

PEAK profile for test_1 (5000 bp, 21482 reads)

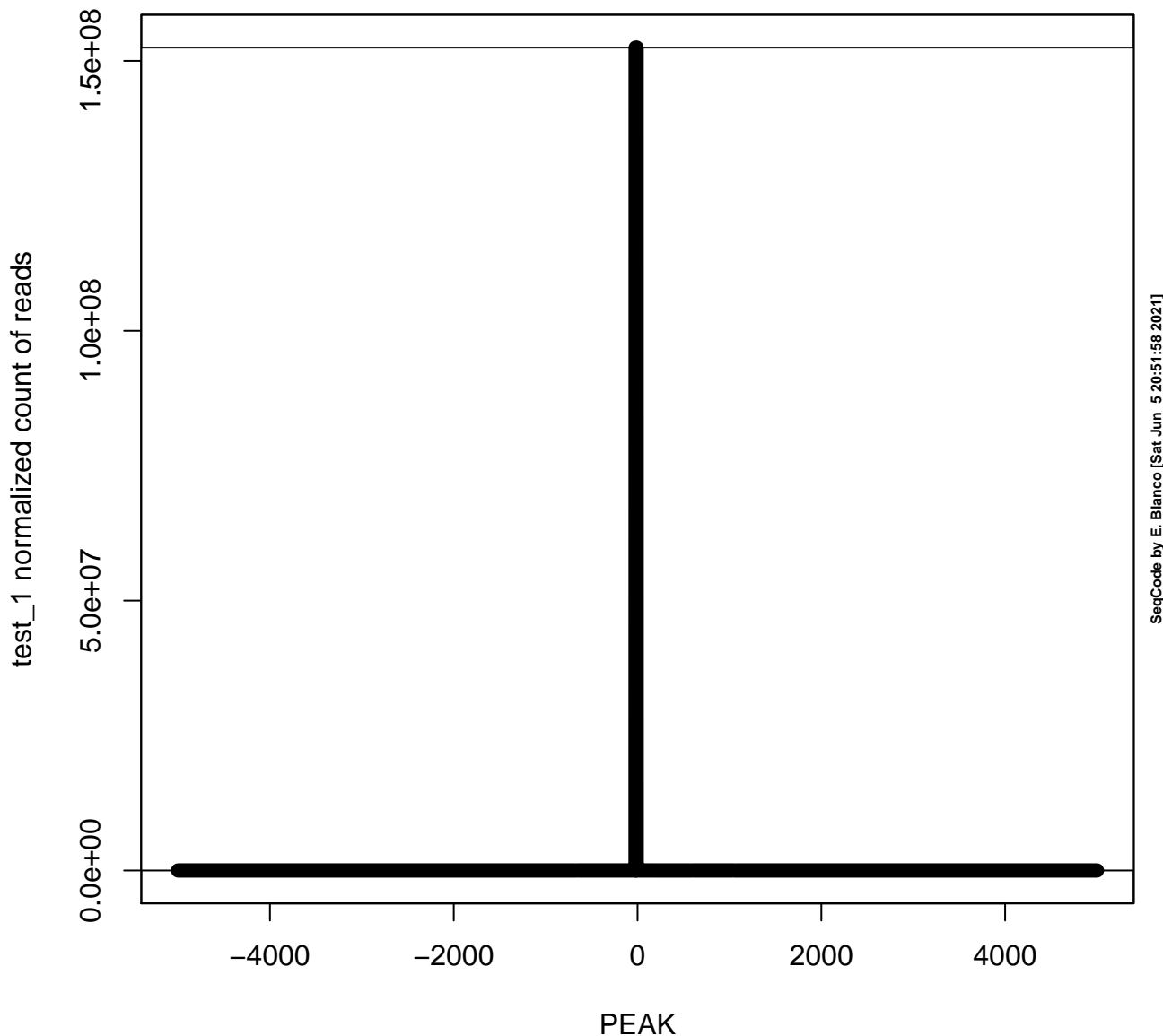


Figure legend. Average distribution of ChIPseq reads around the center of the peaks.

This plot is generated by counting the number of reads along this region for each peak and averaging this value for the number of peaks and the number of mapped reads (in millions).

The X-axis represents the region around the peak center in which the counts were calculated for each peak. The Y-axis represents the intensity of the average ChIP signal normalized by the number of reads of the sample. PEAK represents the center of the peaks.

ChIPseq experiment:

test_1

Number of reads:

21482

Number of peaks:

32

Flanking sequence:

5000

Window factor:

10