



Figure legend. Heatmap of ChIPseq reads along a uniform gene model.

This plot is generated by counting the number of reads along this region for each gene to display these values on different rows of the heatmap. The X-axis represents the metagene and the flanking regions in which the counts were calculated for each gene. The Y-axis represents the list of all genes ranked by the average ChIP intensity on this region. TSS is the Transcription Start Site and TES is the Transcription End Site. On the right, ChIP signal range from high (top) to low (bottom).

ChIPseq experiment:

test_7

Number of genes:

834

RefSeq transcripts:

36671

Number of reads:

1499999

Flanking sequence:

5000

Window factor:

100