

TSS profile for test_3-test_3 (5000 bp, 21482-4640 reads)

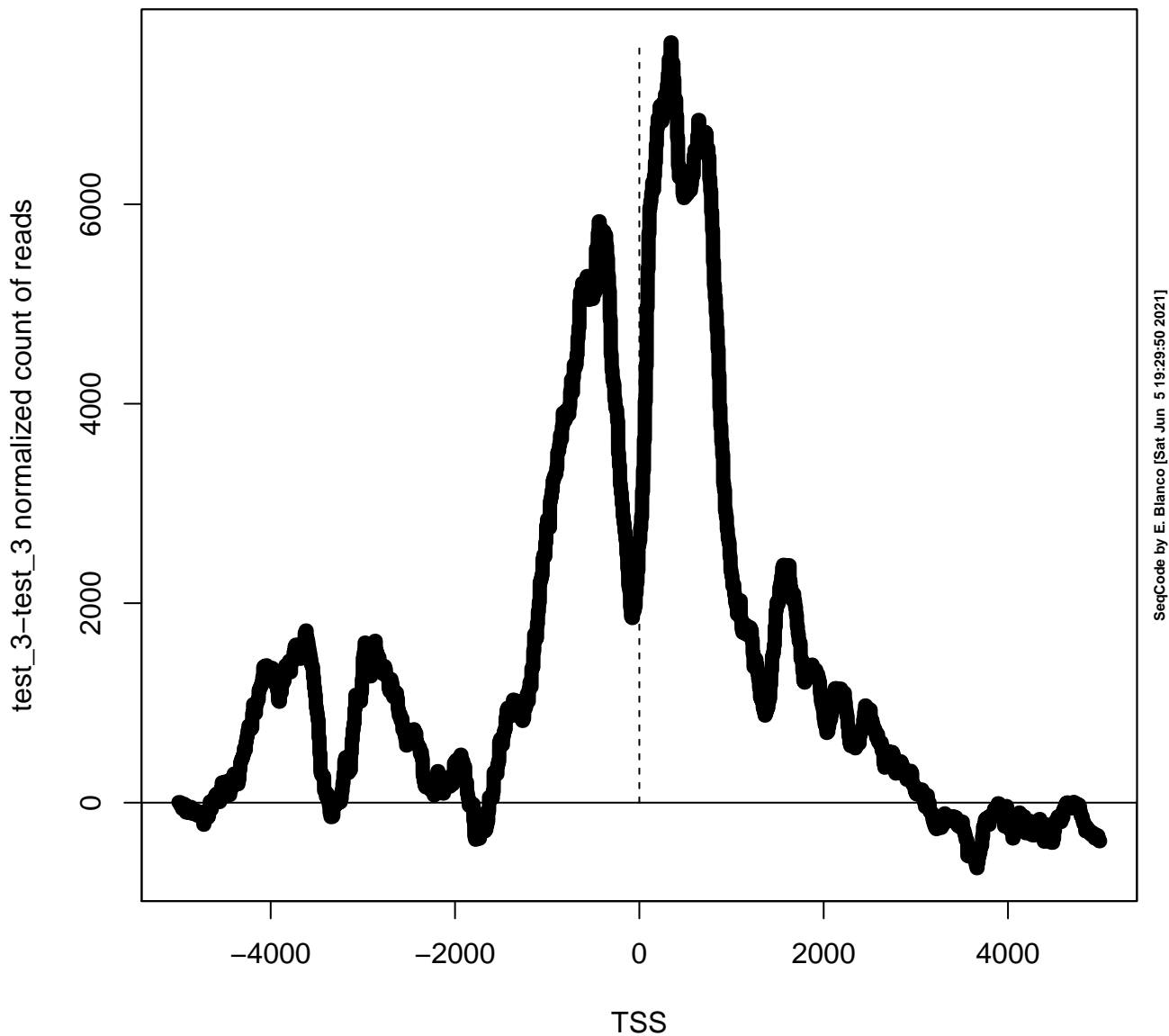


Figure legend. Combined distribution of ChIPseq reads around the TSS of the genes.

This plot is generated by counting the number of reads along this region for each gene and averaging this value from both experiments for the number of genes and reads (in millions). The X-axis represents the region around the TSS in which the counts were calculated for each gene. The Y-axis represents the average ChIP signal intensity subtraction normalized by the number of reads of each sample. TSS is the Transcription Start Site.

ChIPseq experiment 1:

test_3

Number of reads:

21482

ChIPseq experiment 2:

test_3

Number of reads:

4640

Number of genes:

6

Flanking sequence:

5000

RefSeq transcripts:

6

Window factor:

10