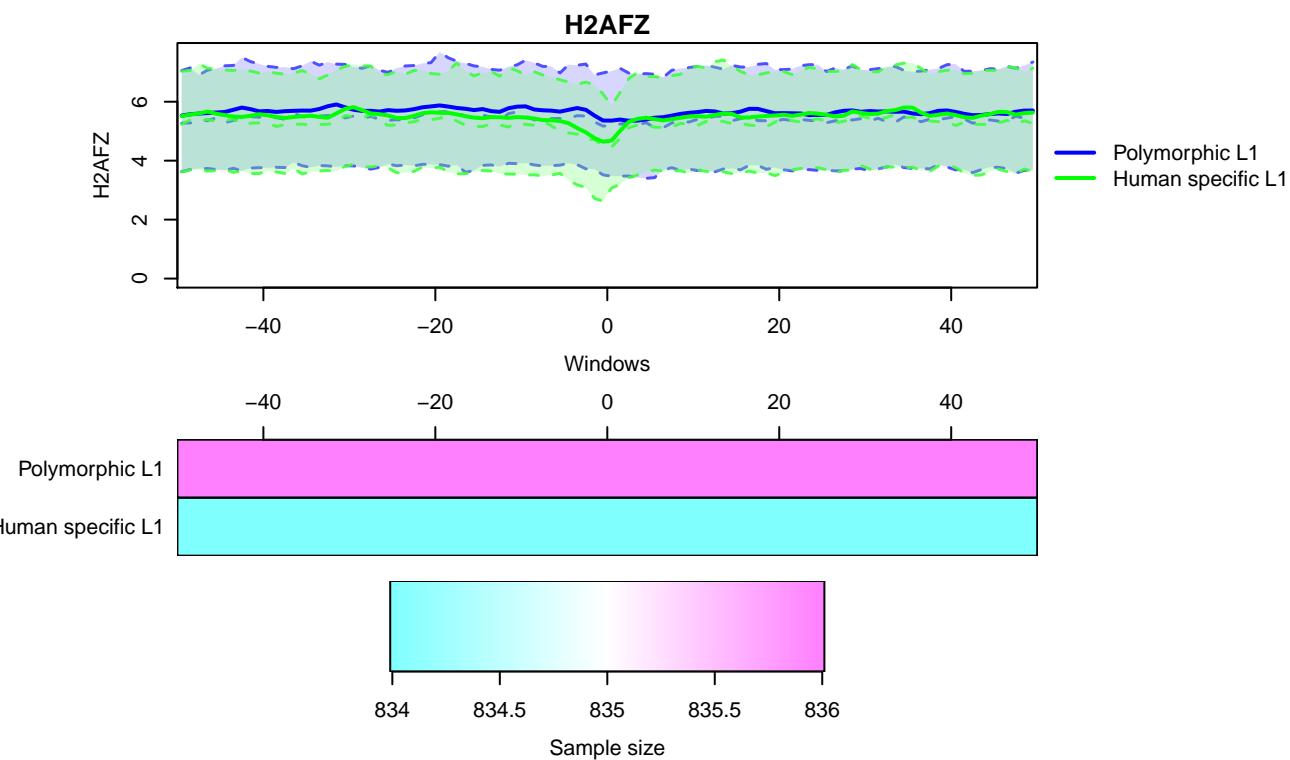
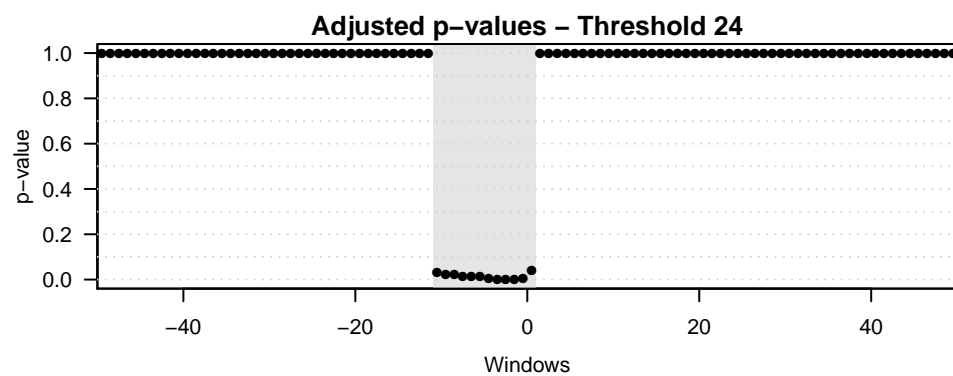
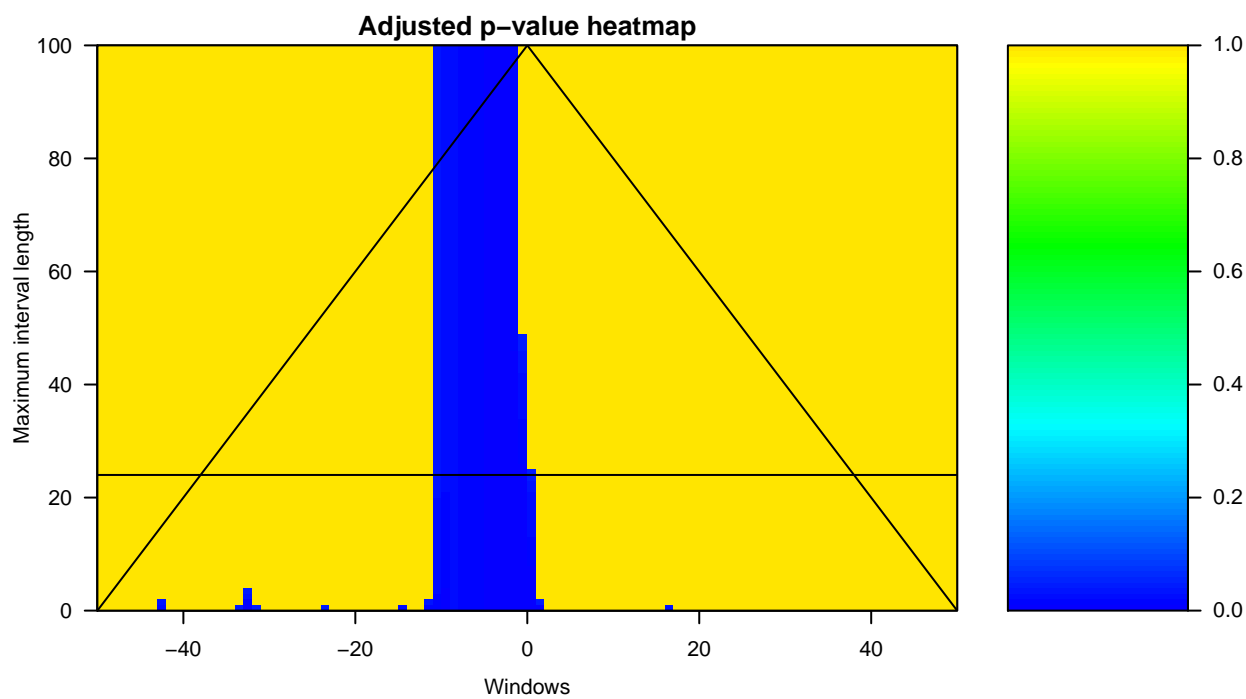
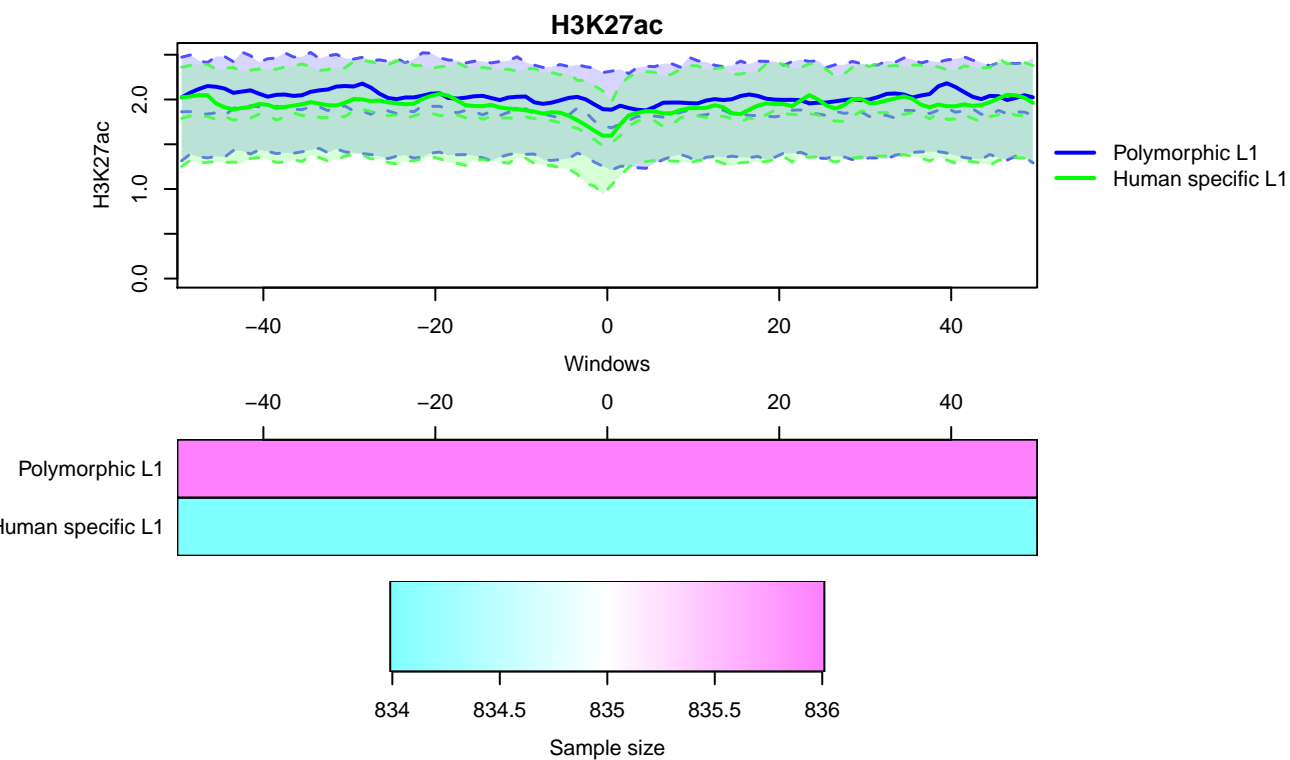
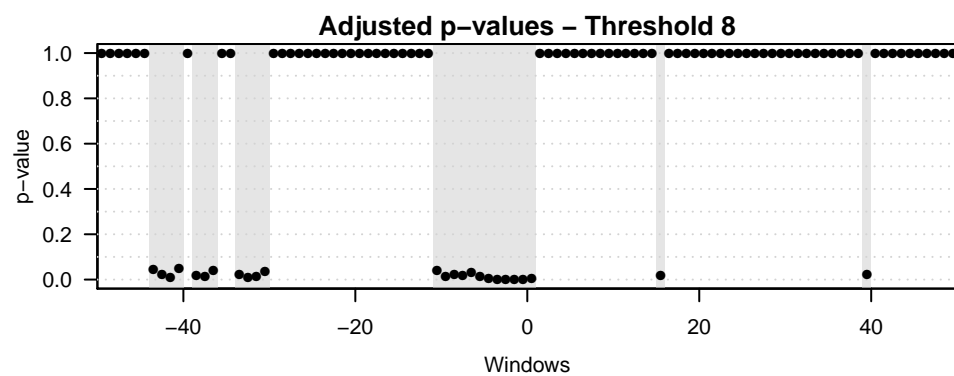
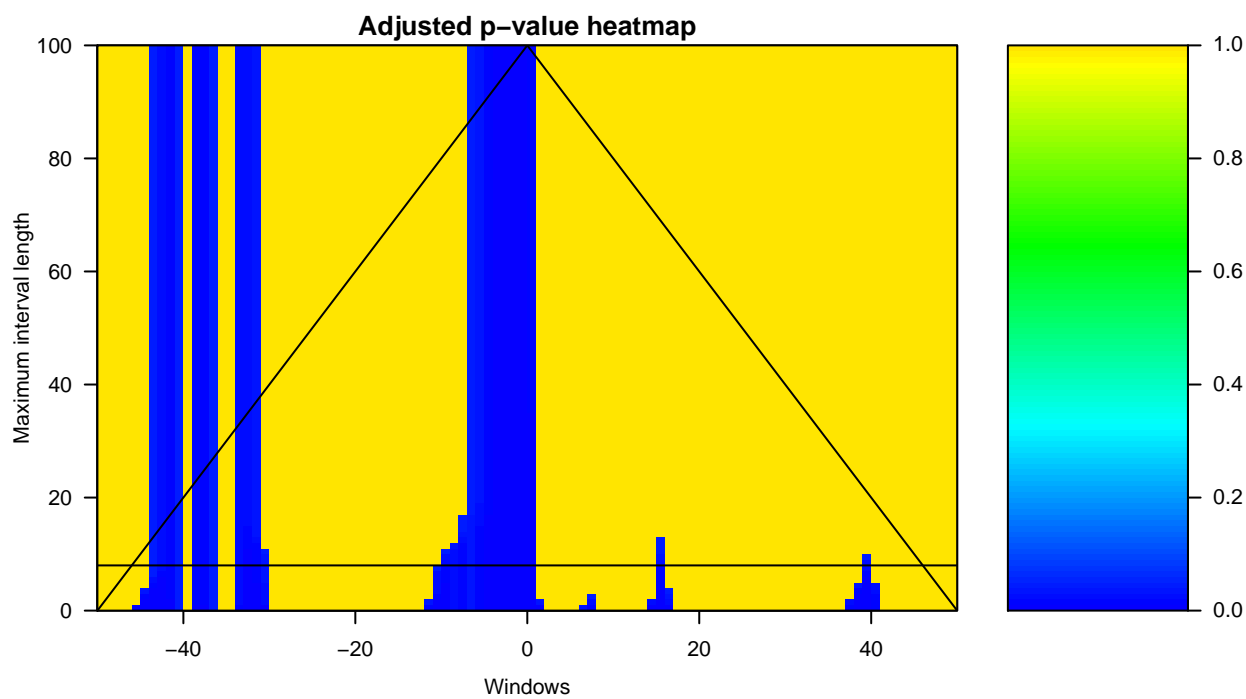


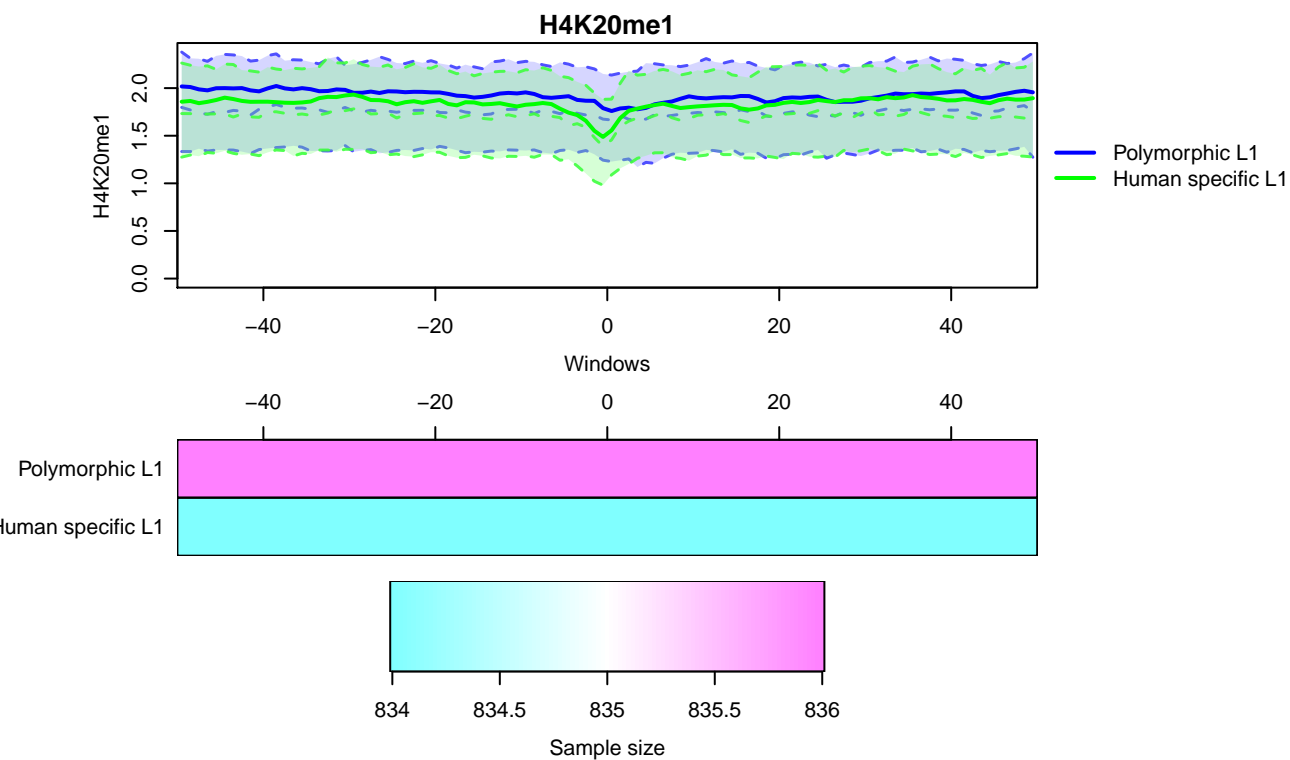
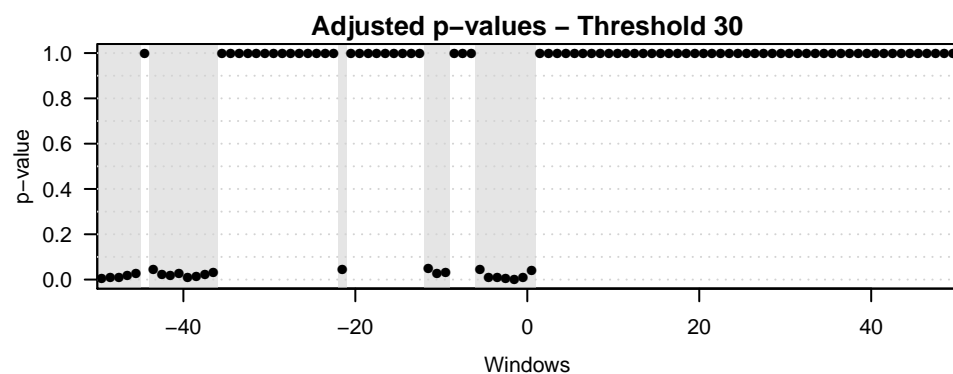
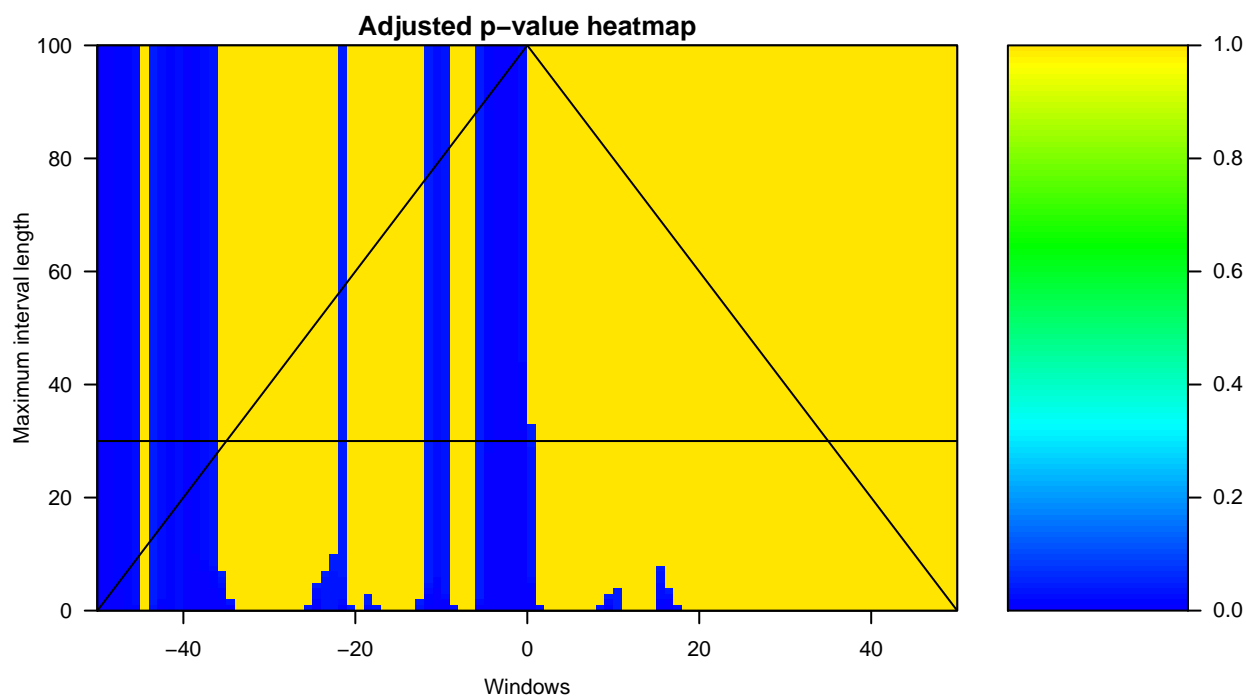
## H2AFZ



