

Transcription Start Site (TSS) Plot

The transcription start site plot (TSS) displays the number of reads that map around the transcription start site of genes within defined regions, such as peaks called during ChIP-seq experiments. This visualization can help identify patterns of chromatin, transcription factor and other protein binding sites along this stretch of the DNA.

You can invoke the creation of the plot on the annotated peak data node. After the peaks are annotated with transcripts, coverage of the reads across the genes overlapped with the regions will be calculated, this information is presented by profile plot (Figure 1) and heatmap (Figure 4).

Select the **Annotated regions** results node then under **Exploratory analysis** in the task menu, select **TSS plot**.

- [TSS profile plot](#)
- [TSS heatmap](#)

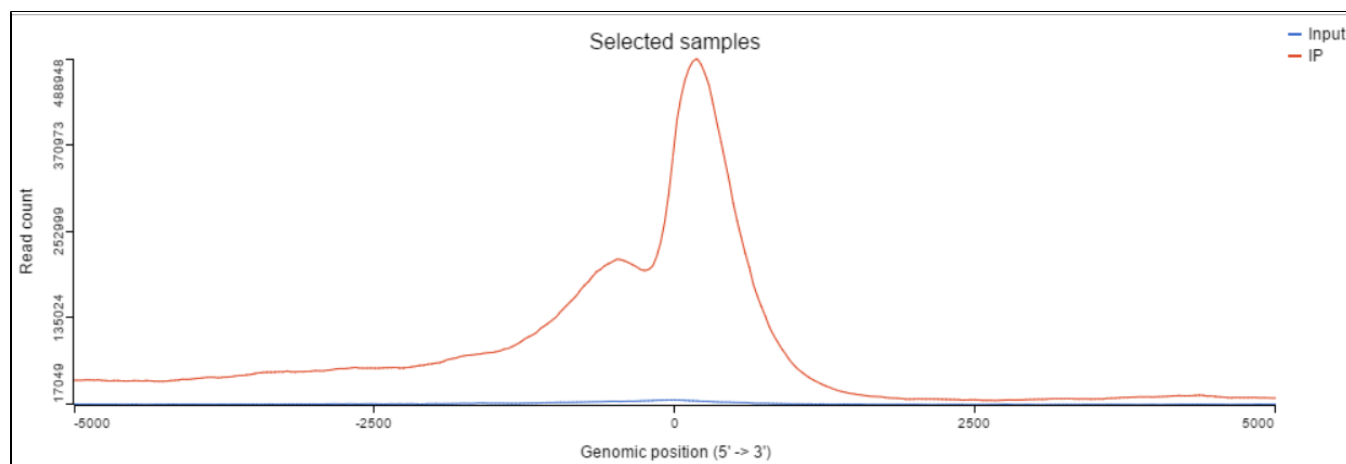


Figure 6. TSS profile plot

TSS profile plot

In the profile plot, the Y-axis is the total read counts, X-axis is the window defined in the annotation task, mid point is the transcription start site (TSS) of all the genes overlapping with the peak regions, the start and end point of X-axis is defined by the promoter upstream/downstream limit specified in the annotate peaks task (Figure 2). Each line represents a selected sample total read counts at each position, all the selected samples are shown in the plot to compare.

Promoter upstream limit

Promoter downstream limit

Select Annotation file

Assembly

Homo sapiens (human) - hg19

Gene/feature annotation

RefSeq Transcripts 80 - 2017-02-06

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Finish

Figure 7. Annotate peaks task dialog

By default, all the samples are selected to display, to remove a sample track, click on the button next to the sample name on the sample control panel (Figure 3); to add a sample in the plot, select the sample name from the **Add sample** drop-down list, a new line will be added on the plot.

Samples

- Add sample - ▼

Input

IP

Figure 8. Sample selection control panel

TSS heatmap

The heatmap is another way to view the overlap between the gene body and peaks detected (Figure 4). The X-axis represents the same information as the profile plot. While the maximum value of the Y-axis varies among different samples. In the heatmap, each row represents a gene, while the color encodes the total read count at each position and the genes are sorted based on total read counts in descending order.

