1. Post-Alignment
    a. Select the sample and download the alignment report which shows mapping statistics of each fastq file within the sample.

    b. Configure settings and click the “View Bam Statistics” button to view aggregated mapping statistics of all the fastq files within the sample selected.

    c. The settings shown below act as a filter, reads which are filtered out are described as “excluded” reads in the charts.
    (note: In the screenshots below for alignment scores, alignment lengths & edit distance, there is no difference between the 2 graphs as all reads pass the default filter settings.)

    Example alignment report:
    https://github.com/paigerollex/gene_cloud_omics/blob/main/output_data/alignment_report.pdf

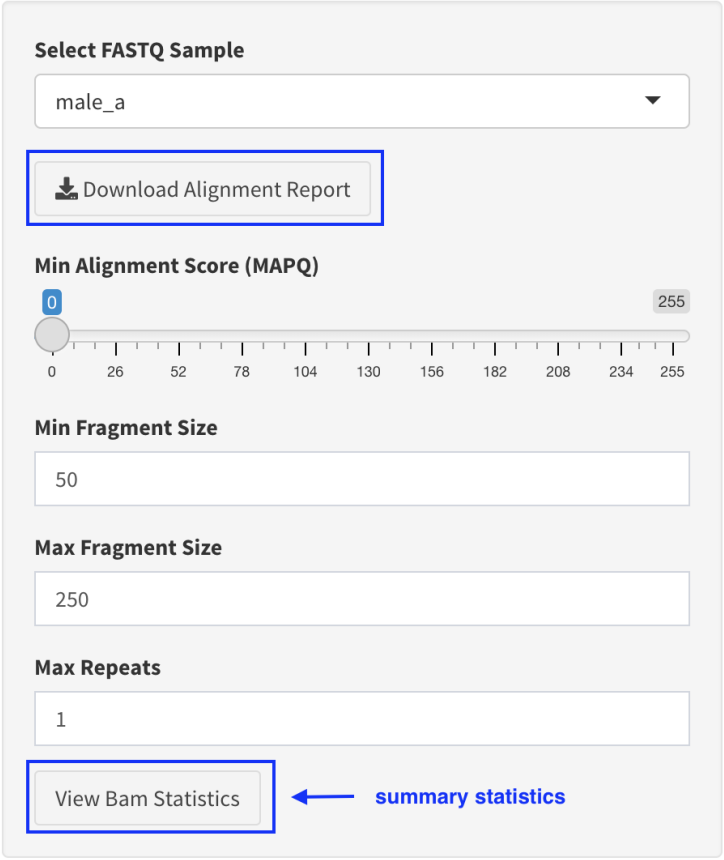


Fig 5.1: Plot settings

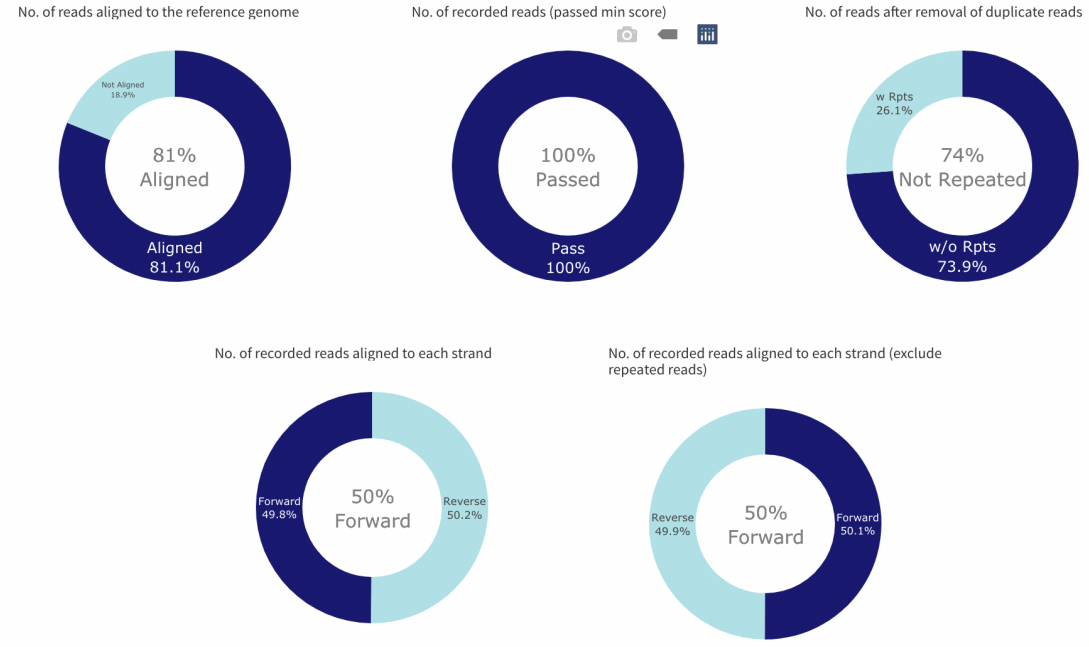


Fig 5.2: Reads aligned

Alignment Scores

```
Average alignment score, after filter: 60
Average alignment score, no filter: 60
```

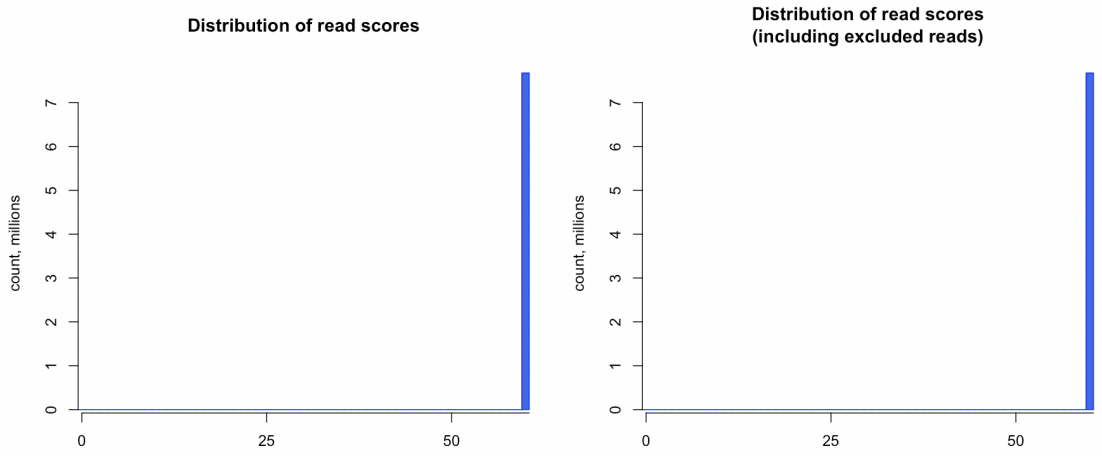


Fig 5.3: Alignment scores

Alignment Length

```
Average aligned length: 72
Average aligned length, no filter: 72
```

