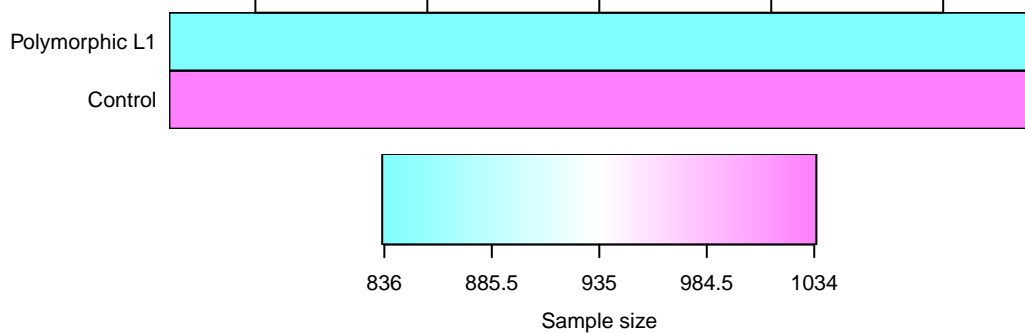
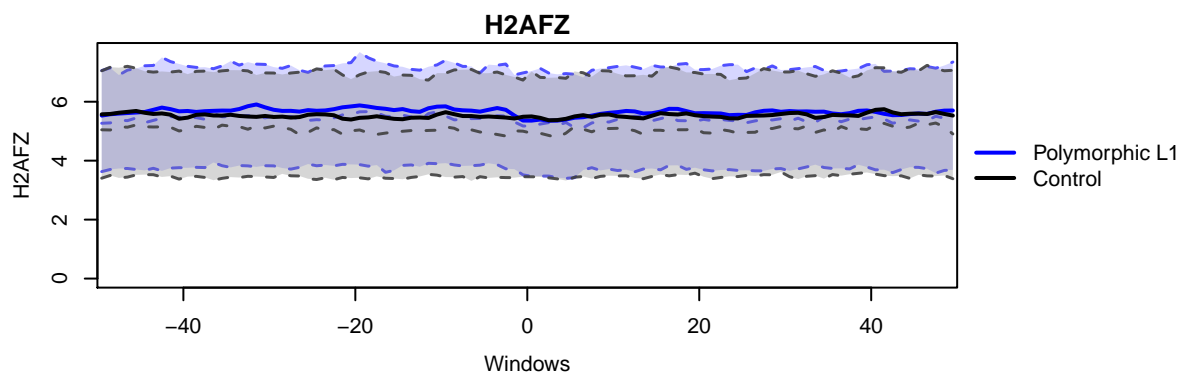
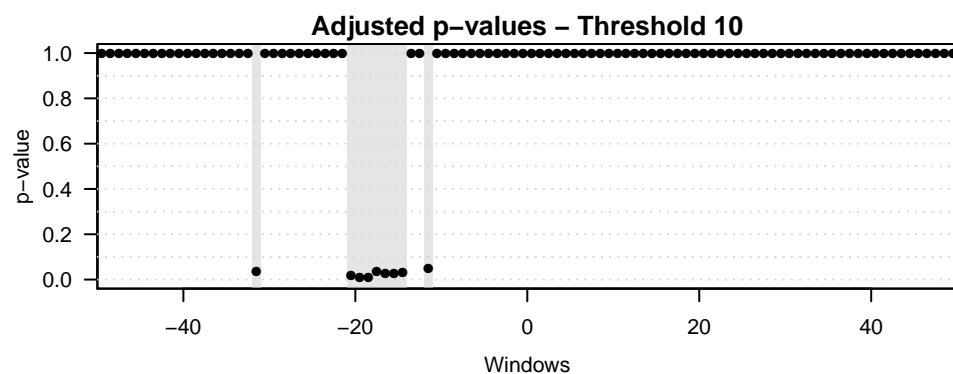
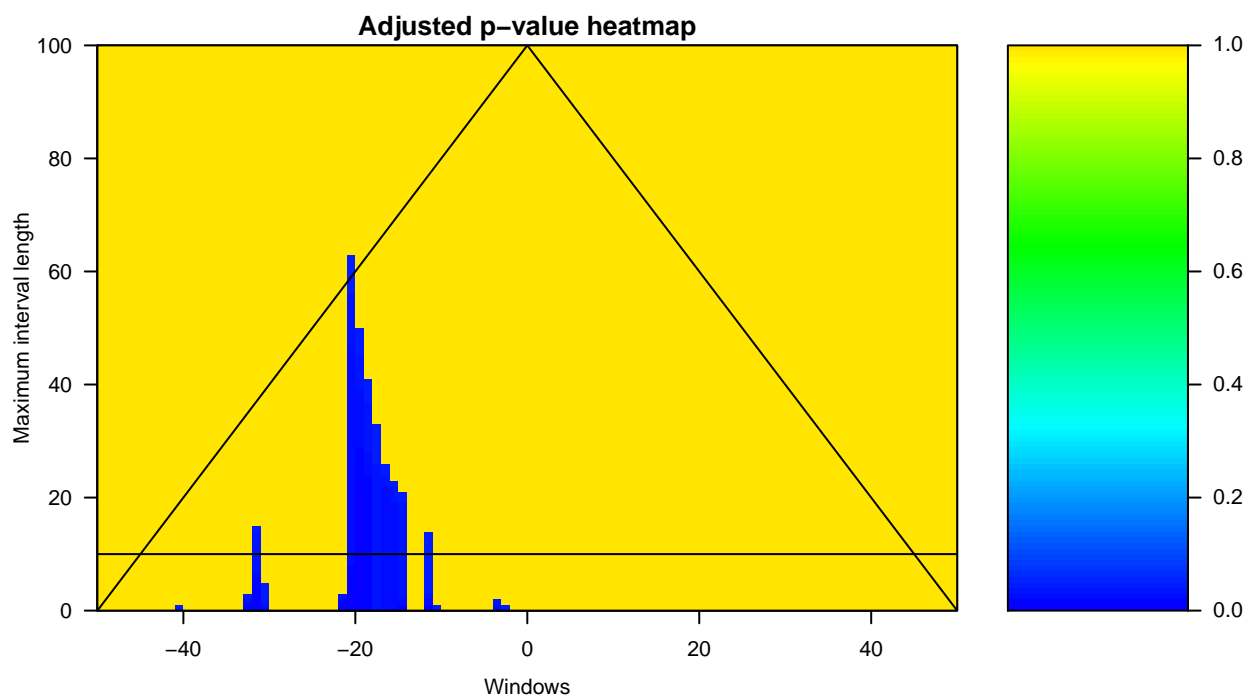
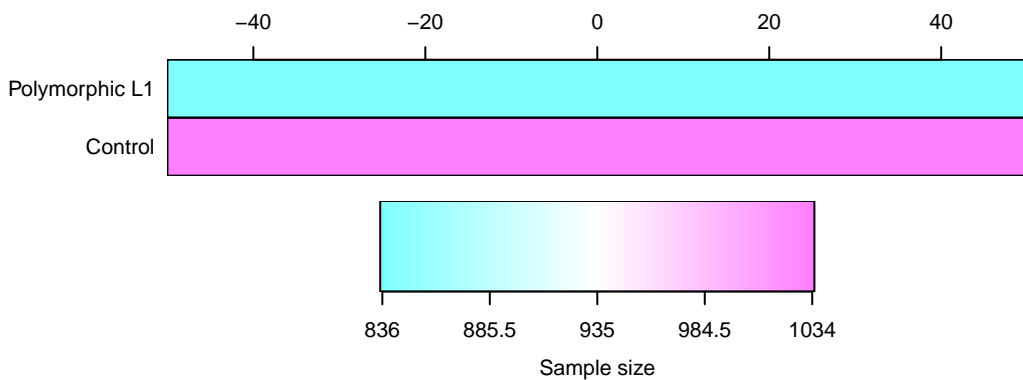
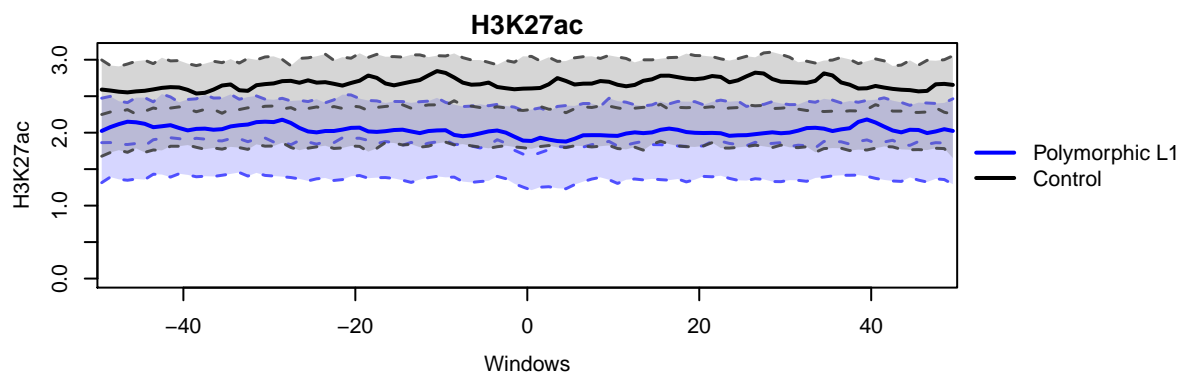
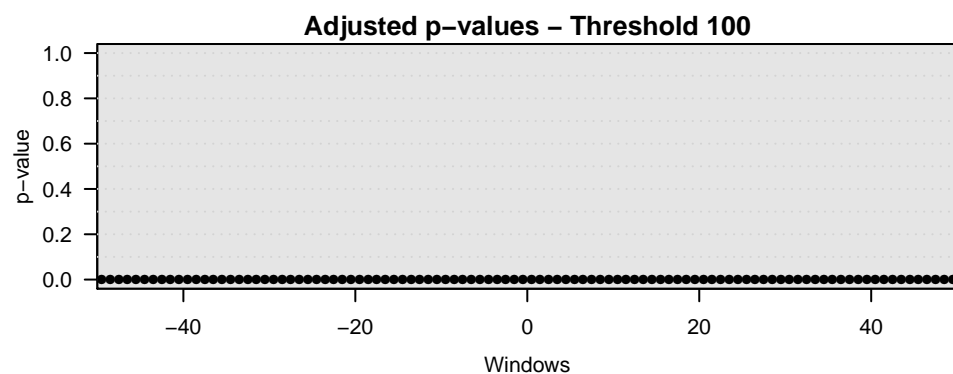
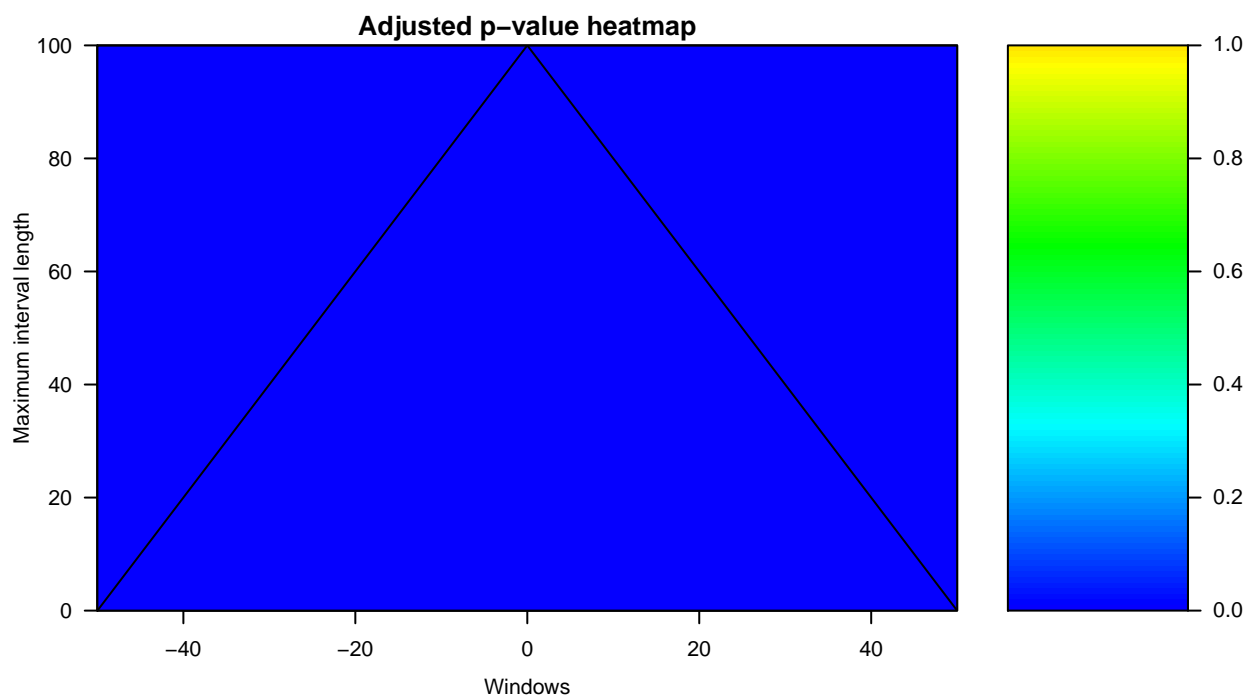


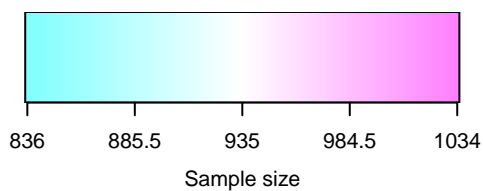
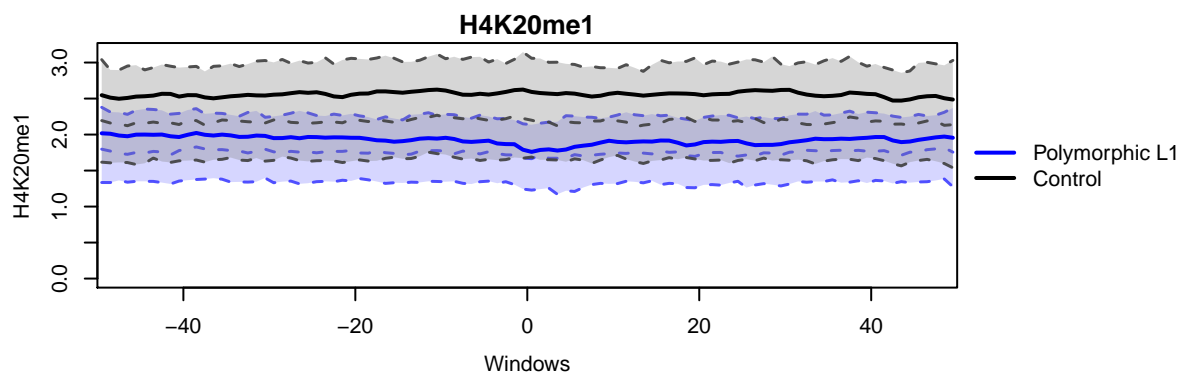
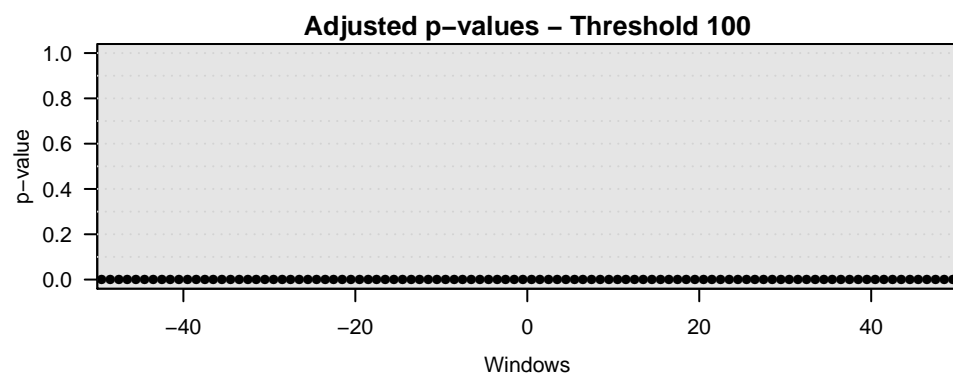
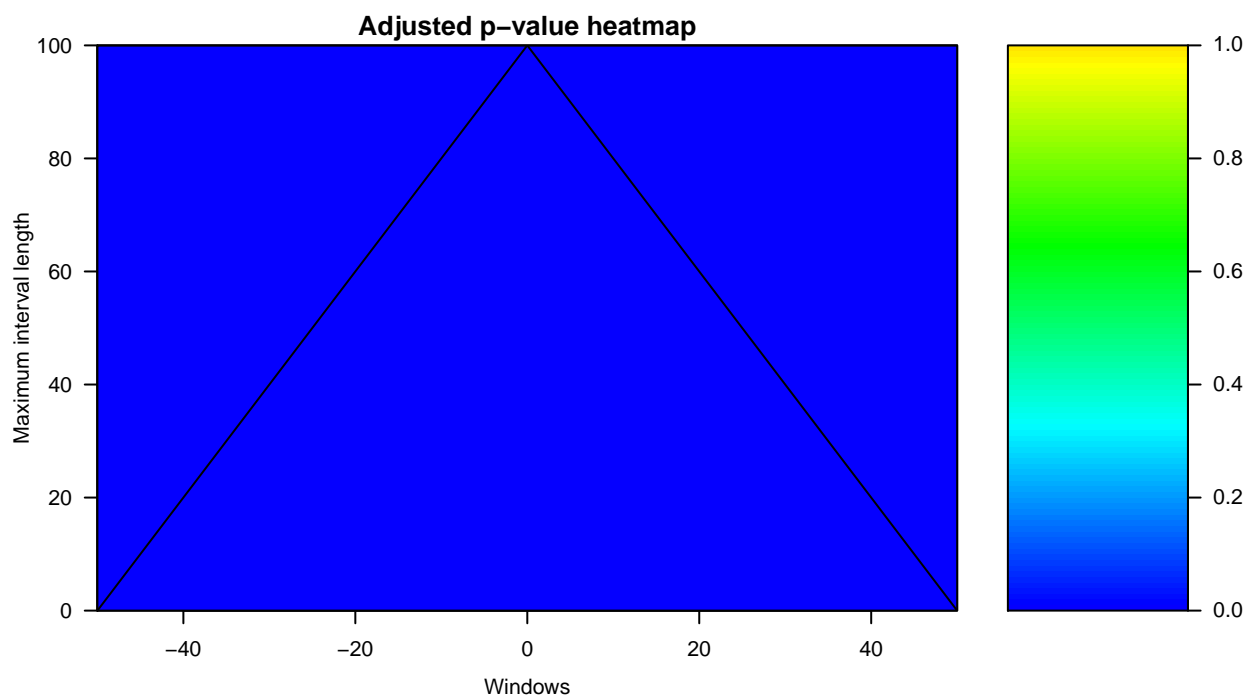
## H2AFZ



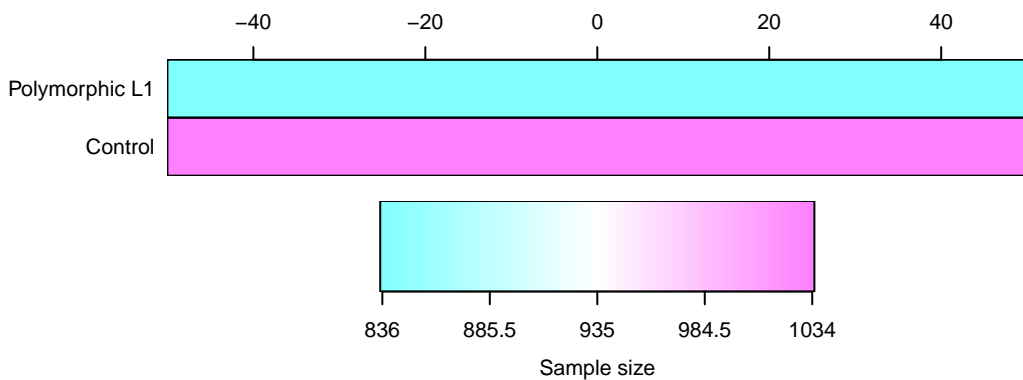
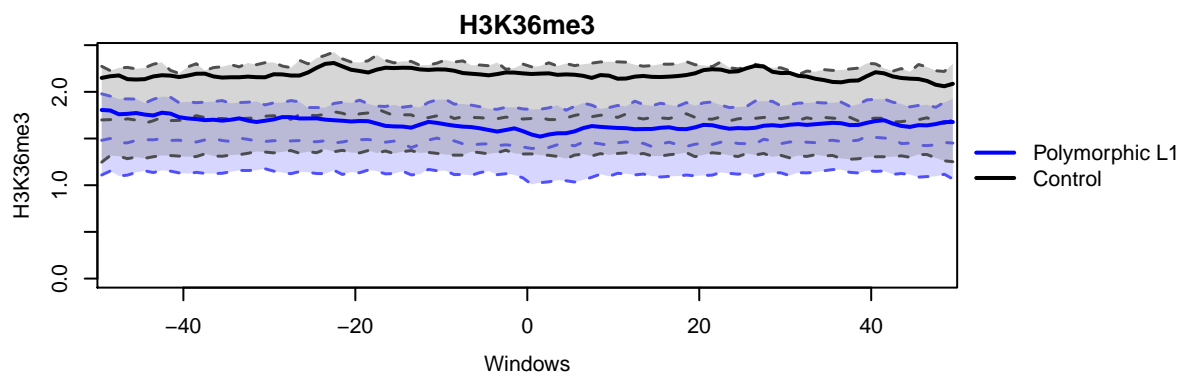
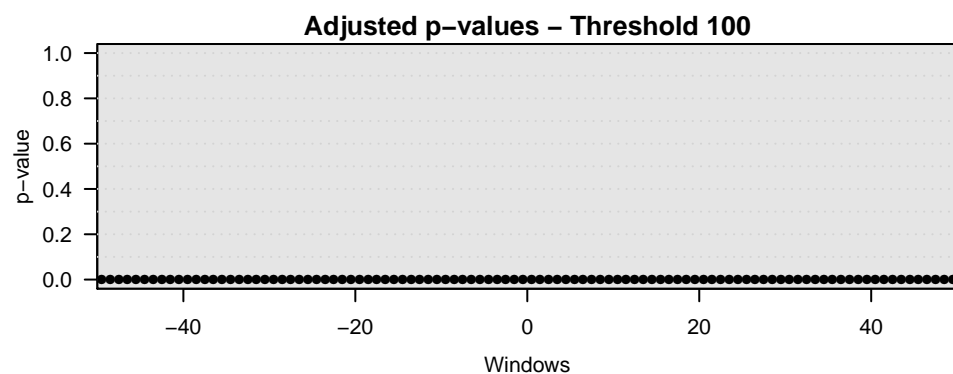
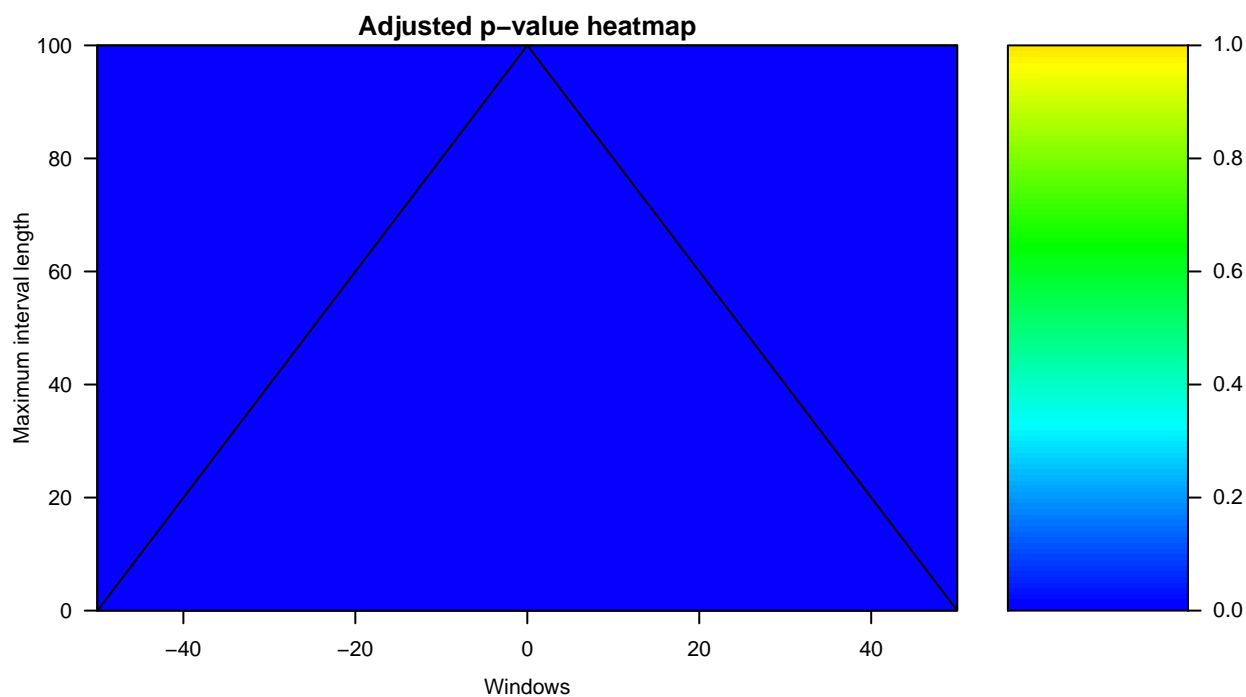
# H3K27ac



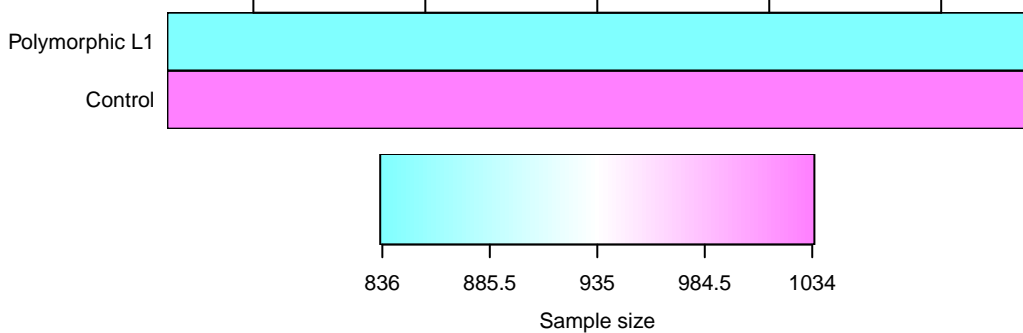
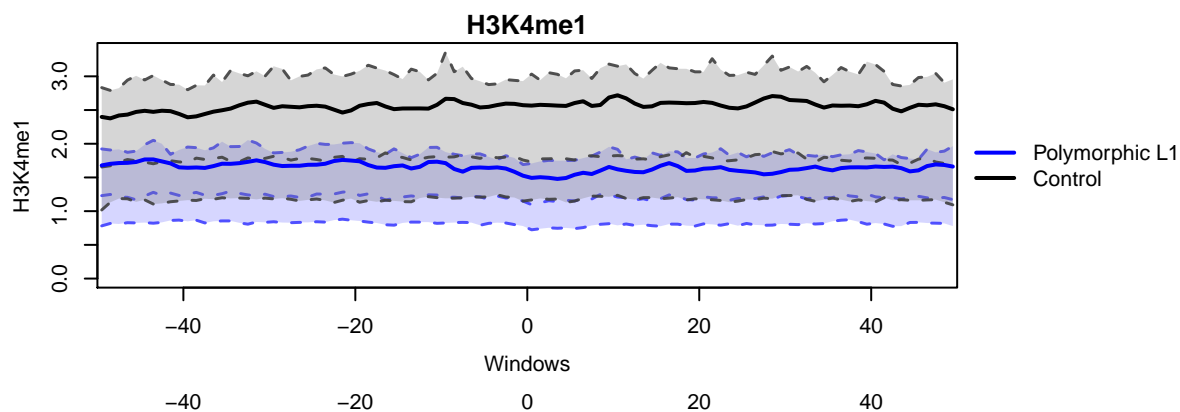
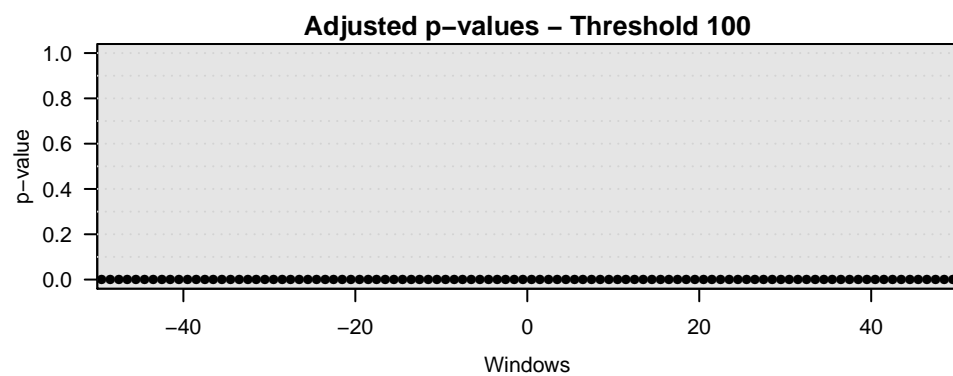
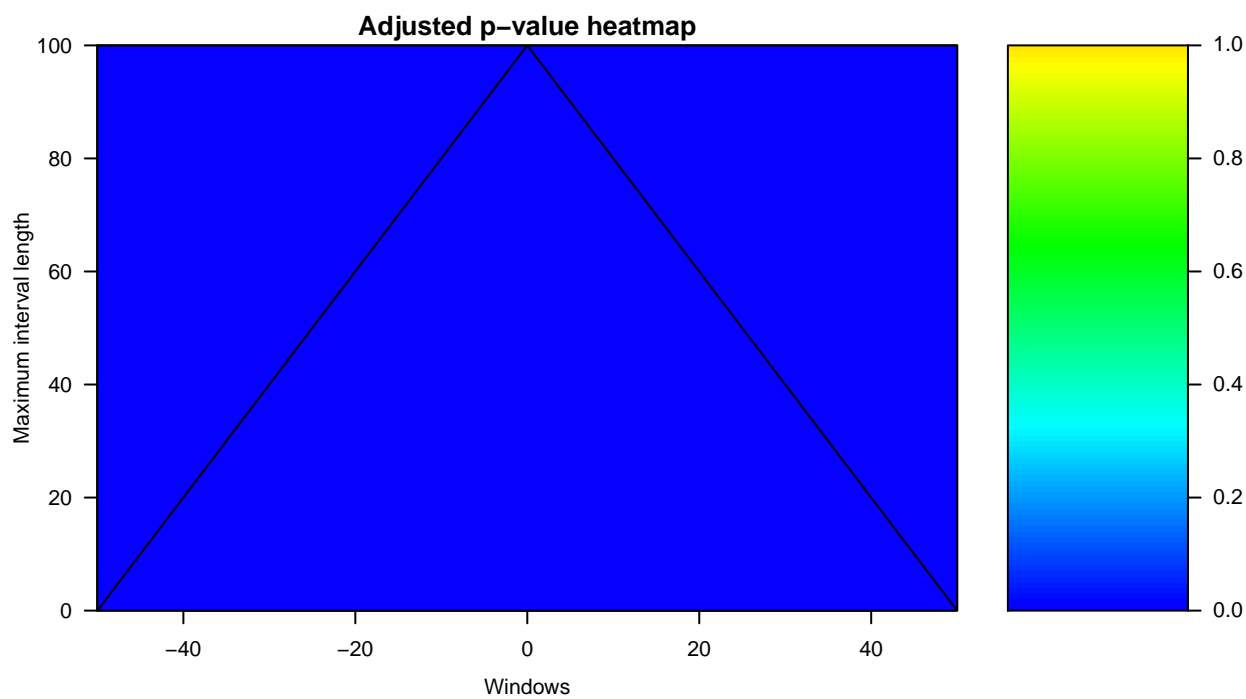
# H4K20me1



