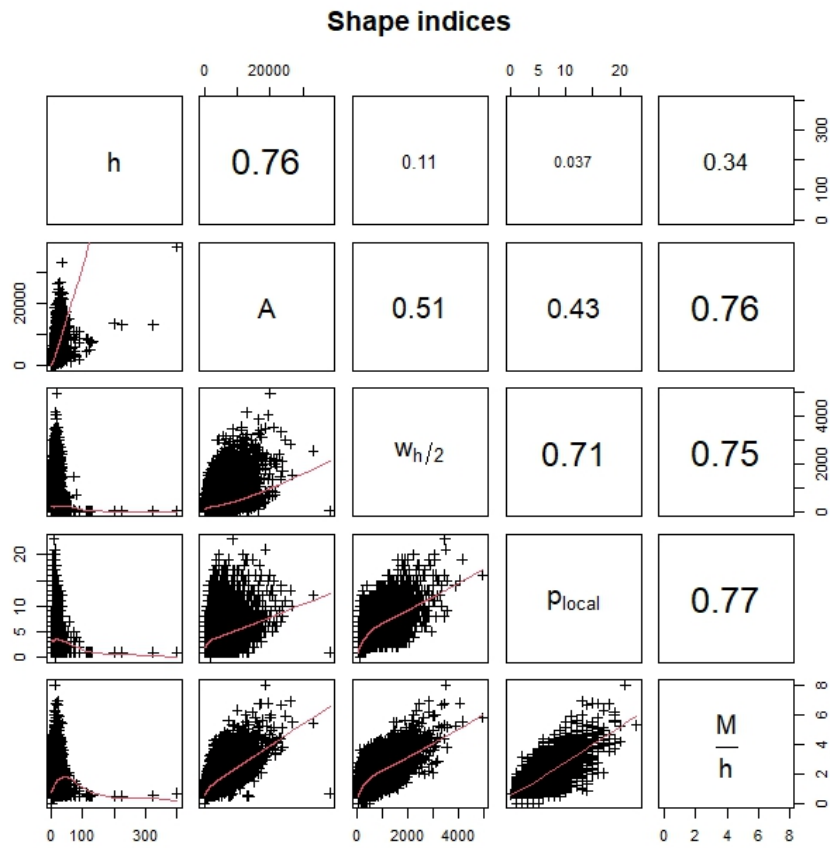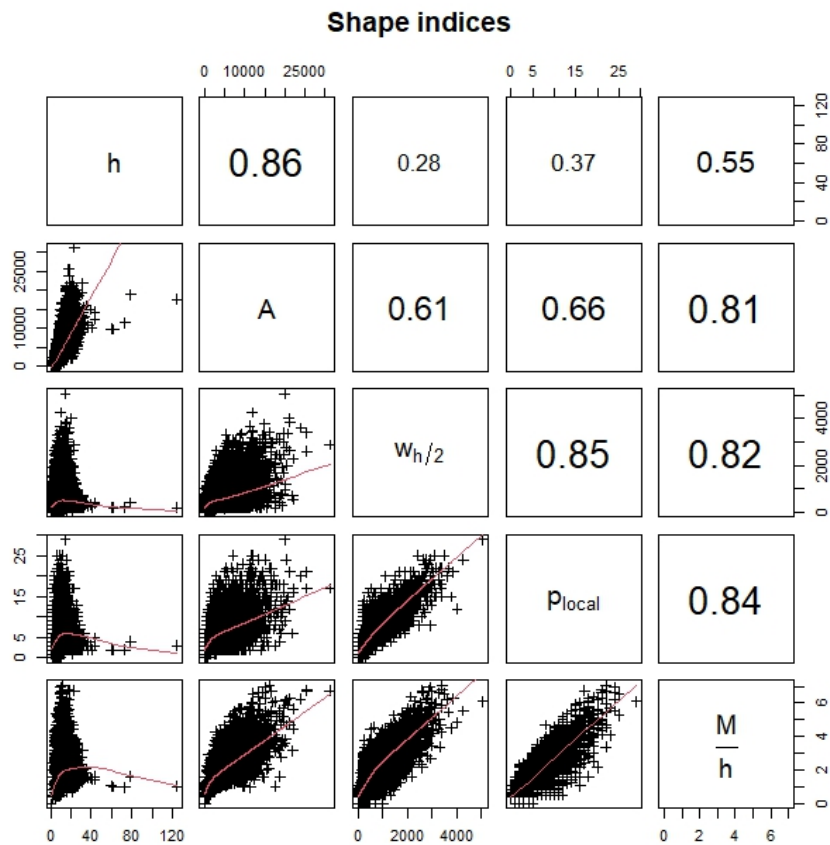**Supplementary figure 1.** Scatter plot representing the Pearson correlation between each of the 5 indices for standardized data of a) Open and b) MonoNuc data.
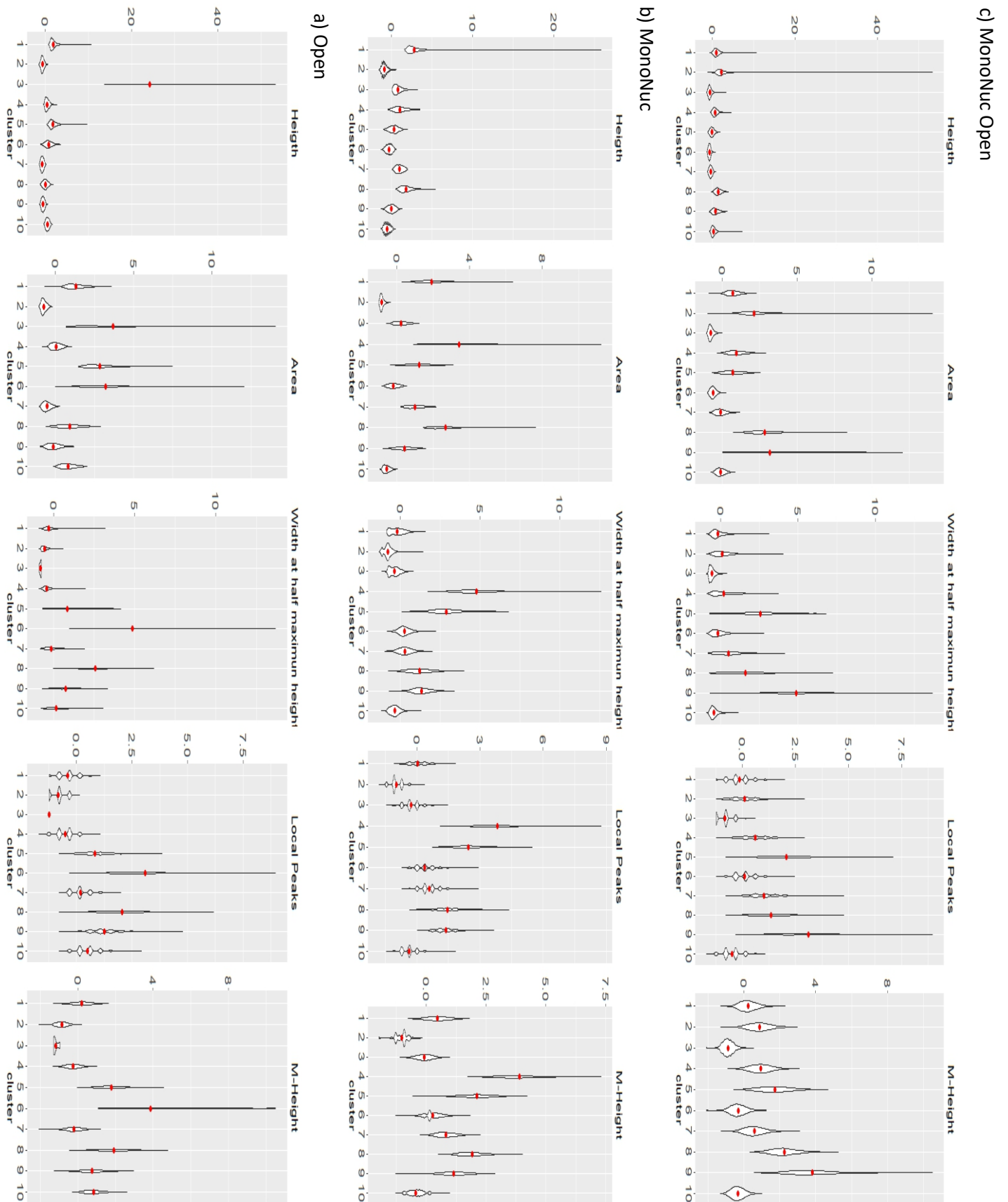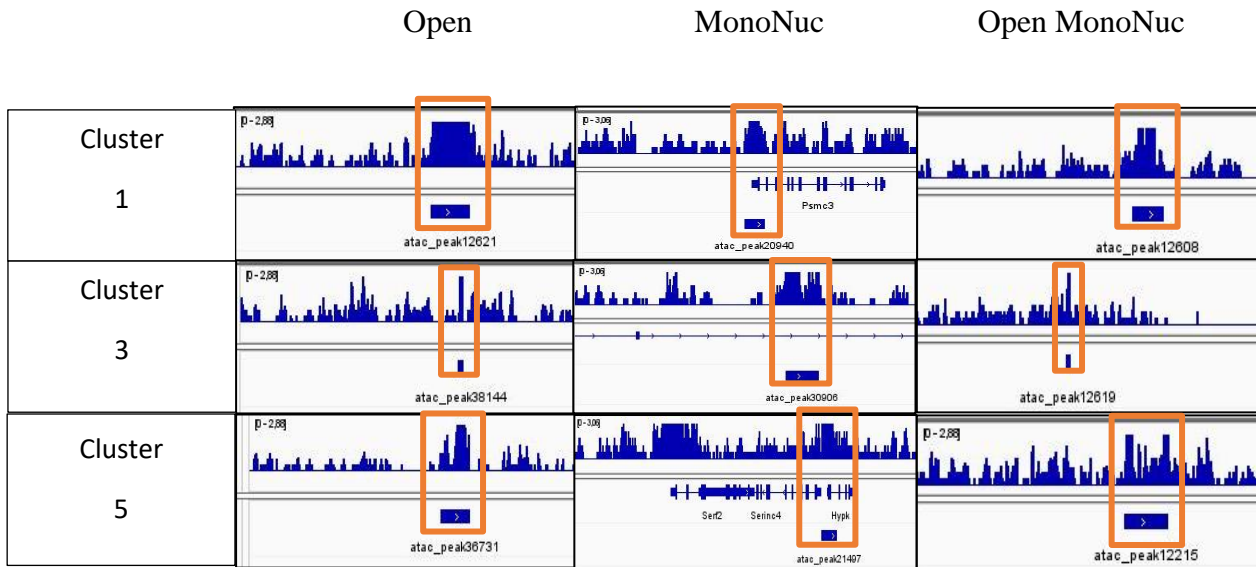
a)

