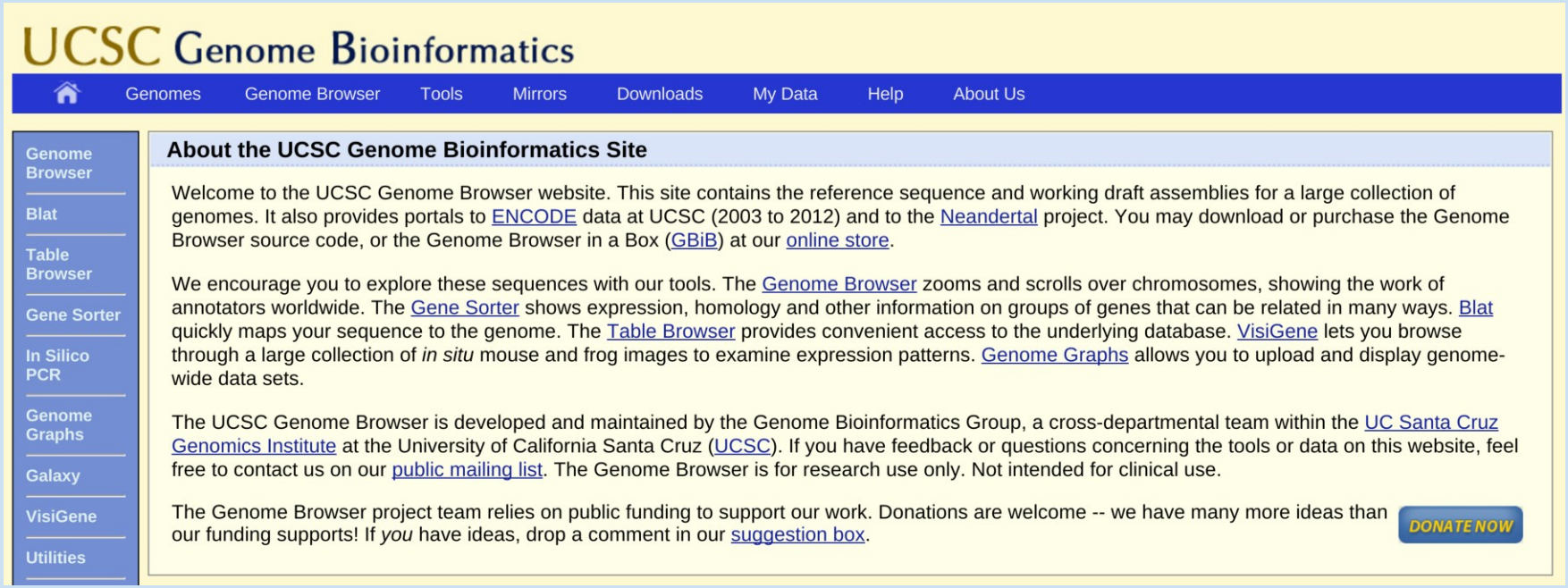
Alignment (3)



Need **efficient** ways to visualize alignment data.