# H3K36me3

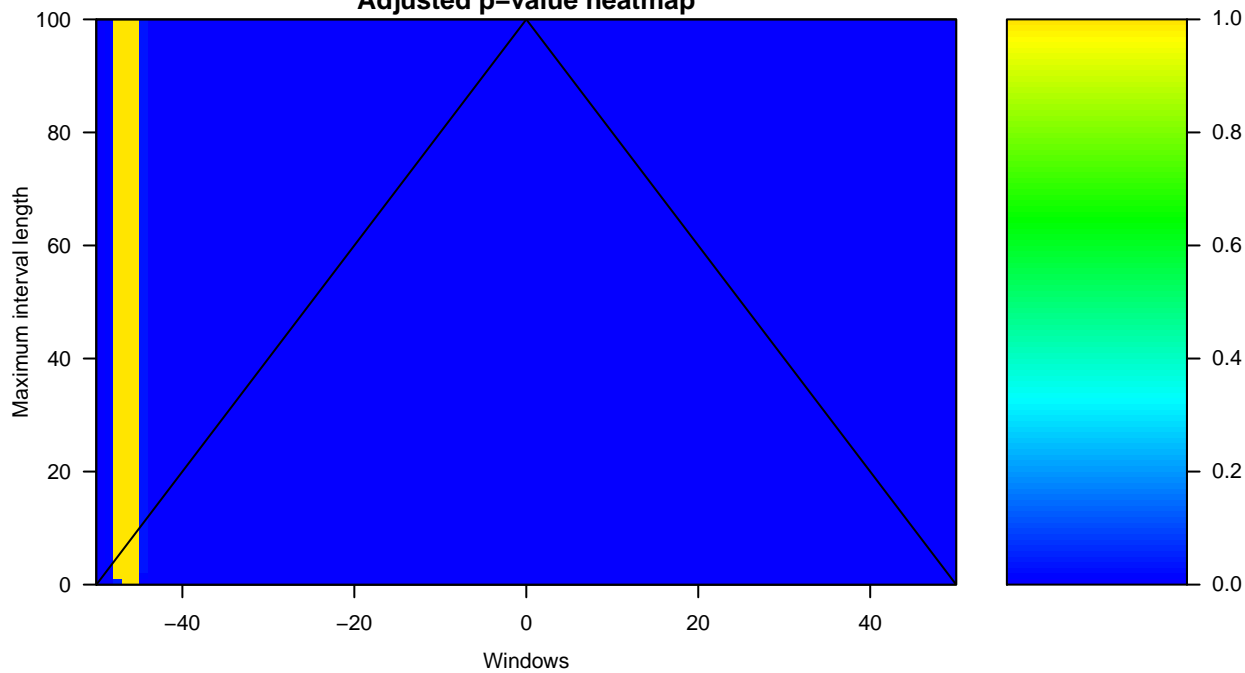


# H3K4me1

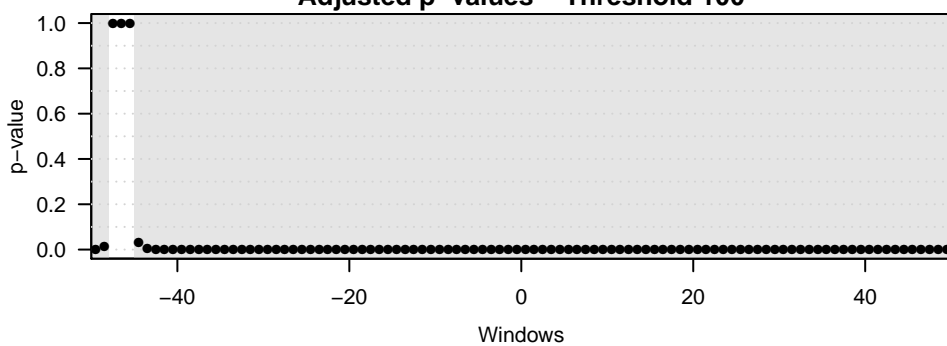


# H3K4me2

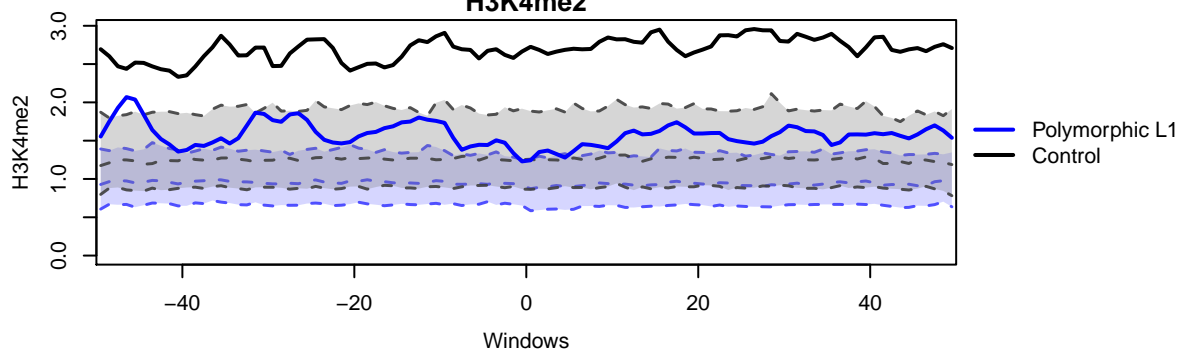
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# H3K4me2



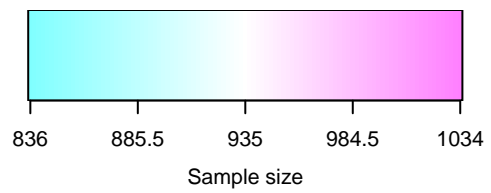
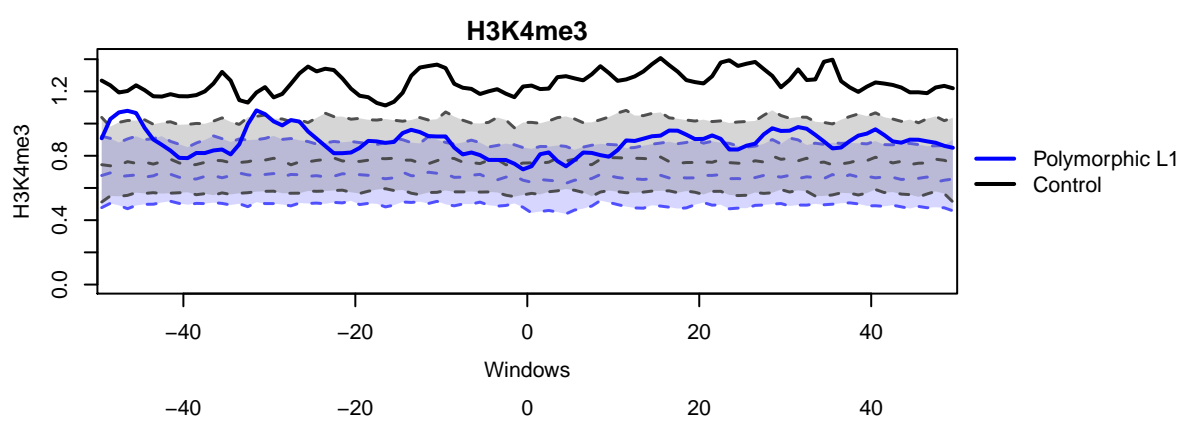
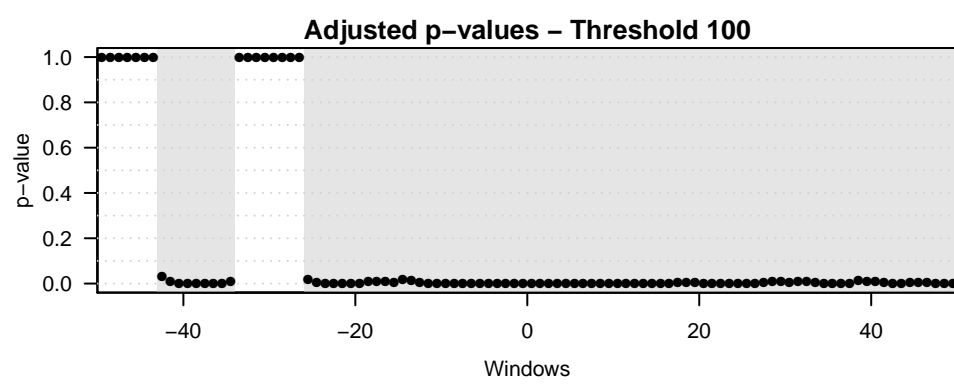
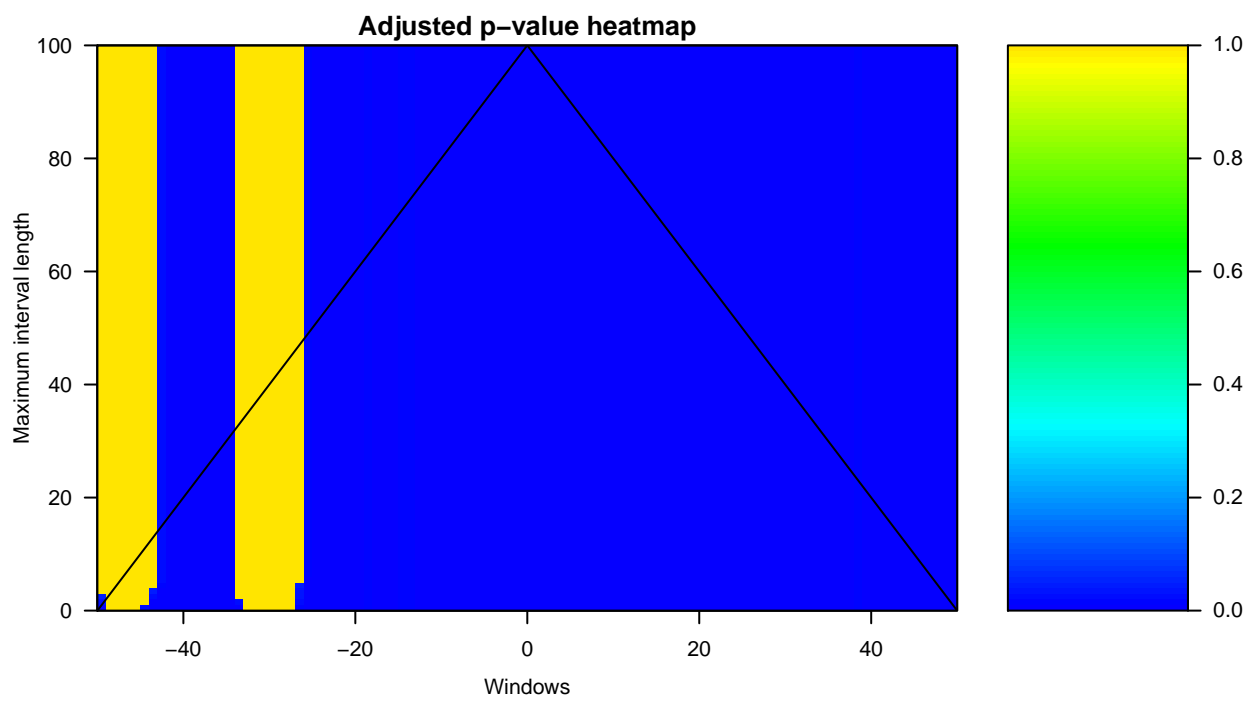
Polymorphic L1

Control

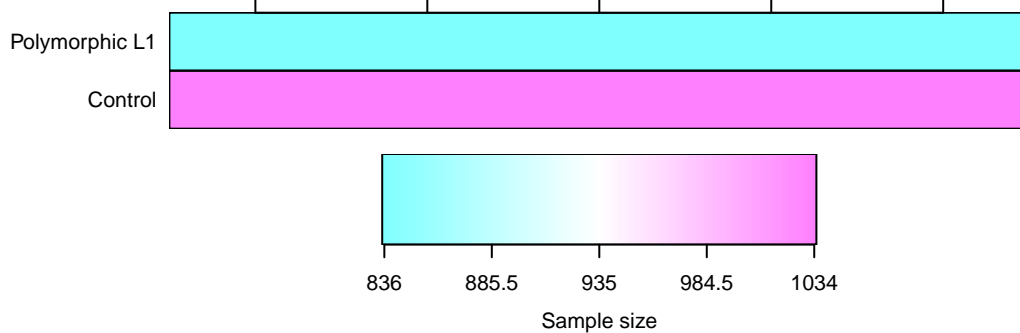
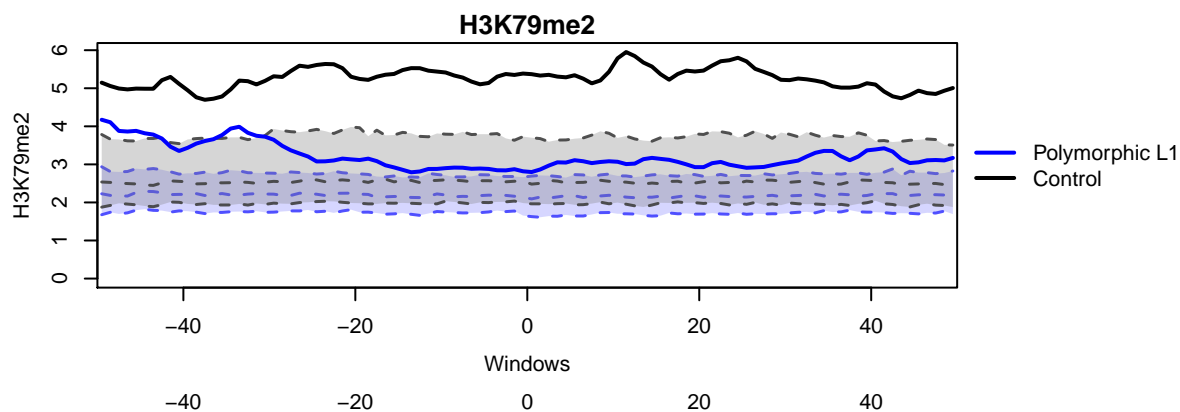
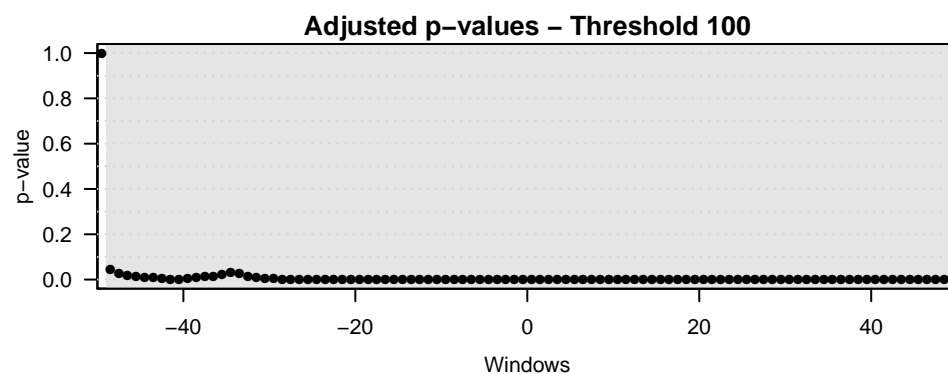
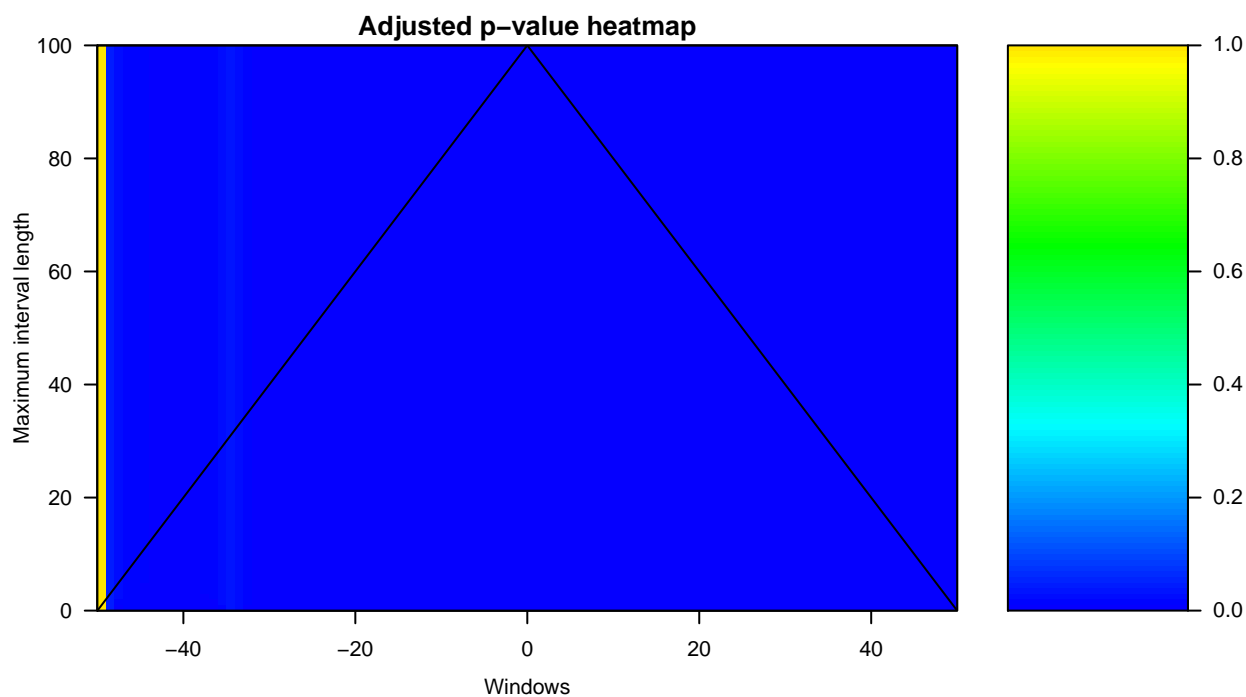
836 885.5 935 984.5 1034

Sample size

# H3K4me3

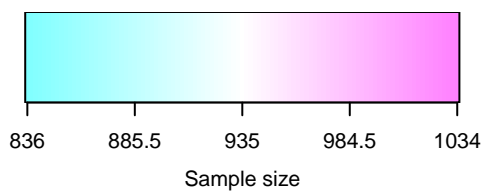
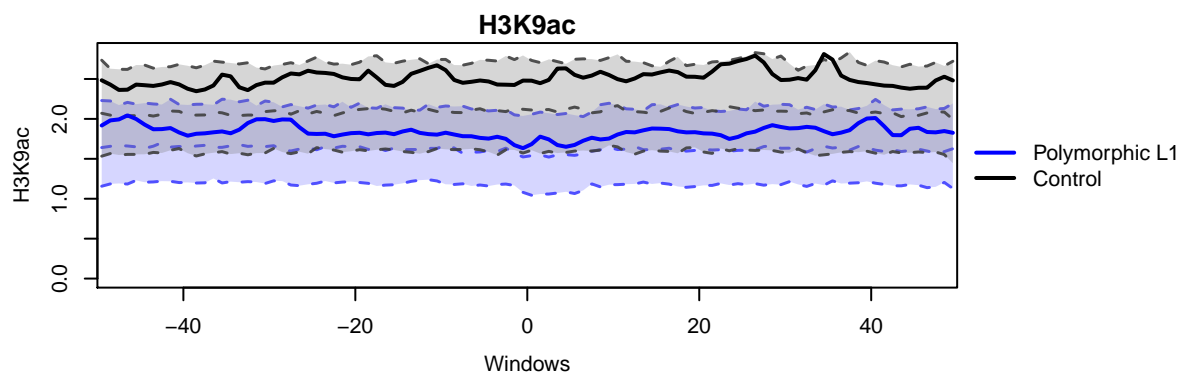
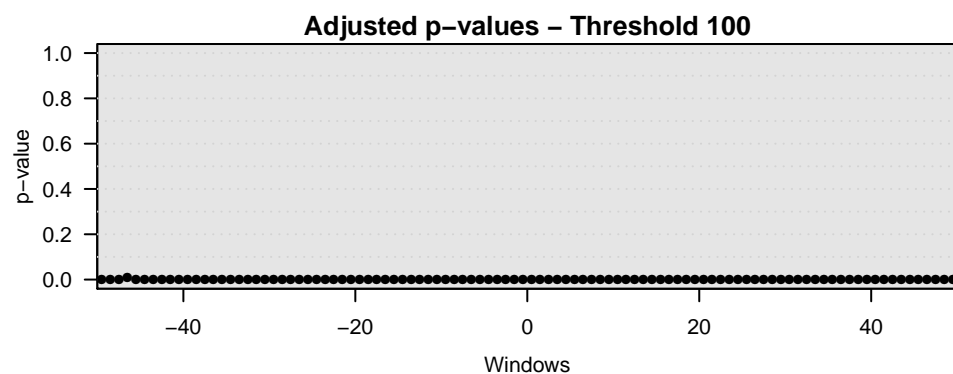
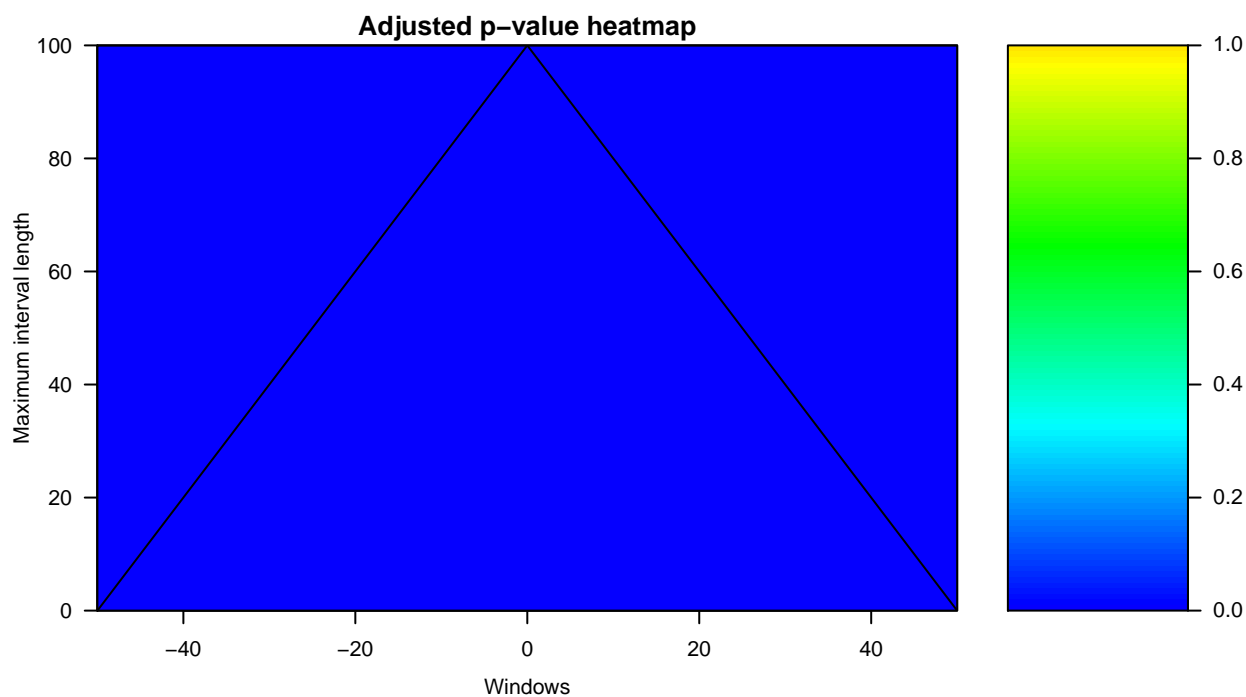


# H3K79me2

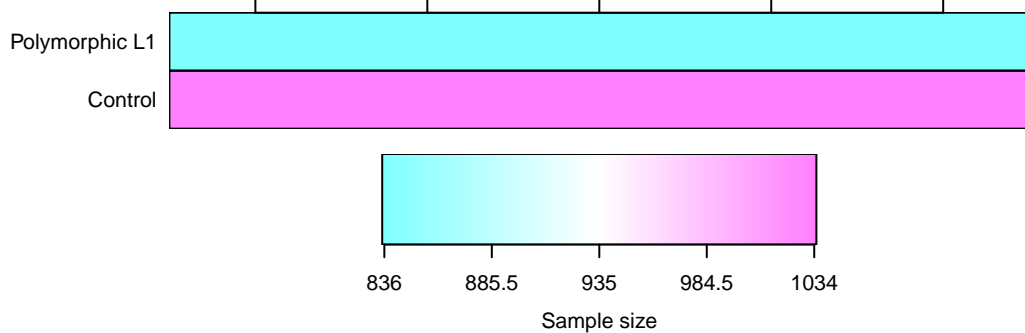
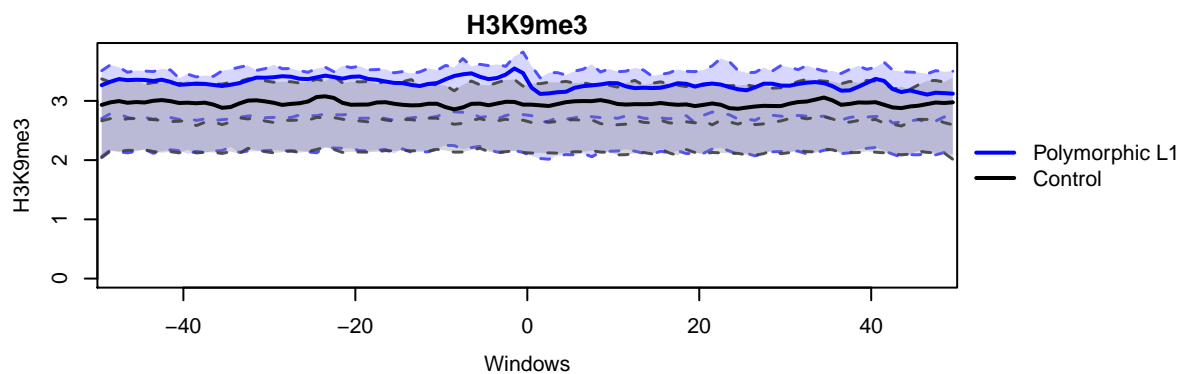
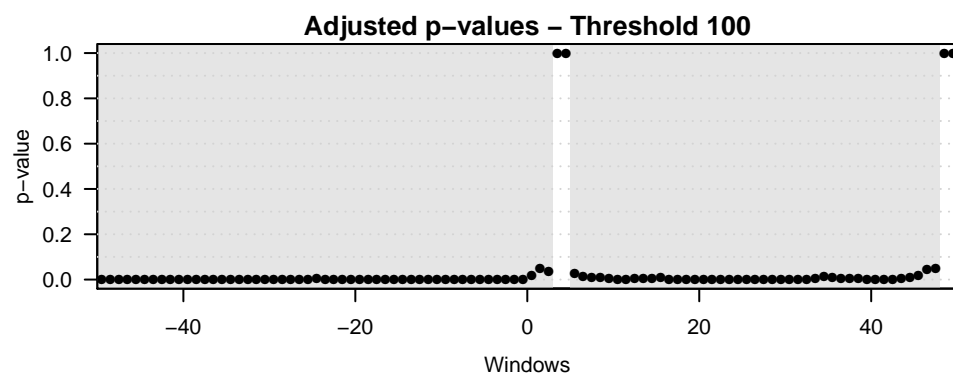
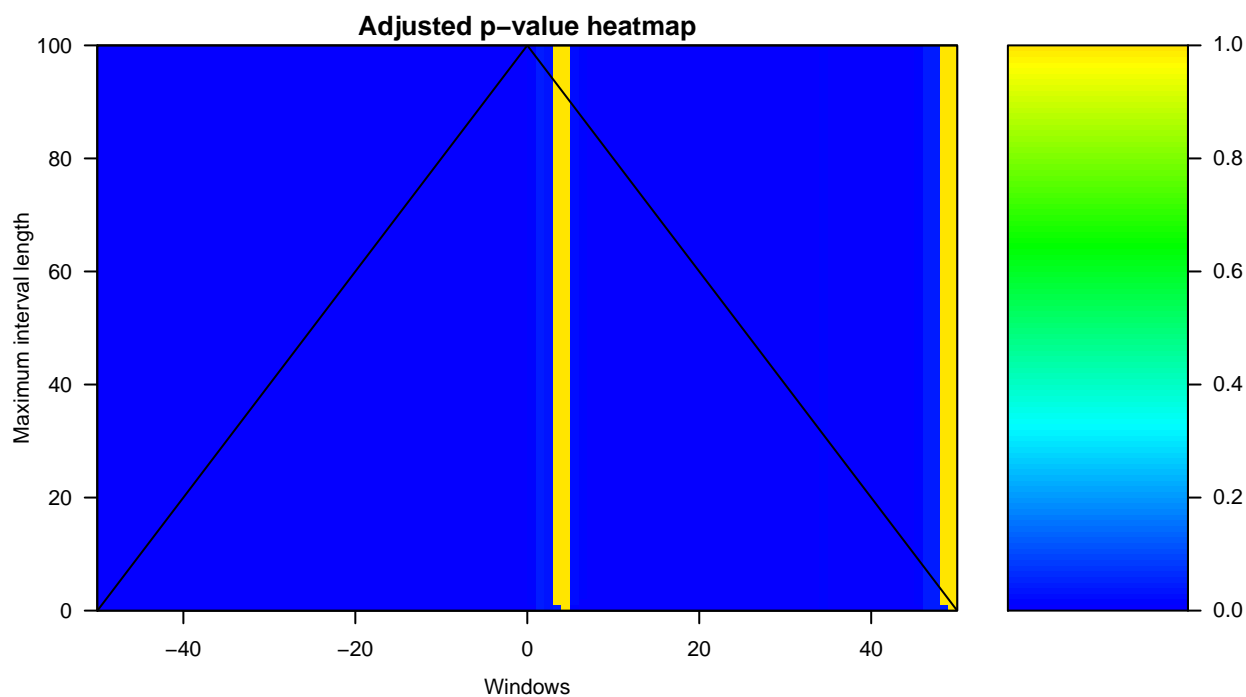




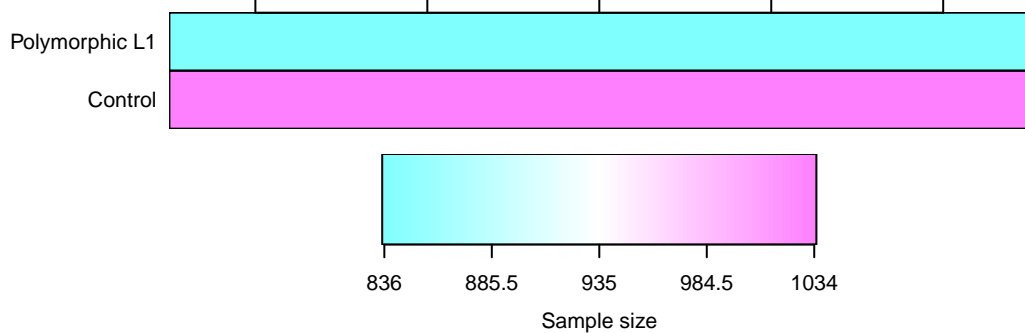
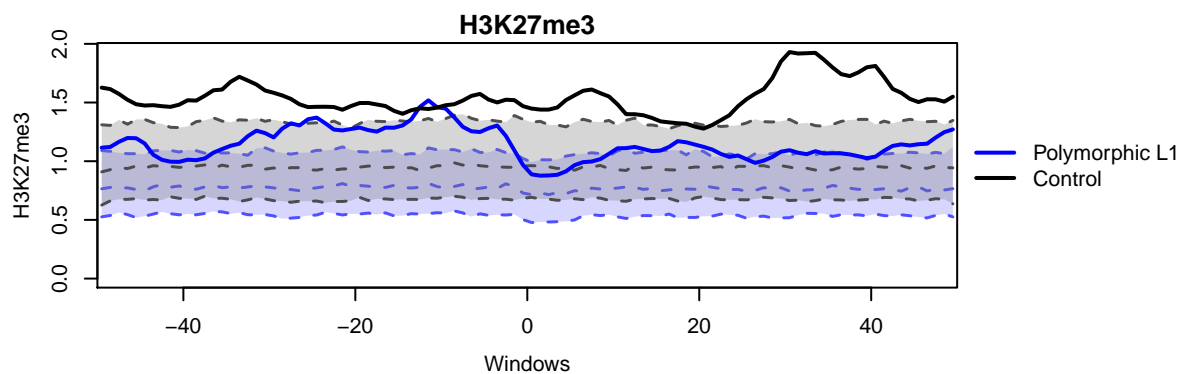
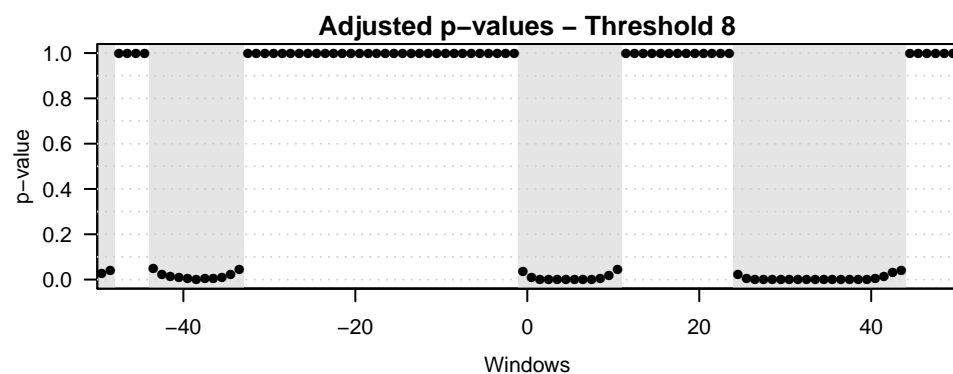
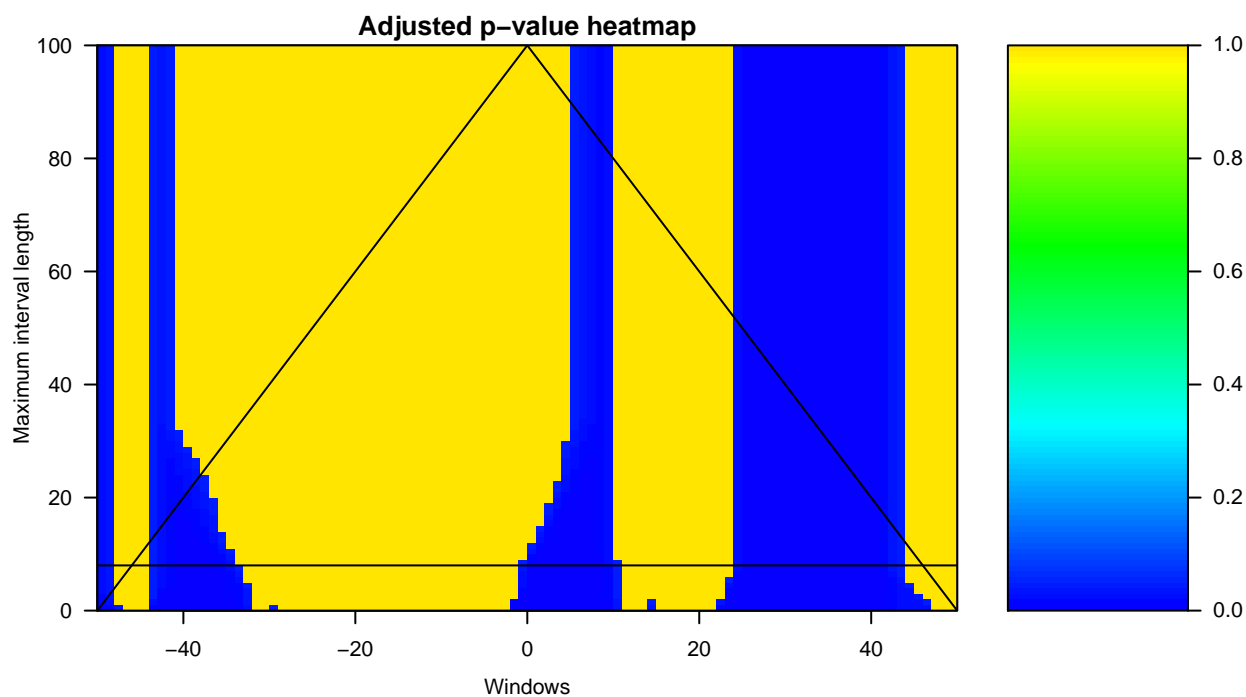
# H3K9ac