b)

Supplementary figure 2. Violin plots representind distribution of the means and standard deviation from standarised data of each of the five indices for the a) Open, b) MonoNuc and c) MonoNuc Open data.

Supplementary figure 3. Representation of some examples of the distinctive morphology of the peaks of clusters 1, 3 and 5 from Open, MonoNuc and Open MonoNuc data.
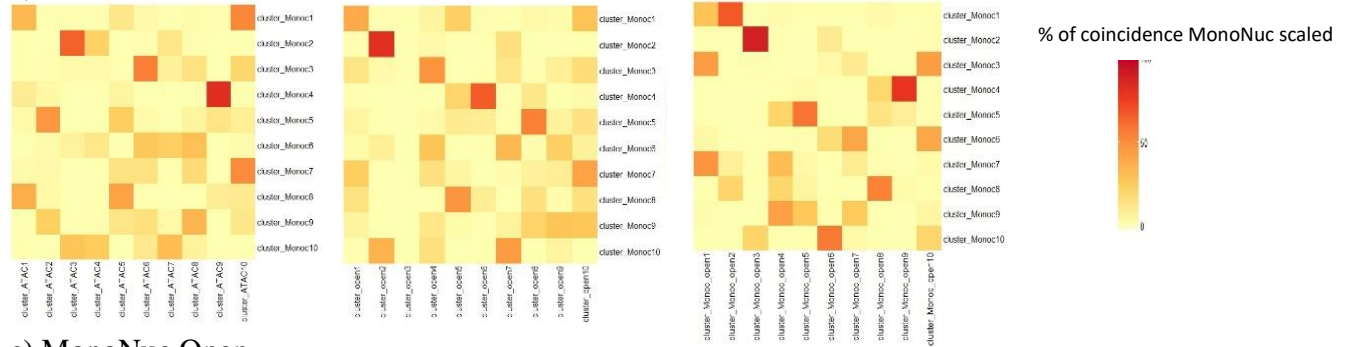
Supplementary figure 4. Heatmaps of coincidence. Number of overlapping regions that share the clusters of the different types of data scaled based on the cluster length of each input. a) Open, b) MonoNuc and c) MonoNuc Open.
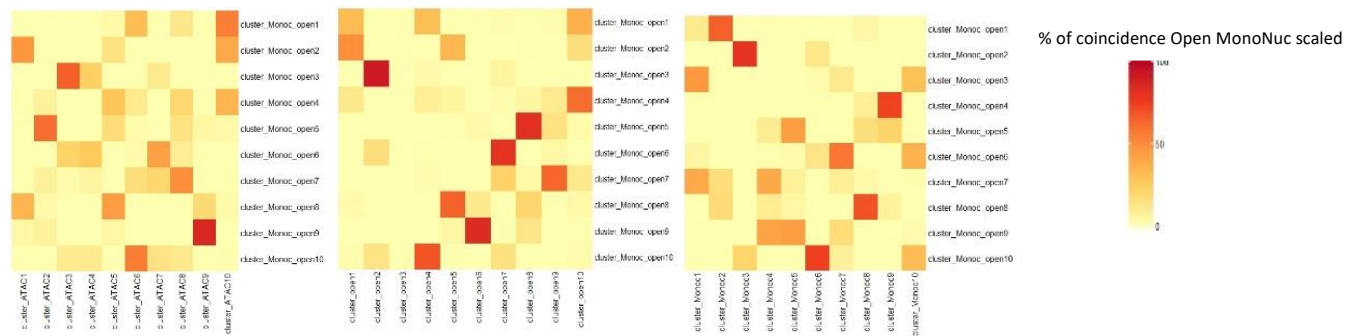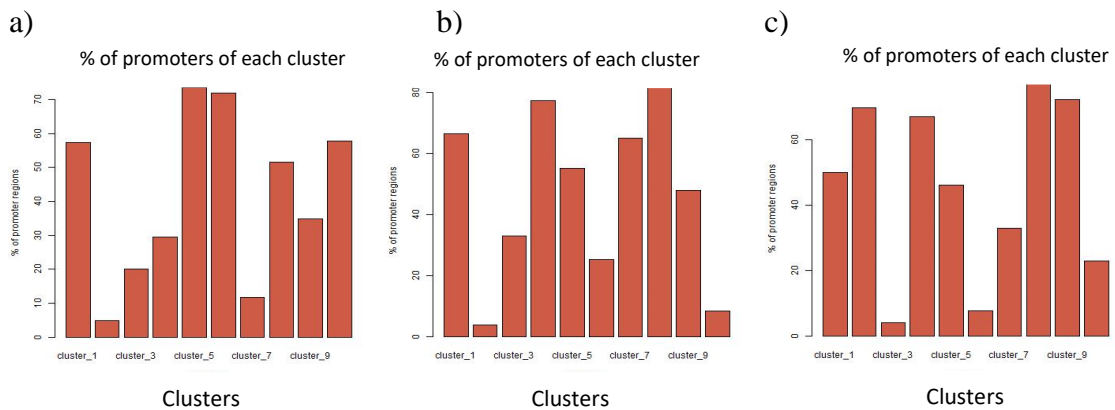
a) Open
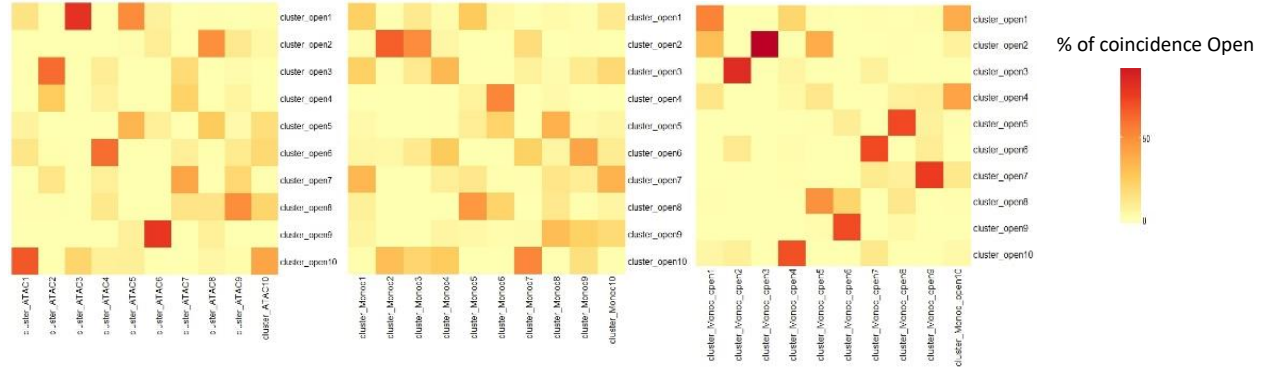
b) MonoNuc

