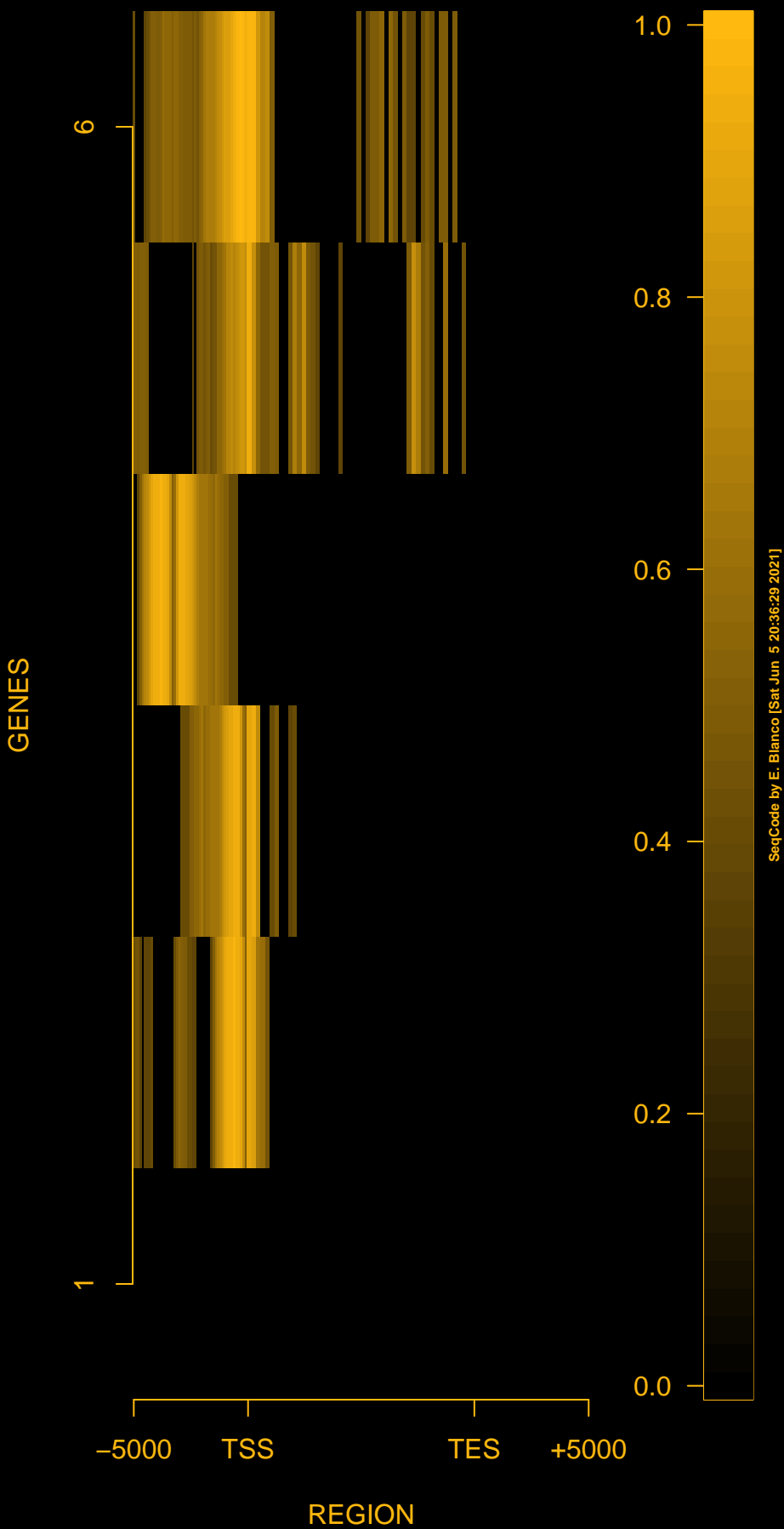**Figure legend. Heatmap of ChIPseq reads along a uniform gene model.**
This plot is generated by counting the number of reads along this region for
each gene to display these values on different rows of the heatmap. The X–
axis represents the metagene and the flanking regions in which the counts
were 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:
test_4

Number of genes:
6

RefSeq transcripts:
6

Number of reads:
21482

Flanking sequence:
5000

Window factor:
100