# H3K9me3

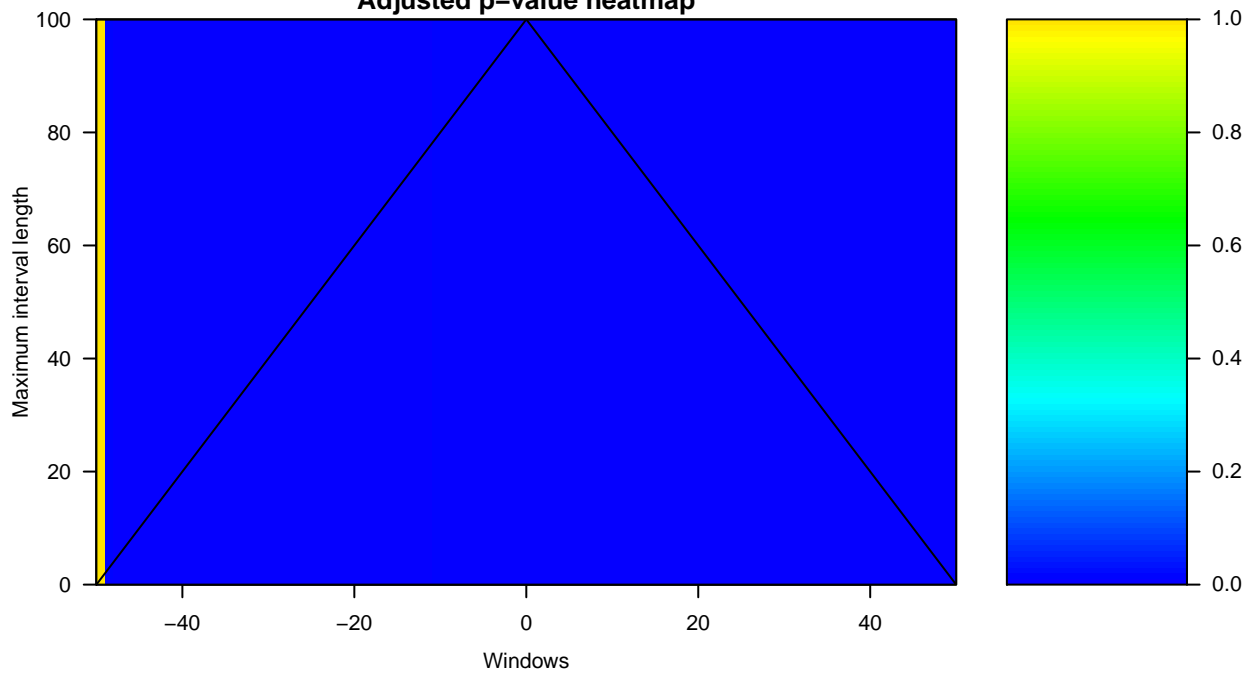


# H3K27me3

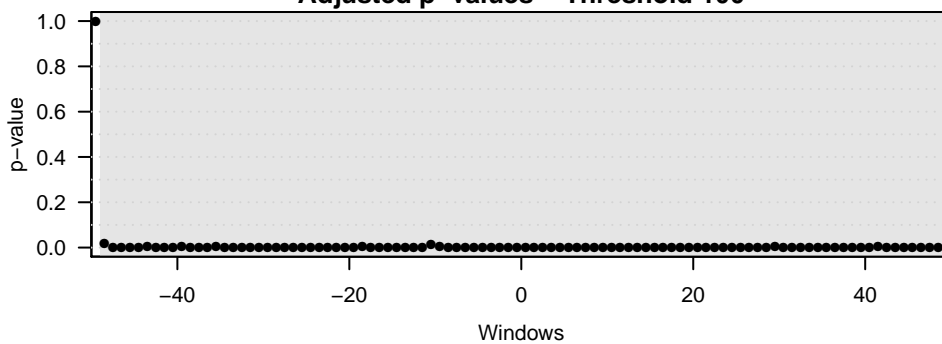


# CTCF

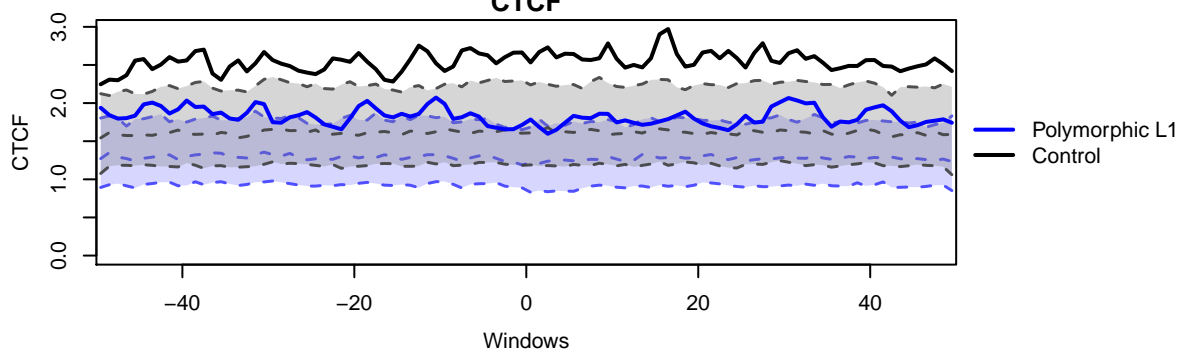
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# CTCF



Polymorphic L1

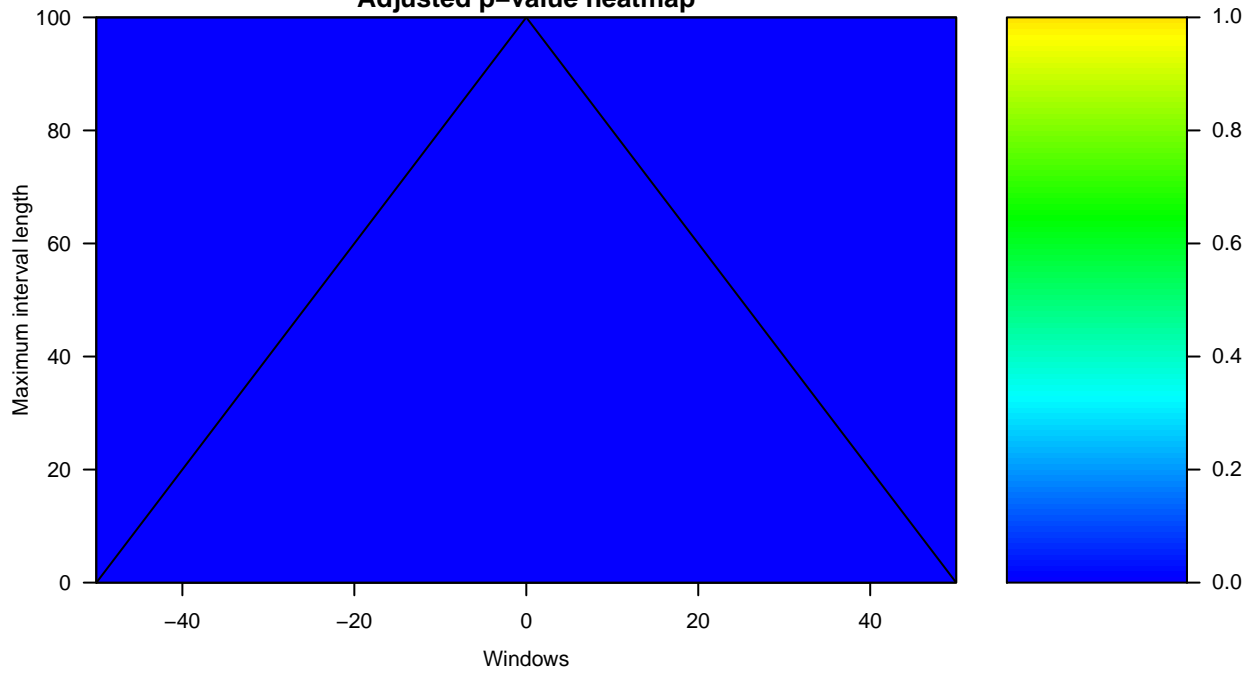
Control

836 885.5 935 984.5 1034

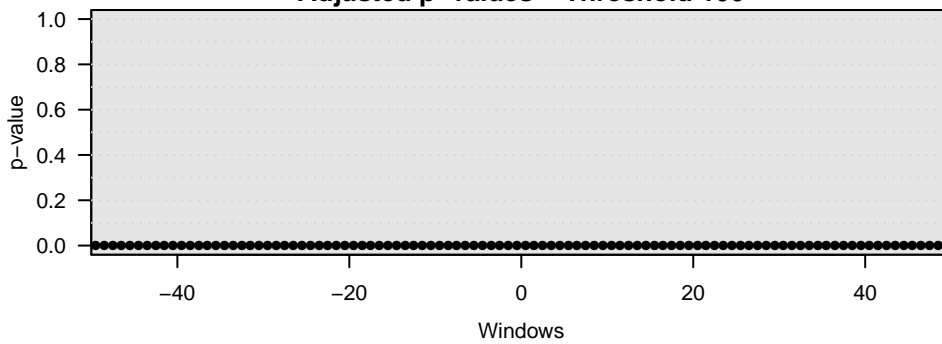
Sample size

# DNase hypersensitive sites

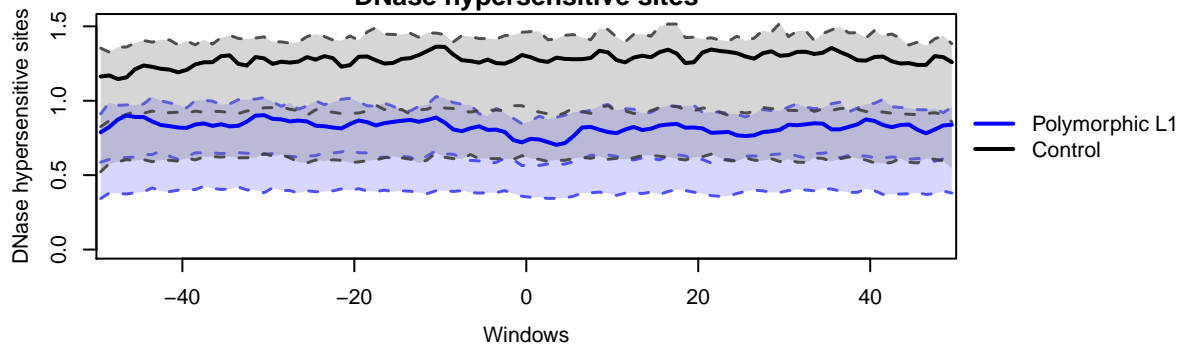
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



## DNase hypersensitive sites



Polymorphic L1

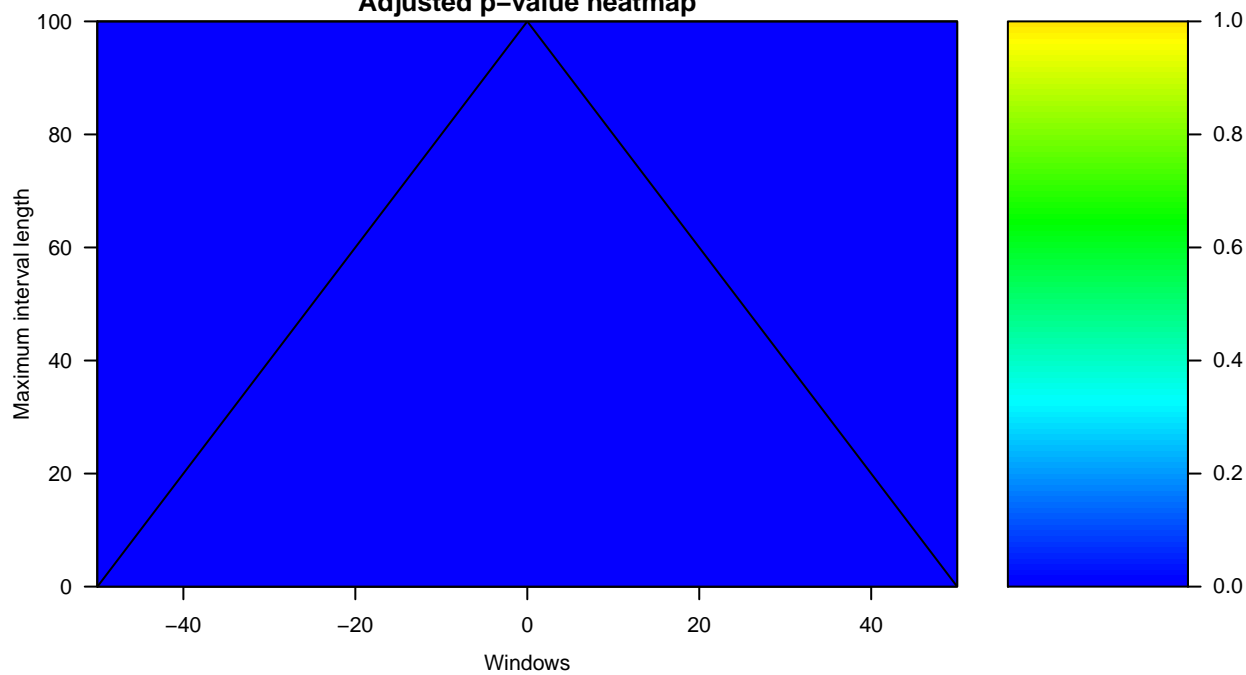
Control

836 885.5 935 984.5 1034

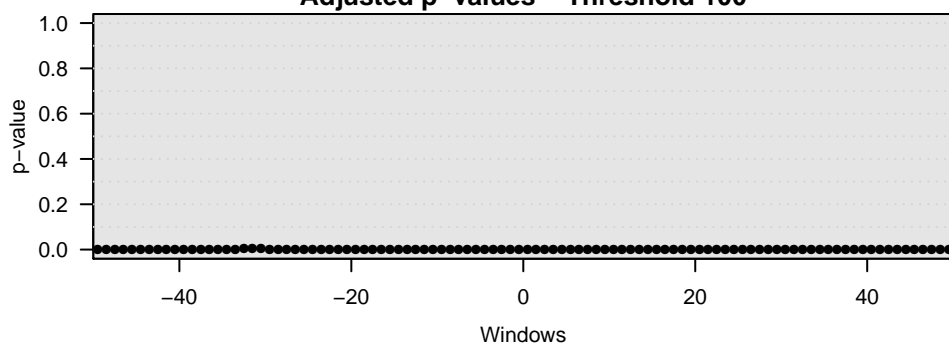
Sample size

# RNA Pol2

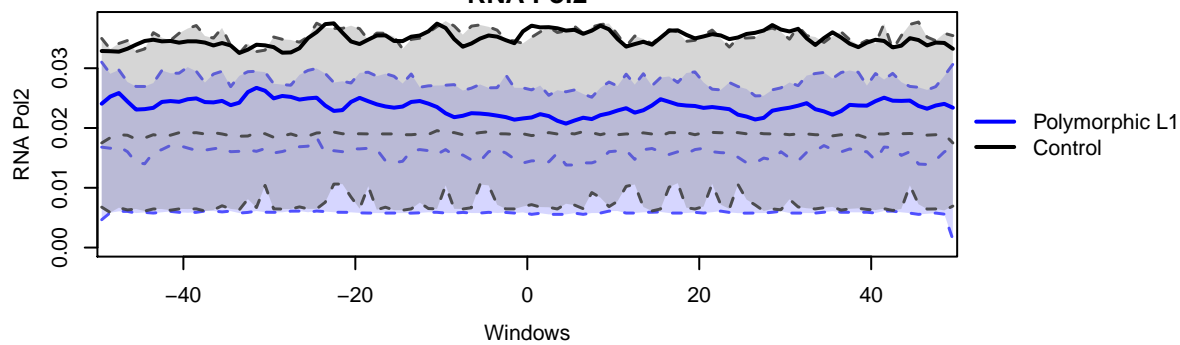
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# RNA Pol2



Polymorphic L1  
Control

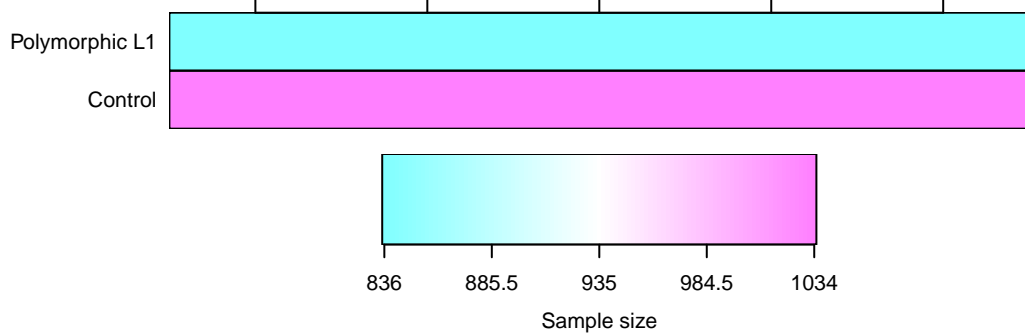
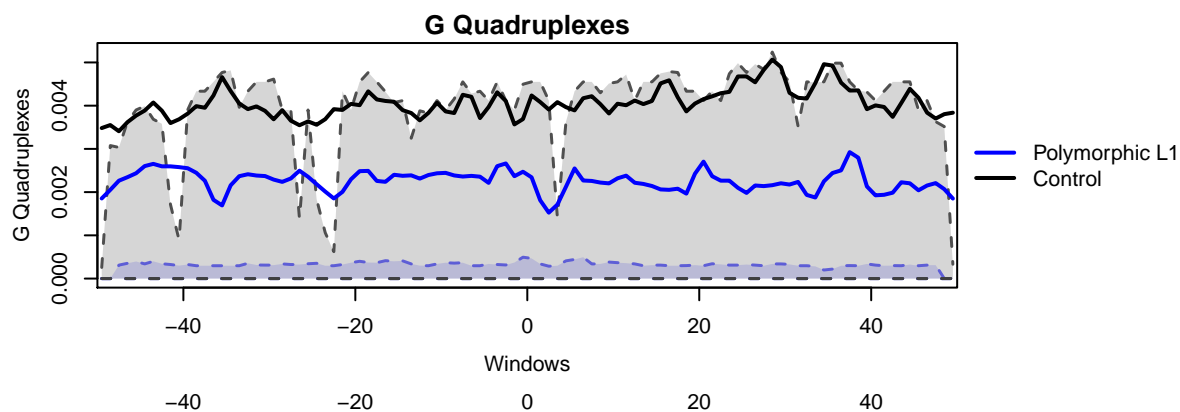
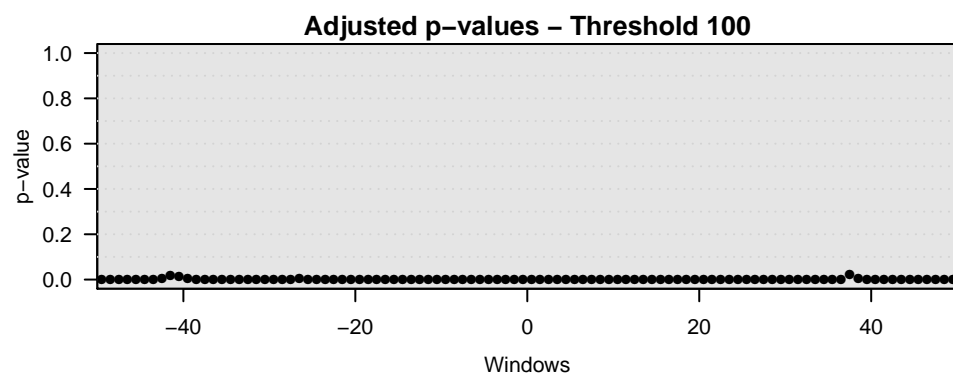
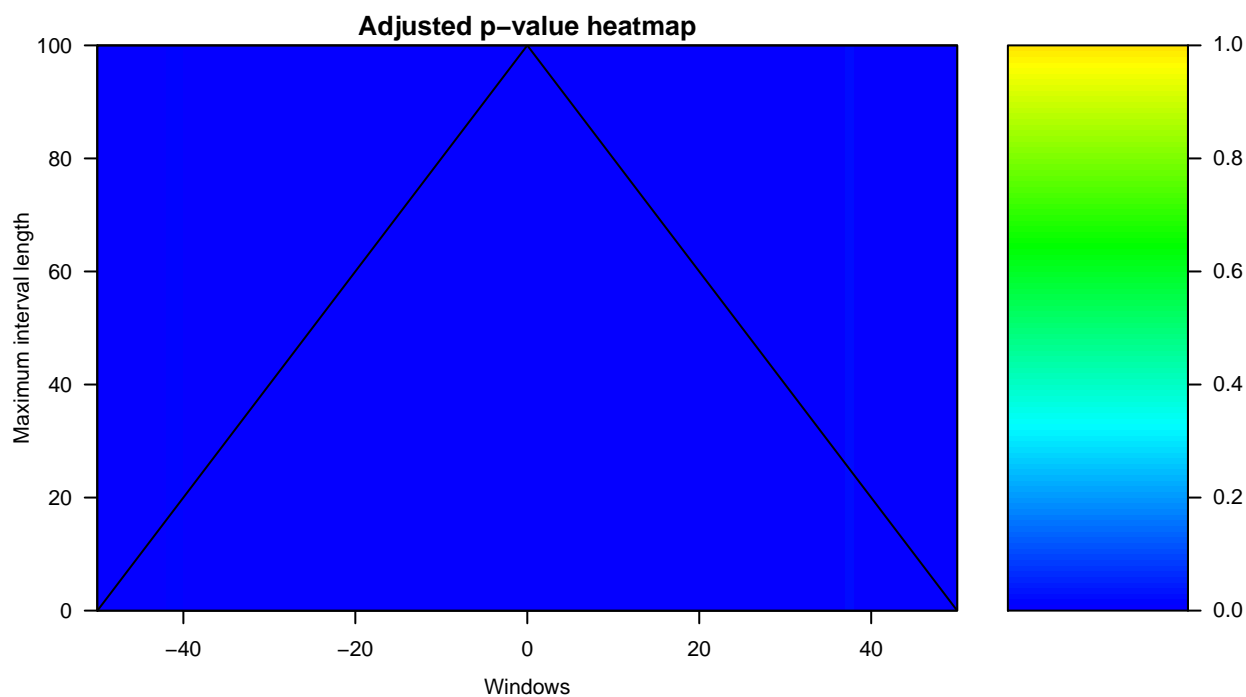
Polymorphic L1

Control

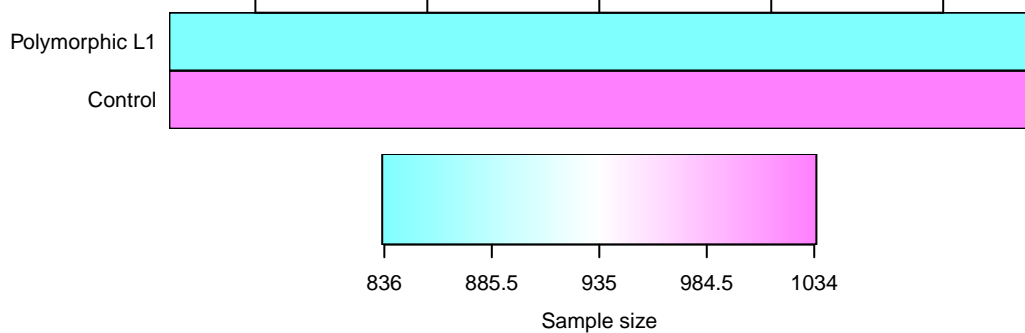
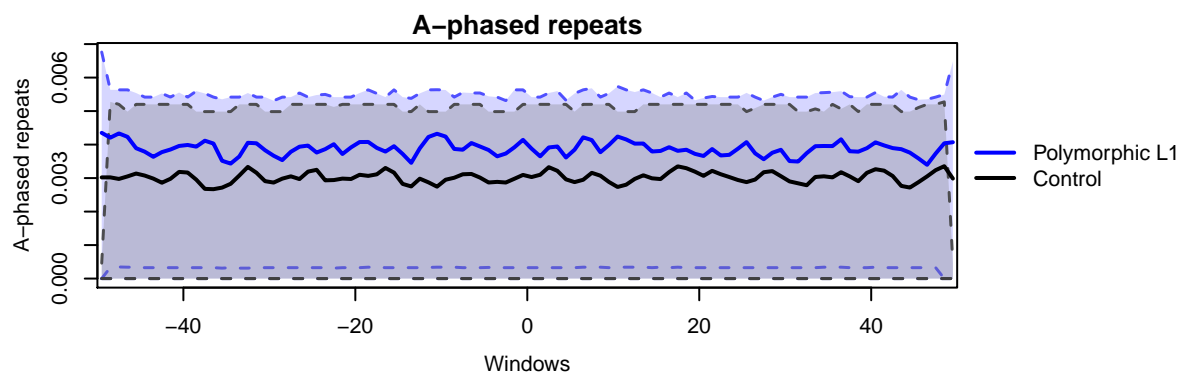
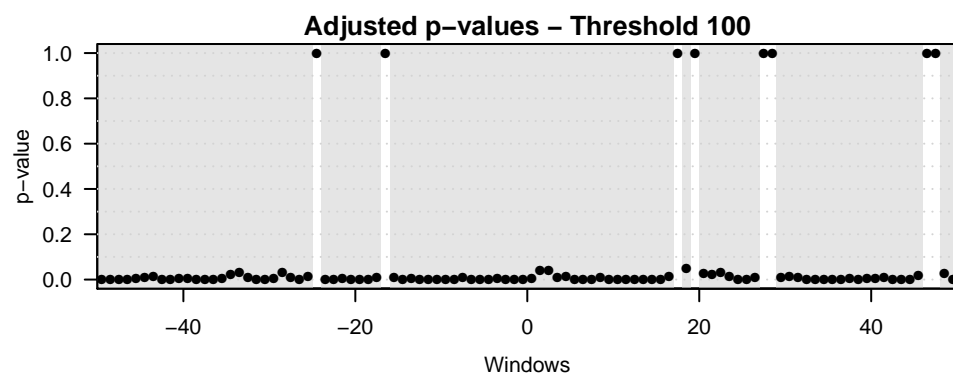
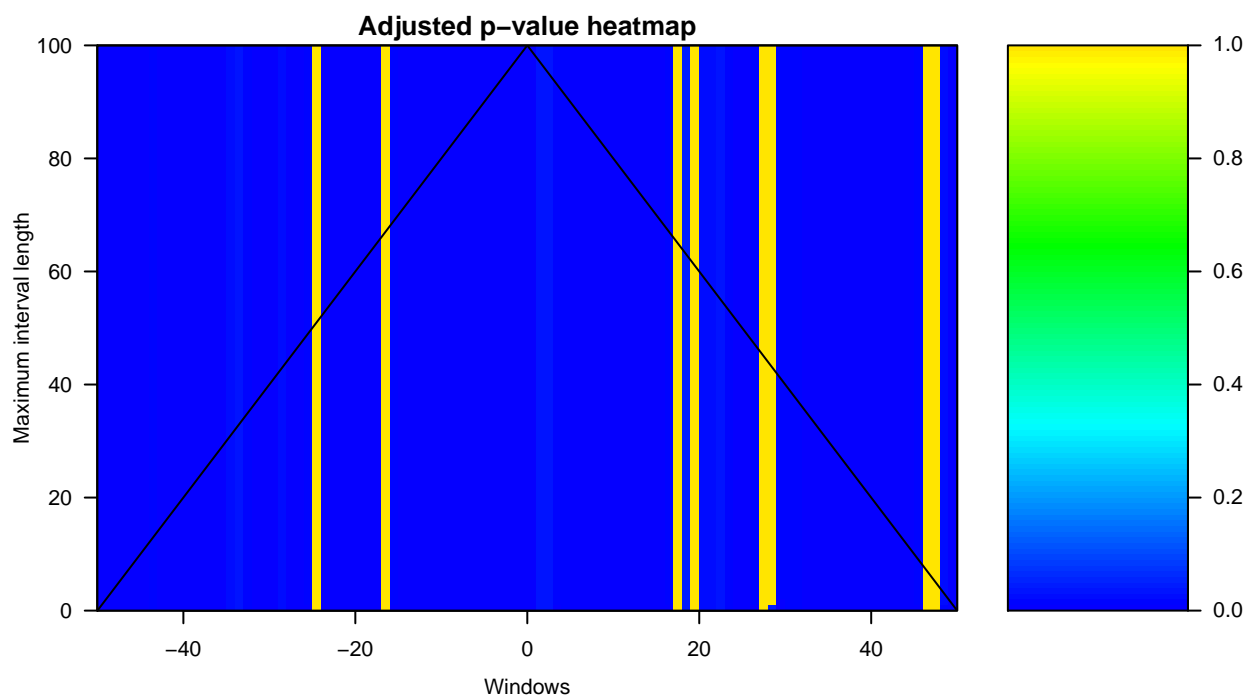
836 885.5 935 984.5 1034

Sample size

# G Quadruplexes

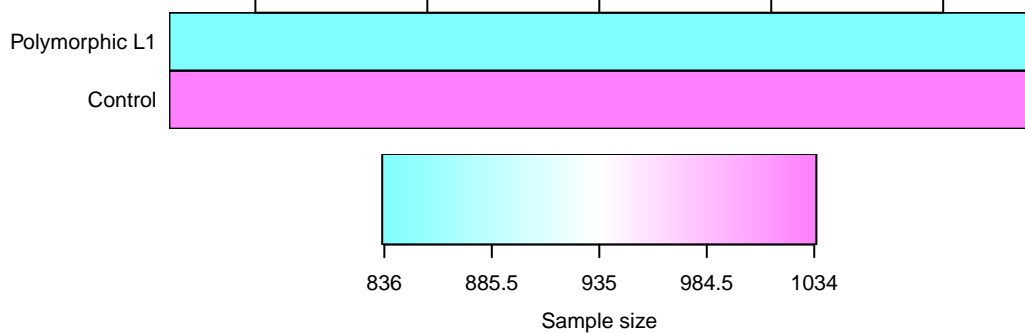
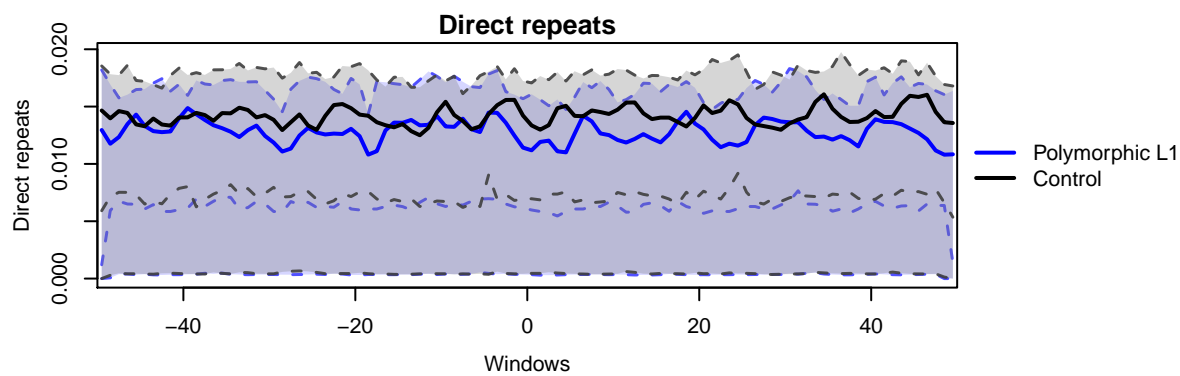
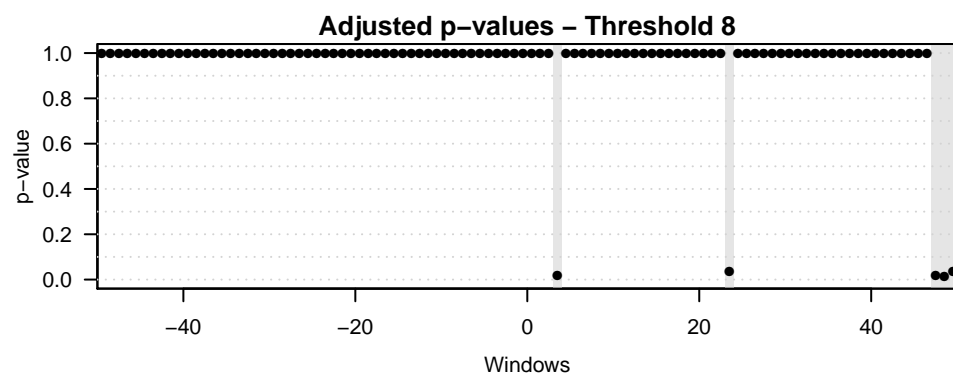
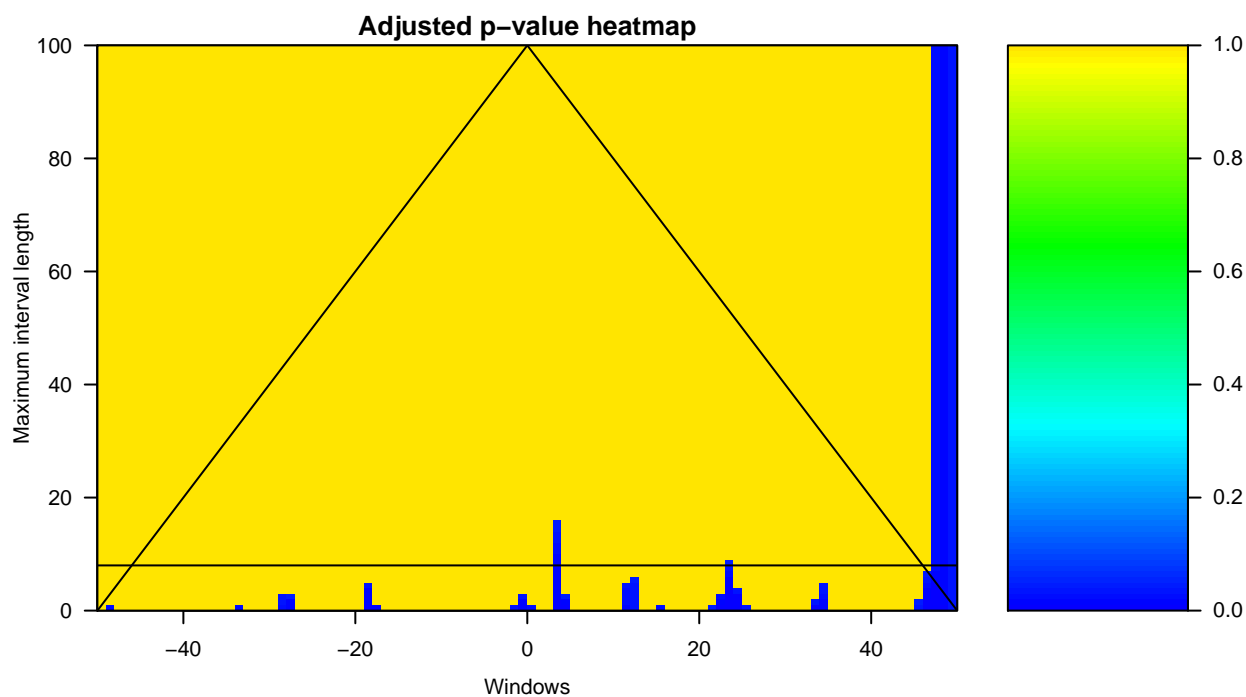


