GENE profile for H2AUb_EwS (5000 bp, 24792275 reads)
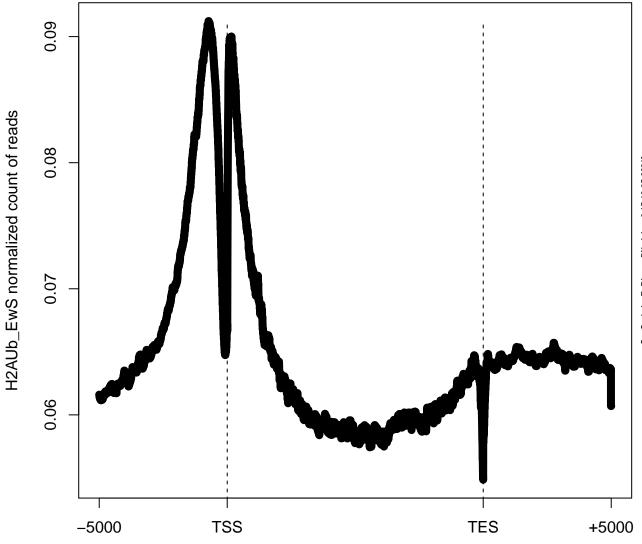

y-axis: H2AUb_EwS normalized count of reads

x-axis: GENE

x-axis labels: −5000, TSS, TES, +5000

y-axis labels: 0.06, 0.07, 0.08, 0.09

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.

<div align="center">

ChIPseq experiment:

H2AUb_EwS

Number of reads:

24792275

Number of genes:

20248

Flanking sequence:

5000

RefSeq transcripts:

78106

Window factor:

10

</div>