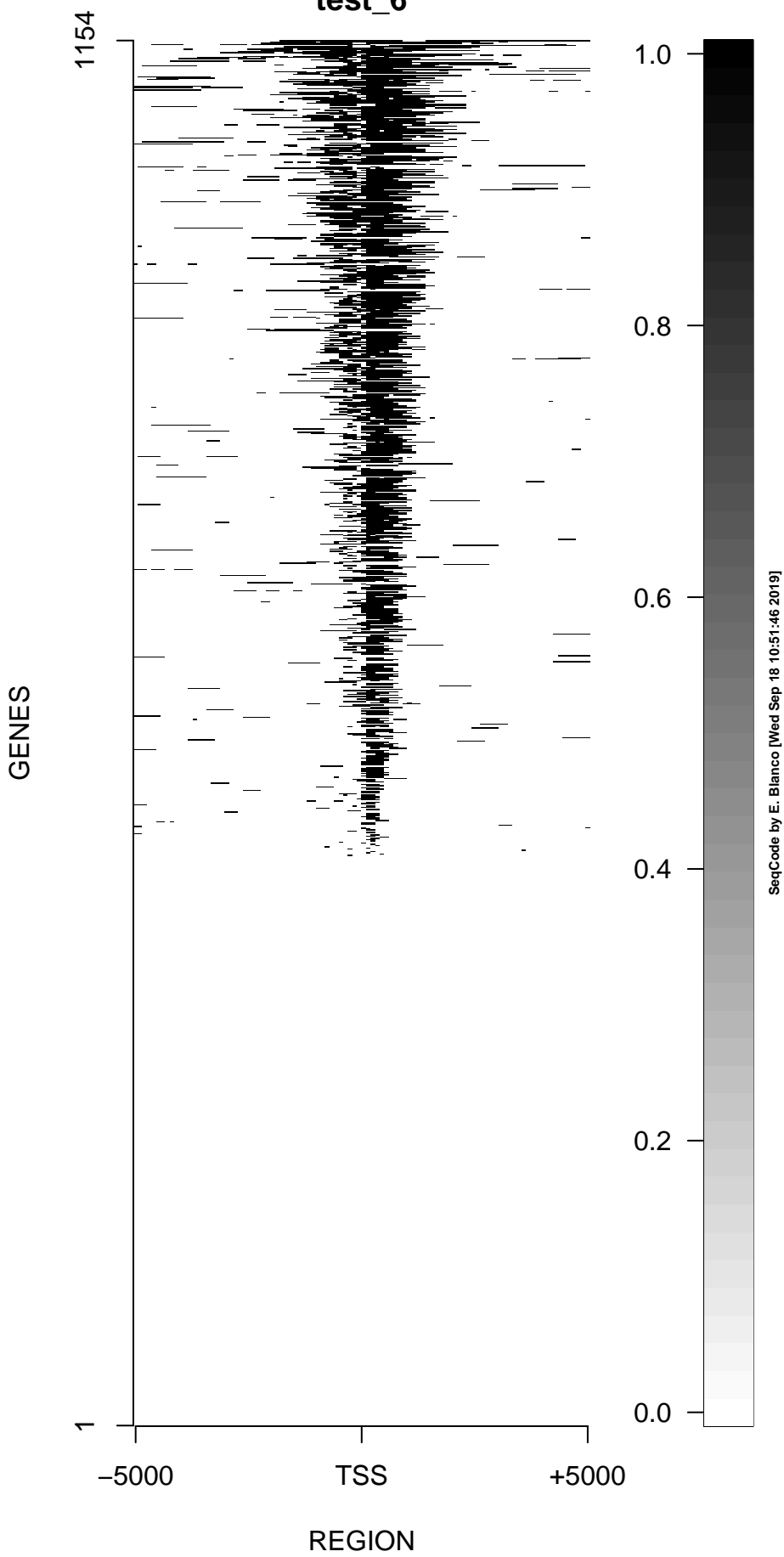test_6

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:
test_6

Number of genes:
1154

RefSeq transcripts:
36671

Number of reads:
1528788

Flanking sequence:
5000

Window factor:
100