c) MonoNuc Open


Supplementary figure 5. Percentage of promoter regions that comforms each cluster for the a) Open, b) MonoNuc and c) MonoNuc Open data. The number of promoter regions based on the classification performed by the logistic prediction model.
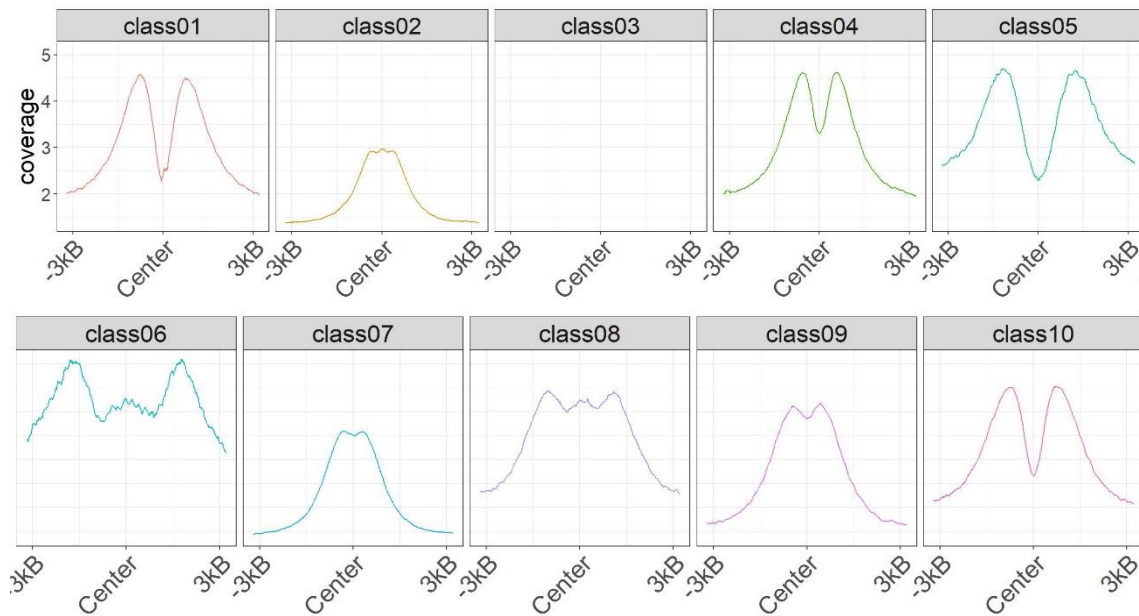
Supplementary figure 6. Distribution of the histone mark signal and de ATAC-seq data of the Open set of data. The plot shows the intensity and coverage of the signal in one centered spot of each region found and extents 3kb upstream and downstream. a) Distribution of the H3K4me1 histone mark, b) Distribution of the H3K4me3 histone mark, c) Distribution of the H3K27ac histone mark, d) Distribution of the ATAC-seq reads over the different clusters.