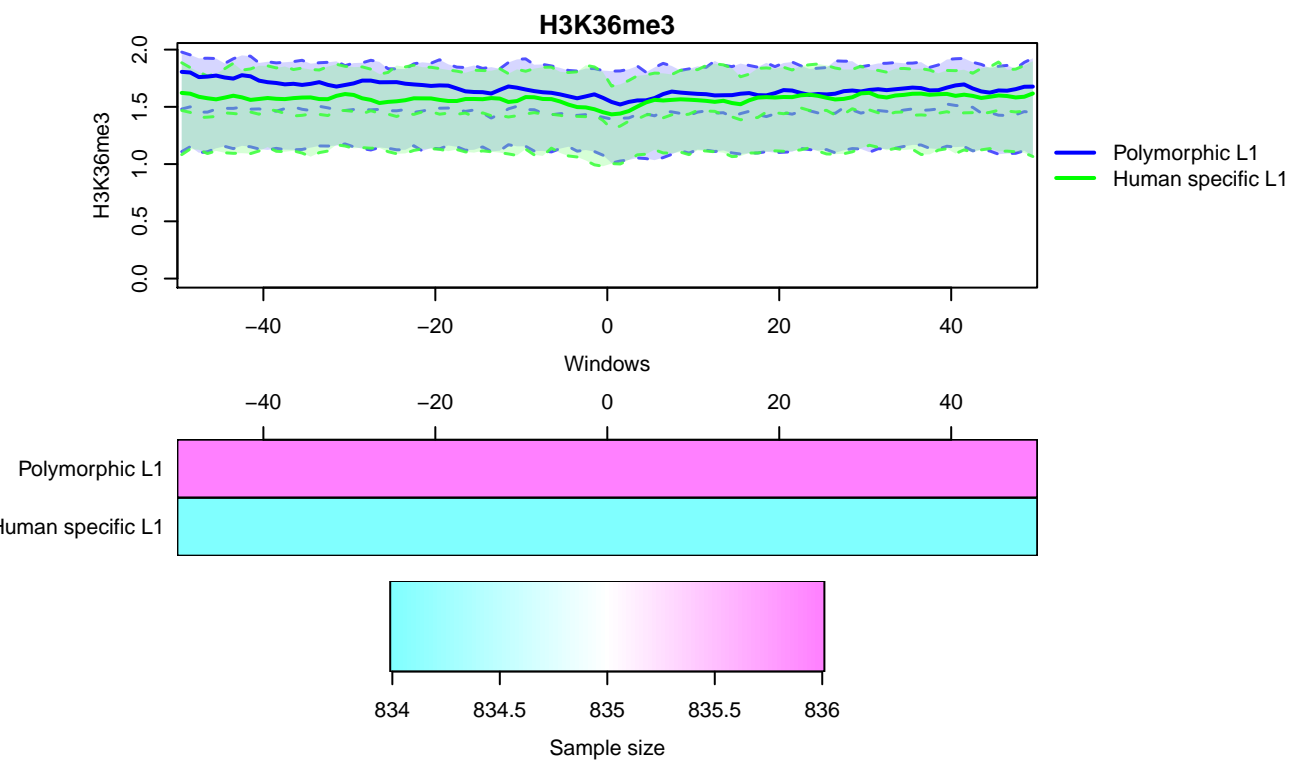
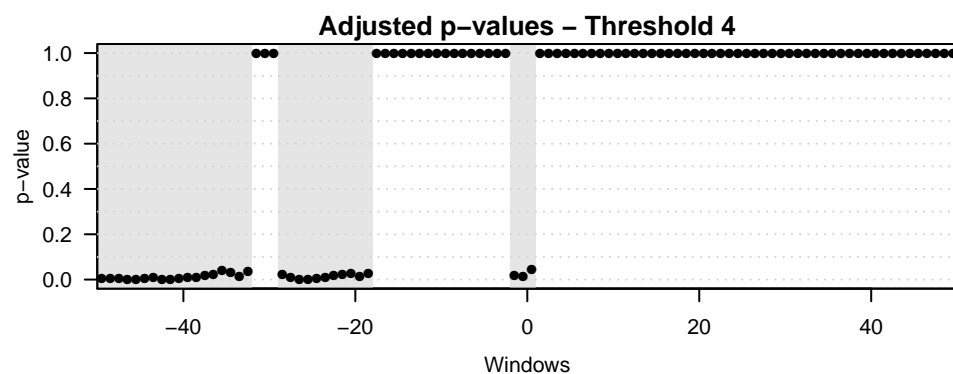
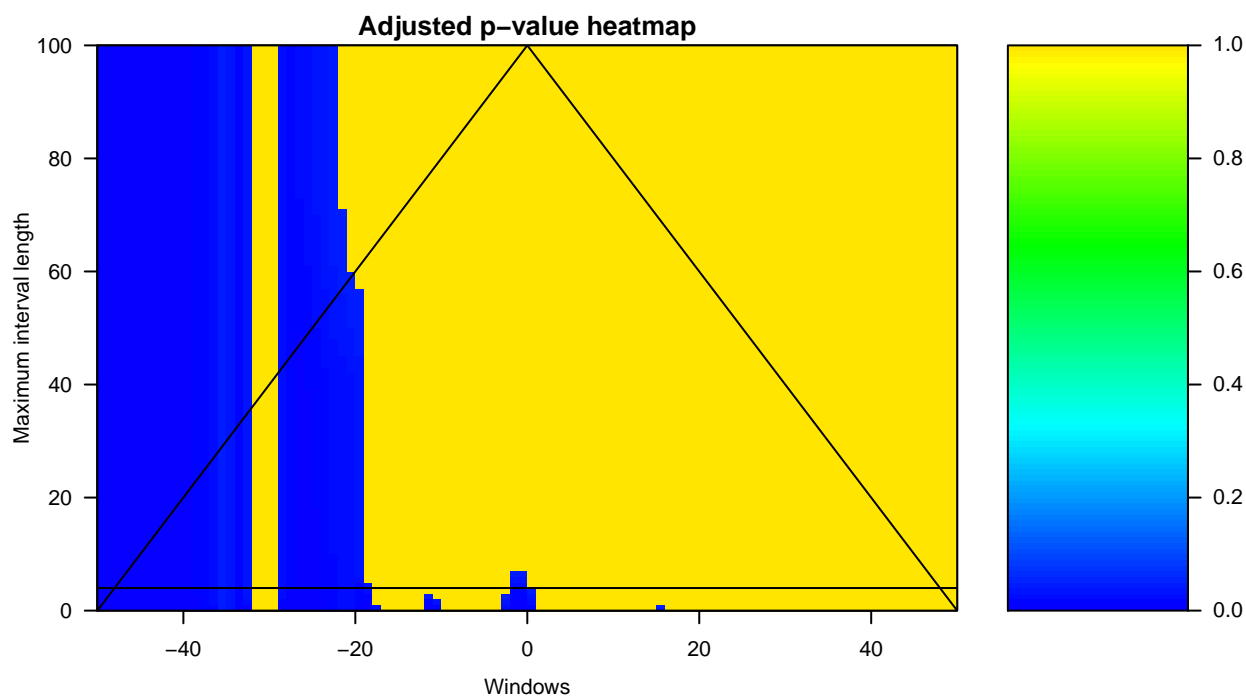
# H3K27ac



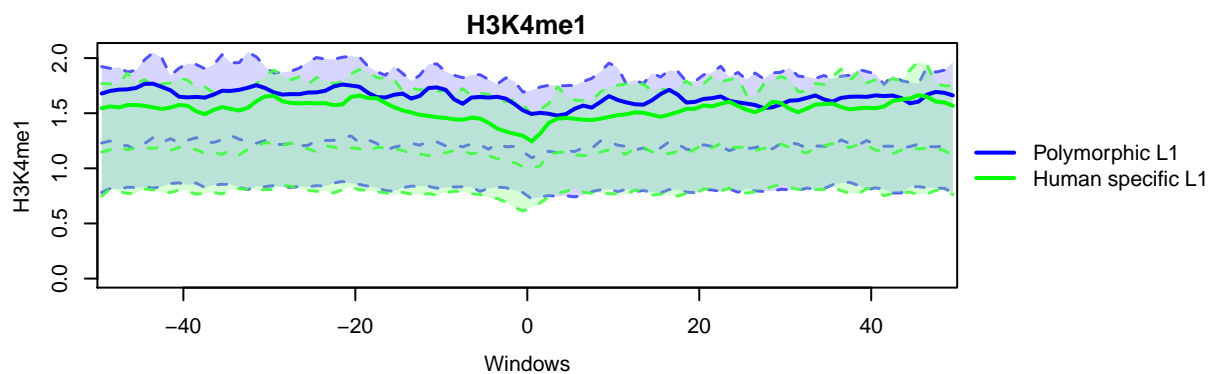
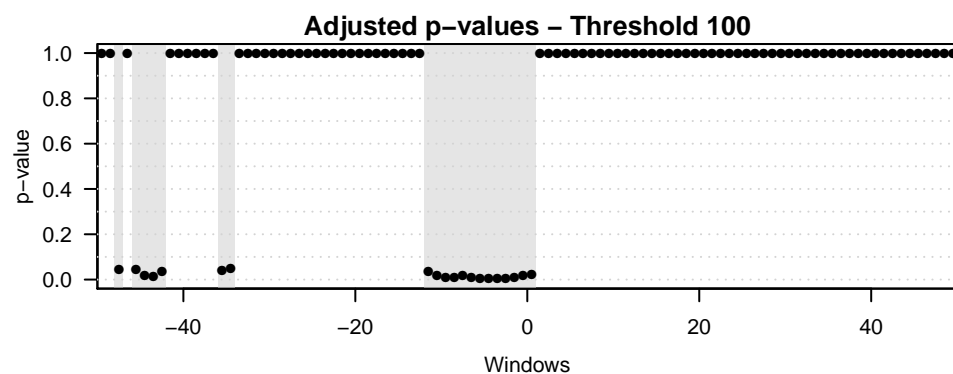
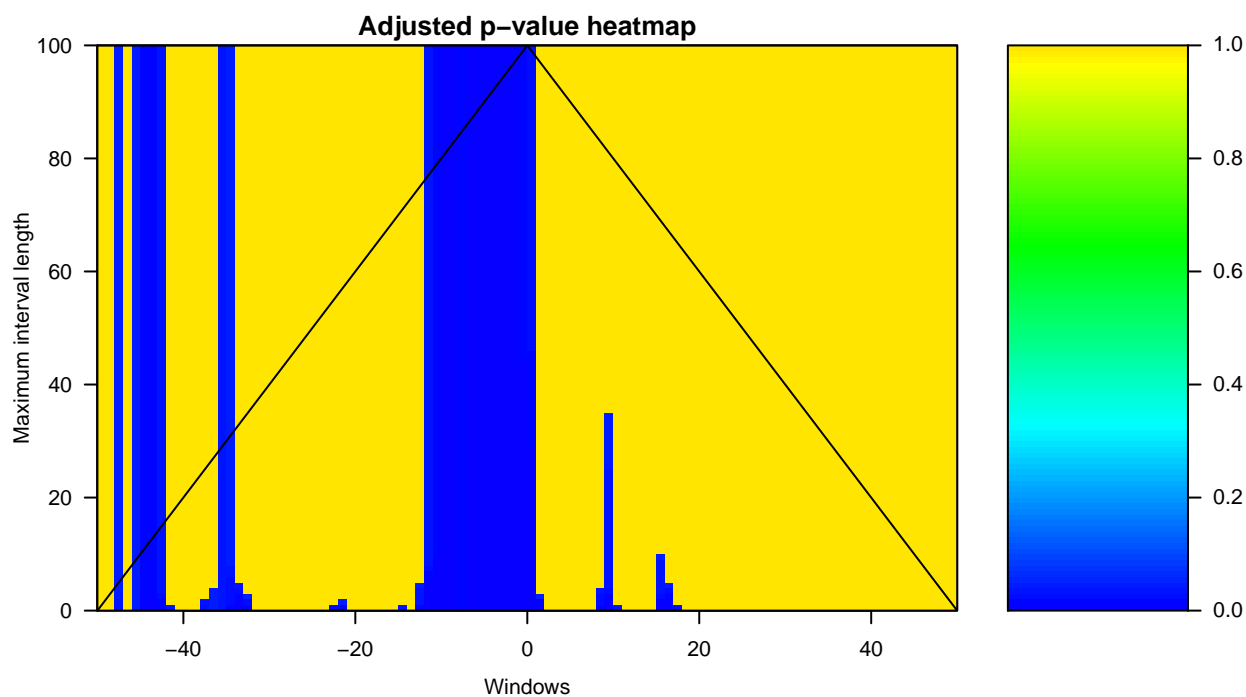
# H4K20me1



# H3K36me3



# H3K4me1



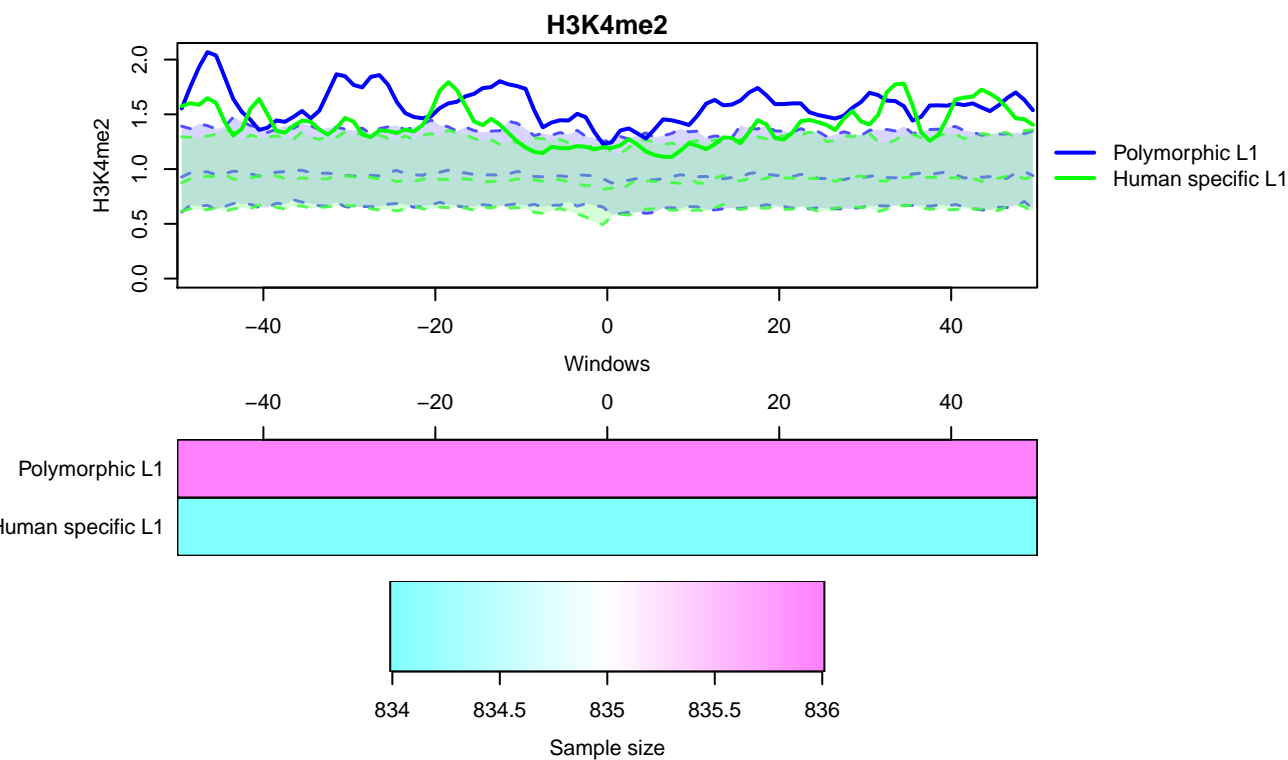
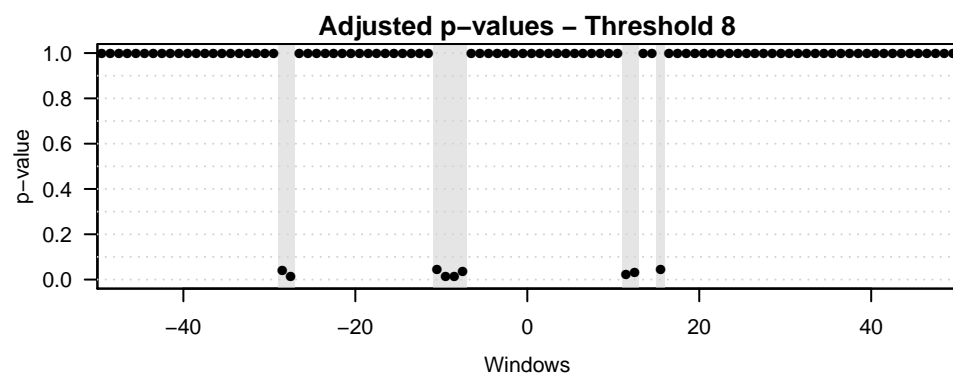
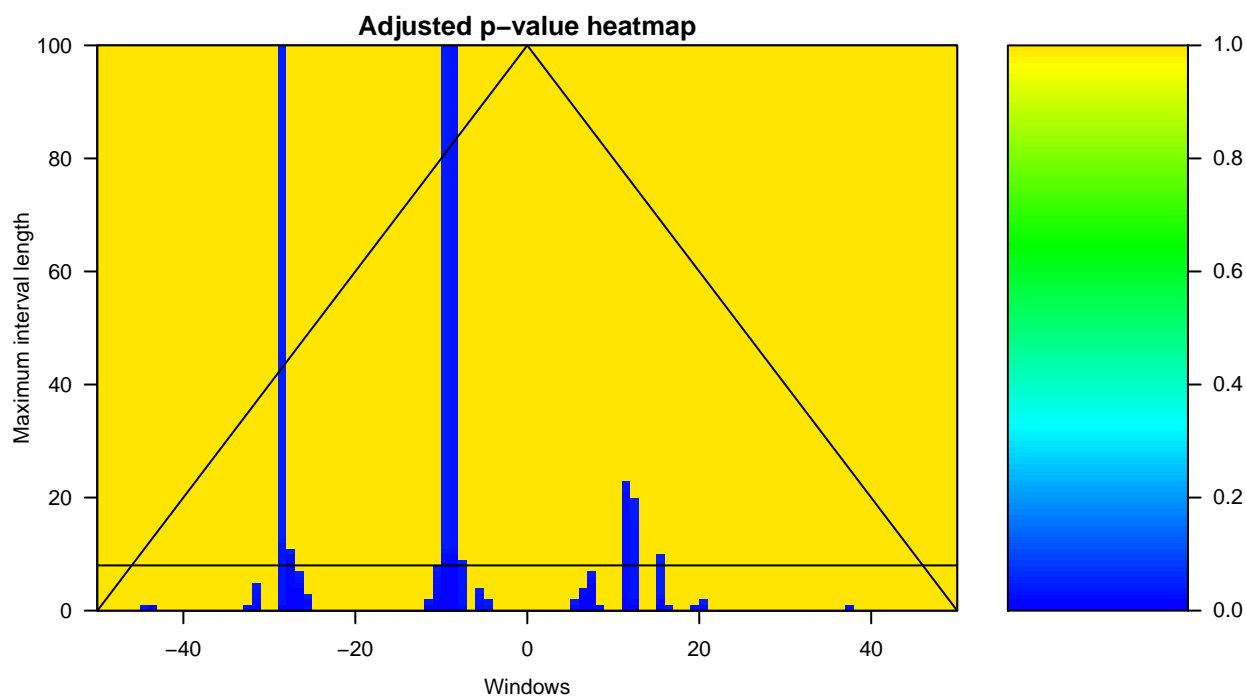
Polymorphic L1

