

GENE profile for test_2 (5000 bp, 1528788 reads)

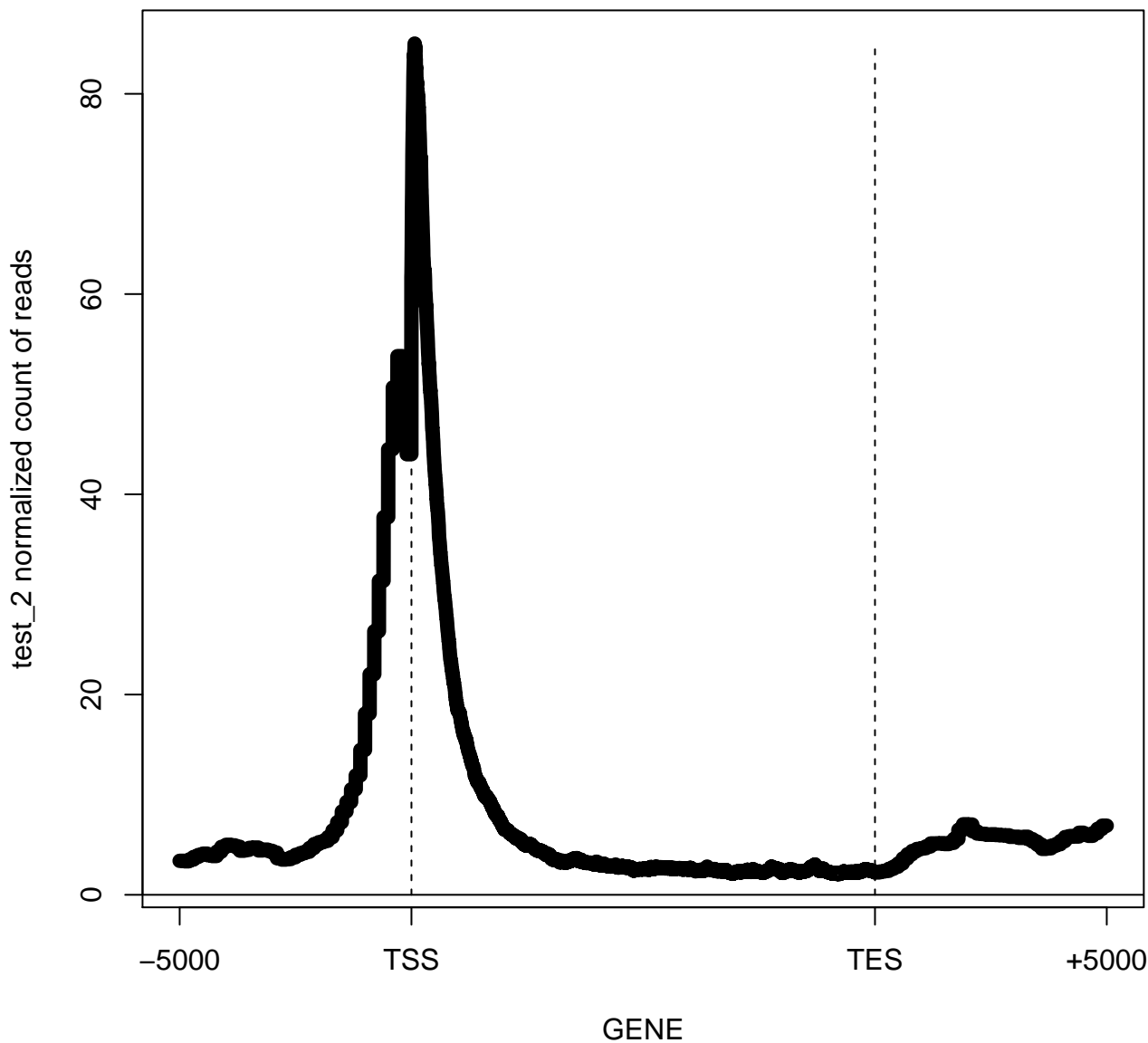


Figure legend. Average distribution of ChIPseq reads along a uniform gene model.

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 metagene and the flanking region 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 and TES is the Transcription End Site.

ChIPseq experiment:

test_2

Number of reads:

1528788

Number of genes:

834

Flanking sequence:

5000

RefSeq transcripts:

36671

Window factor:

100