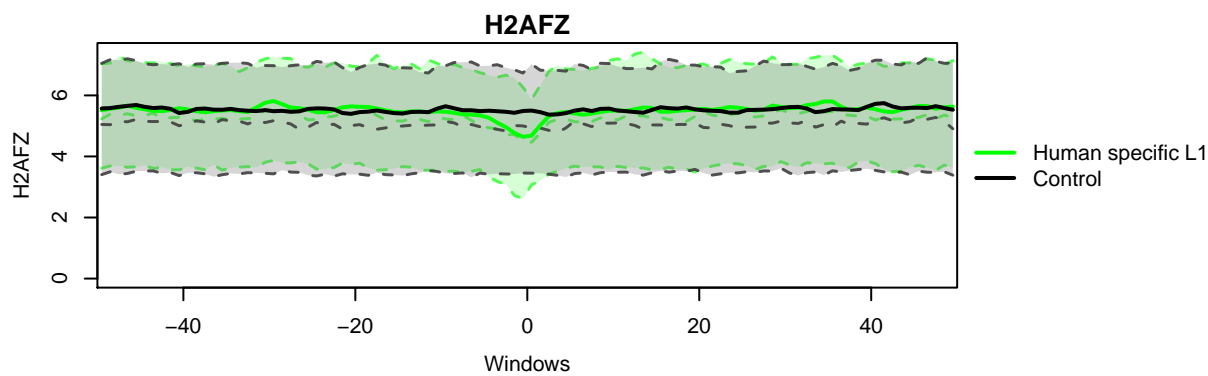
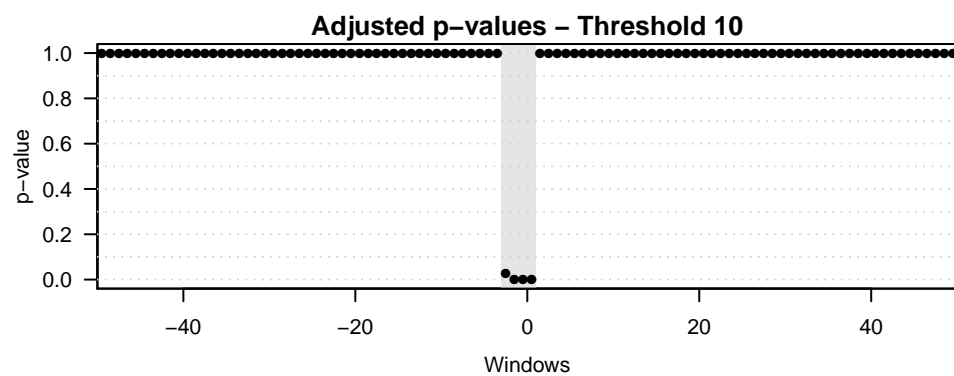
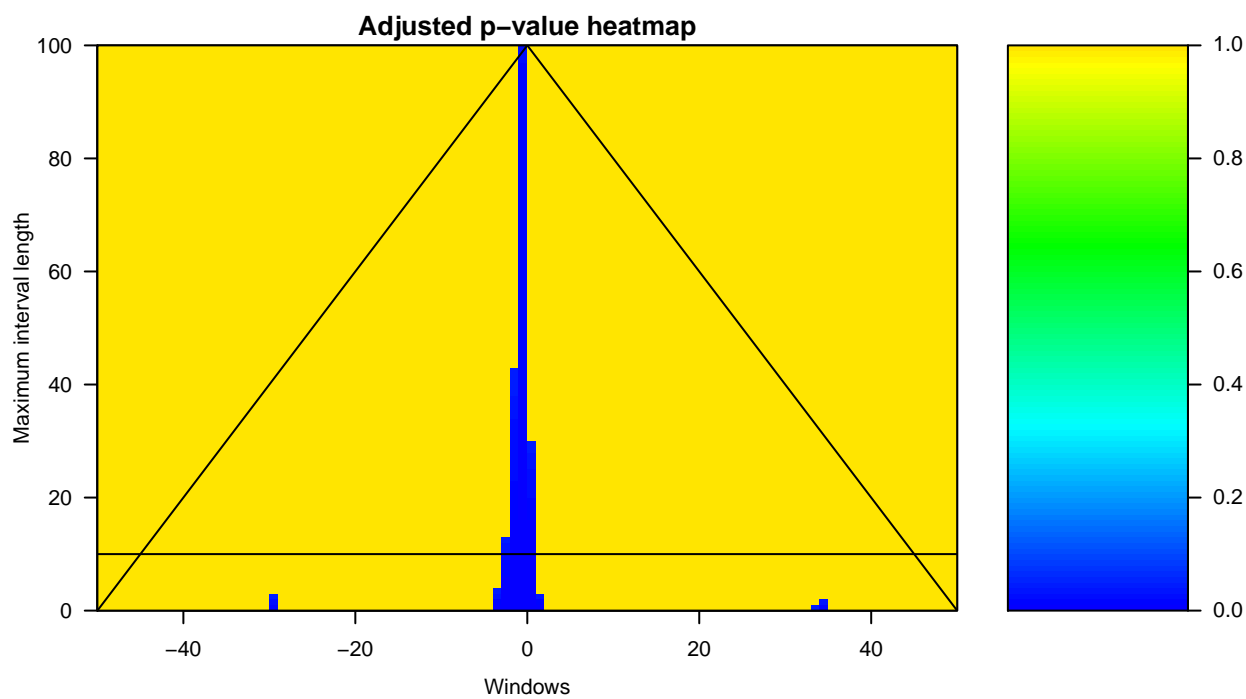
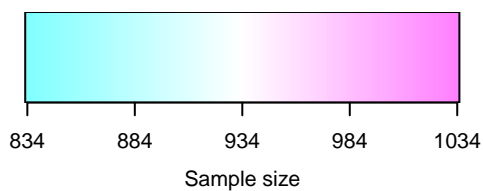


## H2AFZ

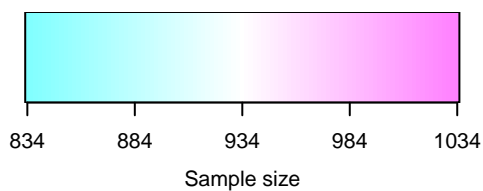
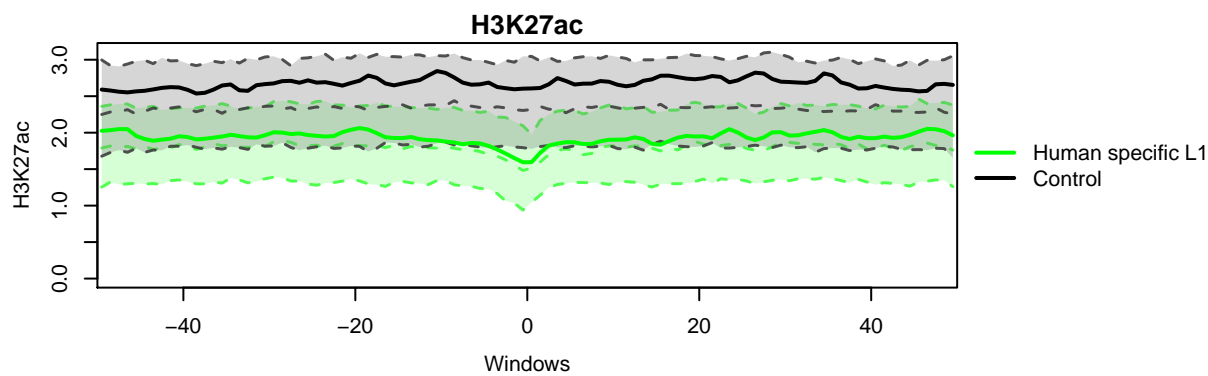
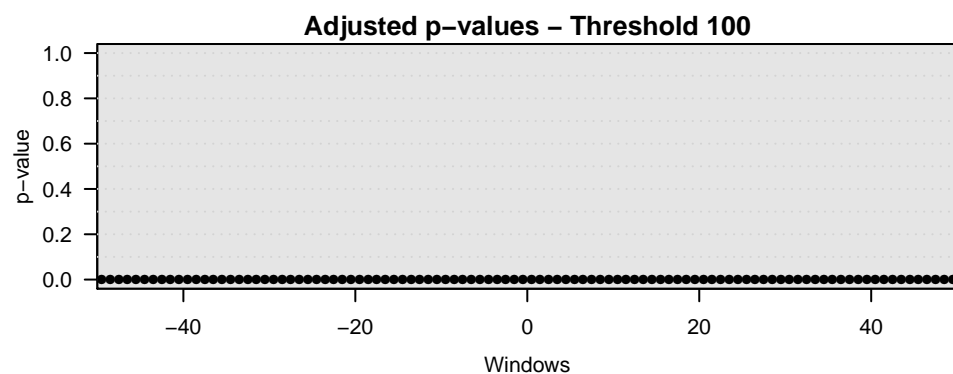
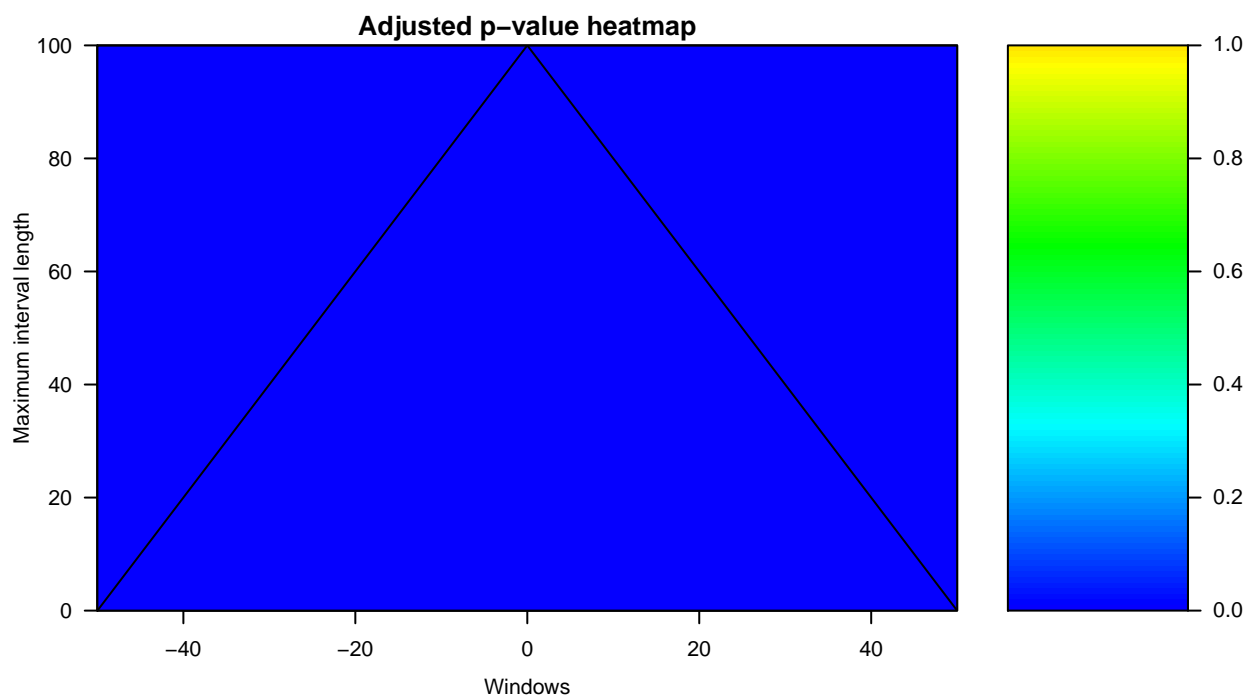


Human specific L1

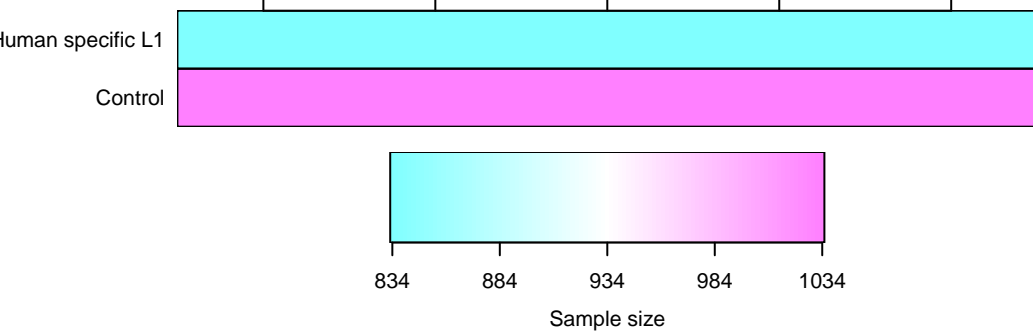
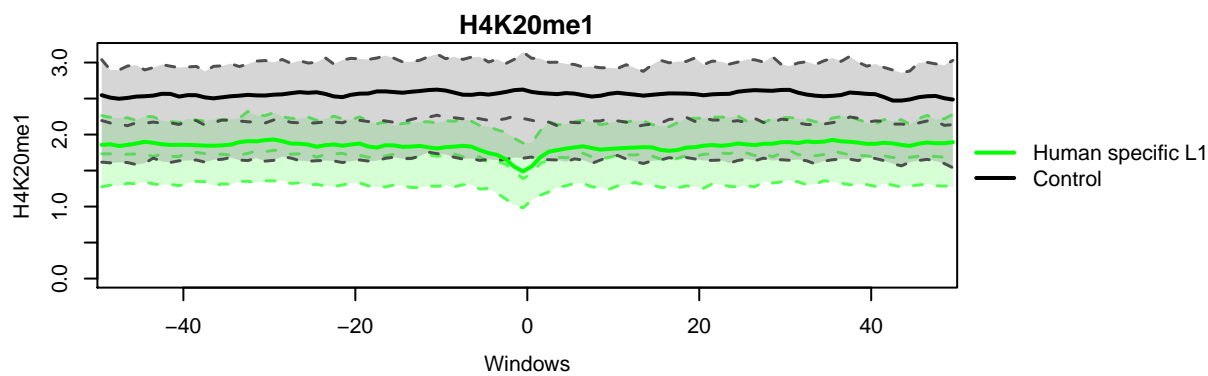
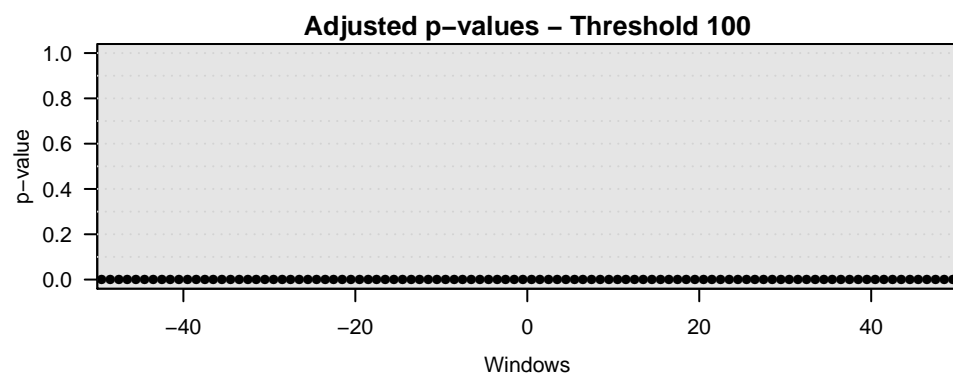
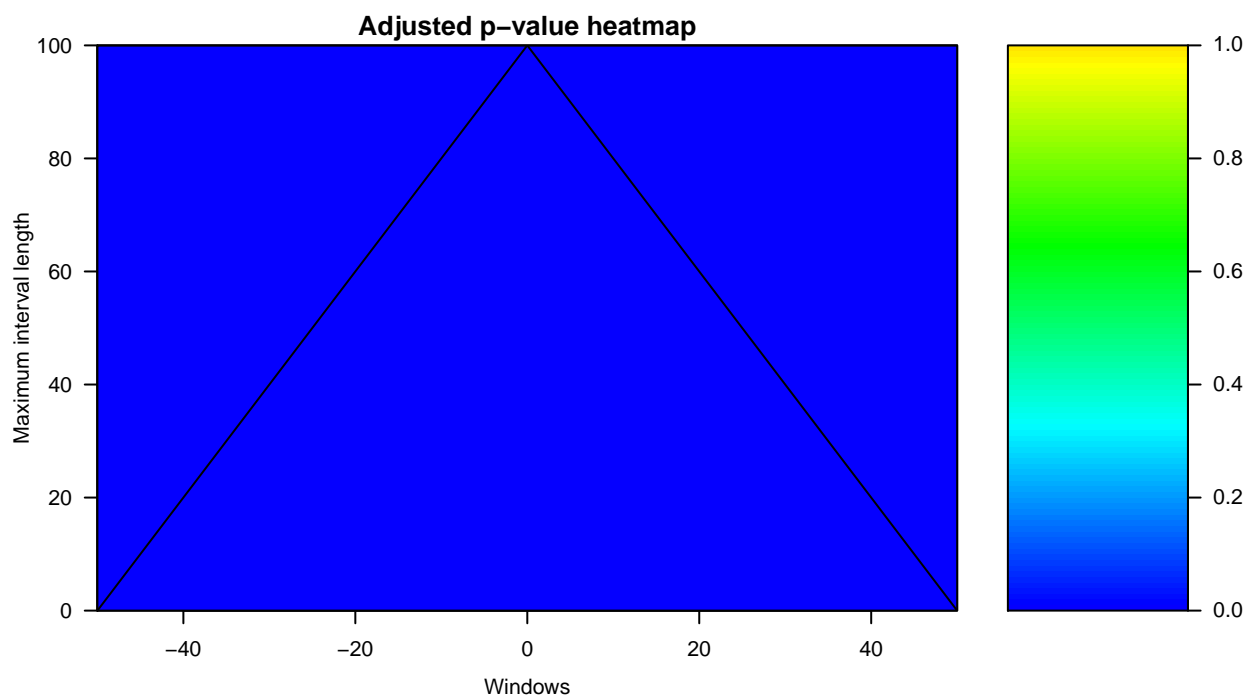
Control



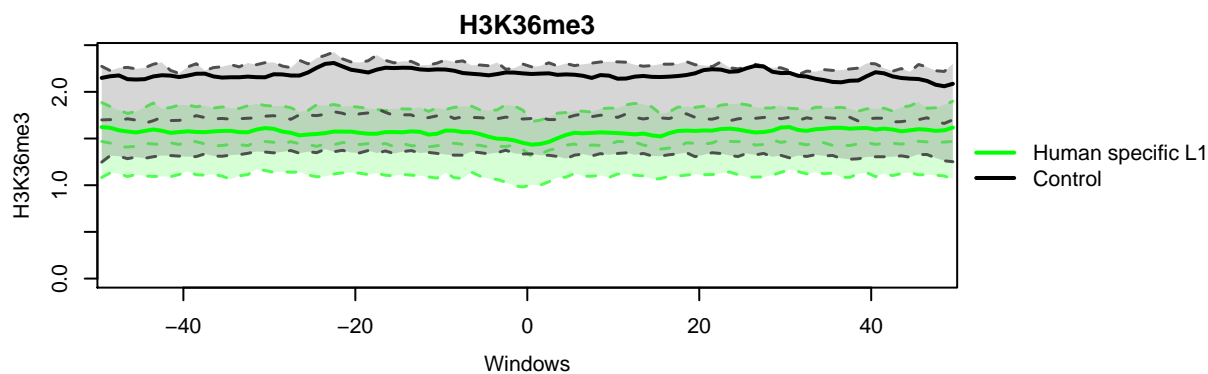
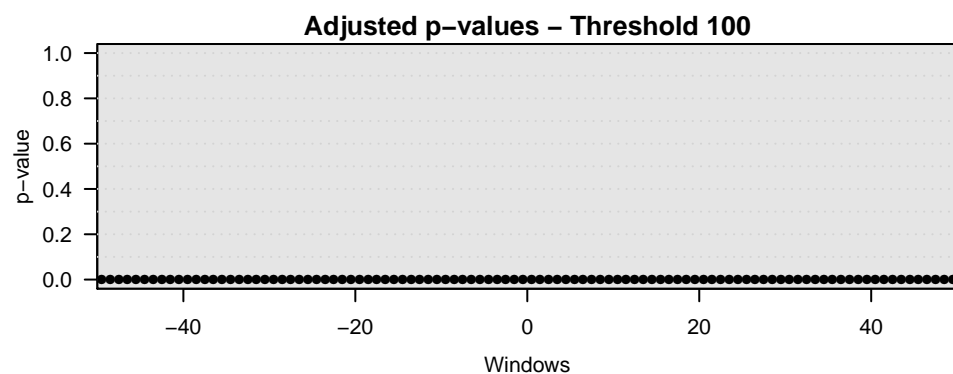
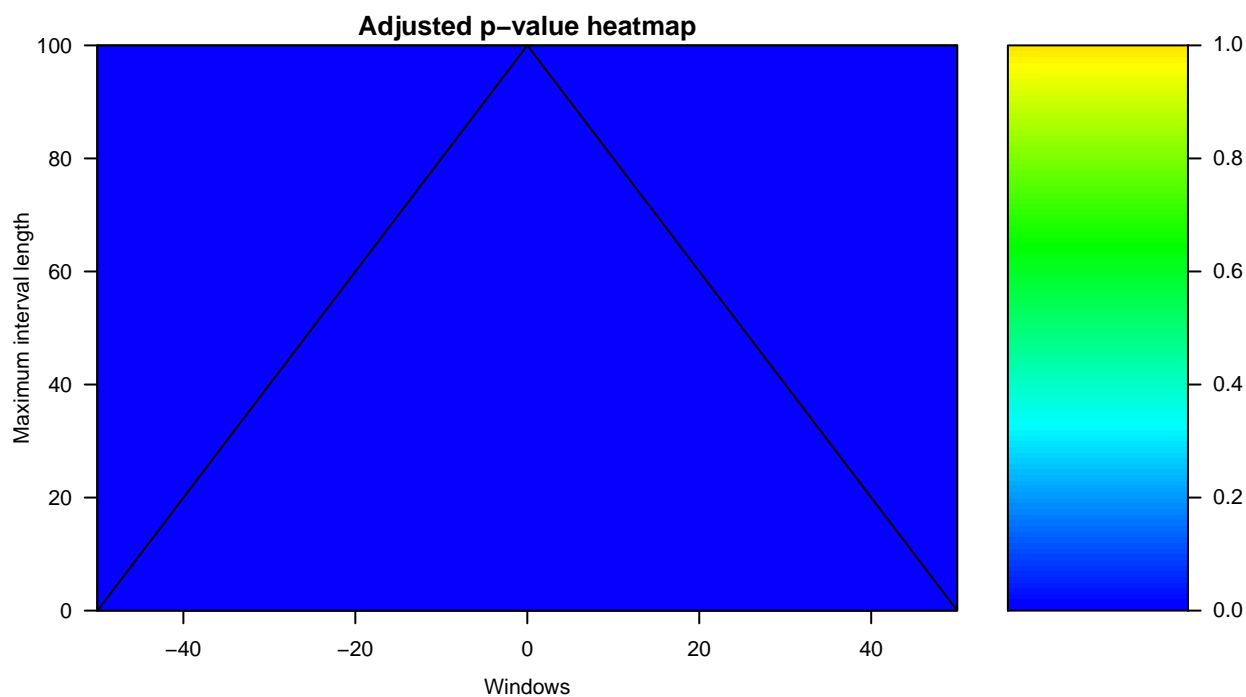
# H3K27ac



# H4K20me1

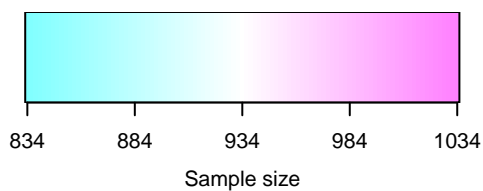


# H3K36me3

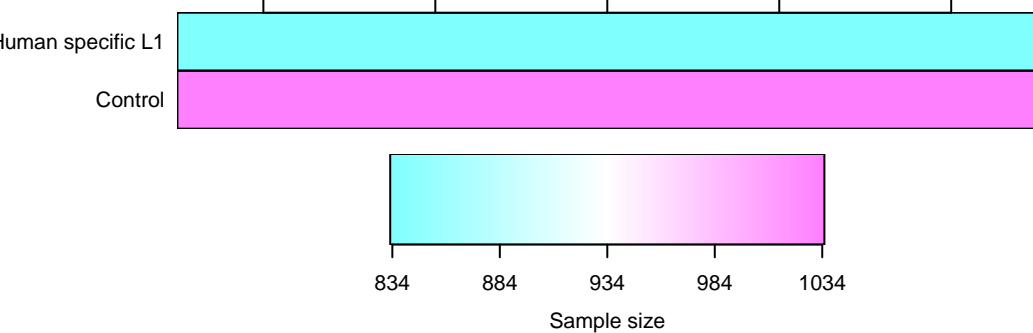
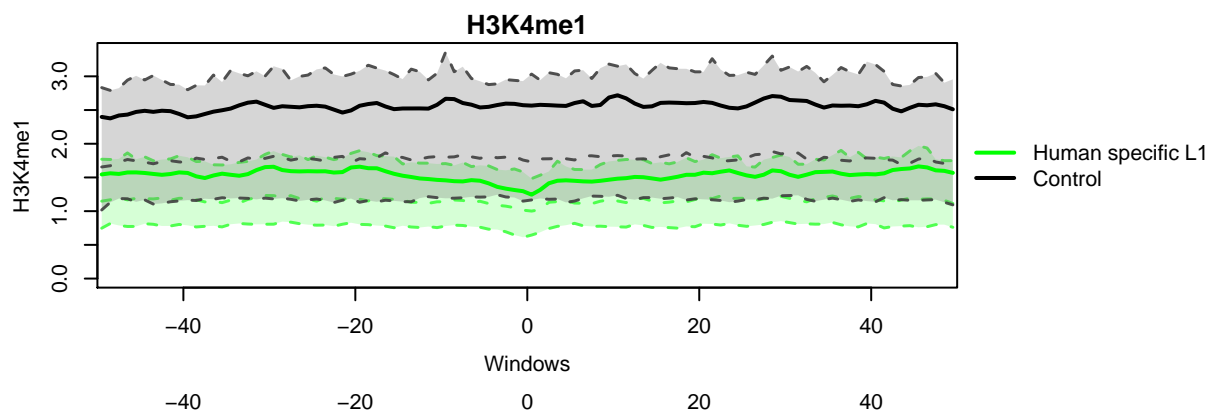
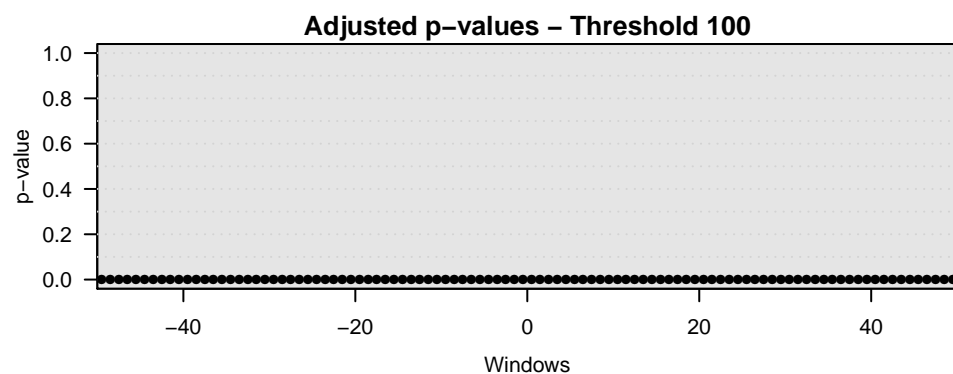
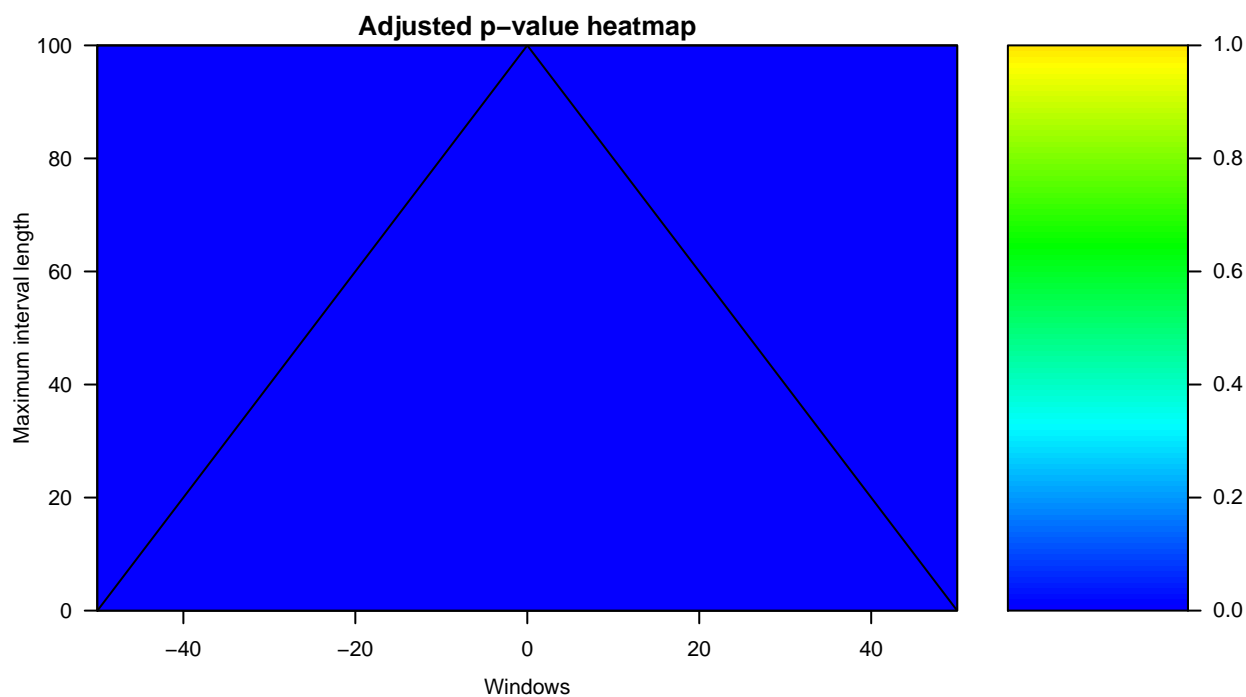


Human specific L1

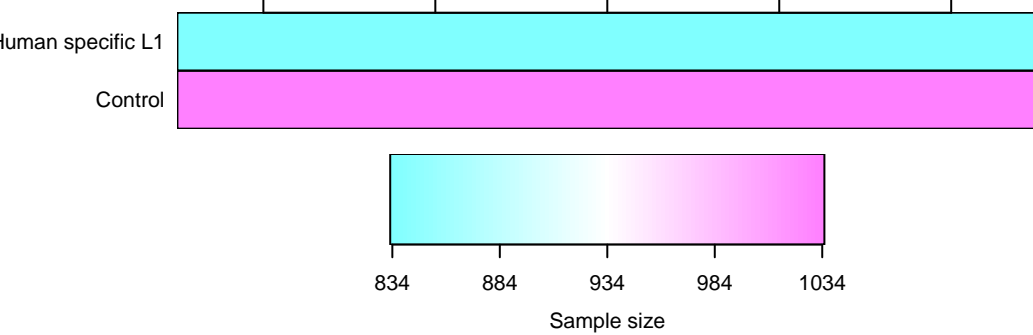
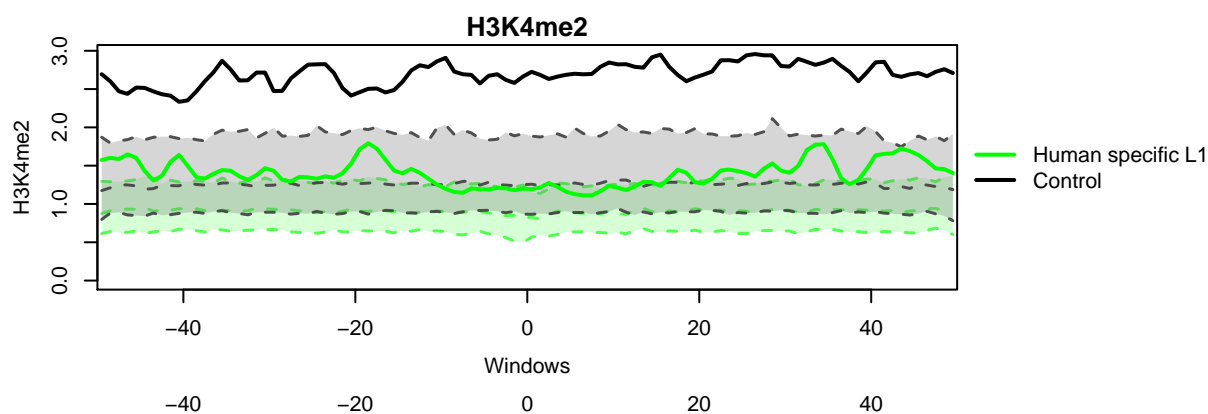
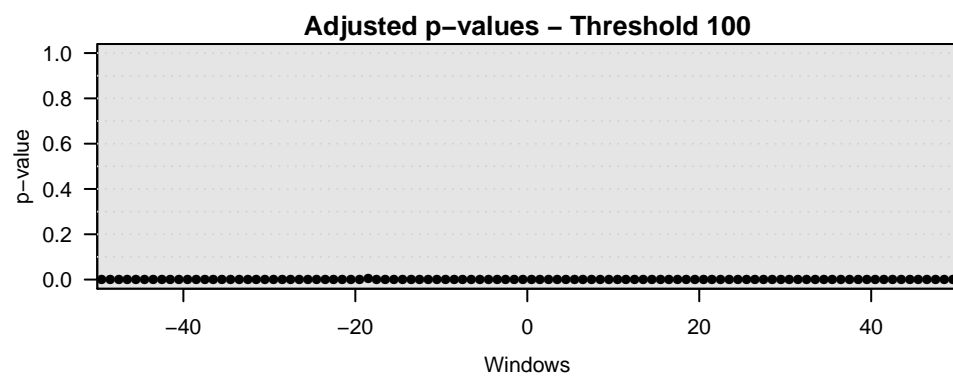
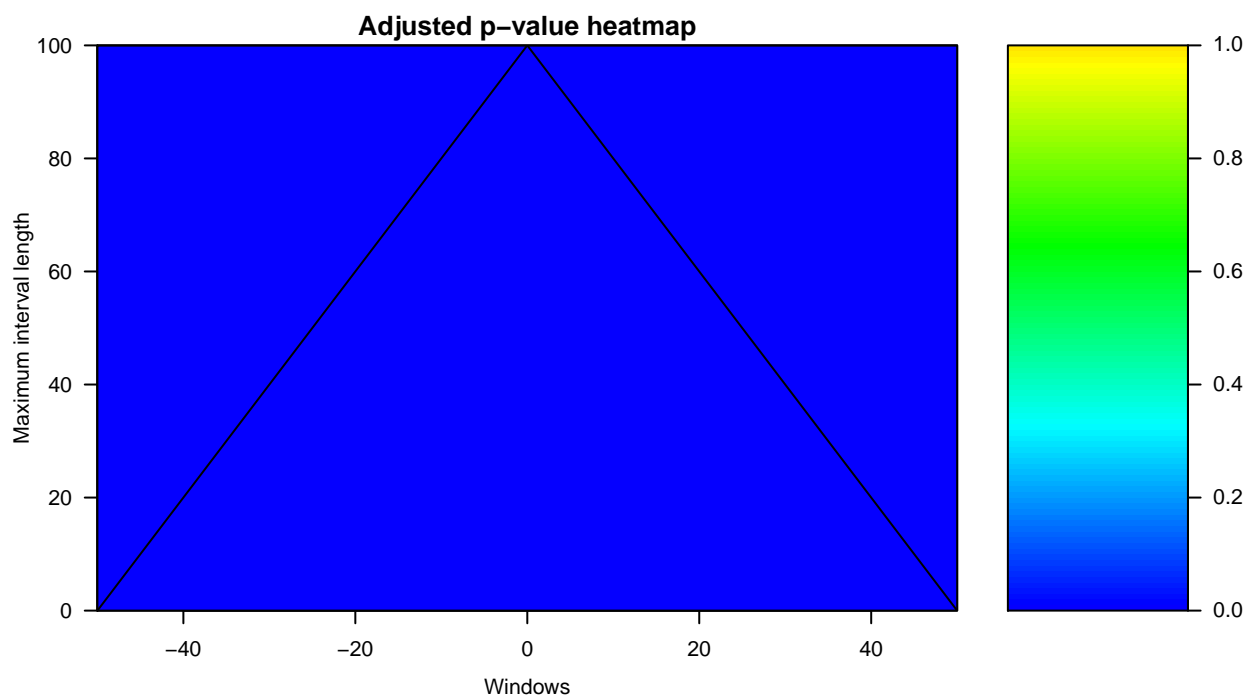
Control



