

TSS profile for test_2 (5000 bp, 4640 reads)

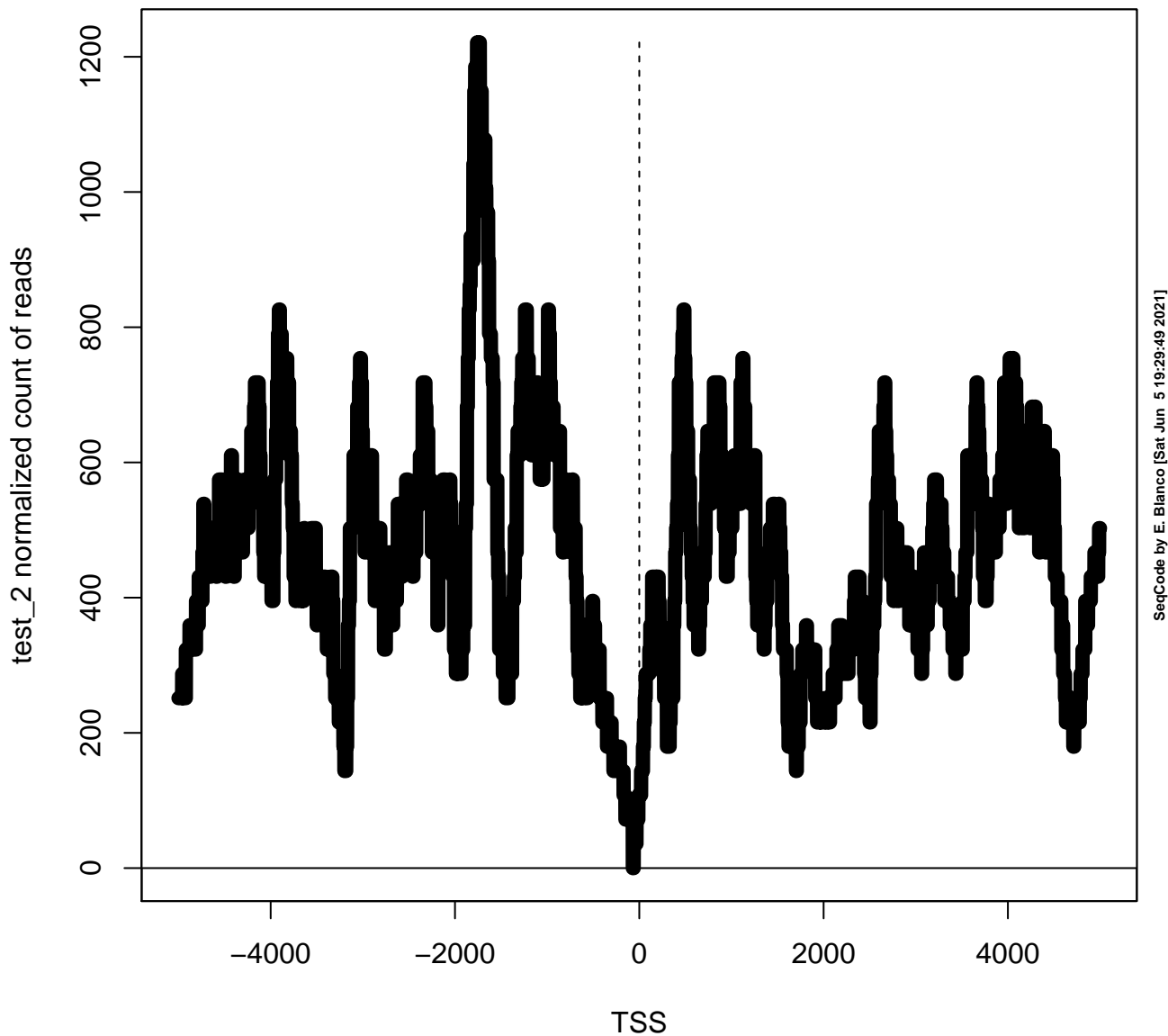


Figure legend. Average distribution of ChIPseq reads around the TSS of the genes.

This plot is generated by counting the number of reads along this region for each gene and averaging this value for the number of genes and the number of mapped reads (in millions). The X-axis represents the region around the TSS in which the counts were calculated for each gene. The Y-axis represents the intensity of the average ChIP signal normalized by the number of reads of the sample. TSS is the Transcription Start Site.

ChIPseq experiment:

test_2

Number of reads:

4640

Number of genes:

6

Flanking sequence:

5000

RefSeq transcripts:

6

Window factor:

10