# A-phased repeats

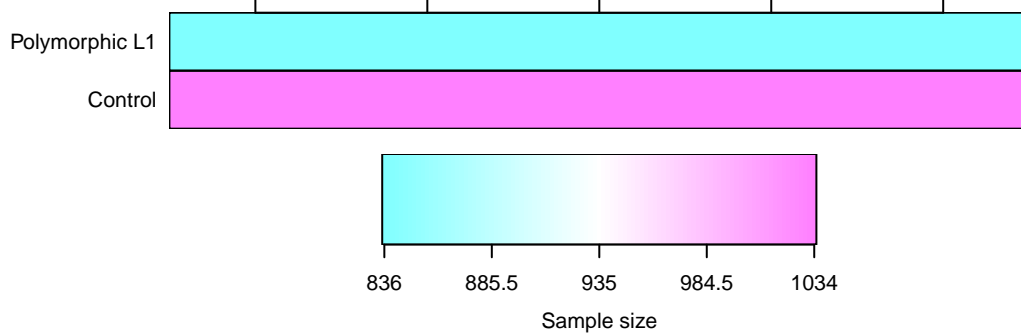
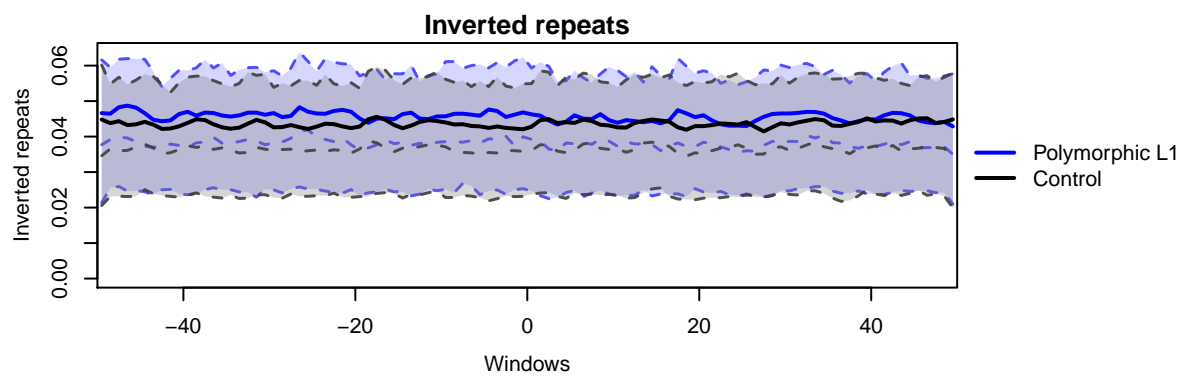
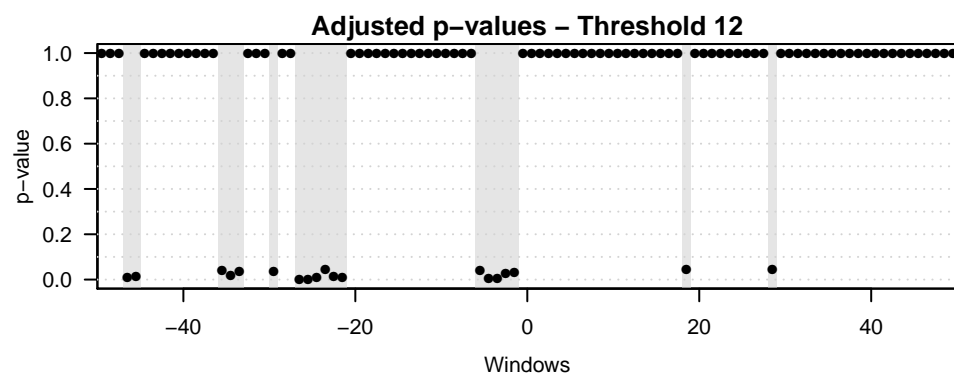
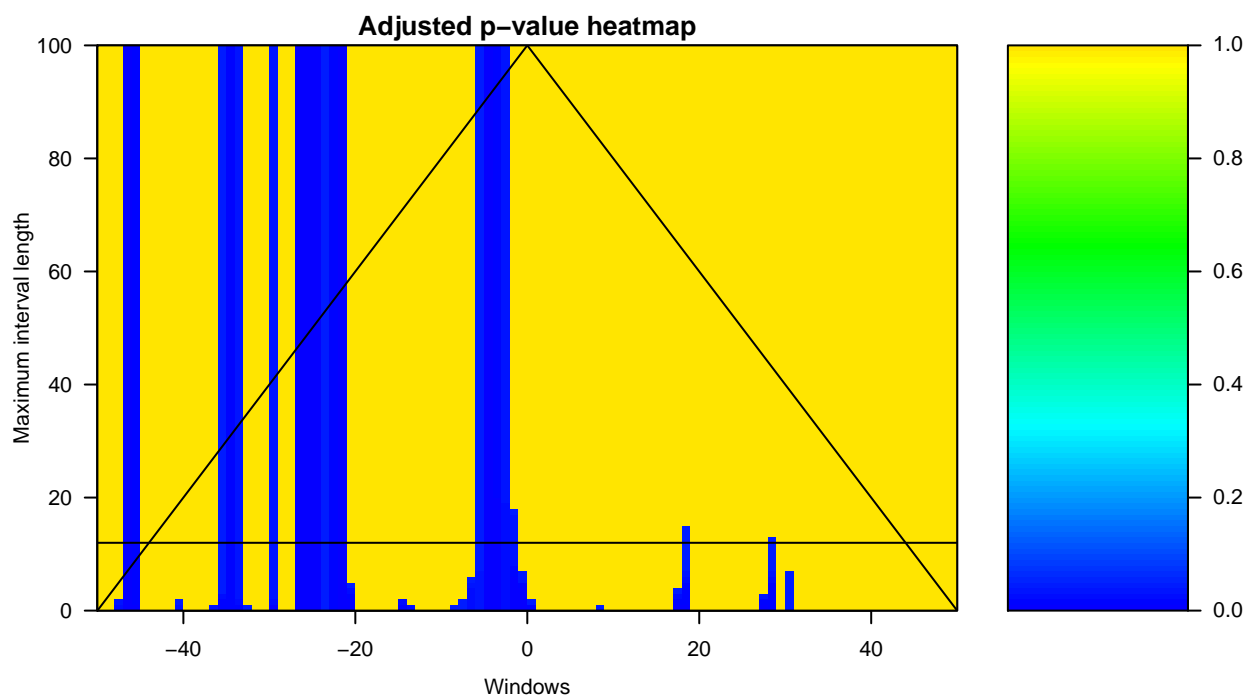




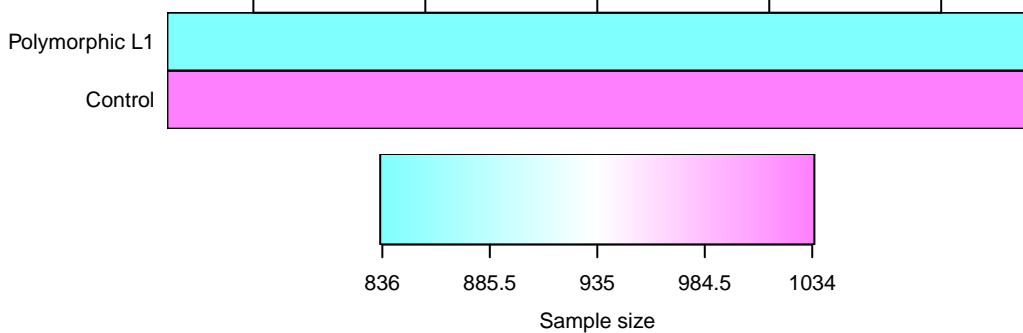
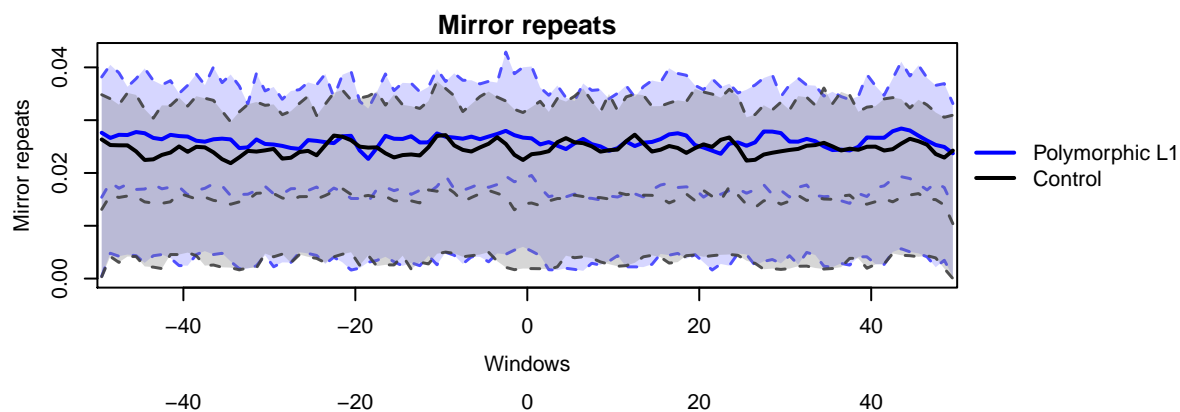
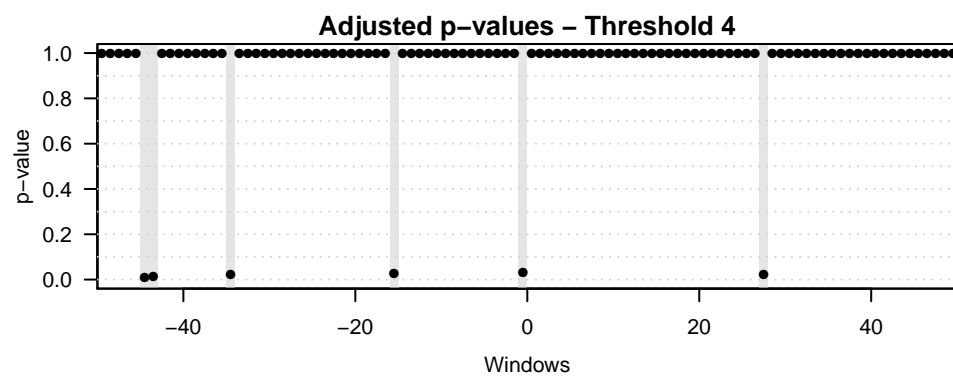
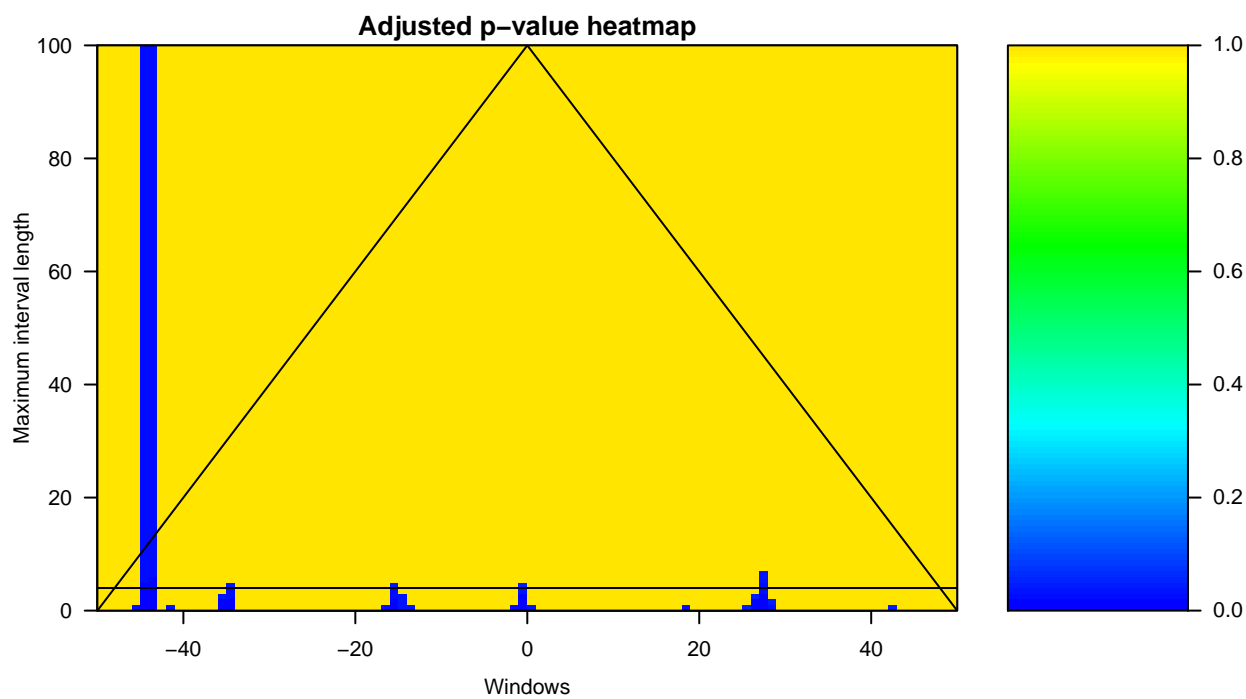
# Direct repeats



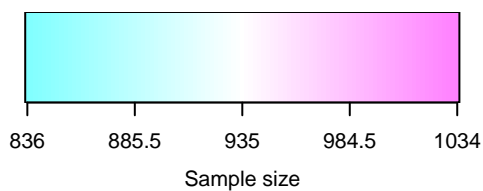
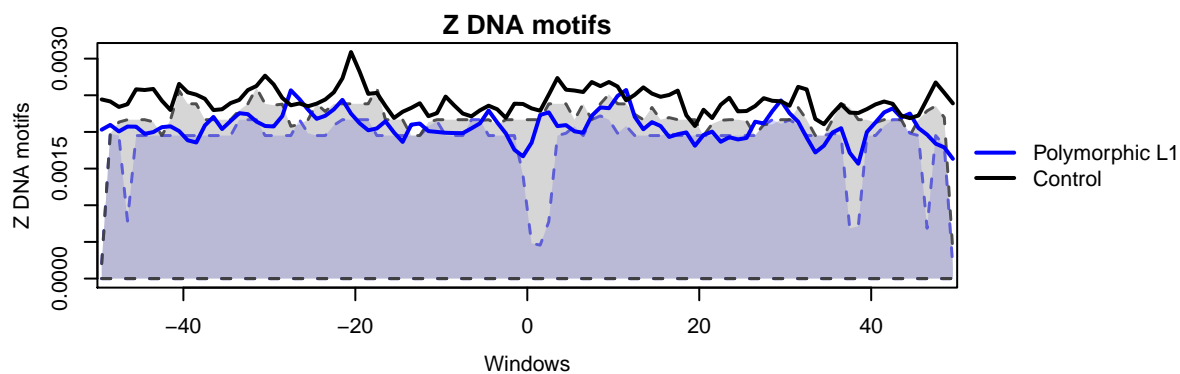
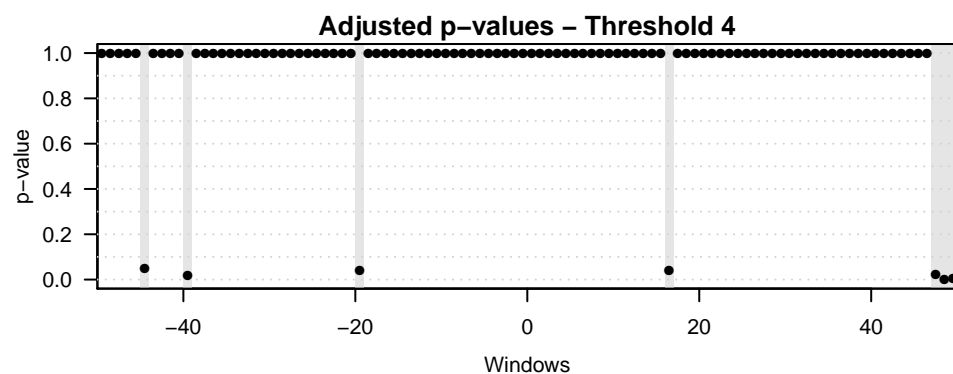
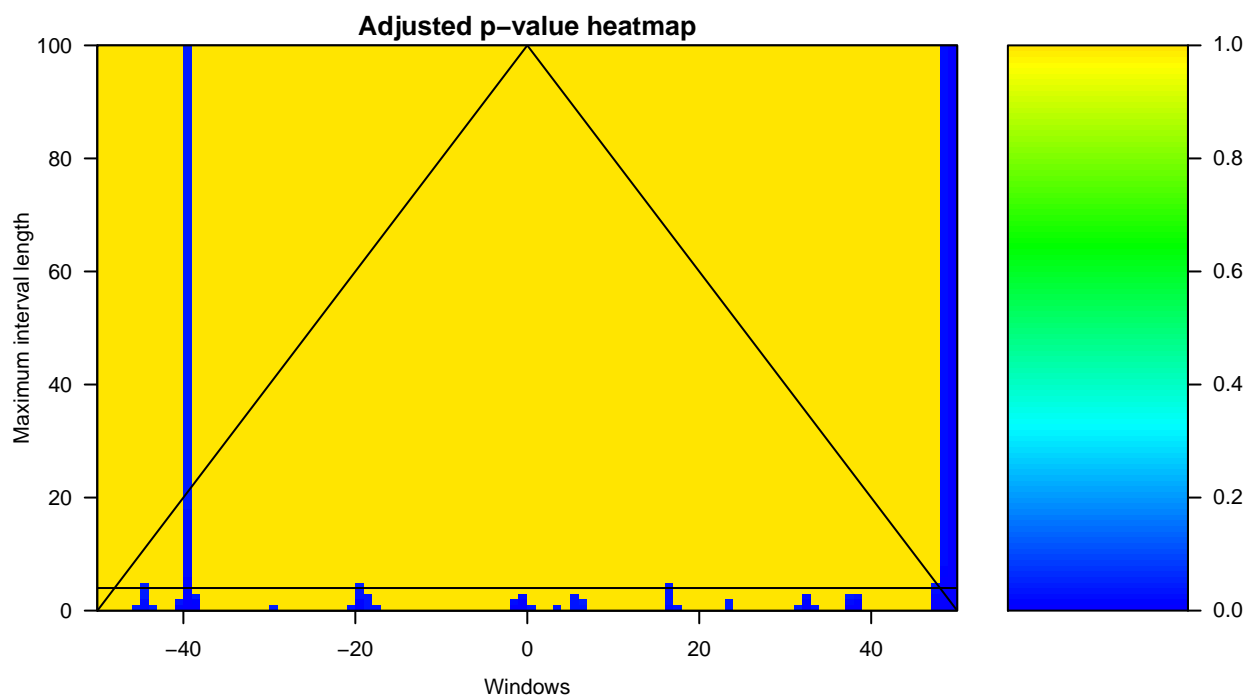
# Inverted repeats



# Mirror repeats

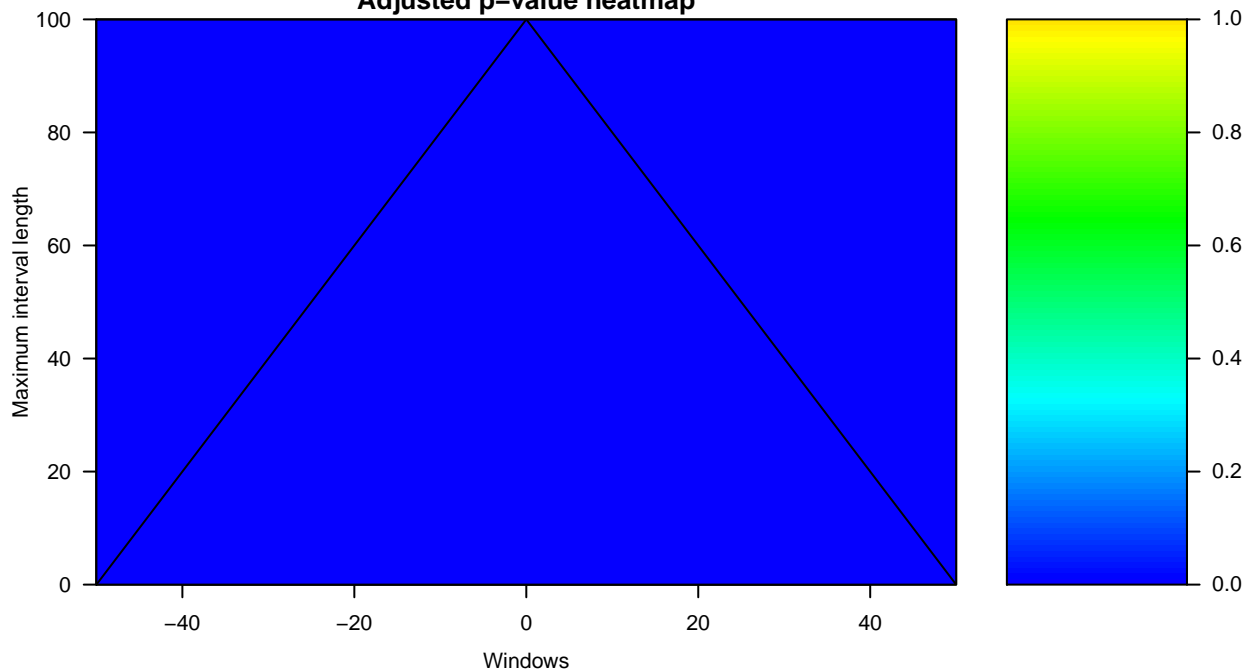


# Z DNA motifs

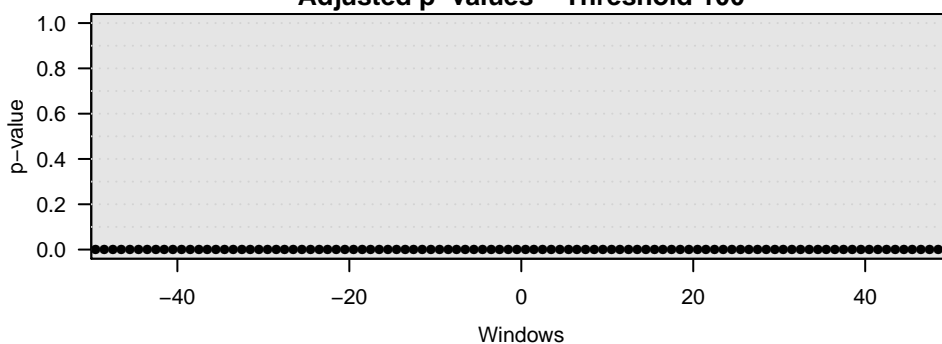


# Most conserved element

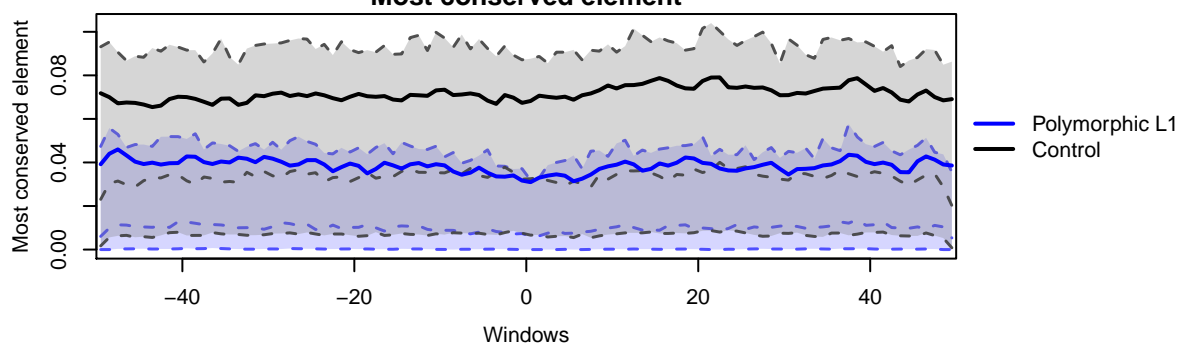
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# Most conserved element



Polymorphic L1

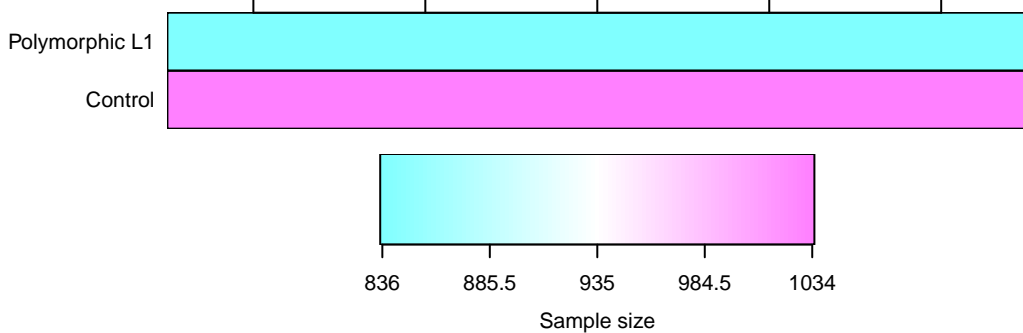
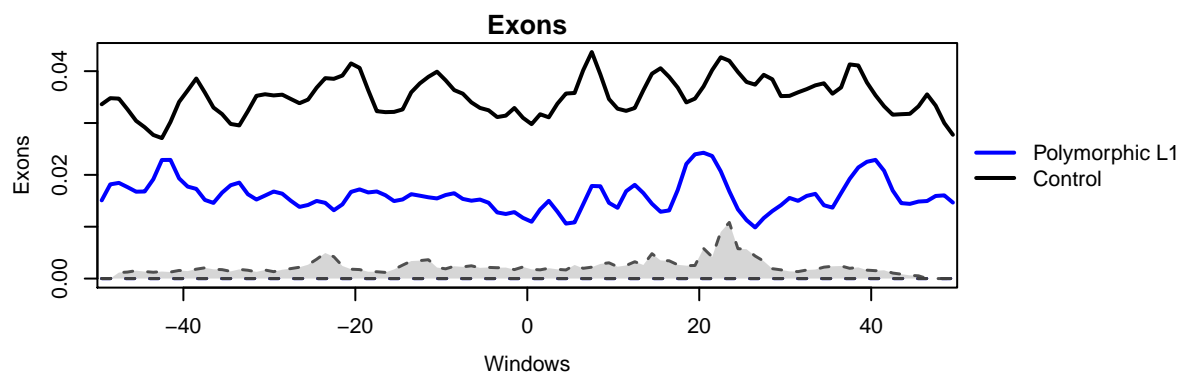
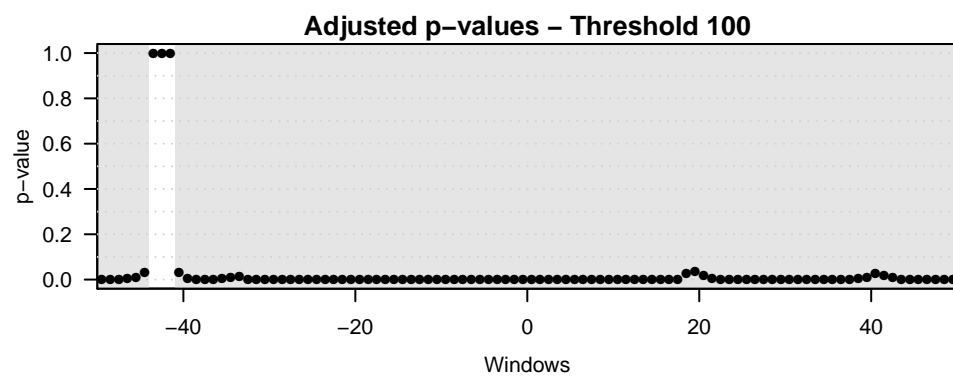
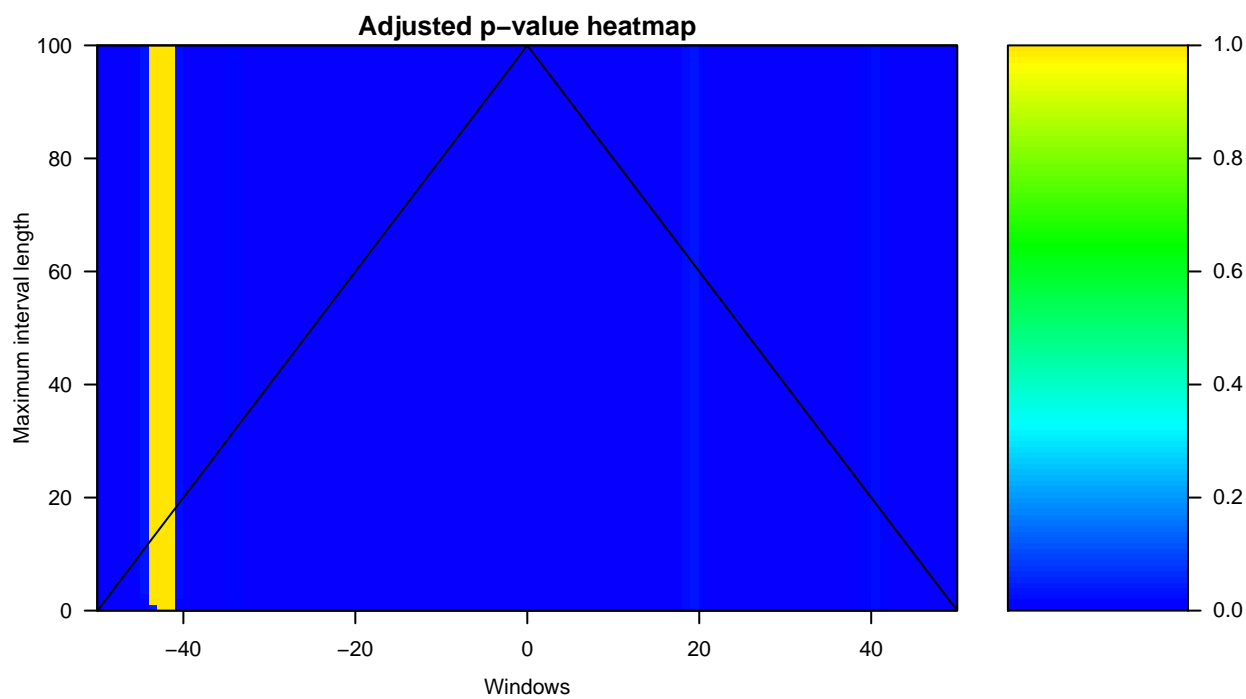
Control