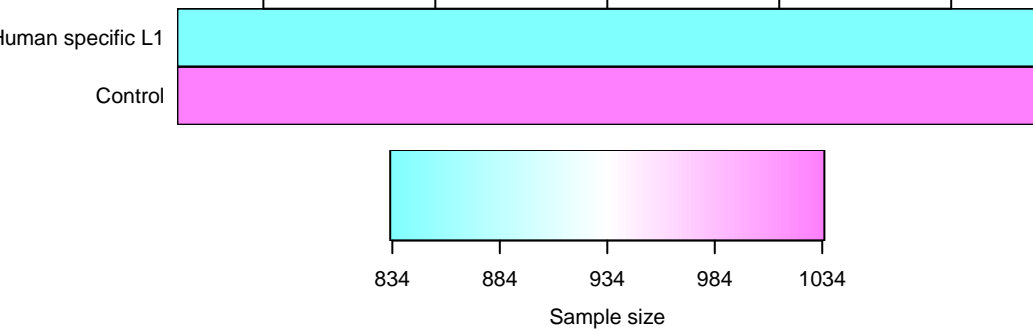
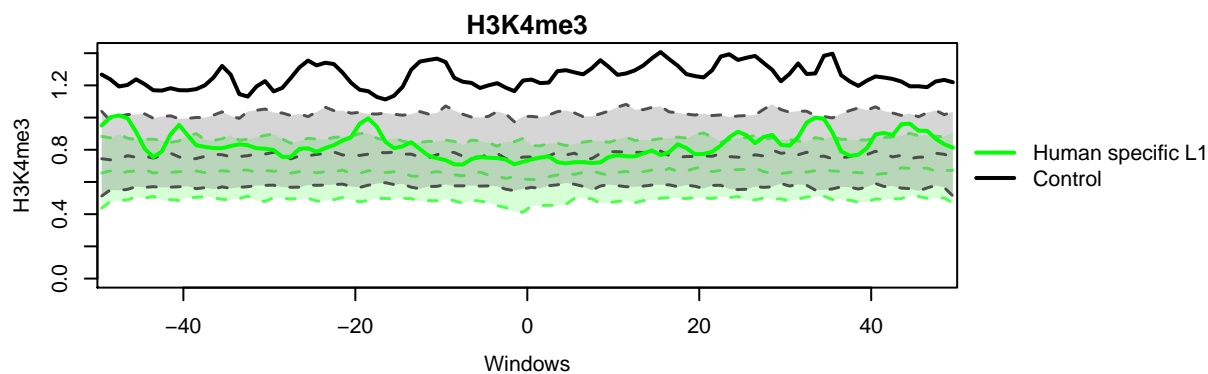
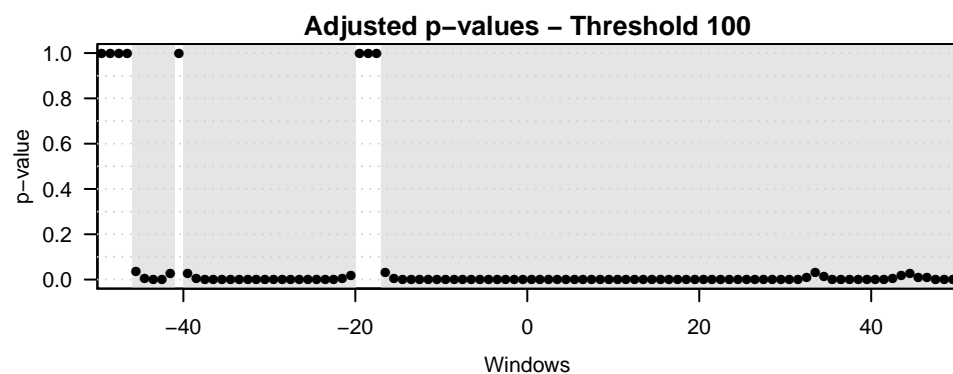
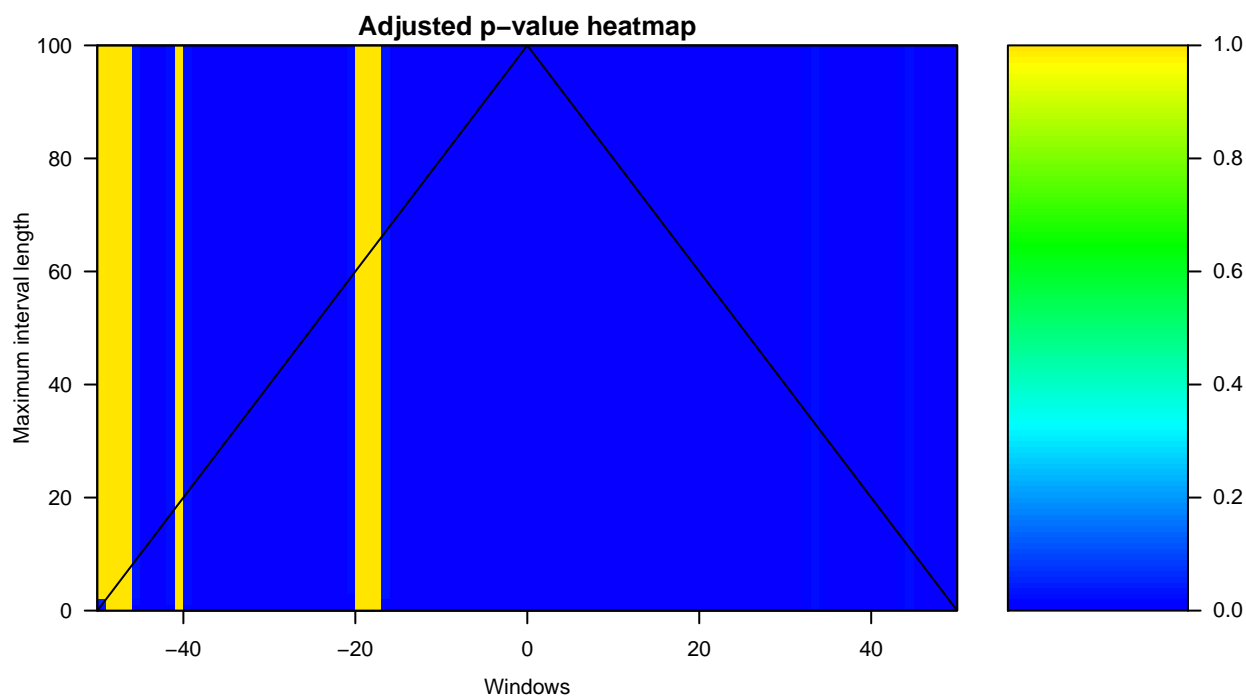
# H3K4me1



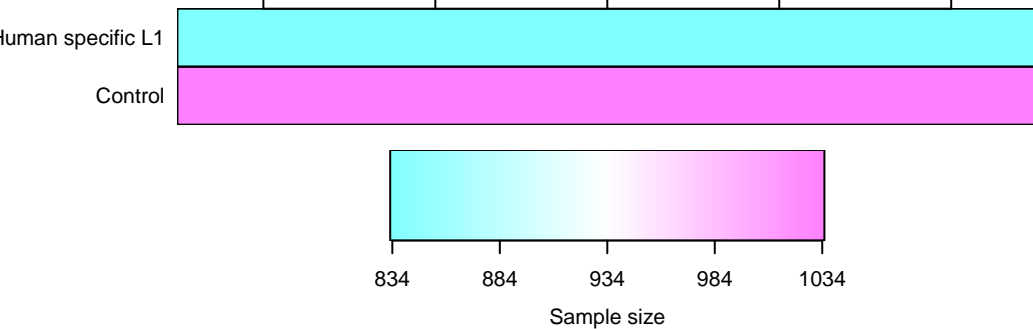
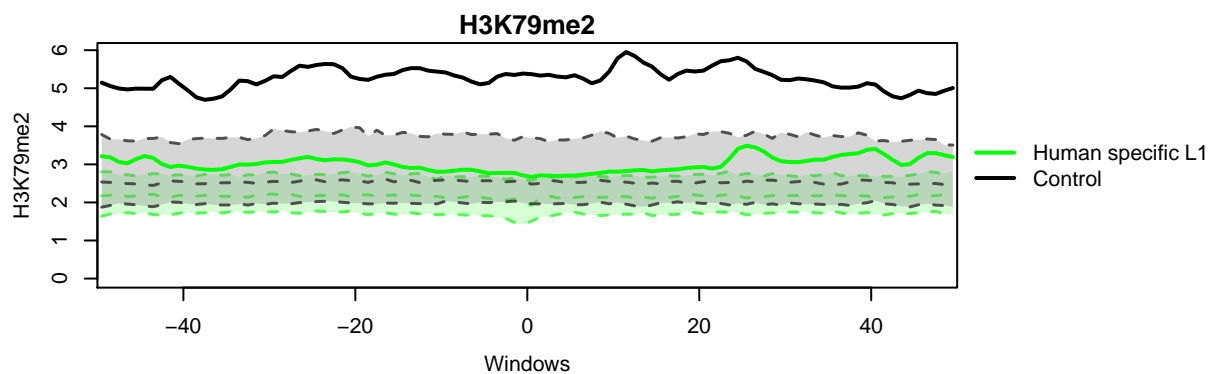
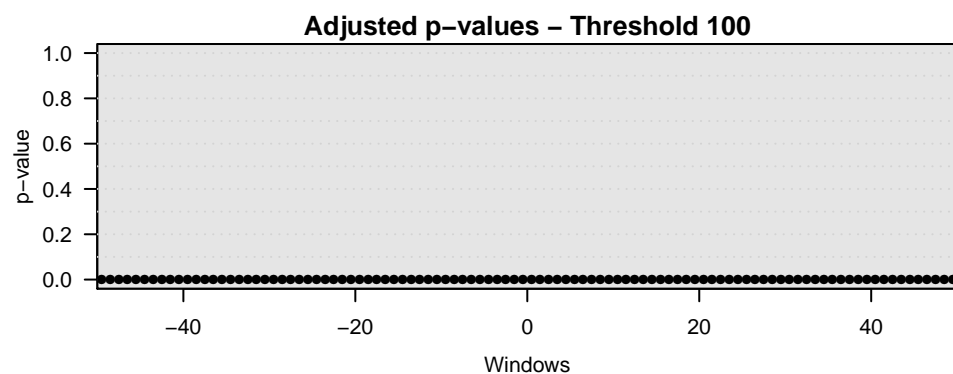
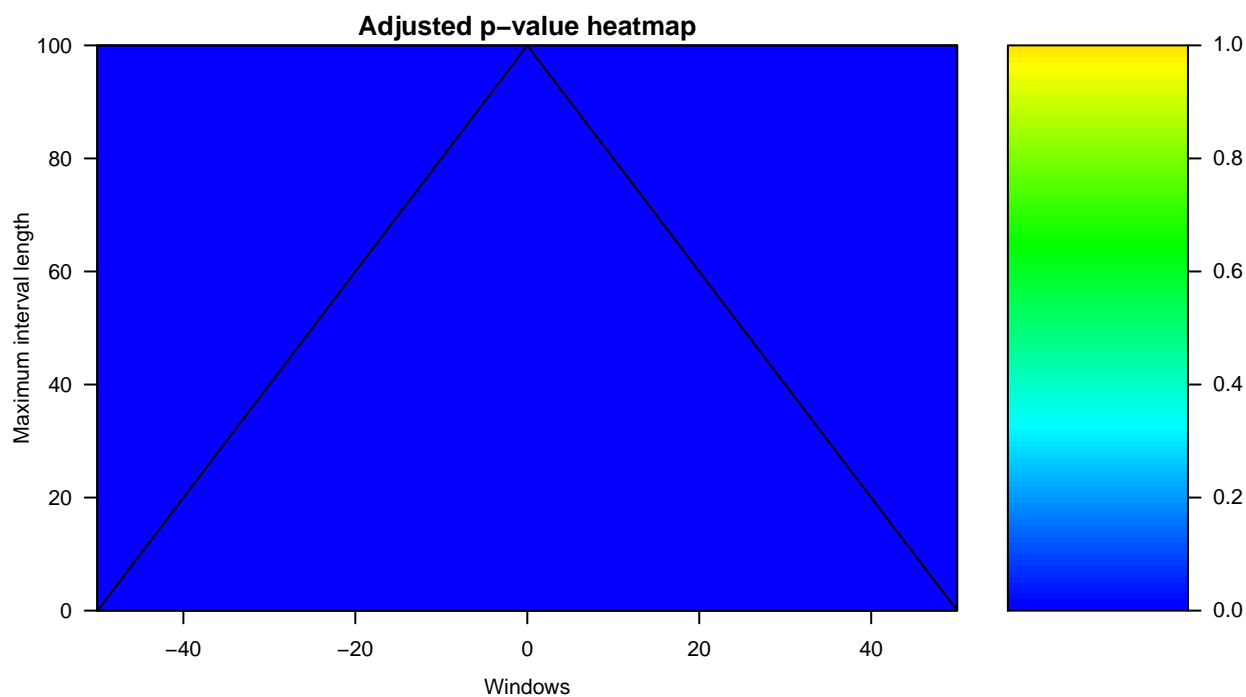
# H3K4me2



# H3K4me3

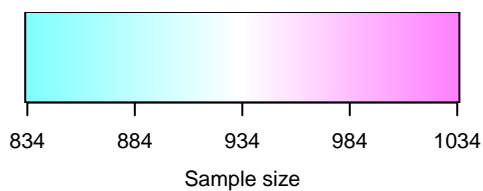
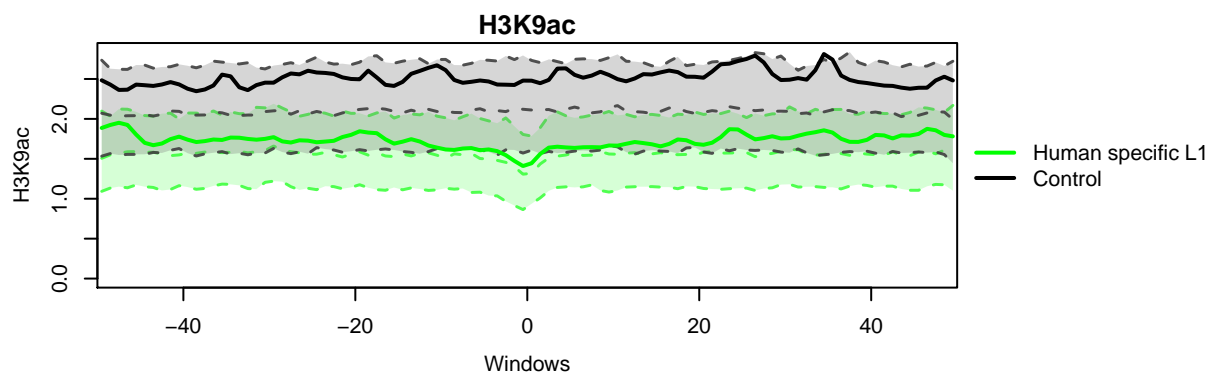
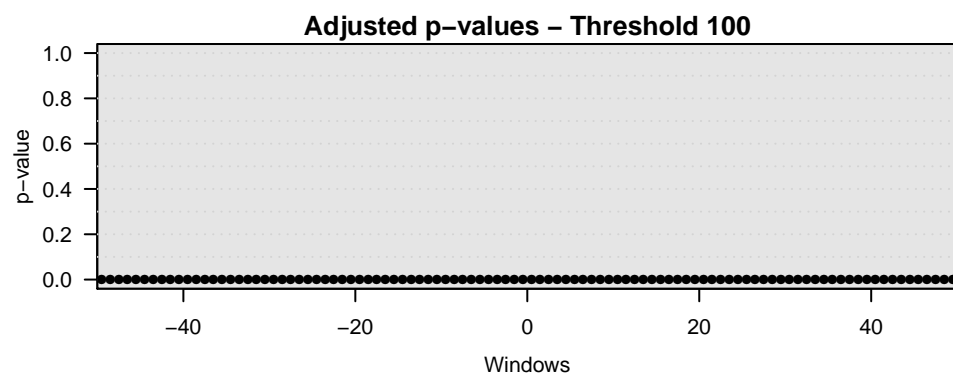
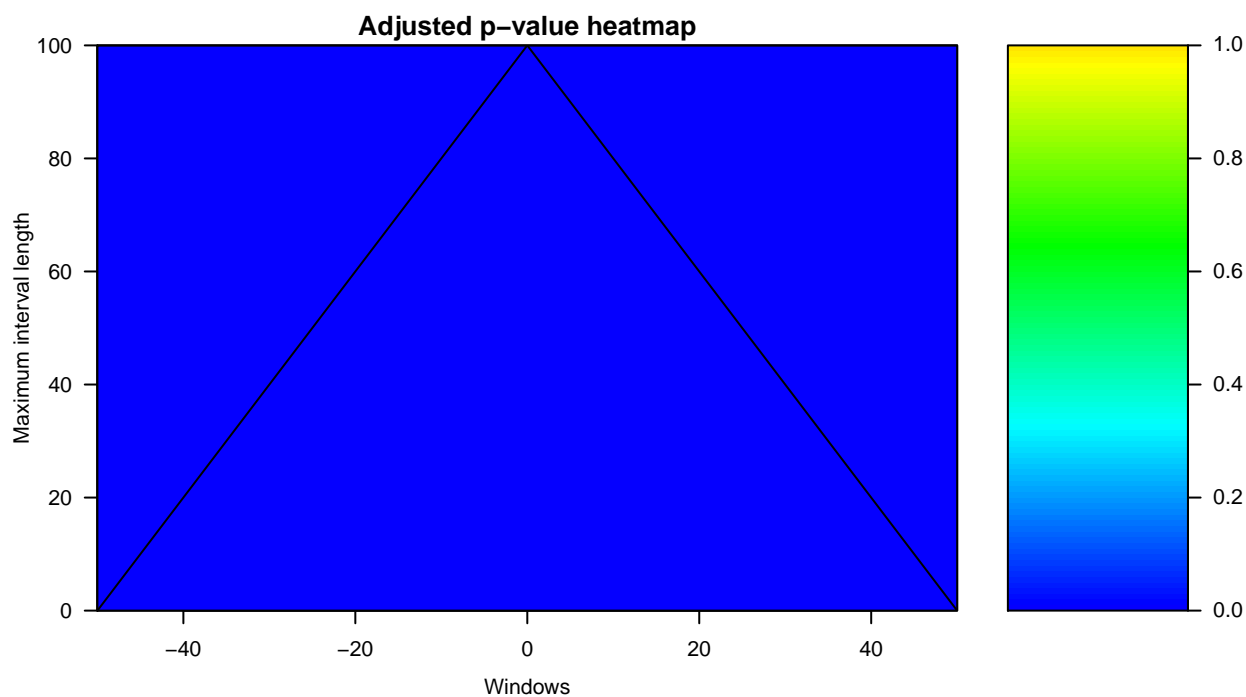


# H3K79me2

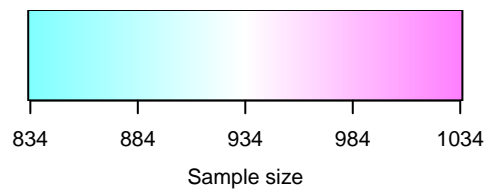
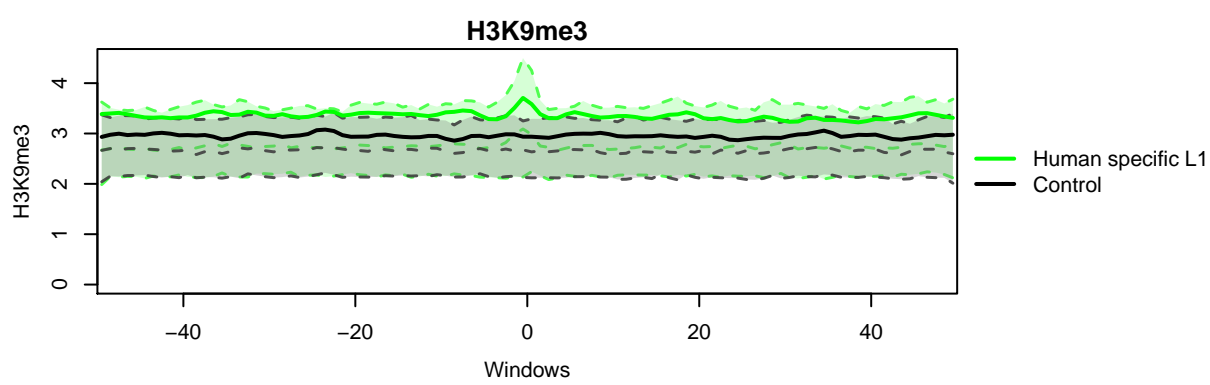
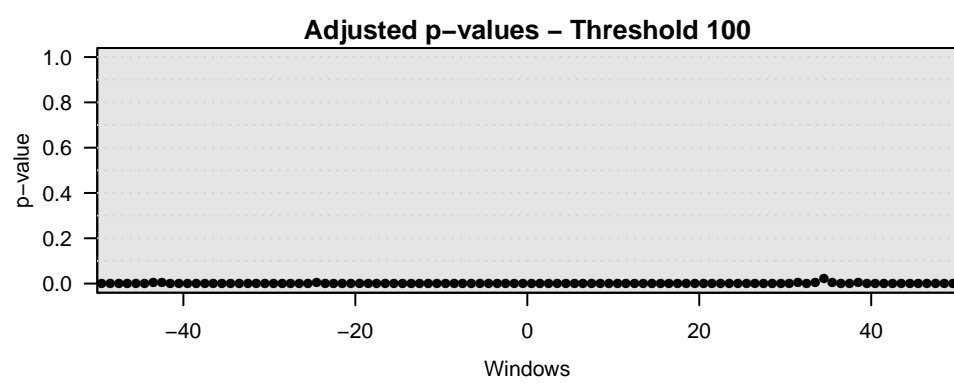
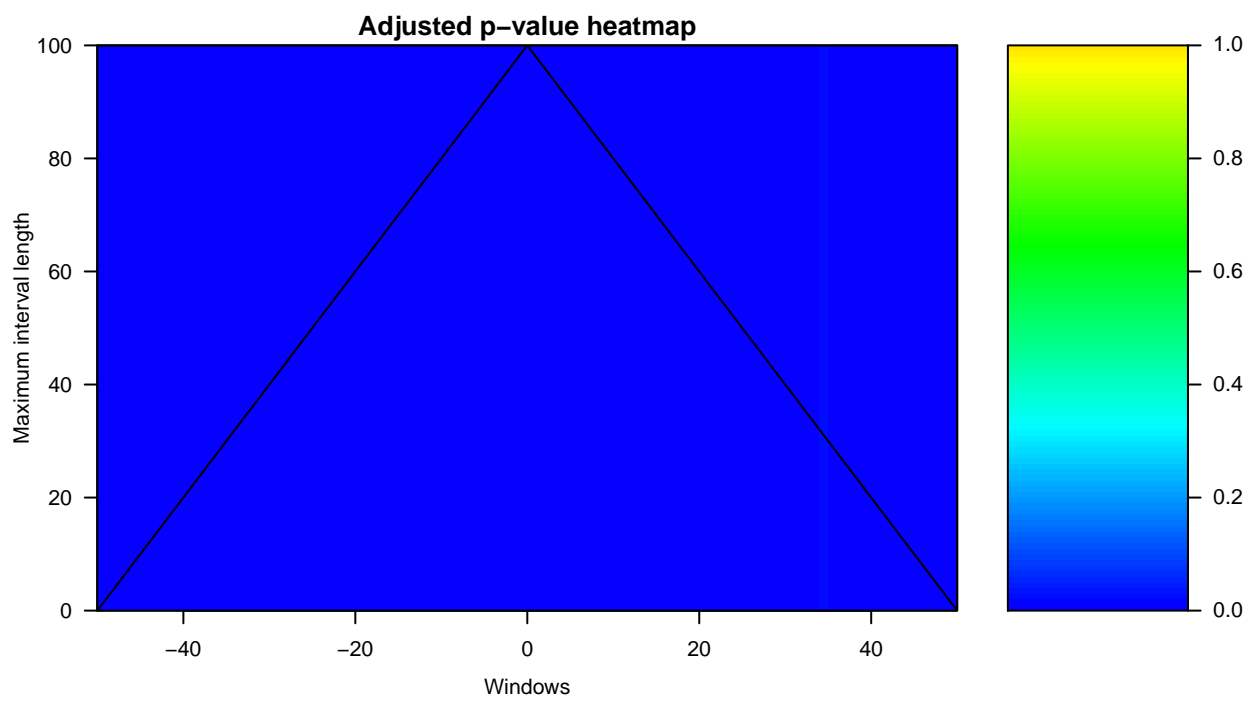




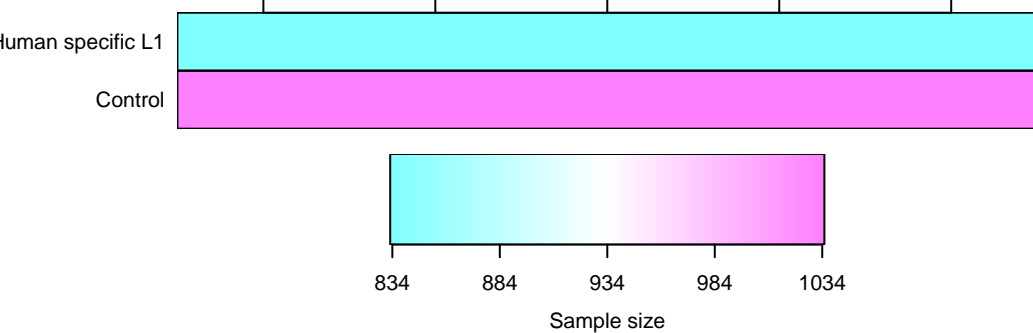
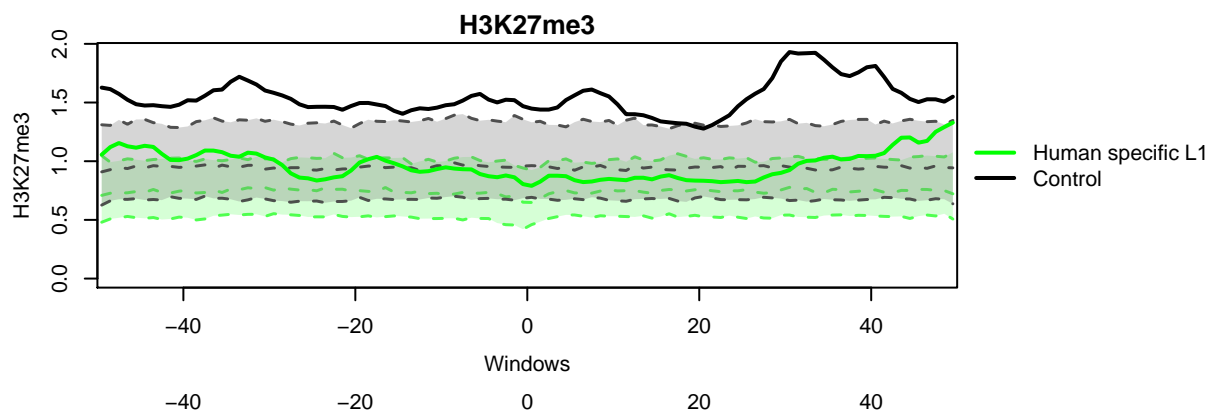
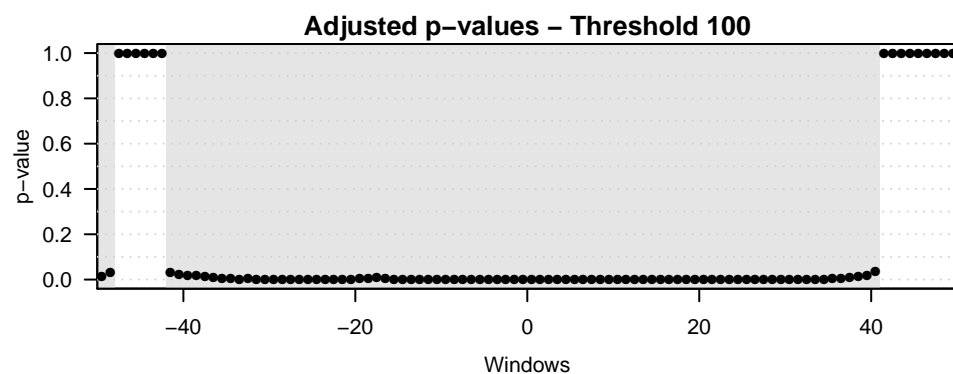
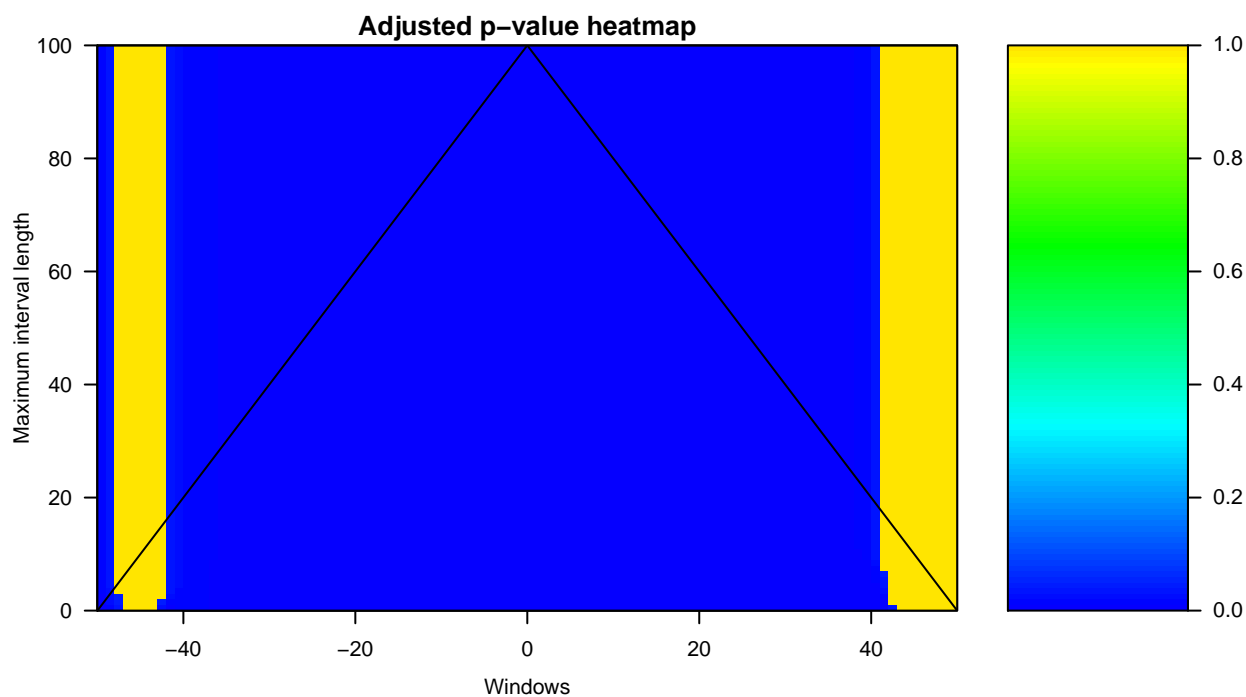
# H3K9ac