Human specific L1

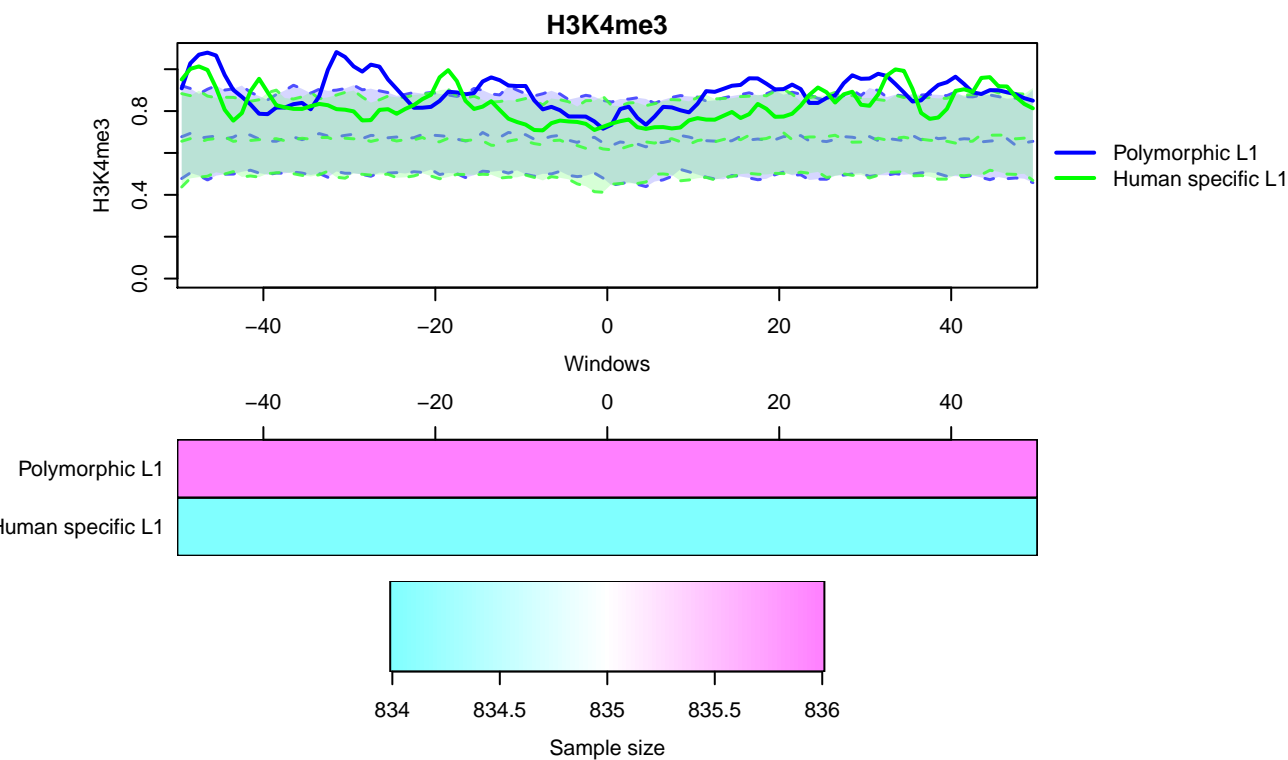
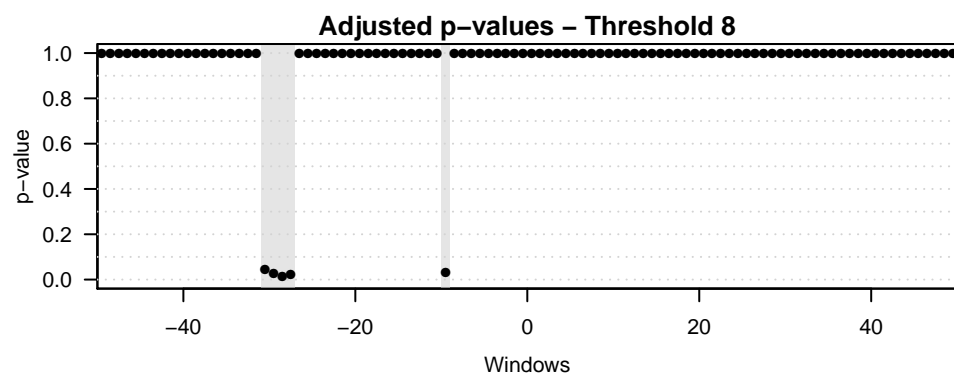
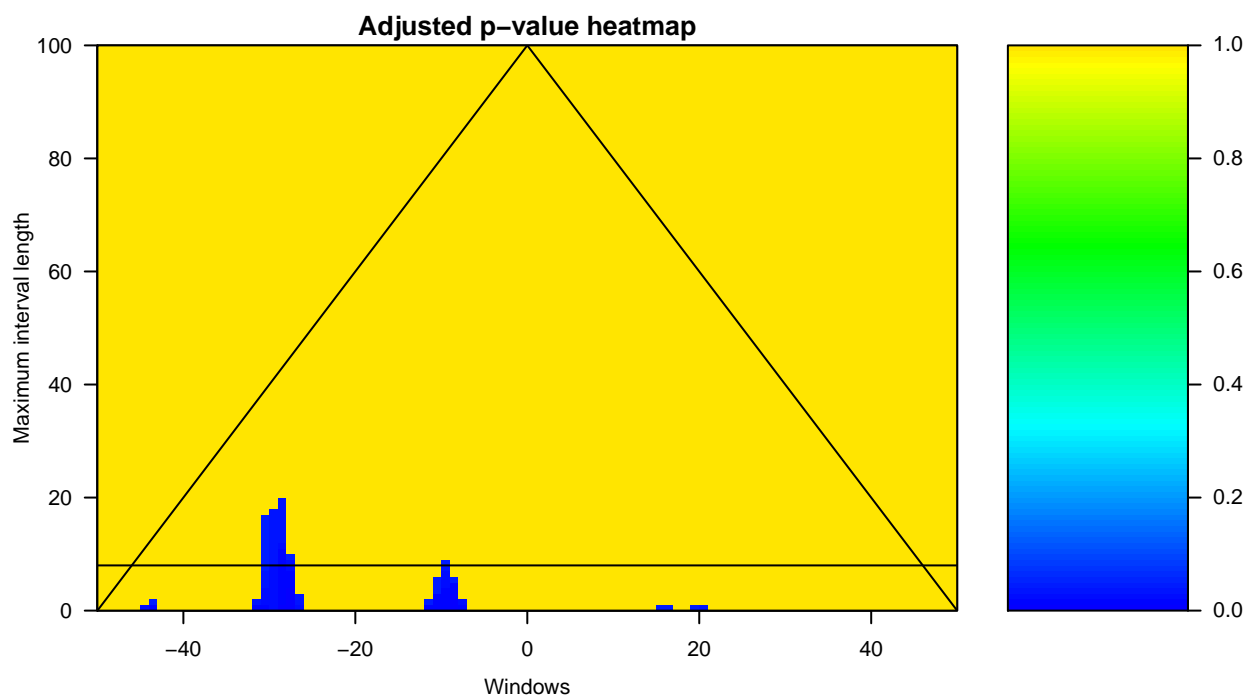
834 834.5 835 835.5 836

Sample size

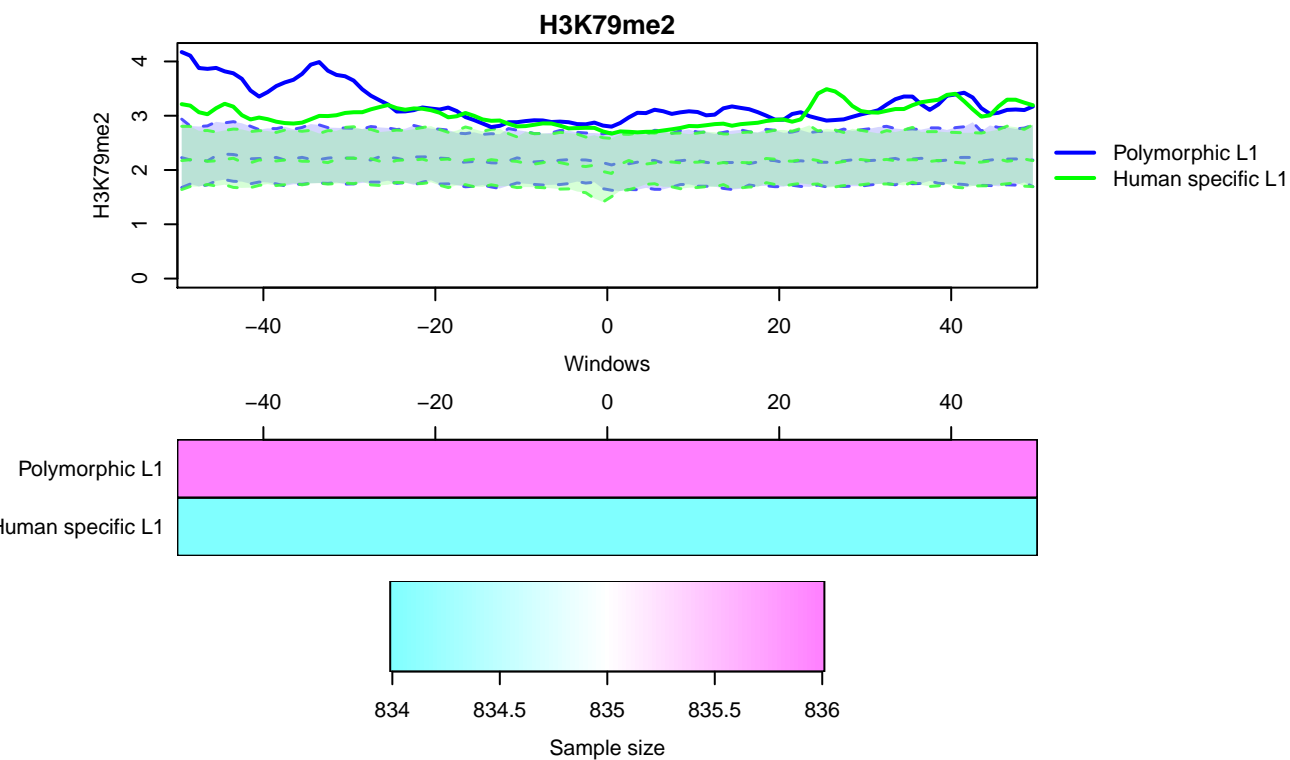
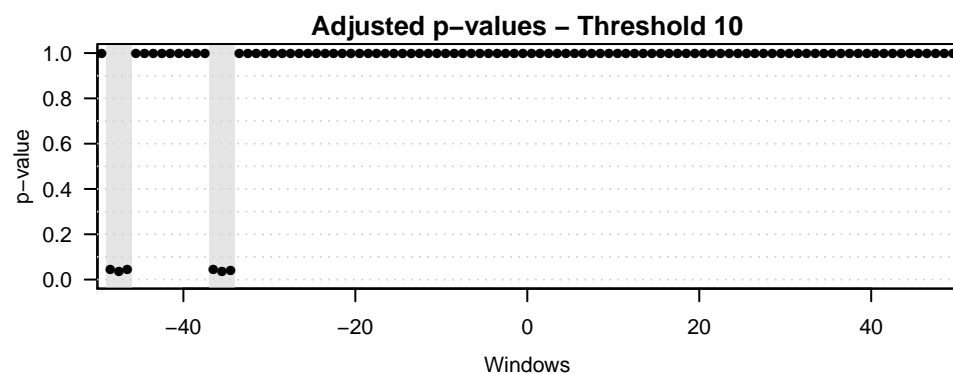
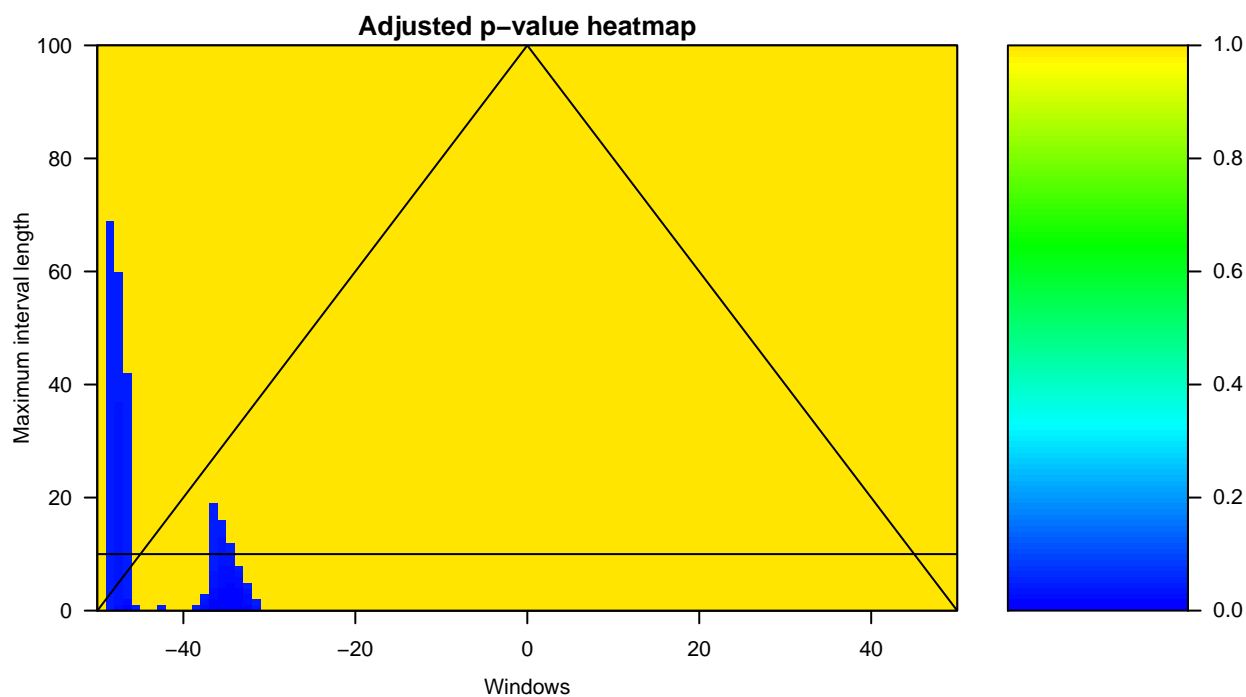
# H3K4me2



# H3K4me3

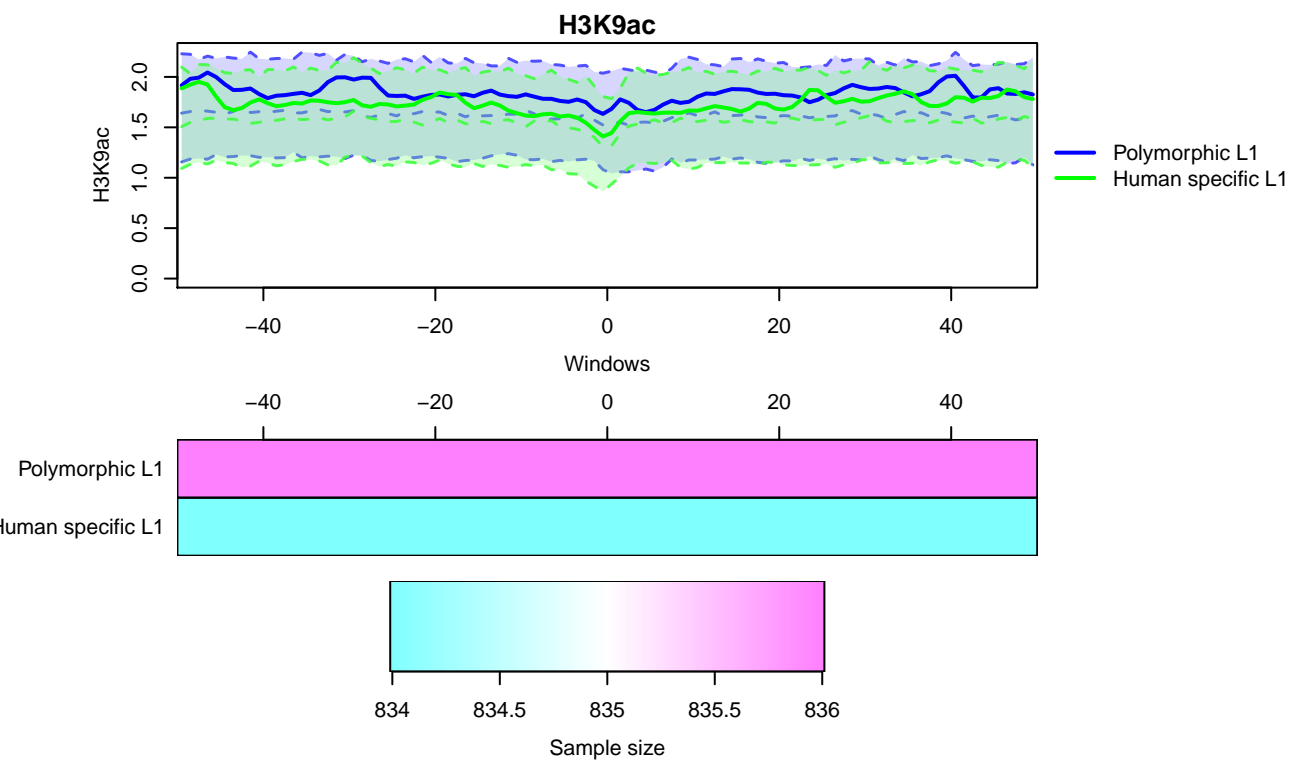
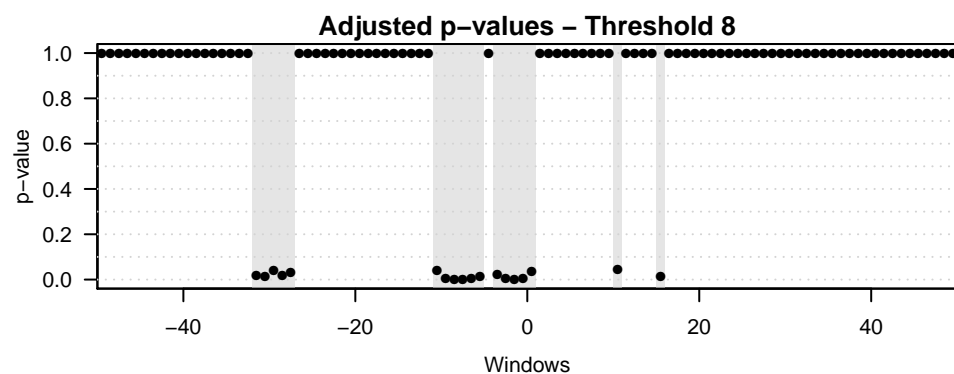
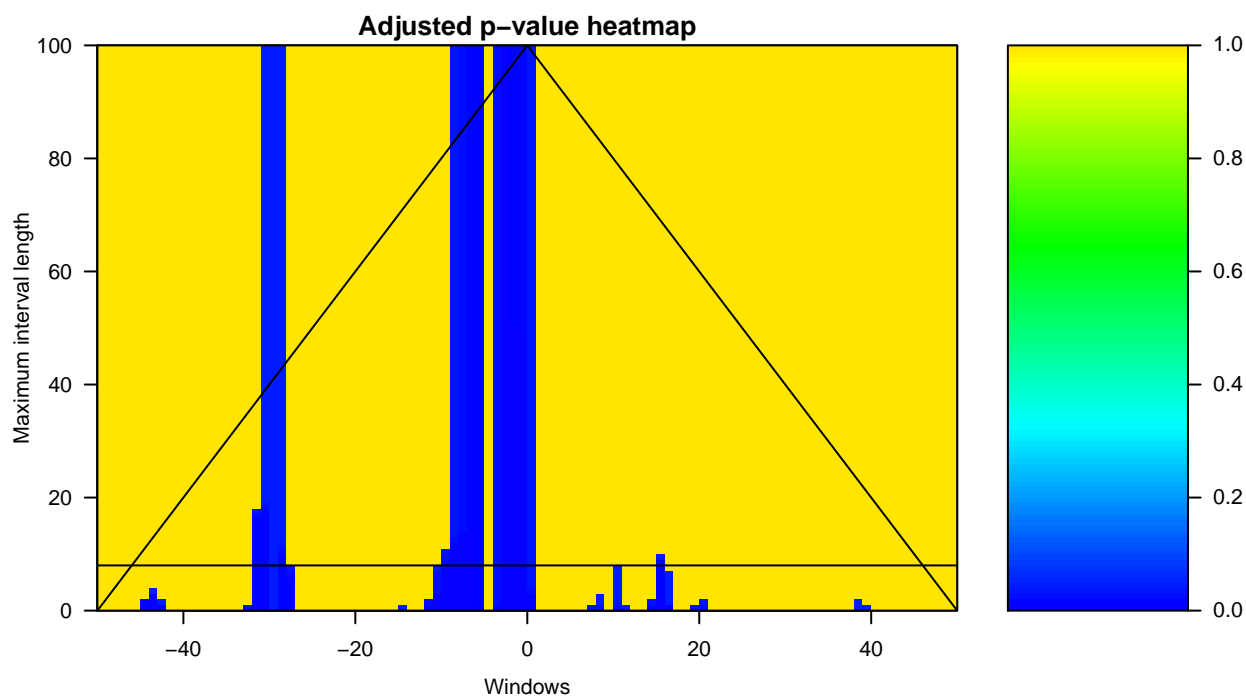