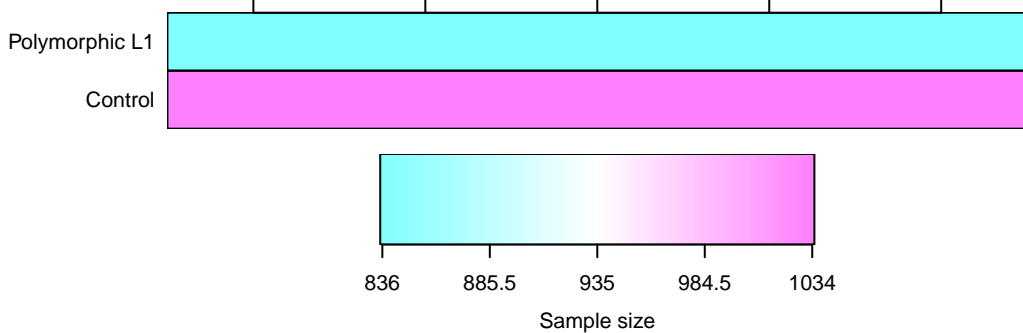
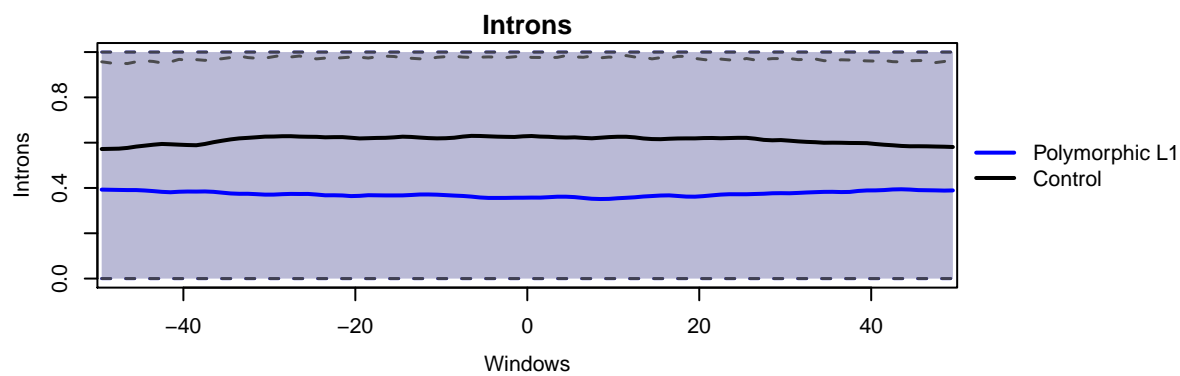
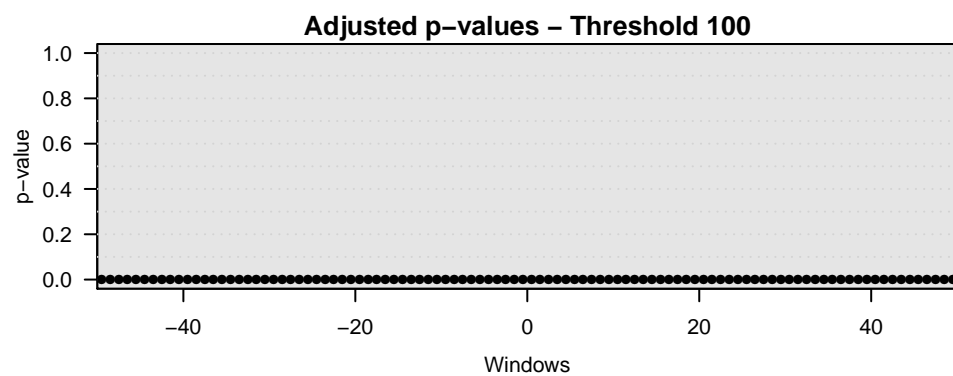
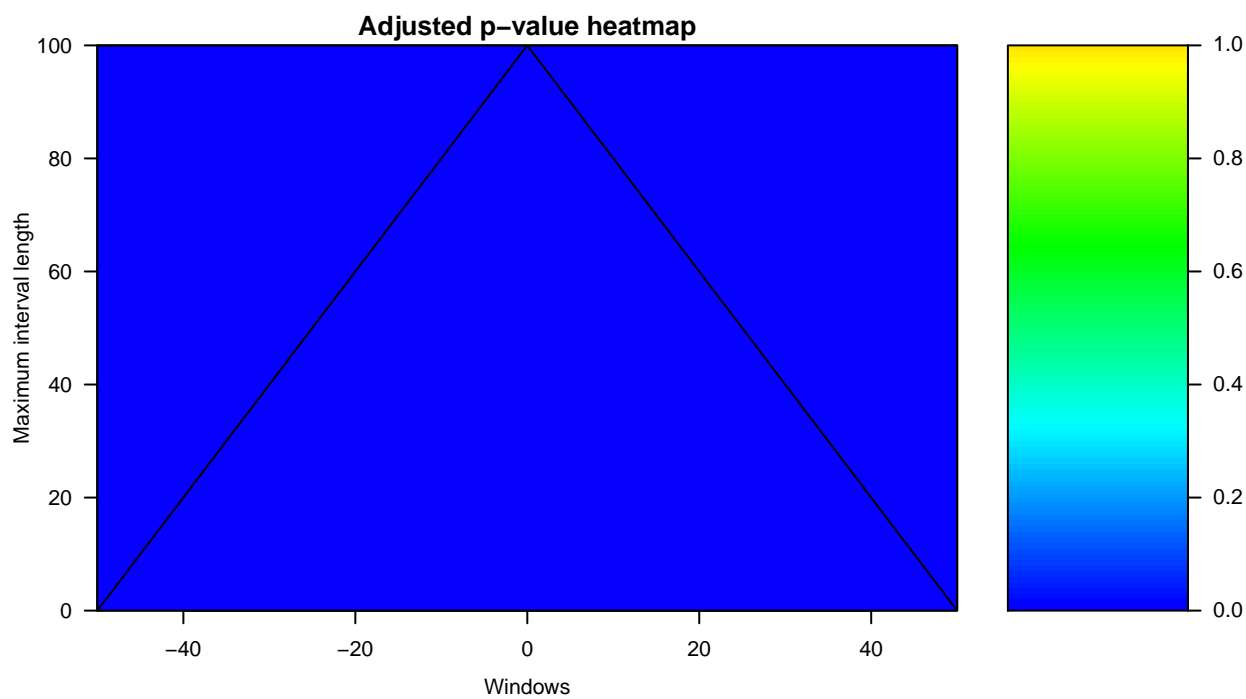
836 885.5 935 984.5 1034

Sample size

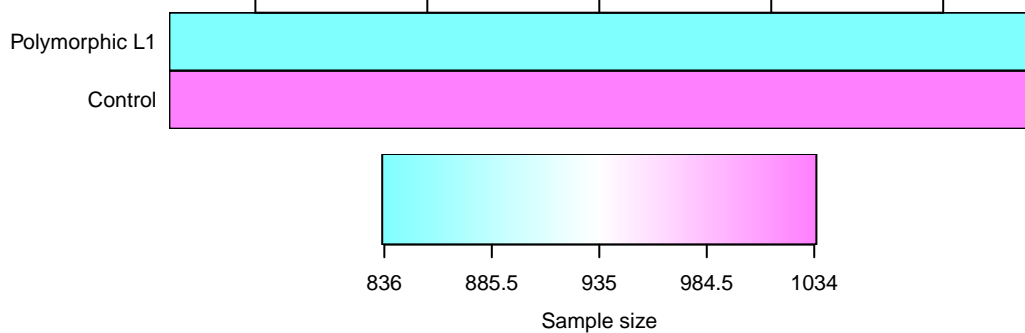
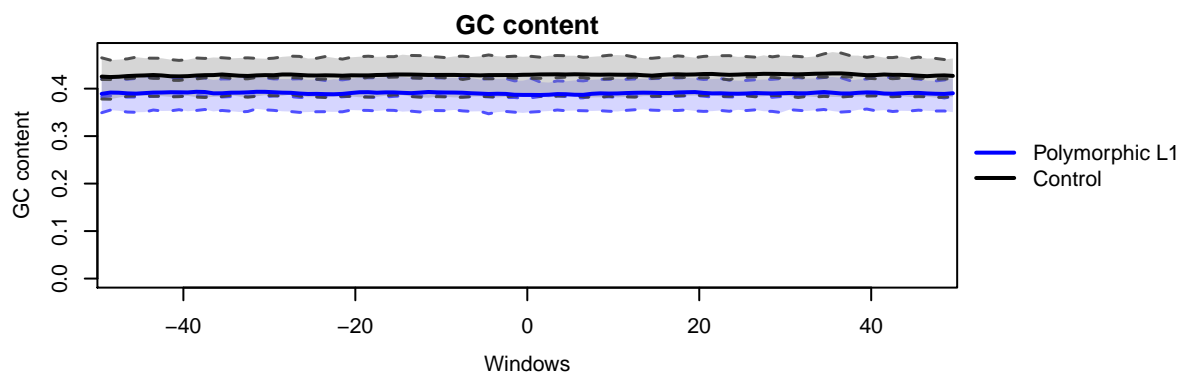
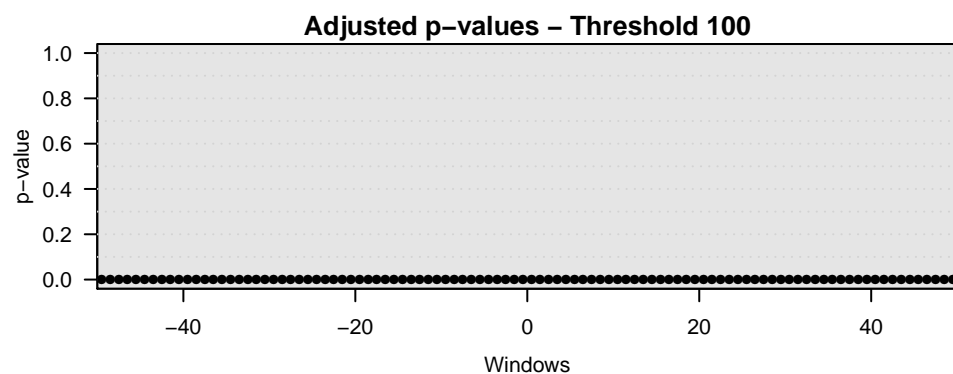
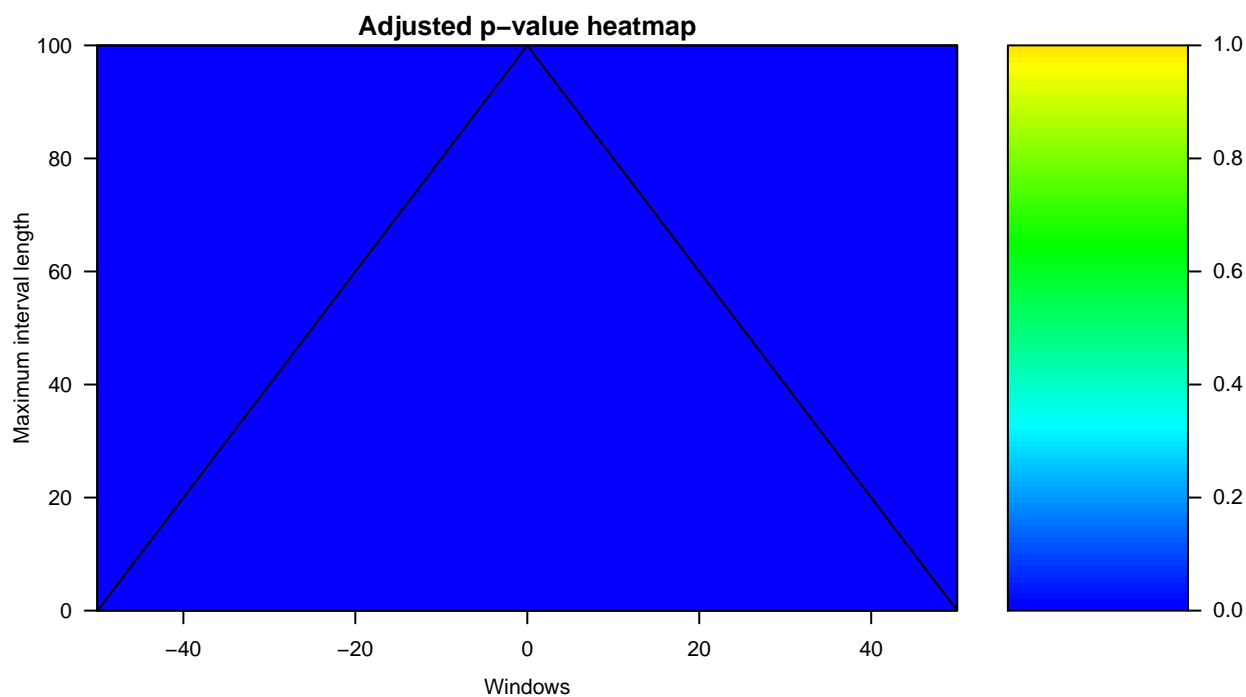
## Exons



# Introns

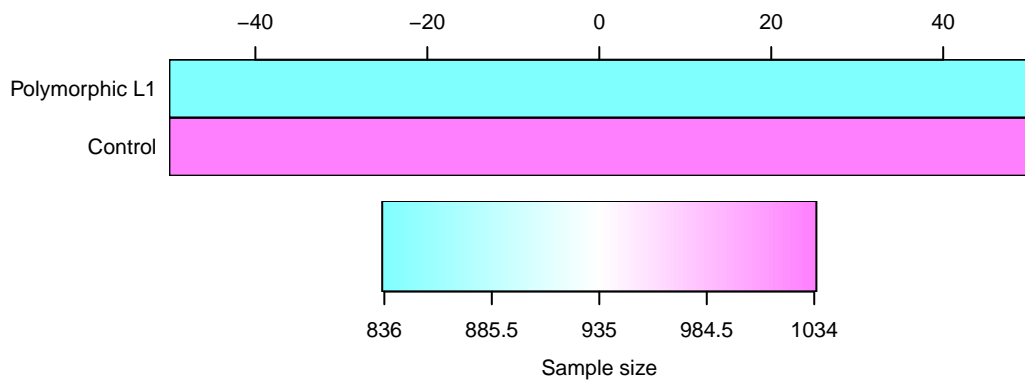
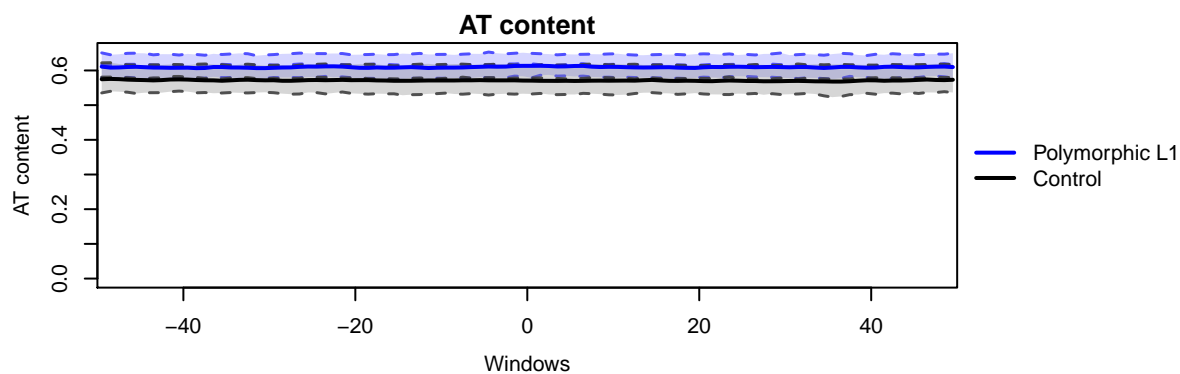
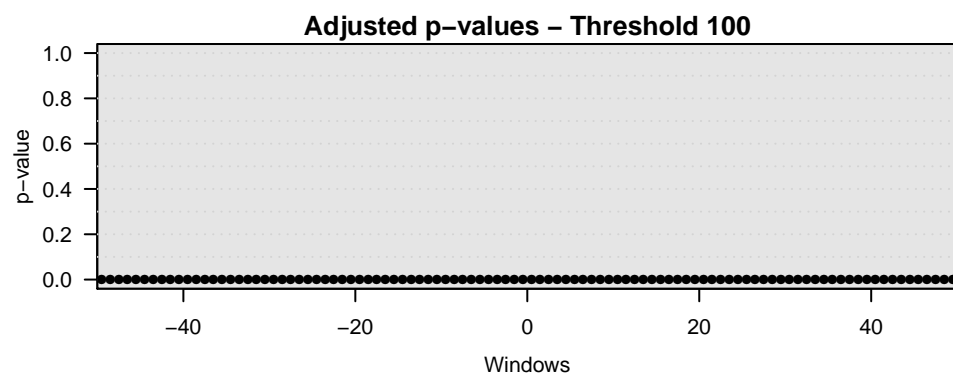
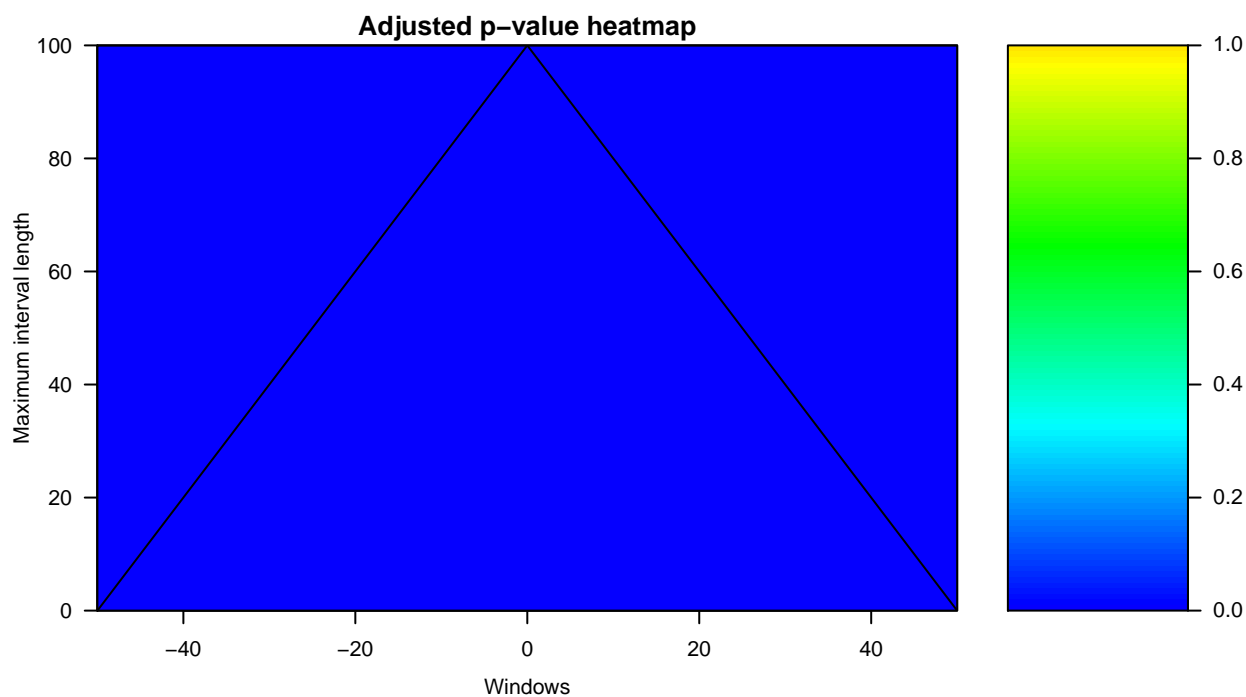


# GC content

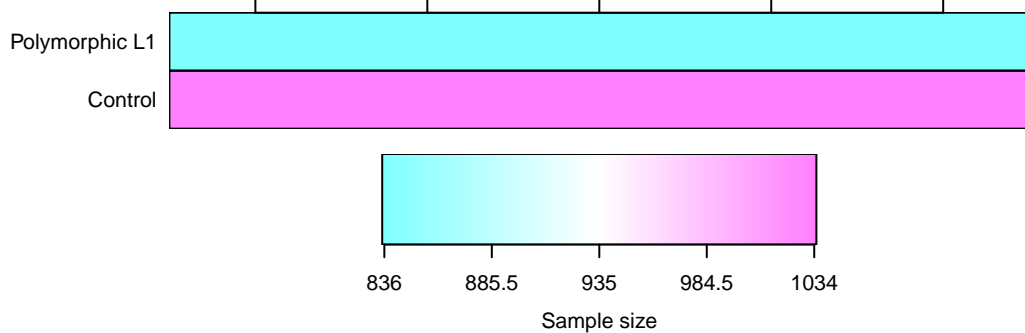
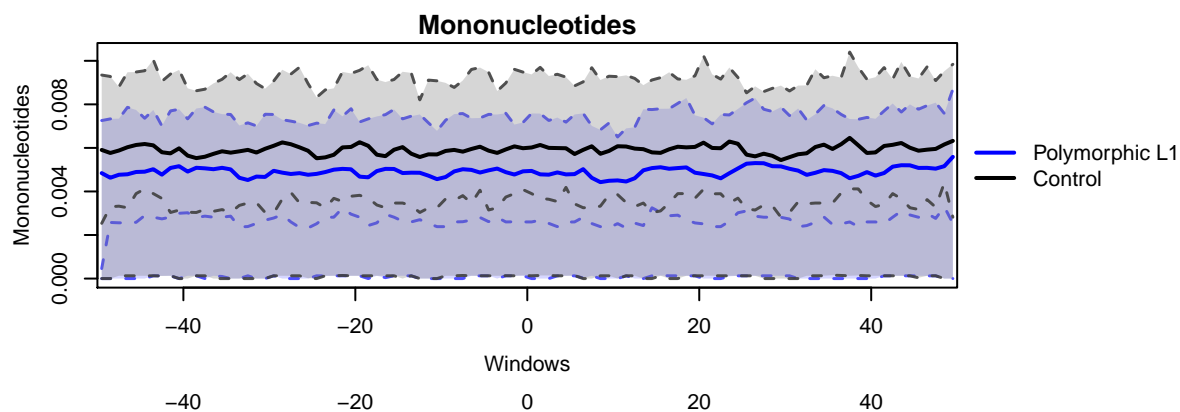
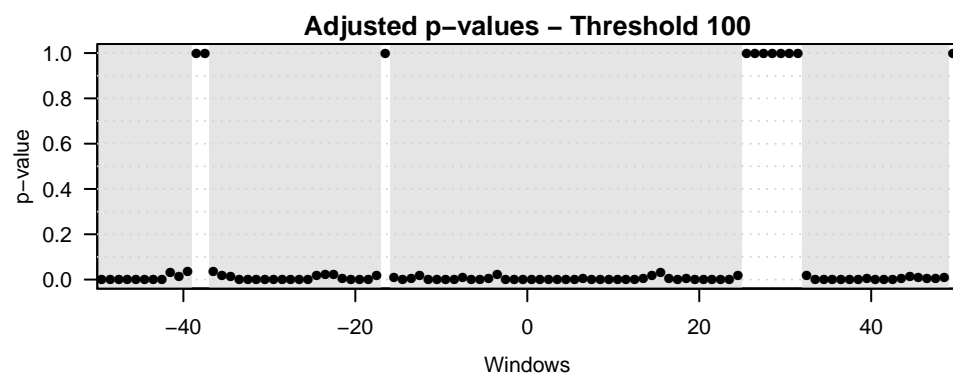
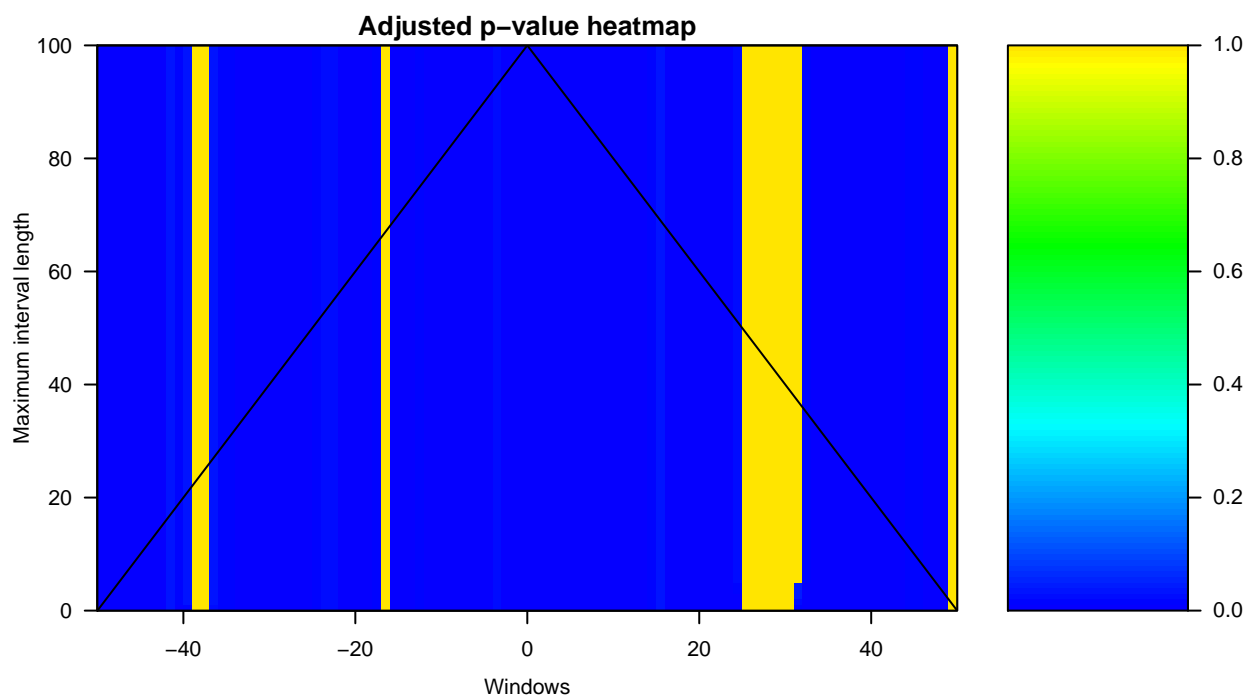




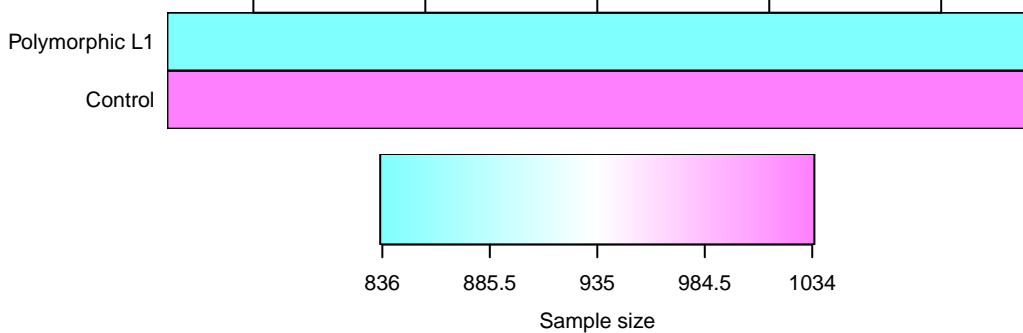
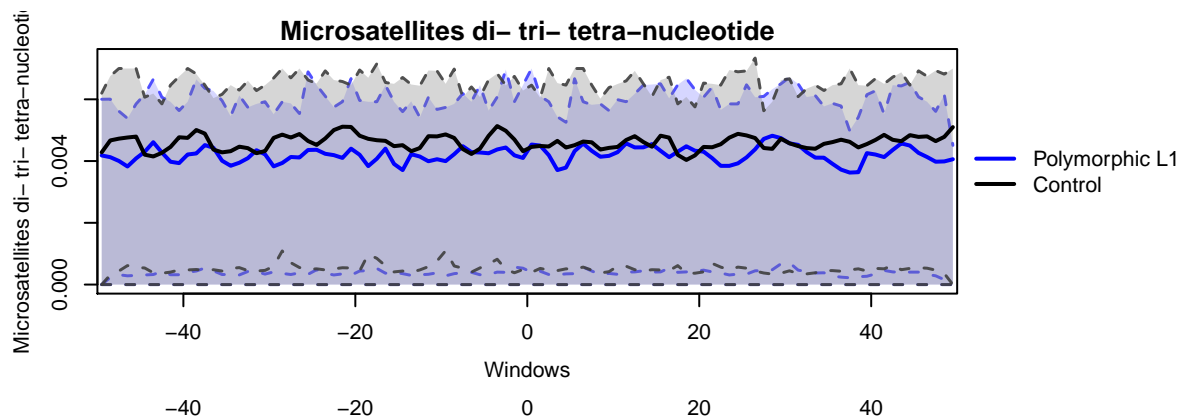
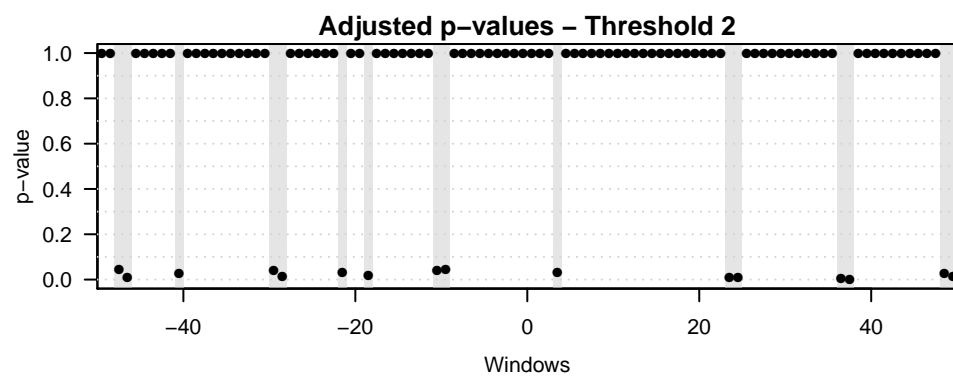
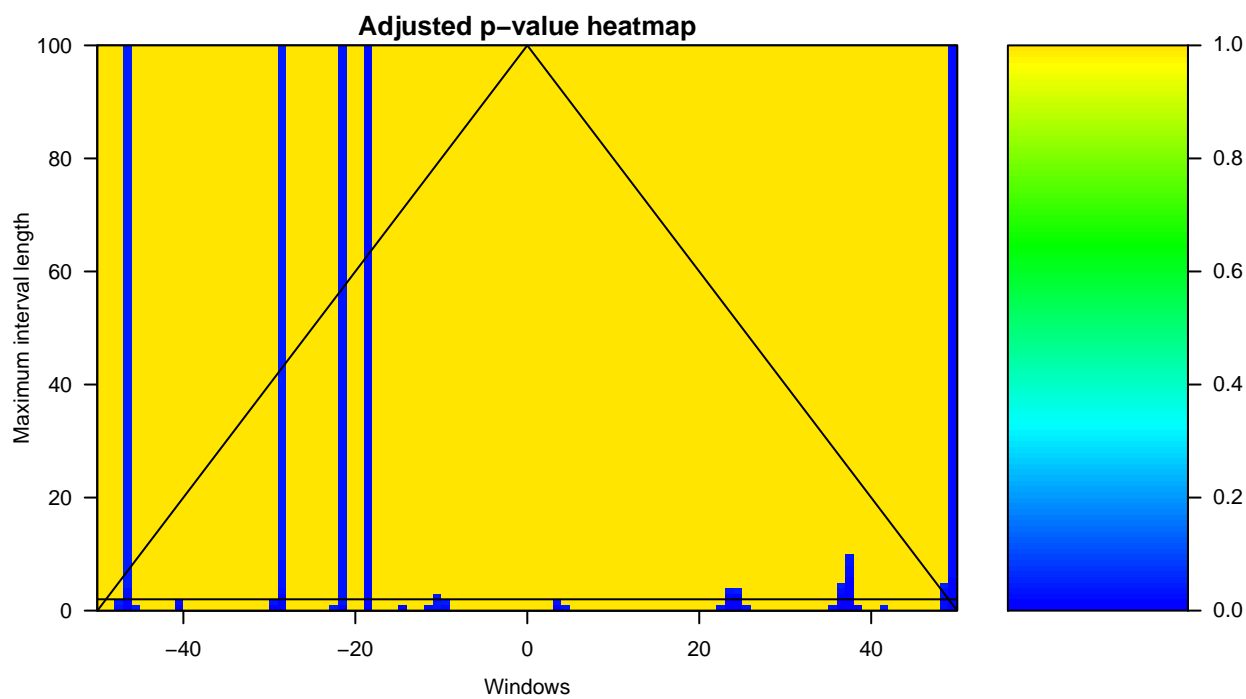
# AT content



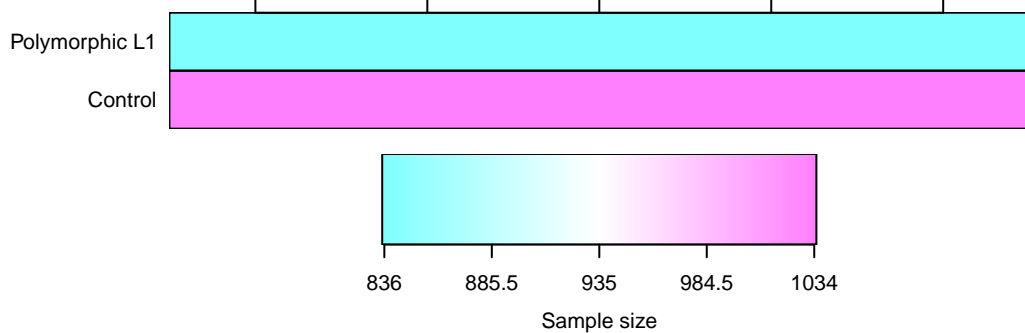
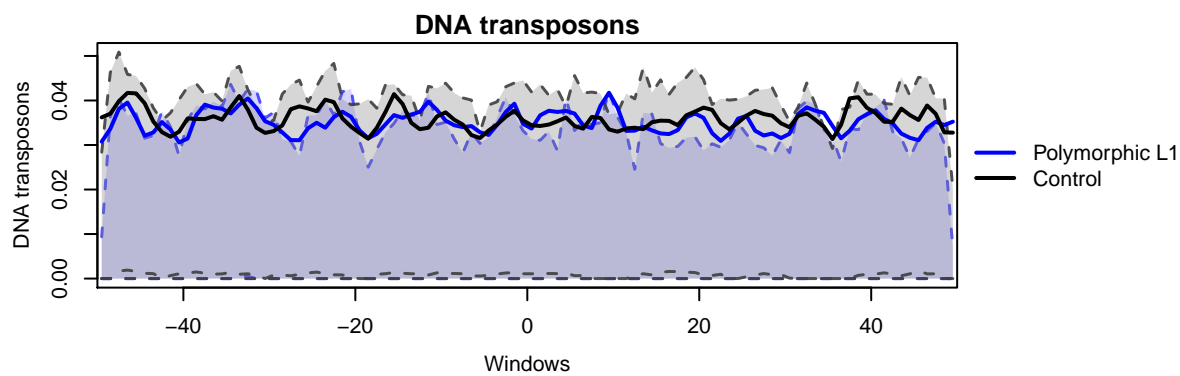
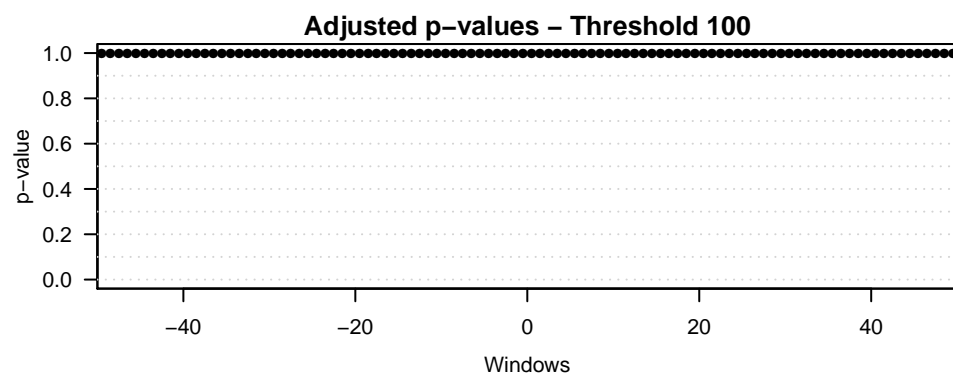
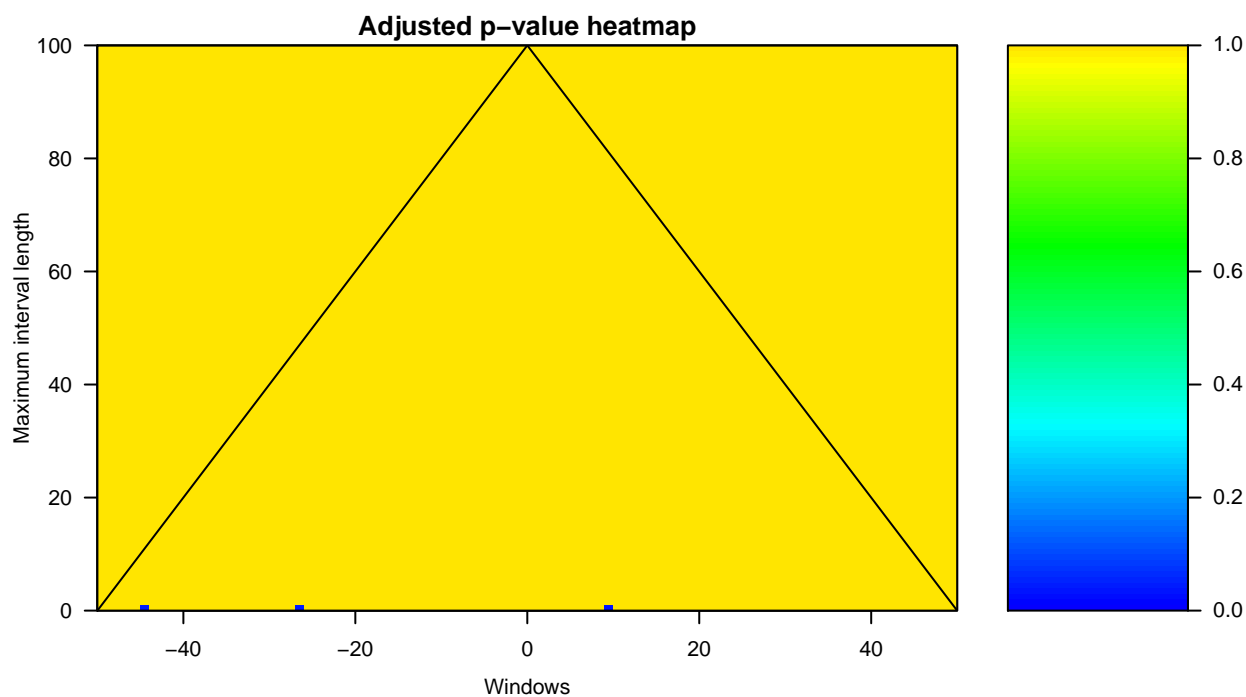
# Mononucleotides