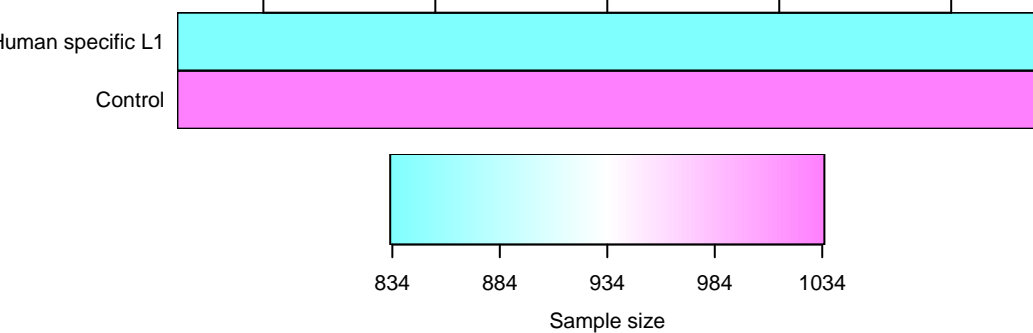
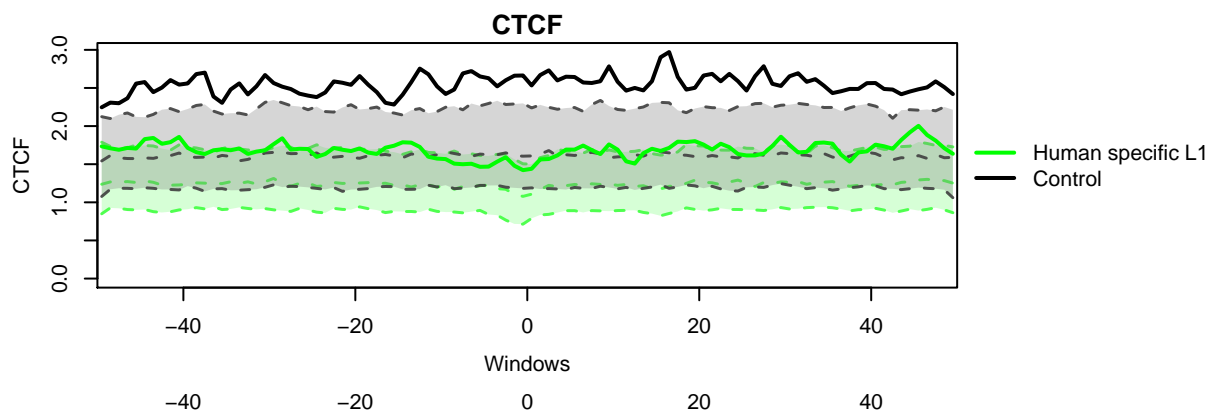
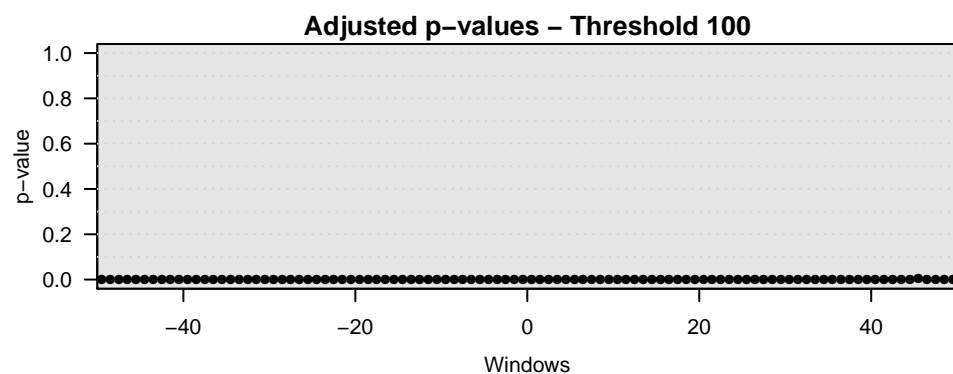
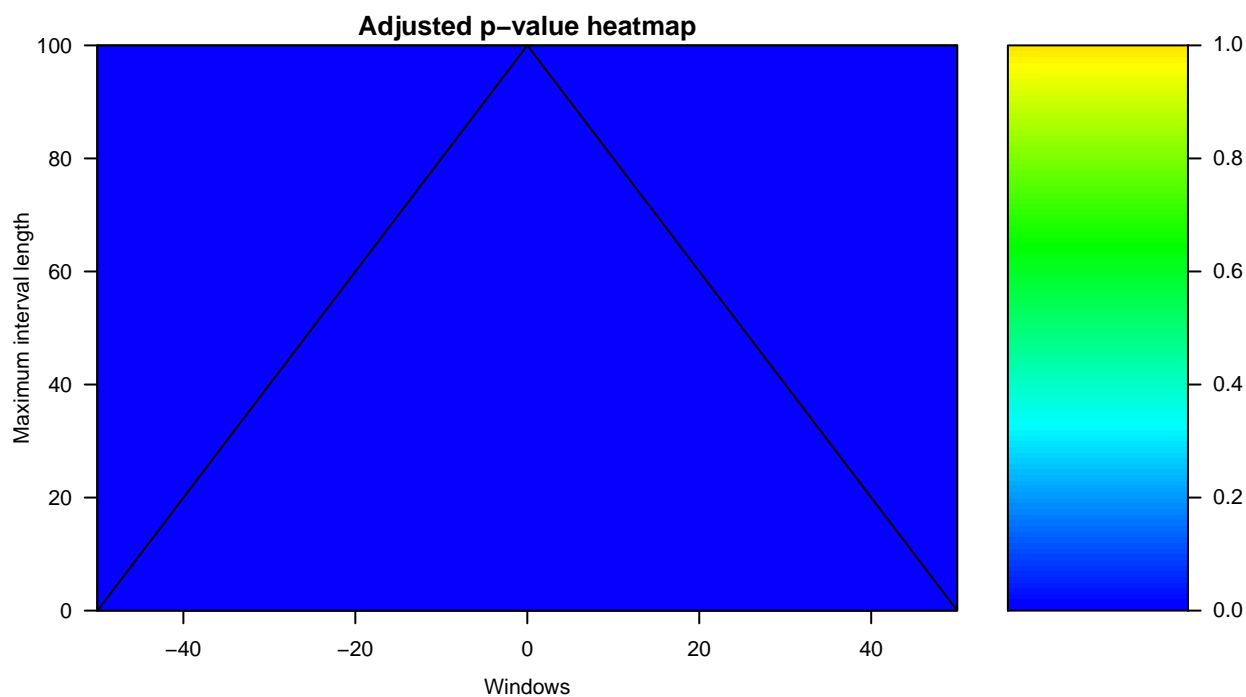
# H3K9me3



# H3K27me3

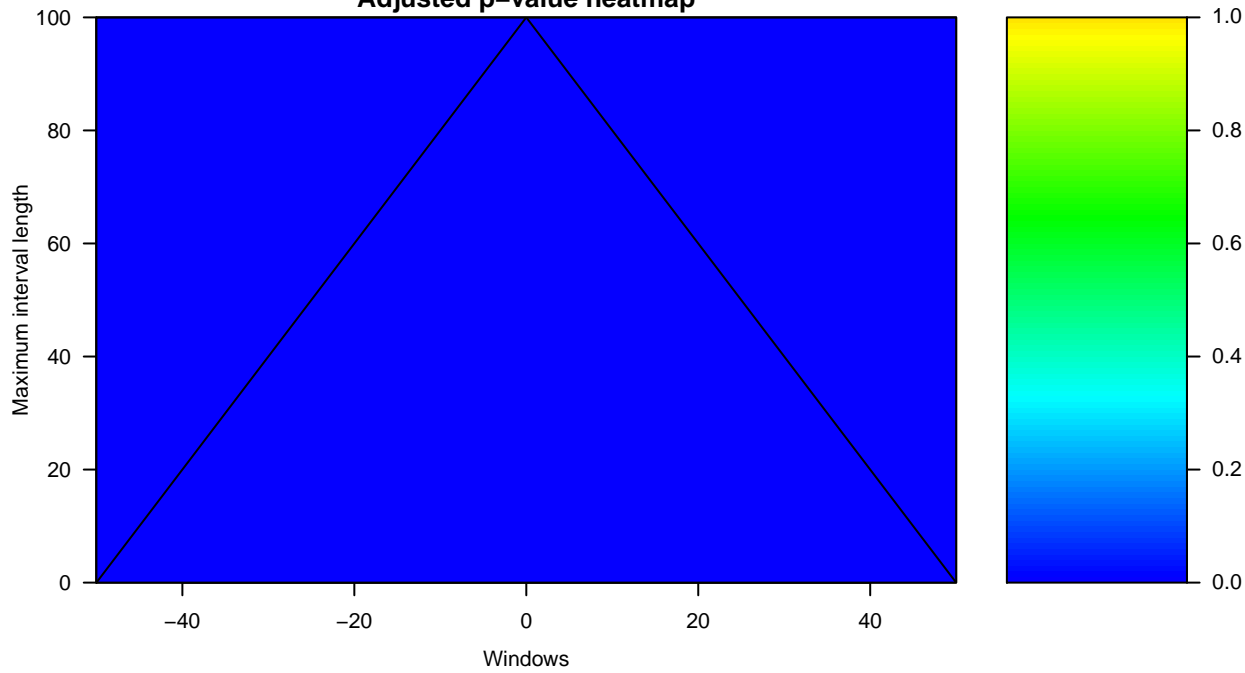


# CTCF

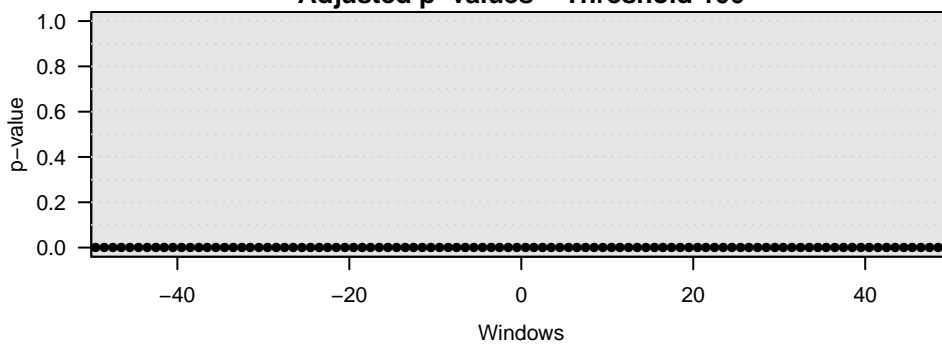


# DNase hypersensitive sites

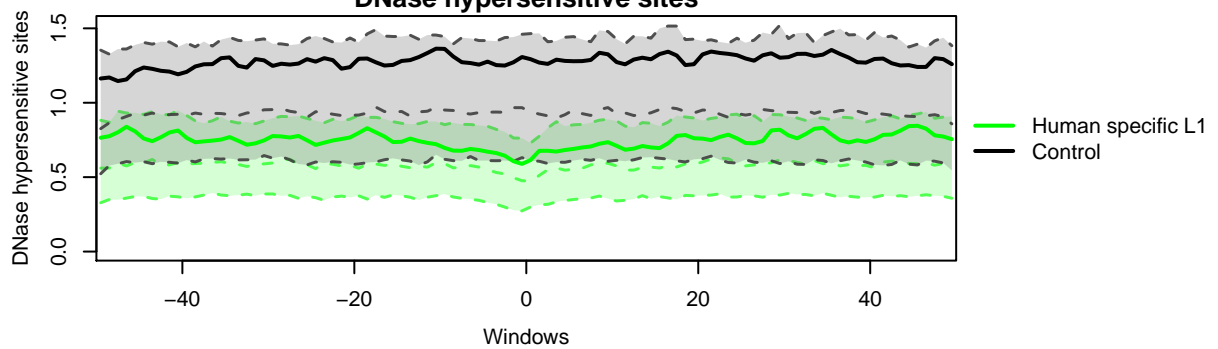
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



## DNase hypersensitive sites



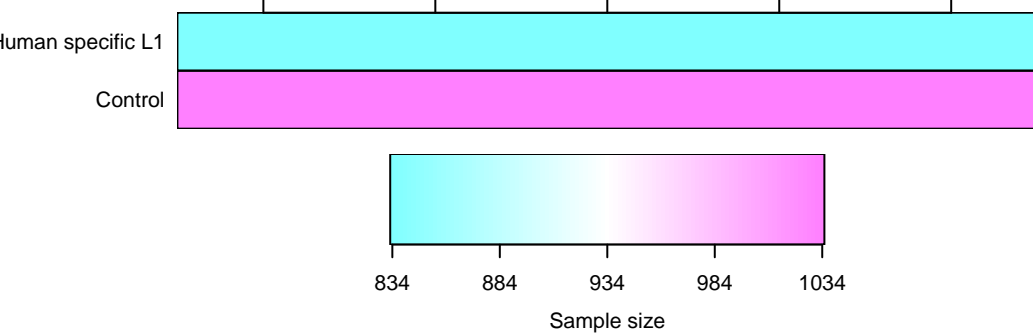
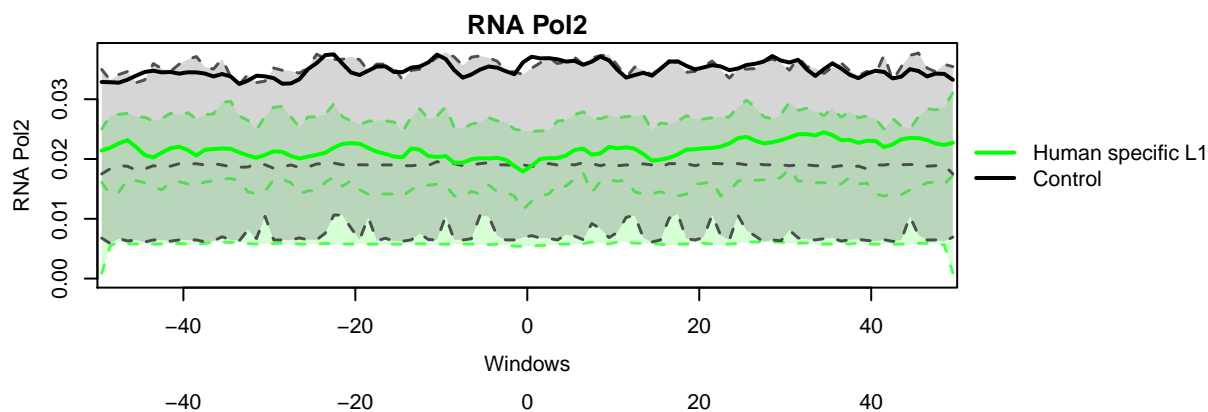
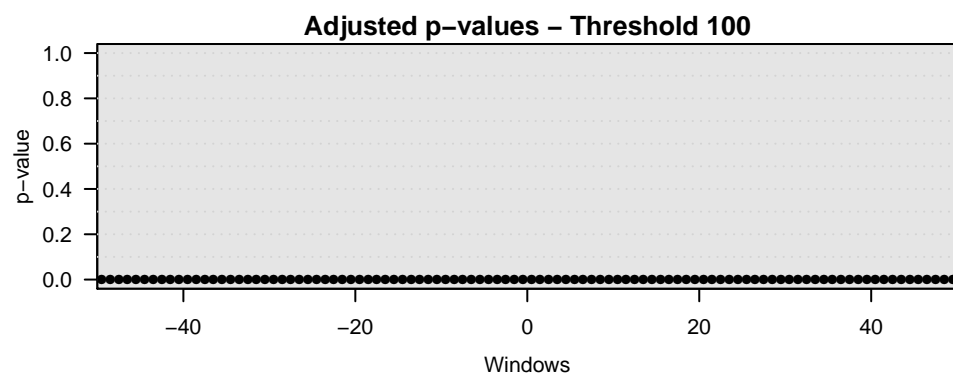
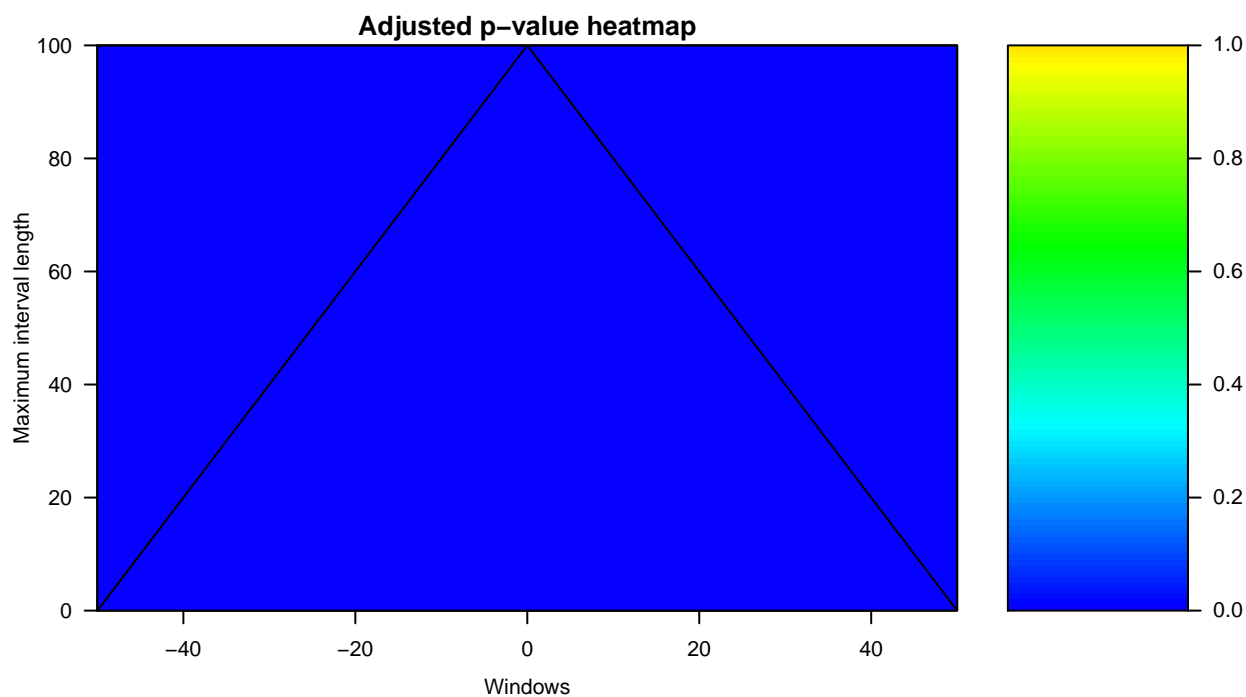
Human specific L1

Control

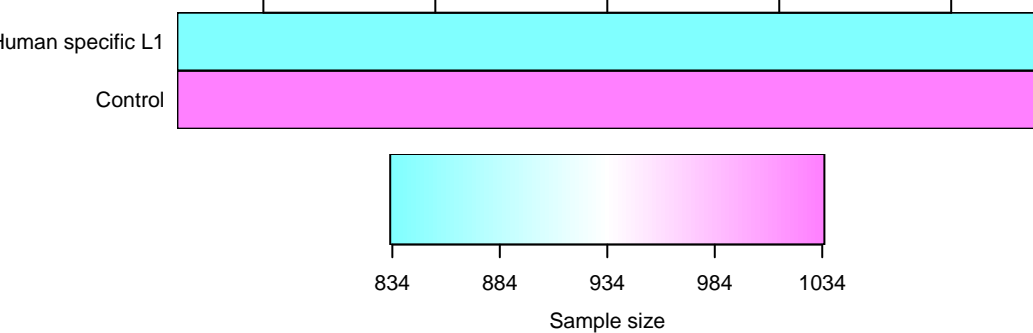
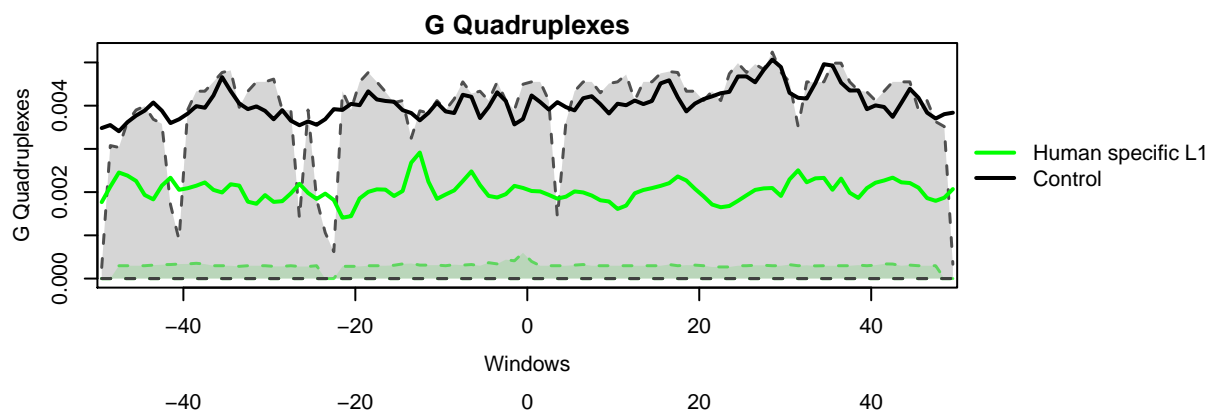
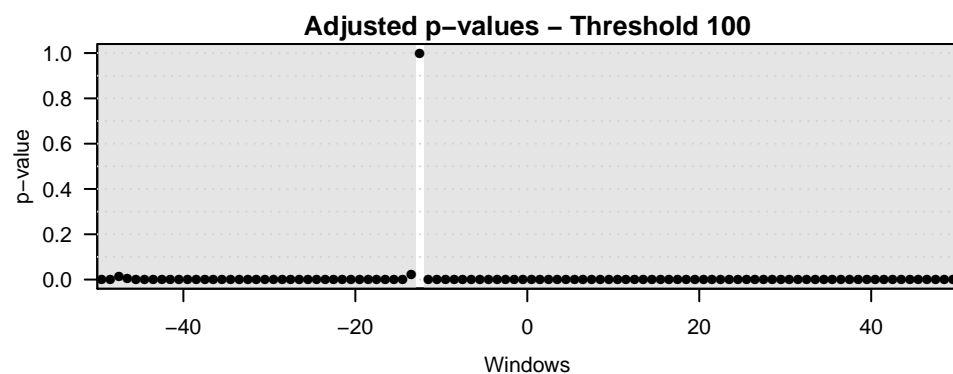
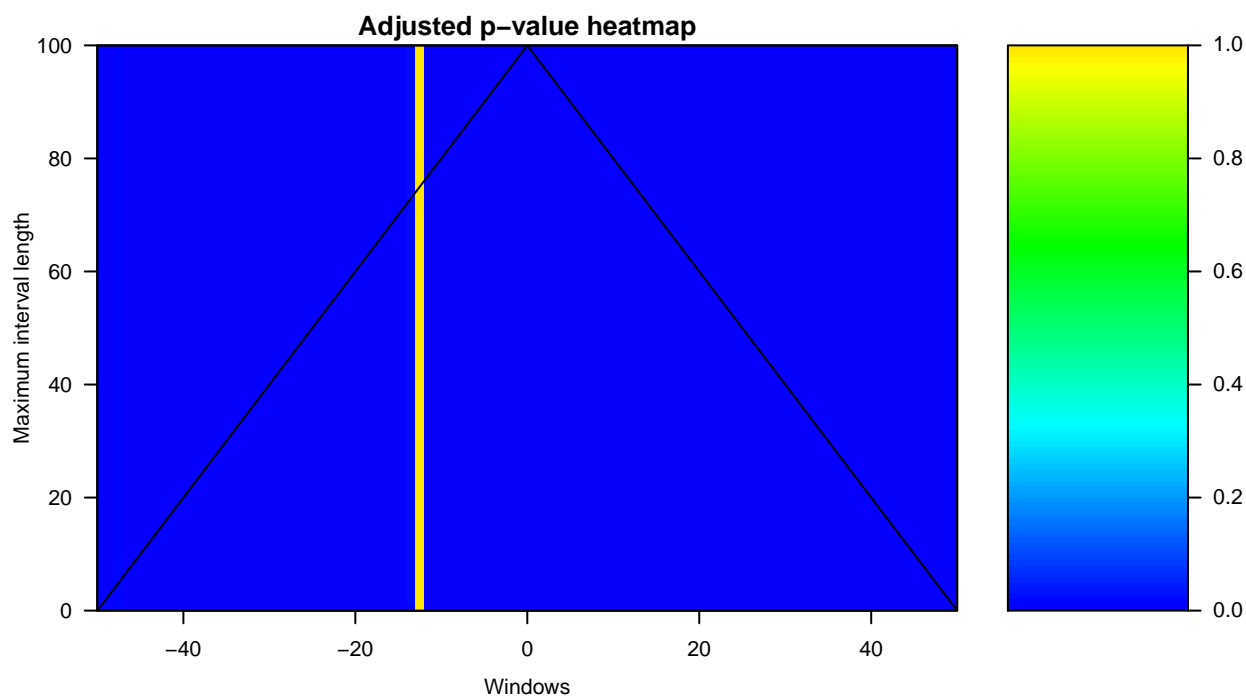
834 884 934 984 1034

Sample size

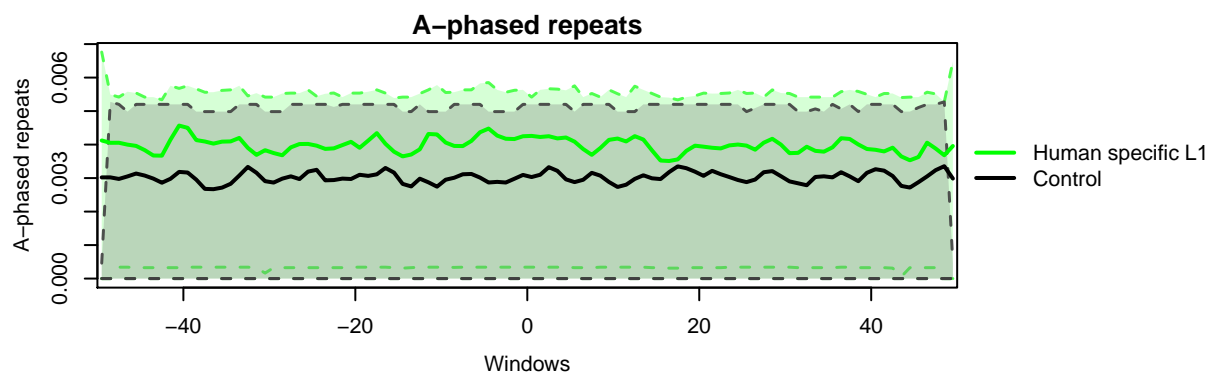
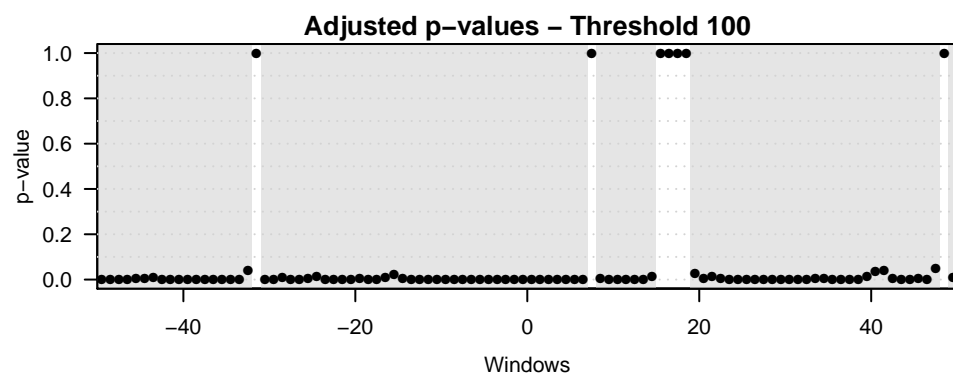
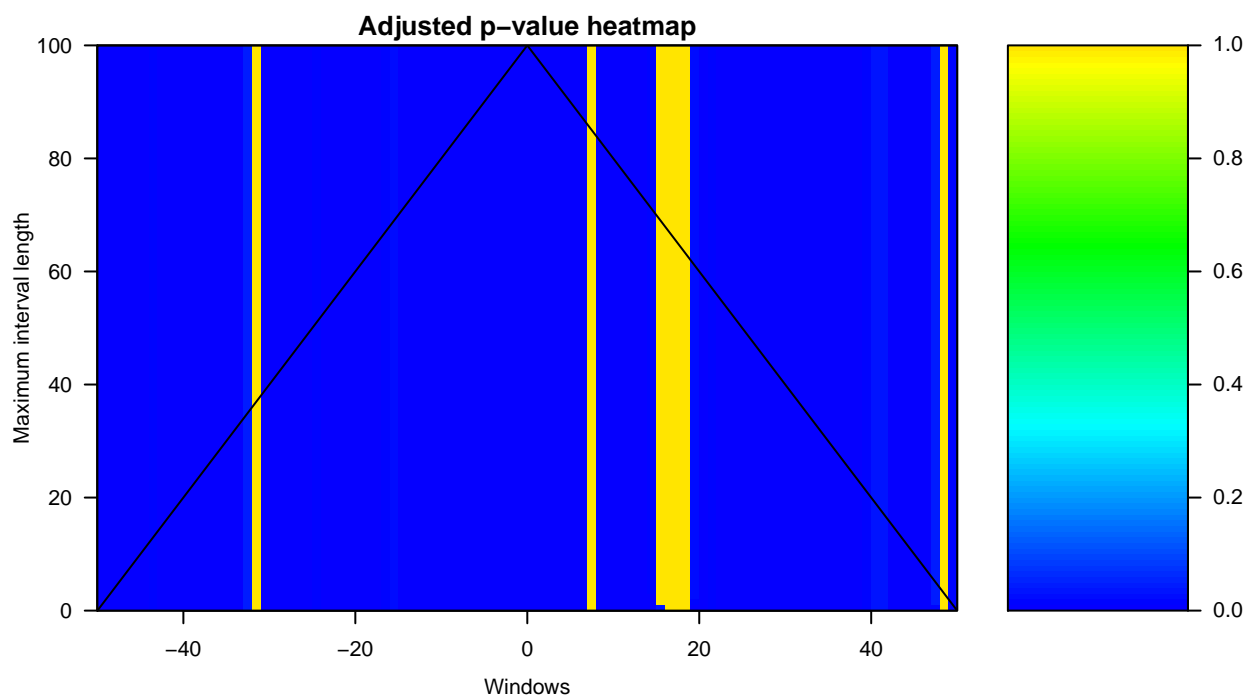
# RNA Pol2



# G Quadruplexes

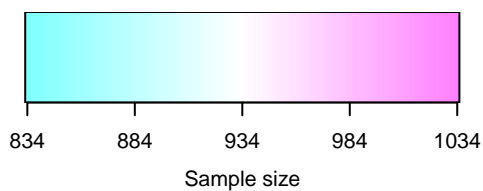


# A-phased repeats



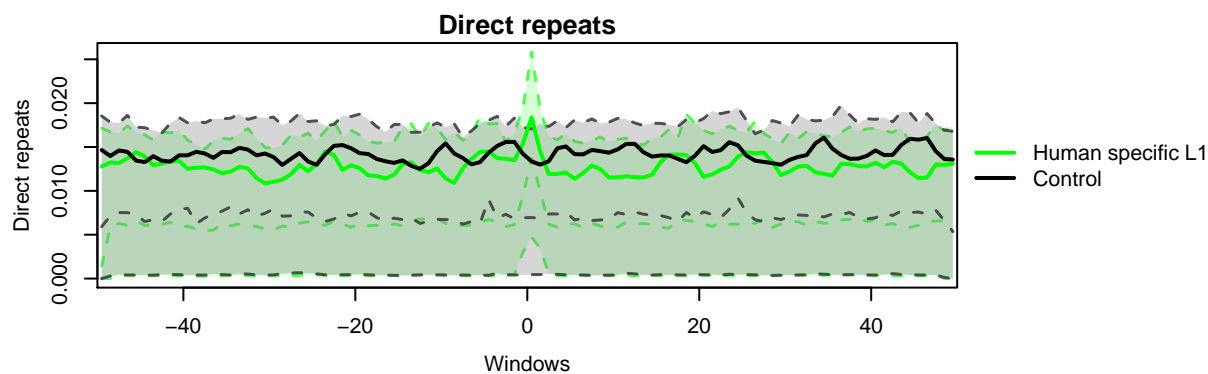
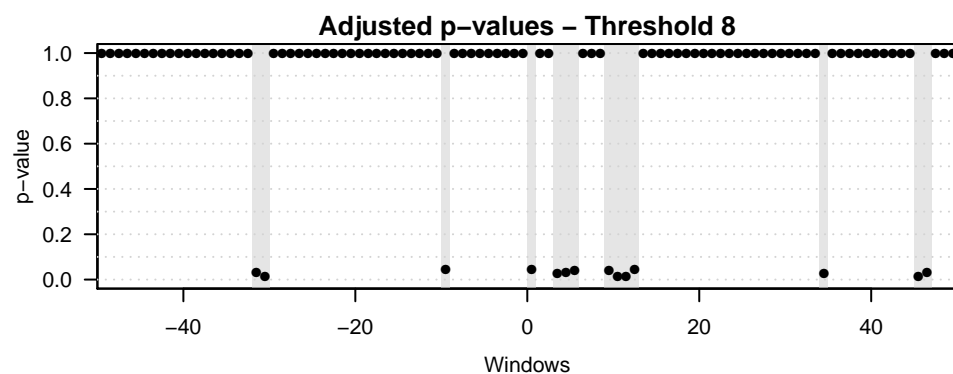
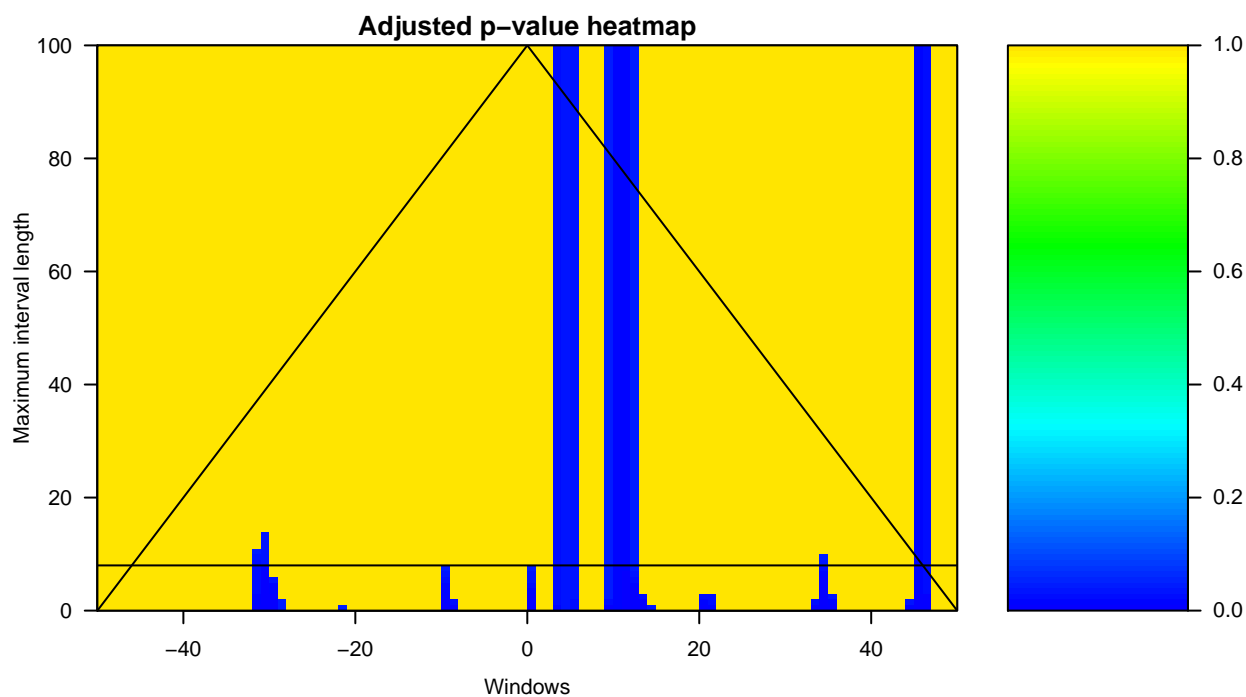
Human specific L1