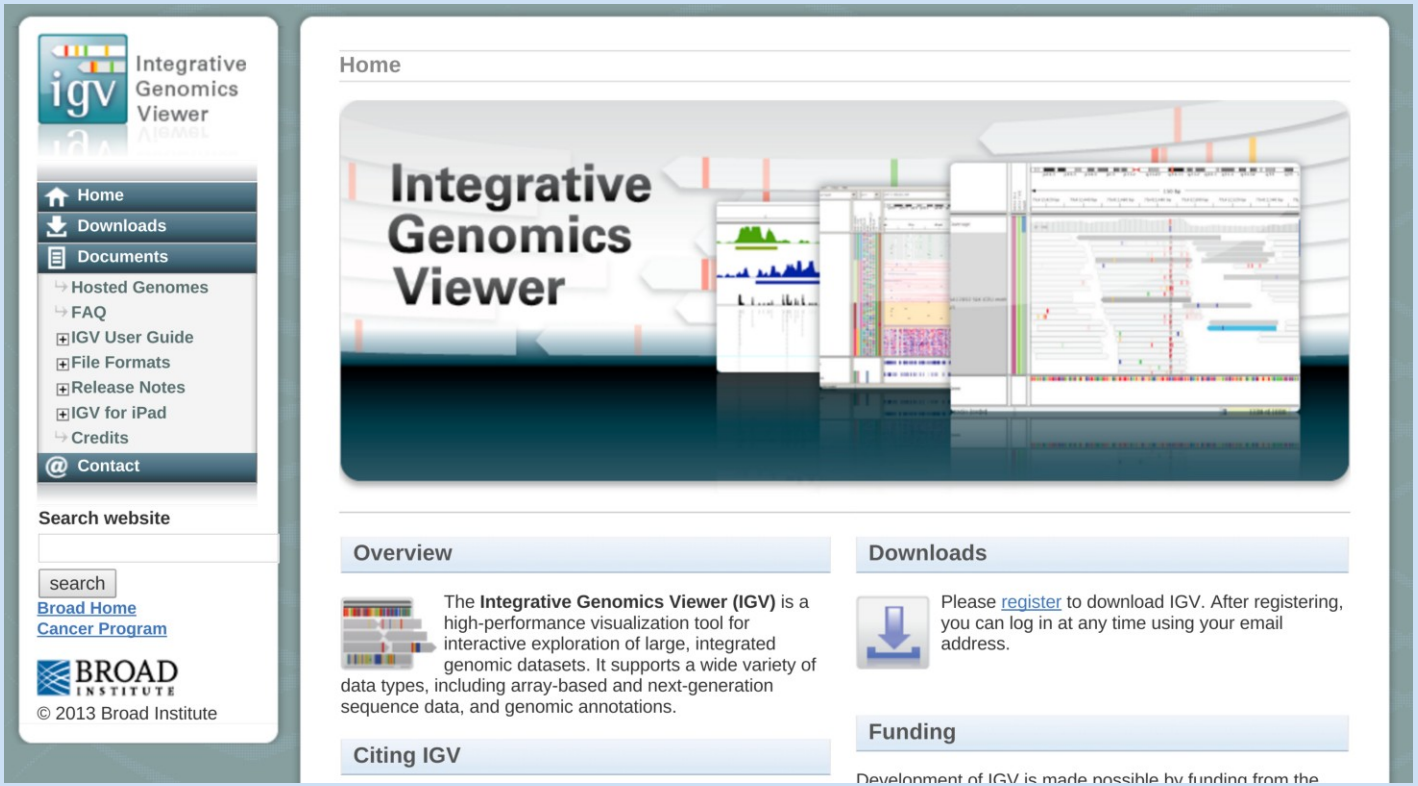
Genome browsers (1)

UCSC genome browser – interactive web service, https://genome-euro.ucsc.edu/index.html



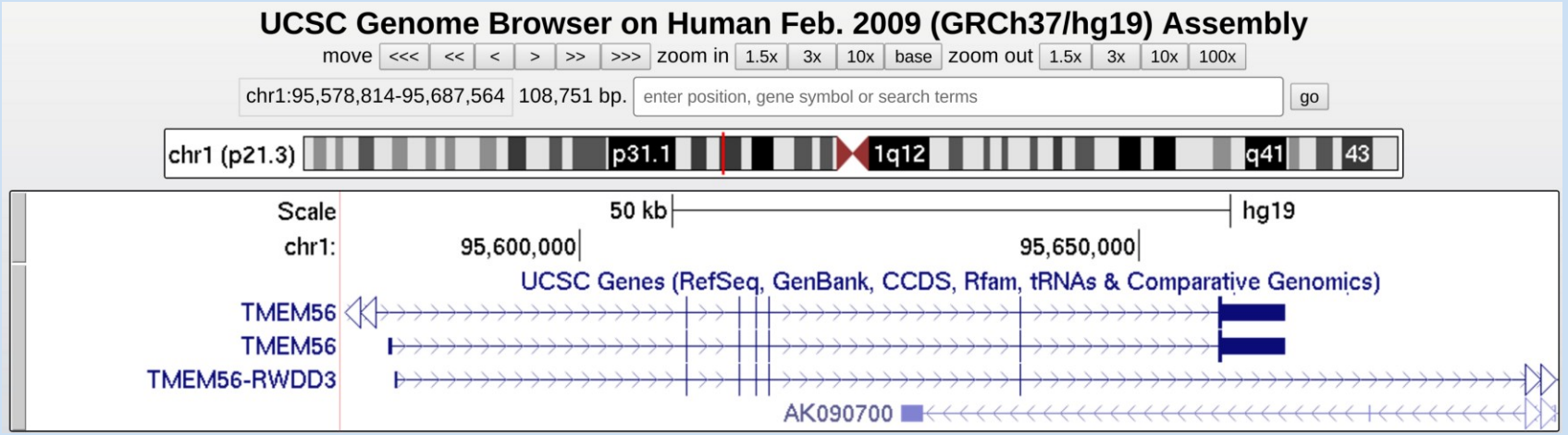
Genome browsers (2)

