PEAK profile for test_2 (5000 bp, 21482 reads)
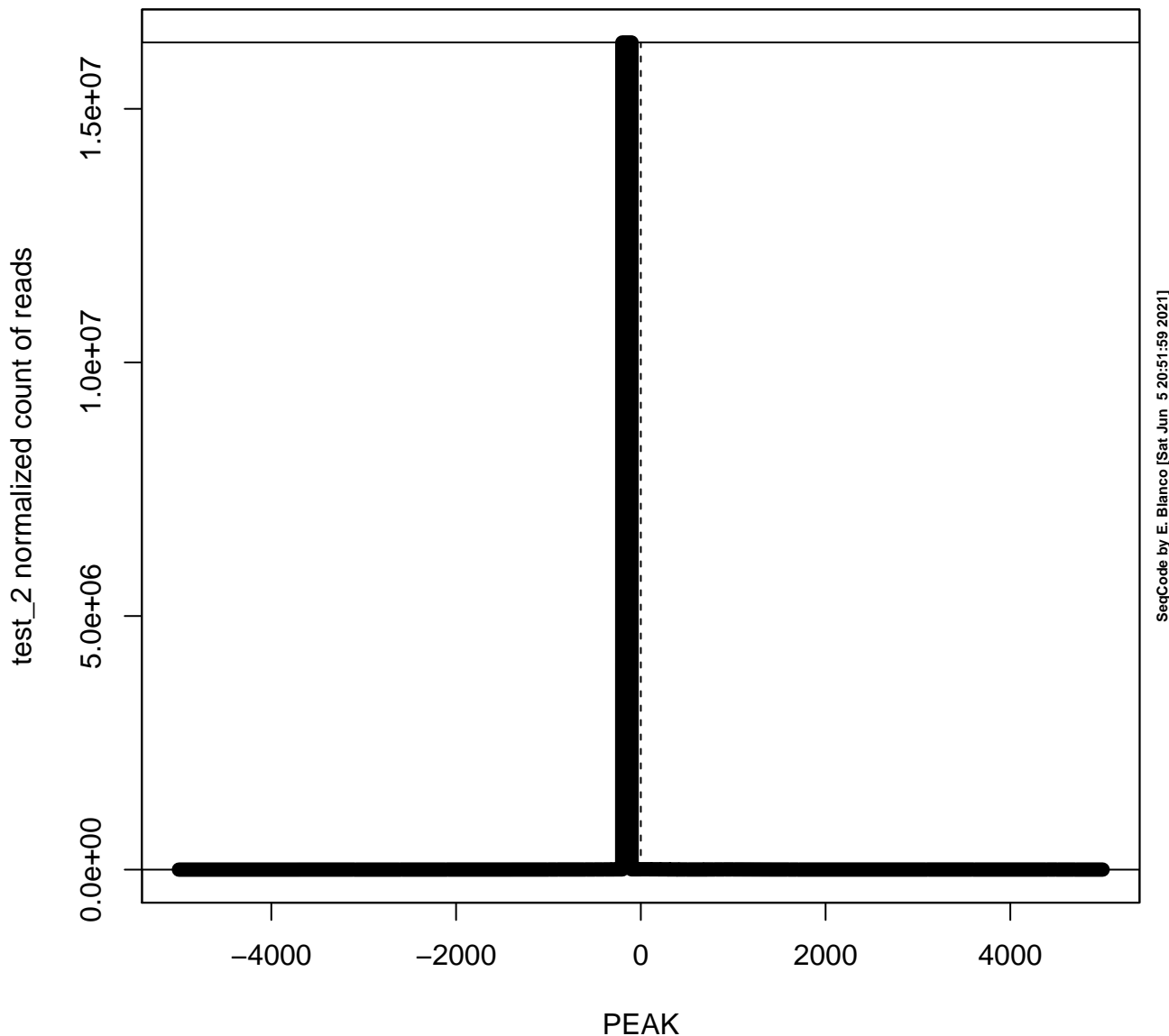

test_2 normalized count of reads

PEAK

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_2

Number of reads:

21482

Number of peaks:

32

Flanking sequence:

5000

Window factor:

100