Control



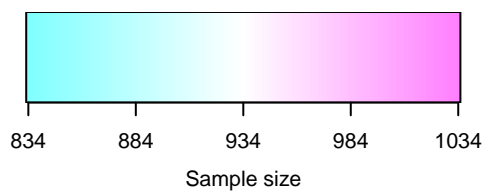


# Direct repeats

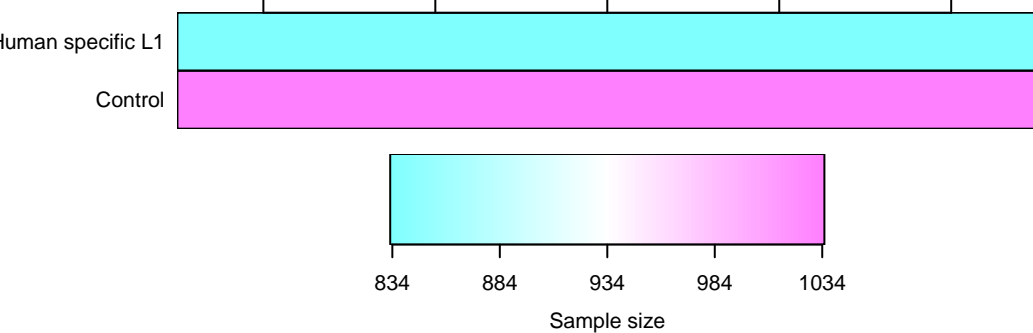
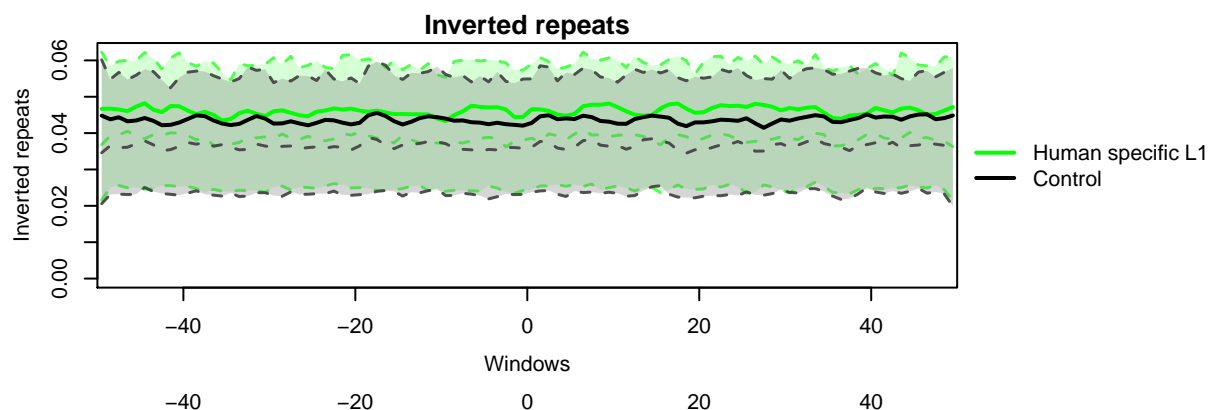
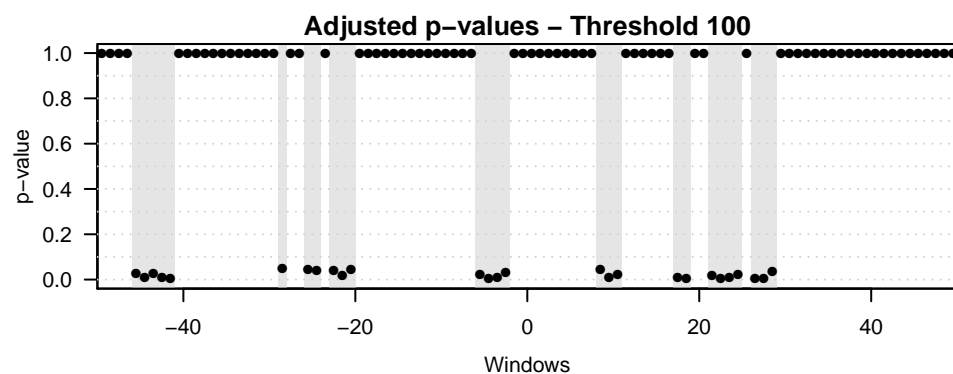
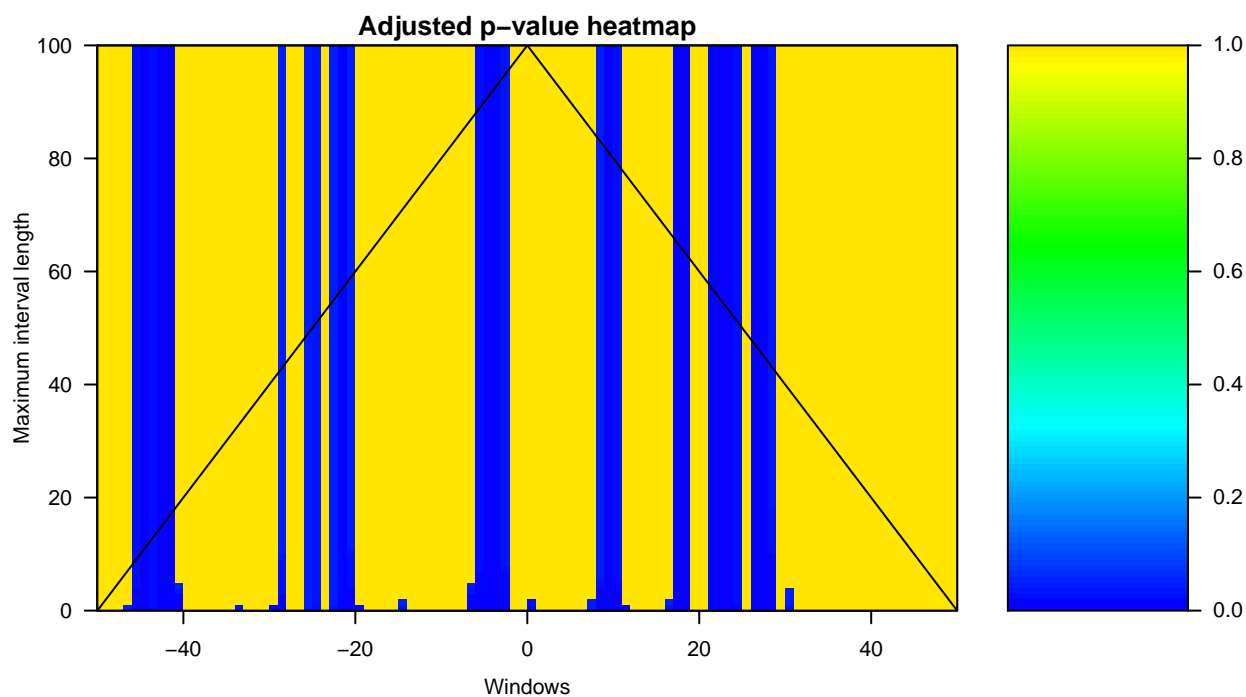


Human specific L1

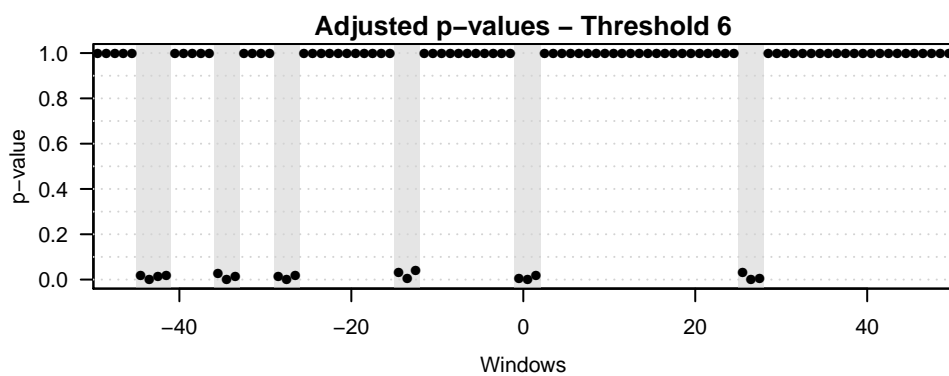
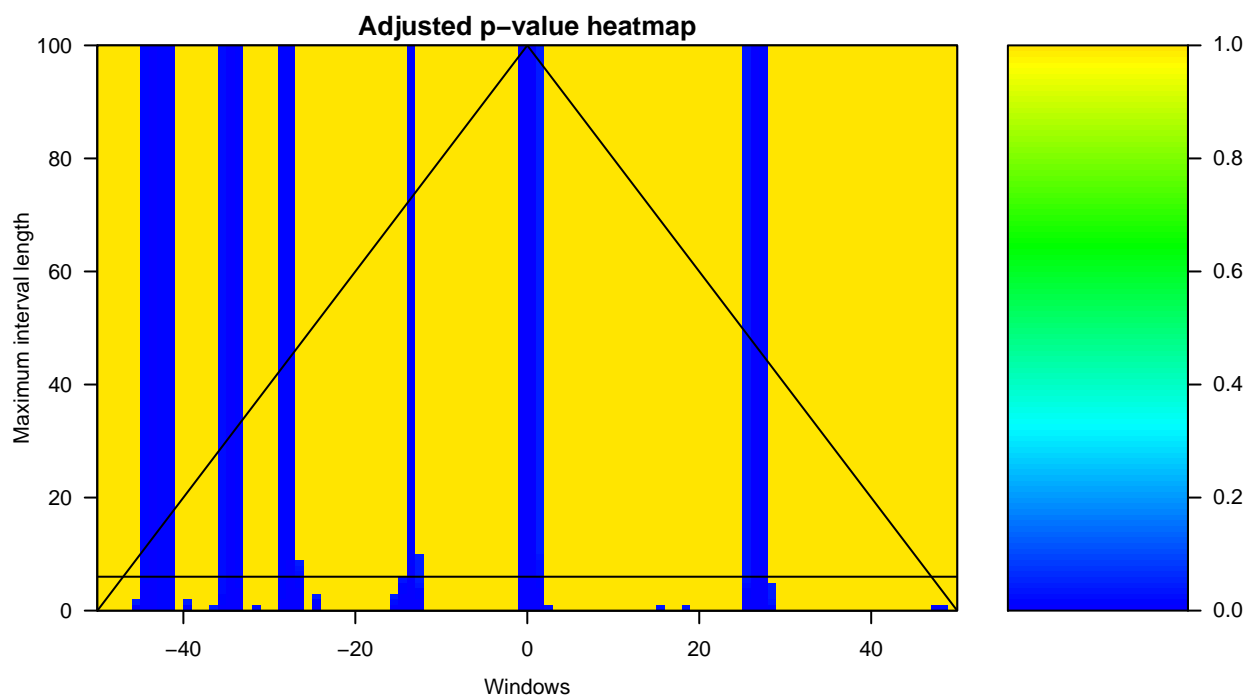
Control



# Inverted repeats

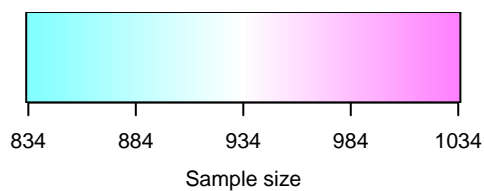


# Mirror repeats

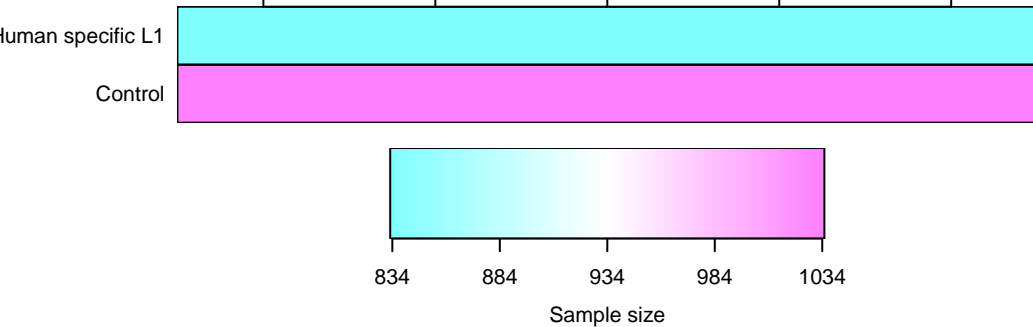
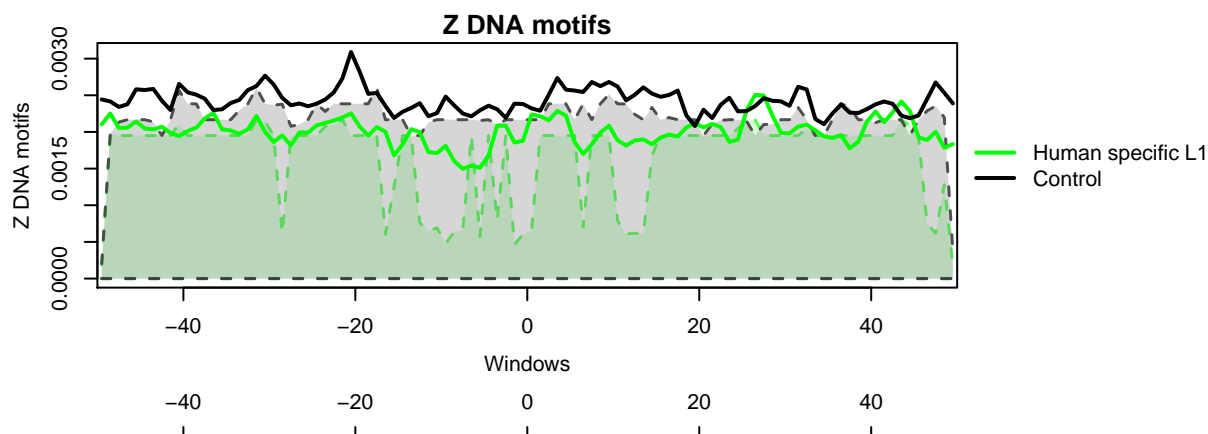
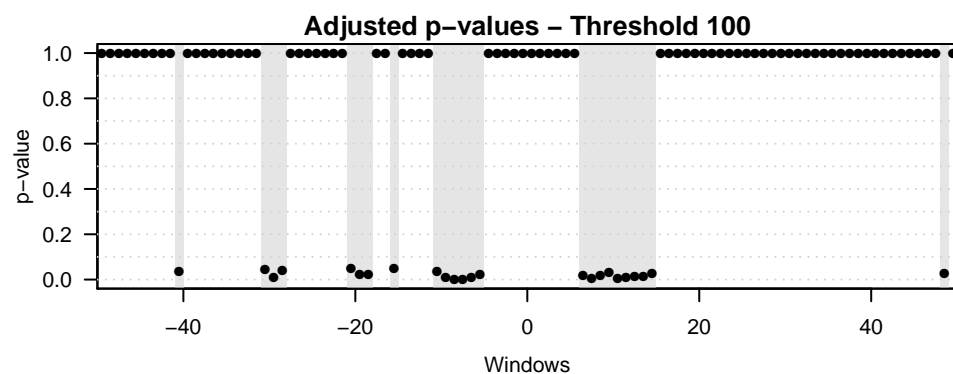
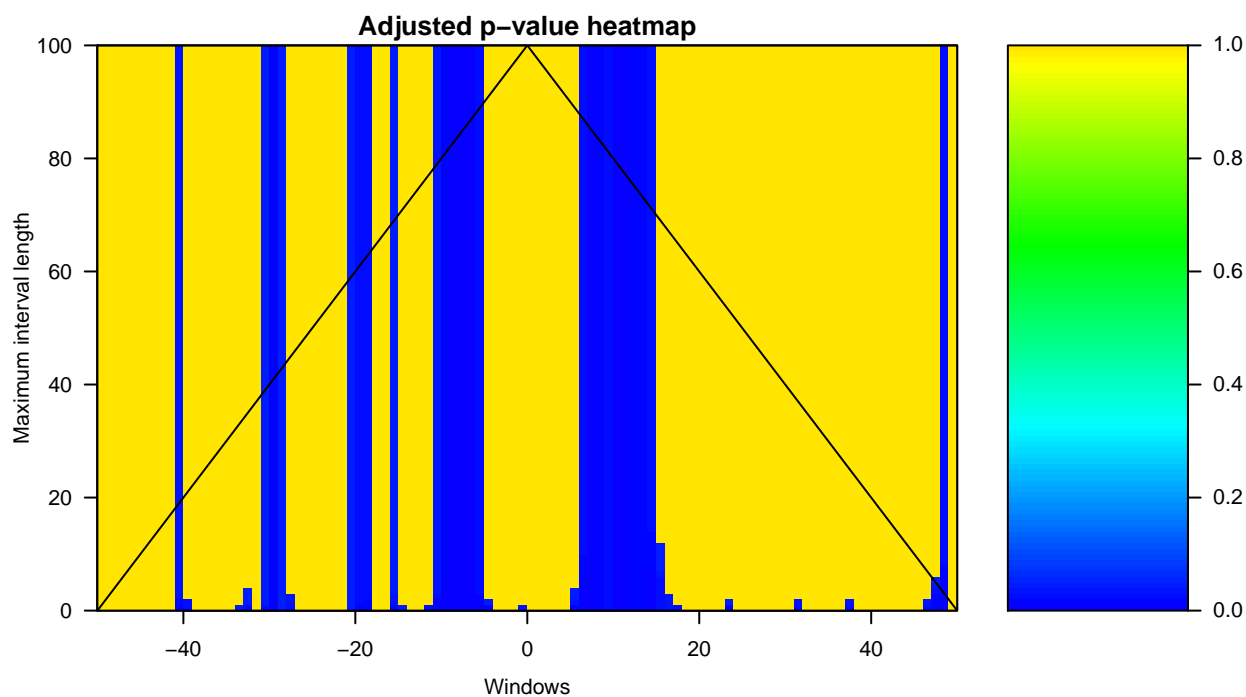


Human specific L1

Control

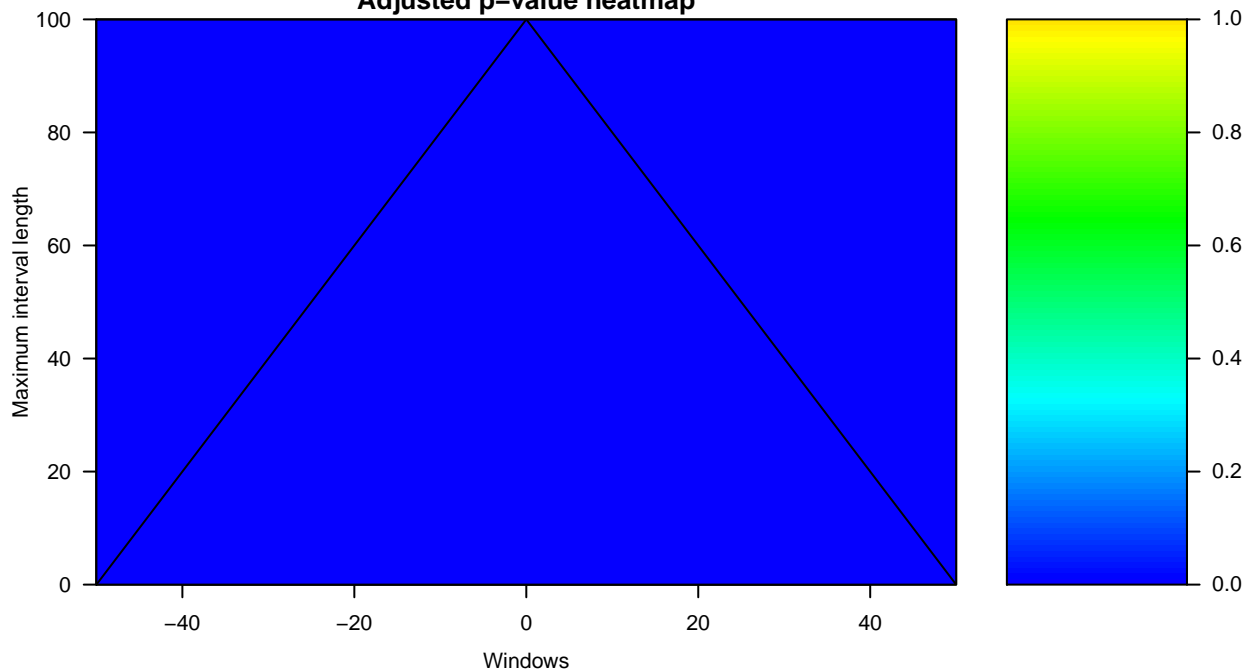


# Z DNA motifs

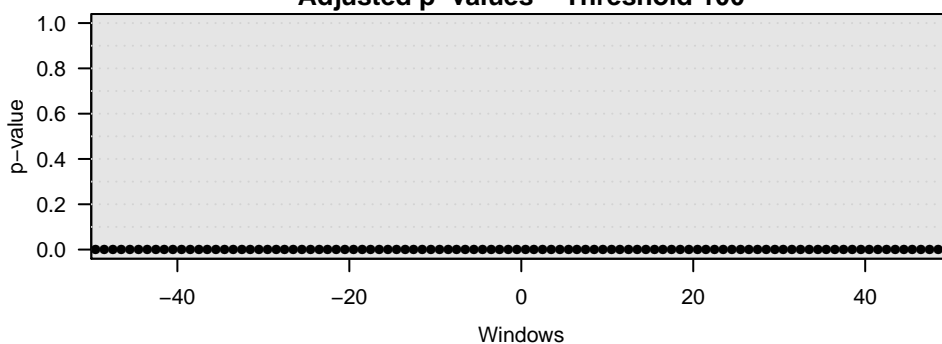


# Most conserved element

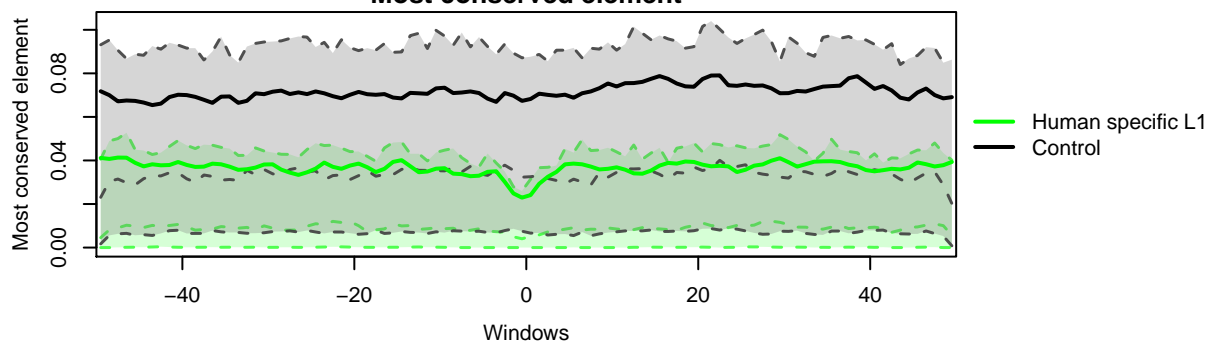
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# Most conserved element



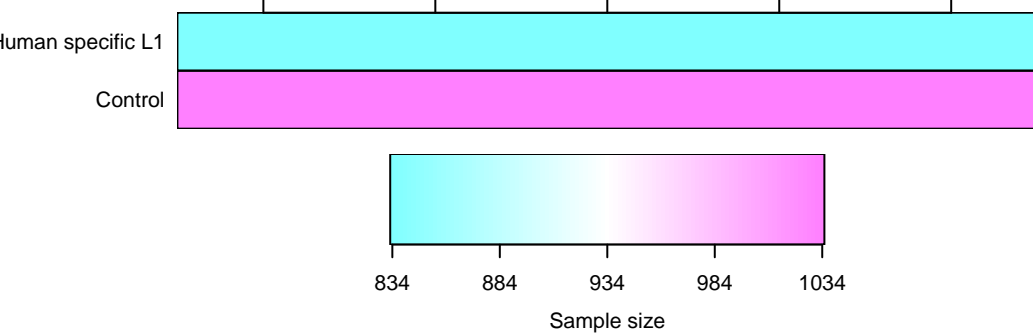
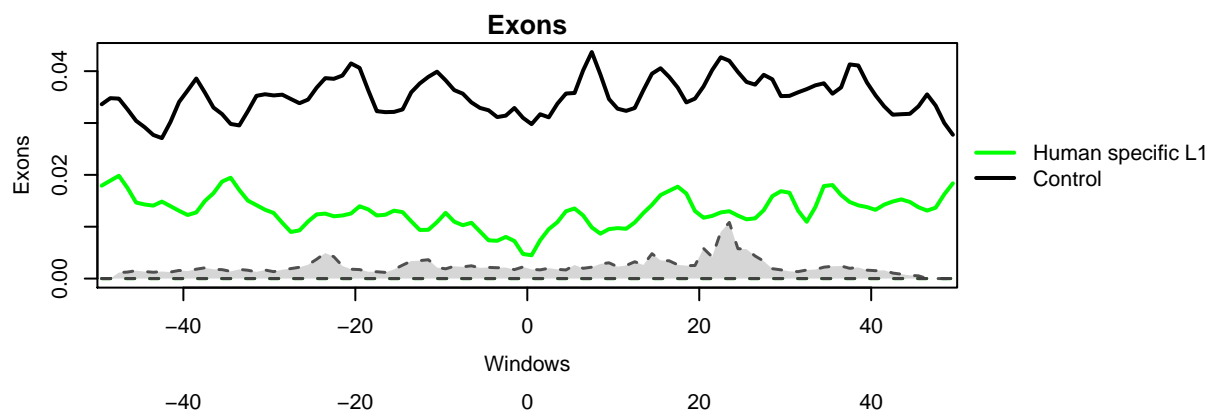
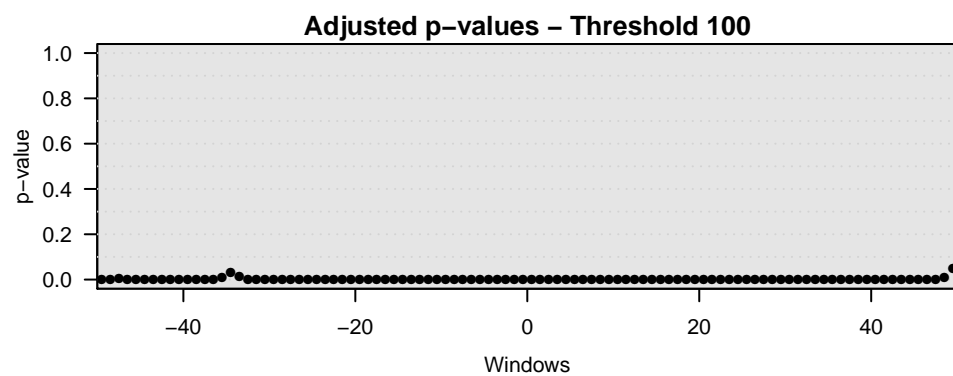
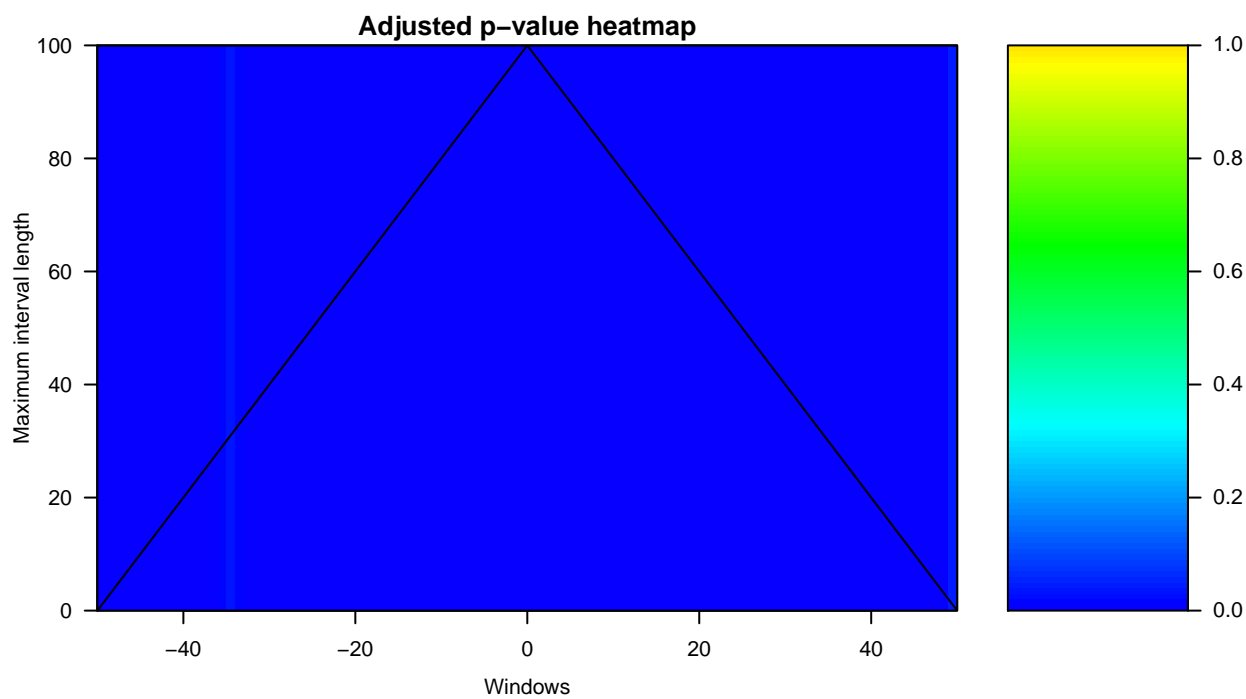
Human specific L1