# H3K79me2

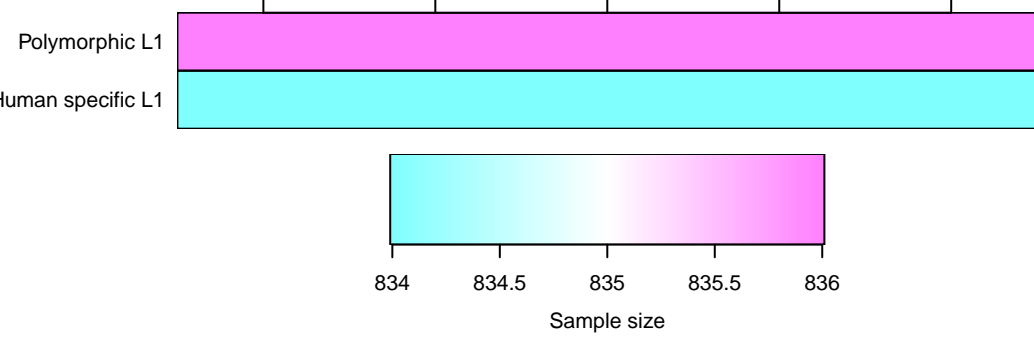
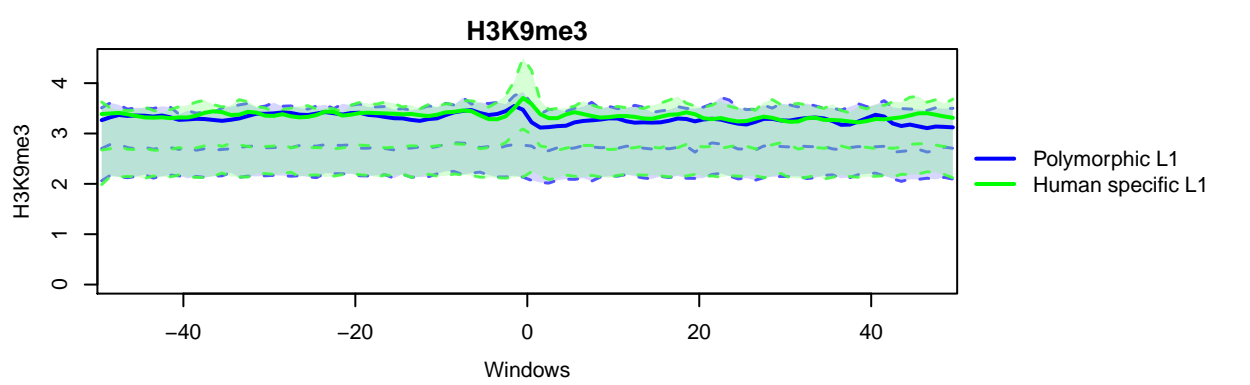
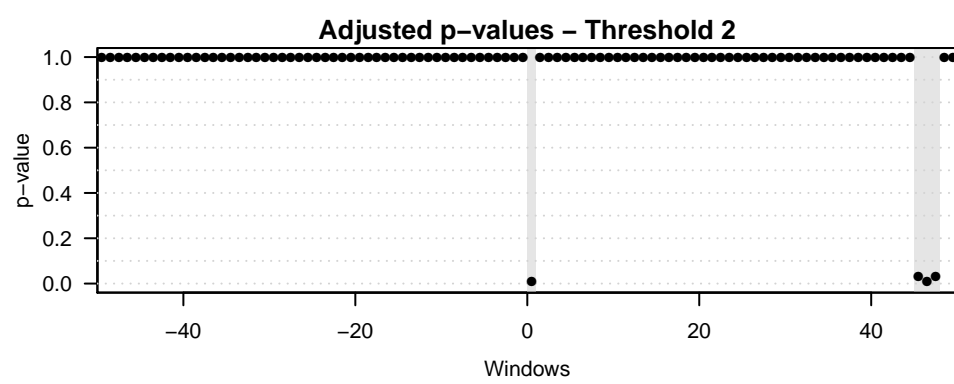
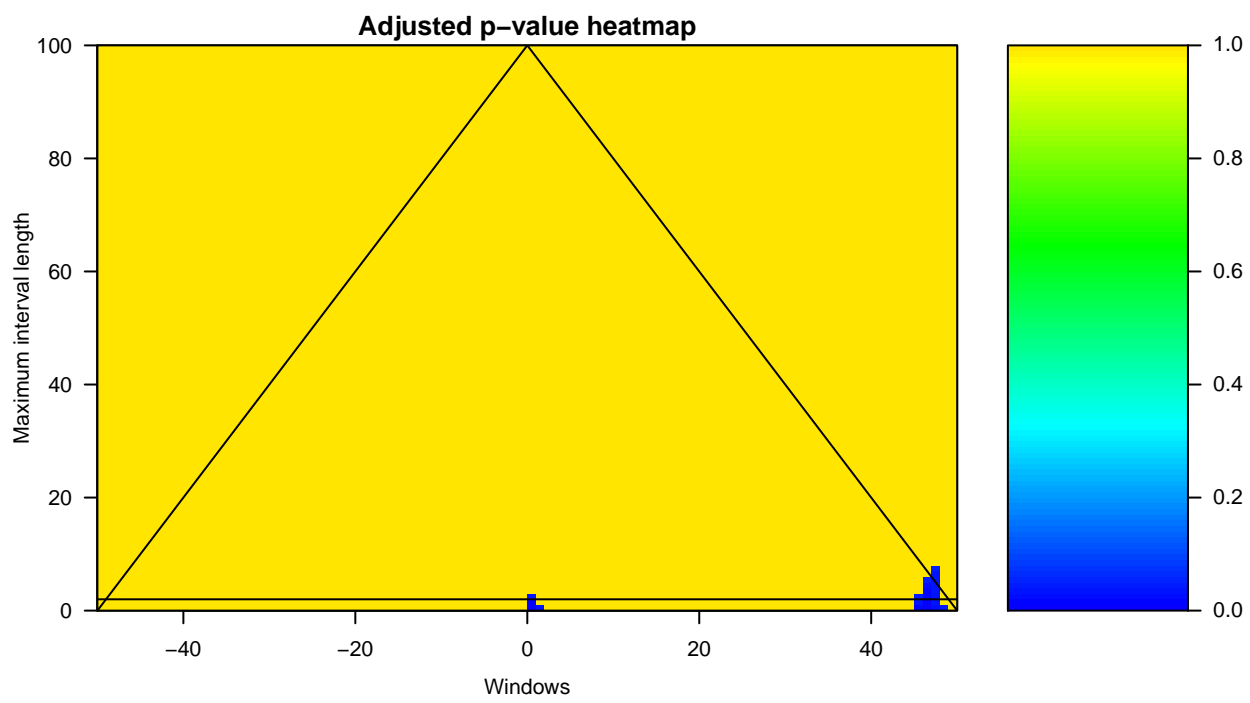




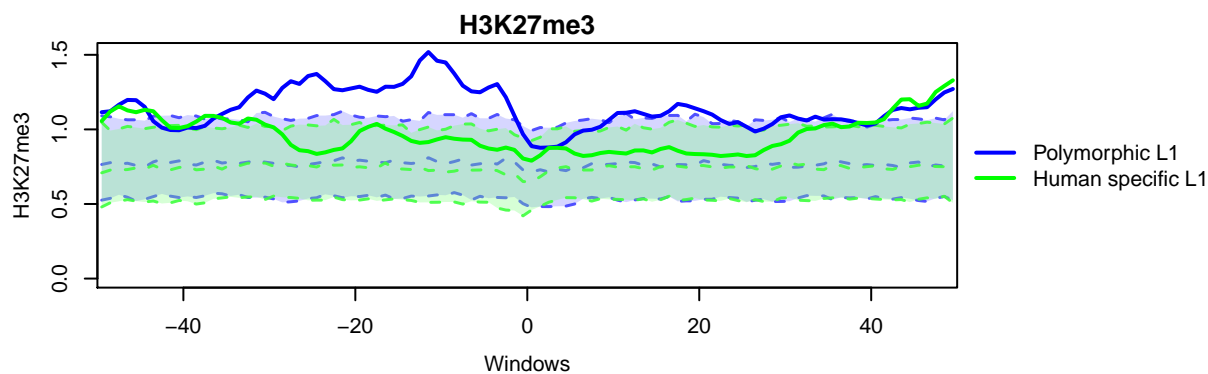
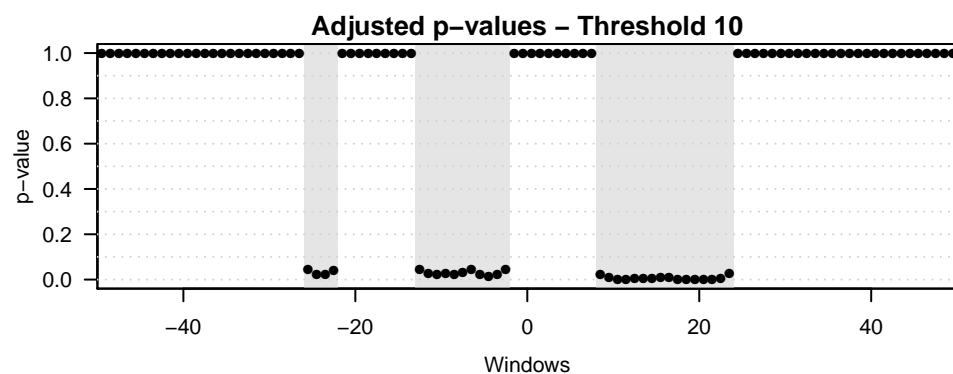
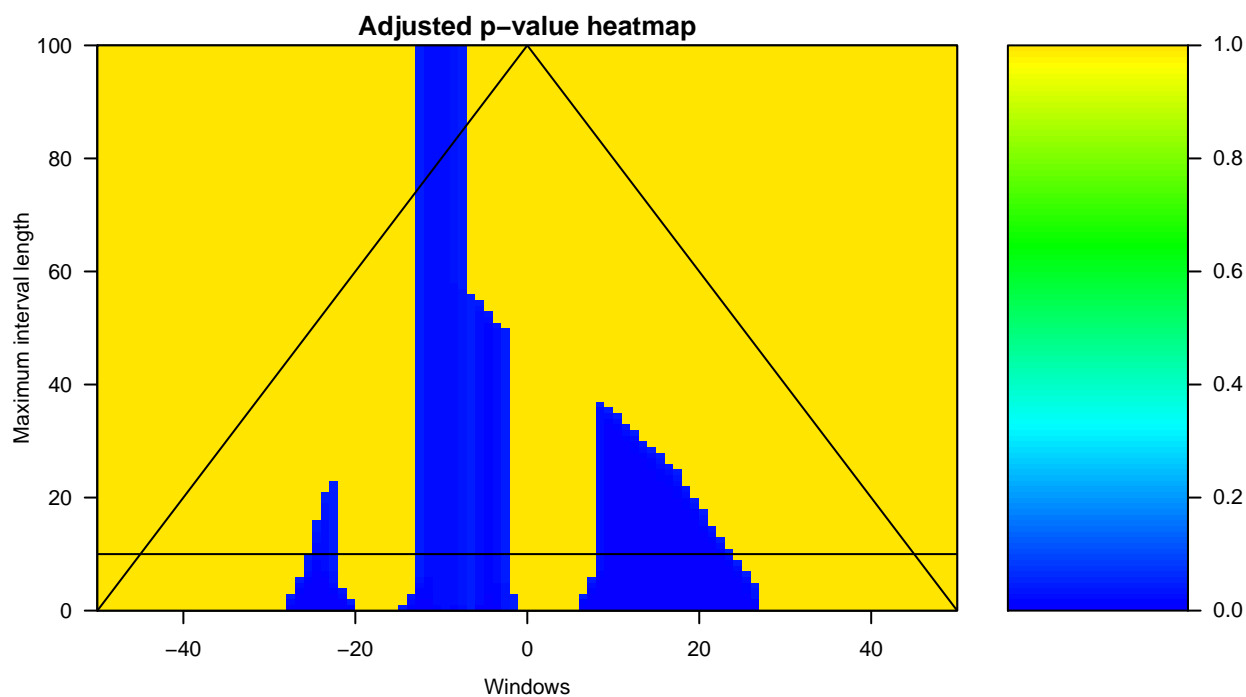
# H3K9ac



# H3K9me3

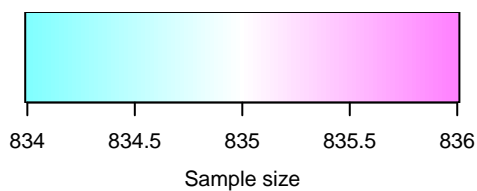


# H3K27me3

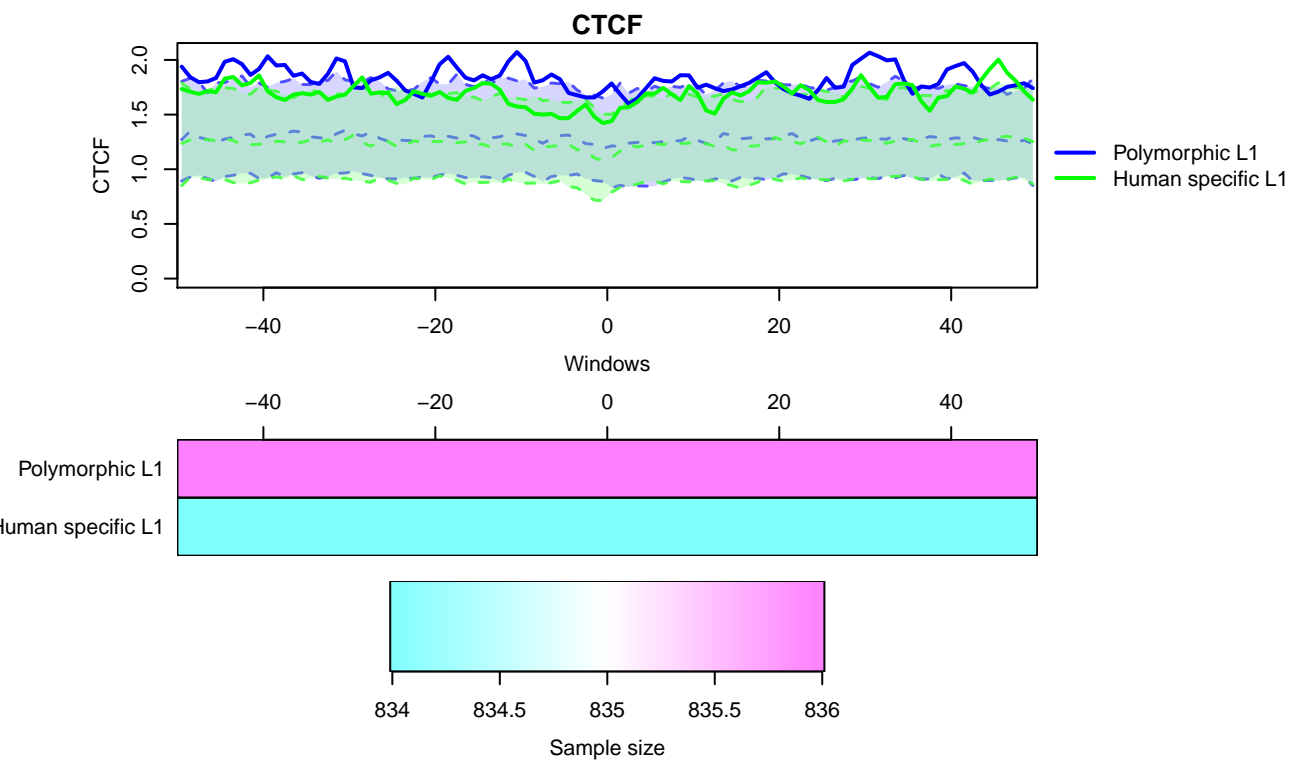
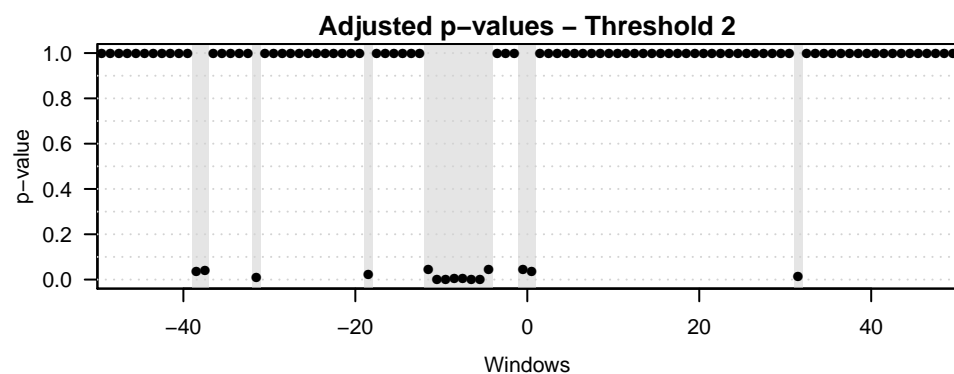
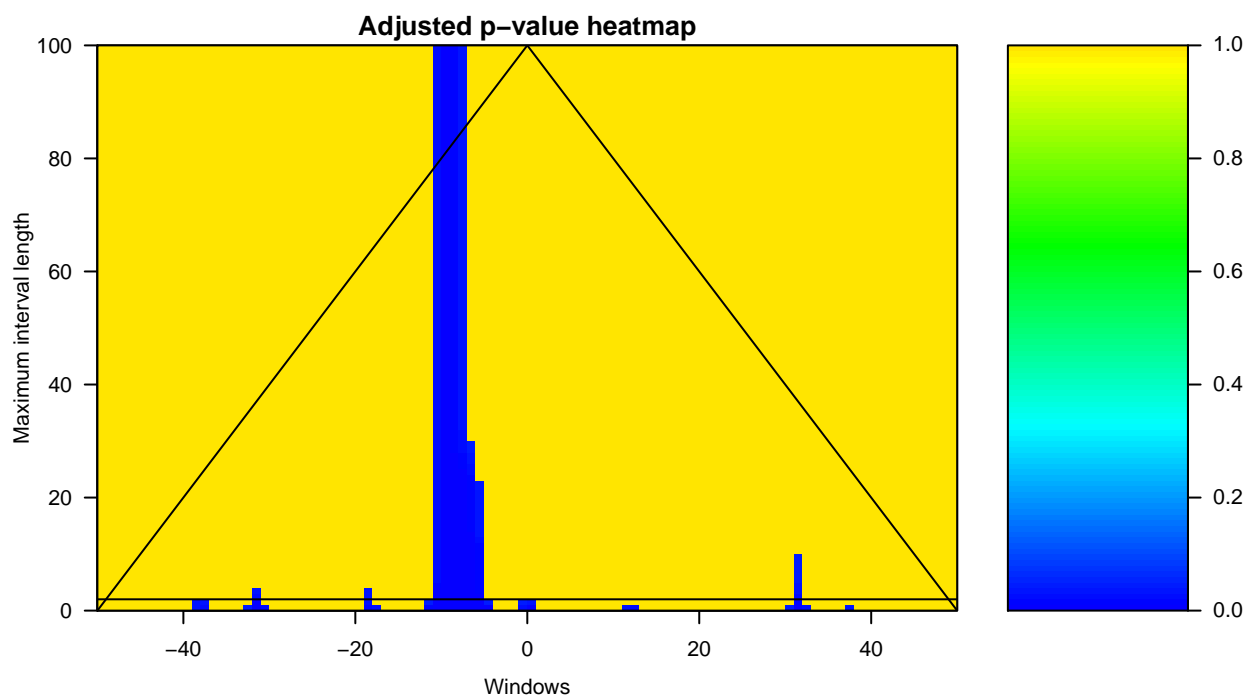