a) Matrix data
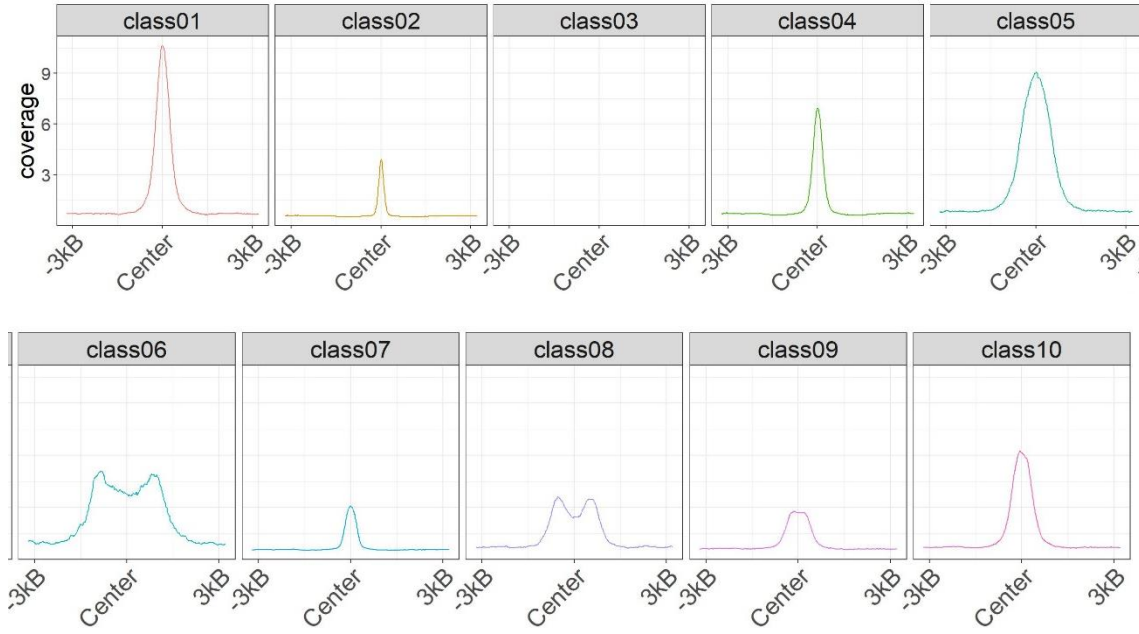
b) H3K4me1

c) H3K4me3

d) H3K27ac

Supplementary figure 7. Distribution of the histone mark signal and de ATAC-seq data of the MonoNuc set of data. The plot shows the intensity and coverage of the signal in one centered spot of each region found and extents 3kb upstream and downstream. a) Distribution of the H3K4me1 histone mark, b) Distribution of the H3K4me3 histone mark, c) Distribution of the H3K27ac histone mark, d) Distribution of the ATAC-seq reads over the different clusters.
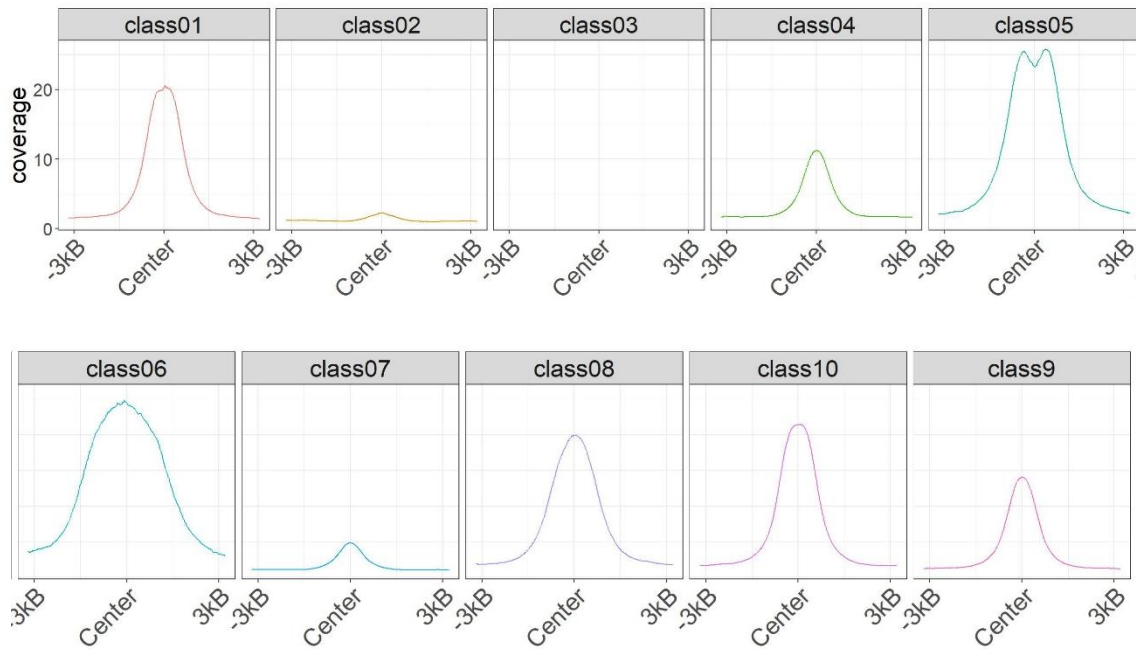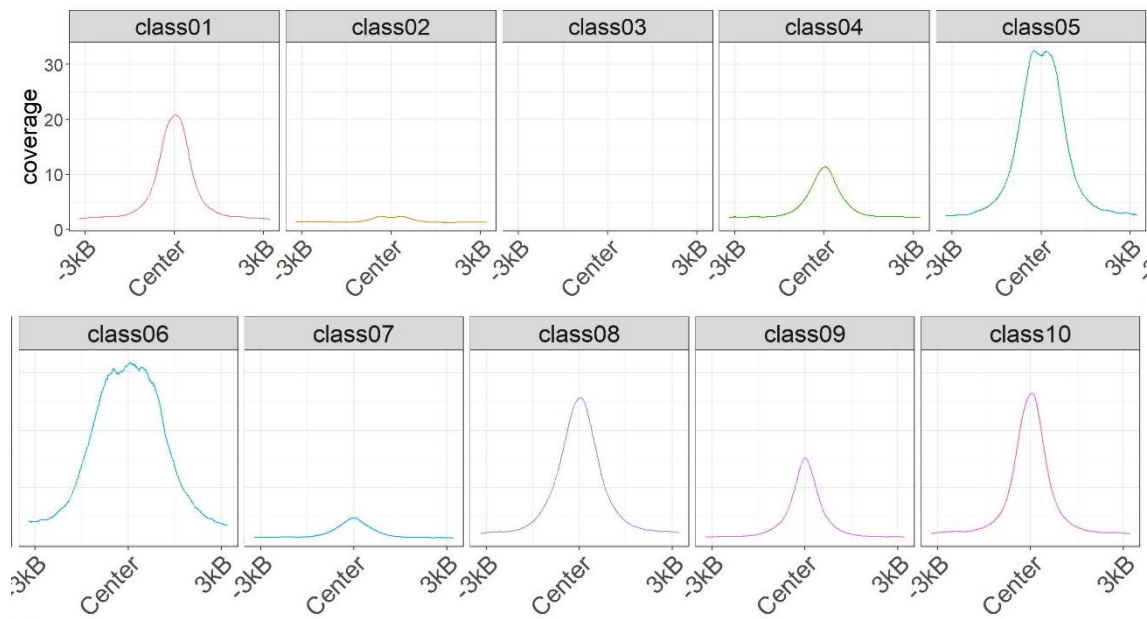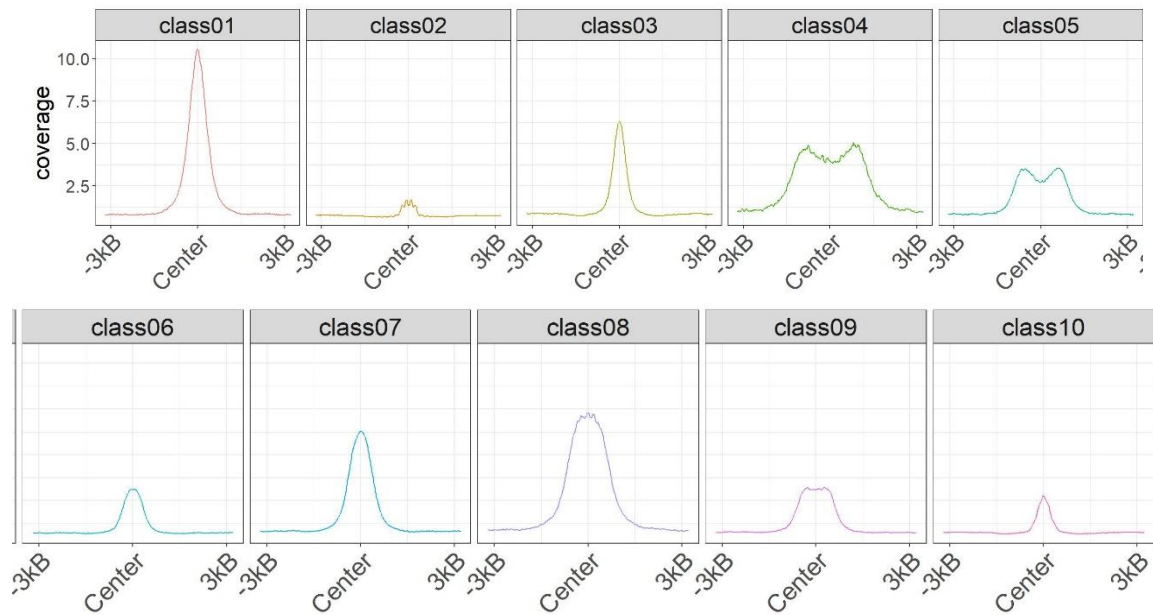
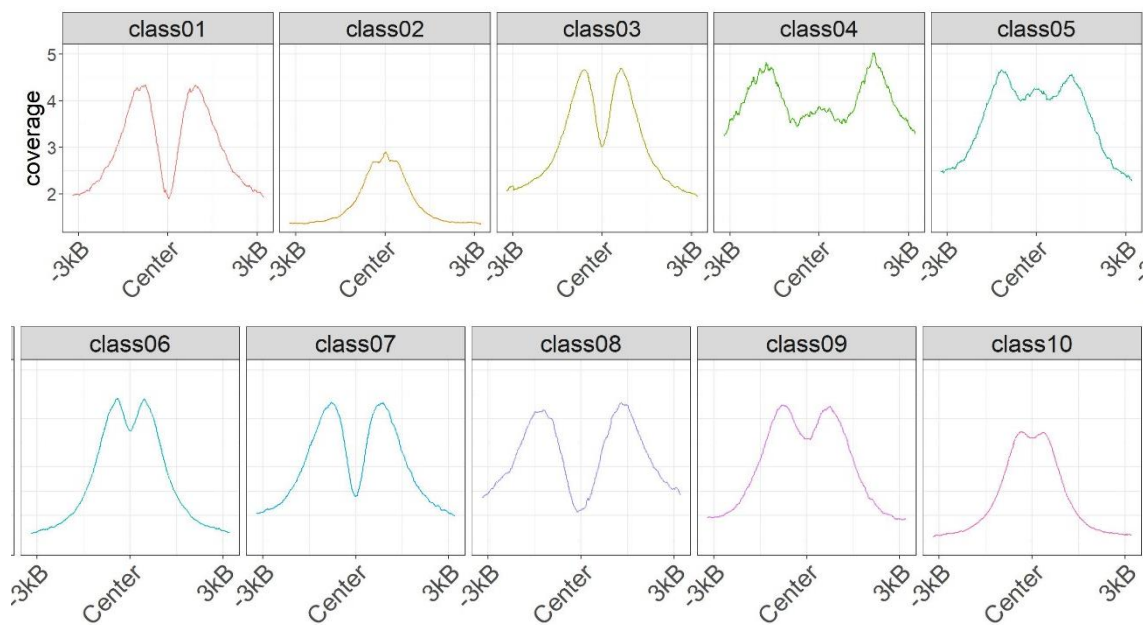a) Matrix data

