

GENE profile for FLI1_EwS (5000 bp, 42095743 reads)

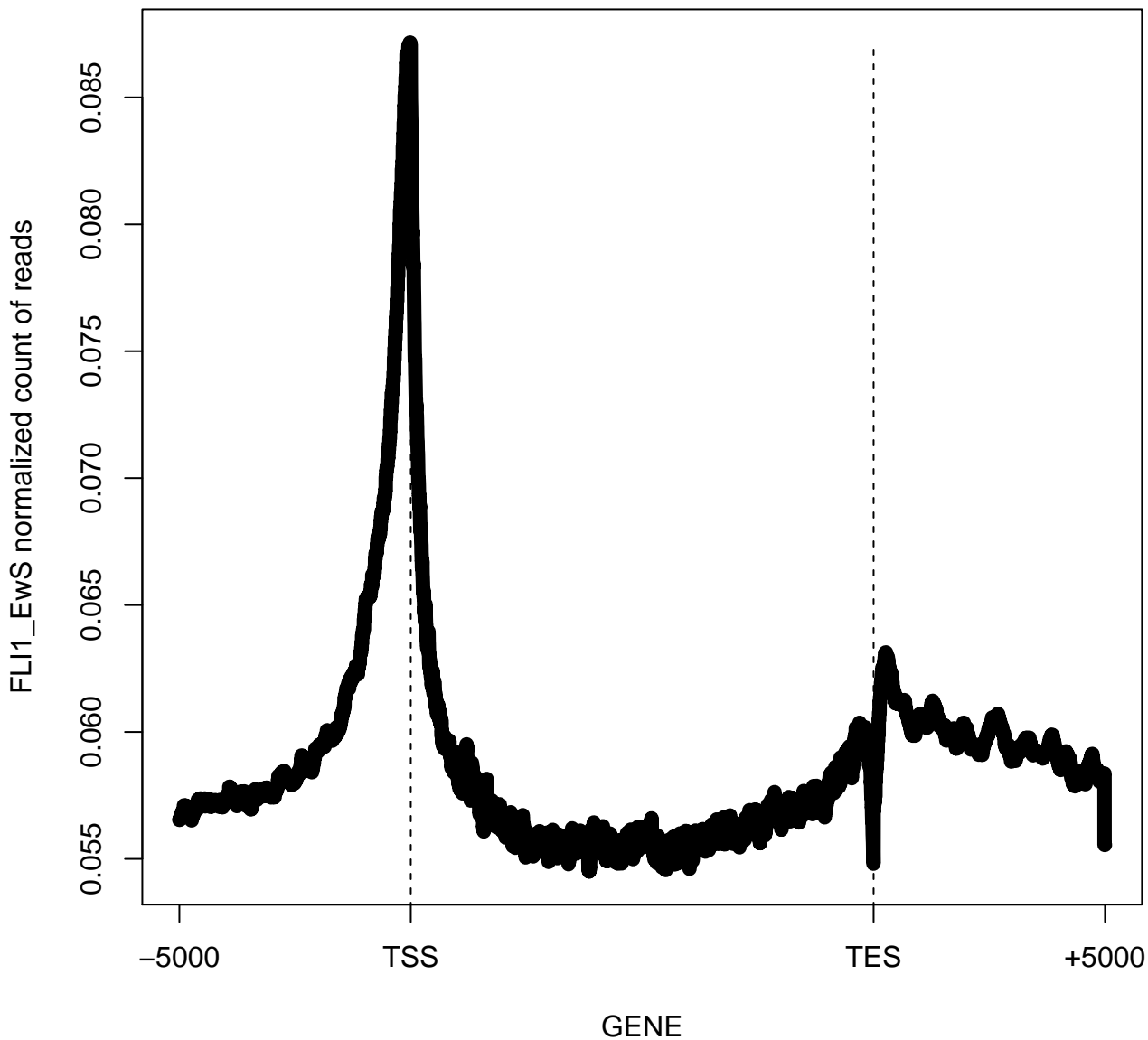


Figure legend. Average distribution of ChIPseq reads along a uniform gene model.

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:

FLI1_EwS

Number of reads:

42095743

Number of genes:

20248

Flanking sequence:

5000

RefSeq transcripts:

78106

Window factor:

10