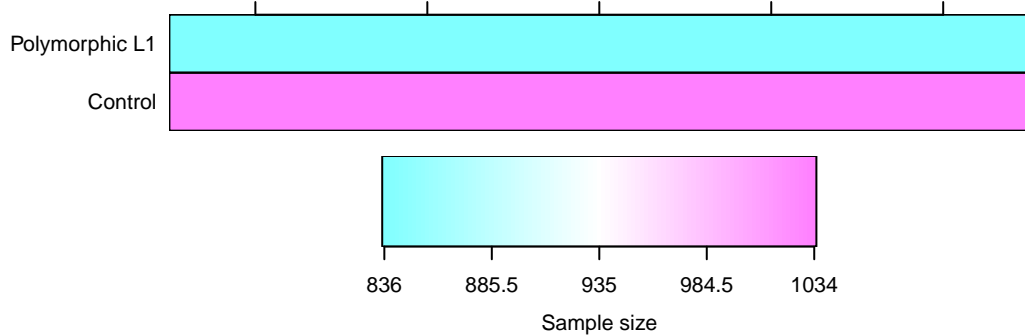
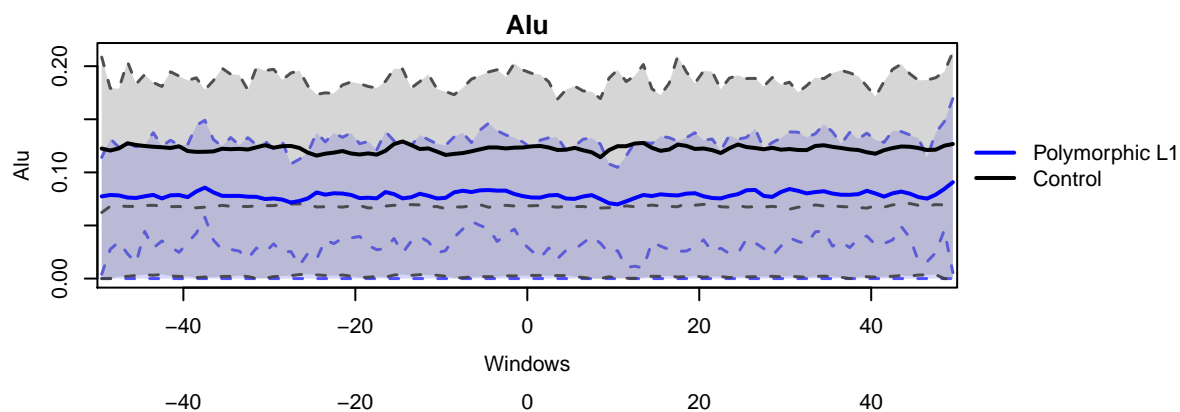
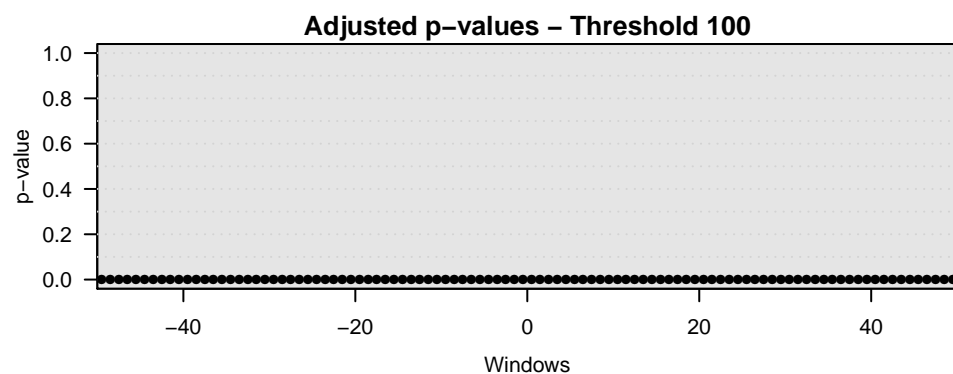
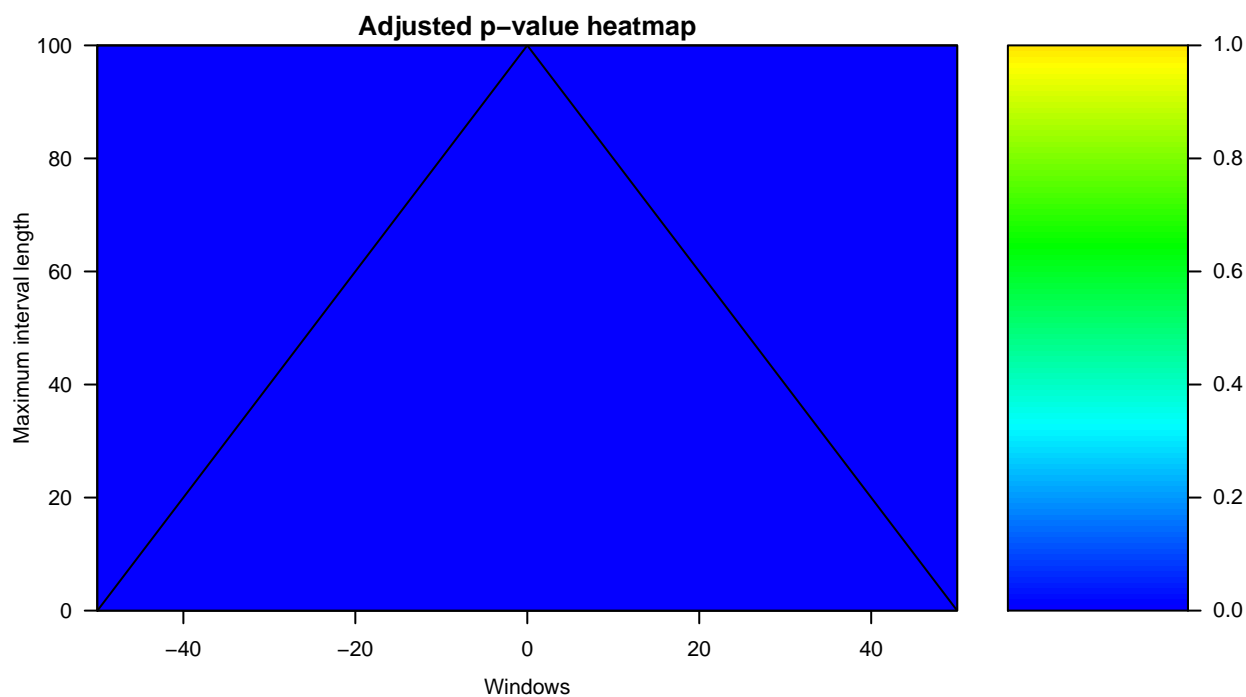
# Microsatellites di- tri- tetra-nucleotide



# DNA transposons

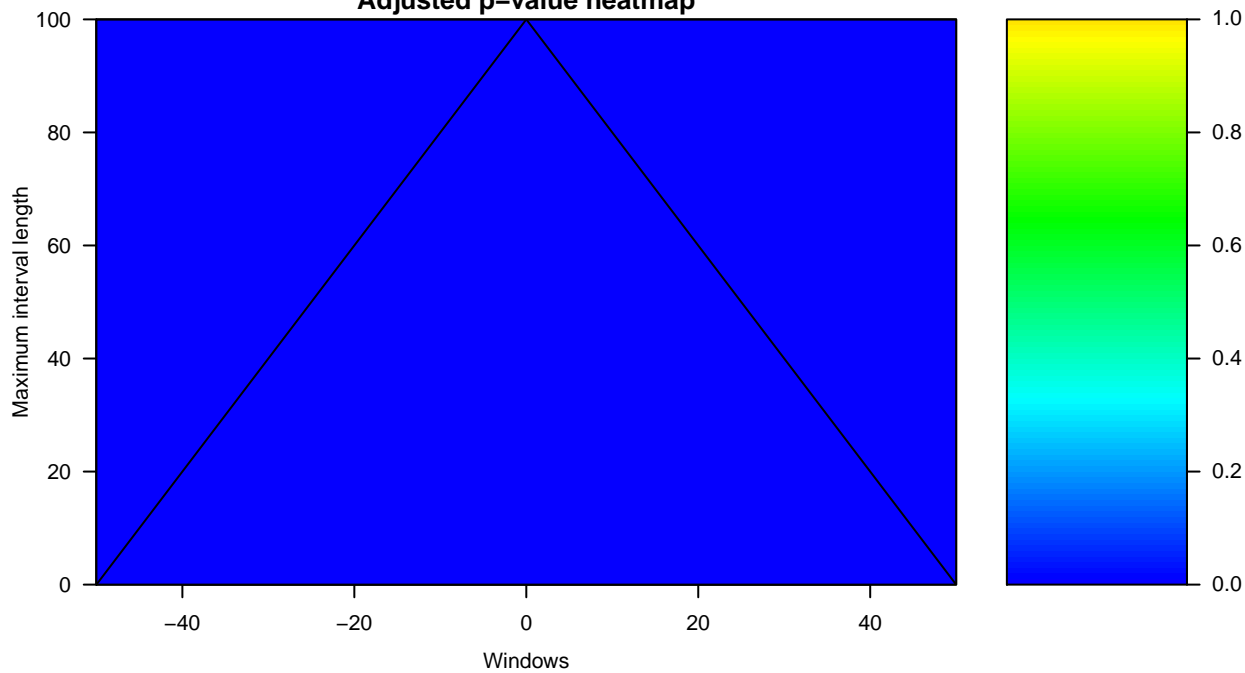


# Alu

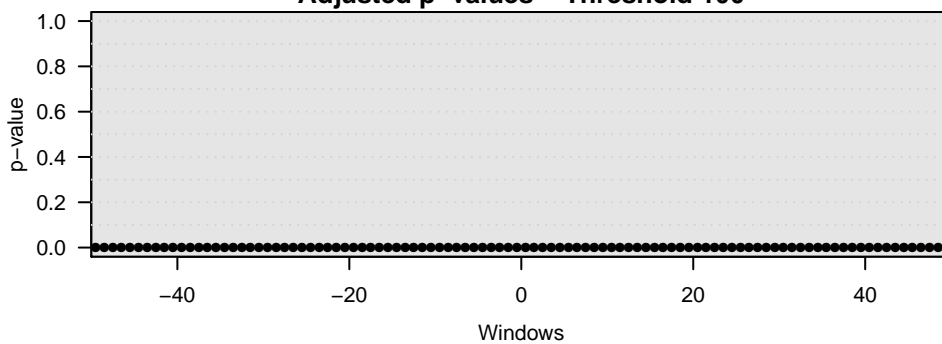


# MIR

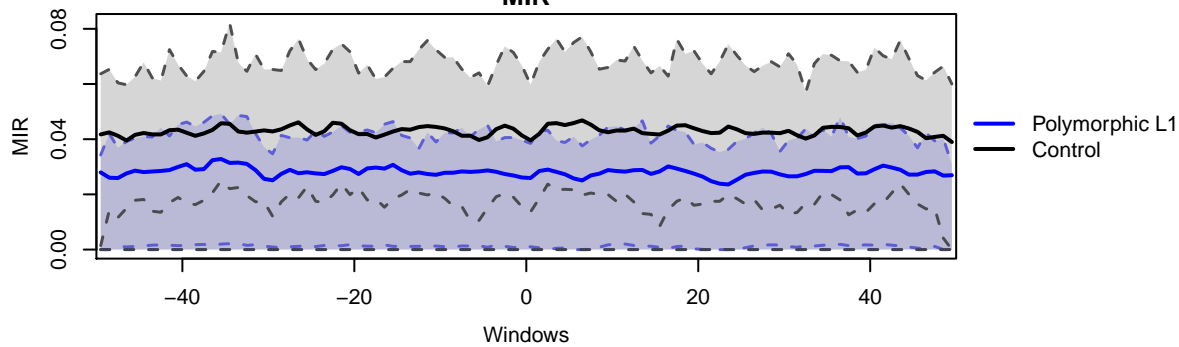
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100

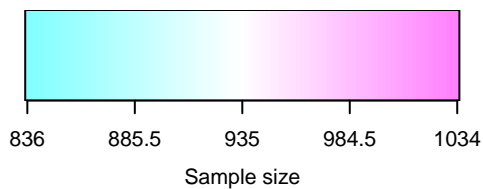


# MIR

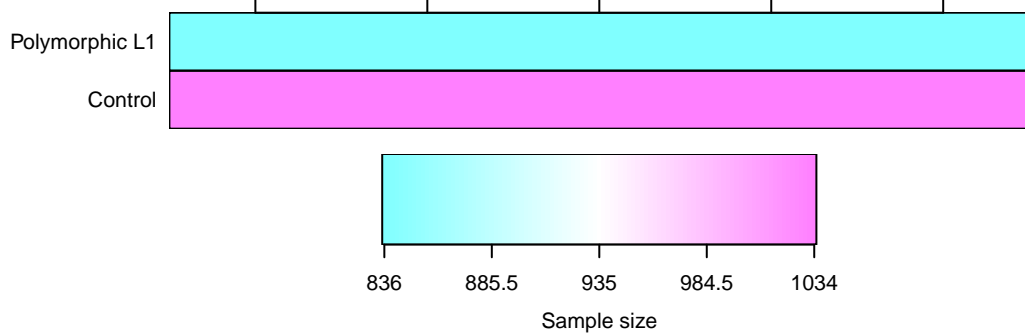
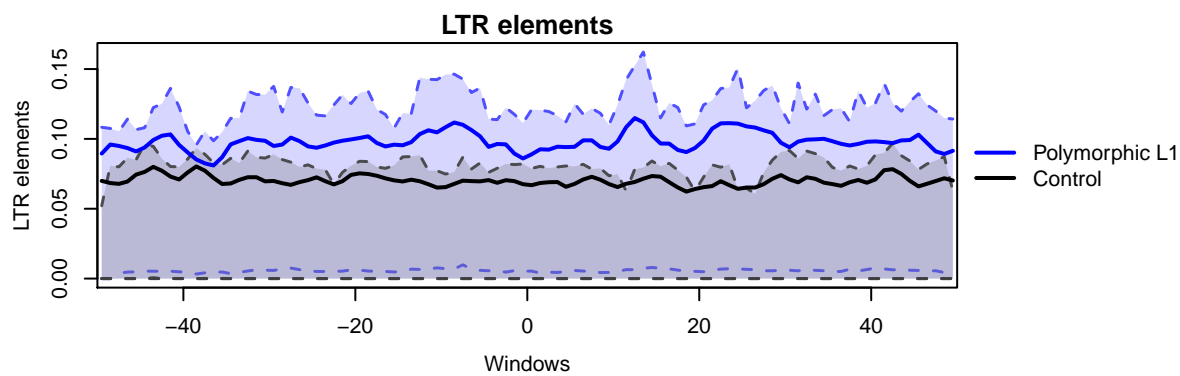
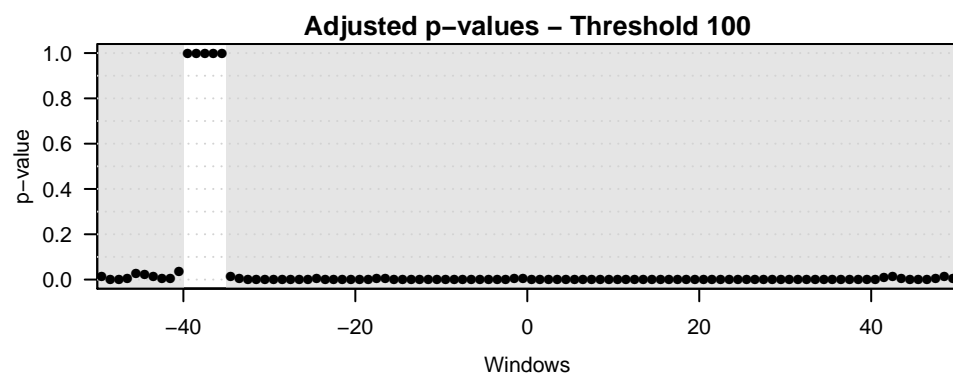
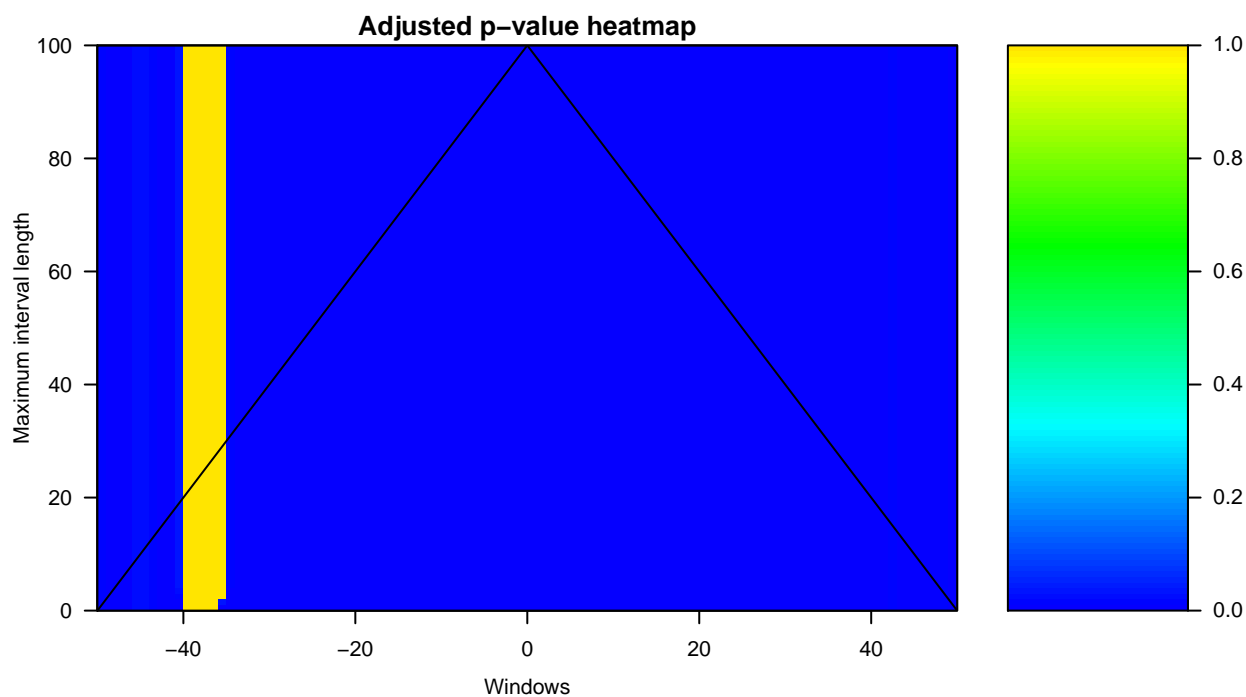


Polymorphic L1

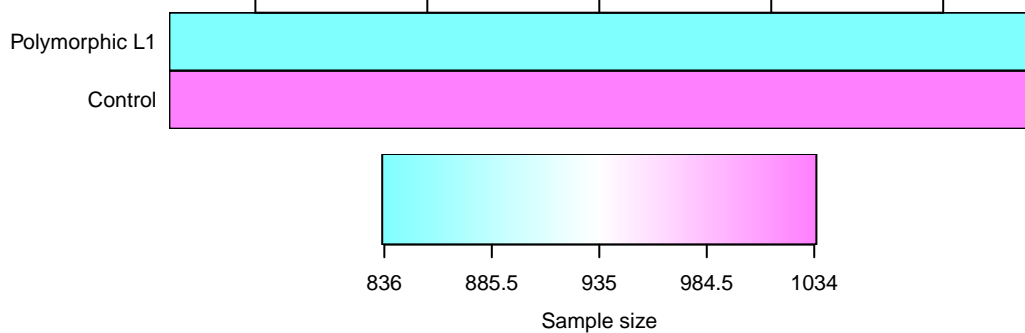
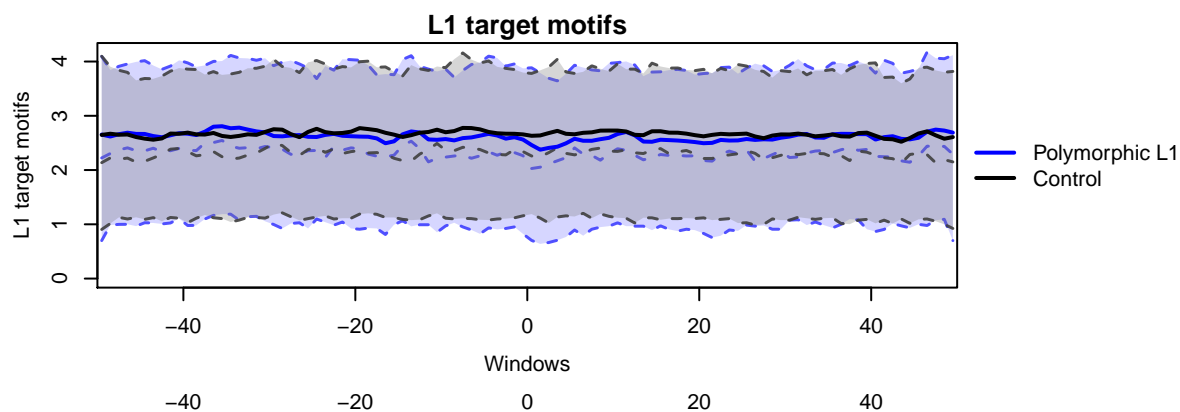
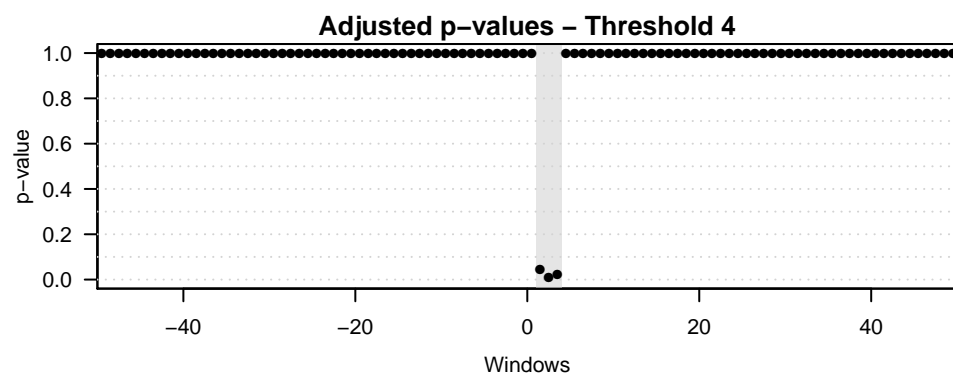
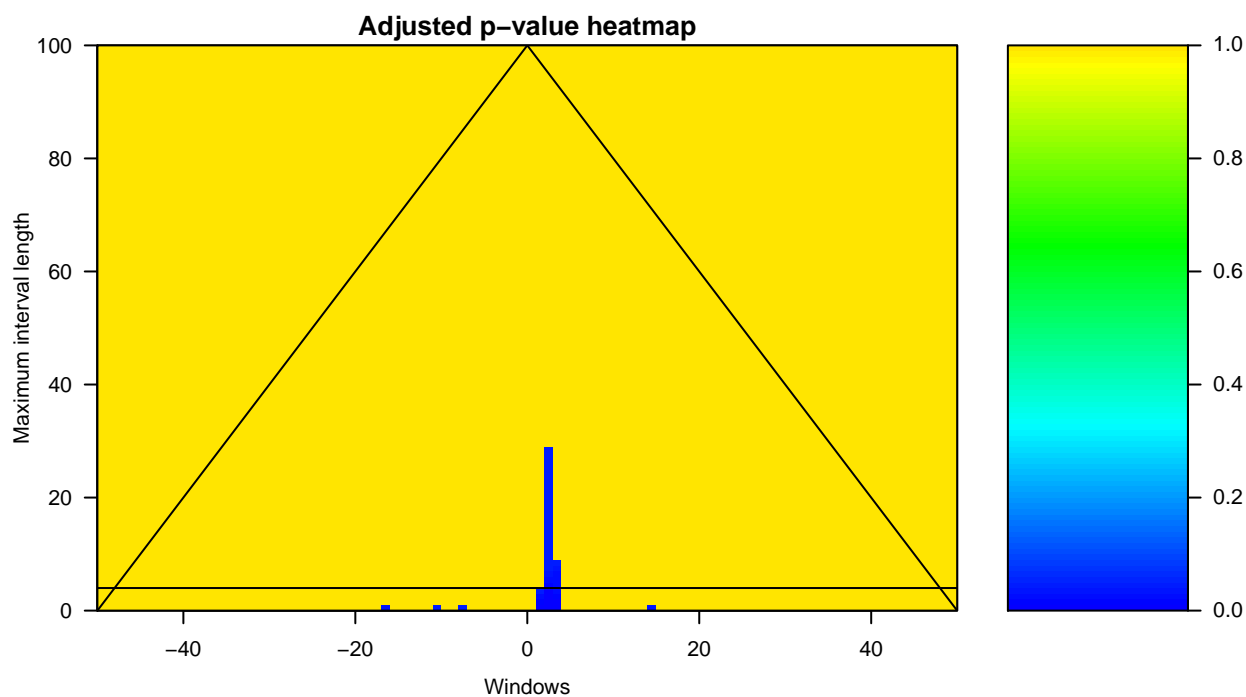
Control



# LTR elements

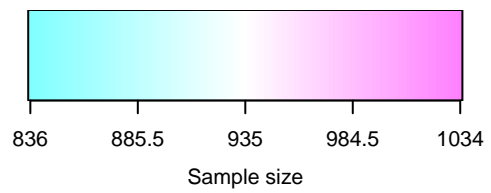
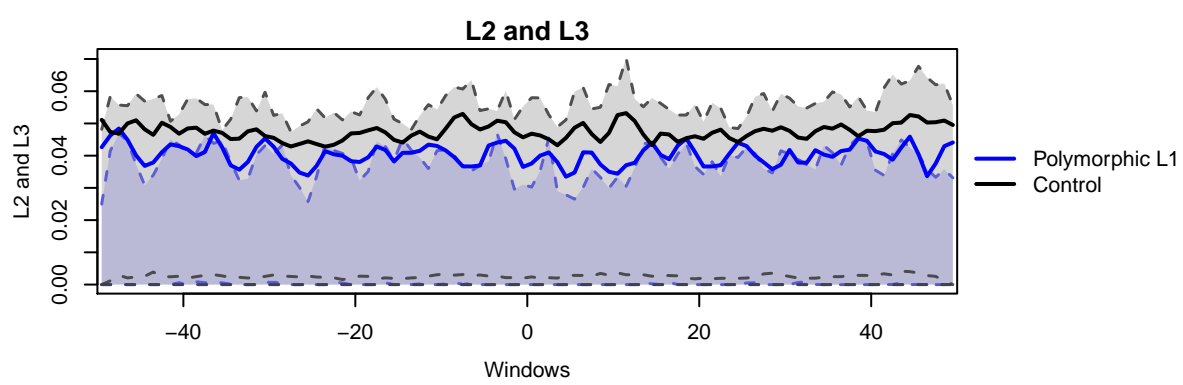
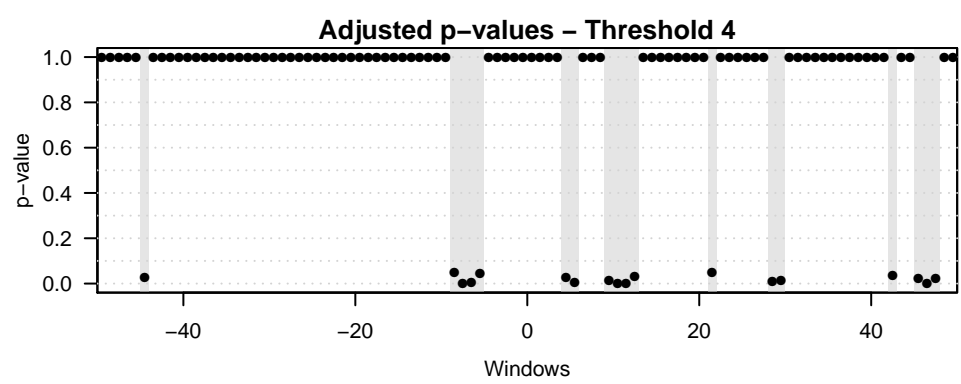
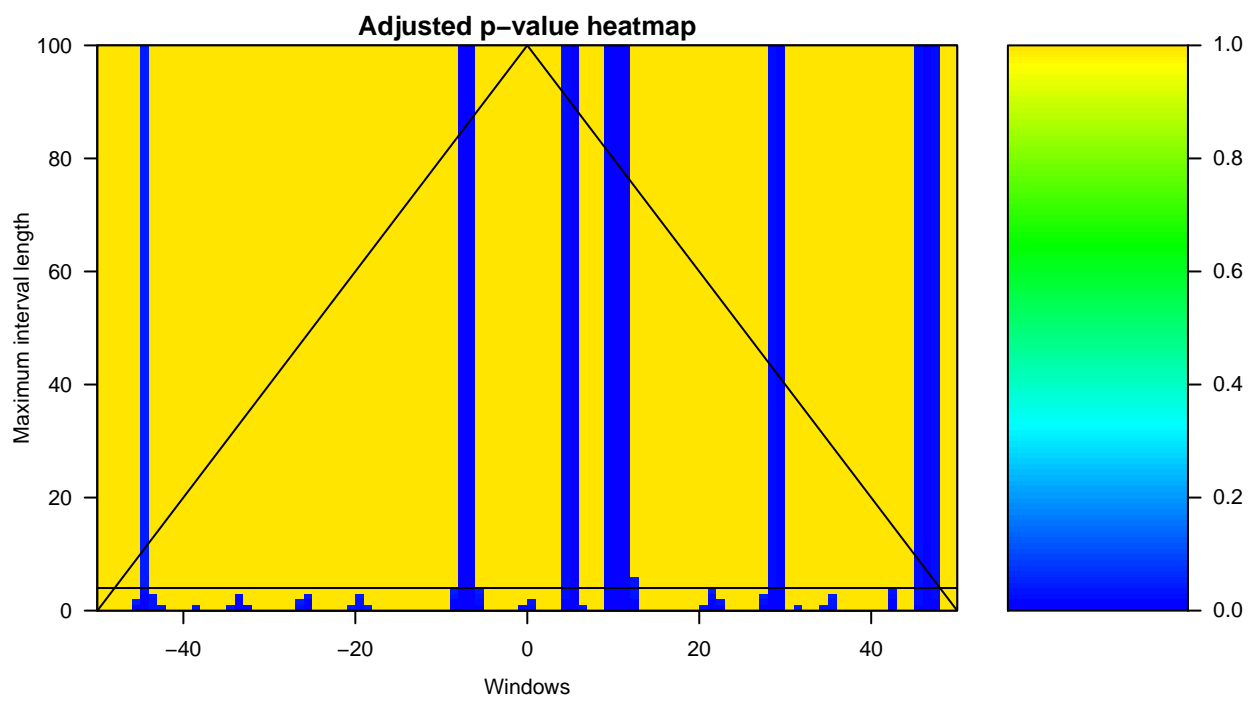