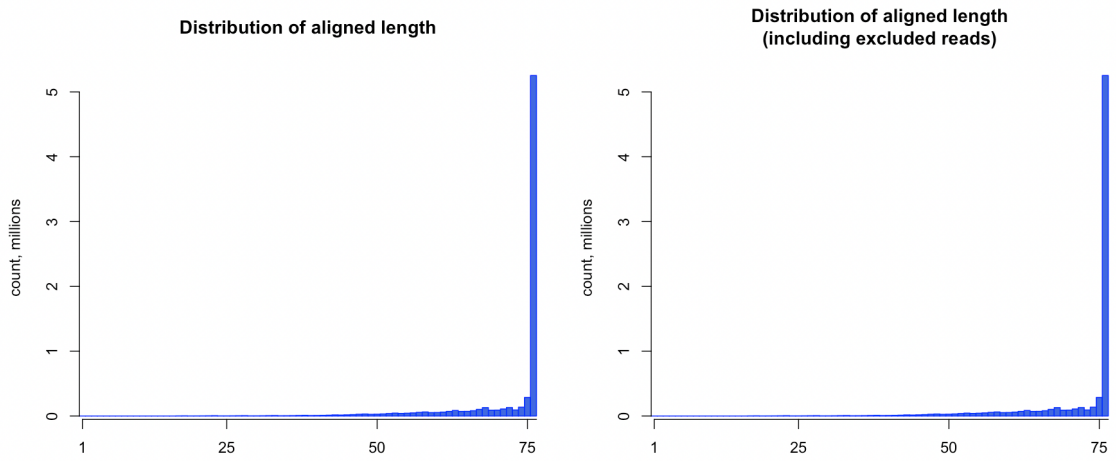


Fig 5.4: Alignment length

Edit Distance

```
Average edit distance, after filter: 0.249203492683443
Average edit distance, no filter: 0.249203492683443
```

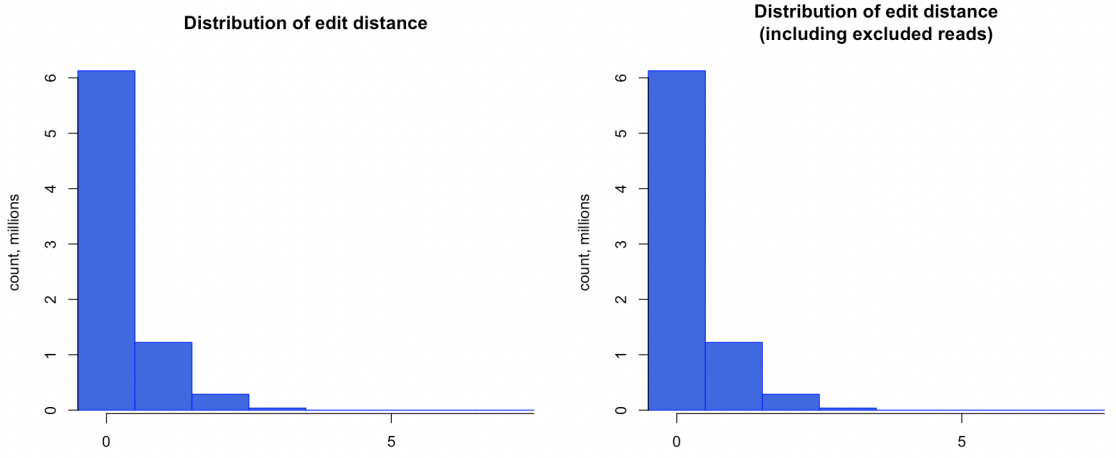


Fig 5.5: Edit distance

2. Genome Browser
    a. Select the sample to view coverage

    b. Select the chromosome from the gene annotation file and the range to plot. At times, some gene ids or transcripts ids of the coverage graph cannot be seen clearly, so you can extend the plot from the right or left.
    (note: Range to plot changes with the chromosome selected to plot)