Control

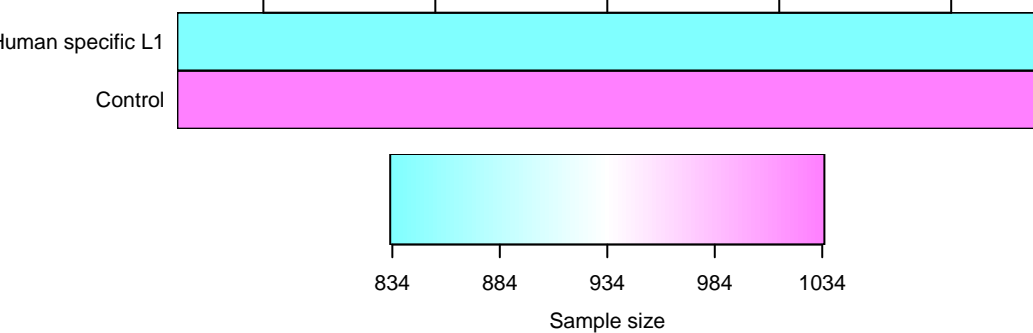
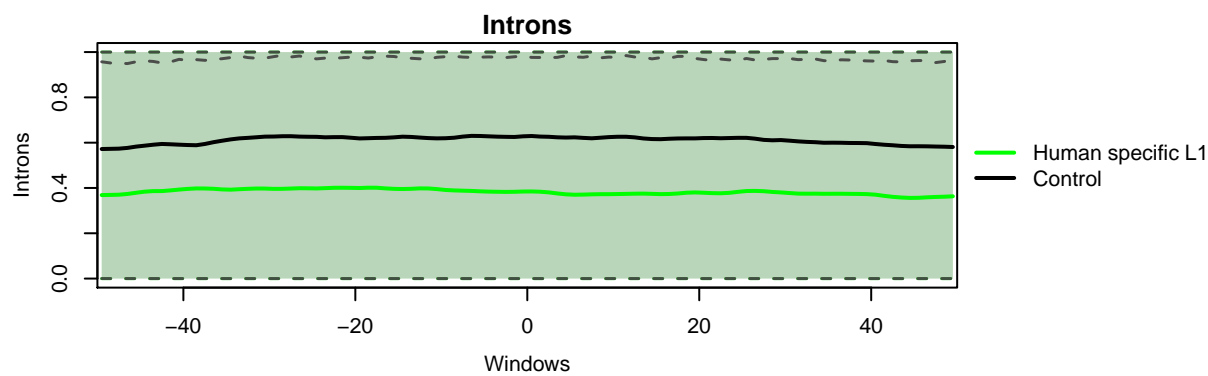
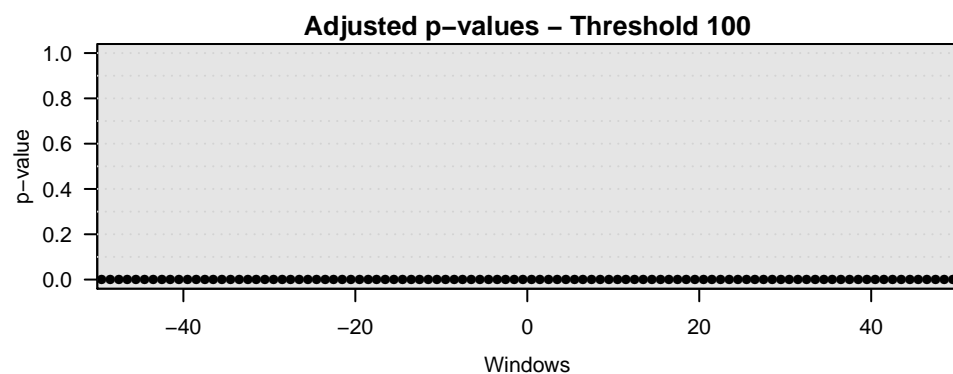
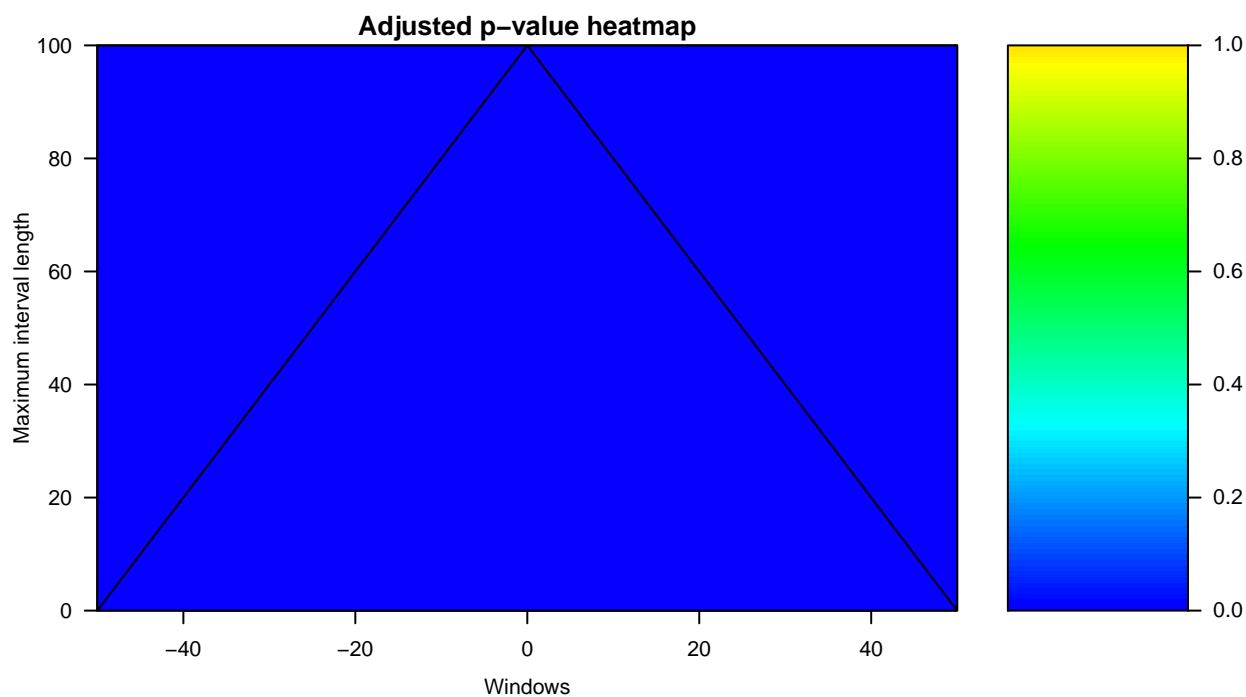
834 884 934 984 1034

Sample size

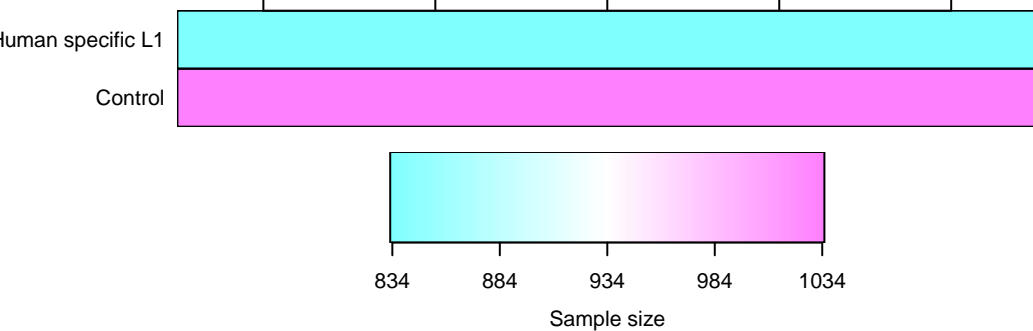
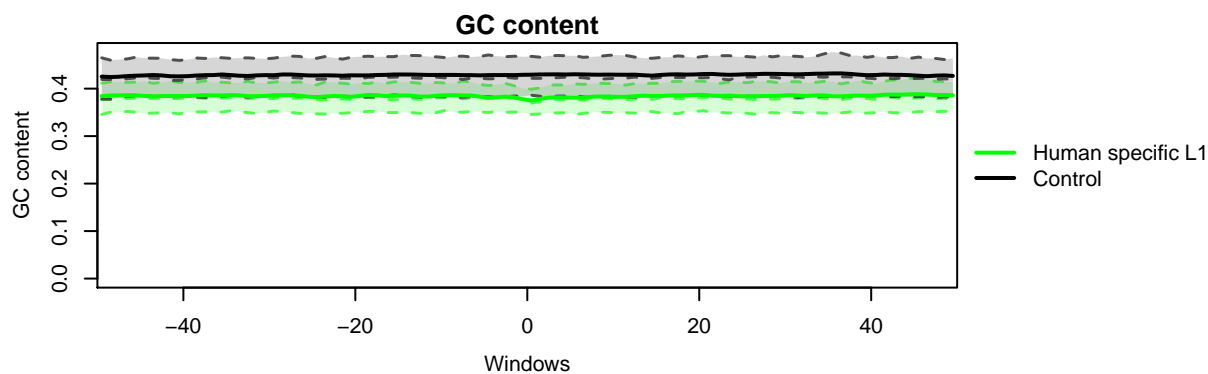
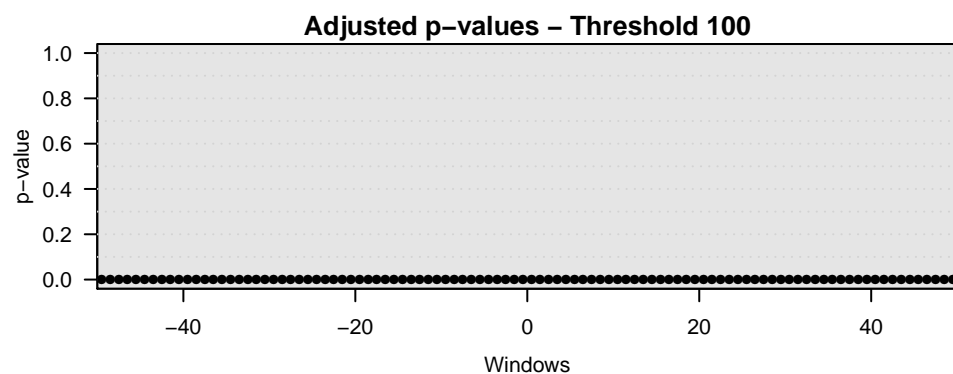
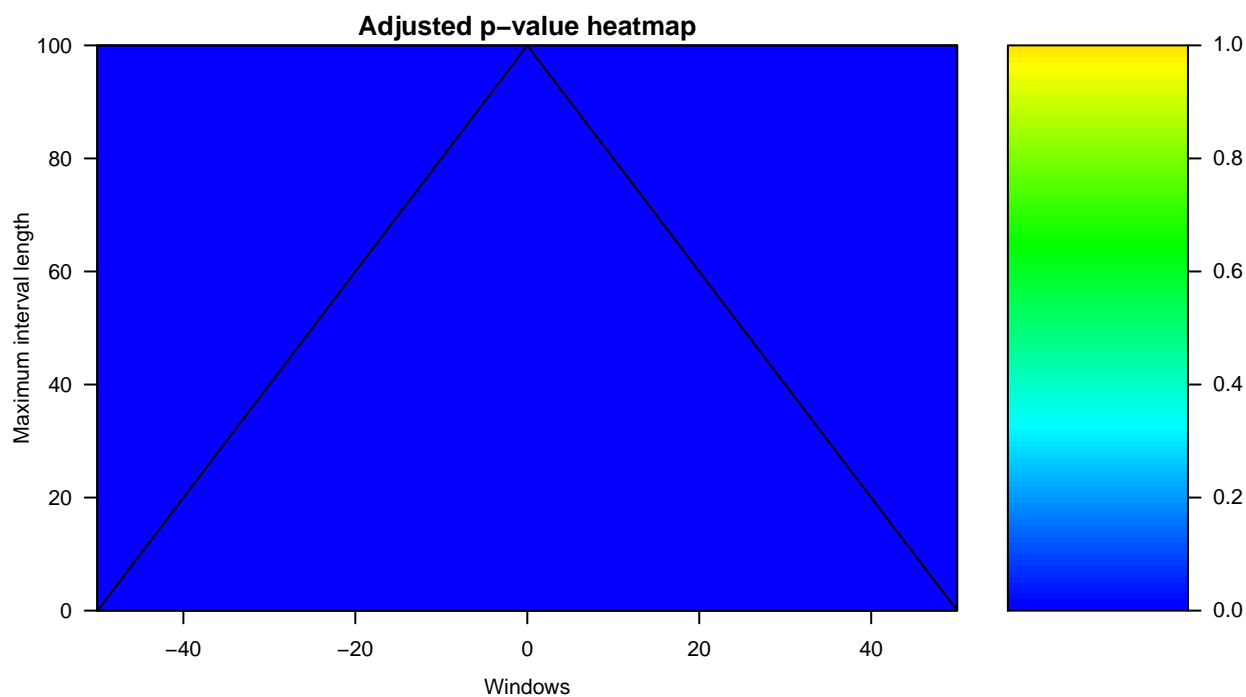
## Exons



# Introns

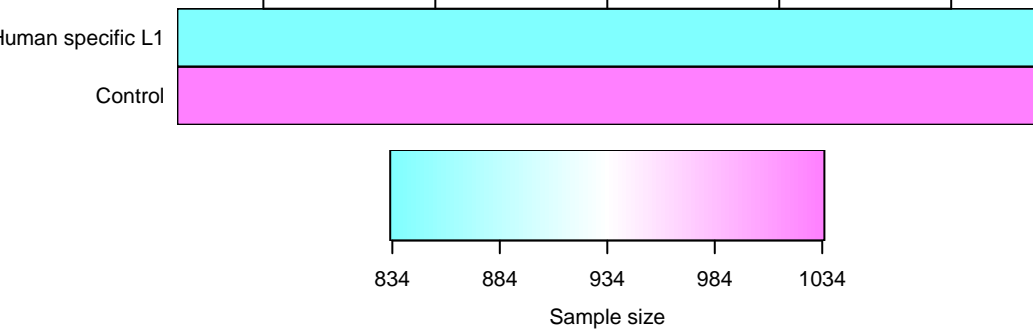
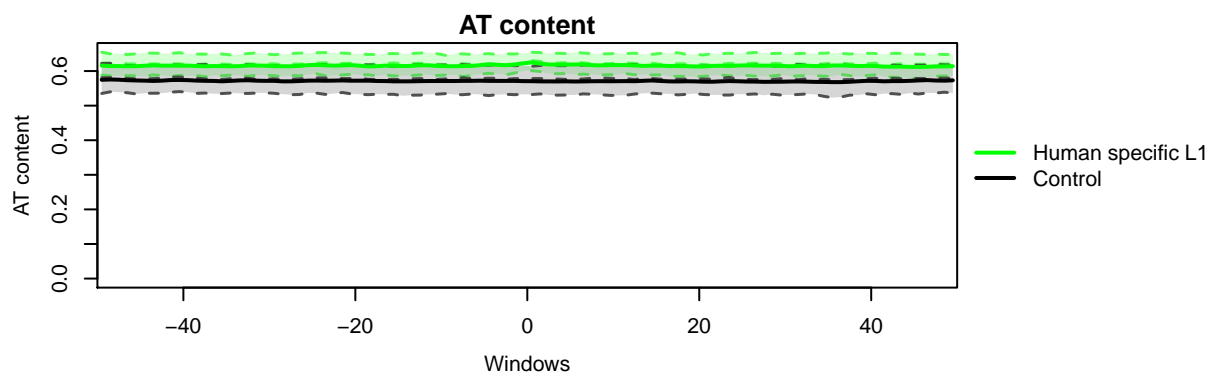
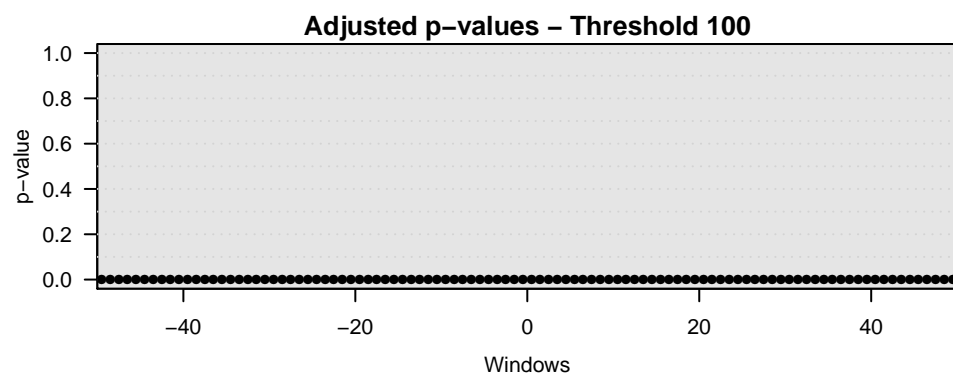
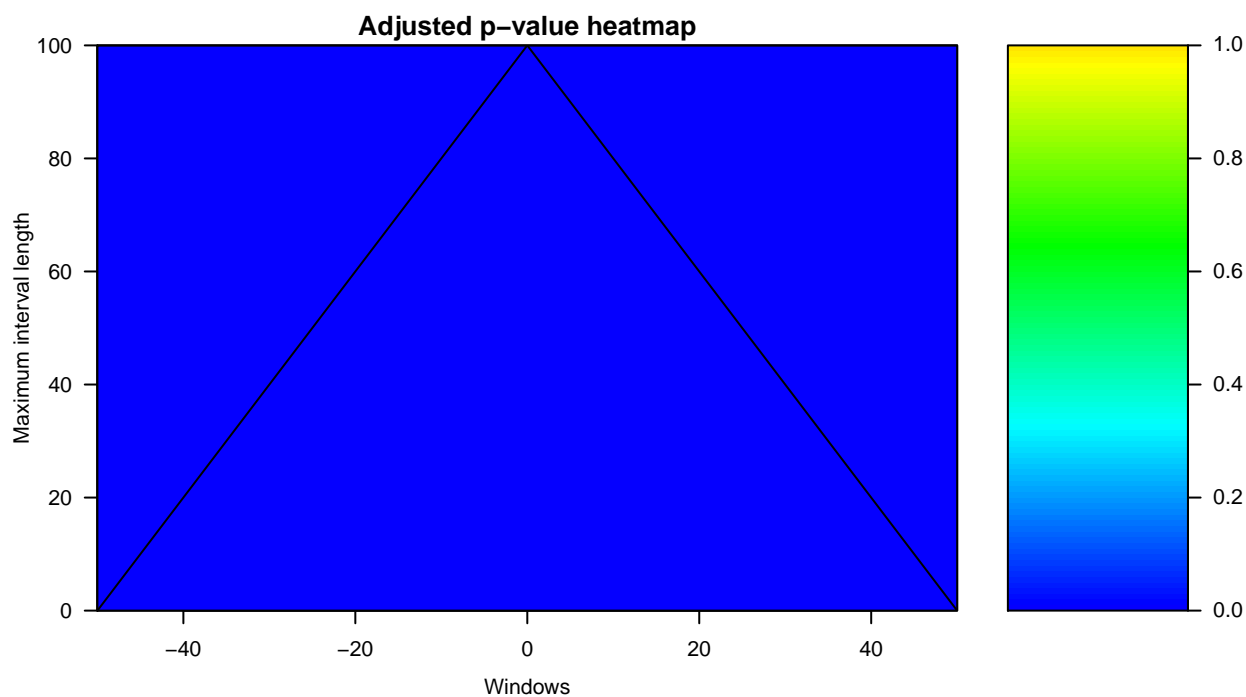


# GC content

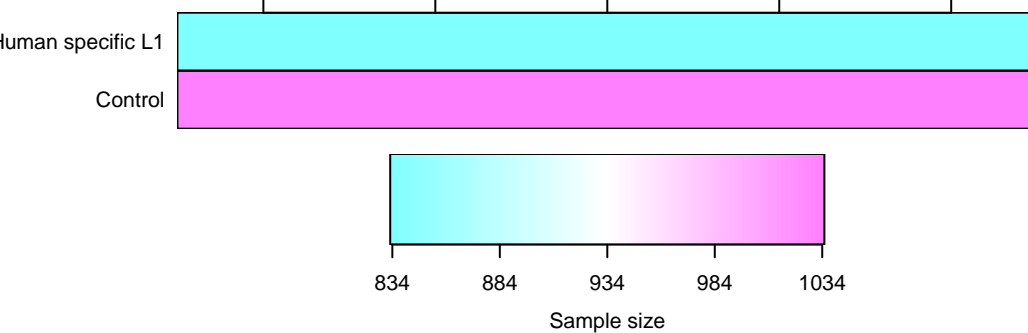
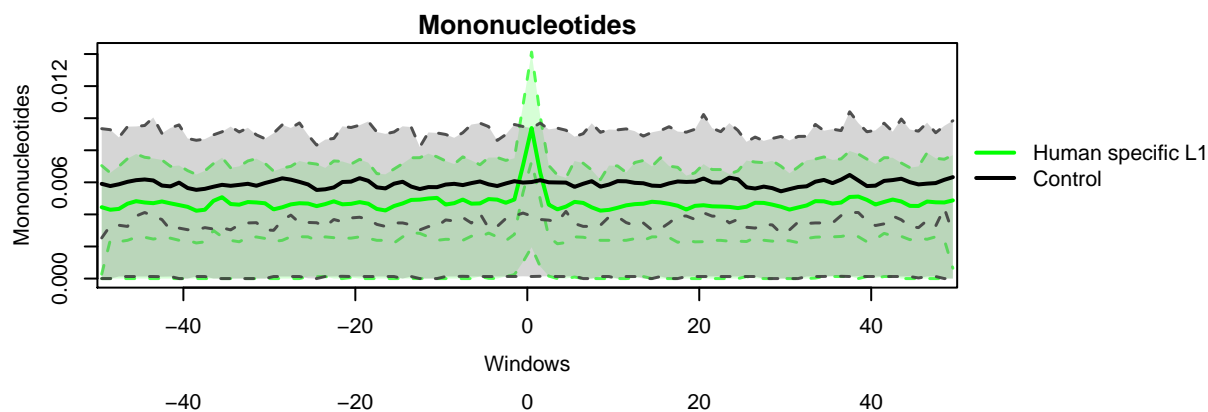
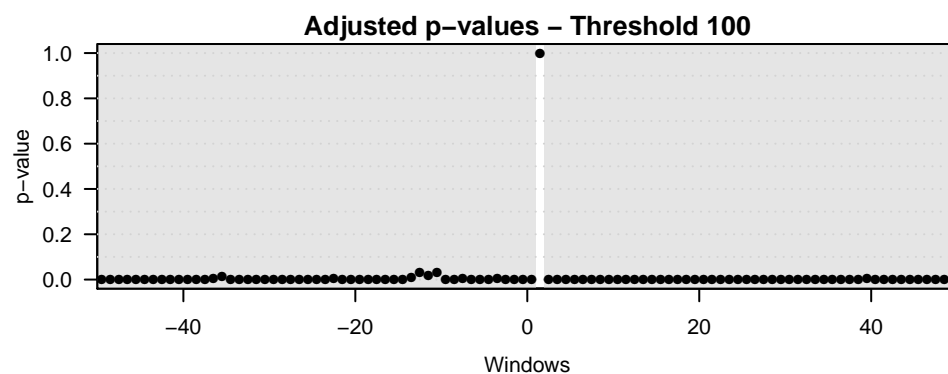
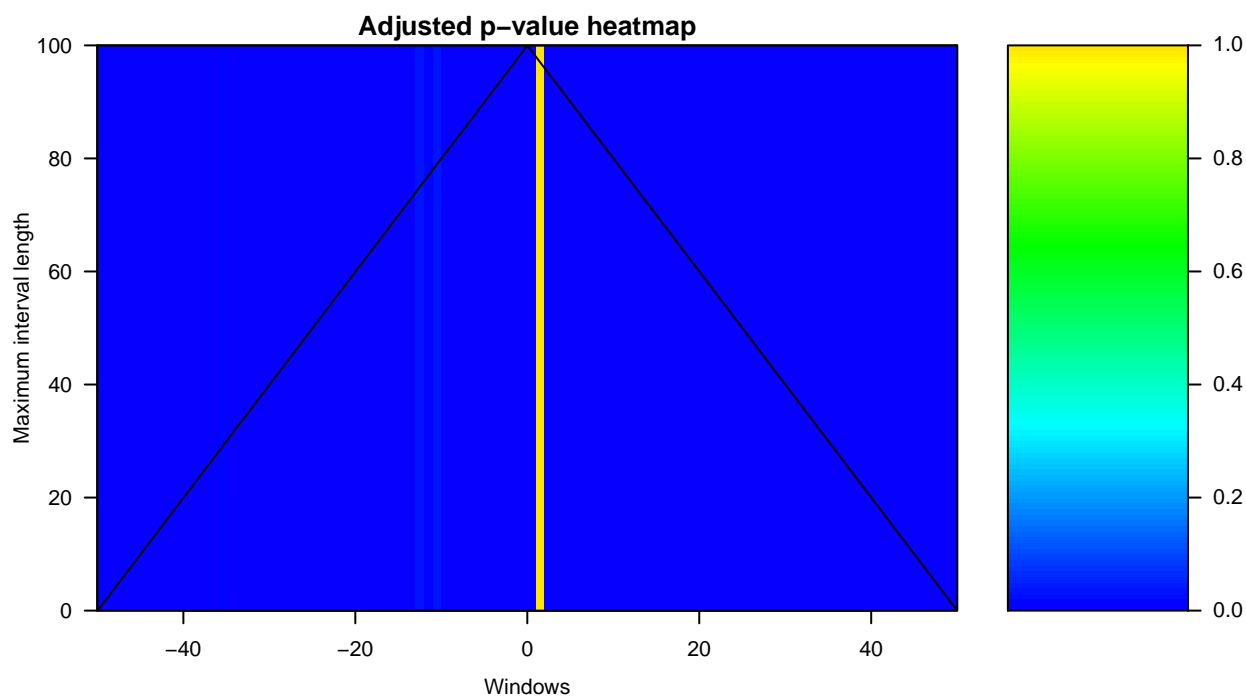




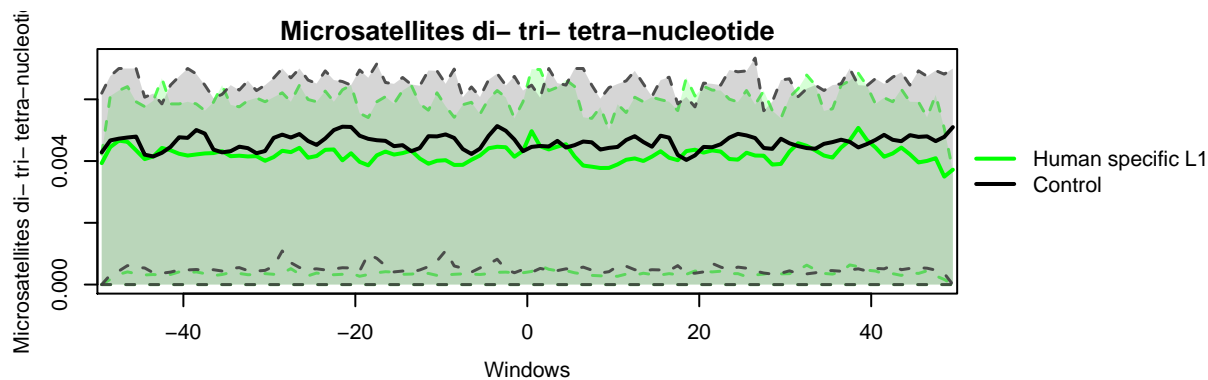
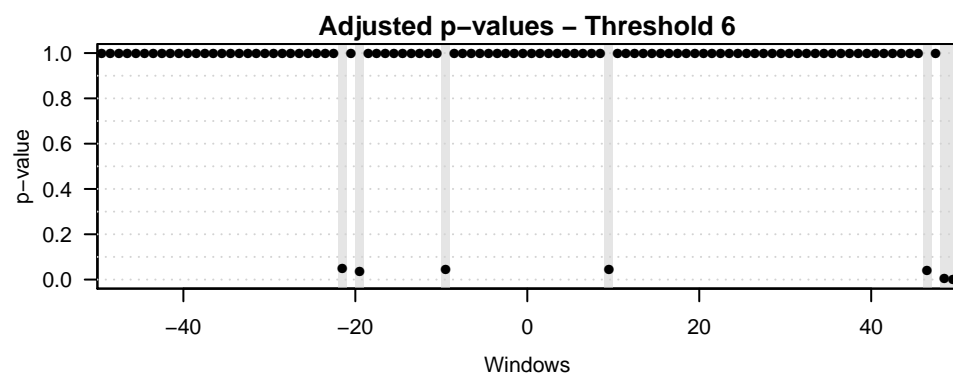
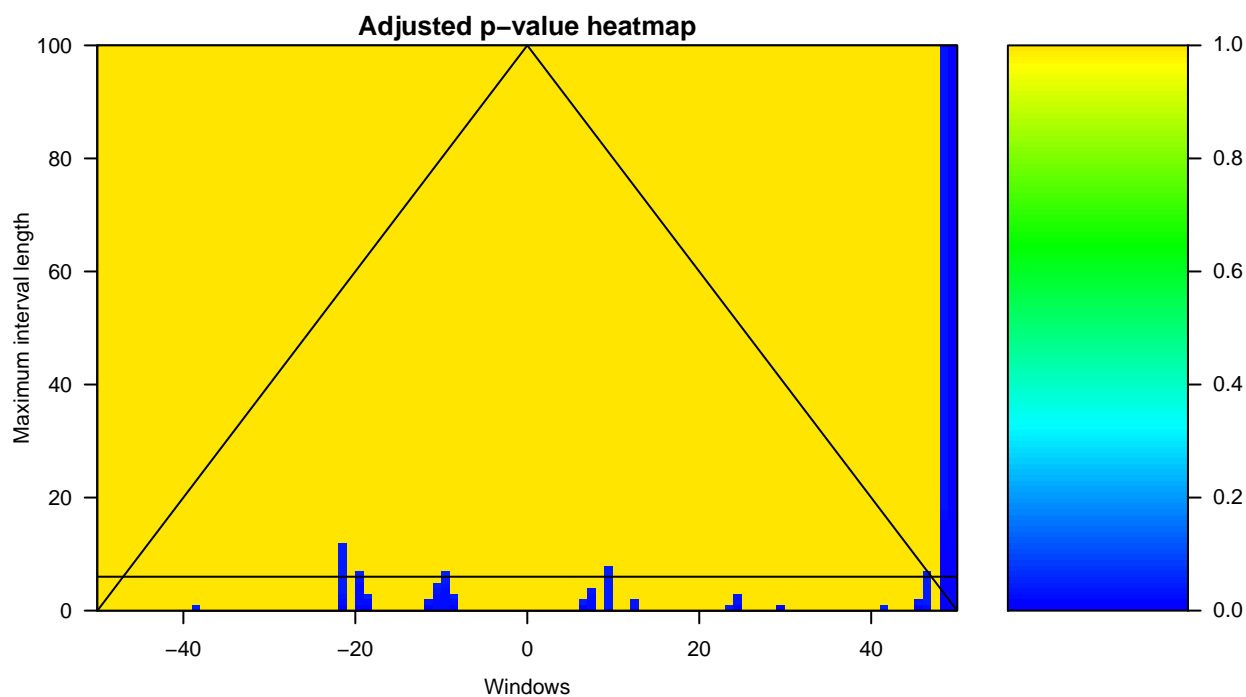
# AT content



# Mononucleotides



# Microsatellites di- tri- tetra-nucleotide



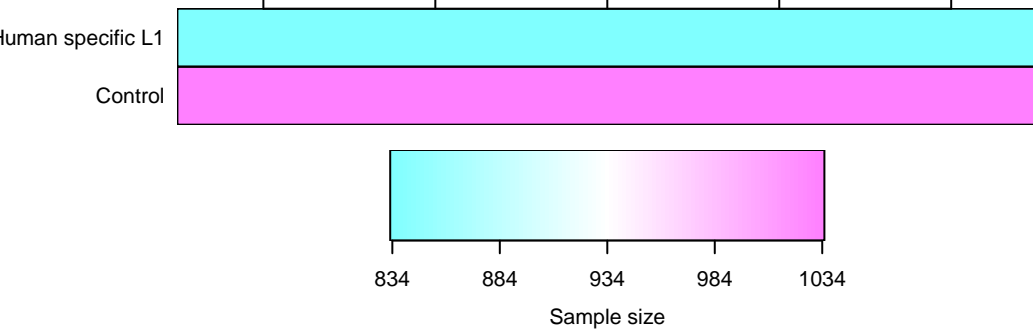
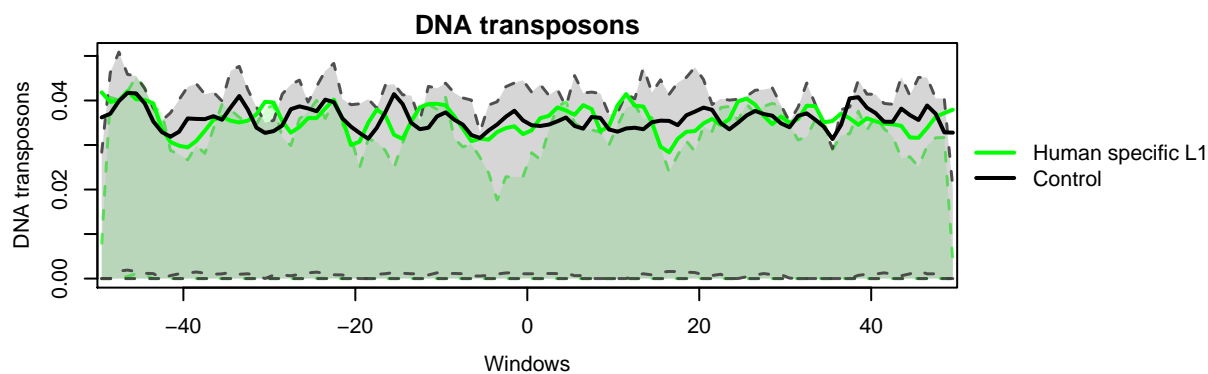
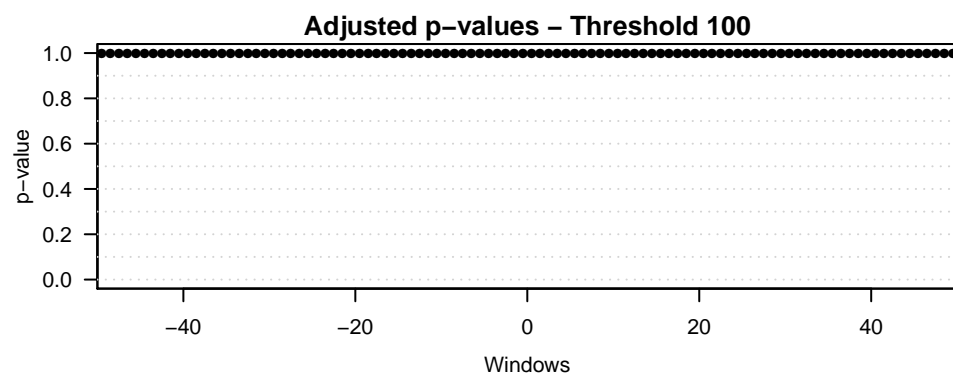
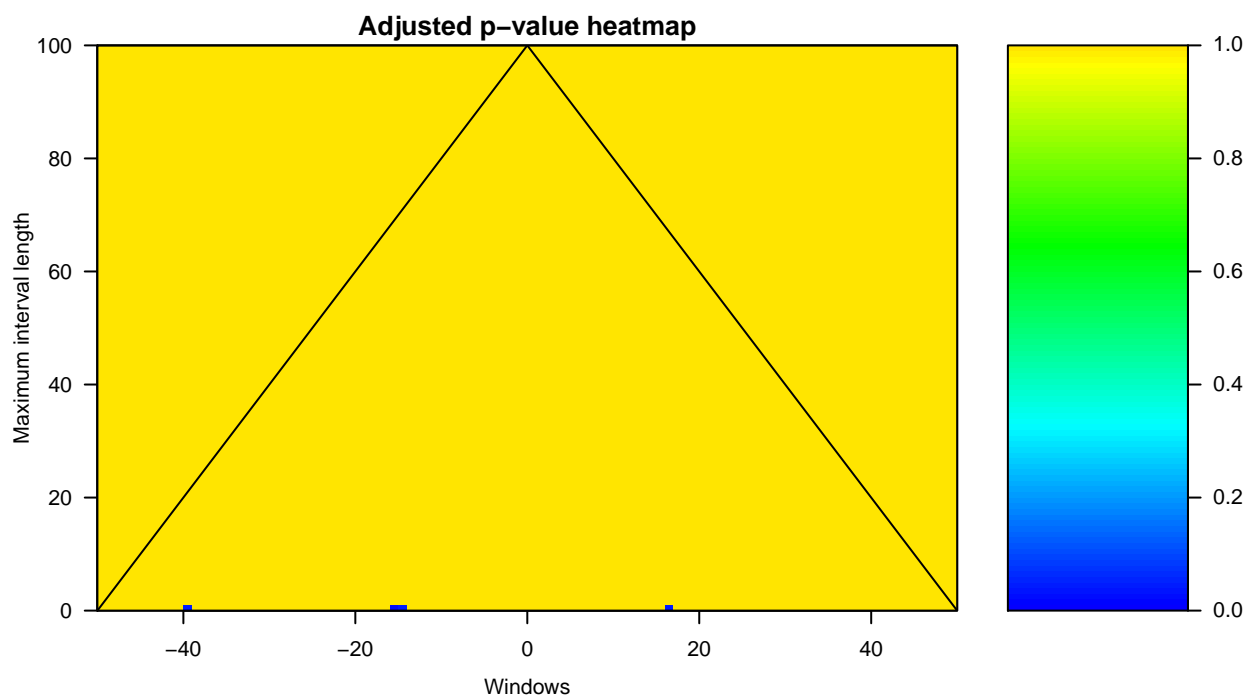
Human specific L1