IGV – integrative genome viewer, to install locally
https://www.broadinstitute.org/igv/

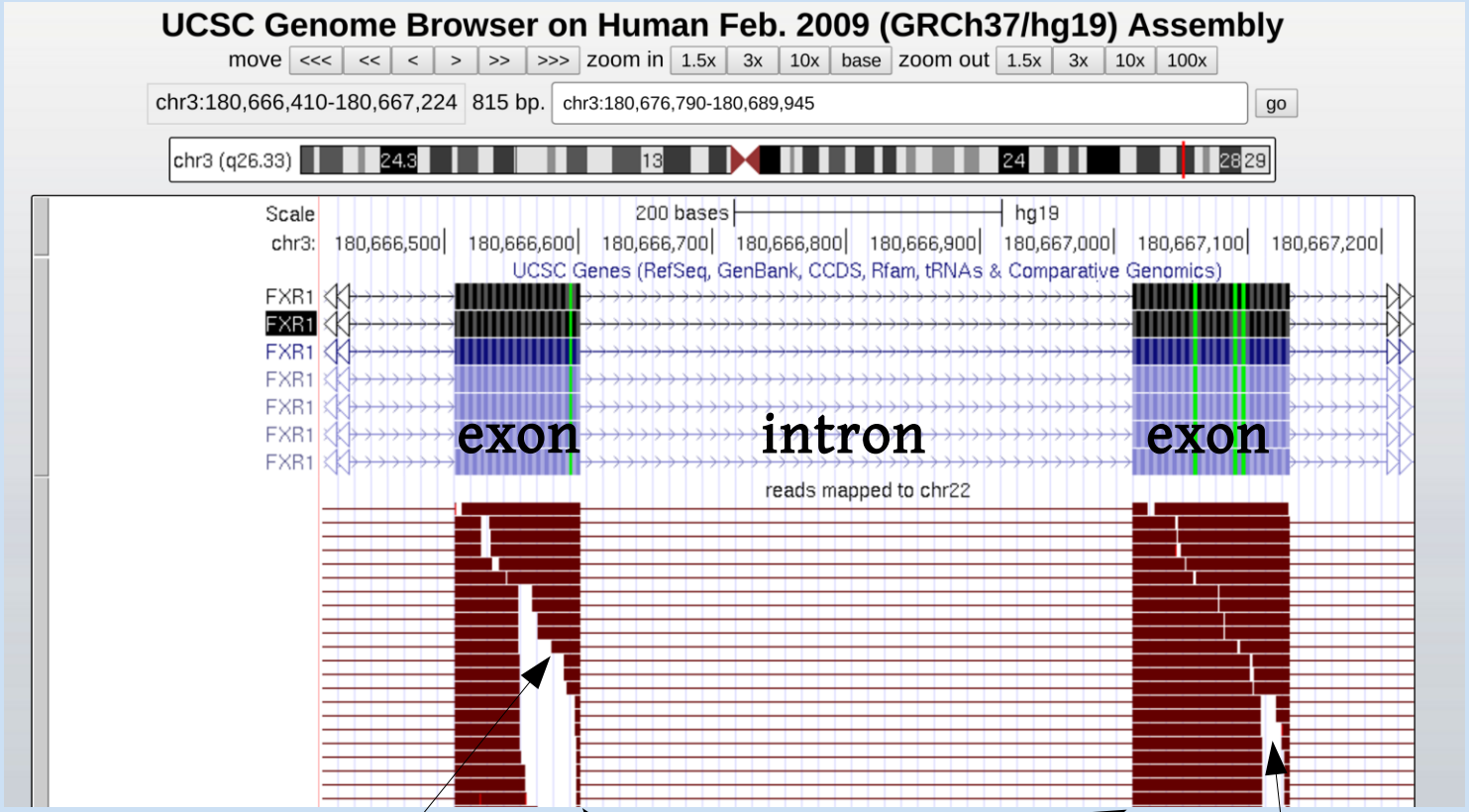


Genome browsers (3)

Concept – move around the genome to zoom-in on the areas of interest.



