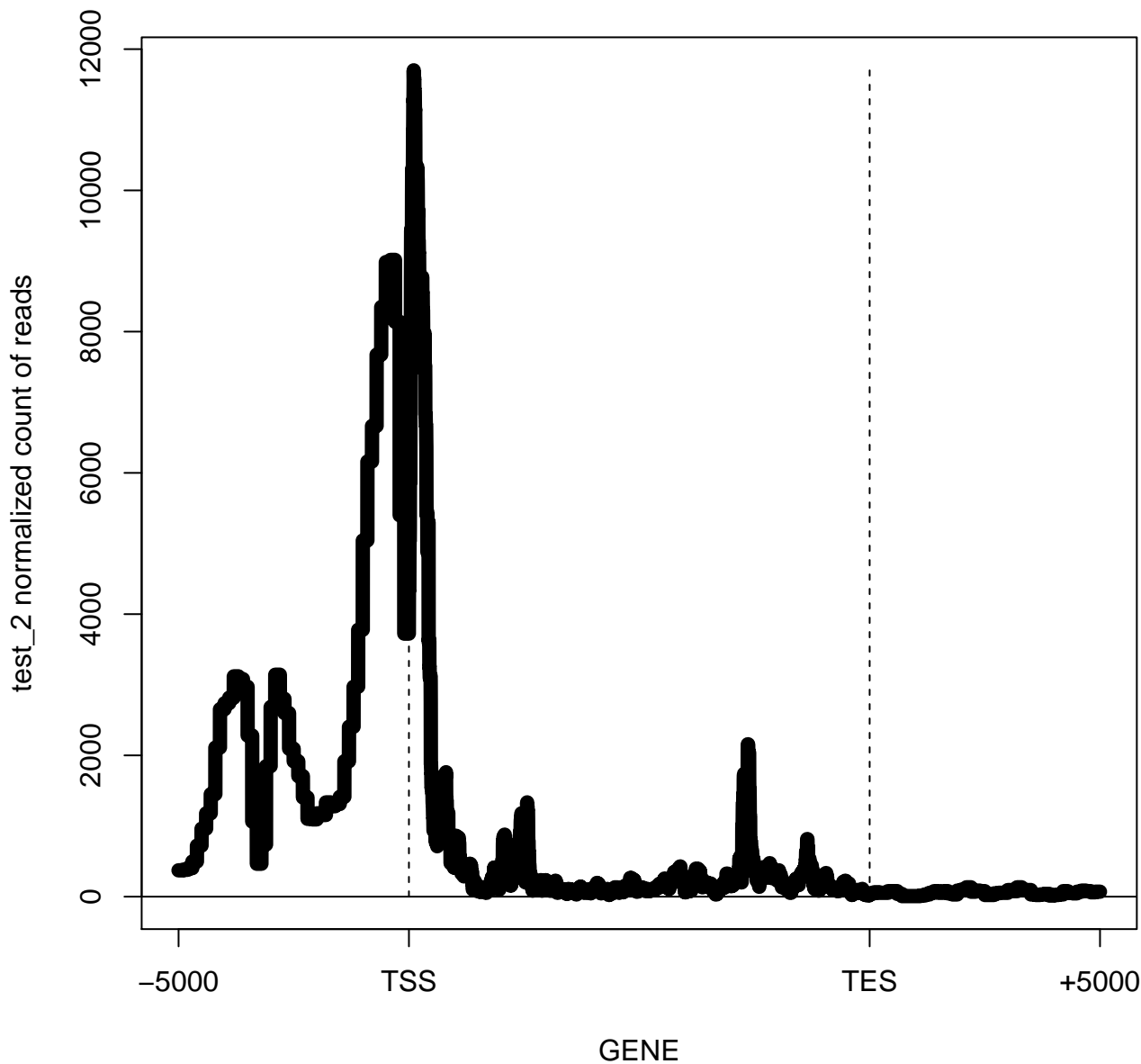


# GENE profile for test\_2 (5000 bp, 21482 reads)



**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:

*21482*

Number of genes:

*6*

Flanking sequence:

*5000*

RefSeq transcripts:

*6*

Window factor:

*100*