Control

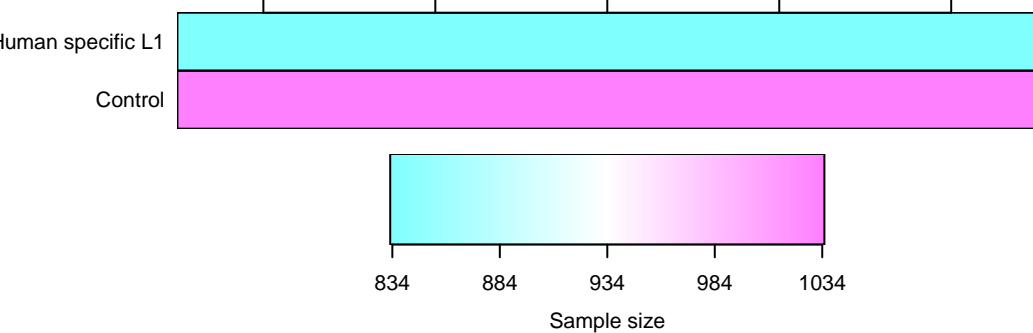
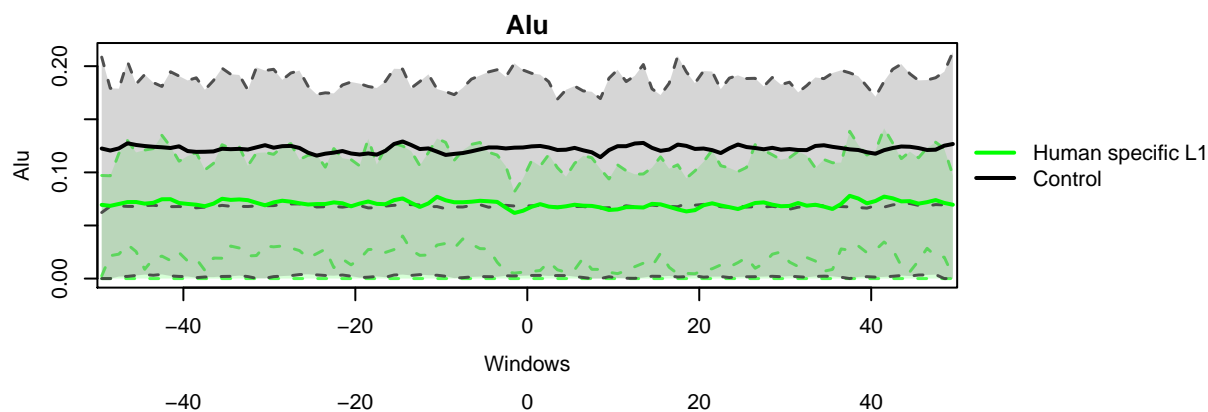
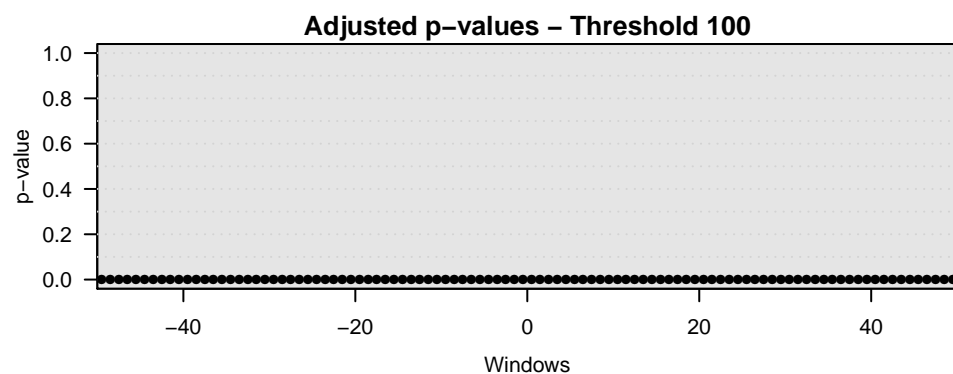
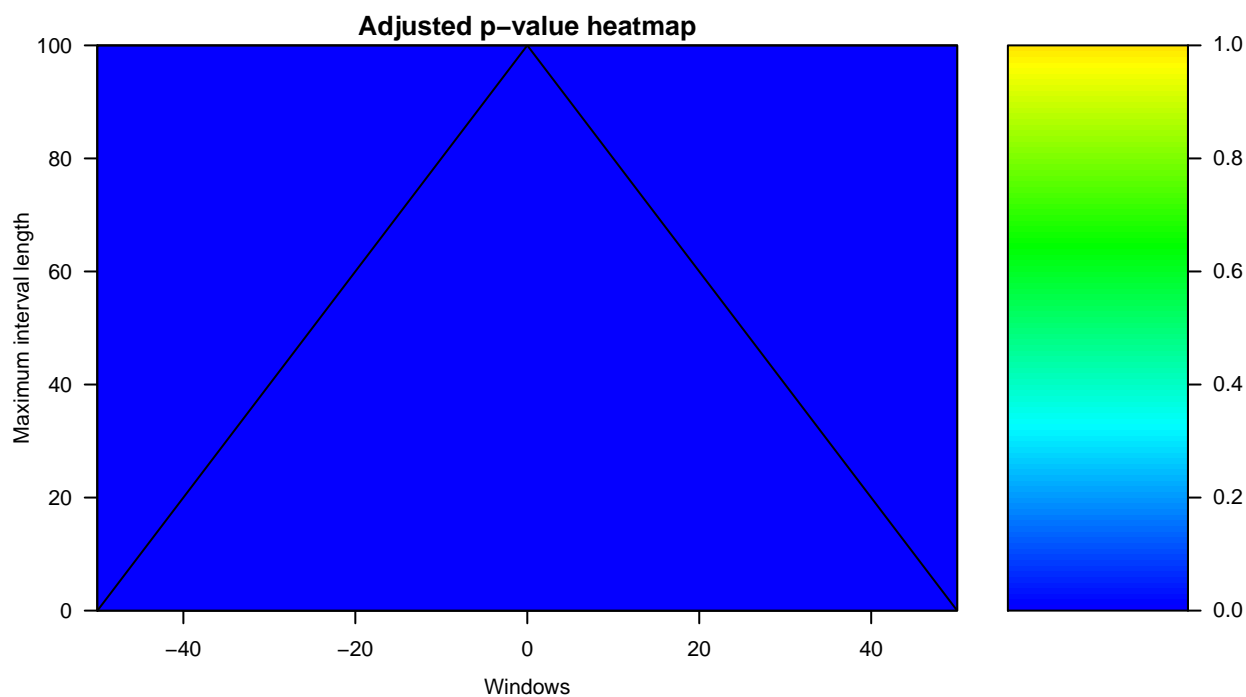
834 884 934 984 1034

Sample size

# DNA transposons

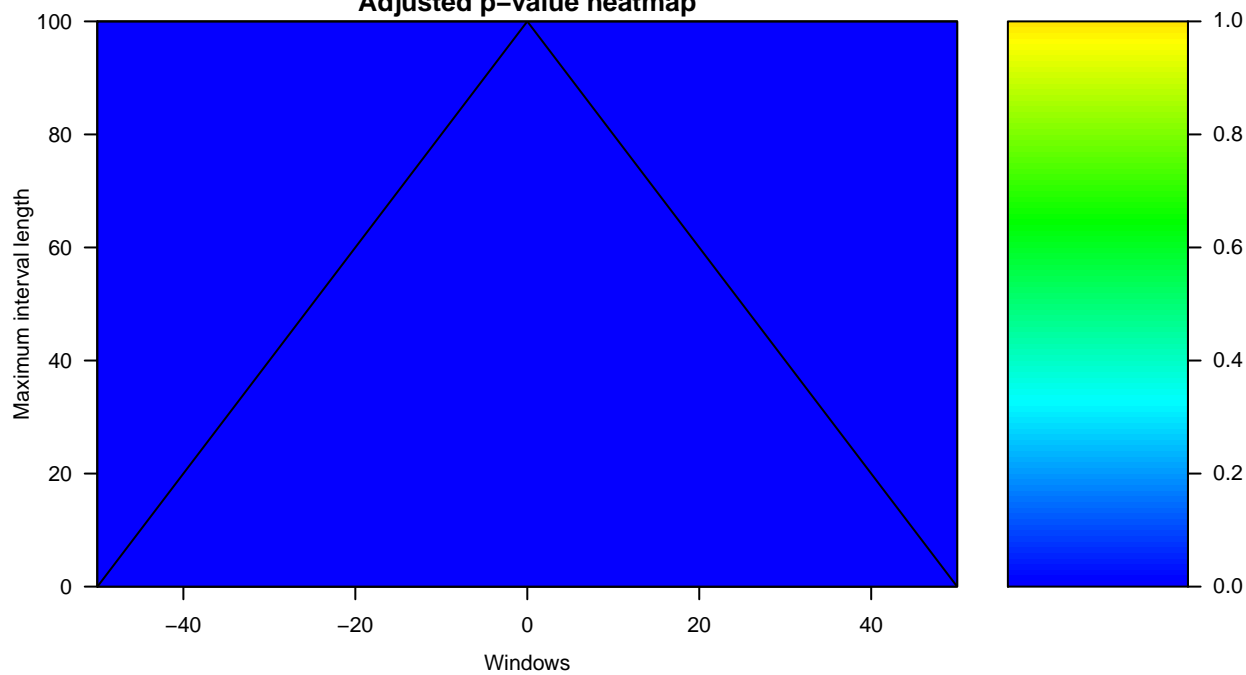


# Alu

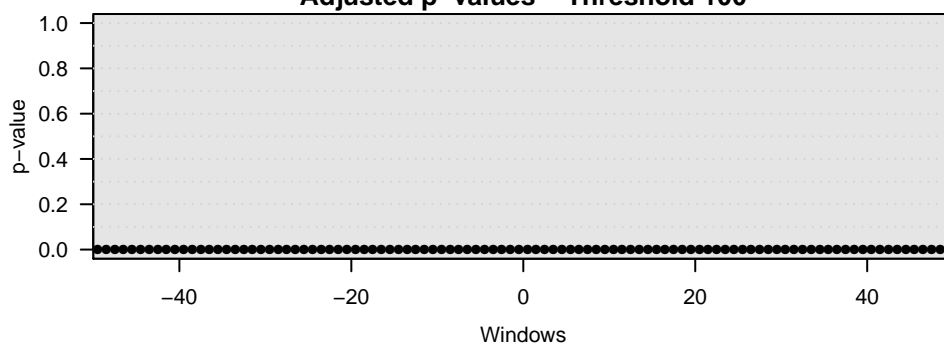


# MIR

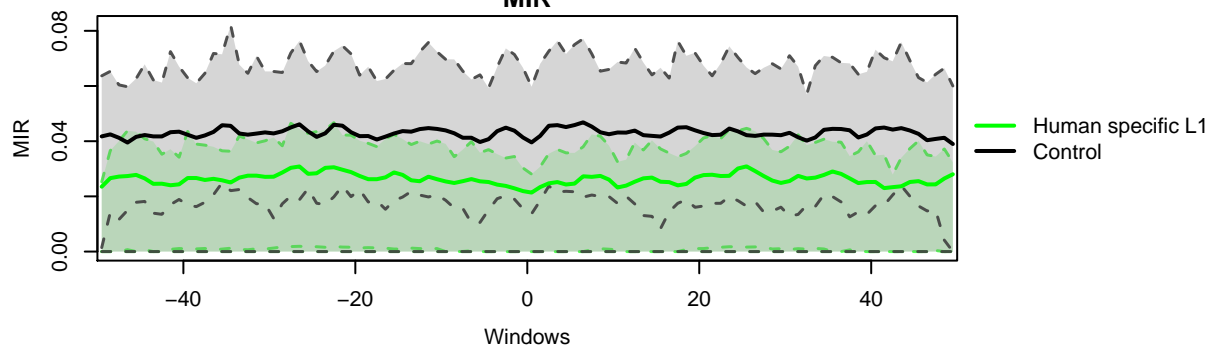
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# MIR



Human specific L1

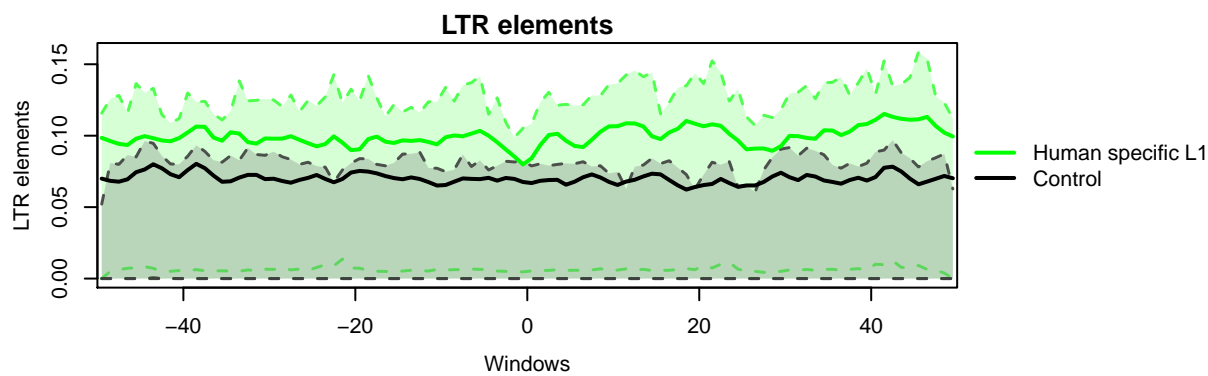
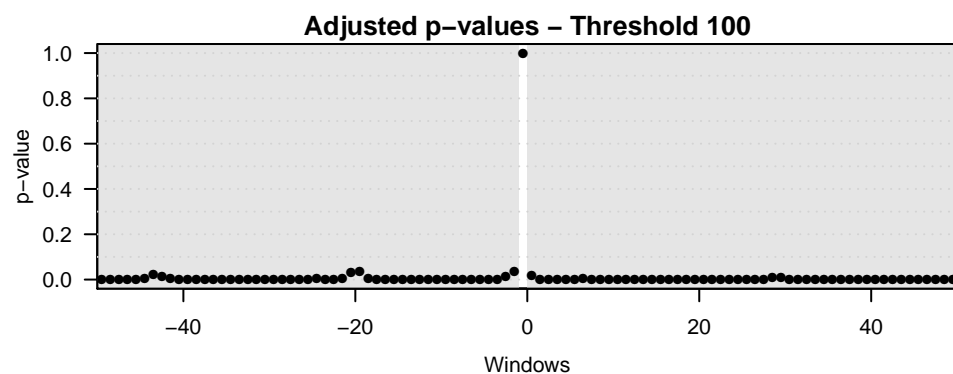
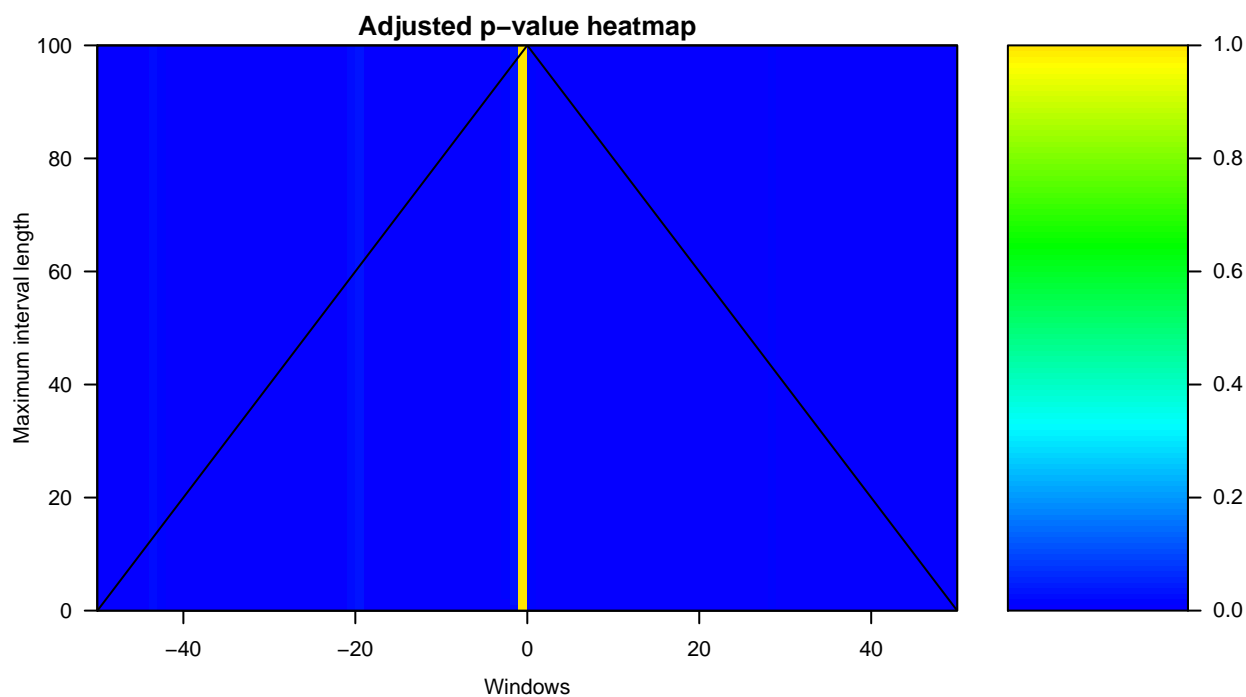
Control



834 884 934 984 1034

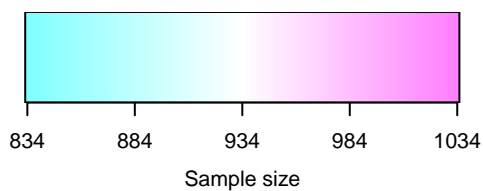
Sample size

# LTR elements

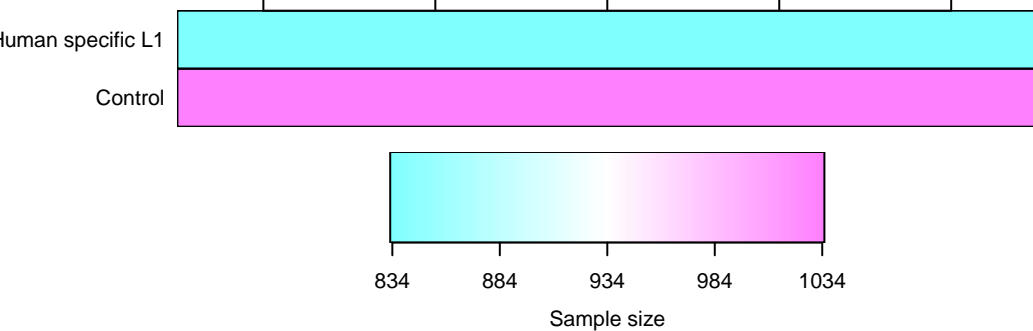
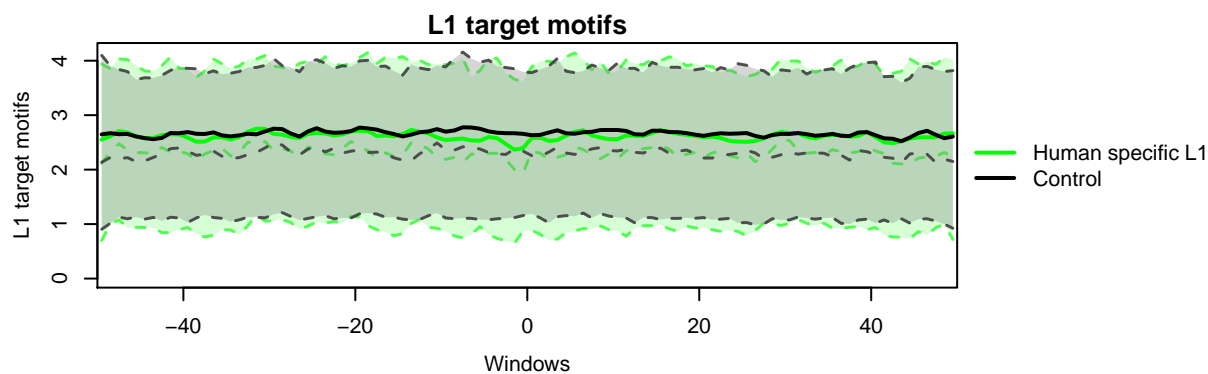
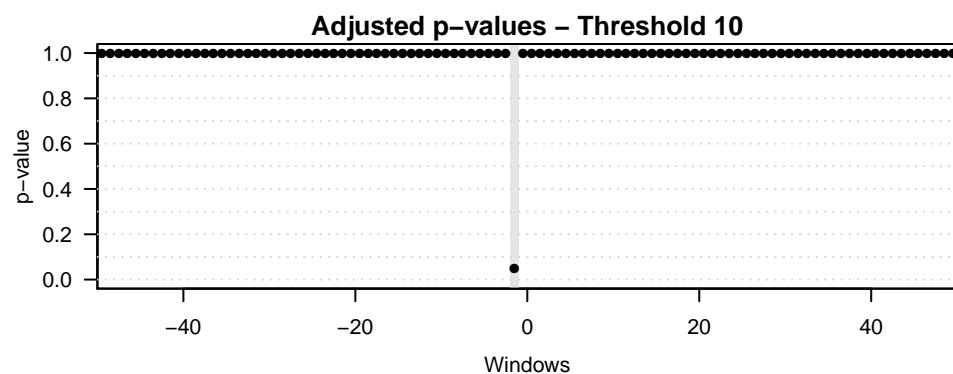
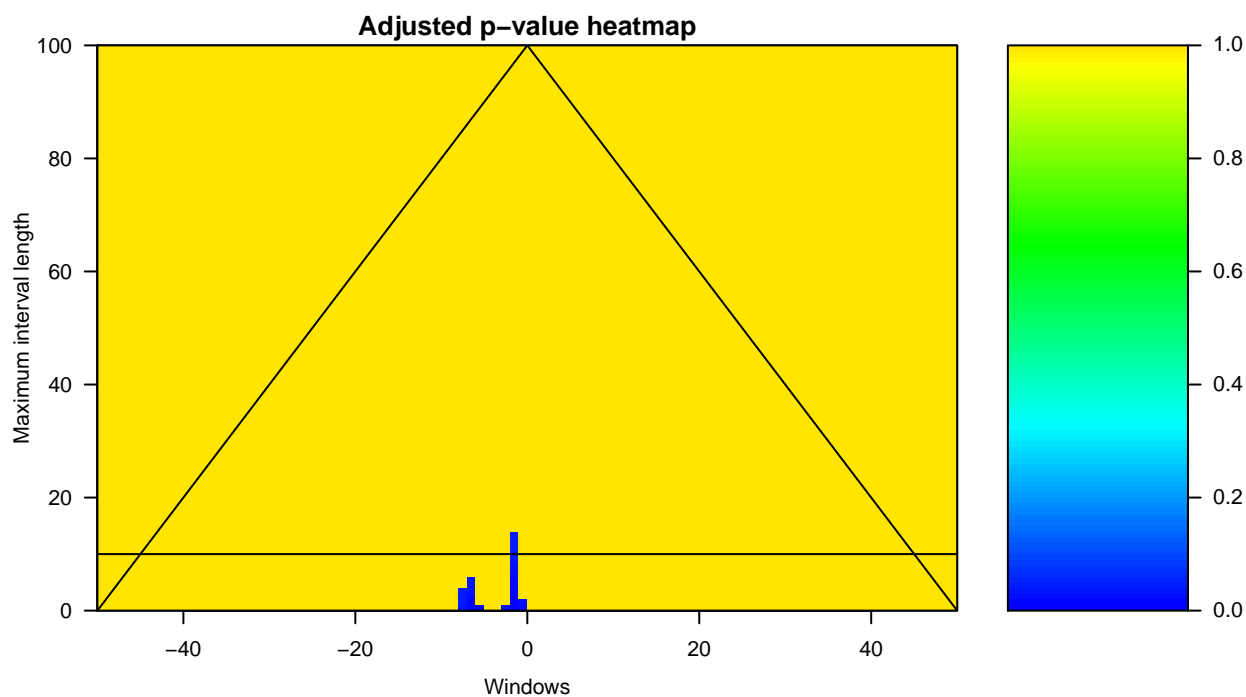


Human specific L1

Control

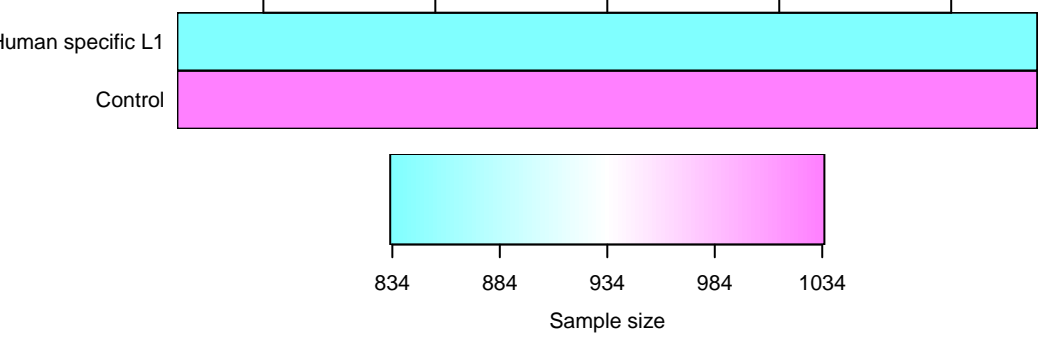
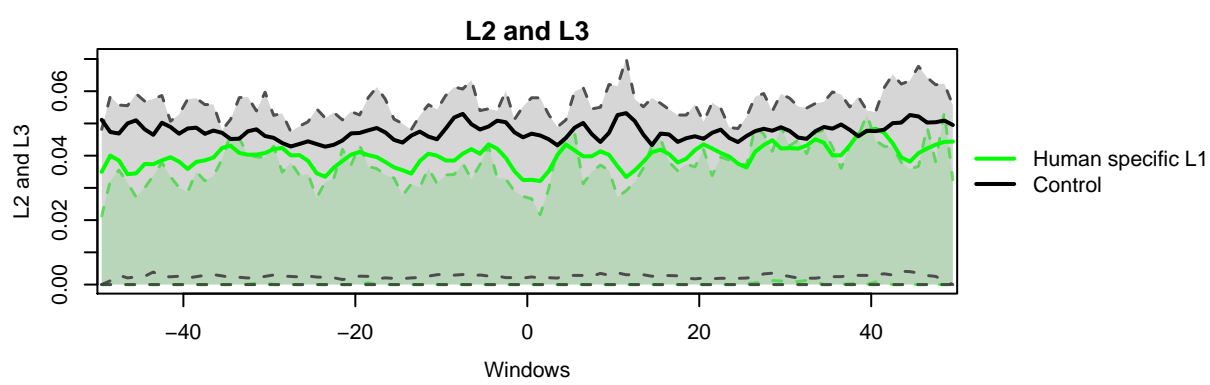
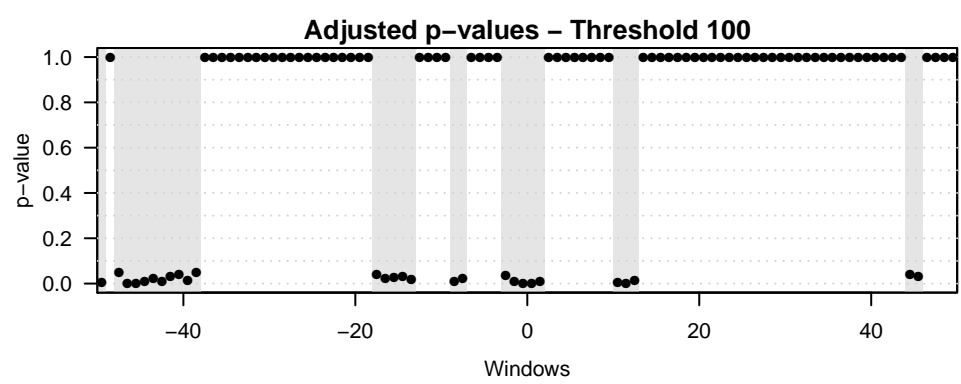
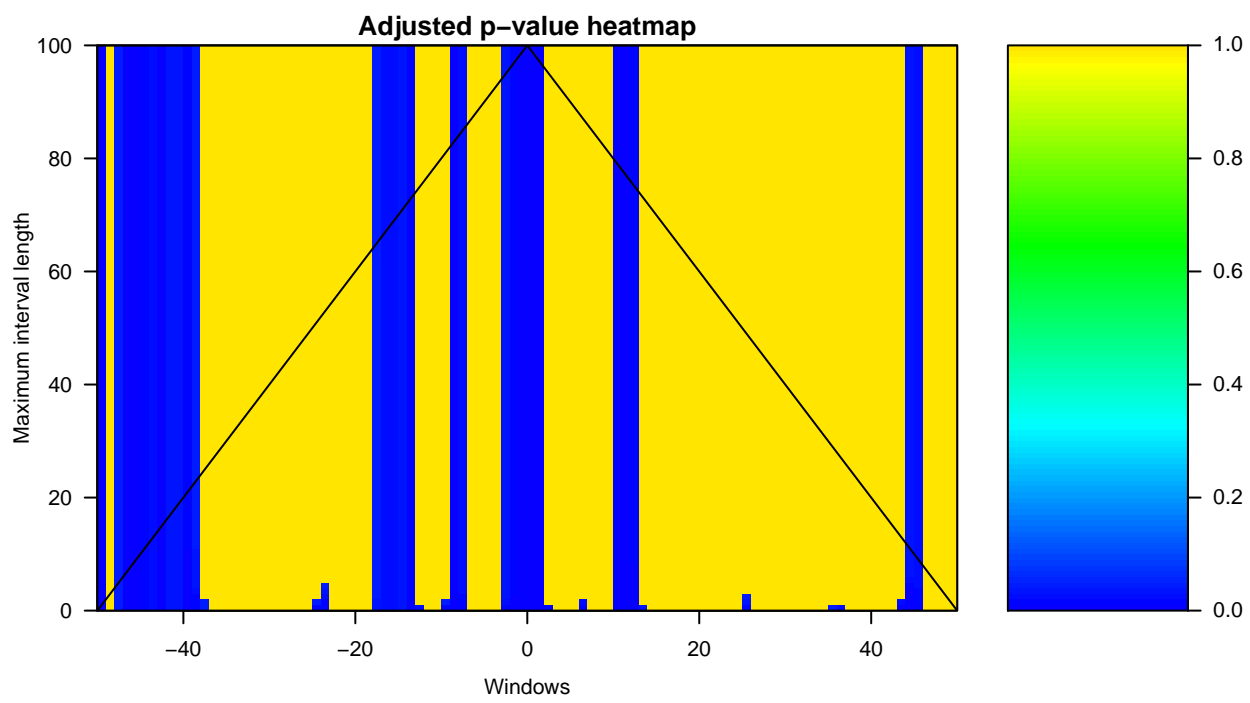