Visualizing BAM files (1)

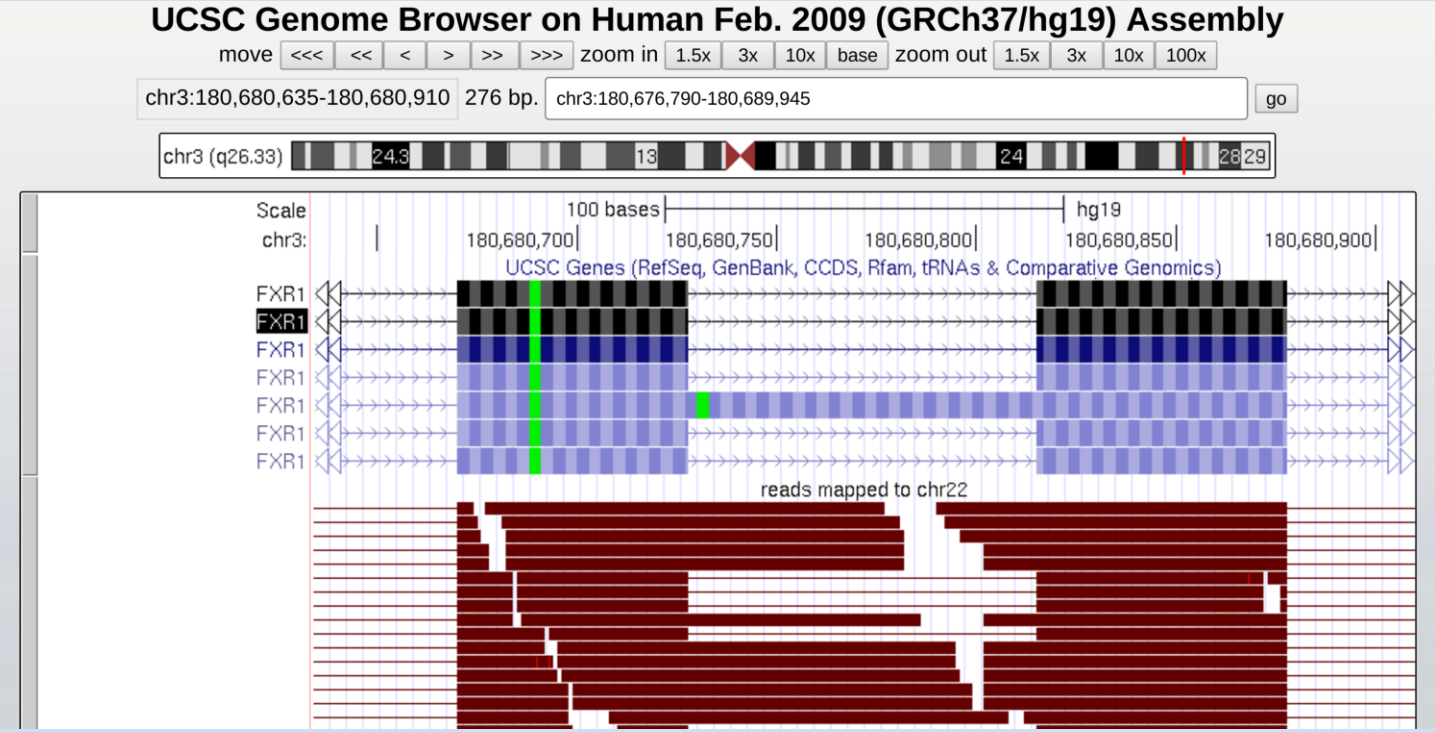


Part of a read mapped to an exon

Read was split here

Part of a read mapped to an exon

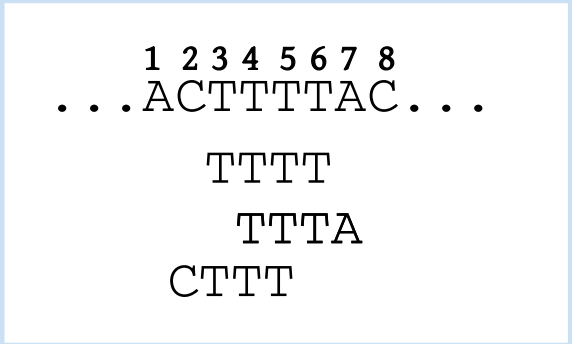
Visualizing BAM files (2)



Some reads fully map to this intron – indication of a splicing event called intron retention (which can also be seen in the annotation).