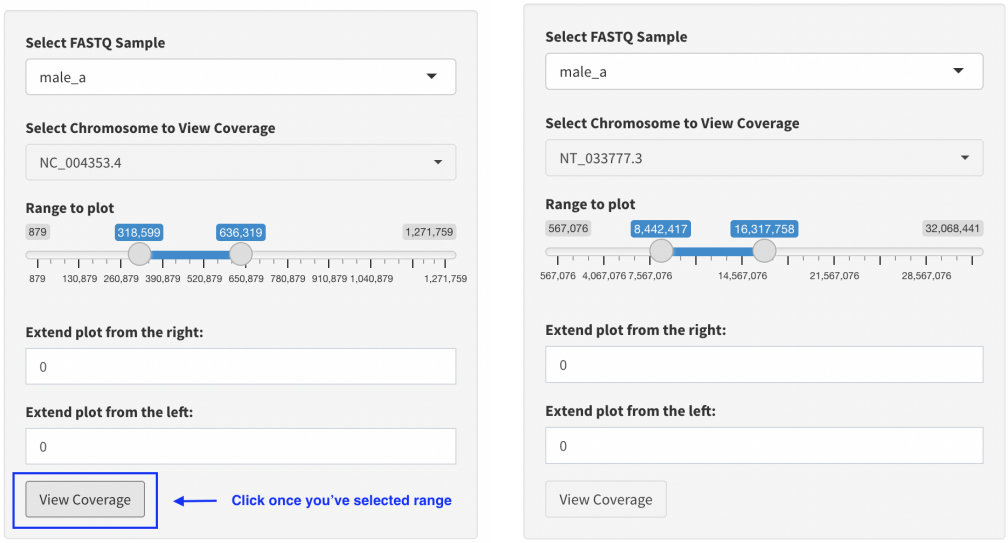
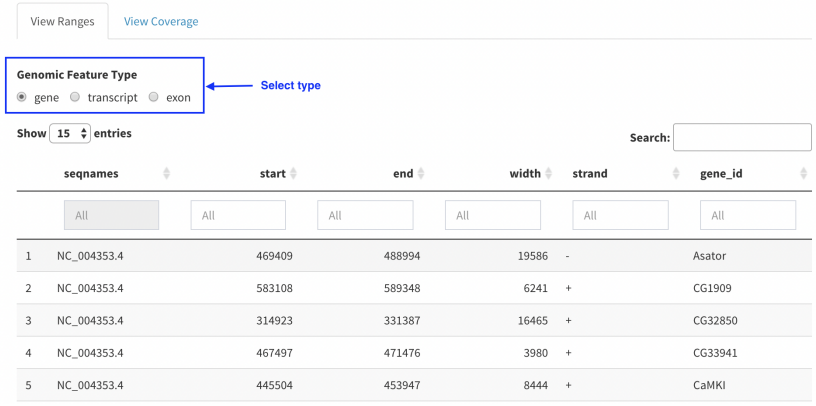


Fig 5.6: Ranges of different chromosomes

    c. Based on the selected chromosome and range to plot, you can view additional information about the genes, transcripts and exons plotted in the graph.



	seqnames	start	end	width	strand	gene_id
	All	All	All	All	All	All
1	NC_004353.4	469409	488994	19586	-	Asator
2	NC_004353.4	583108	589348	6241	+	CG1909
3	NC_004353.4	314923	331387	16465	+	CG32850
4	NC_004353.4	467497	471476	3980	+	CG33941
5	NC_004353.4	445504	453947	8444	+	CaMKI

Fig 5.7: Genes plotted

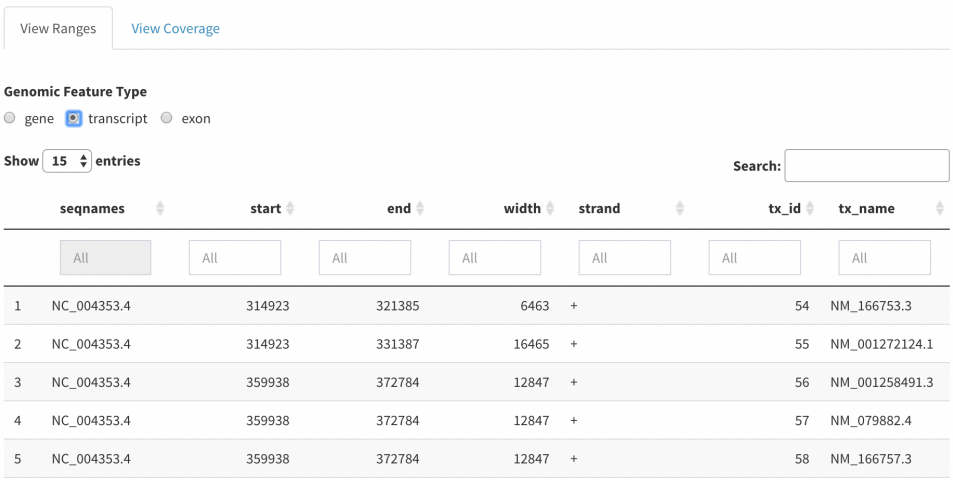


Fig 5.8: Transcripts plotted

d. Click “View Coverage” button

e. Coverage plot:
   i. On the left gray rectangle are fastq identifiers within the sample.