# L1 target motifs

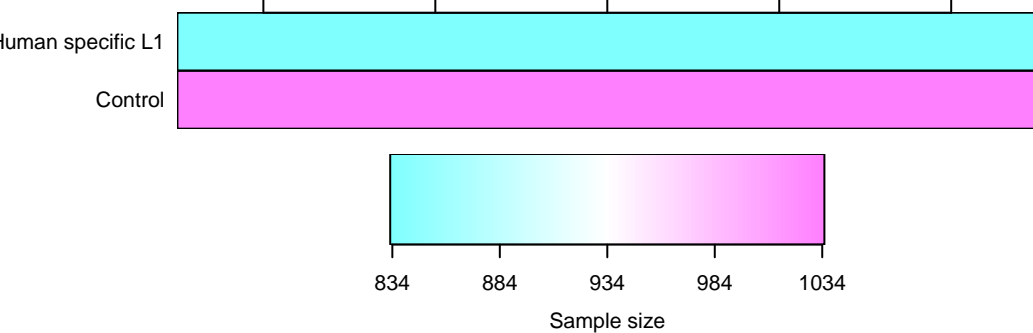
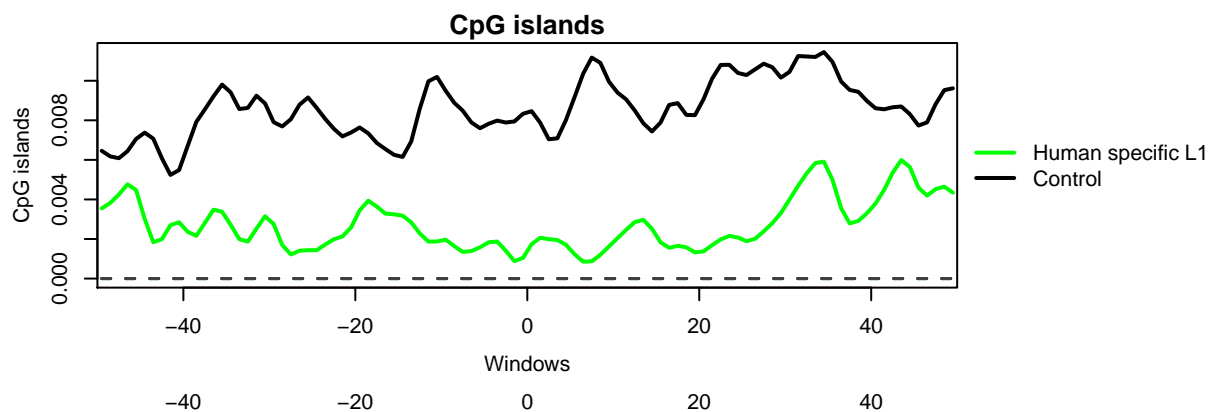
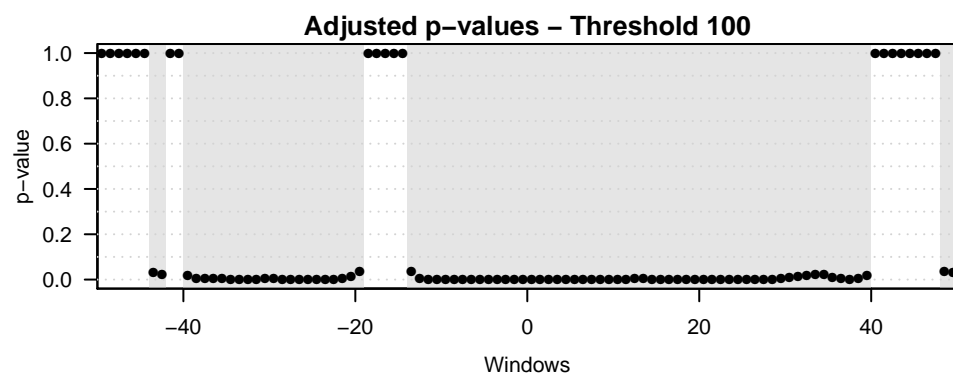
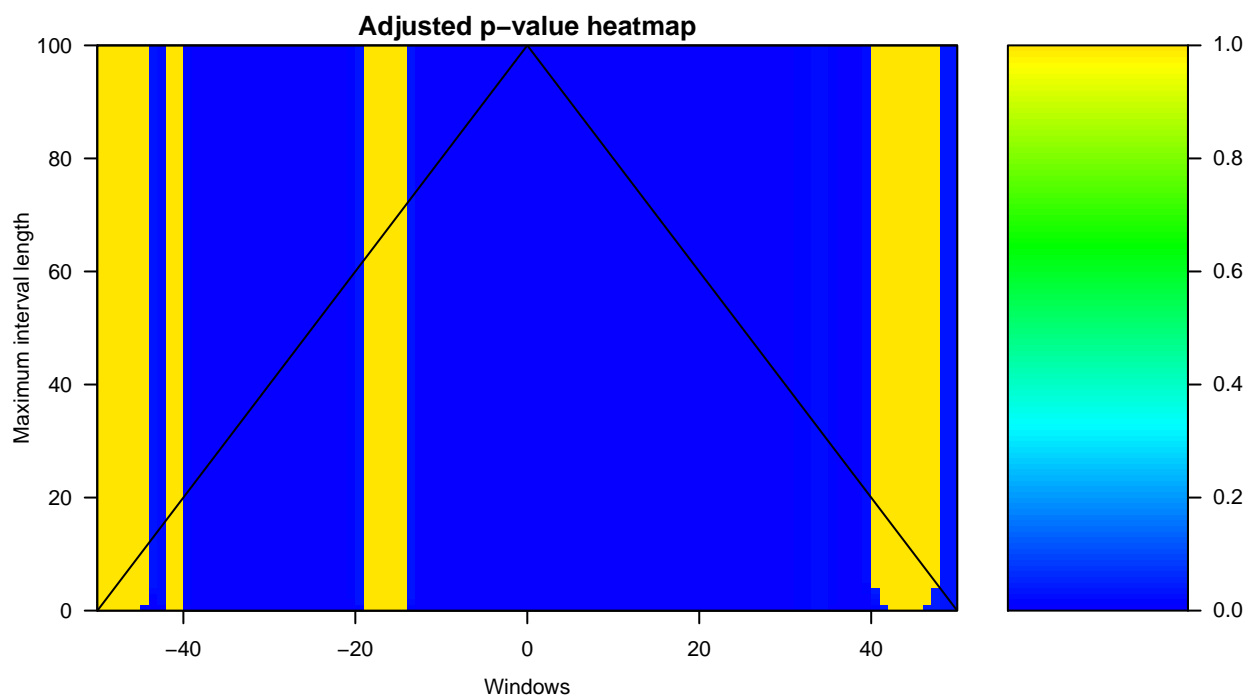




# L2 and L3

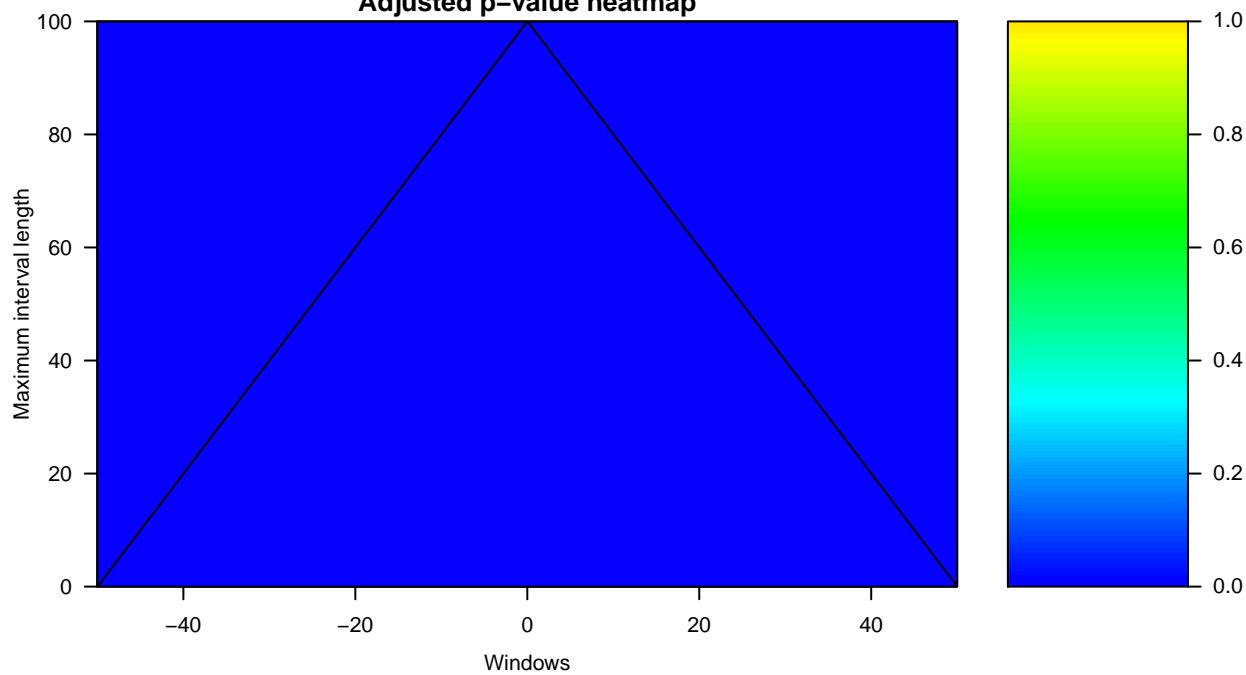


# CpG islands

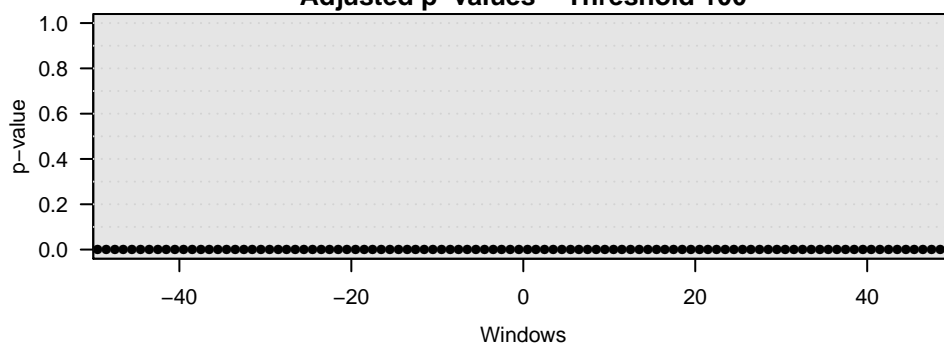


# 5-hydroxymethylcytosine

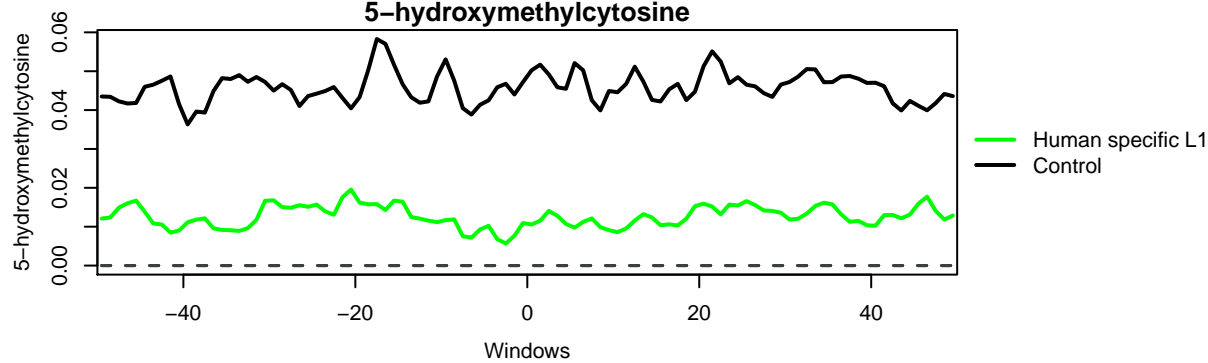
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100

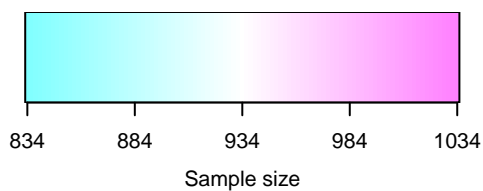
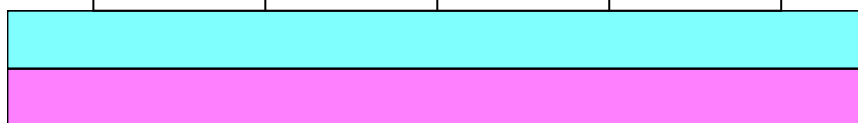


# 5-hydroxymethylcytosine



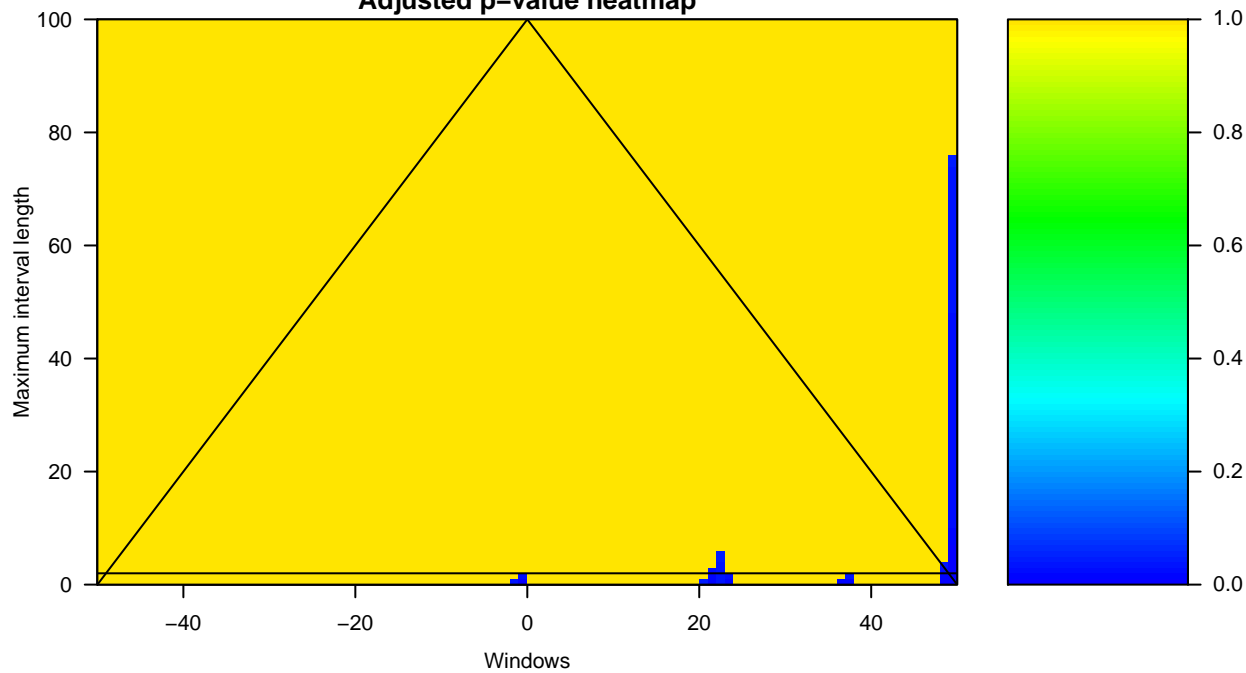
Human specific L1

Control

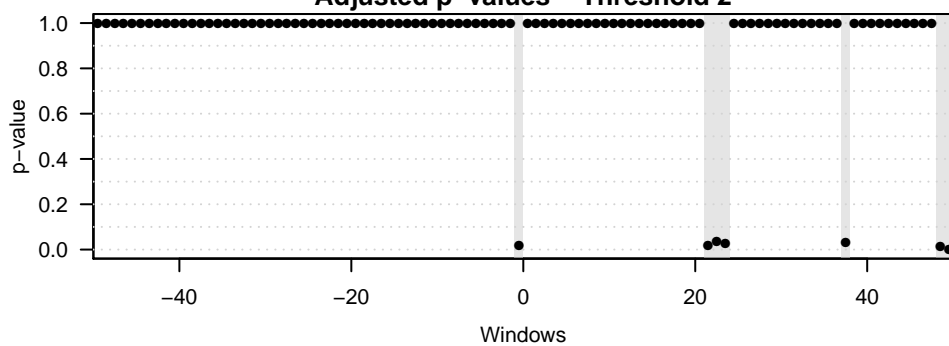


# Sperm hypomethylation

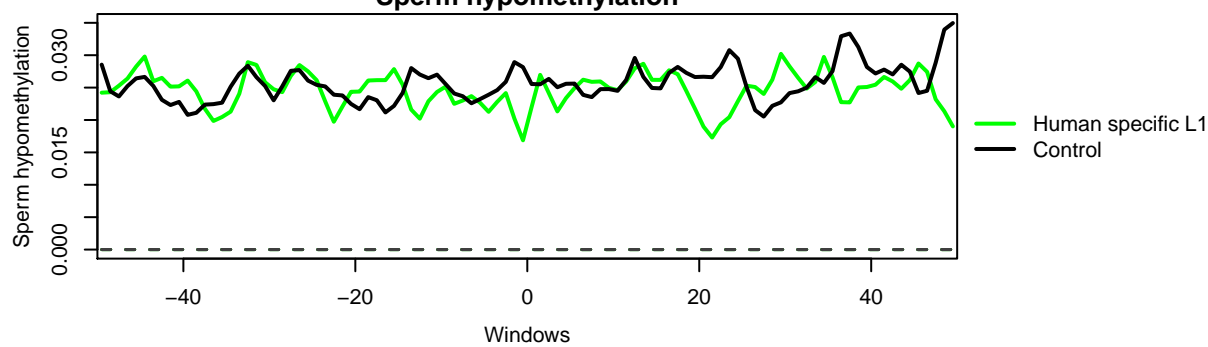
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 2

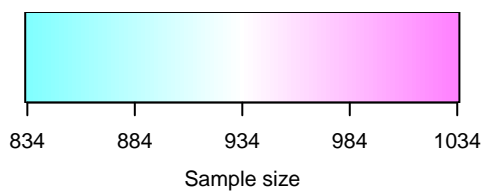


# Sperm hypomethylation

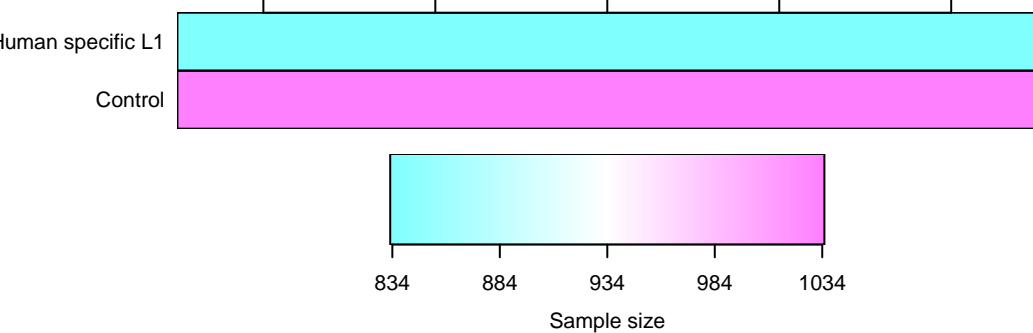
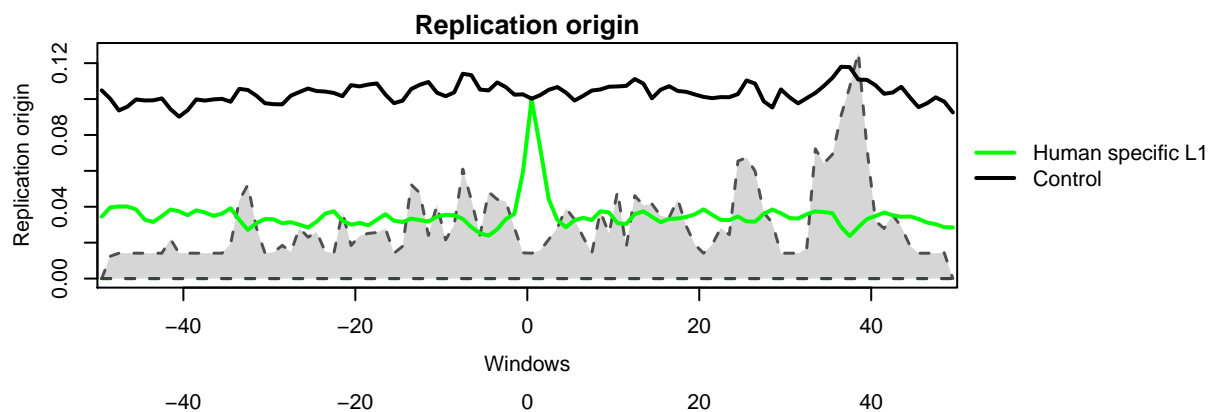
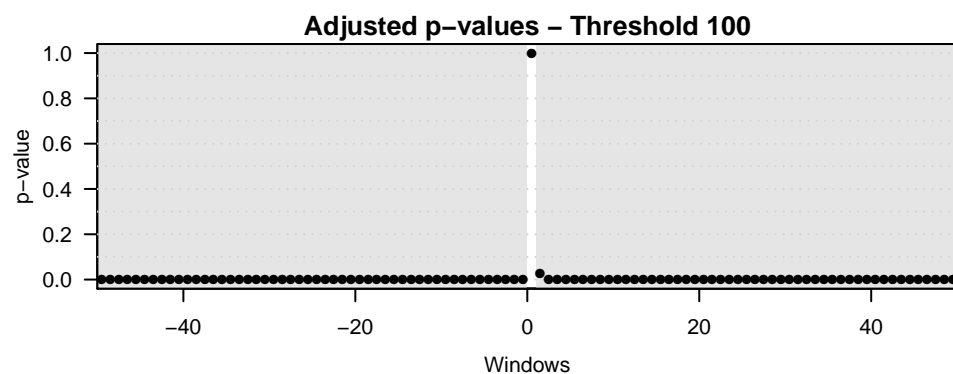
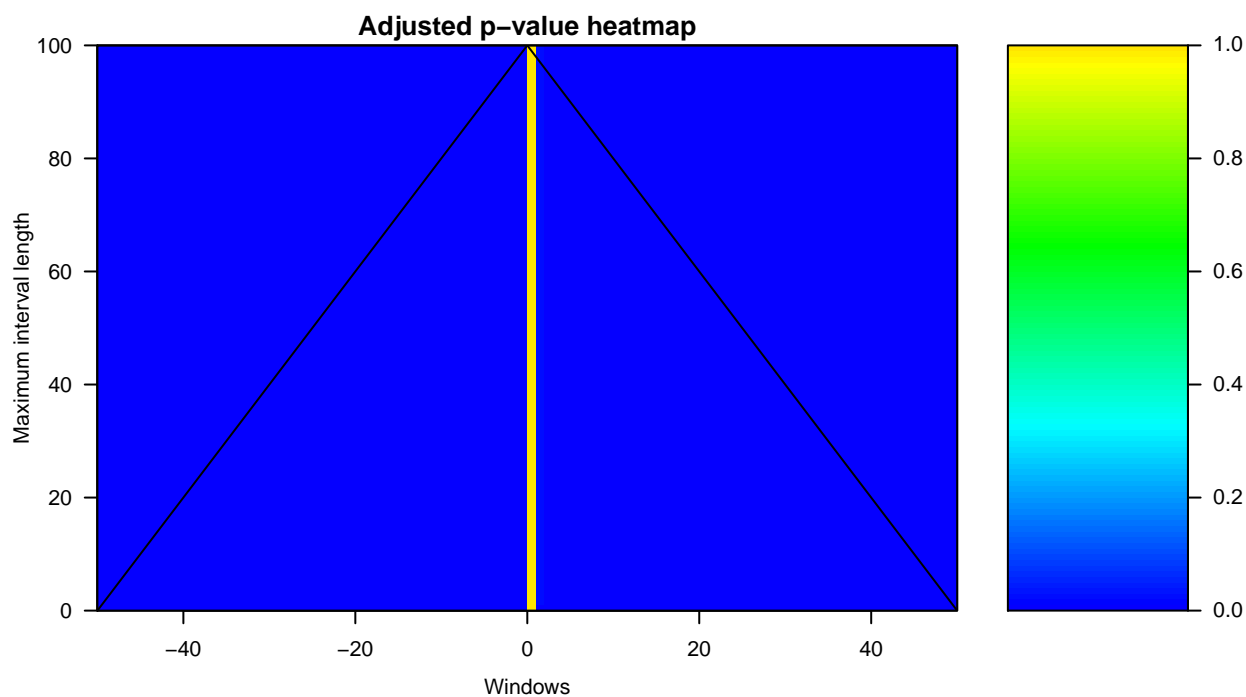


Human specific L1

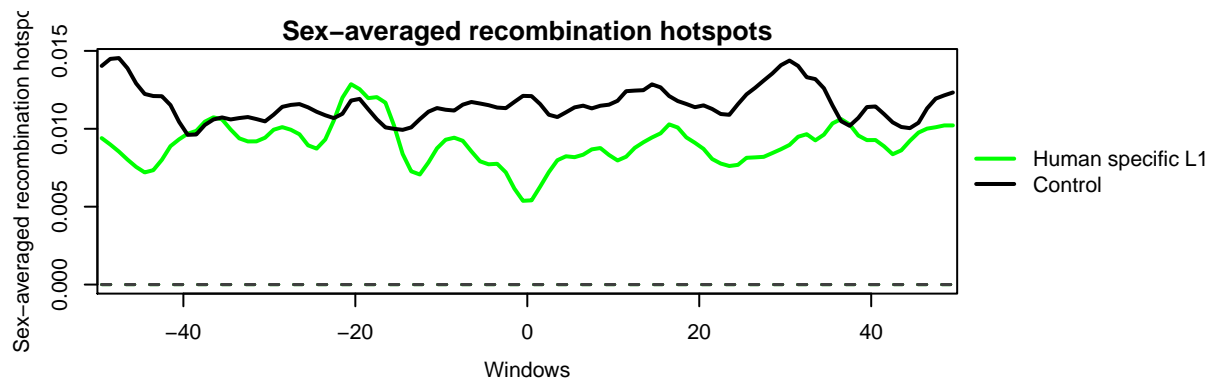
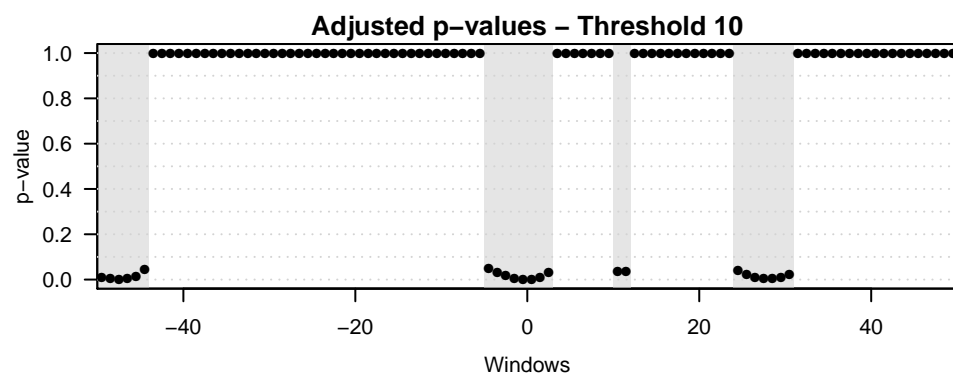
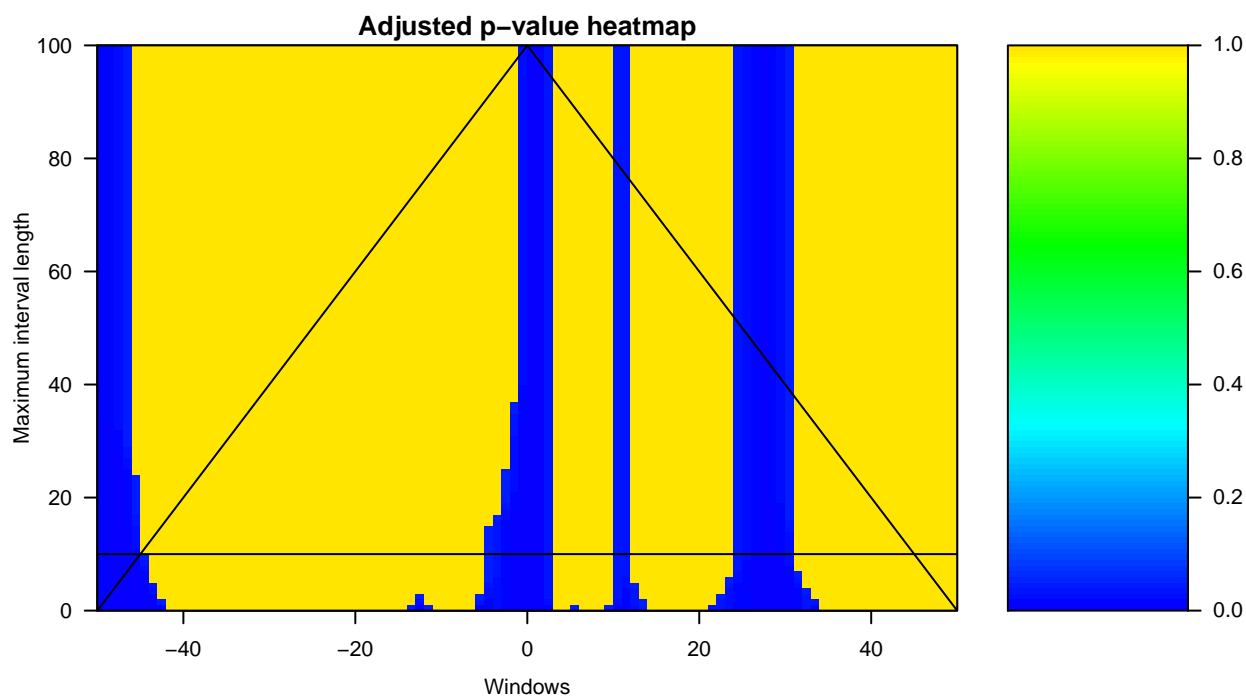
Control



# Replication origin



# Sex-averaged recombination hotspots



Human specific L1

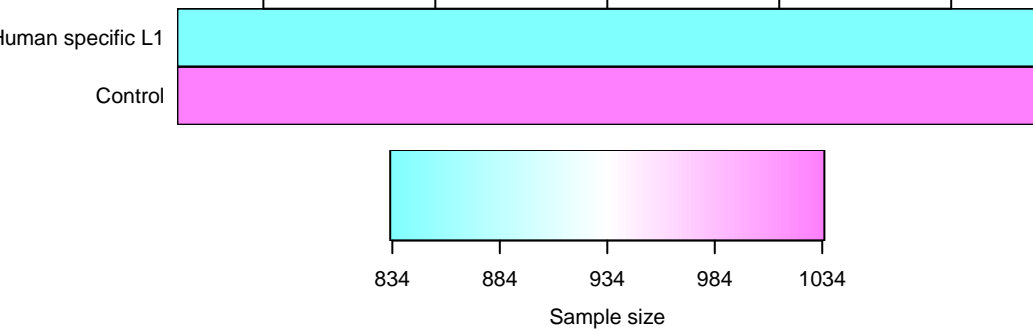
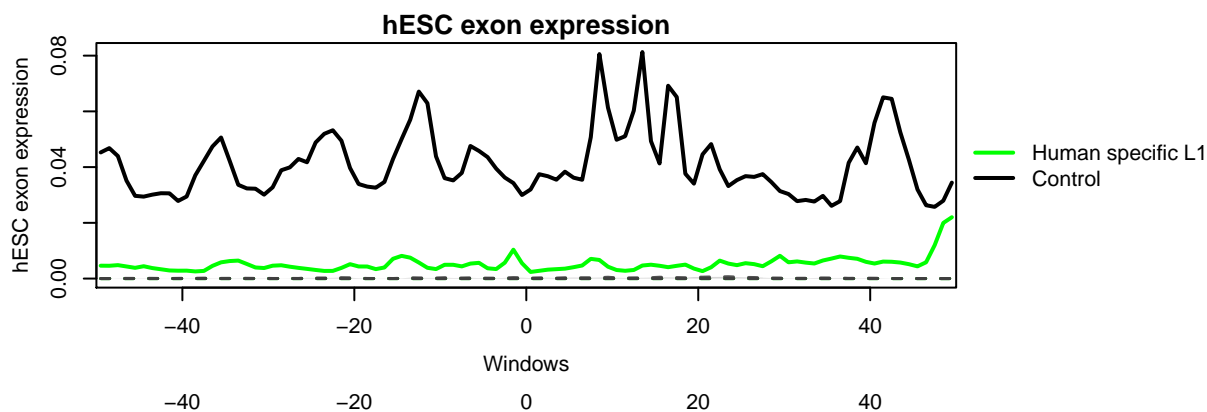
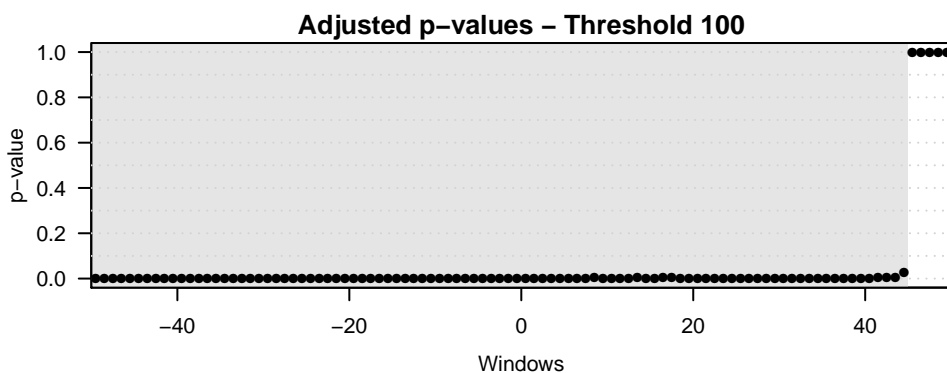
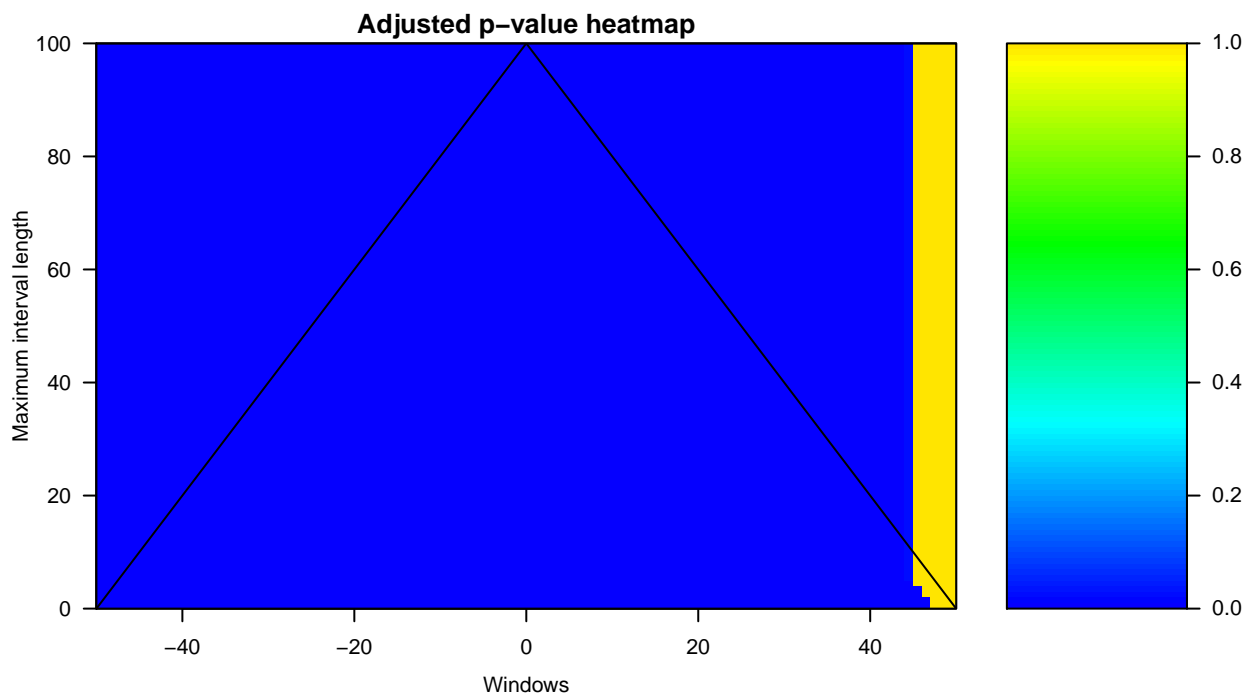
Control