Polymorphic L1

Human specific L1

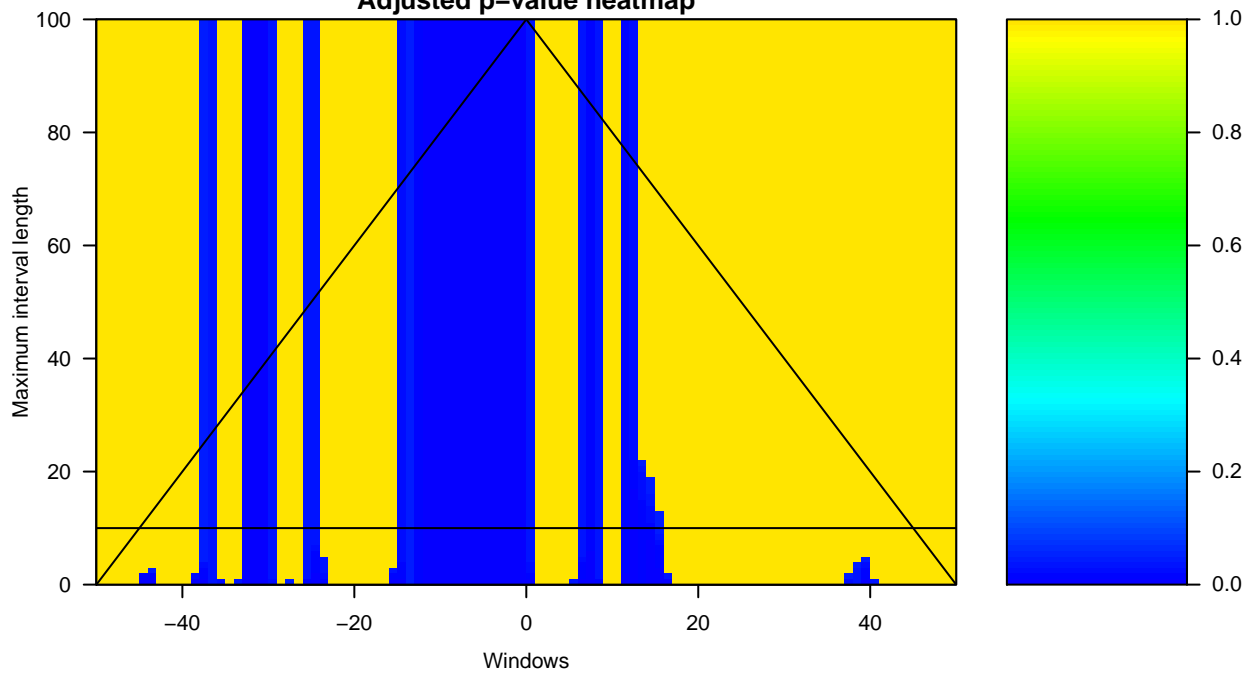


CTCF

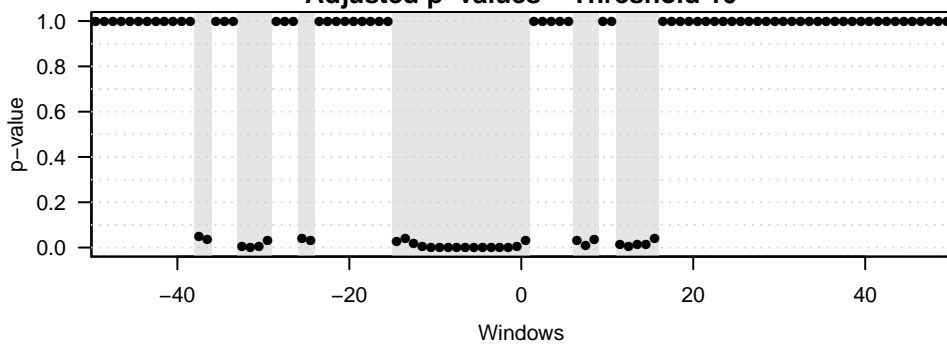


# DNase hypersensitive sites

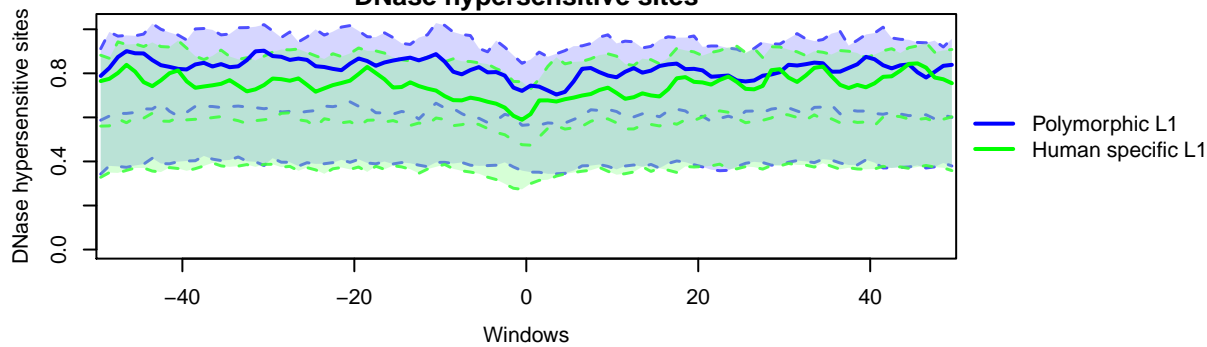
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 10

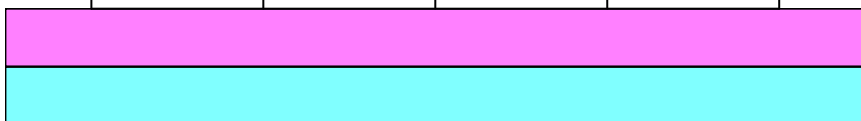


## DNase hypersensitive sites



Polymorphic L1

Human specific L1

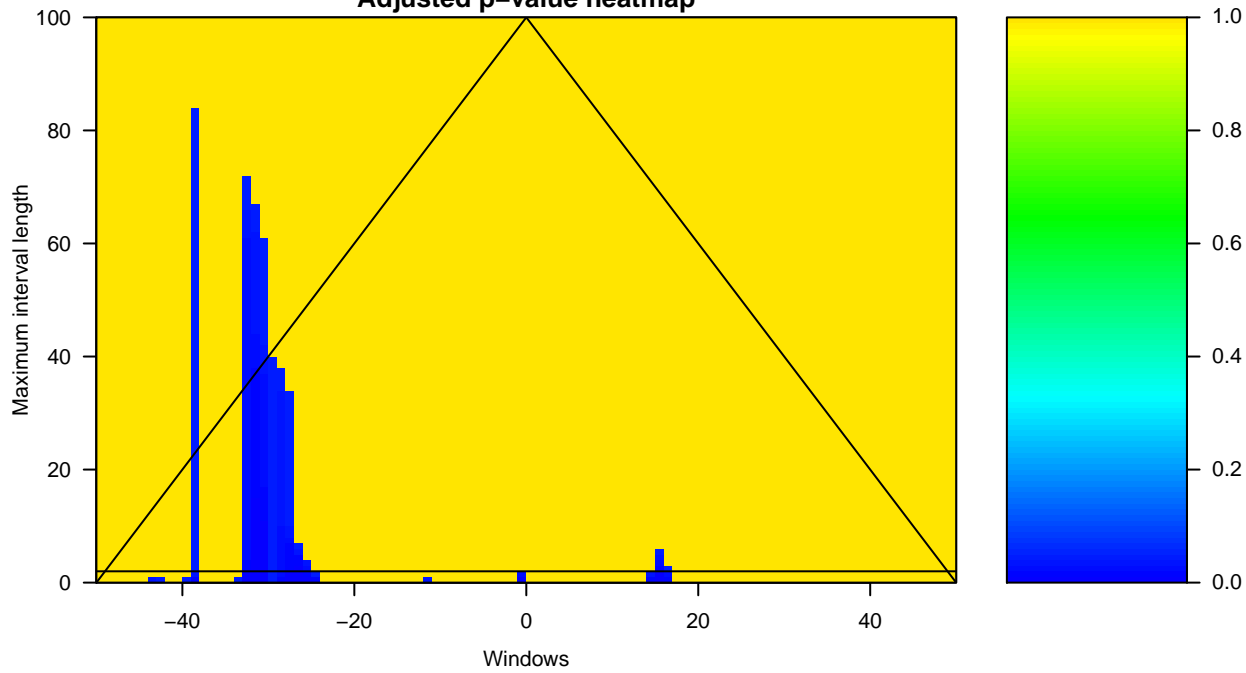


834 834.5 835 835.5 836

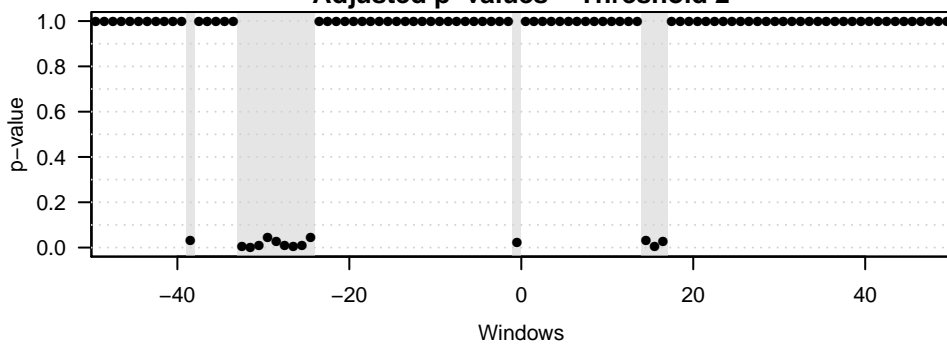
Sample size

# RNA Pol2

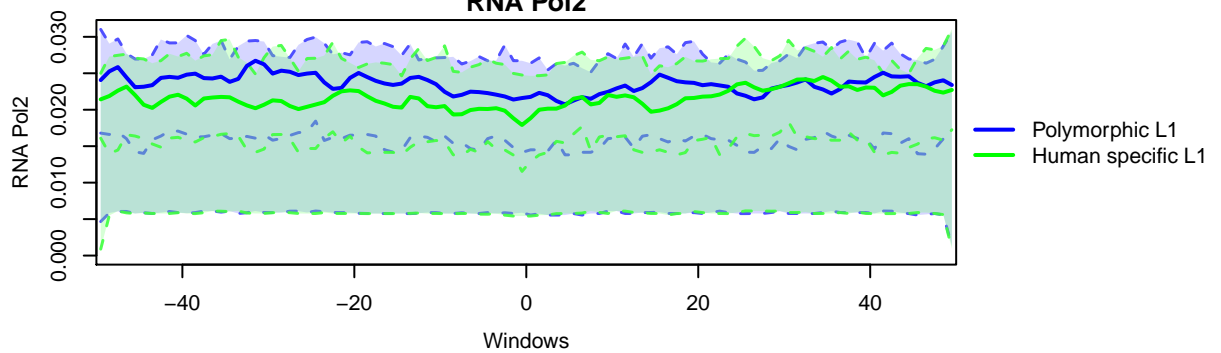
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 2



# RNA Pol2



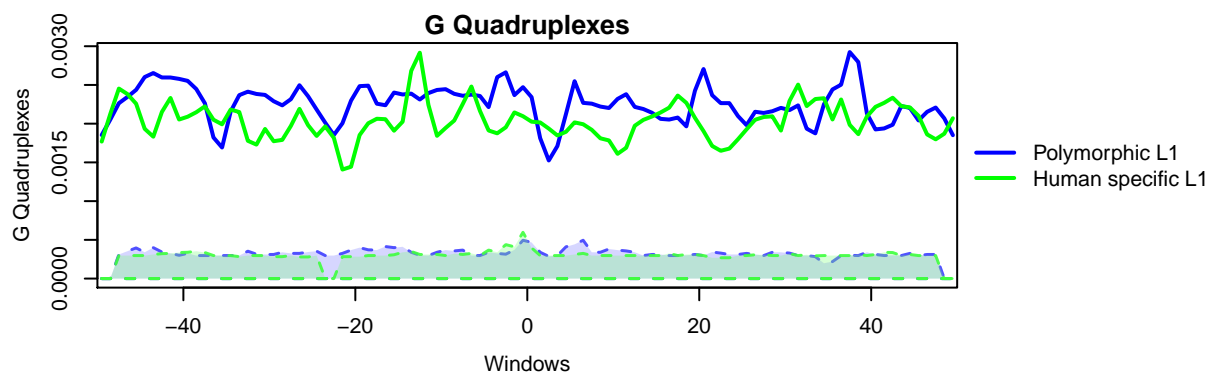
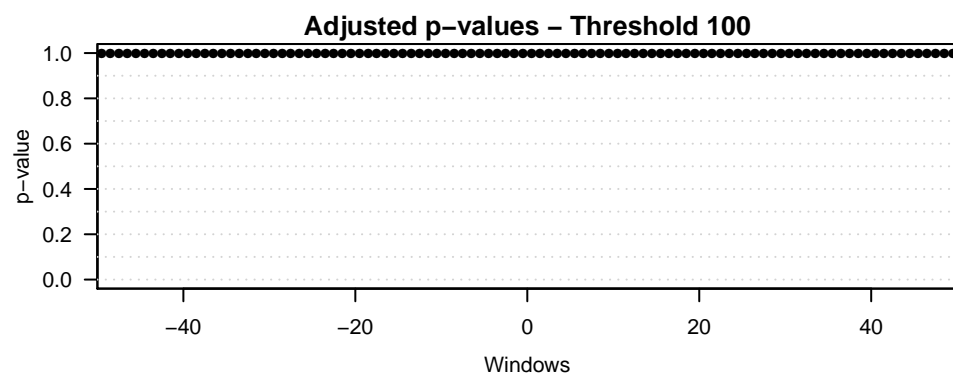
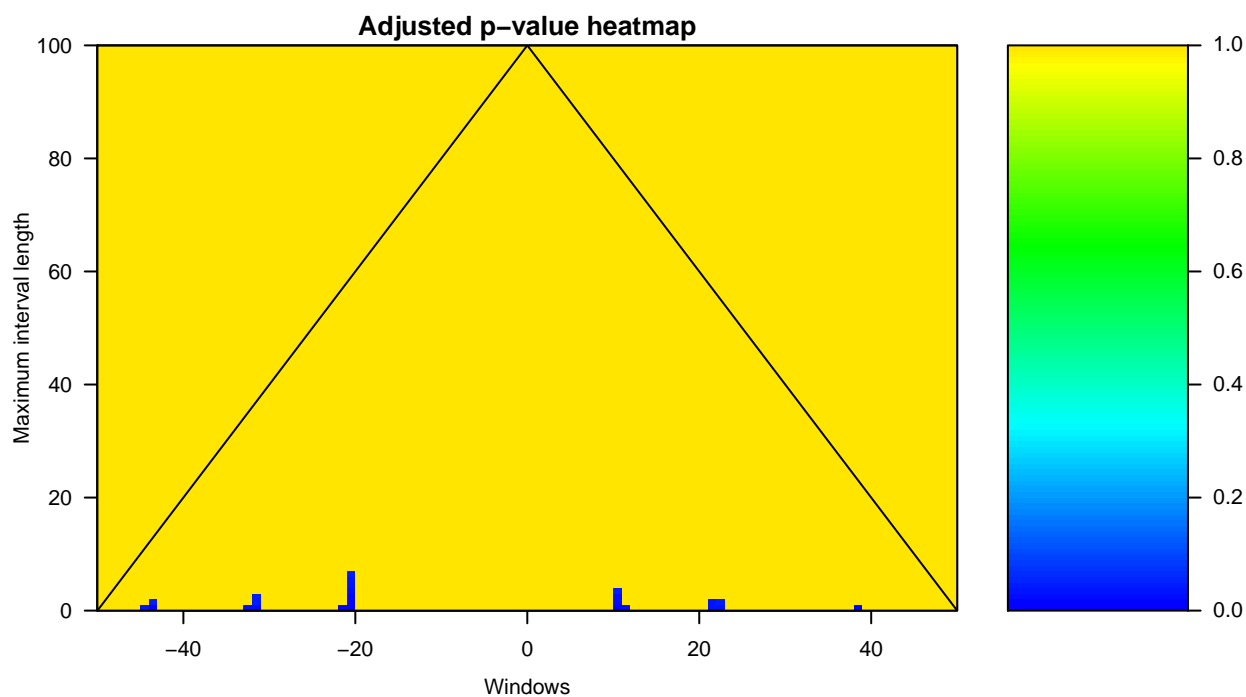
Polymorphic L1

