test_6

PEAKS

REGION

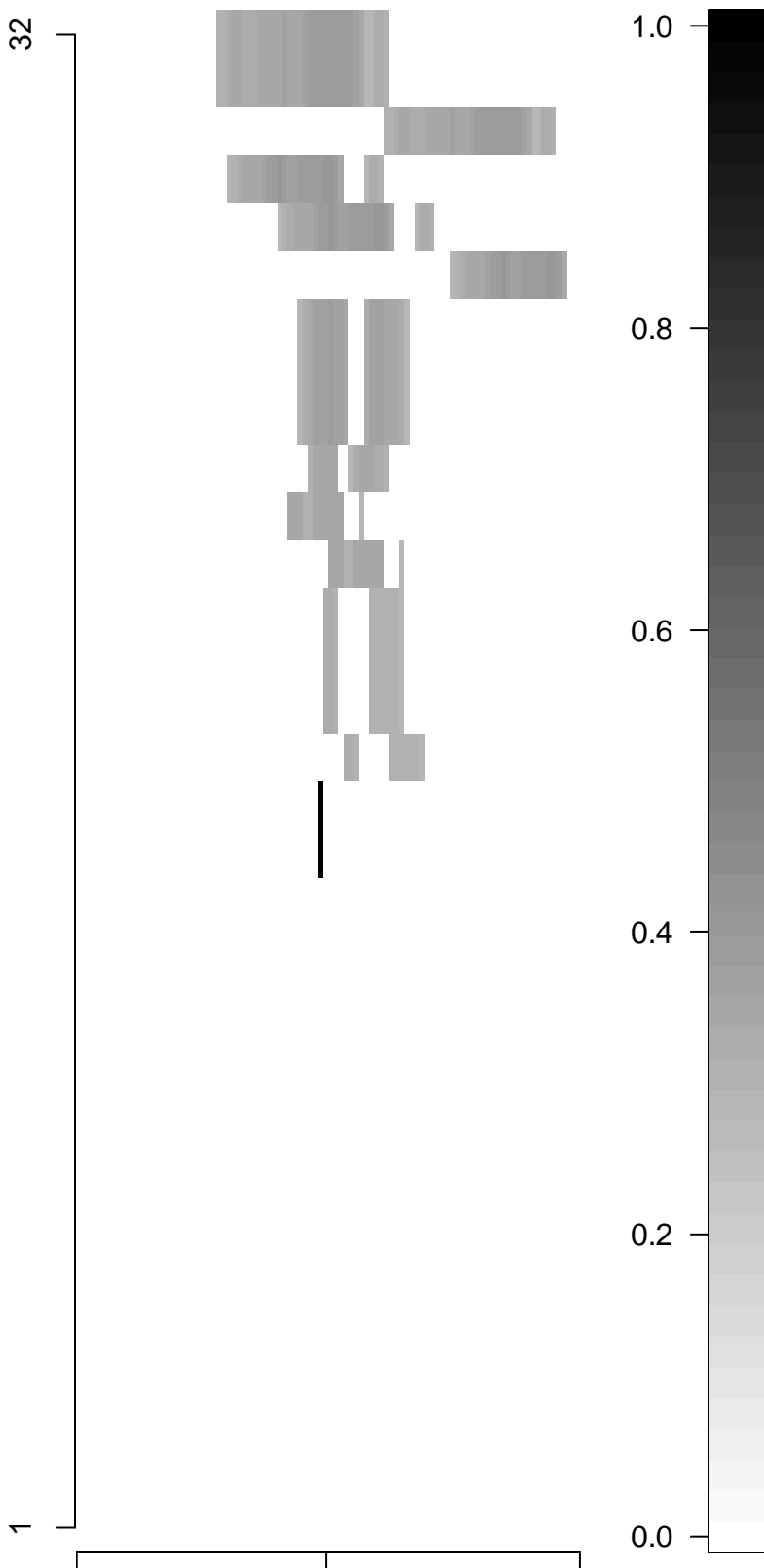−5000   PEAK   +5000

32

1

1.0

0.8

0.6

0.4

0.2

0.0

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Figure legend. Heatmap 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 to display these values on different rows of the heatmap. The X–axis represents the region around the peak center in which the counts were calculated for each peak. The Y–axis represents the list of peaks ranked by the average ChIP intensity on this region. PEAK represents the center of the peaks. On the right, ChIP signal range from high (top) to low (bottom).

ChIPseq experiment:

test_6

Number of peaks:

32

Number of reads:

21482

Flanking sequence:

5000

Window factor:

100

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