   ii. Empty transcript names in gene annotation file: coverage plot will only show genes within the selected range.
   (note: Often the case when downloading directly from NCBI)

   iii. No empty transcript names in gene annotation file: coverage plot will show both genes and transcripts within the selected range.
   (note: Often the case when downloading directly from Ensembl)

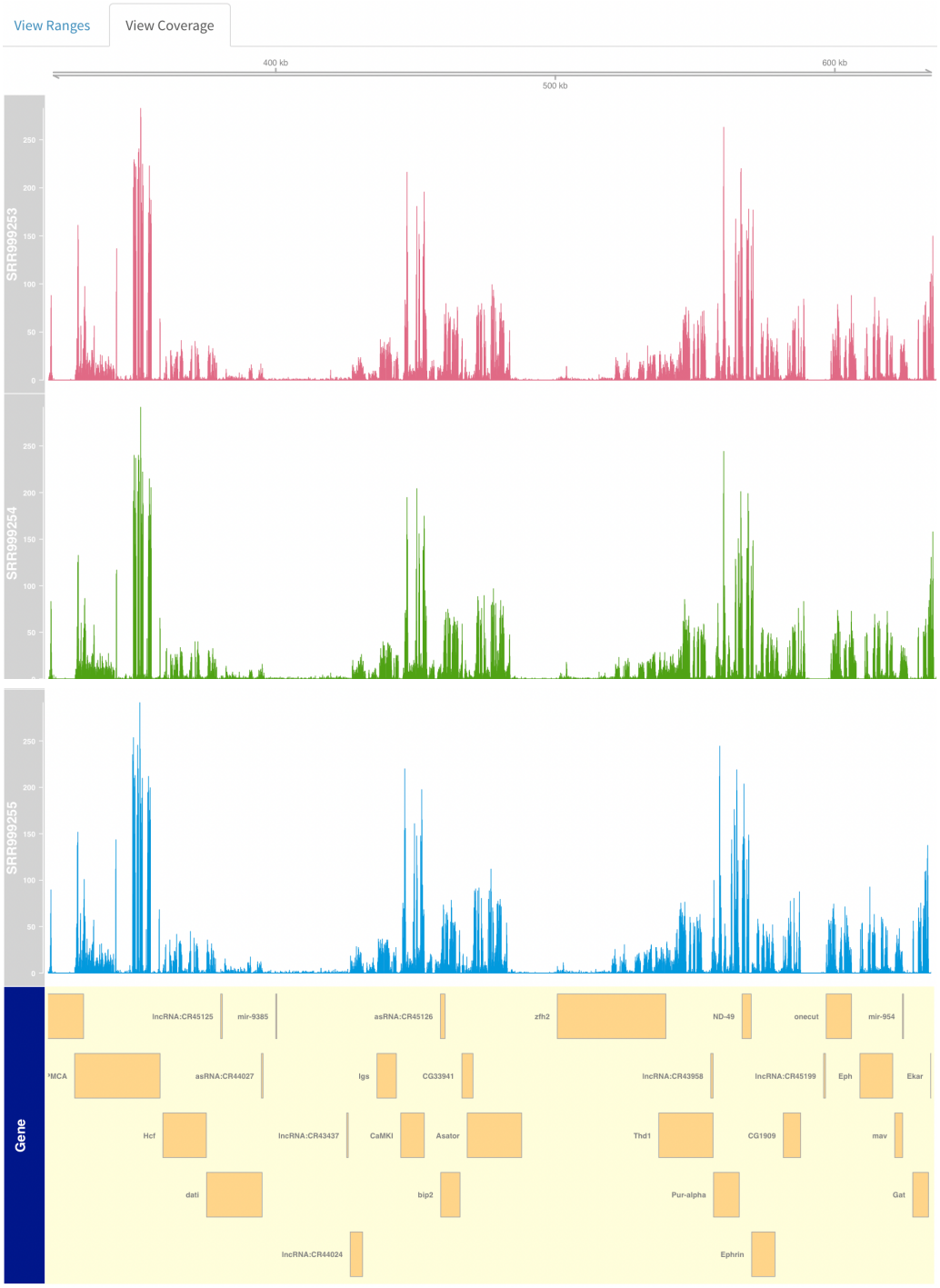


Fig 5.9: Coverage plot with genes (NCBI files)