Human specific L1

834 834.5 835 835.5 836

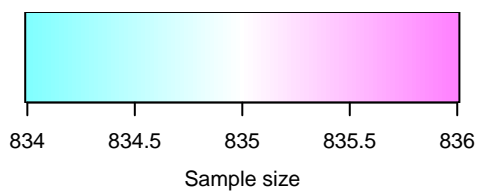
Sample size

# G Quadruplexes

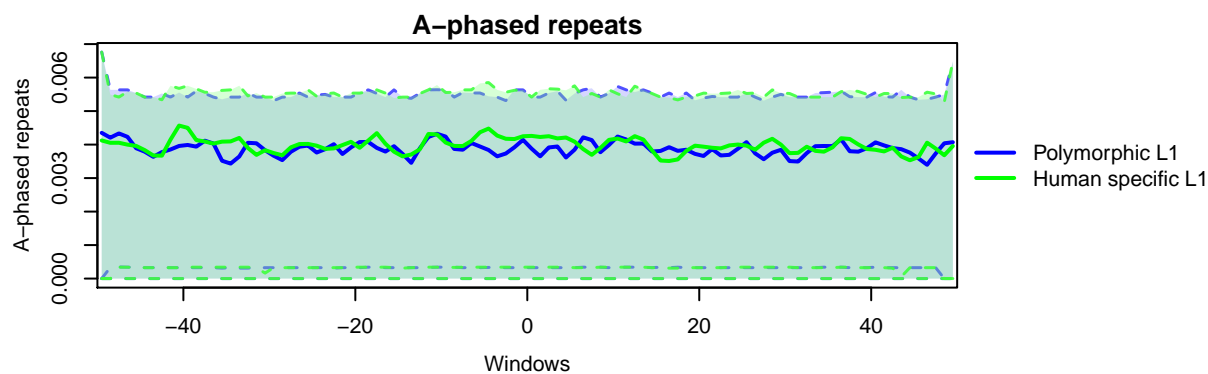
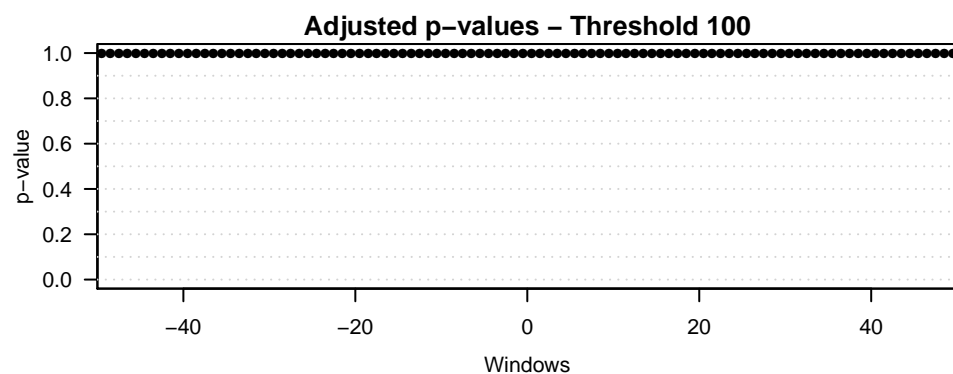
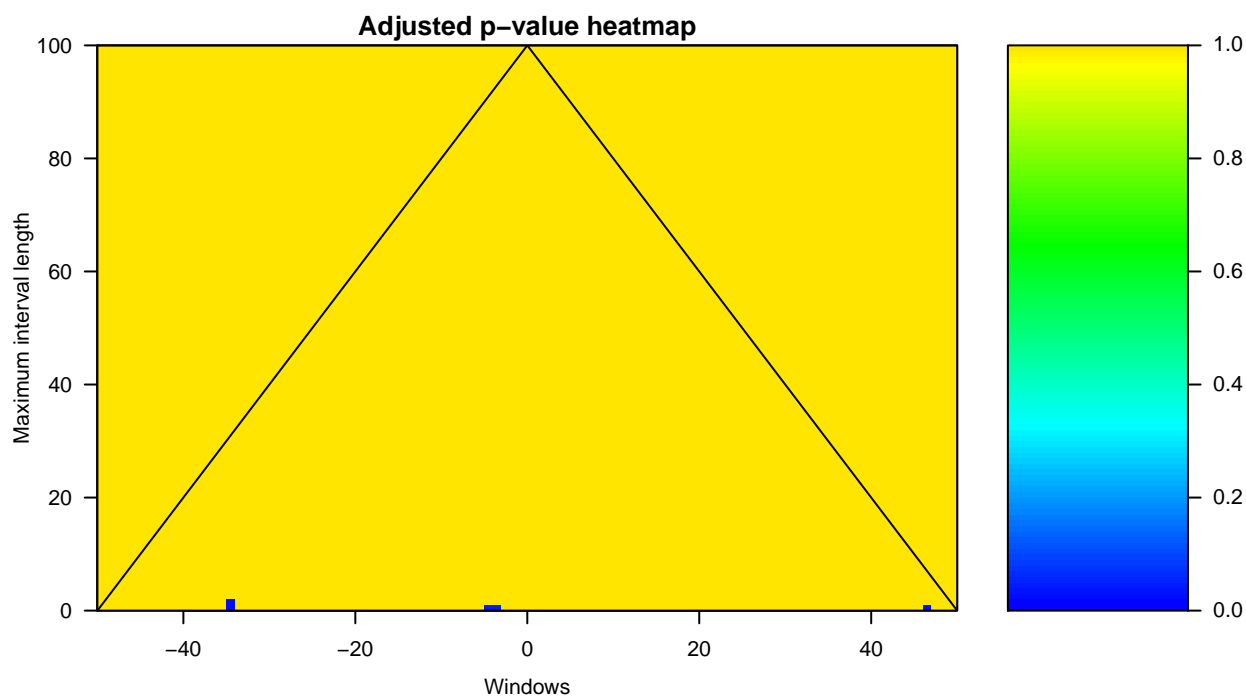


Polymorphic L1

Human specific L1

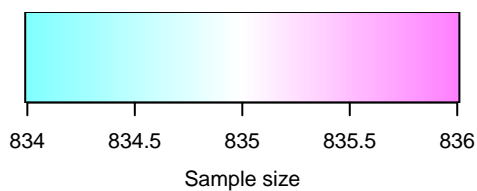


# A-phased repeats



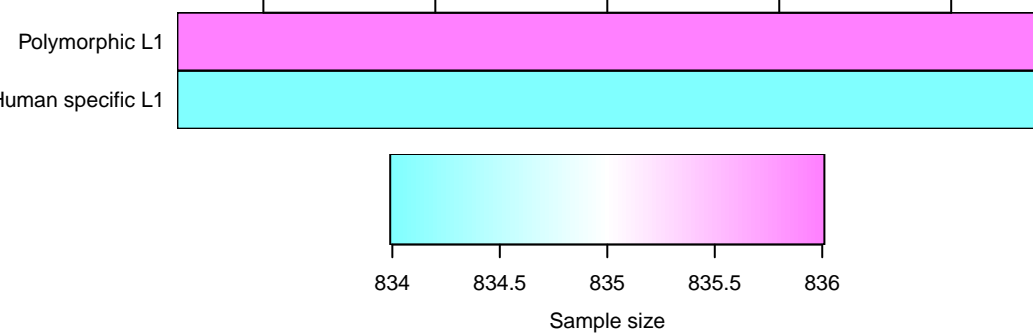
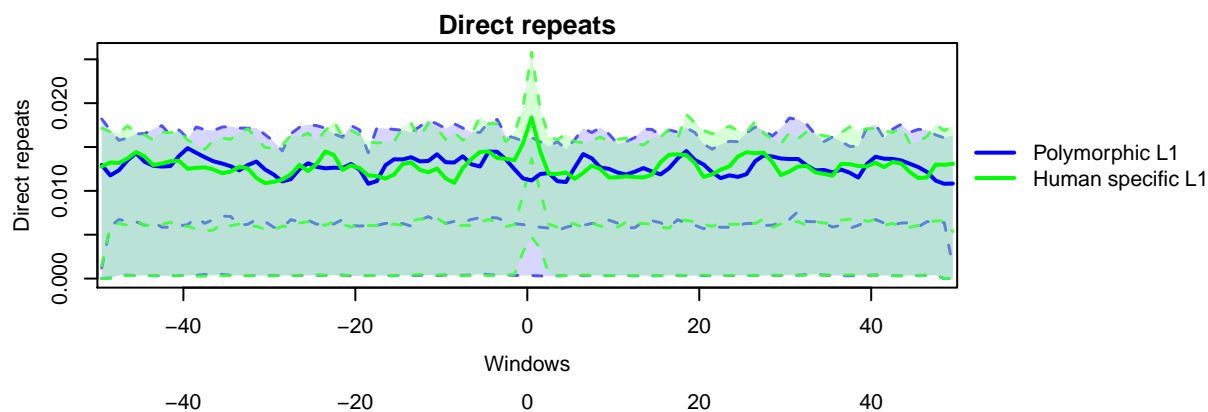
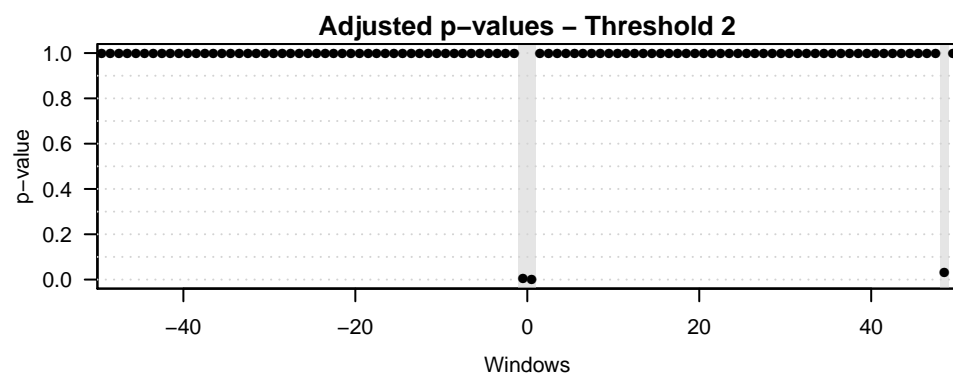
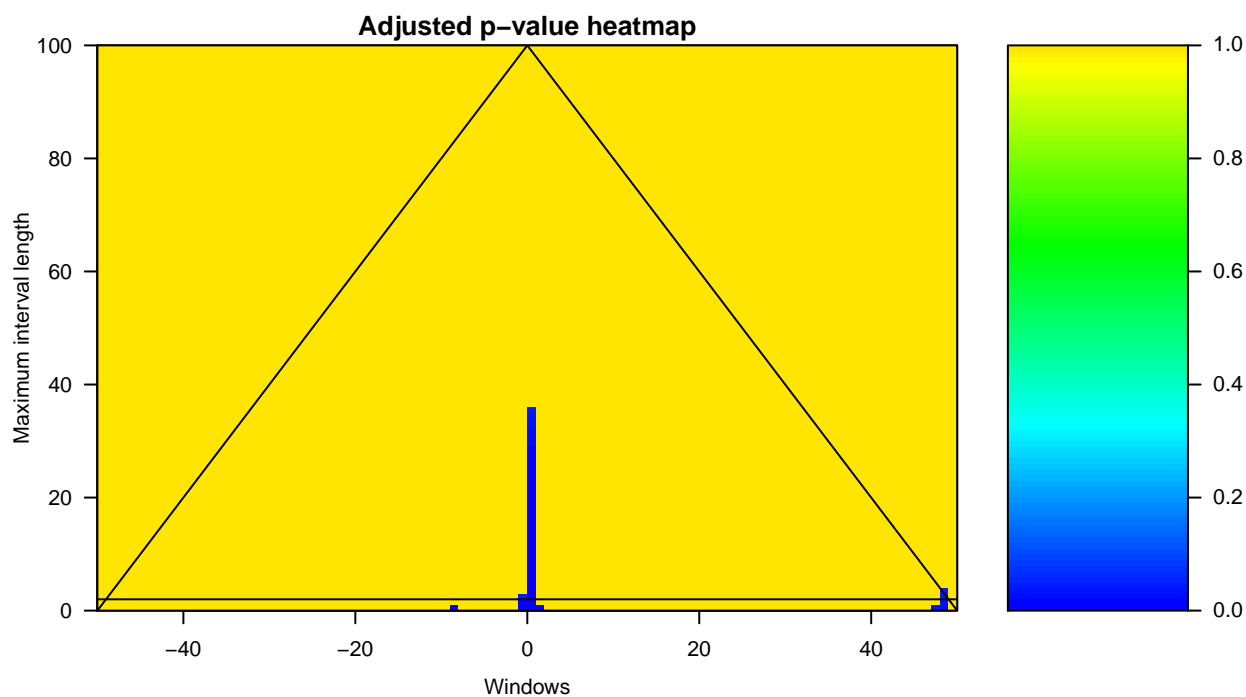
Polymorphic L1

Human specific L1

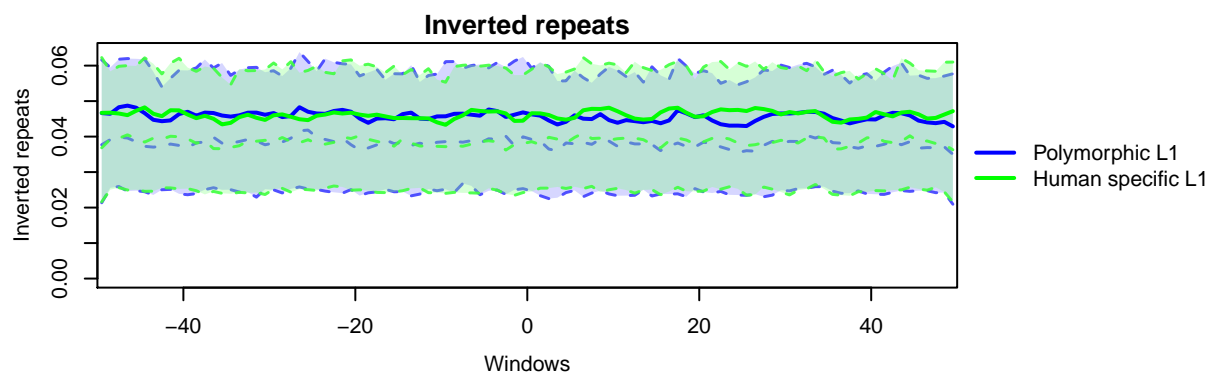
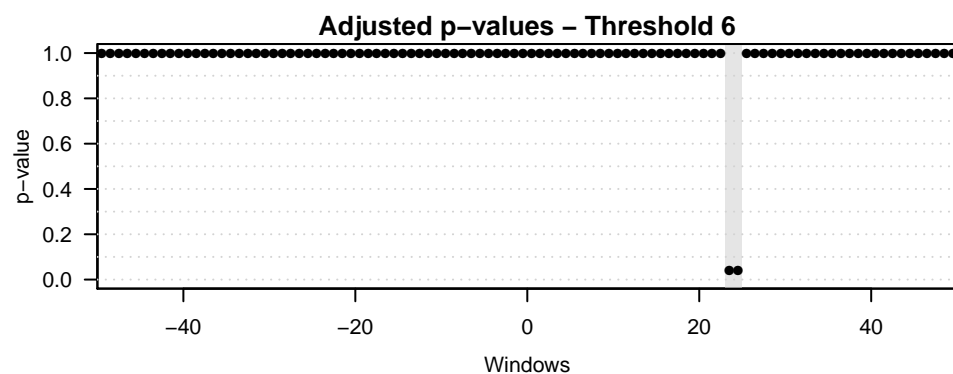
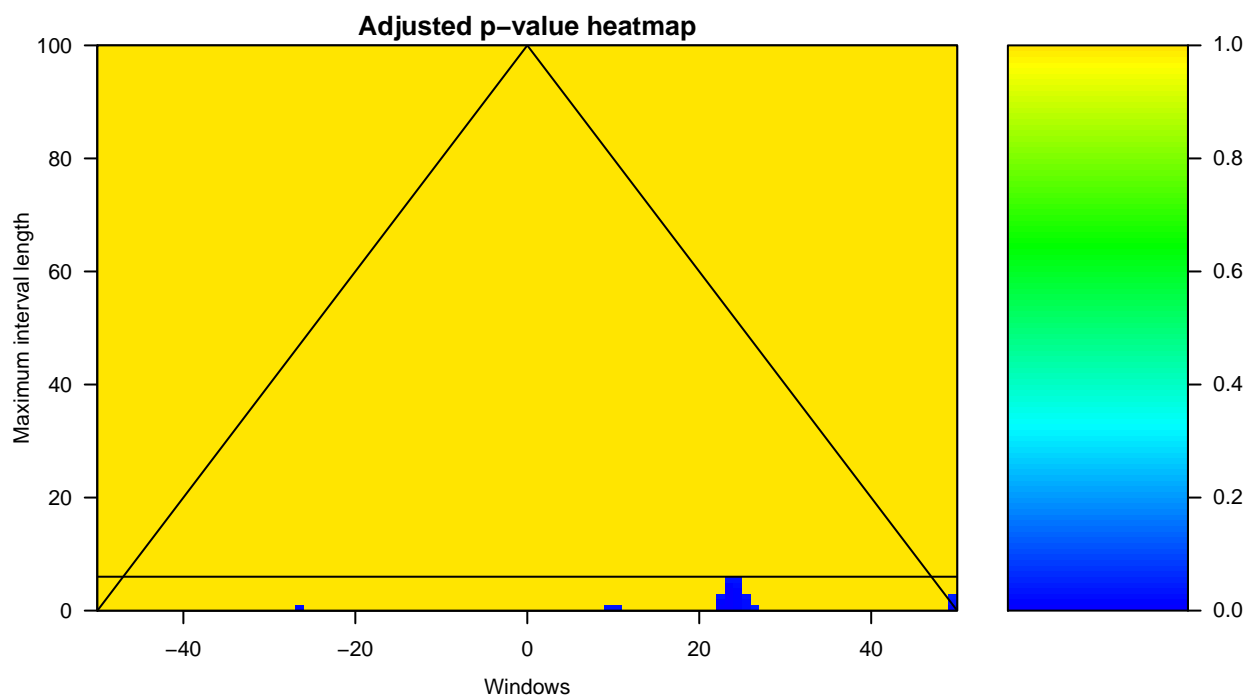




# Direct repeats



# Inverted repeats



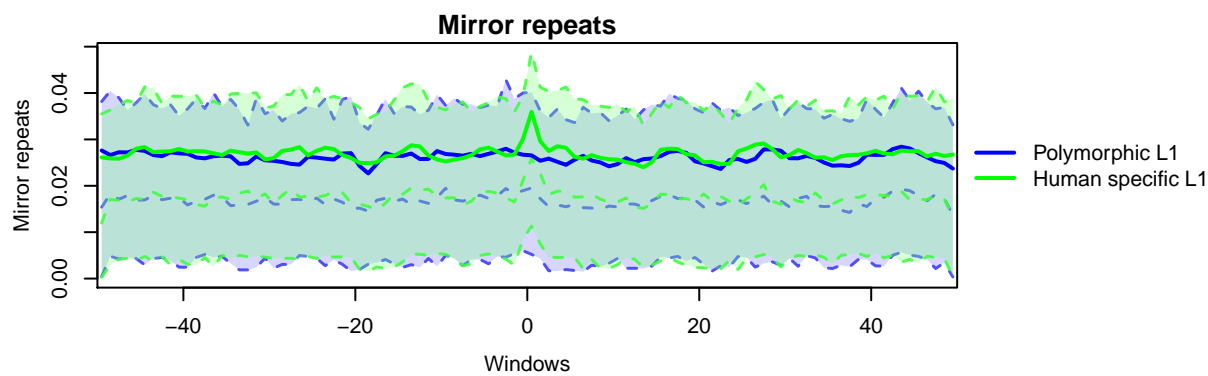
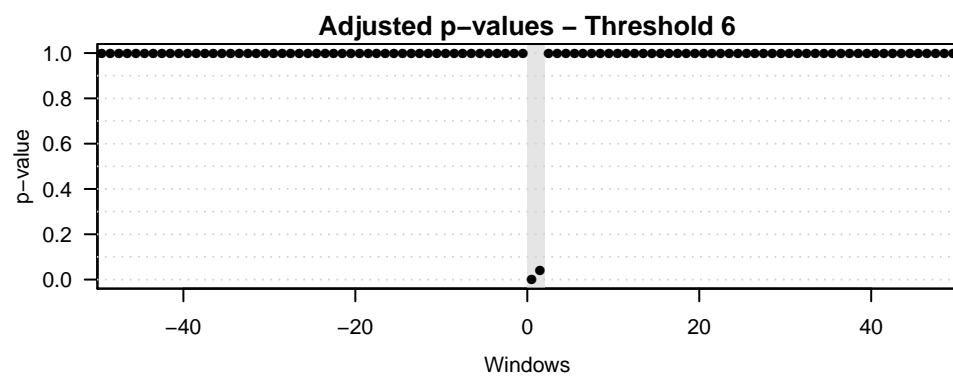
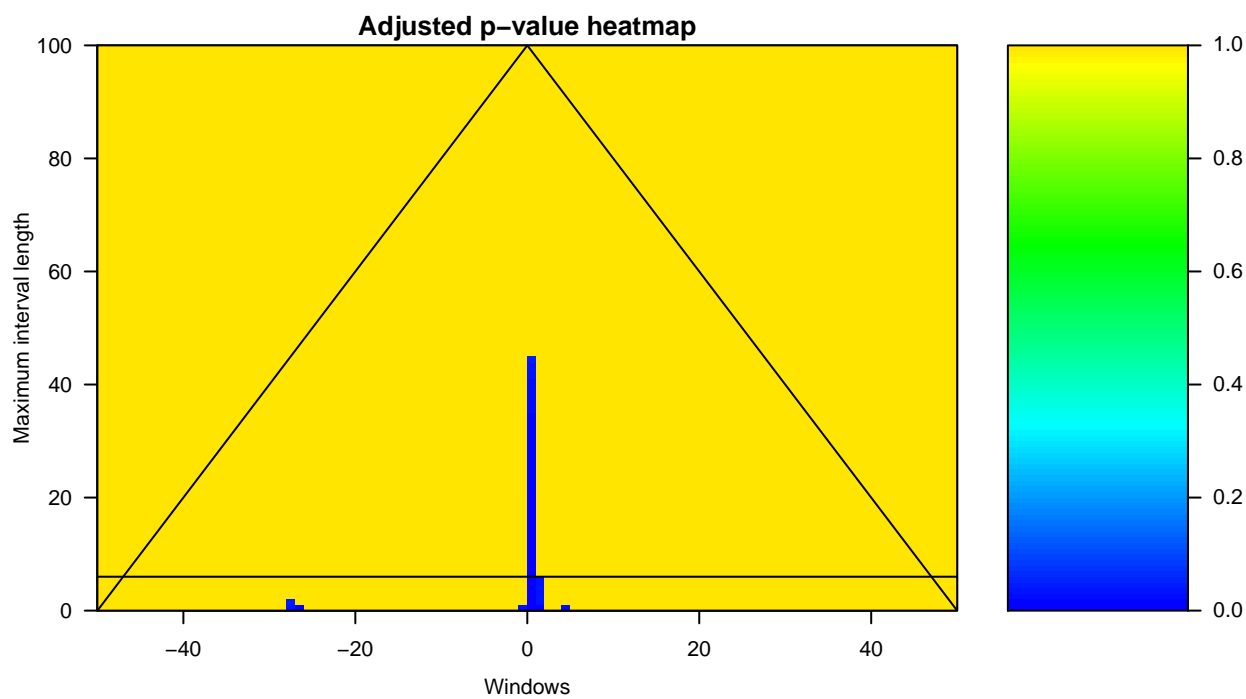
Polymorphic L1