b) H3K4me1

c) H3K4me3

d) H4K27ac

Supplementary figure 8. Distribution of the histone mark signal and the ATAC-seq data of the Open MonoNuc set of data. The plot shows the intensity and coverage of the signal in one centered spot of each region found and extents 3kb upstream and downstream. a) Distribution of the H3K4me1 histone mark, b) Distribution of the H3K4me3 histone mark, c) Distribution of the H3K27ac histone mark, d) Distribution of the ATAC-seq reads over the different clusters.
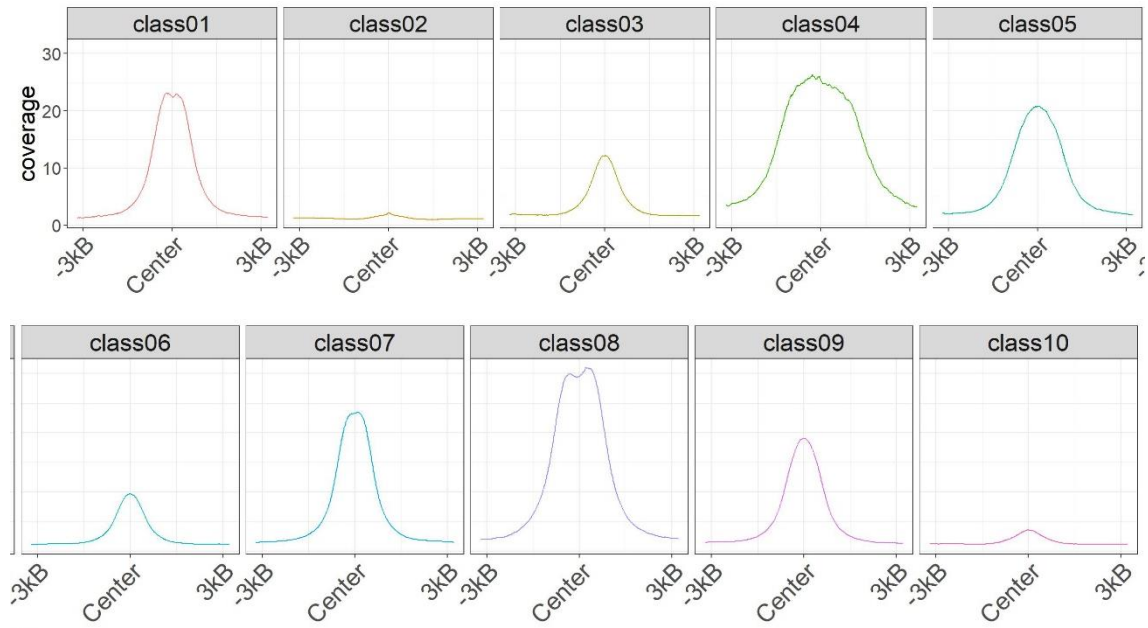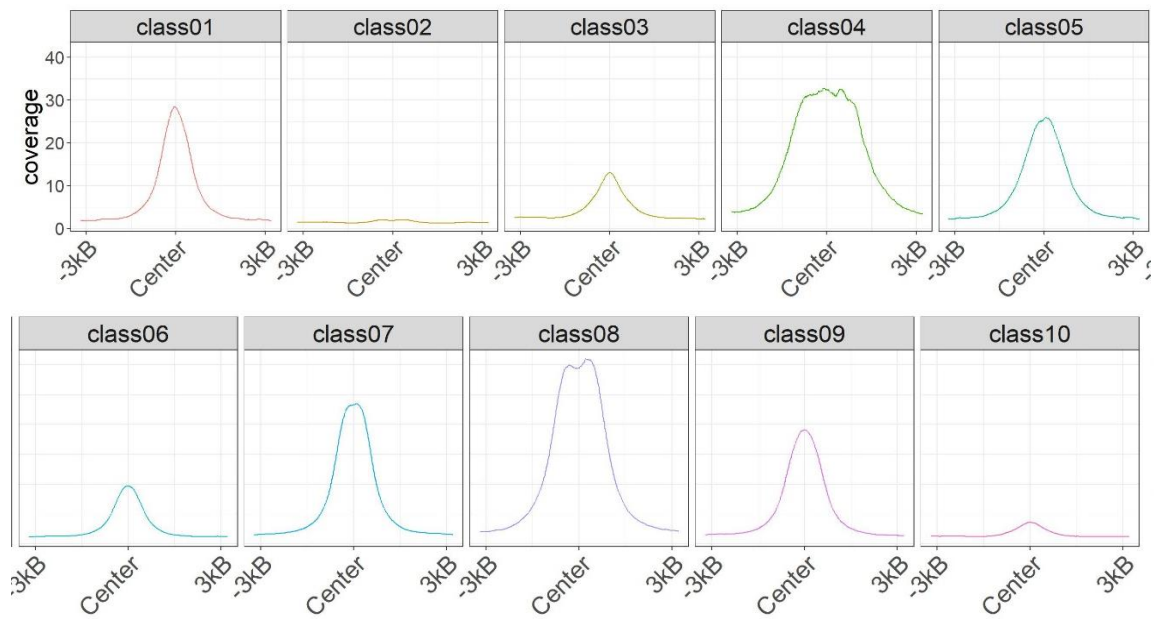
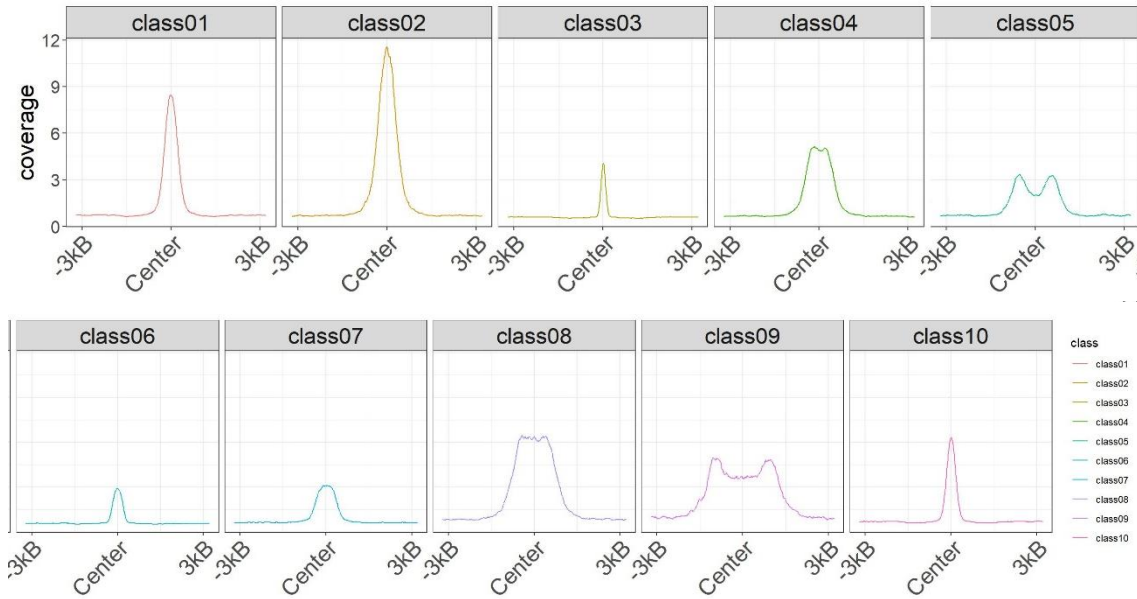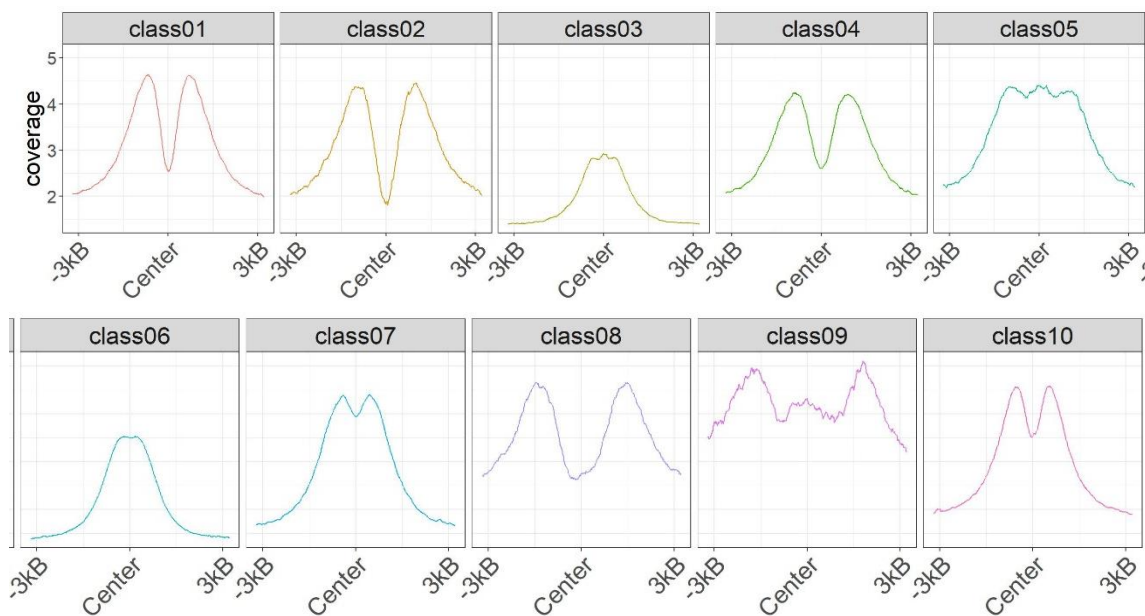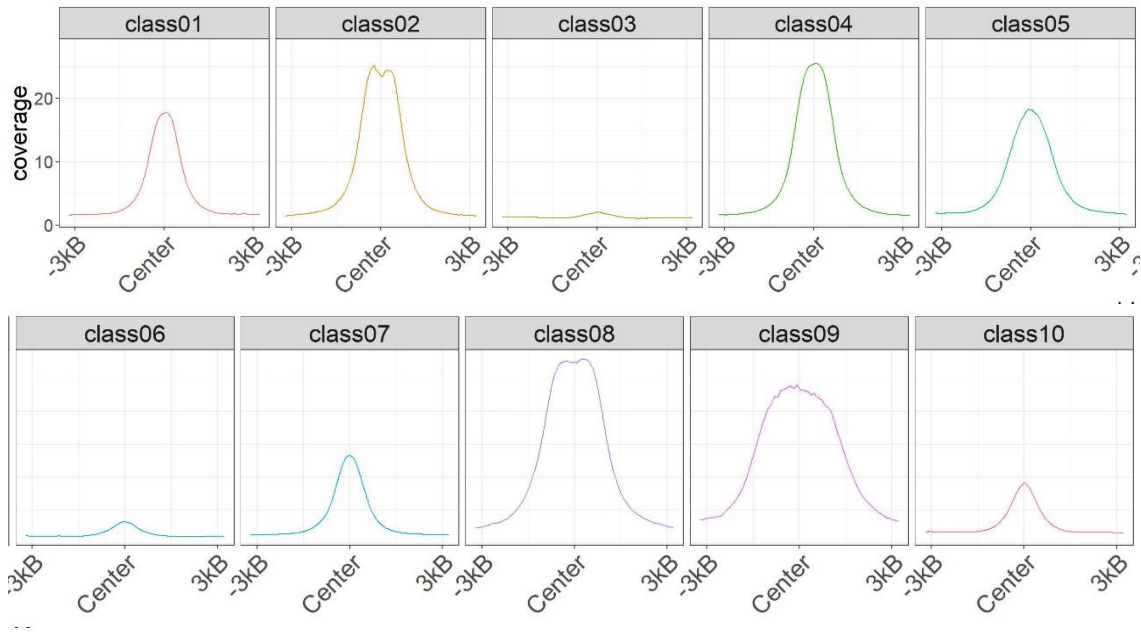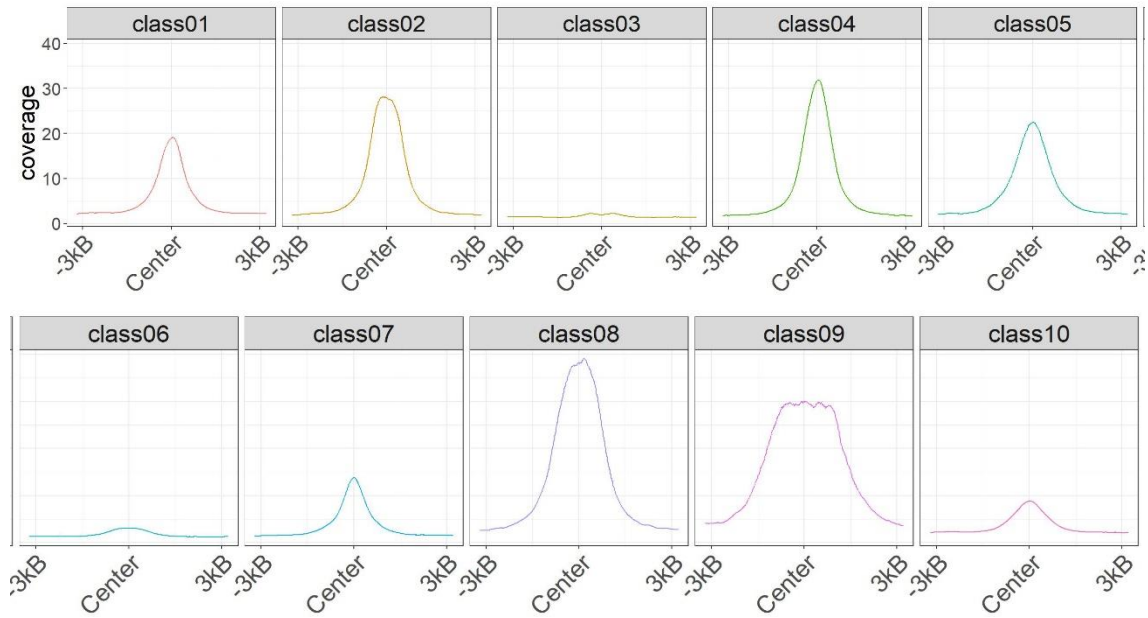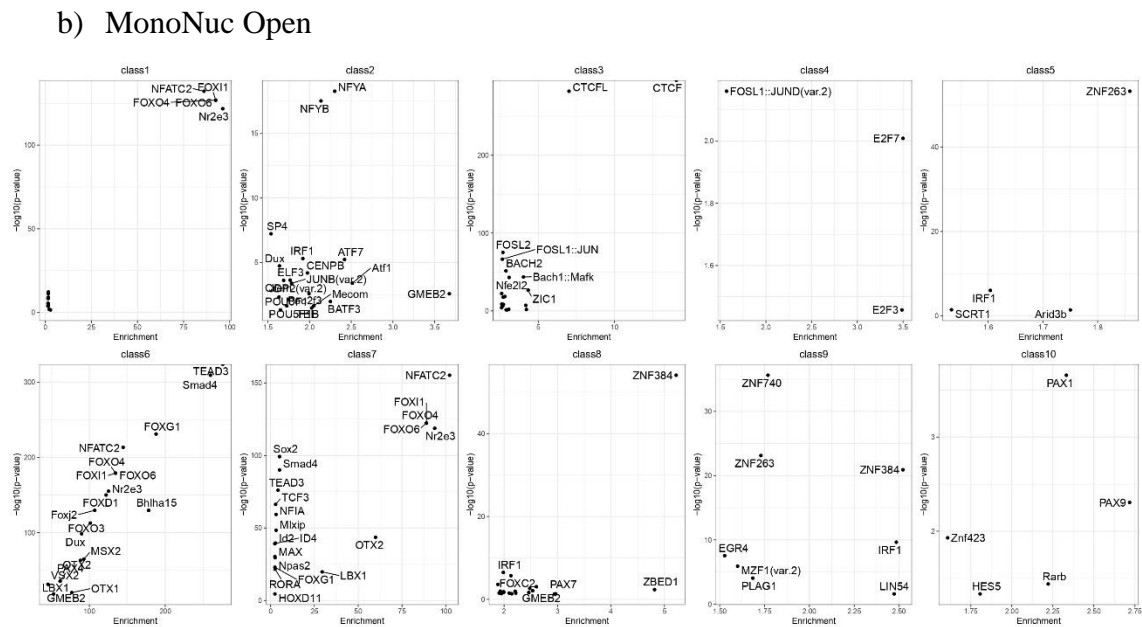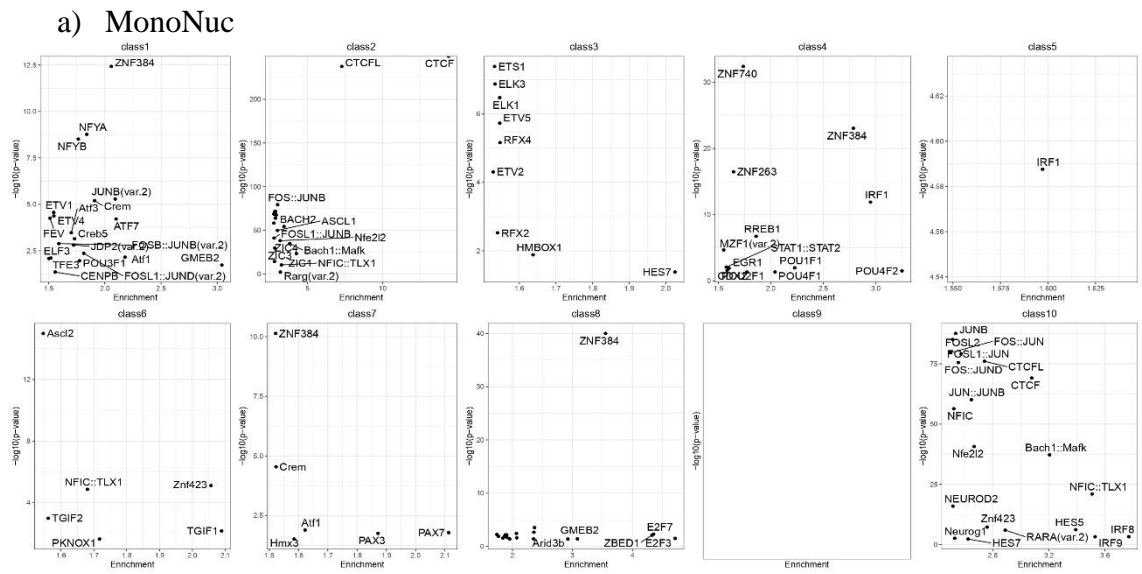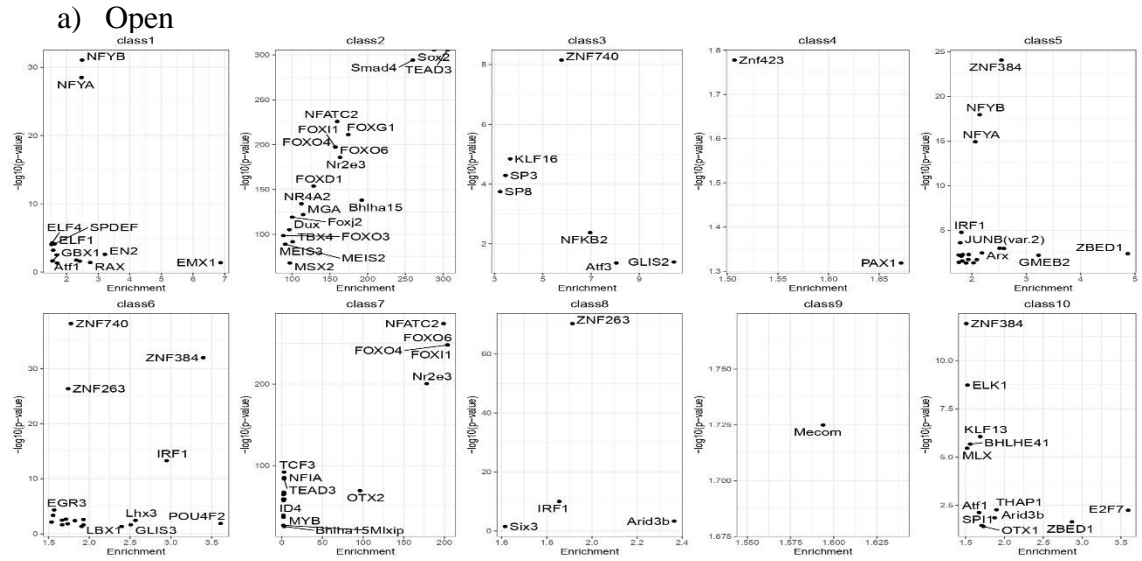a) Matrix data

