Suz12_mESC

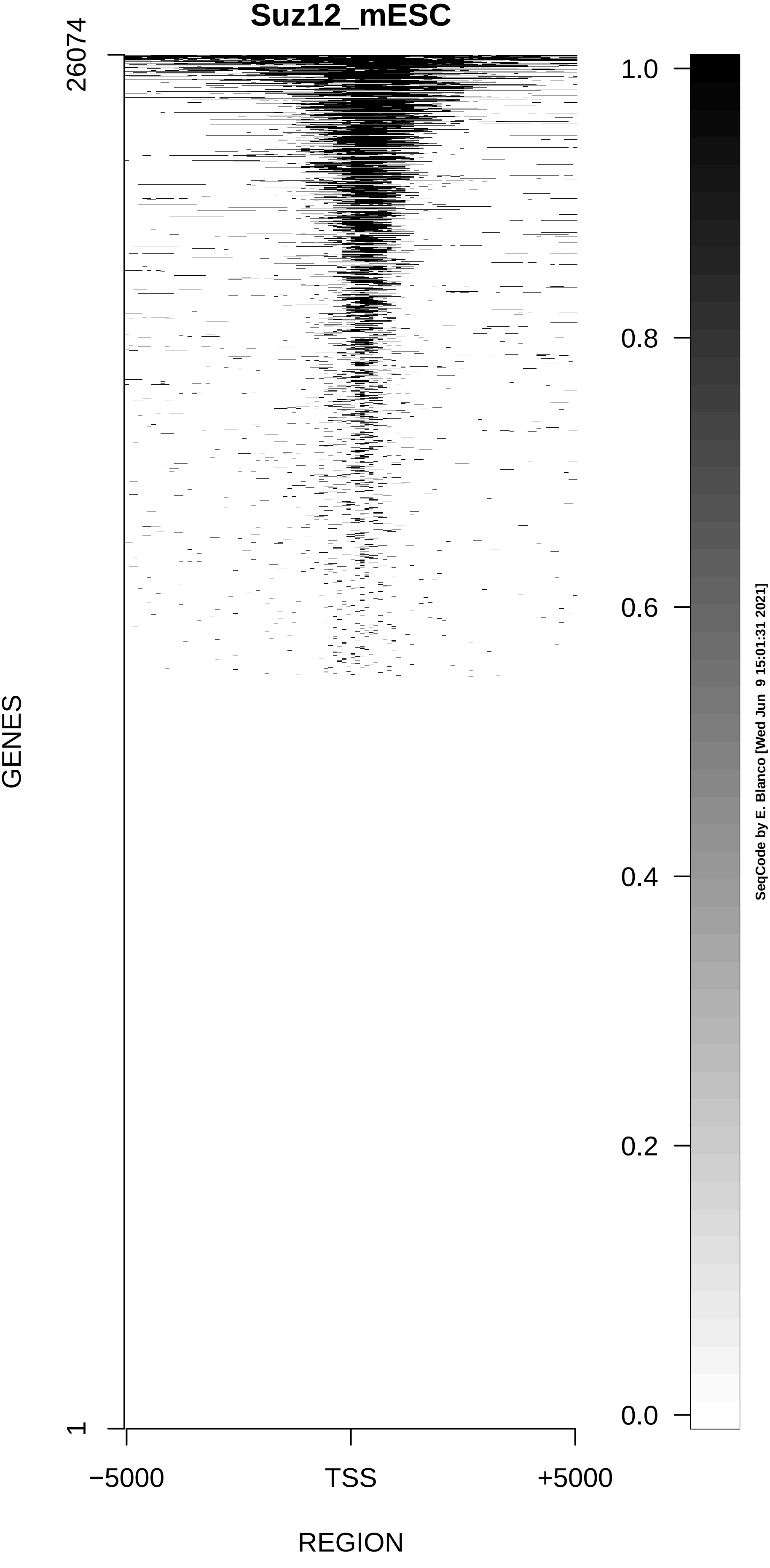
26074
1
GENES
−5000
TSS
+5000
REGION
1.0
0.8
0.6
0.4
0.2
0.0
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Figure legend. Heatmap of ChIPseq reads around the TSS of the genes. This plot is generated by counting the number of reads along this region for each gene to display these values on different rows of the heatmap. The X−axis represents the region around the TSS in which the counts were calculated for each gene. The Y−axis represents the list of genes ranked by the average ChIP intensity on this region. TSS is the Transcription Start Site. On the right, ChIP signal range from high (top) to low (bottom).

ChIPseq experiment:
Suz12_mESC
Number of genes:
26074
RefSeq transcripts:
46881

Number of reads:
15977085
Flanking sequence:
5000
Window factor:
100

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