Human specific L1

834 834.5 835 835.5 836

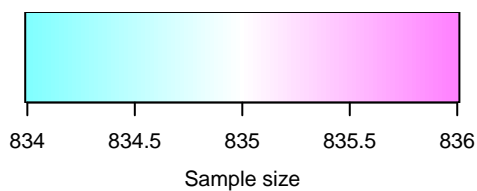
Sample size

# Mirror repeats

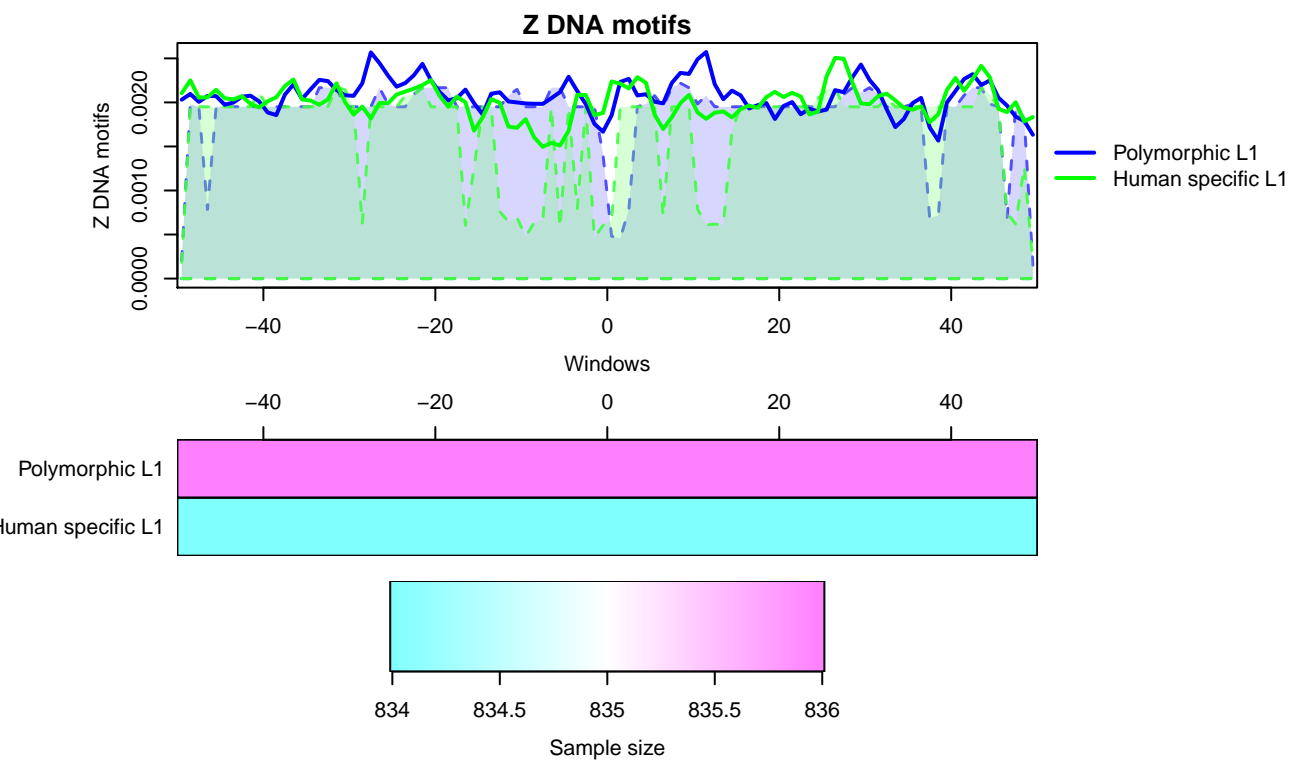
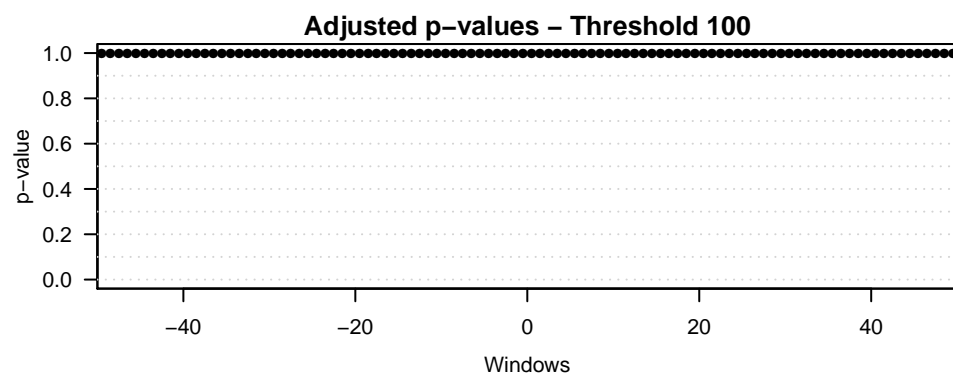
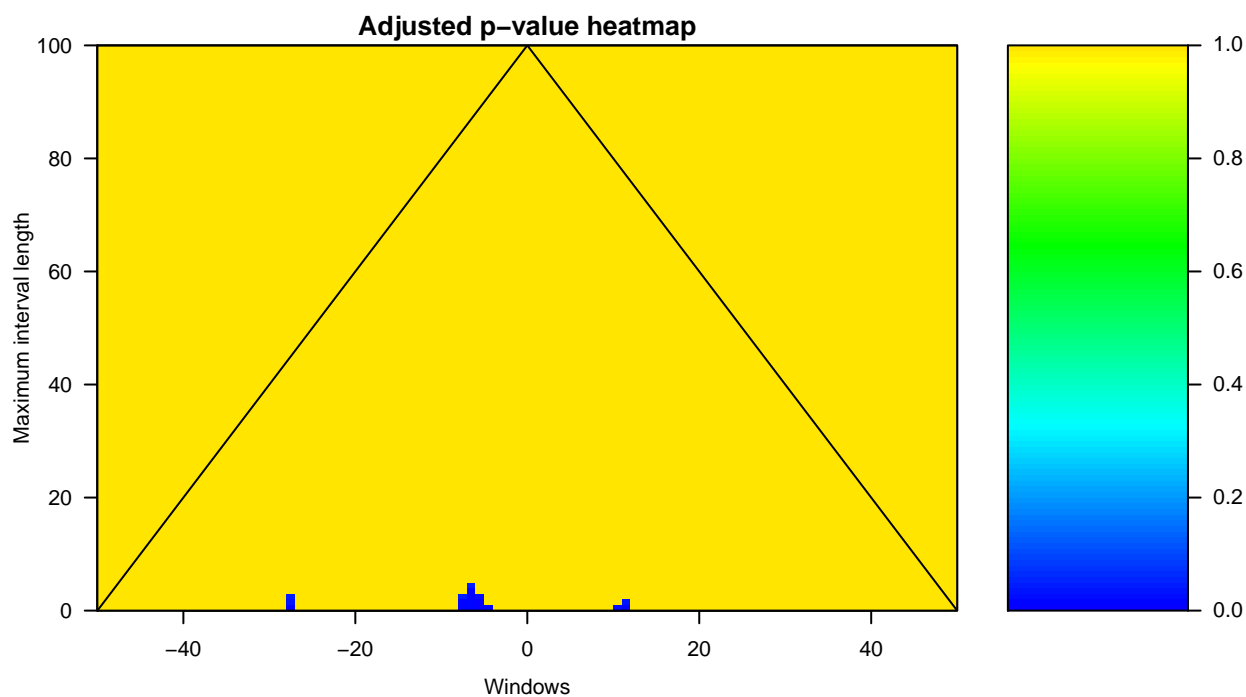


Polymorphic L1

Human specific L1

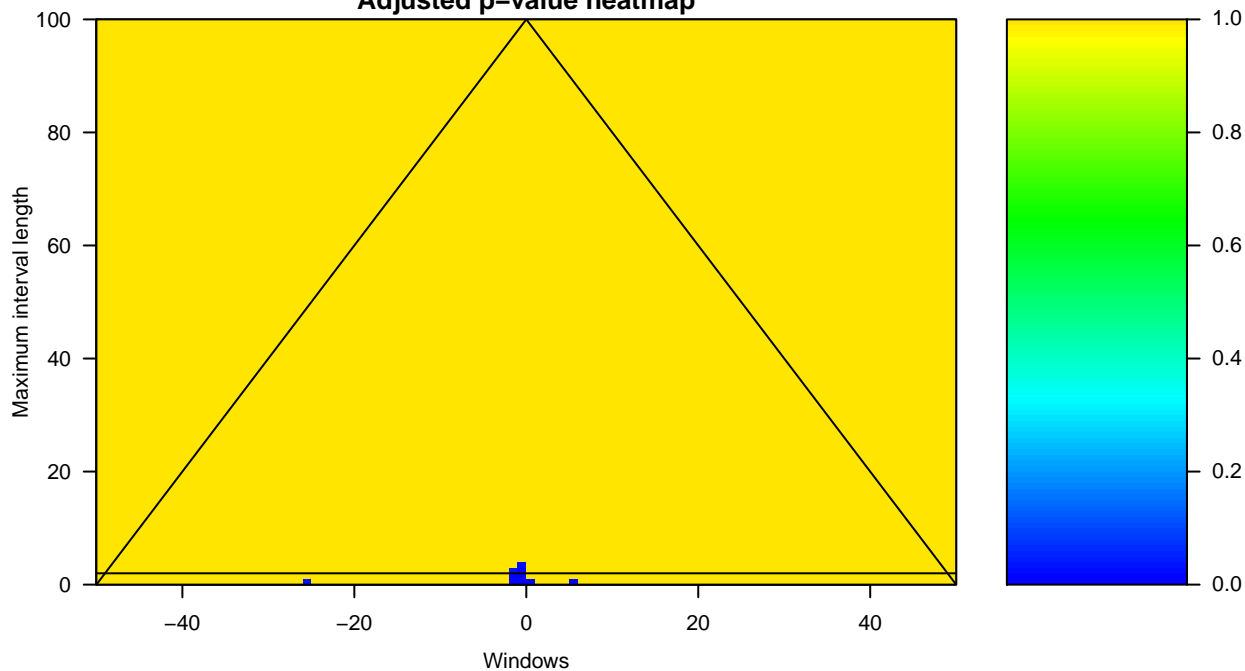


# Z DNA motifs

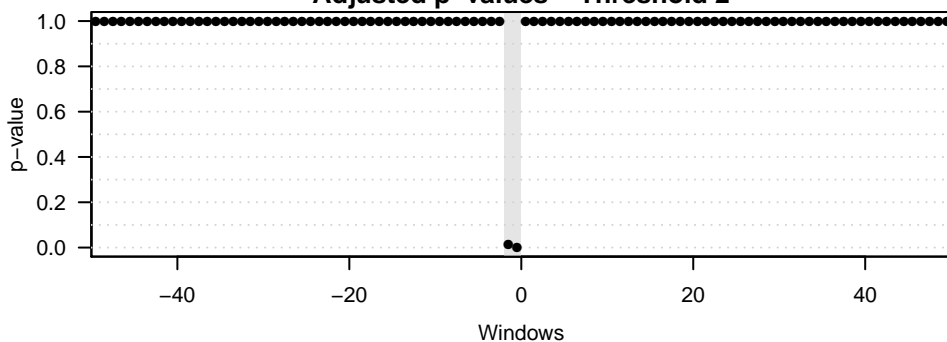


# Most conserved element

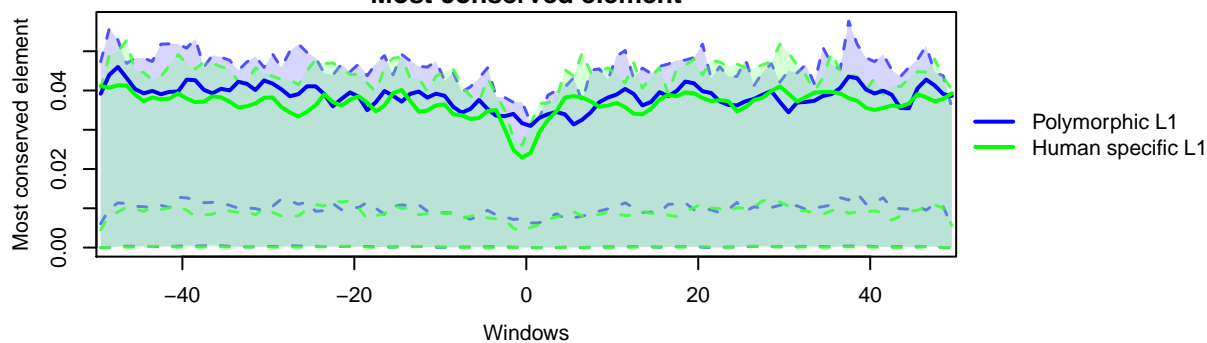
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 2



# Most conserved element



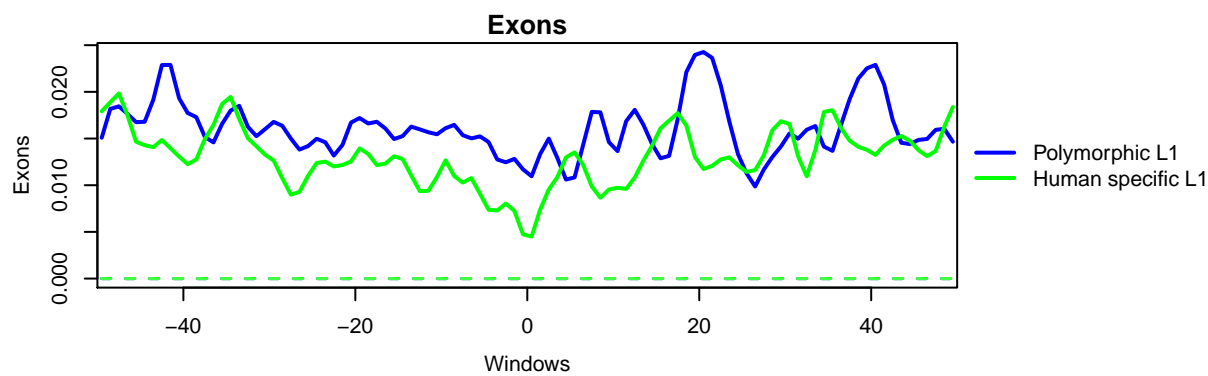
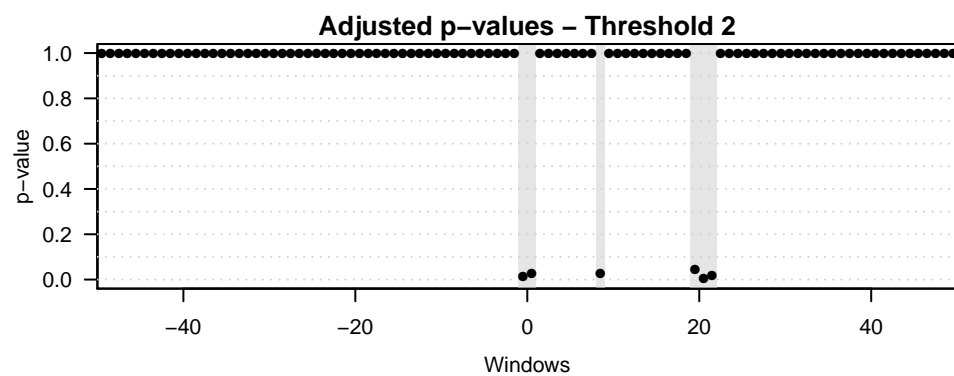
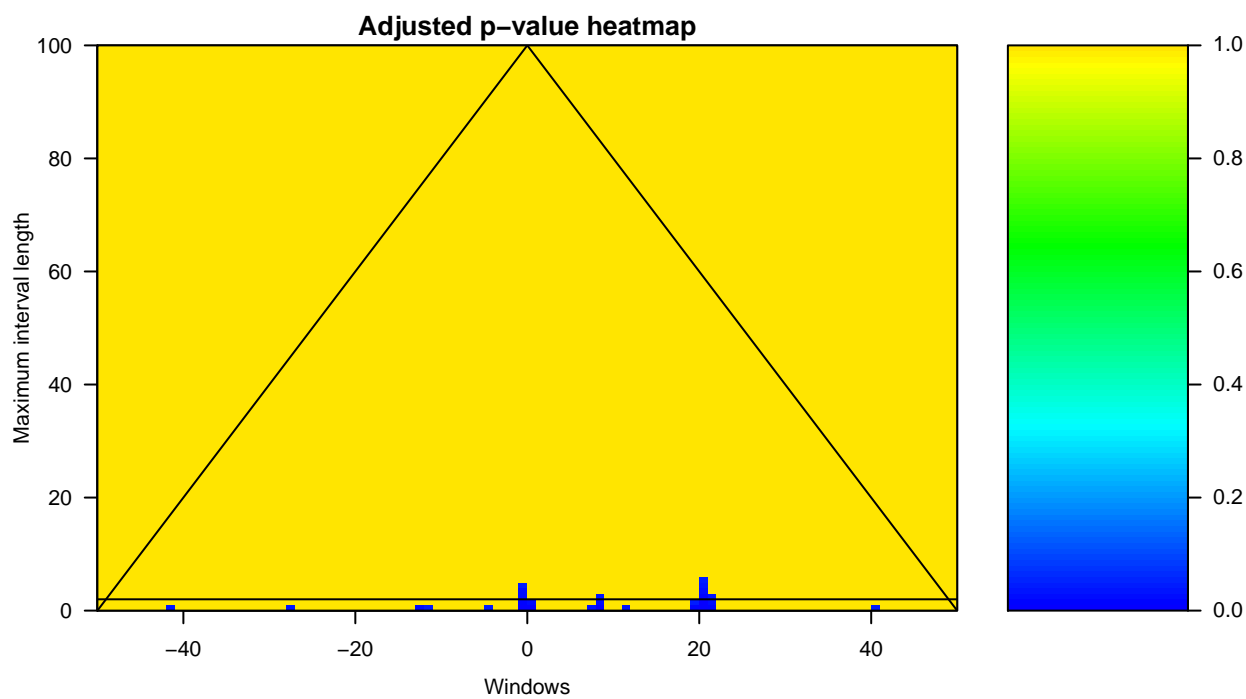
Polymorphic L1