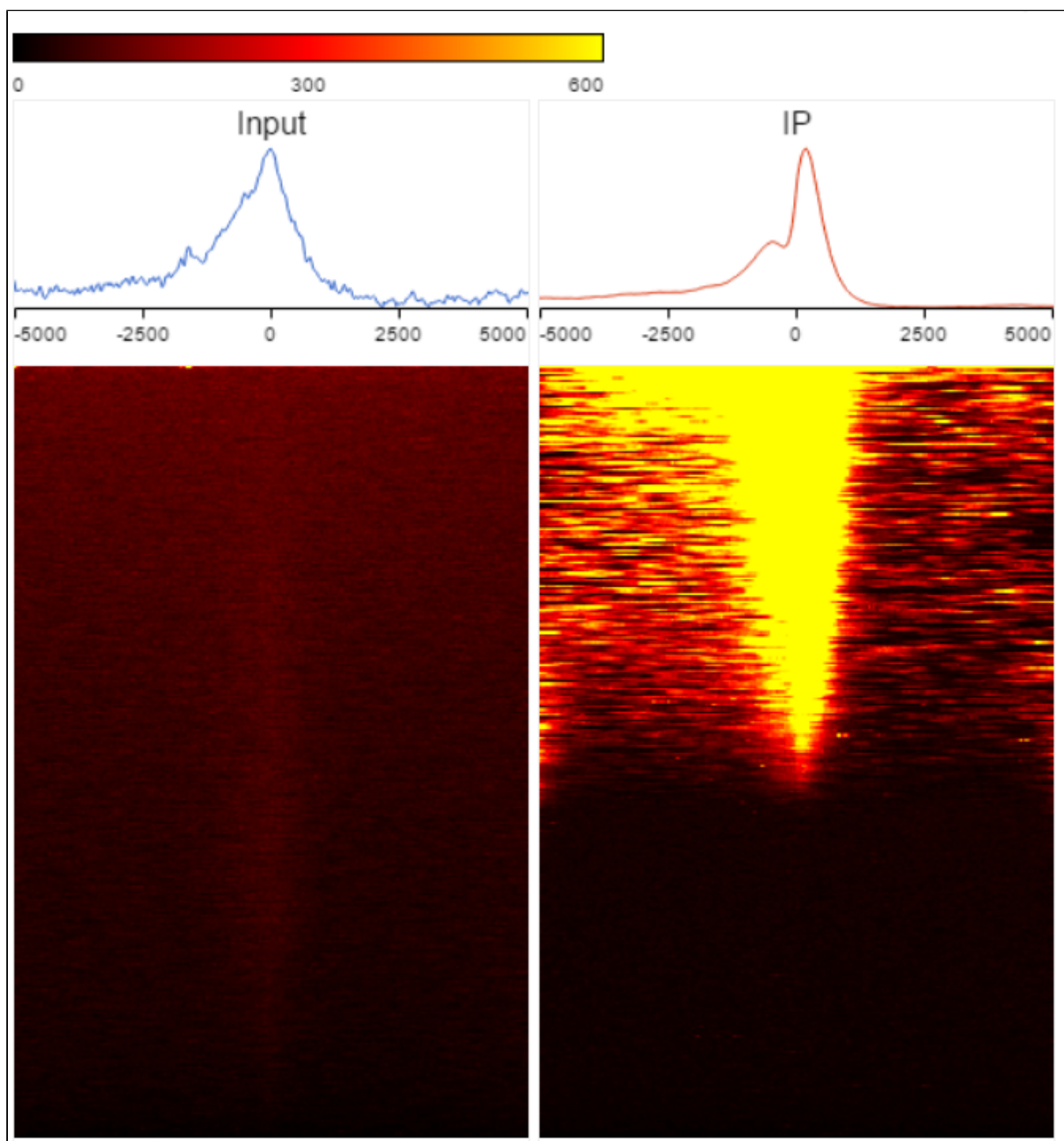


Figure 9. TSS heatmap

The color and color scale on the heatmap can be customized using the control panel on the left (Figure 5). You can change the number of heatmaps per row, with a higher number decreasing the heatmap size. For the heat map colors, changing the *Low* and *High* values will change the color scale of the heatmap. You can also change the color of the profile line by selecting *Customize sample colors*.

Heat maps per row

Heat map colors

Low

▼

≤ 0

Middle
☒

▼

300

High

▼

≥ 600

Customize sample colors

Figure 10. TSS heatmap control panel

Additional Assistance

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



Your Rating: ☆☆☆☆☆ Results: ★★★★★ 30 rates