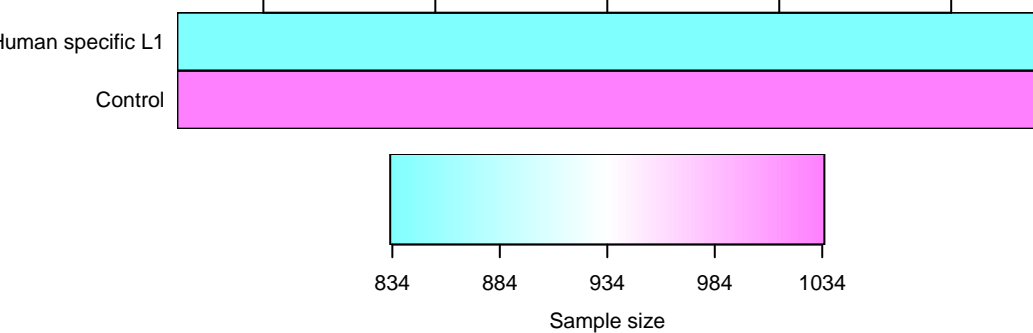
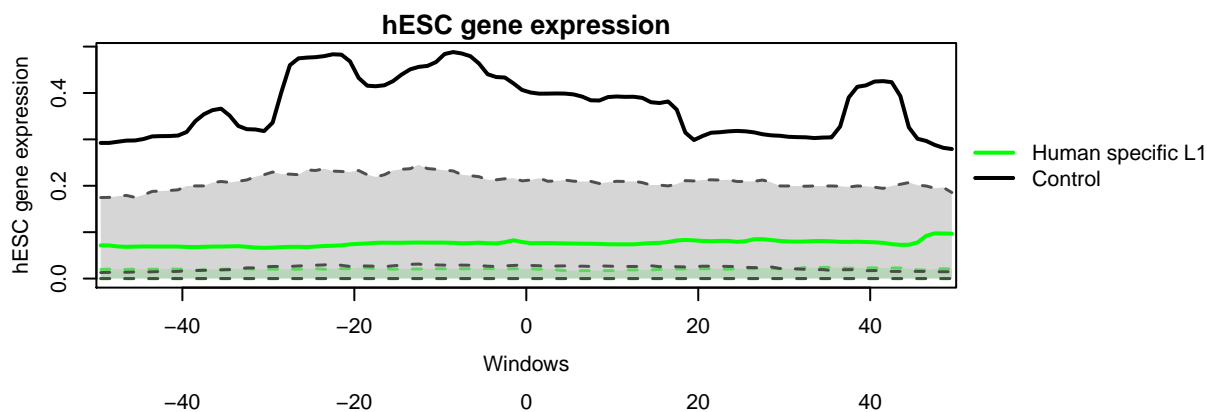
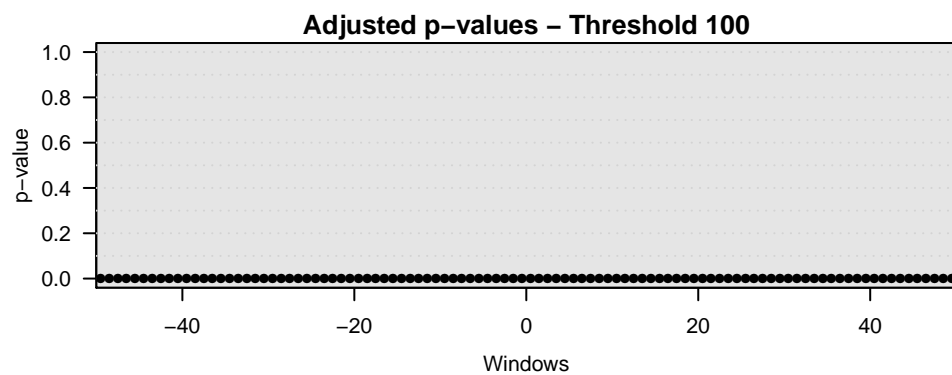
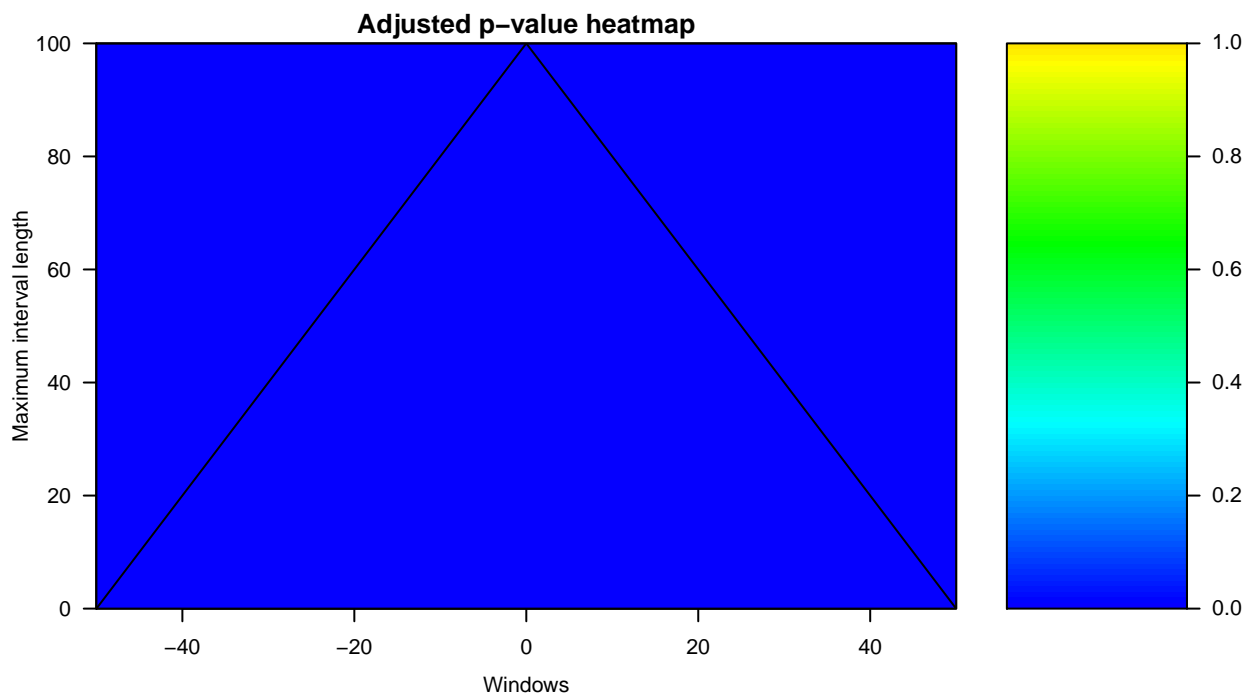
834 884 934 984 1034

Sample size

# hESC exon expression

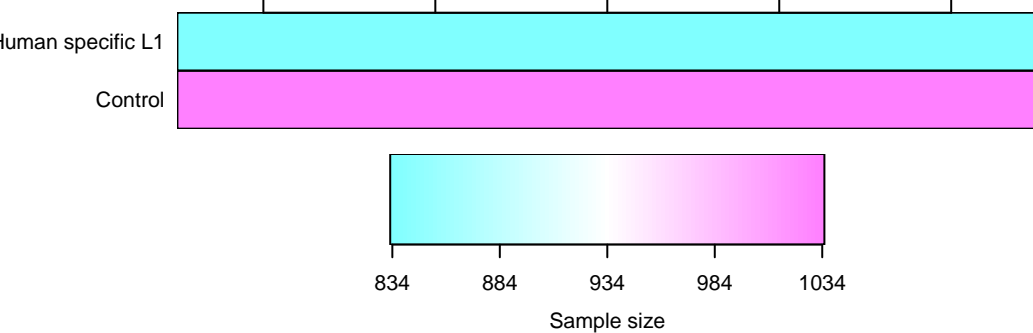
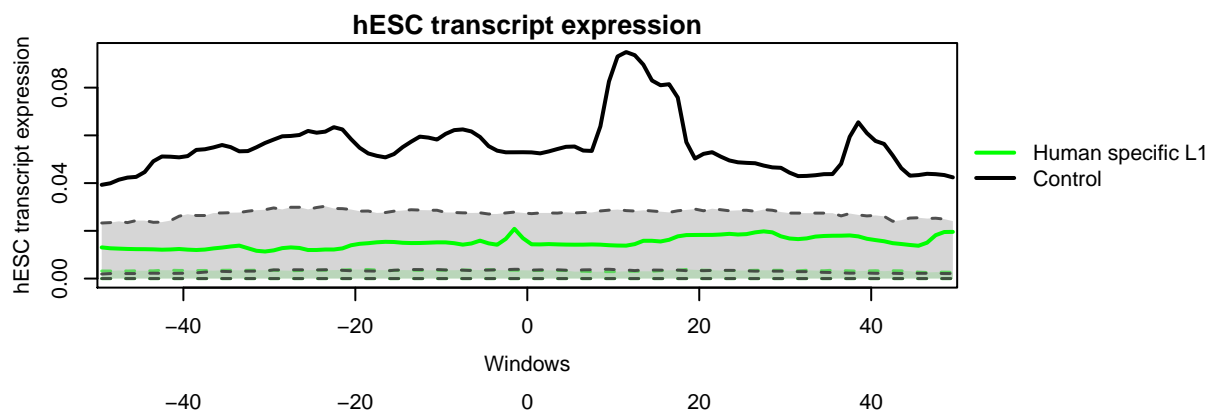
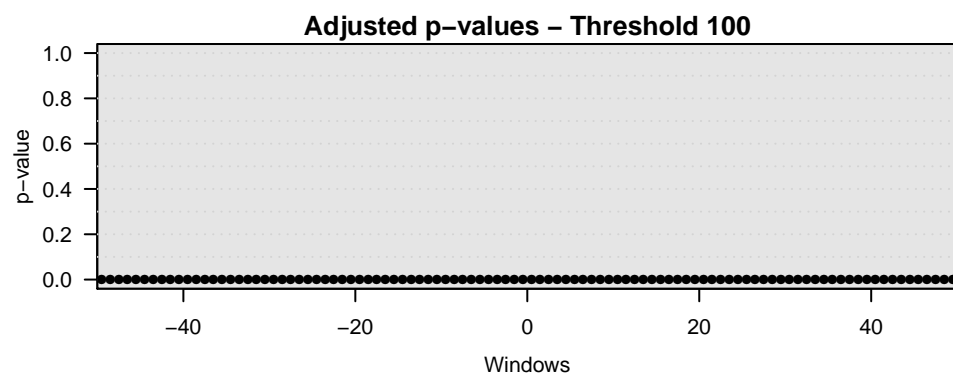
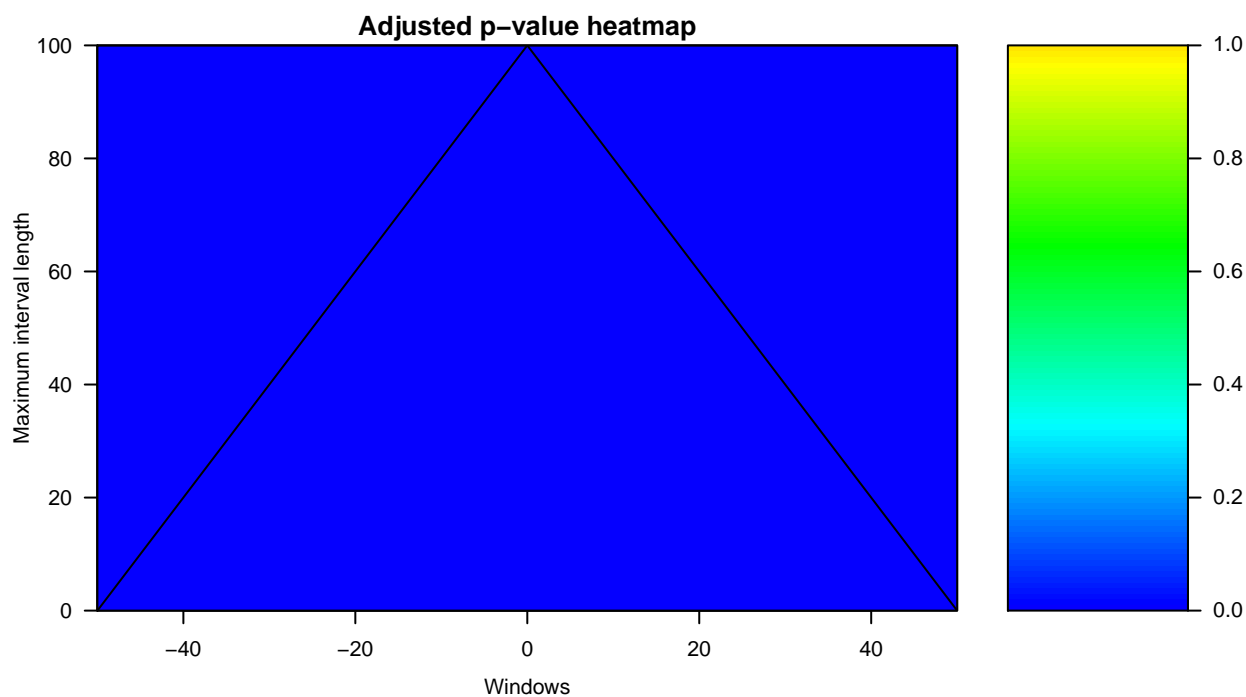


# hESC gene expression

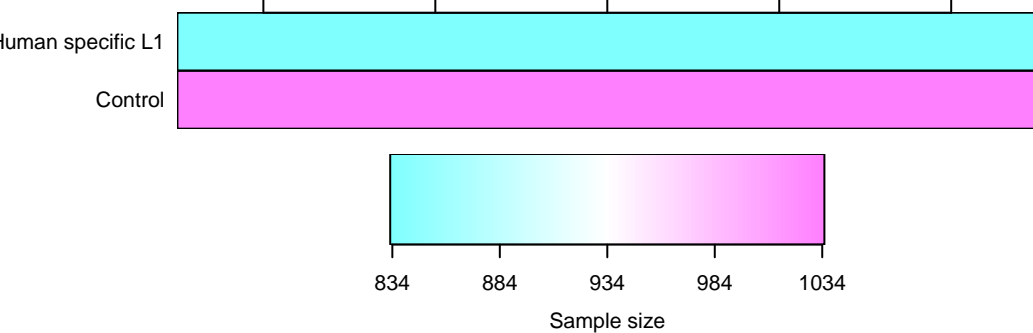
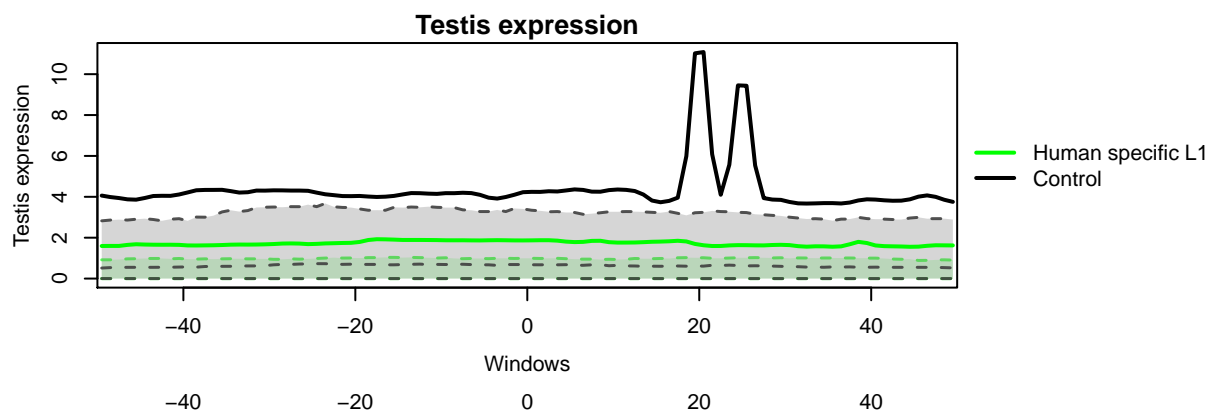
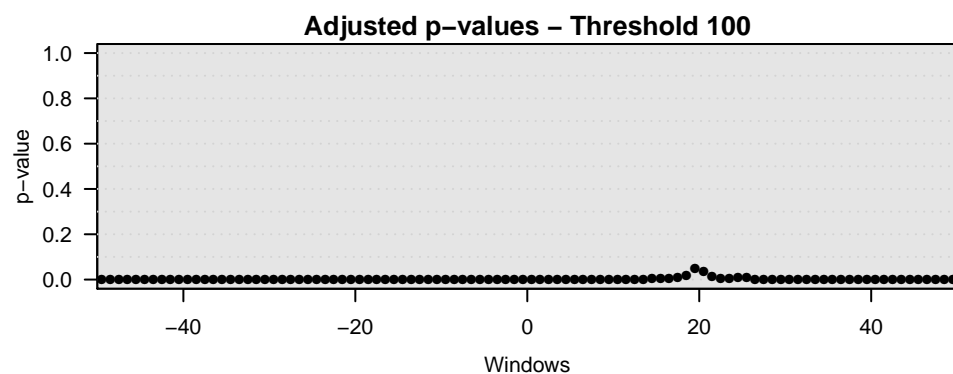
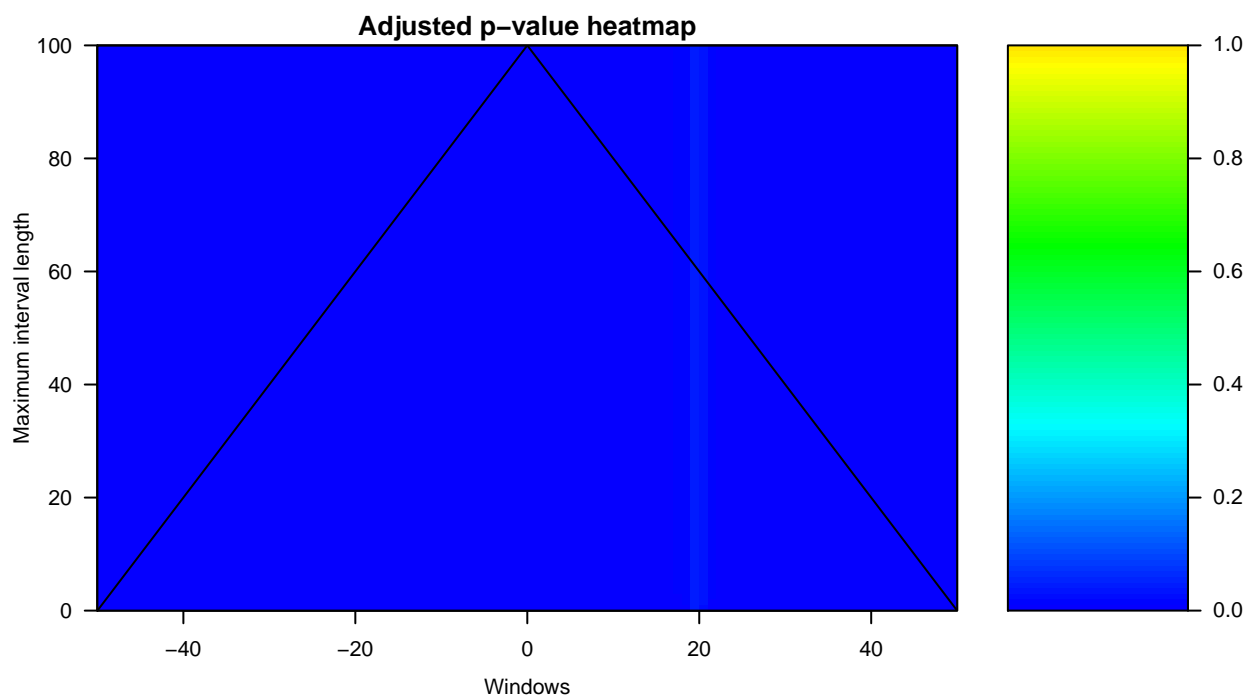




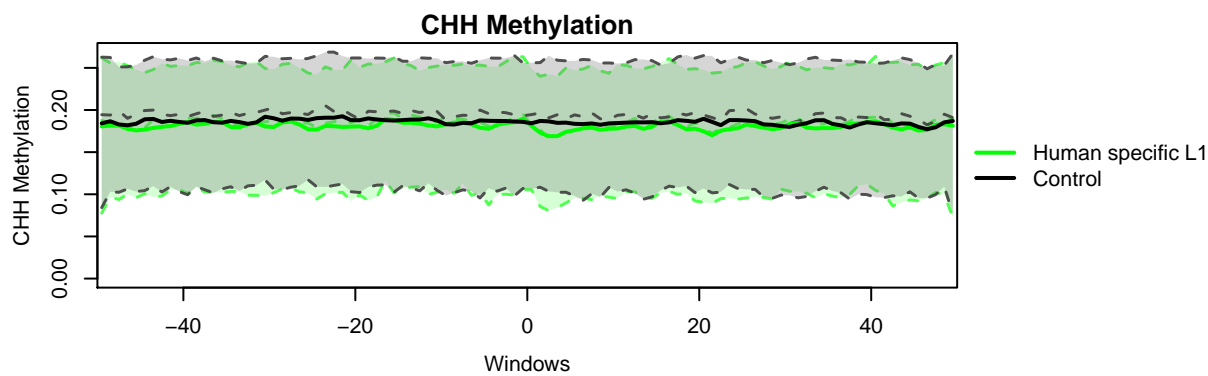
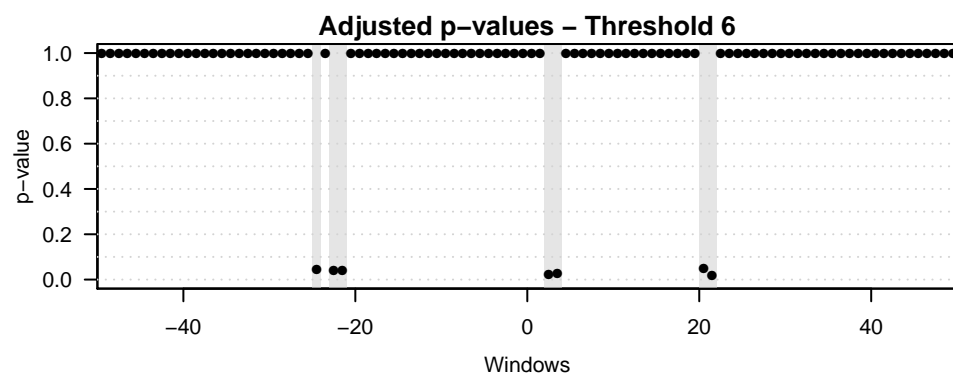
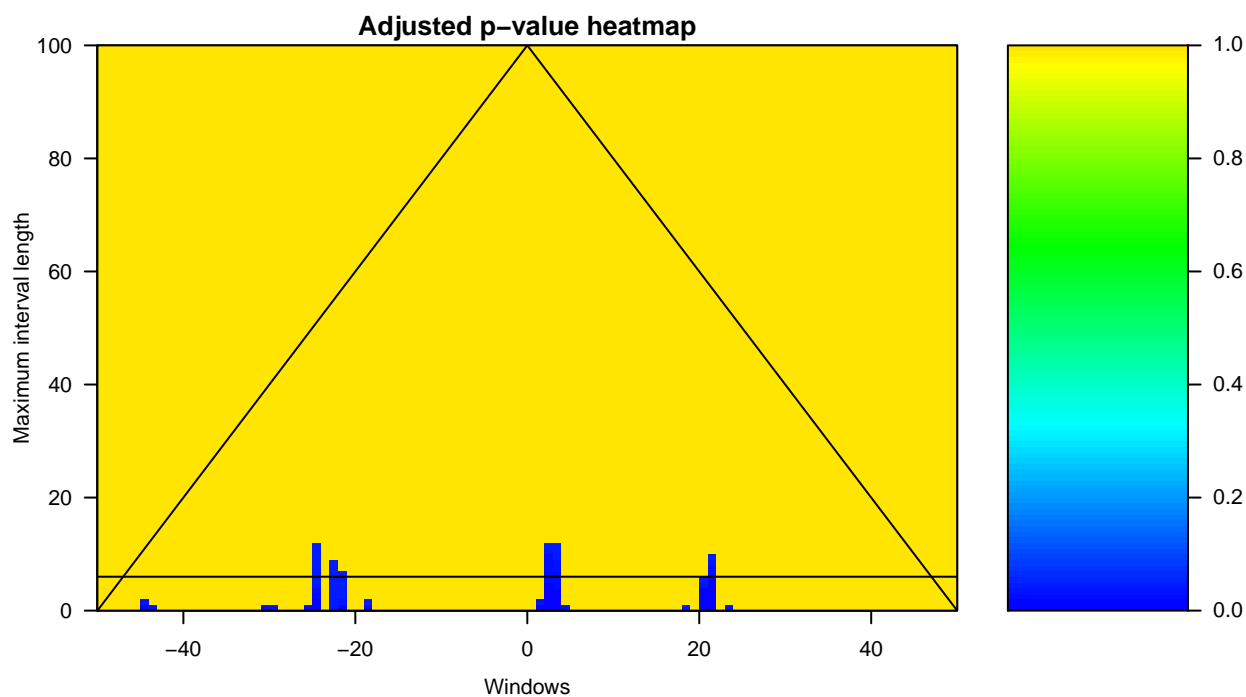
# hESC transcript expression



# Testis expression

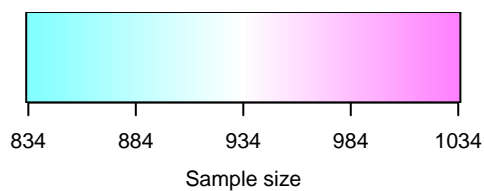


# CHH Methylation

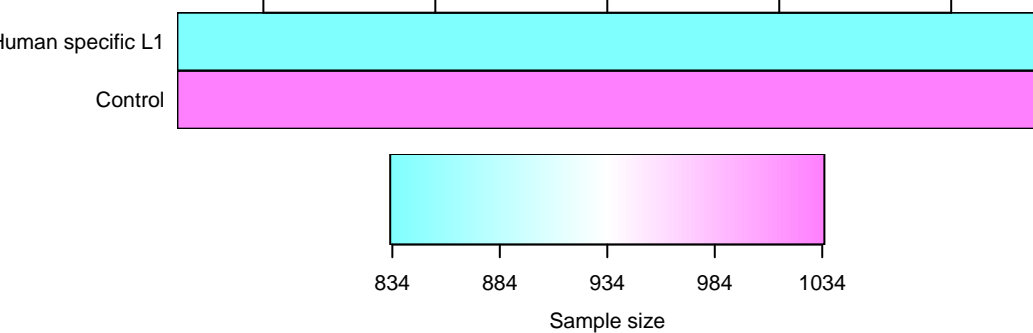
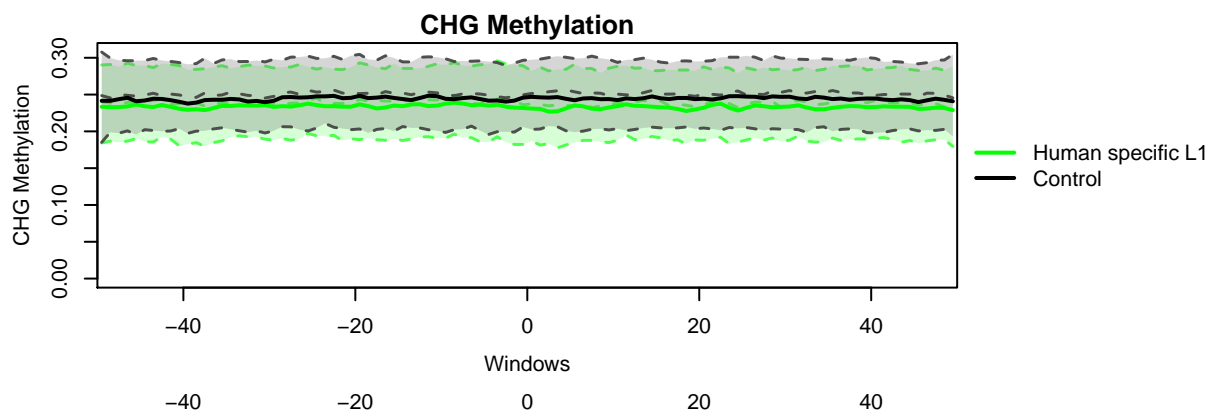
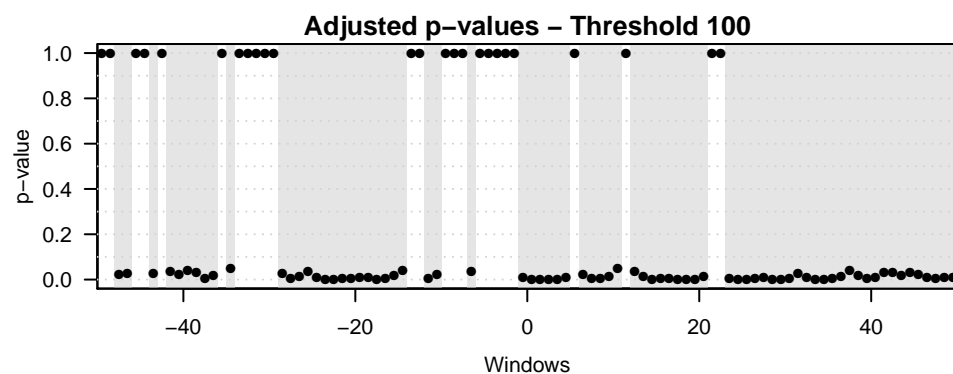
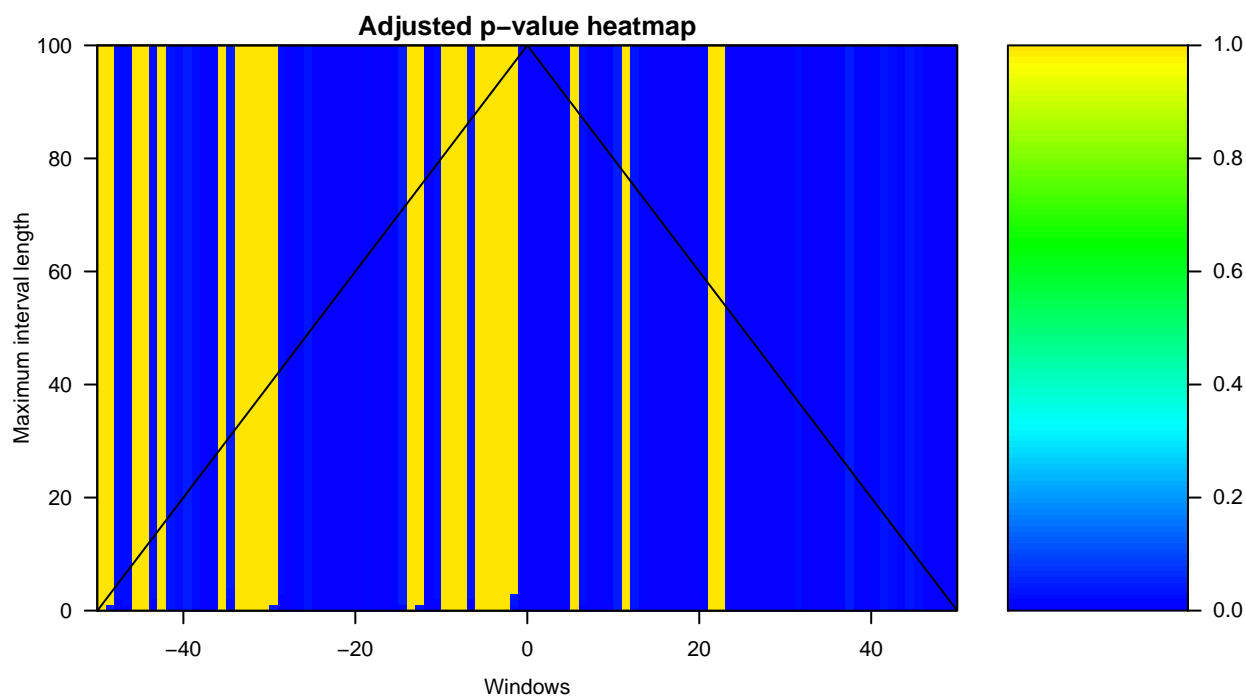


Human specific L1

Control



# CHG Methylation



# CPG Methylation