Wiggle and BigWig files

Wiggle file – per position, number of reads mapped to this position a.k.a. **coverage**.

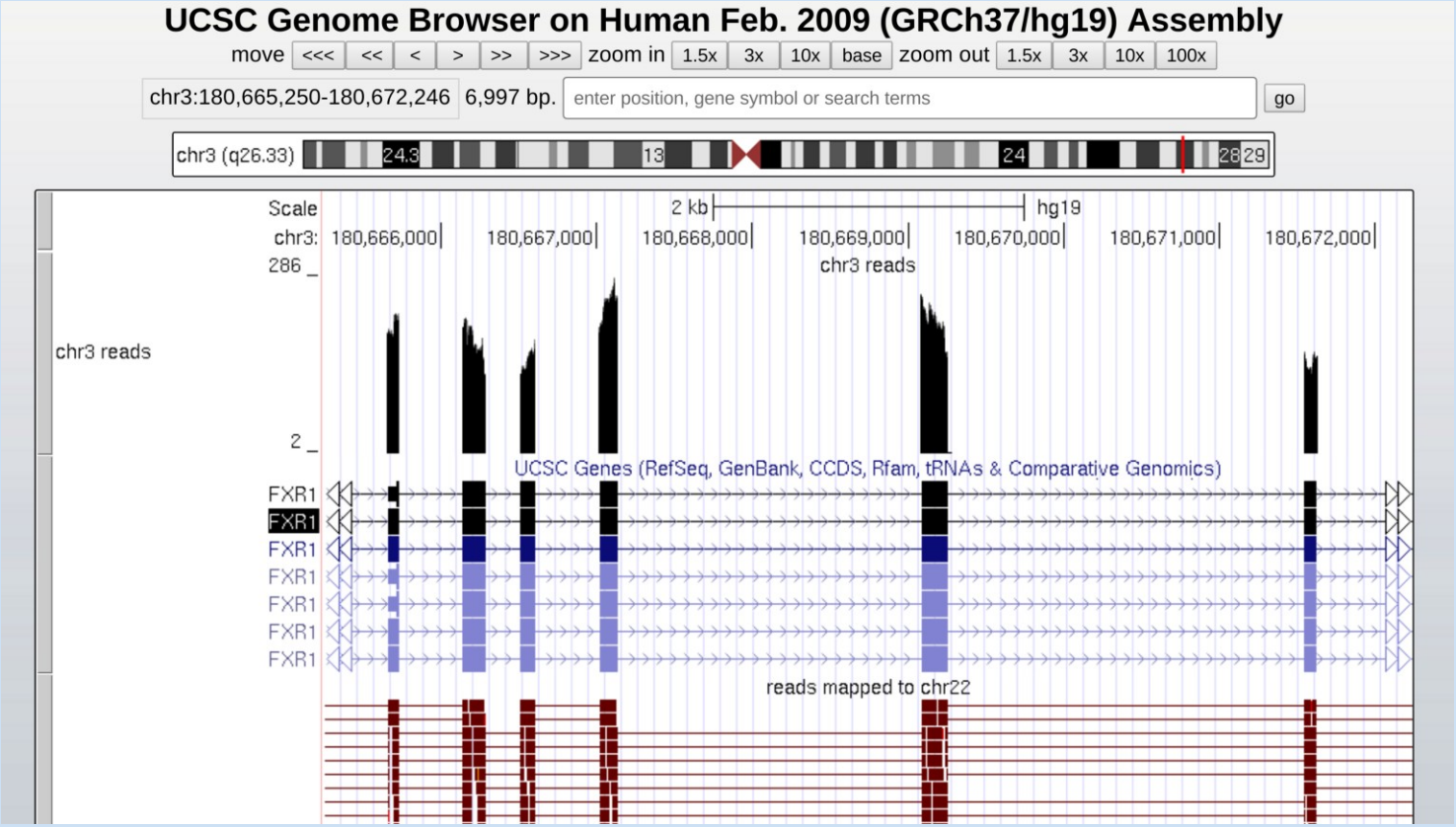


Wiggle file:

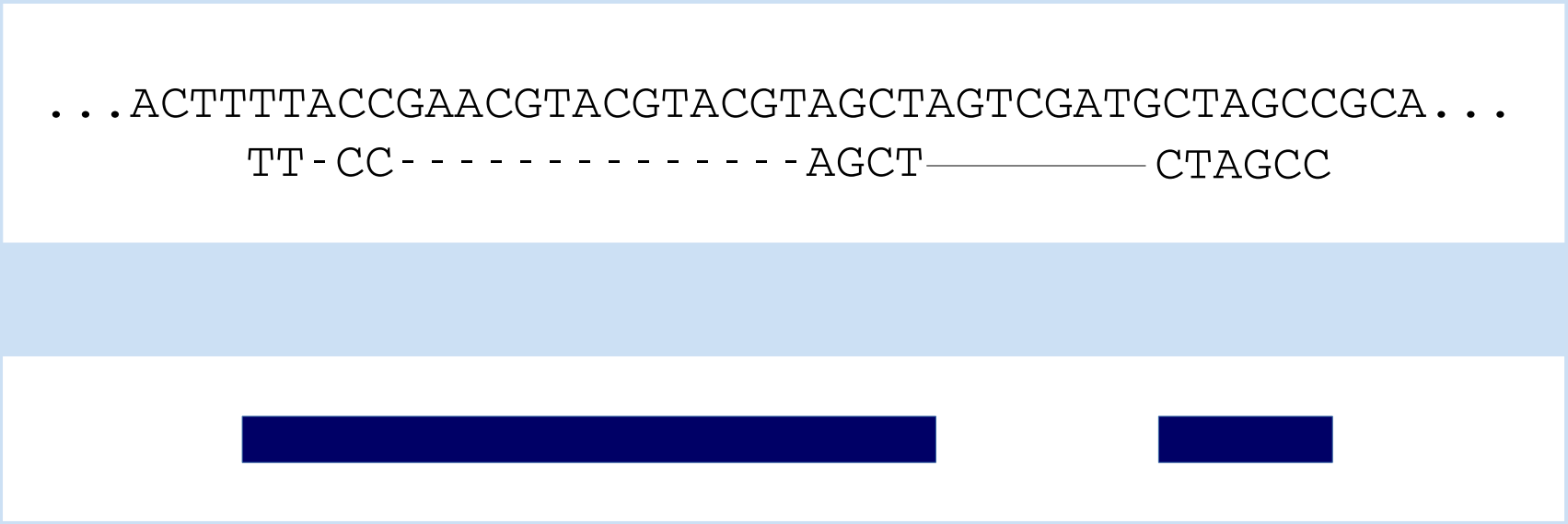
```
chromosome=chrN
1   0
2   1
3   2
4   3
5   4
6   2
7   1
8   0
...
```

BigWig – binary Wiggle file.

Visualising BigWig files

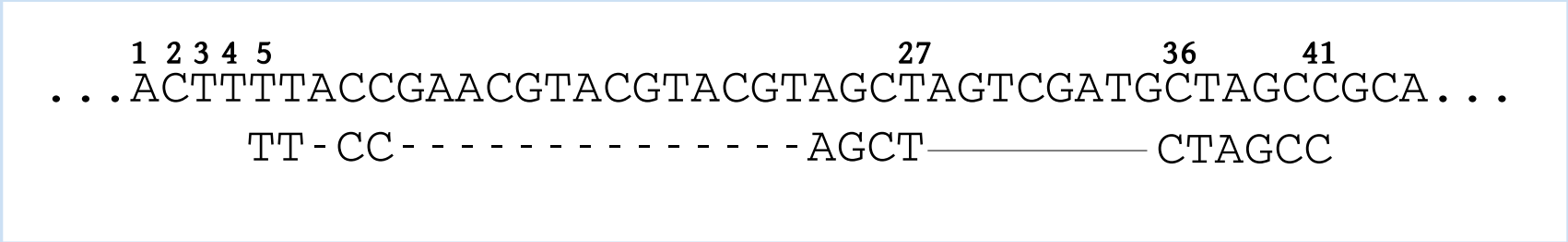


BED files



BED files are rarely used to visualise raw RNA-Seq data.

BED and BEDPE files



BAM

BED file:

```
chrN  5  27
chrN  36 41
```

BEDPE file:

```
chrN  5  27    chrN  36    41
```

BEDPE file retains the connection between ends, but is not supported by the majority of genome browsers.

Demo

https://genome-euro.ucsc.edu/cgi-bin/hgTracks?hgS_doOtherUser=submit&hgS_otherUserName=pulyakhina&hgS_otherUserSessionName=2016%2DRNAseq_course