


# Visualizing gene expression in Chromosome view

From the DESeq2 task report, we can browse to any gene in the *Chromosome view*.

- Click  in the SELENOM row to open *Chromosome view* (Figure 1)

13				TIMP3	8.66E-13	3.41E-11	417.64	417.64	84.88
14				EIF3L	1.12E-12	4.11E-11	0.49	-2.02	320.89
15				MICALL1	1.35E-12	4.6E-11	2.16	2.16	859.48
16				SELENOM	9.23E-12	2.95E-10	61.48	61.48	65.48
17				C22orf23	1.24E-11	3.73E-10	2.84	2.84	125.00

Figure 5. Browsing to a location in Chromosome View

A new tab will open showing SELENOM in the *Chromosome view* (Figure 2).

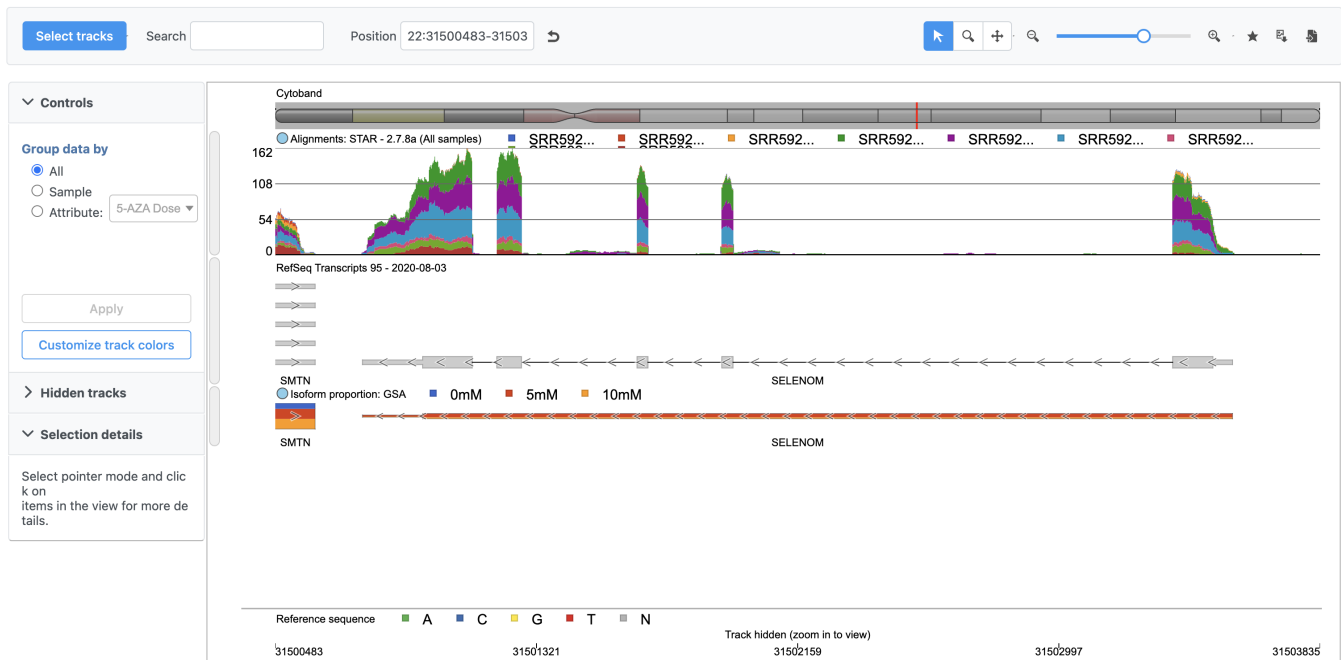


Figure 6. Viewing SELM in Chromosome view

*Chromosome View* shows reference genome, annotation, and data set information together aligned at genomic coordinates.

Each track has *Configure track*  and *Move track*  buttons that can be used to modify each track.

The top track shows average number of total count normalized reads for each of the three treatment groups in a stacked histogram. The second track shows the RefSeq annotation.

We can add tracks from any data node using *Select Tracks*.

- Click **Select tracks**

A pop-up dialog showing the pipeline allows us to choose which data to display as tracks in *Chromosome view* (Figure 3).