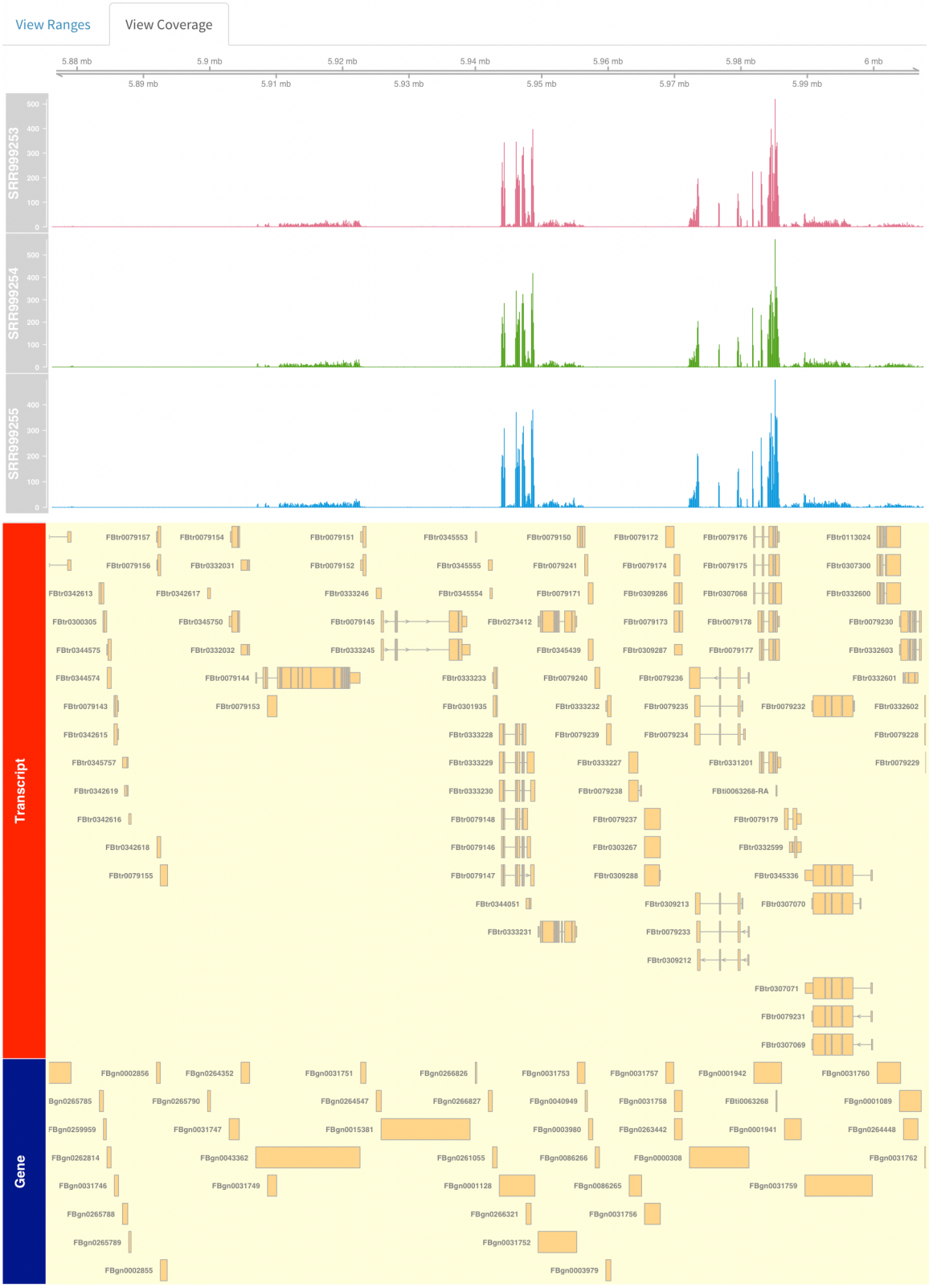


Fig 5.10: Coverage plot with genes & transcripts (Ensembl files)