b) H3K4me1

c) H3K4me3

d) H3K27ac

Supplementary figure 9. Most significative transcription factors associated to found motifs for each cluster of the a) Open, b) MonoNuc and c) Open MonoNuc data. The transcription factors shown are filtered by enrichment and p-value (Enr > 1.5, p-value < 0.05)
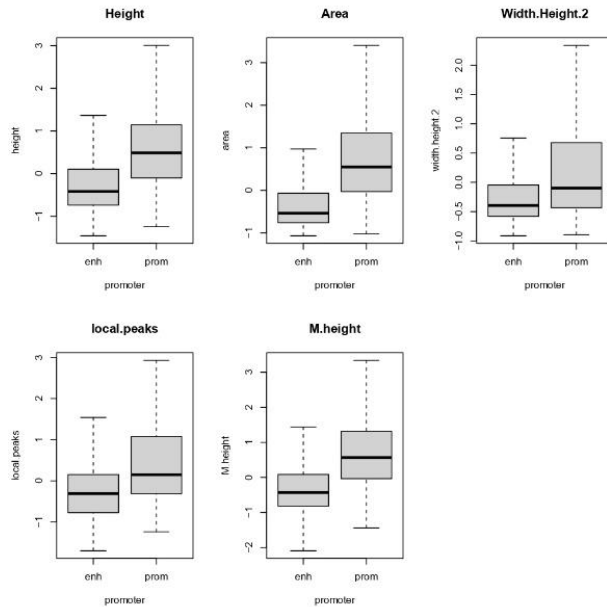
a) Open

a) MonoNuc

b) MonoNuc Open

Supplementary figure 10. Relevant information and graphics about the prediction model of Open data. a) Distribution of the five morphological indices depending on the nature of the classified region promoter or enhancer. b) Representation of the area under the curve evaluation method. ROC Curve representing sensibility over. c) Confusion matrix for model validation predictions being on the x axis and observations on y axis. d) Percentaje comparing the promoter regions predicted by the model for each cluster versus the true percentaje of true promoter regions of each cluster.