# L1 target motifs

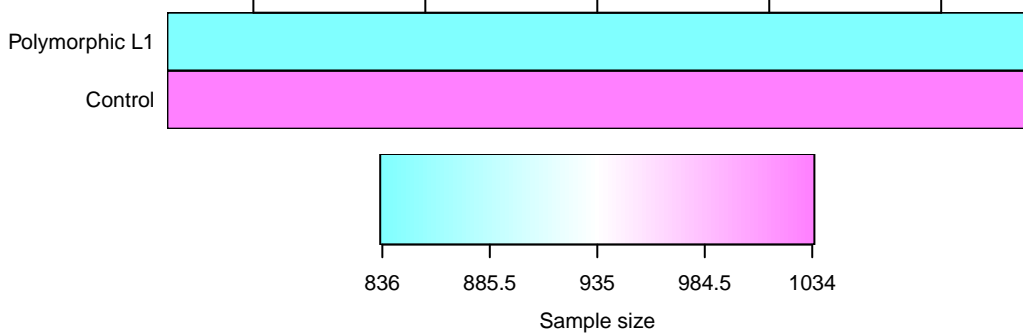
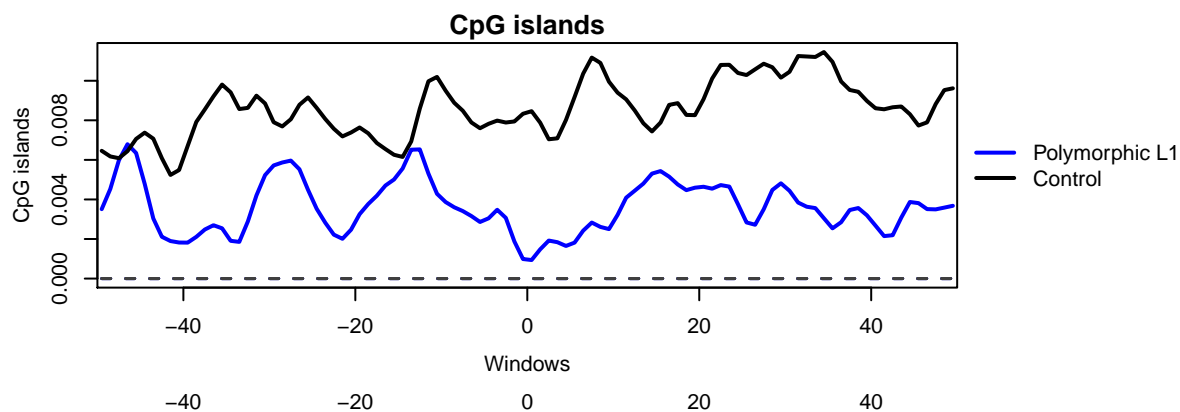
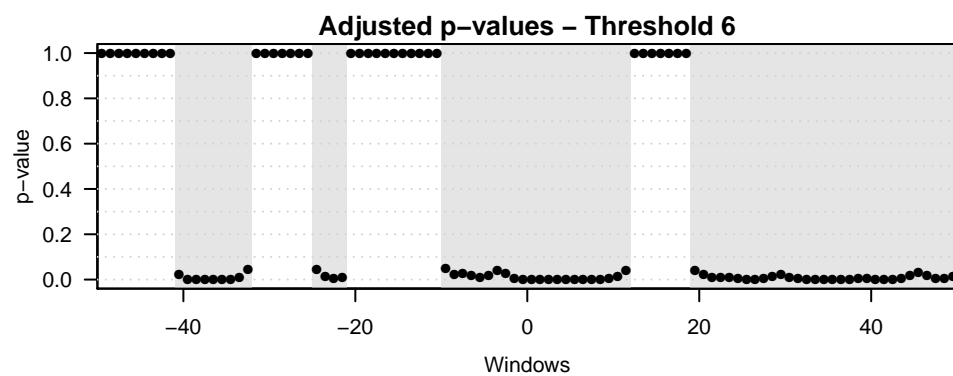
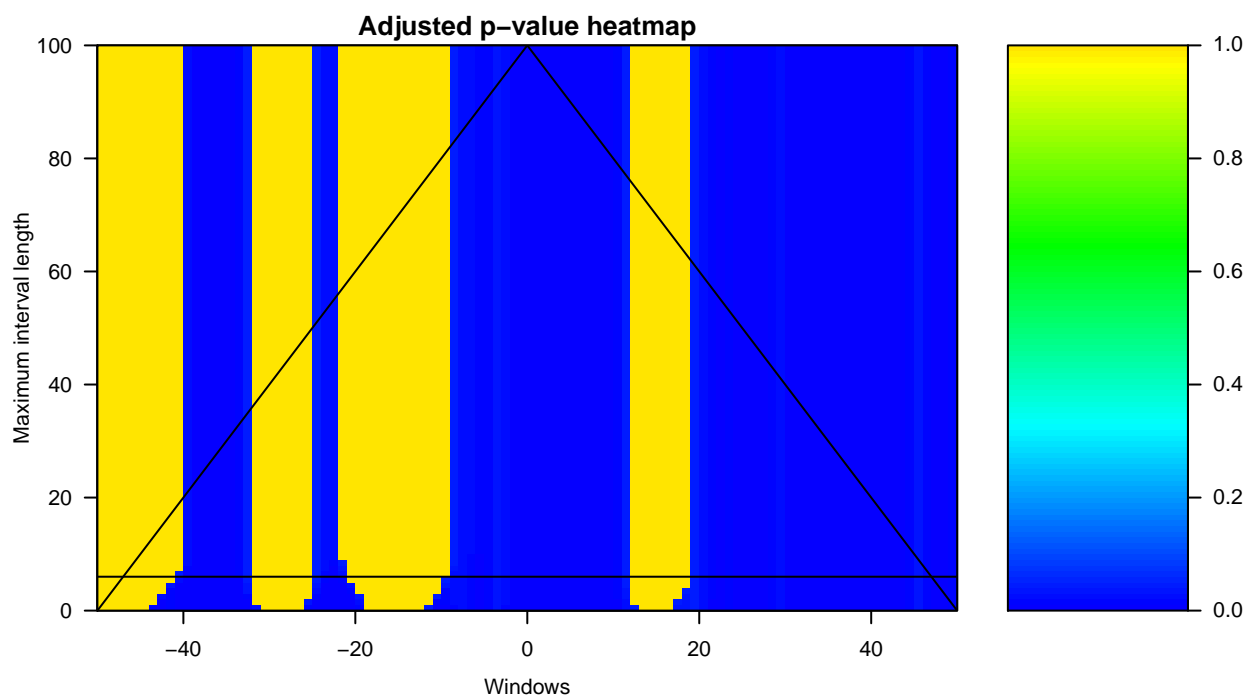




# L2 and L3

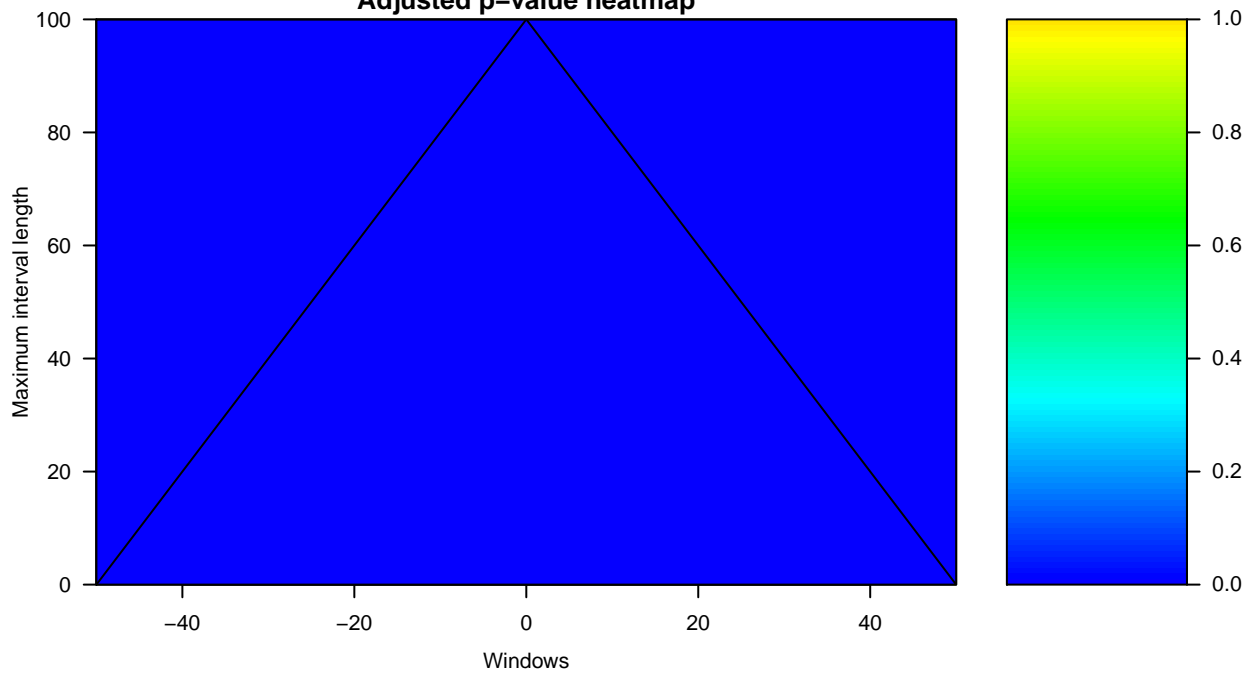


# CpG islands

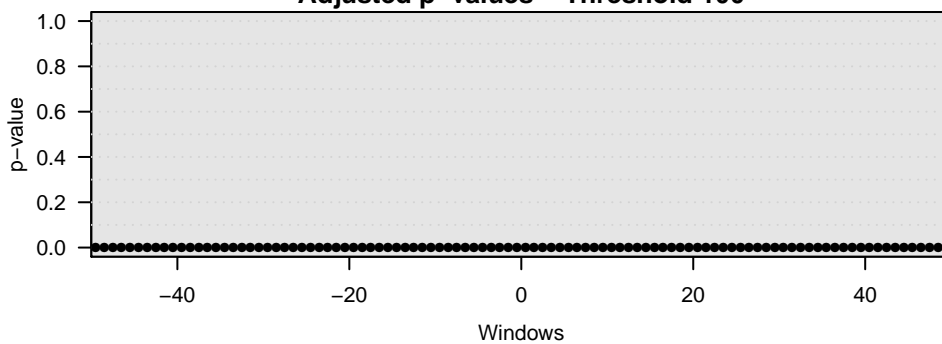


# 5-hydroxymethylcytosine

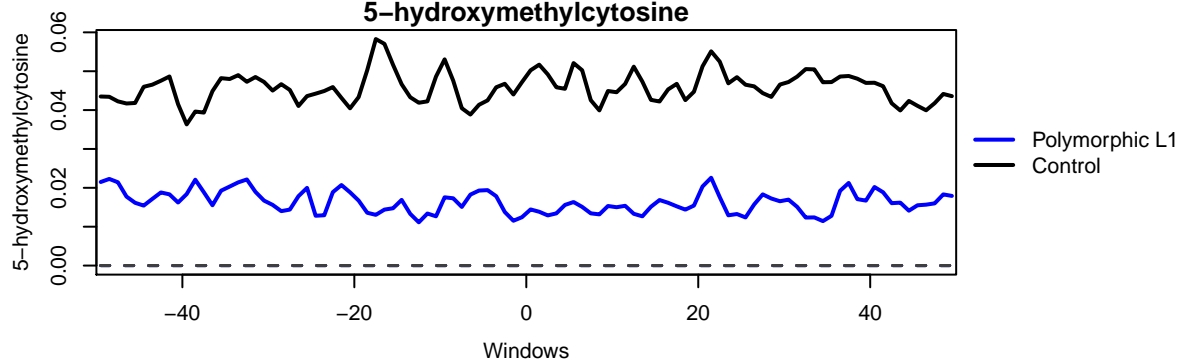
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100

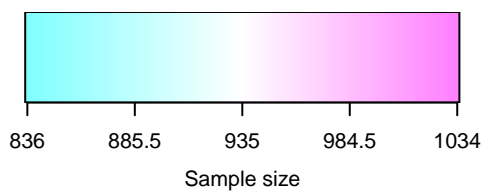


# 5-hydroxymethylcytosine



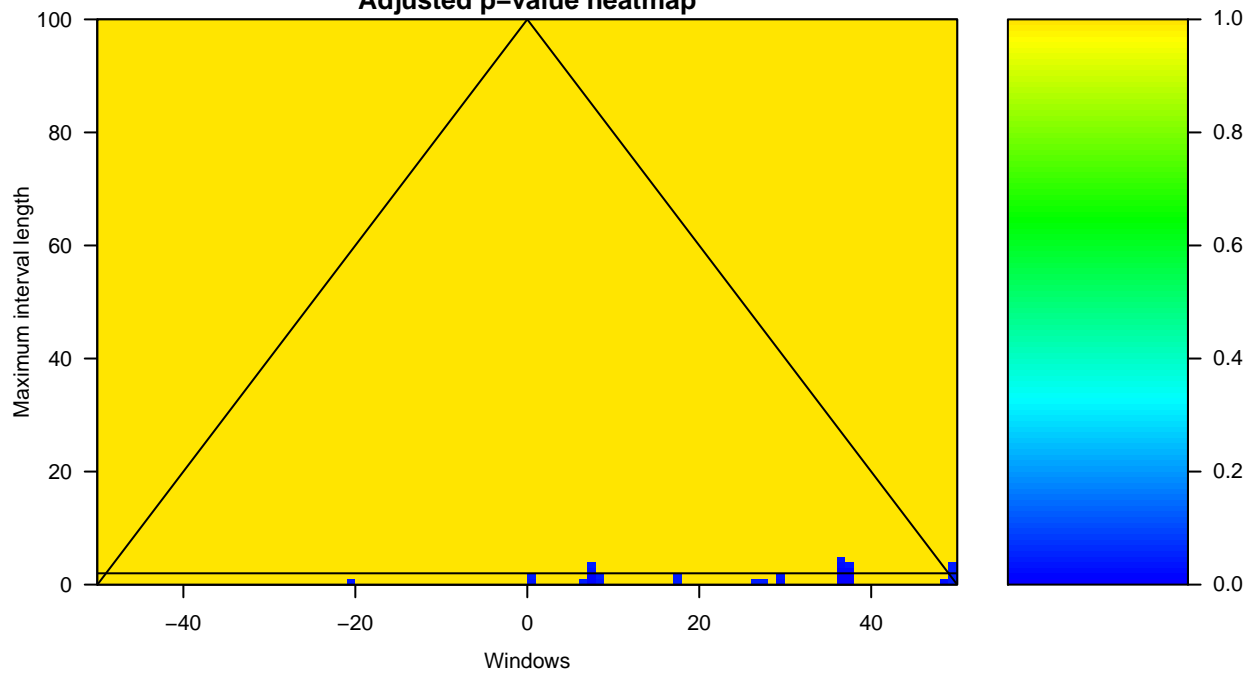
Polymorphic L1

Control

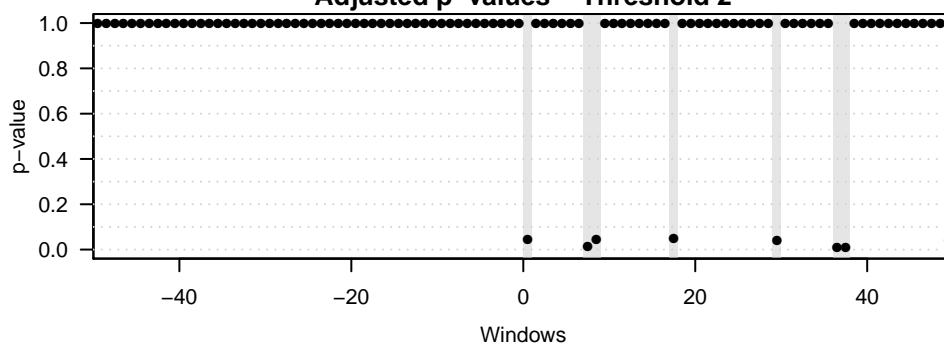


# Sperm hypomethylation

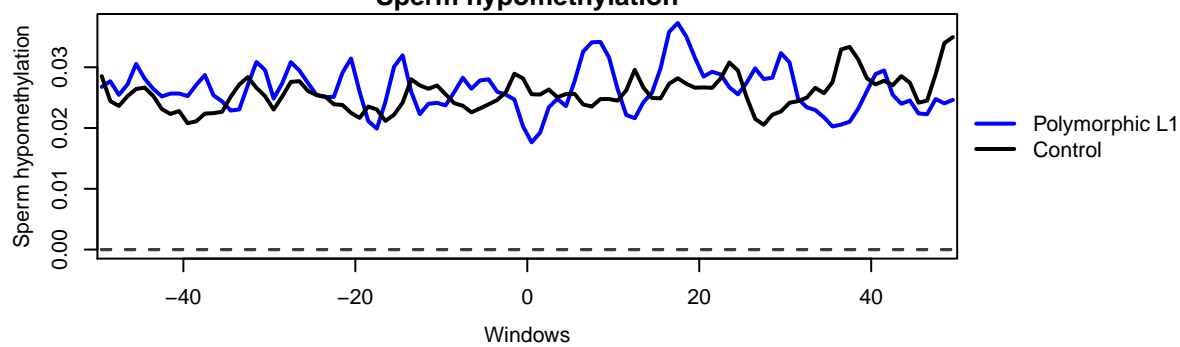
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 2

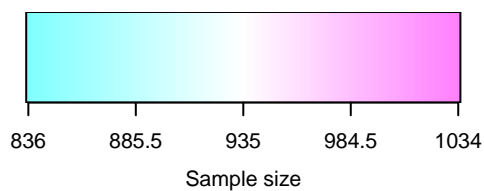


# Sperm hypomethylation



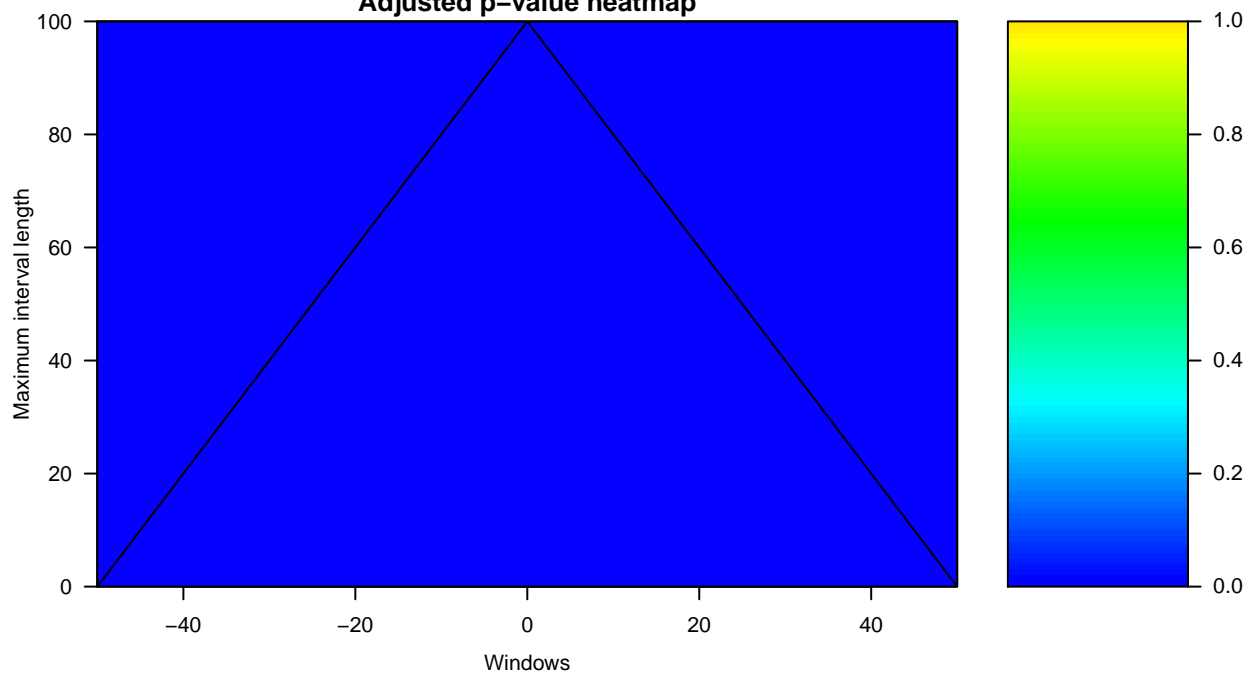
Polymorphic L1

Control

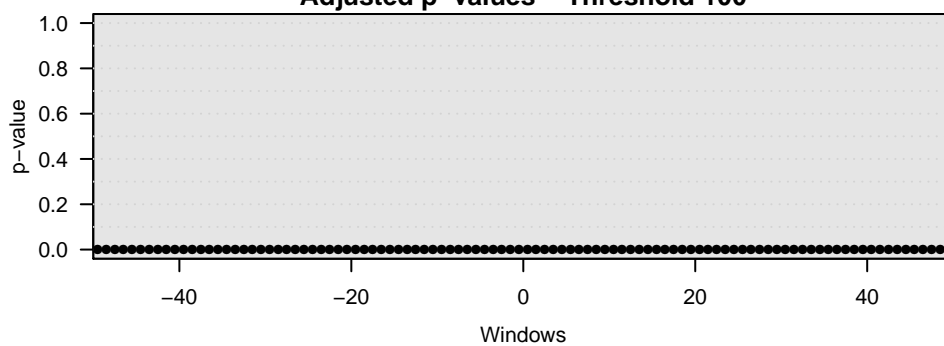


# Replication origin

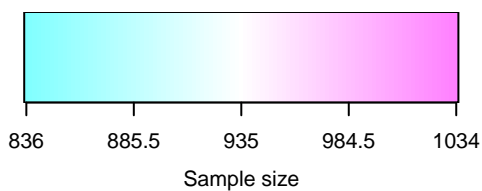
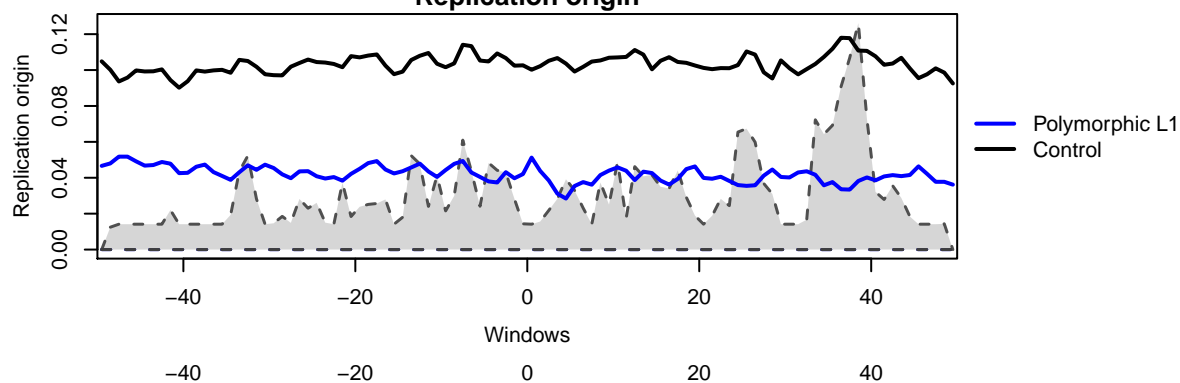
## Adjusted p-value heatmap



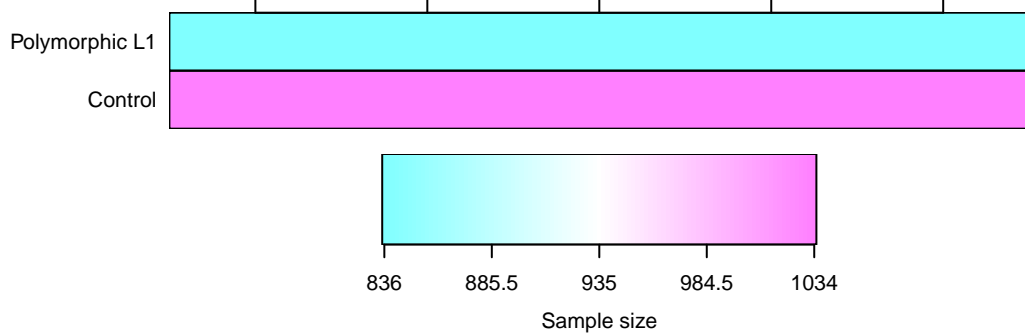
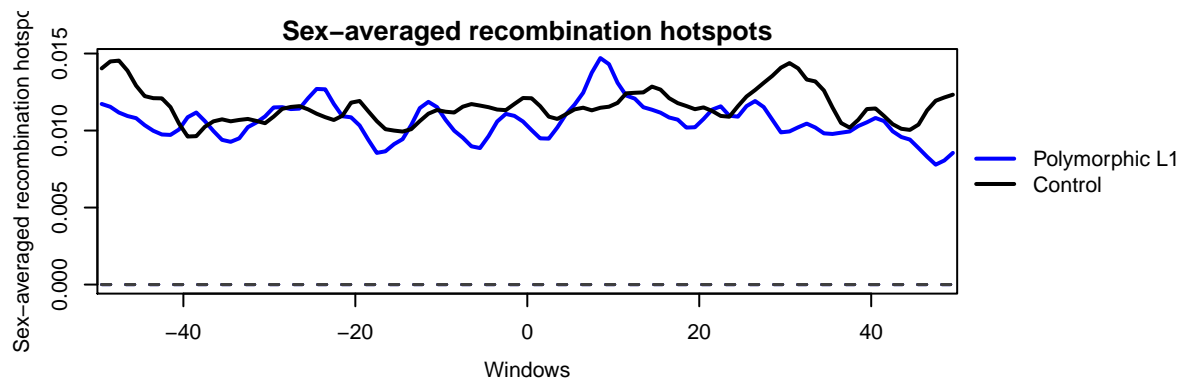
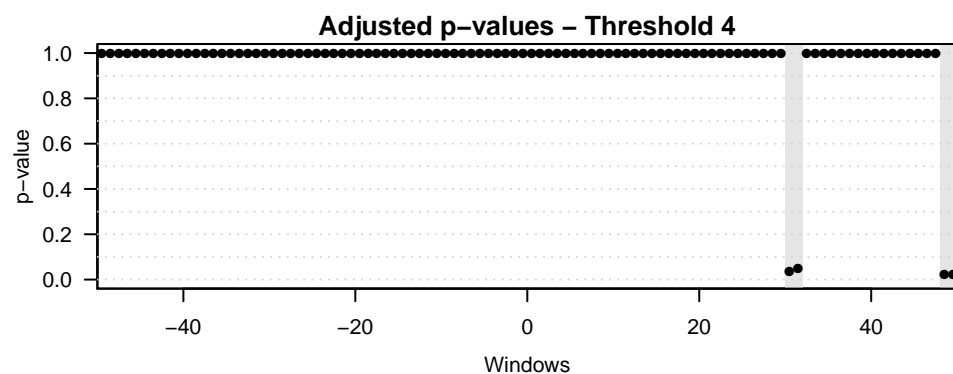
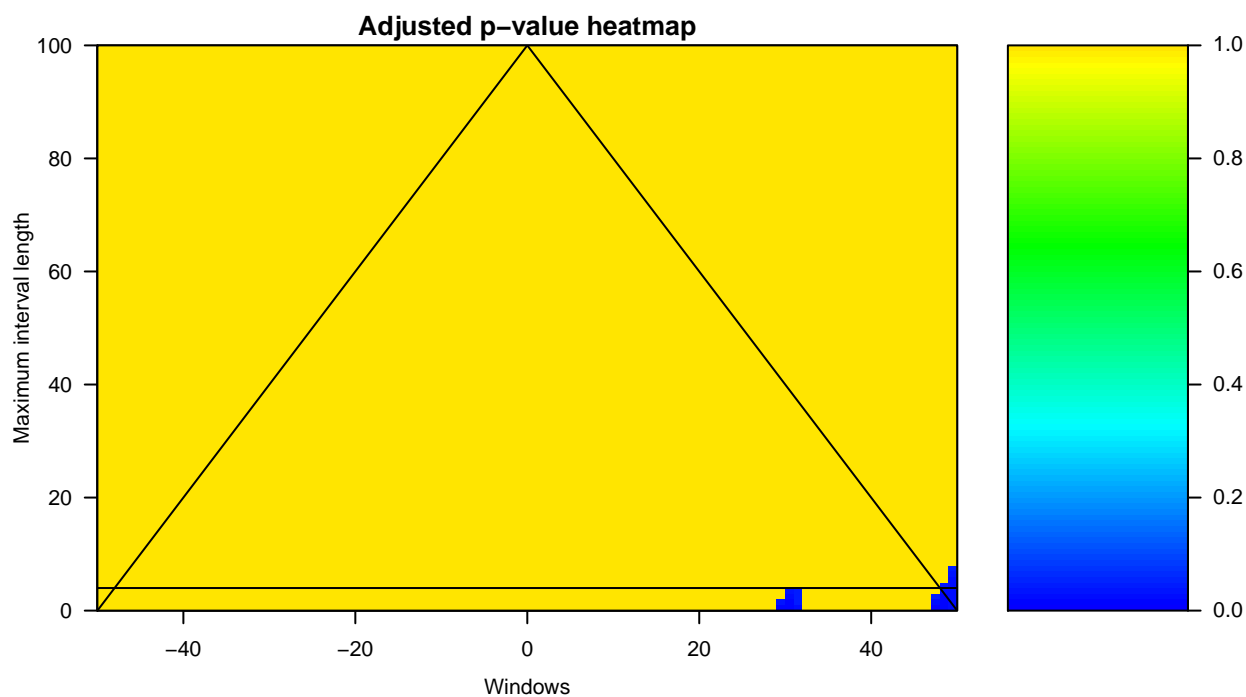
## Adjusted p-values – Threshold 100



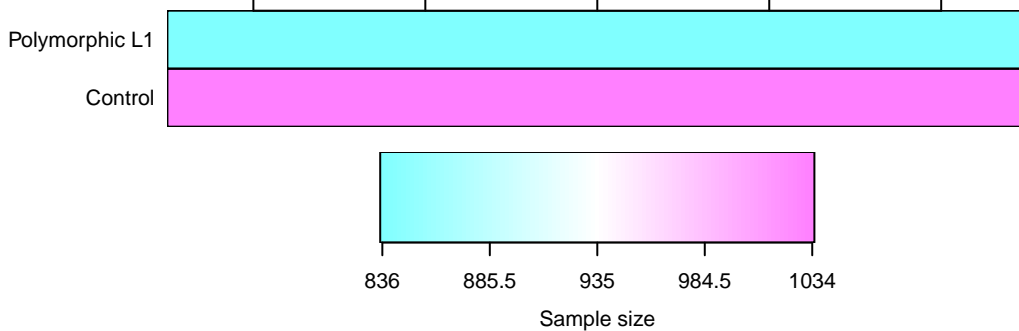
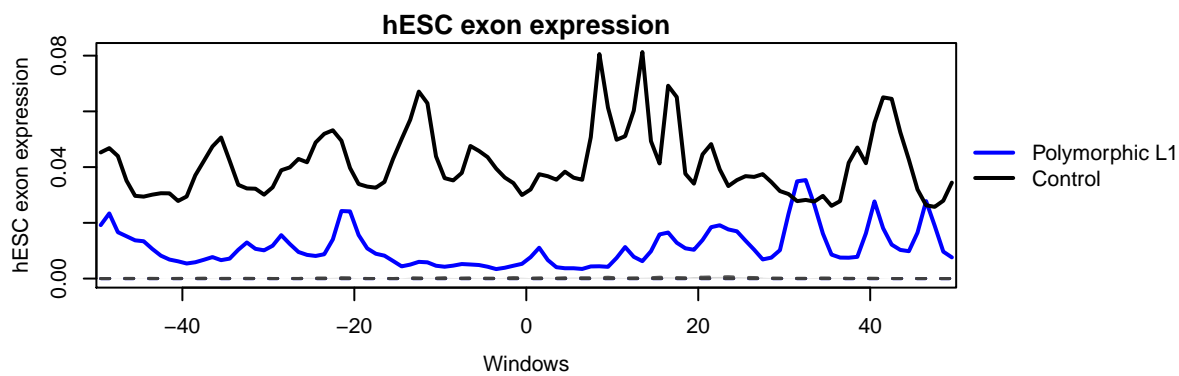
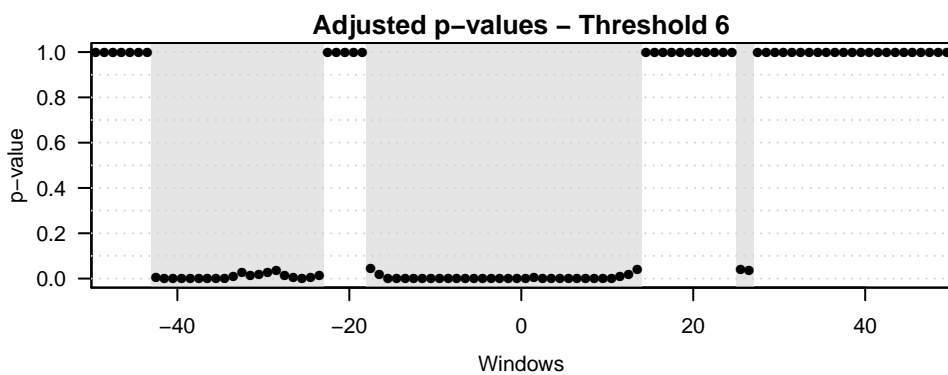
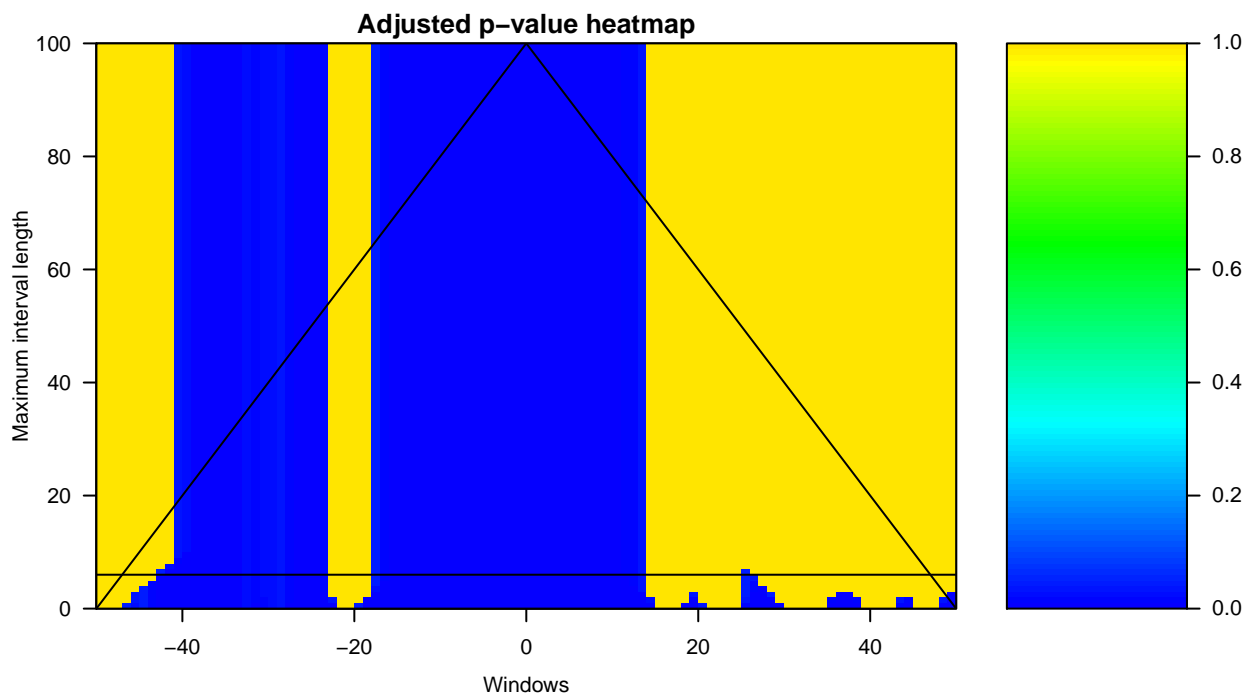
# Replication origin



