TSS profile for RING1B_EwS (5000 bp, 25718321 reads)
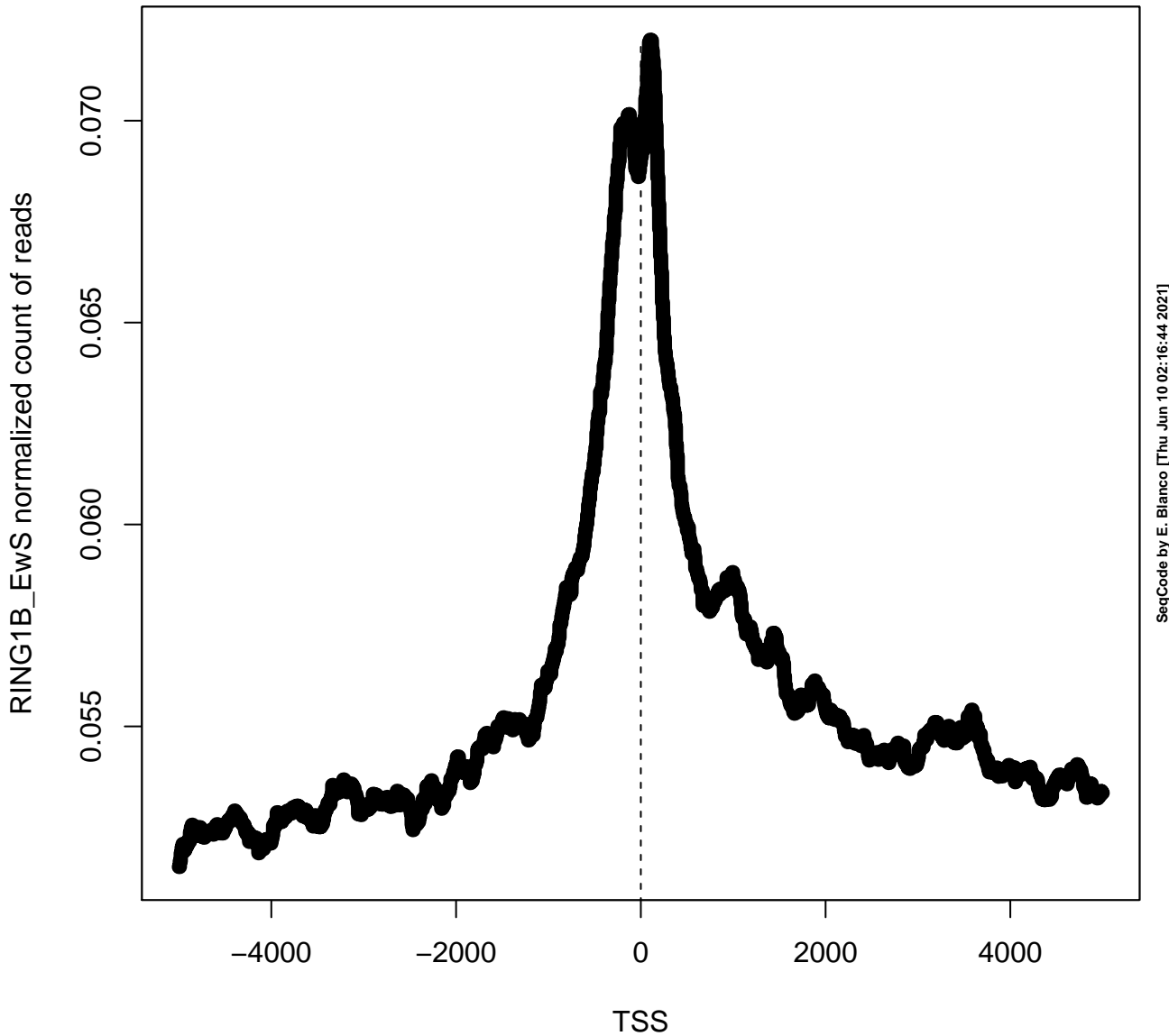

RING1B_EwS normalized count of reads

TSS

Figure legend. Average 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 for the number of genes and the number of mapped 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 intensity of the average ChIP signal normalized by the number of reads of the sample. TSS is the Transcription Start Site.

ChIPseq experiment:

RING1B_EwS

Number of reads:

25718321

Number of genes:

28237

Flanking sequence:

5000

RefSeq transcripts:

78106

Window factor:

10