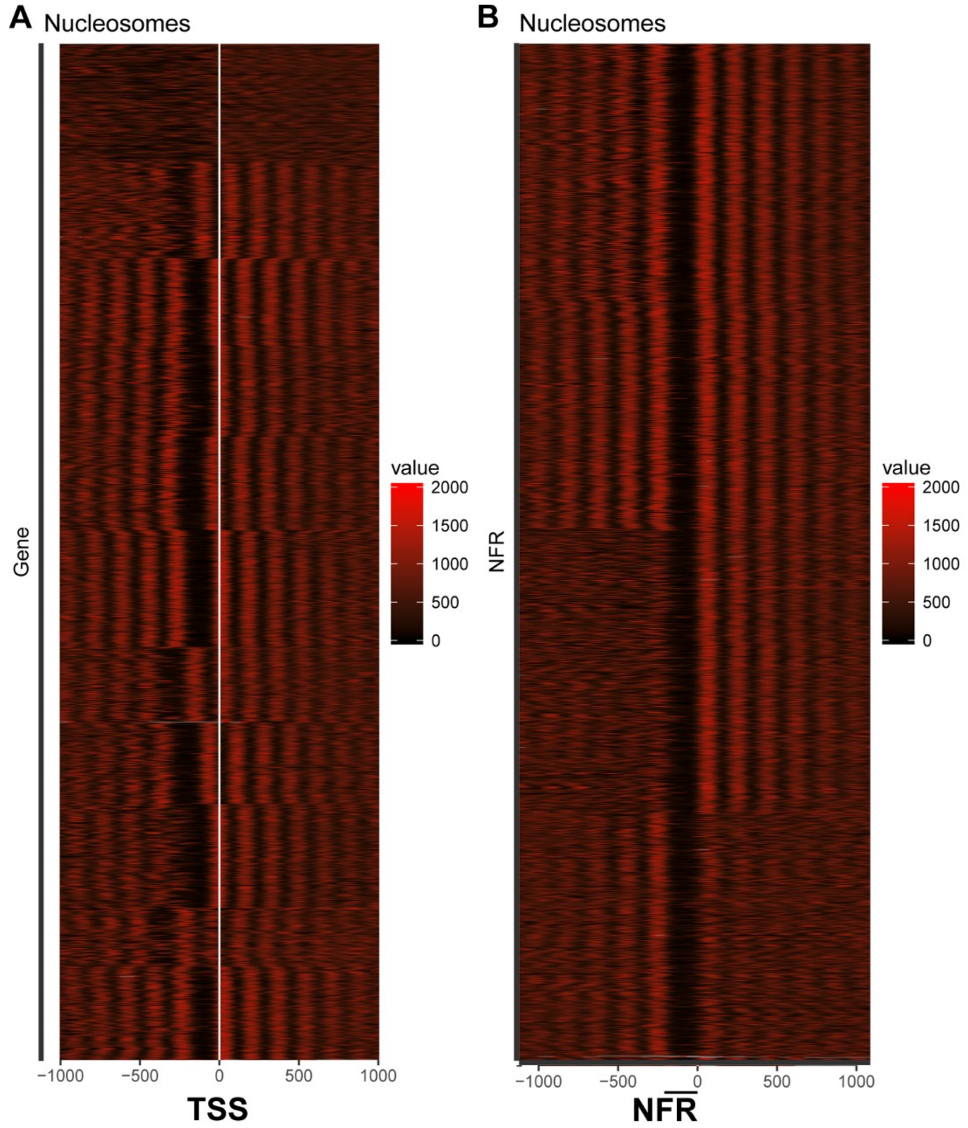

Figure S3 – The relationship of TSS to NFR distance and the +1 nucleosome at genes downstream of GCBS's is displayed here. Heatmaps were generated using SeqPlots and transferred to the statistical R-environment for further analysis. A) Using K-means clustering analysis, the traces were grouped into 13 clusters of similar structure. The heatmap displays the relative nucleosome density around the TSS, highlighted by the white line in the middle. This includes nucleosomes 1 kbp up- and downstream. The intensity of the heatmap is proportional to the normalised read-depth indicated in the figure. B) The same nucleosome data as displayed in A) was used, but now aligned at the accompanying NFR. K-means clustering of the data in this orientation resulted in the identification of 4 clusters. The e intensity of the heatmap as a function of normalised reads is indicated in the figure. The bar at the bottom indicates the orientation of the NFR at these genomic positions.