a)

b)

c)

d)
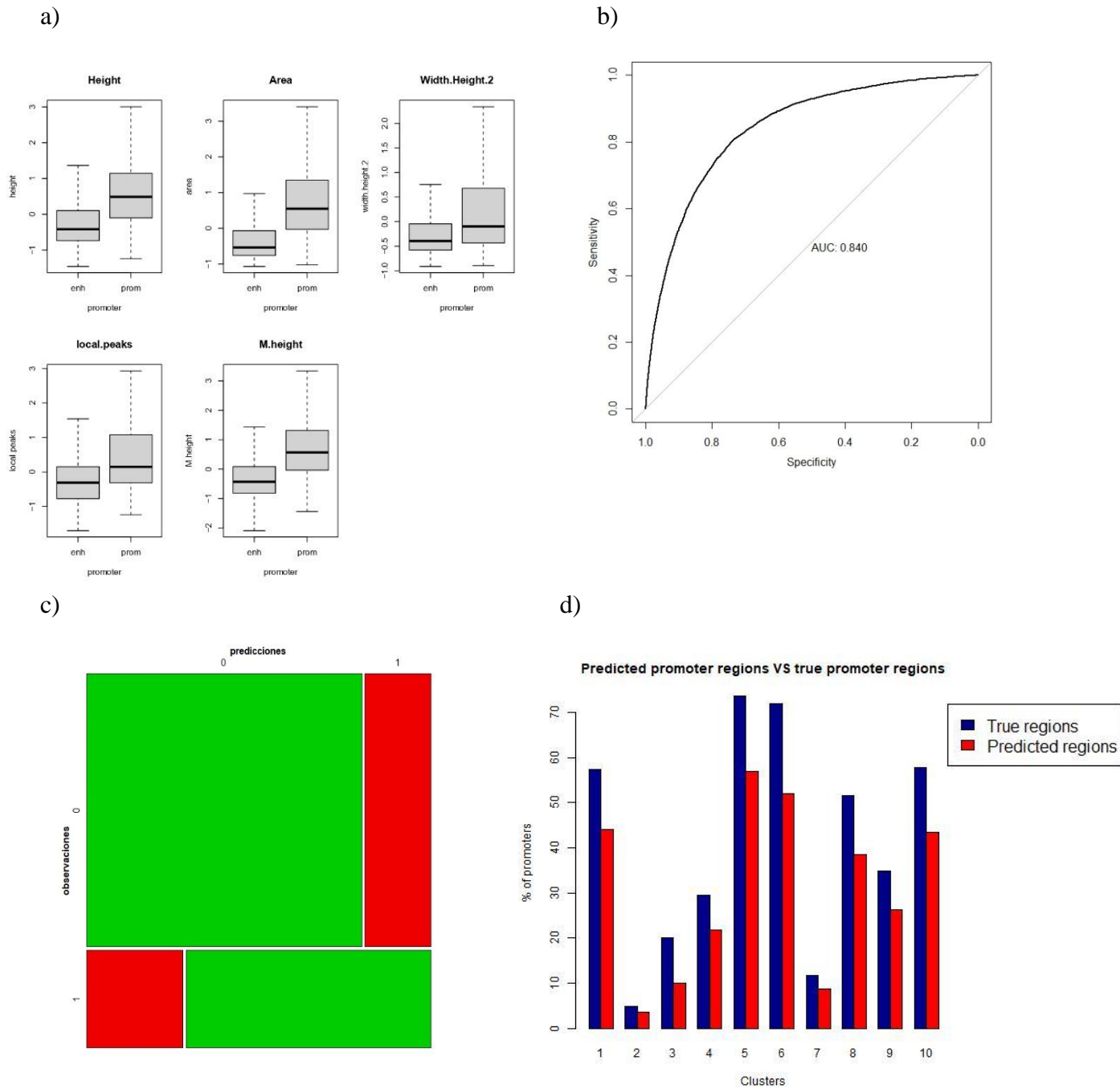
Supplementary figure 11. Relevant information and graphics about the prediction model of MonoNuc data. a) Distribution of the five morphological indices depending on the nature of the classified region promoter or enhancer. b) Representation of the area under the curve evaluation method. ROC Curve representing sensibility over. c) Confusion matrix for model validation predictions being on the x axis and observations on y axis. d) Percentaje comparing the promoter regions predicted by the model for each cluster versus the true percentaje of true promoter regions of each cluster.
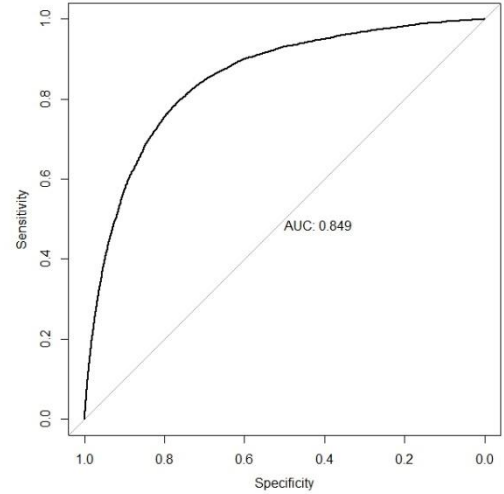
a)

b)

c)

d)
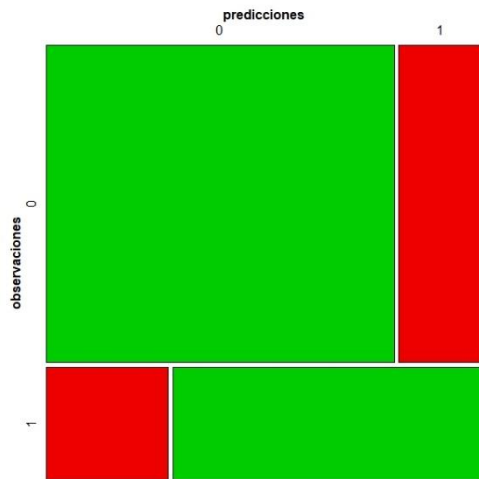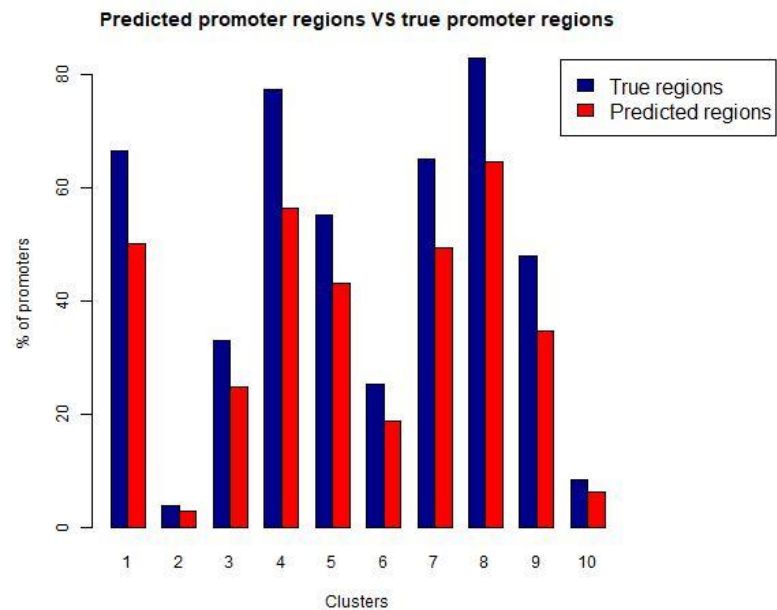
Supplementary figure 12. Relevant information and graphics about the prediction model of Open MonoNuc data. a) Distribution of the five morphological indices depending on the nature of the classified region promoter or enhancer. b) Representation of the area under the curve evaluation method. ROC Curve representing sensibility over. c) Confusion matrix for model validation predictions being on the x axis and observations on y axis. d) Percentaje comparing the promoter regions predicted by the model for each cluster versus the true percentaje of true promoter regions of each cluster.

a)

b)

c)

d)