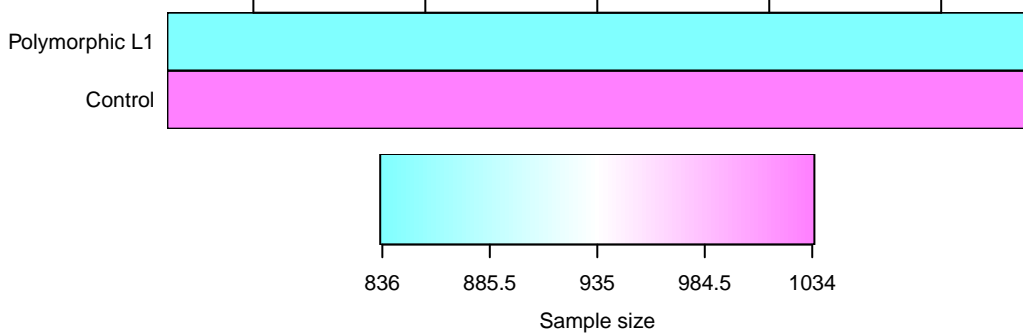
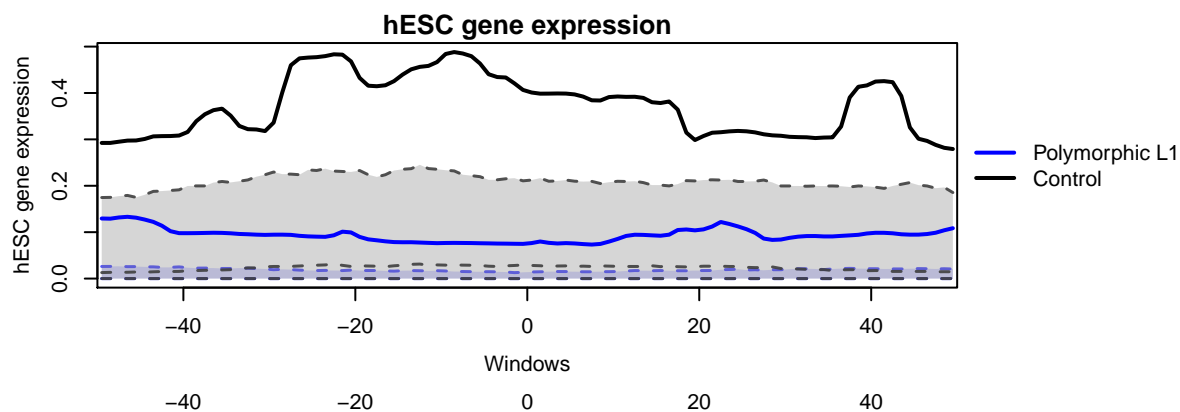
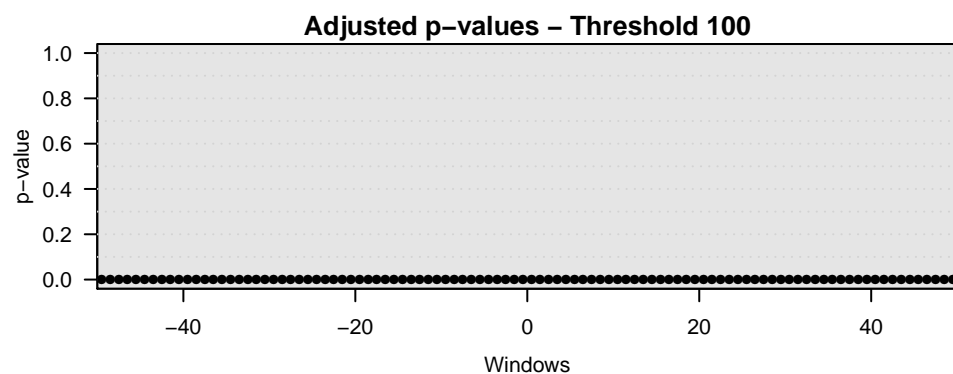
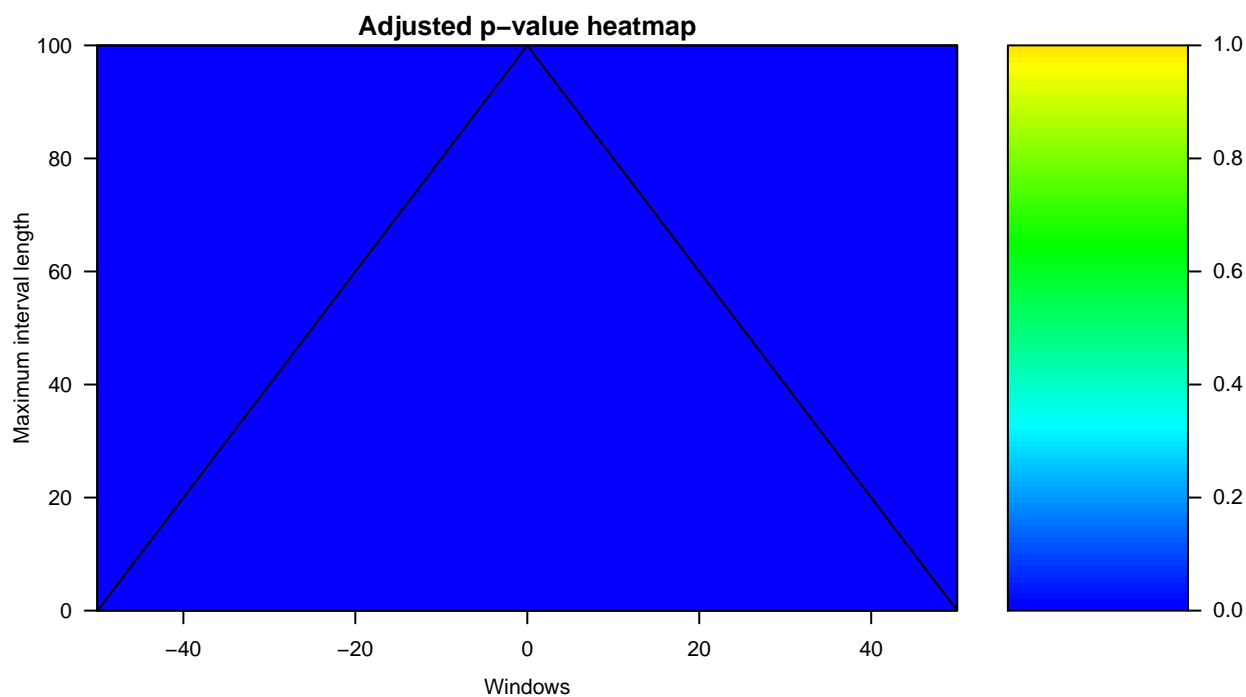
# Sex-averaged recombination hotspots



# hESC exon expression

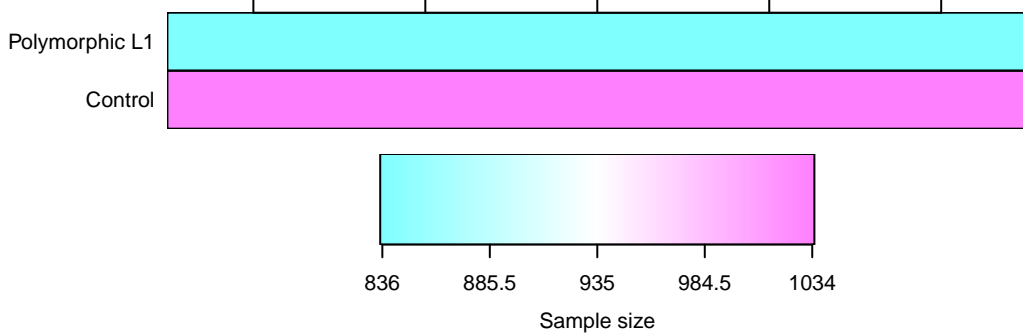
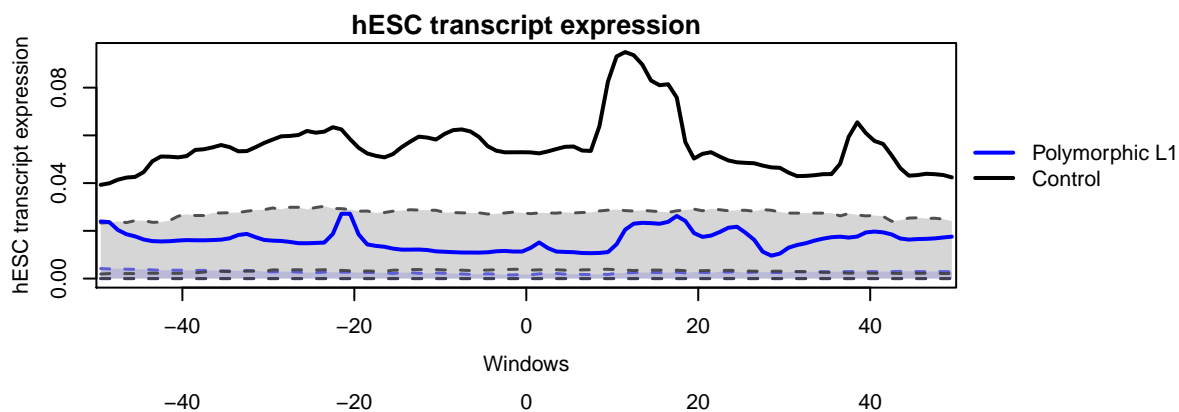
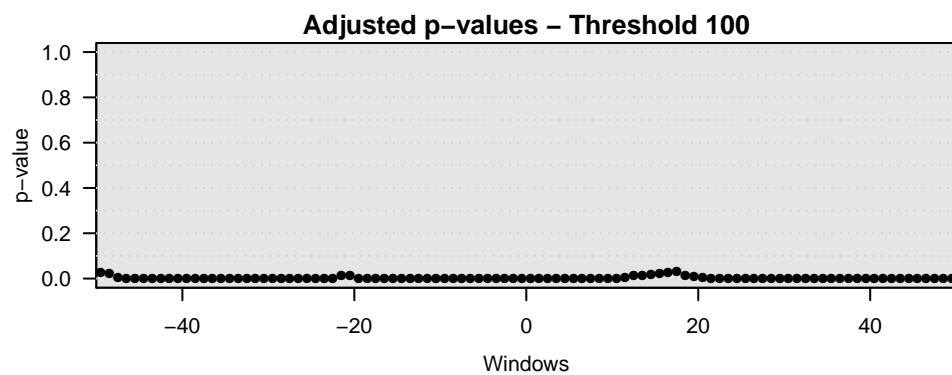
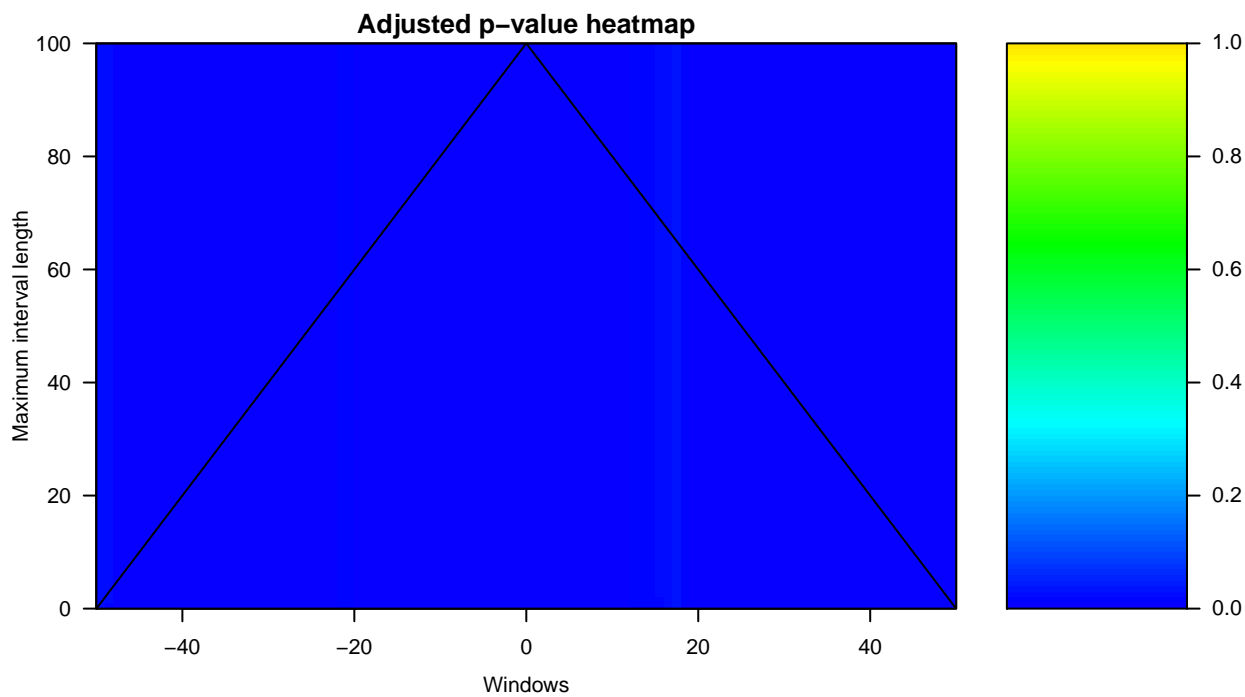


# hESC gene expression

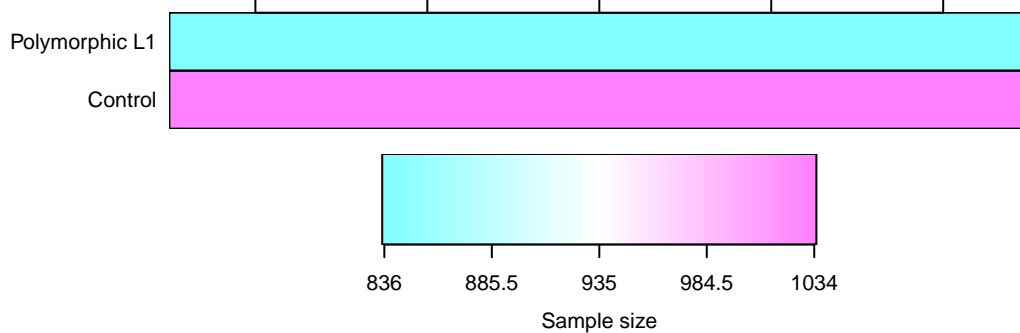
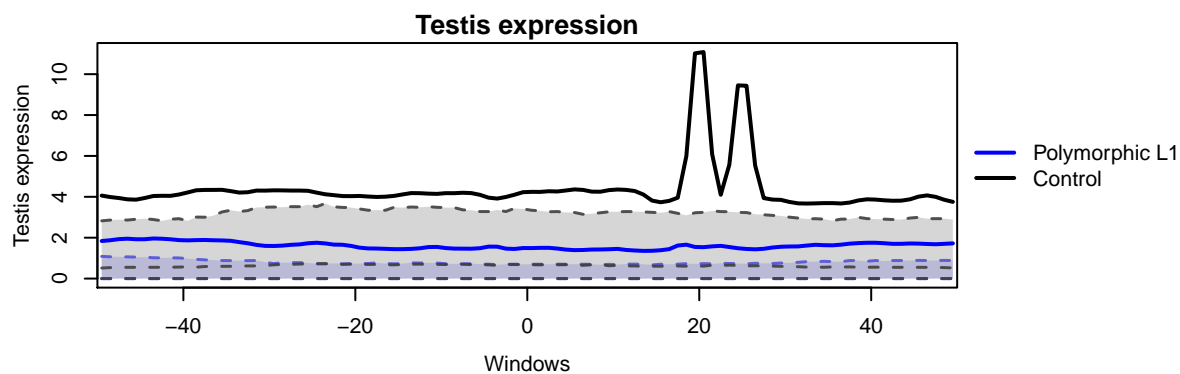
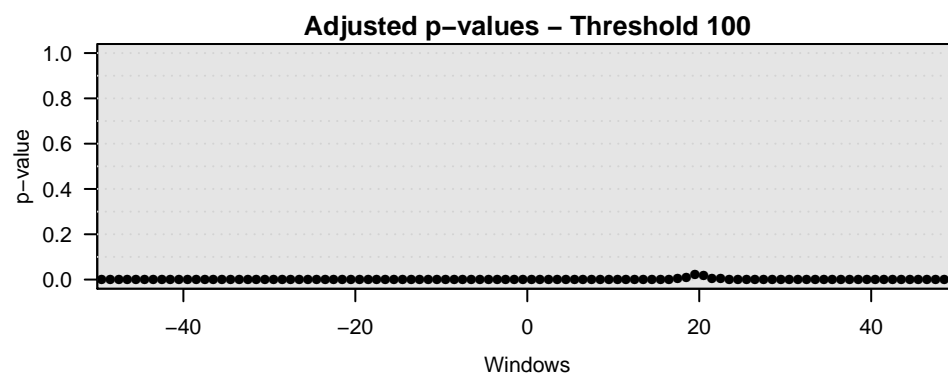
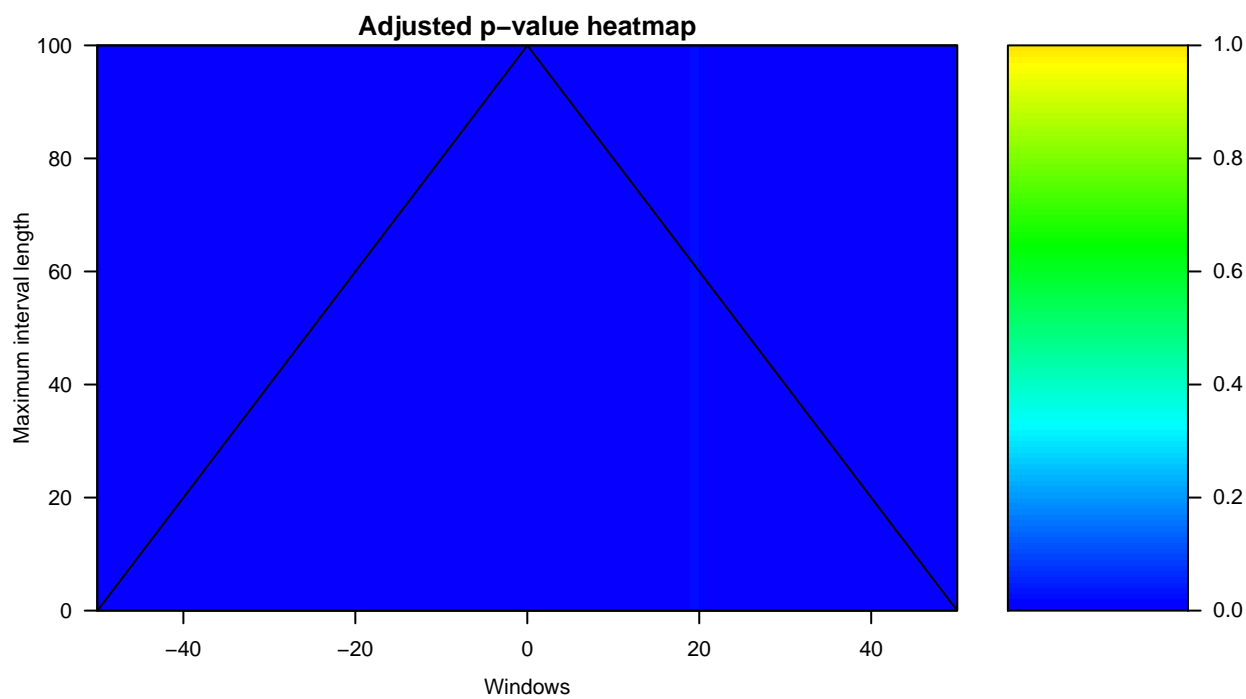




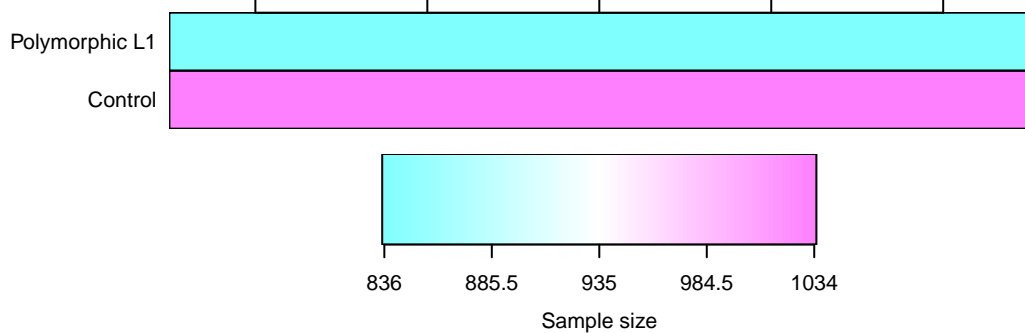
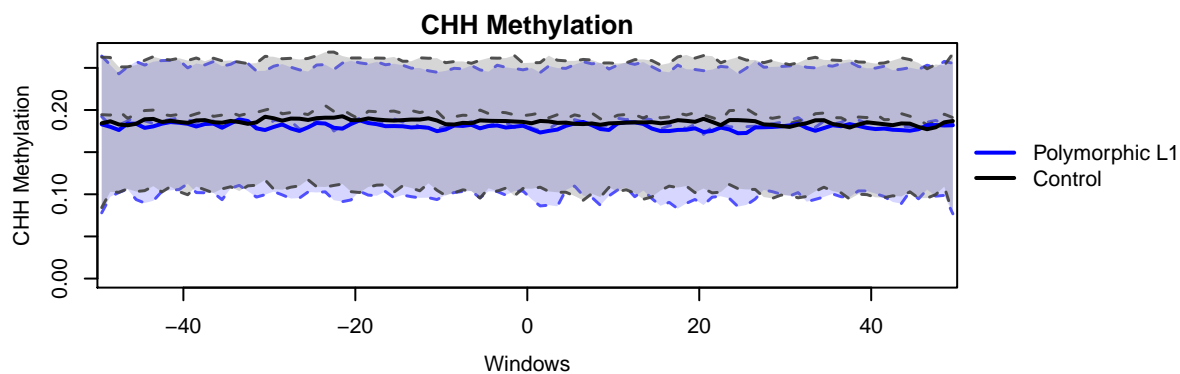
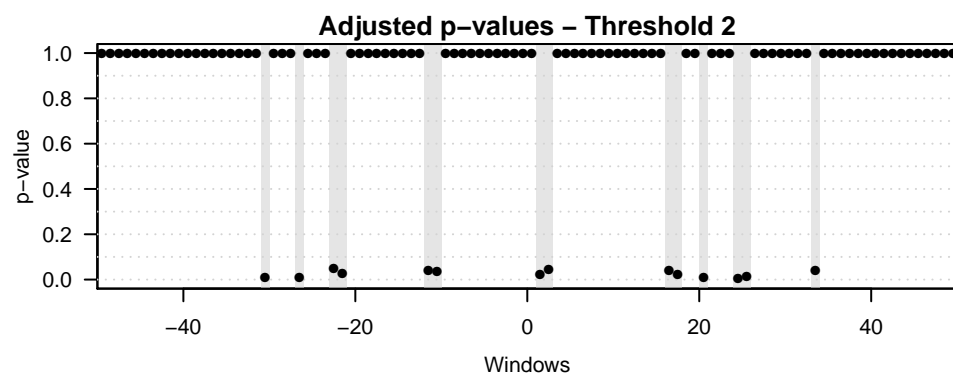
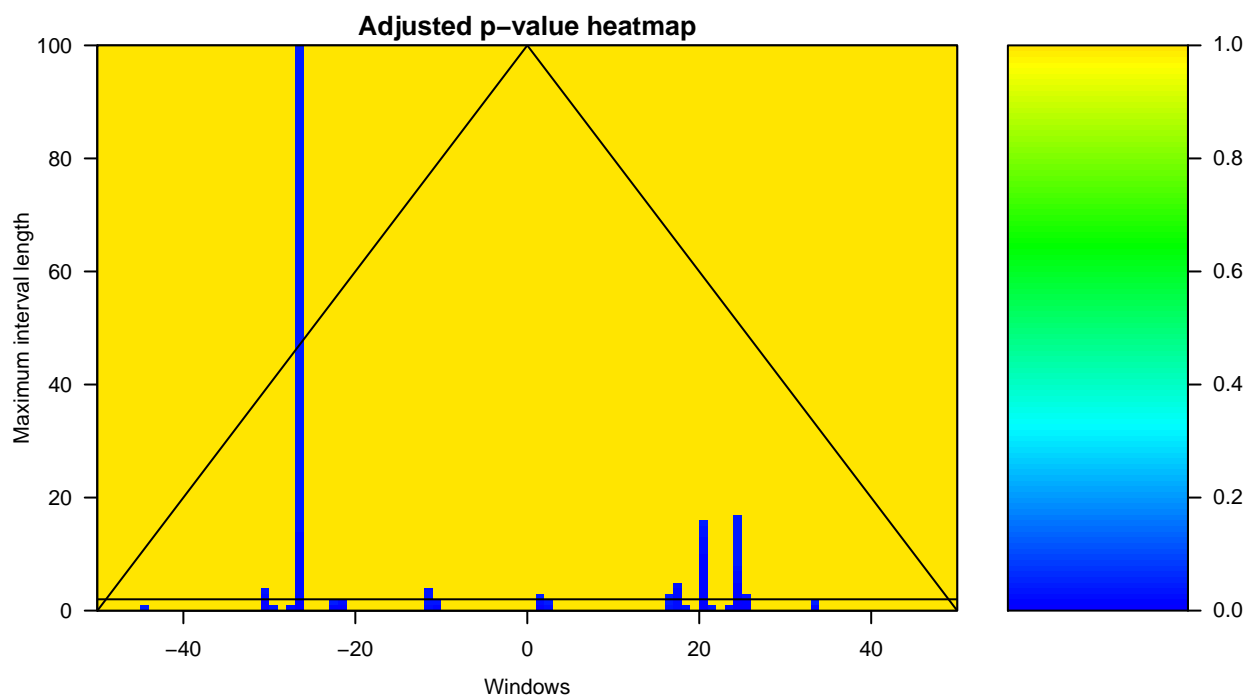
# hESC transcript expression



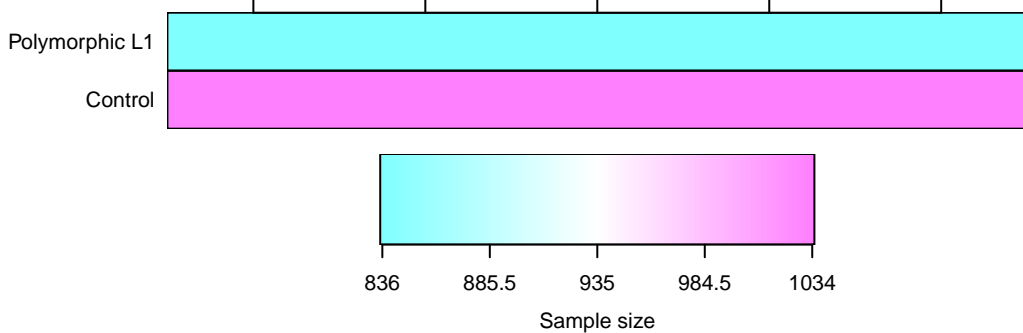
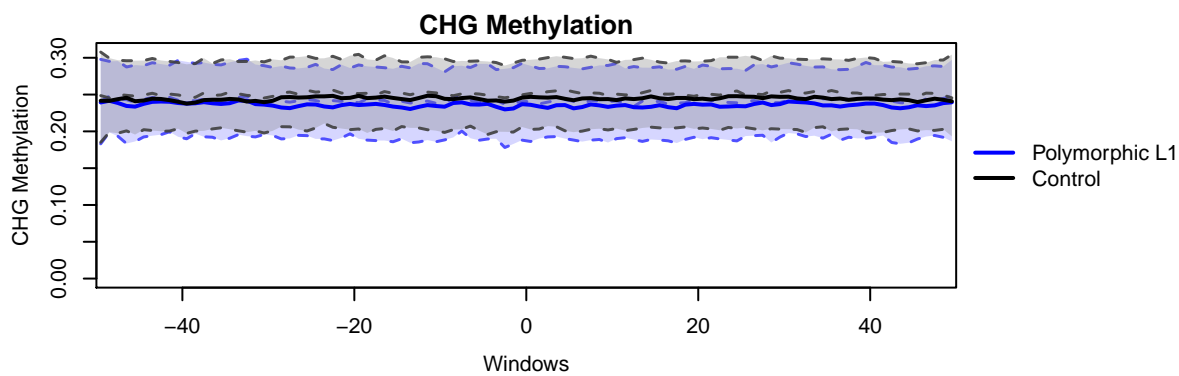
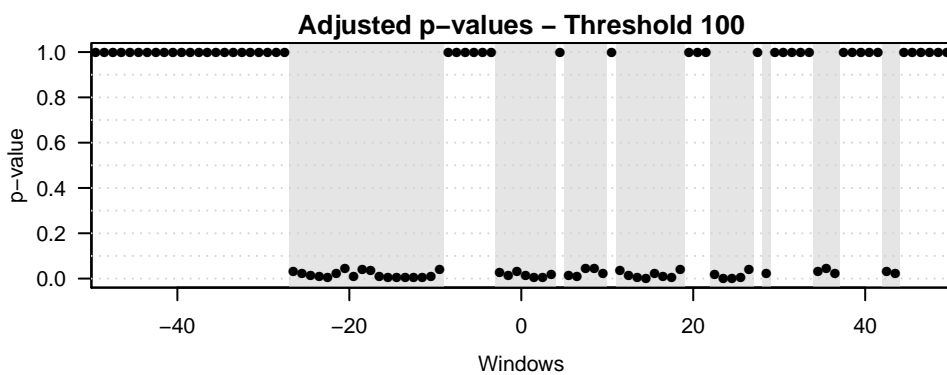
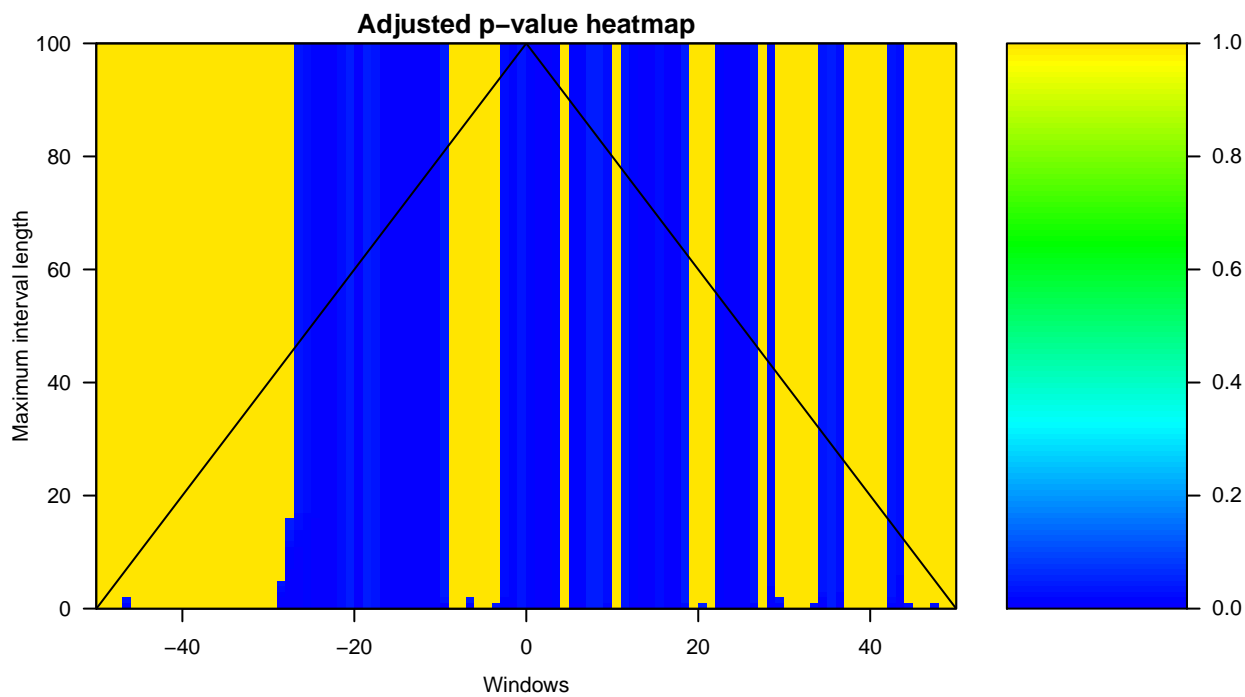
# Testis expression



# CHH Methylation



# CHG Methylation



# CPG Methylation