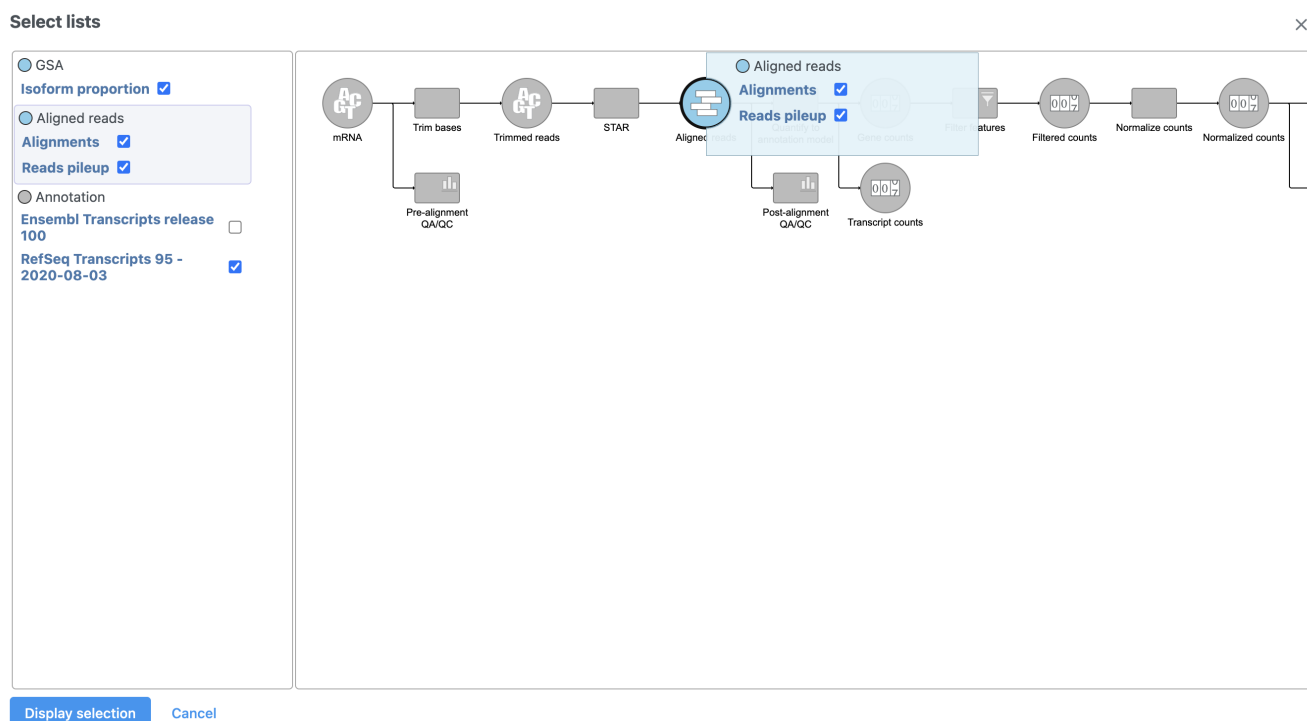


Figure 7. Choosing tracks to display in Chromosome view

- Click **Reads pileup** under *Aligned reads* on the left-hand side of the dialog
- Click **Display tracks** to make the change

The reads pileup track is now included (Figure 4).

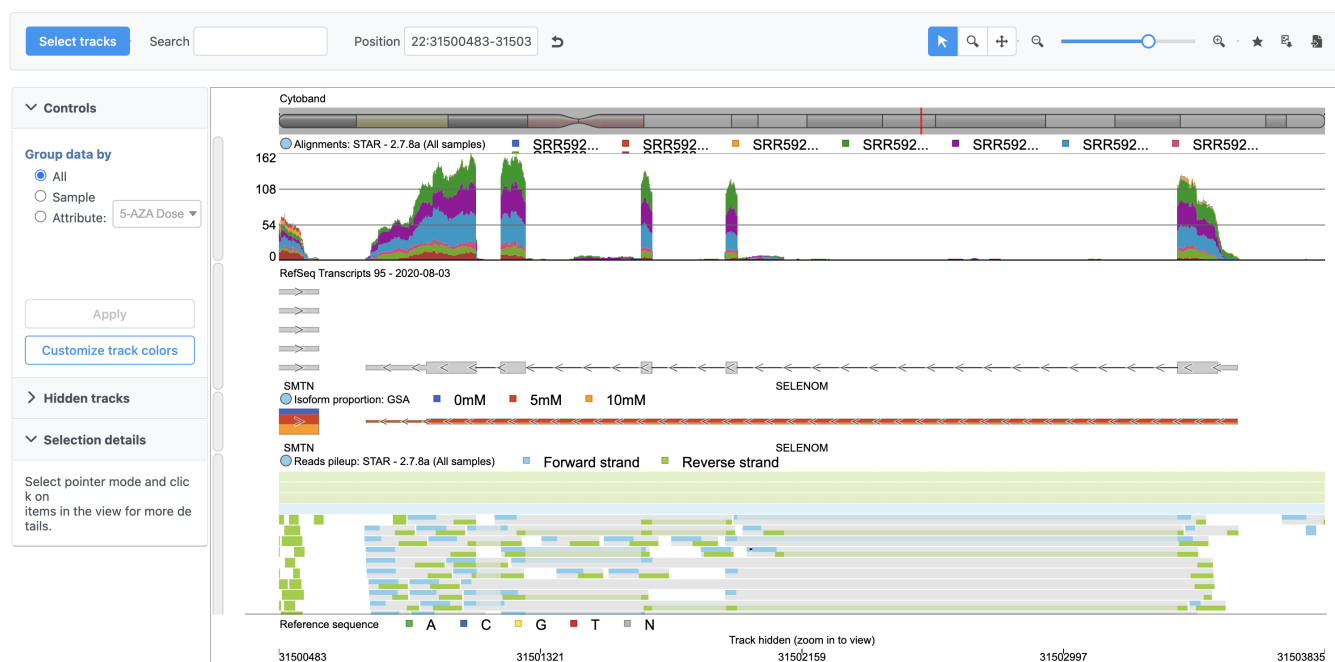


Figure 8. The reads pileup track shows every read in its aligned position on the reference genome

To learn more about *Chromosome view*, please consult the [Chromosome View](#) user guide.

[« Viewing a dot plot for a gene](#) [Generating a hierarchical clustering heatmap](#) »

## Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



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