

# INPUT\_EwS

20248

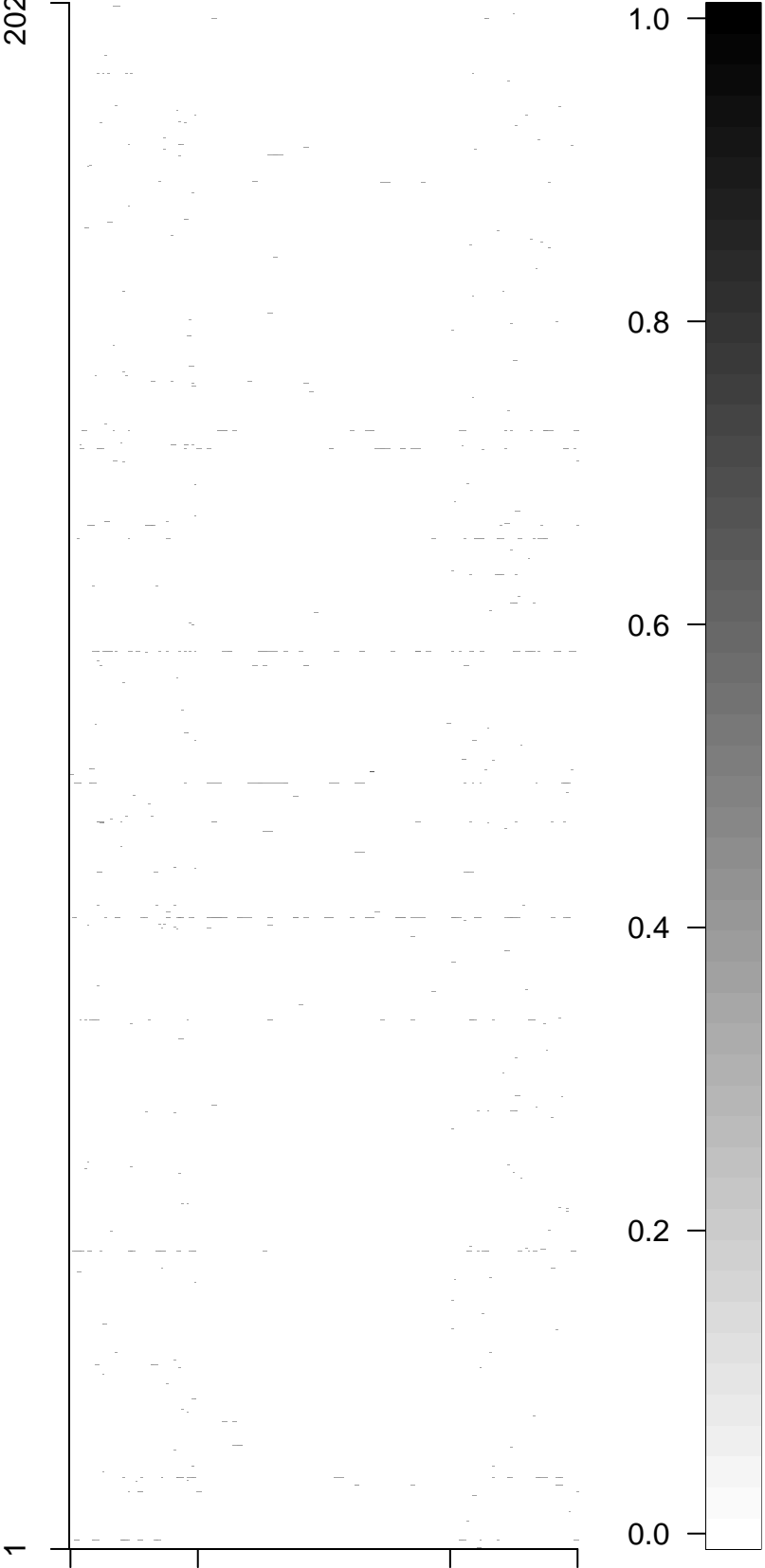
GENES

-5000 TSS TES +5000

REGION

1.0  
0.8  
0.6  
0.4  
0.2  
0.0

SeqCode by E. Bianco [Thu Jun 10 02:02:06 2021]



**Figure legend. Heatmap of ChIPseq reads along a uniform gene model.**

This plot is generated by counting the number of reads along this region for each gene to display these values on different rows of the heatmap. The X-axis represents the metagene and the flanking regions in which the counts were calculated for each gene. The Y-axis represents the list of all genes ranked by the average ChIP intensity on this region. TSS is the Transcription Start Site and TES is the Transcription End Site. On the right, ChIP signal range from high (top) to low (bottom).

ChIPseq experiment:

*INPUT\_EwS*

Number of genes:

20248

RefSeq transcripts:

78106

Number of reads:

26616797

Flanking sequence:

5000

Window factor:

100