Human specific L1

834 834.5 835 835.5 836

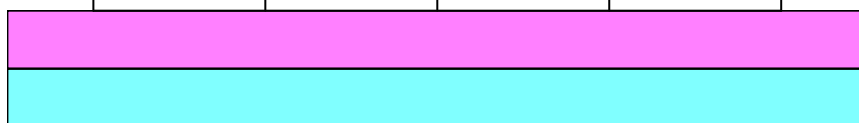
Sample size

## Exons



Polymorphic L1

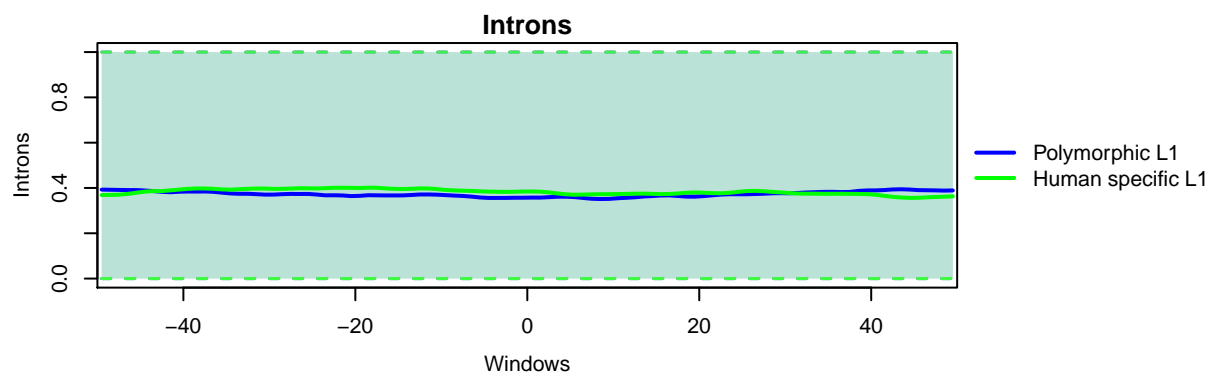
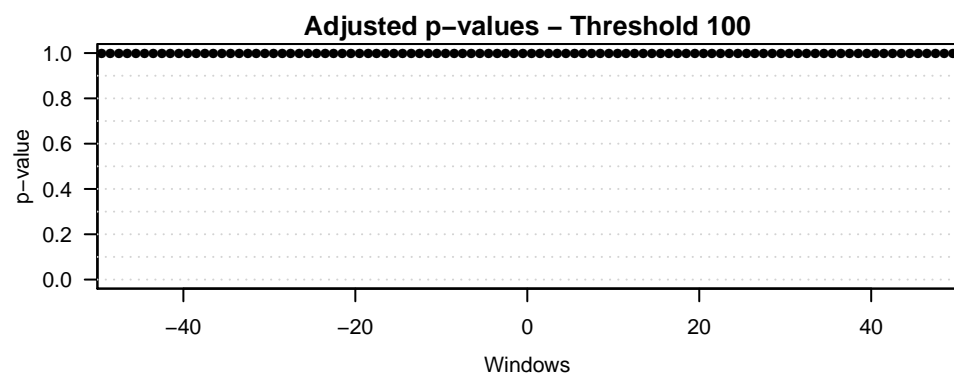
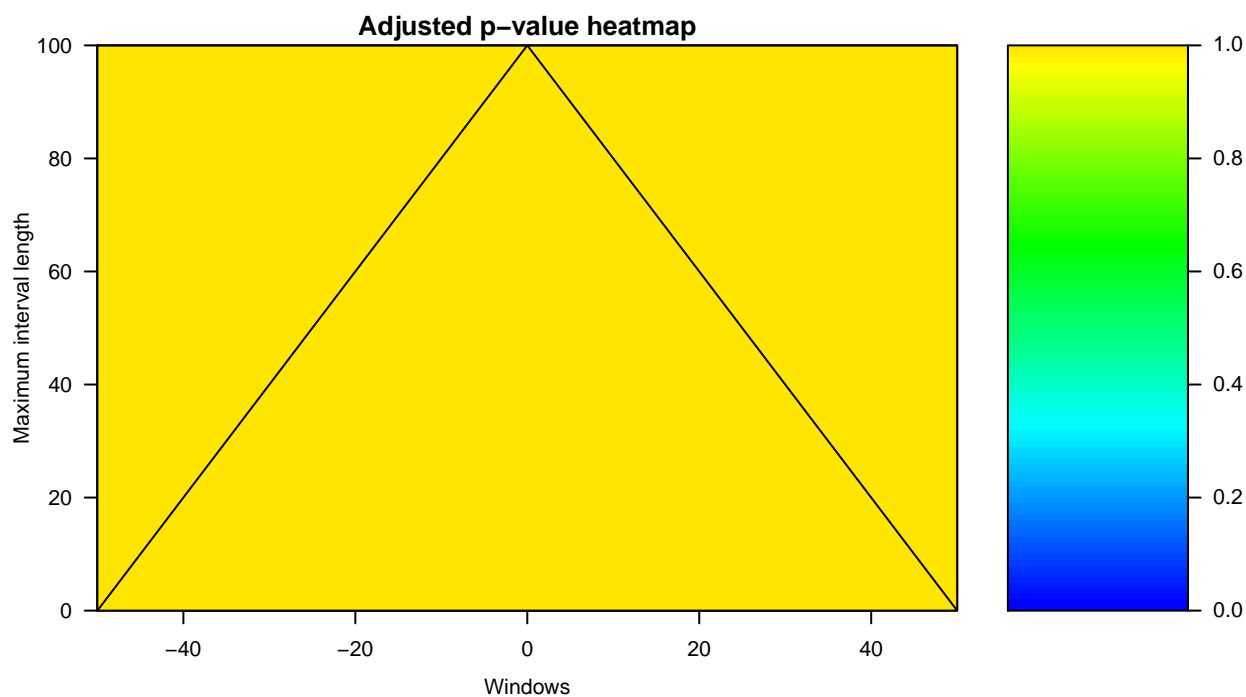
Human specific L1



834 834.5 835 835.5 836

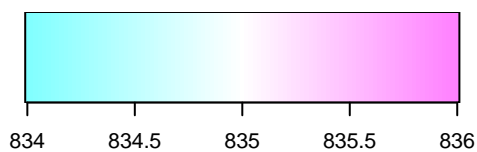
Sample size

# Introns



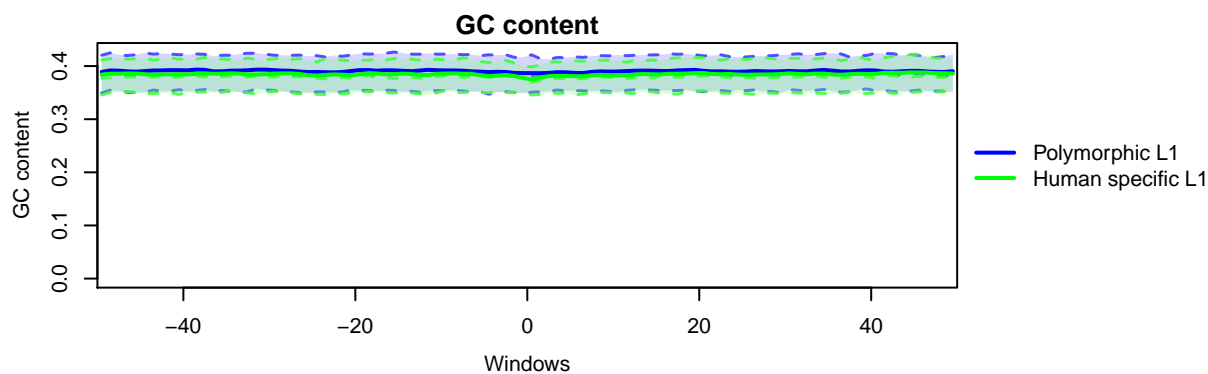
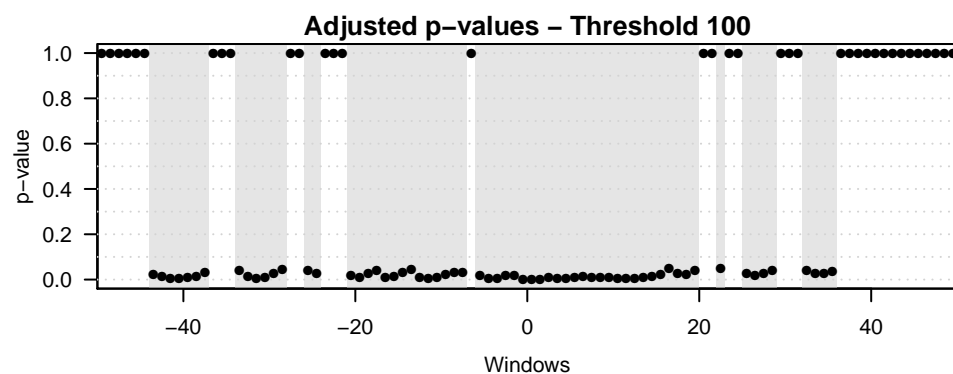
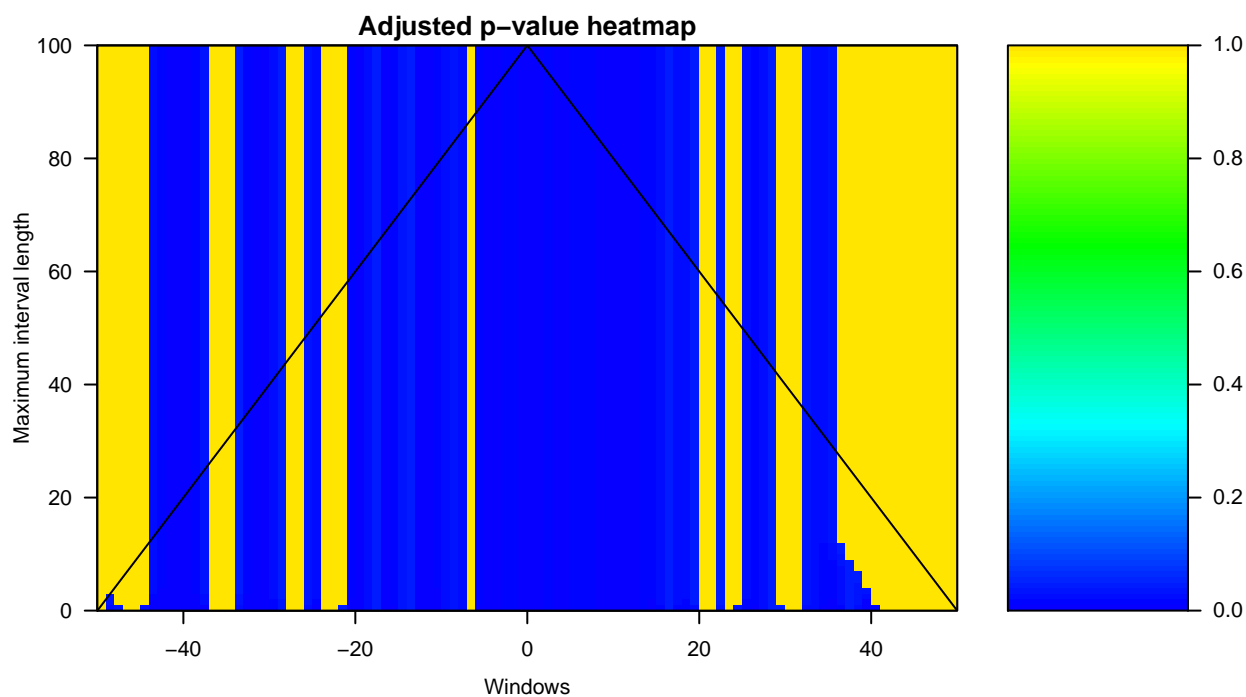
Polymorphic L1

Human specific L1



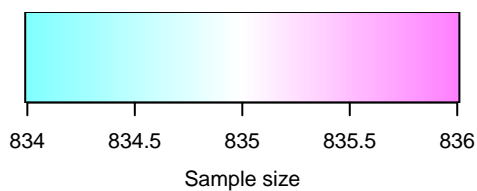
Sample size

# GC content



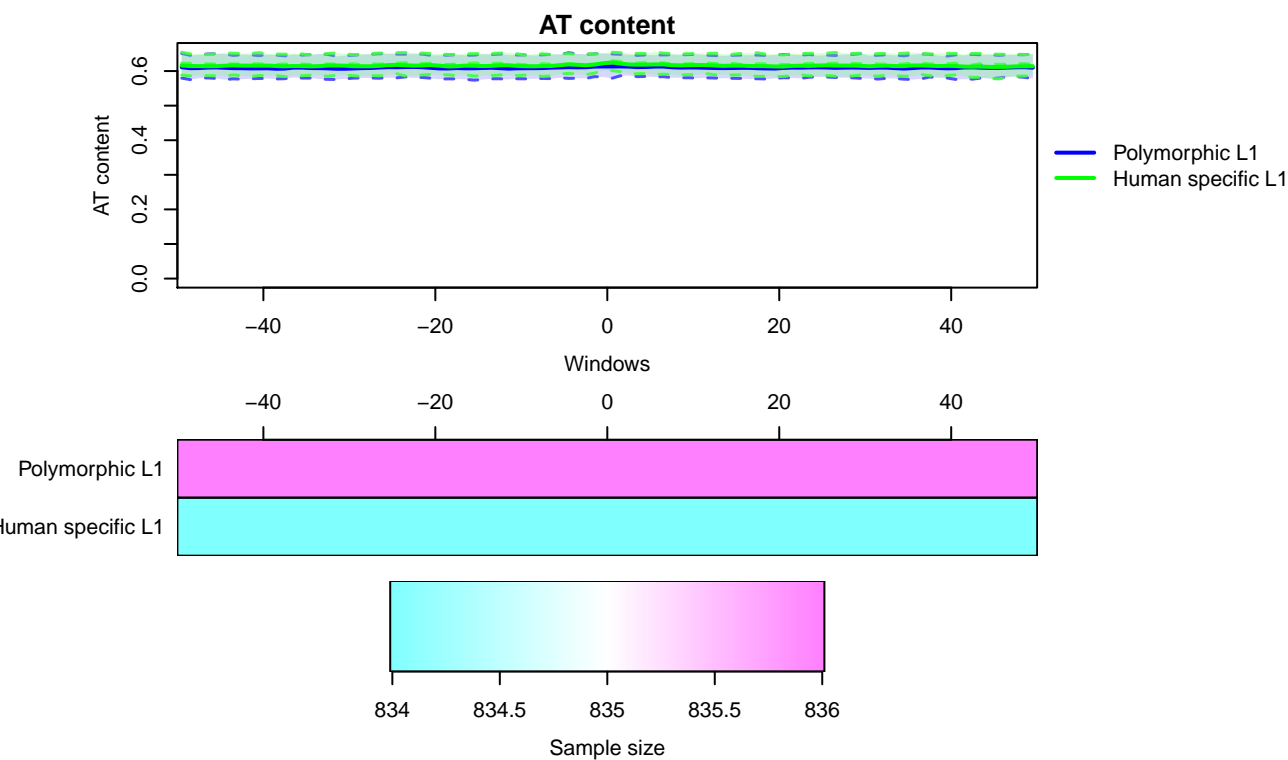
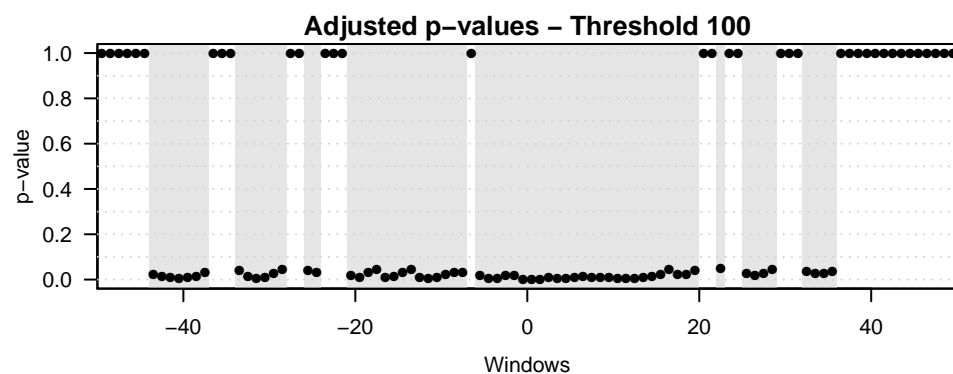
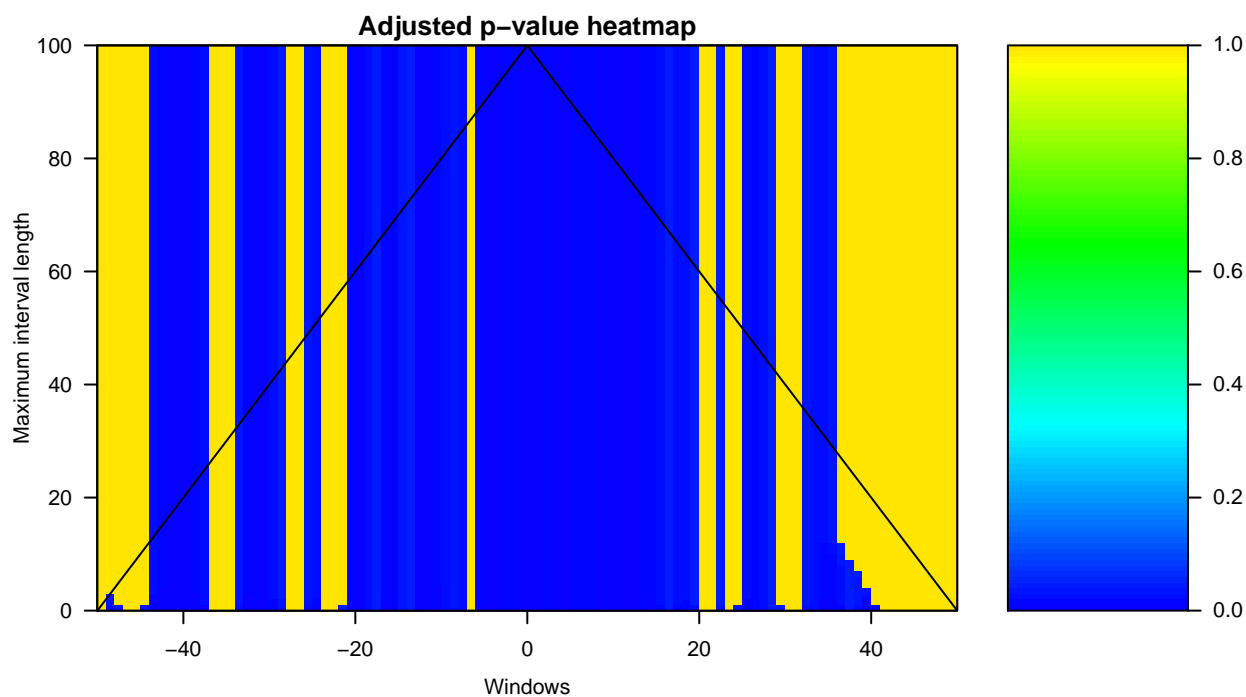
Polymorphic L1

Human specific L1

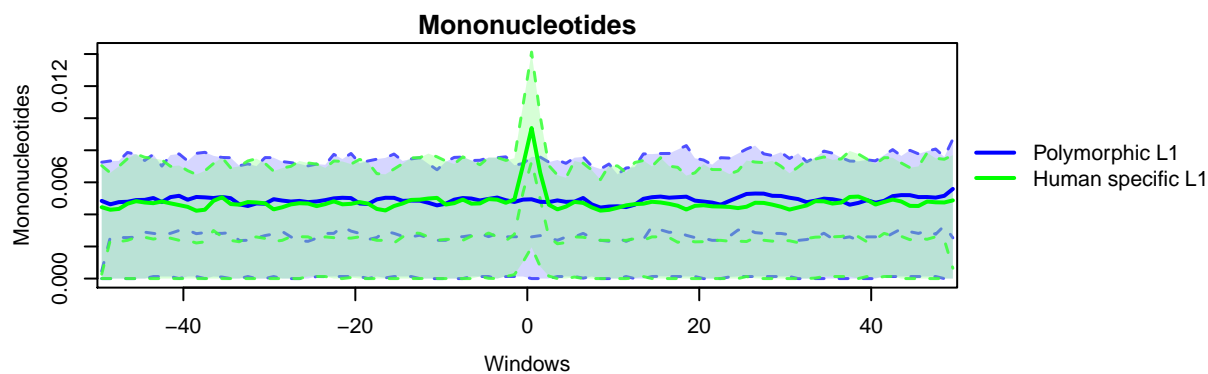
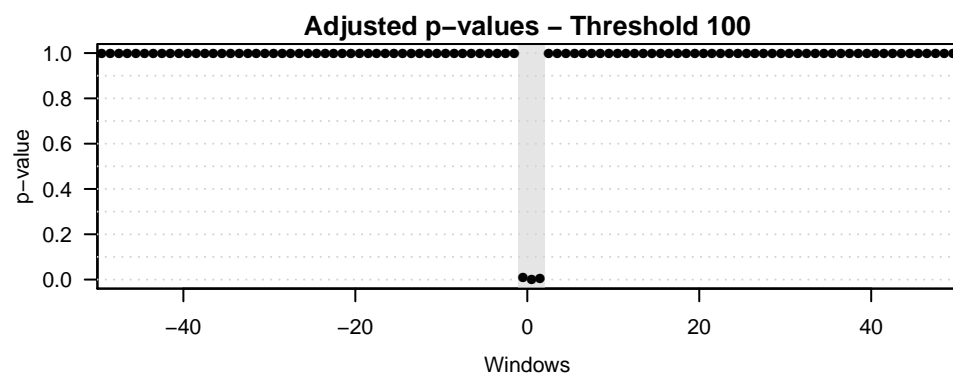
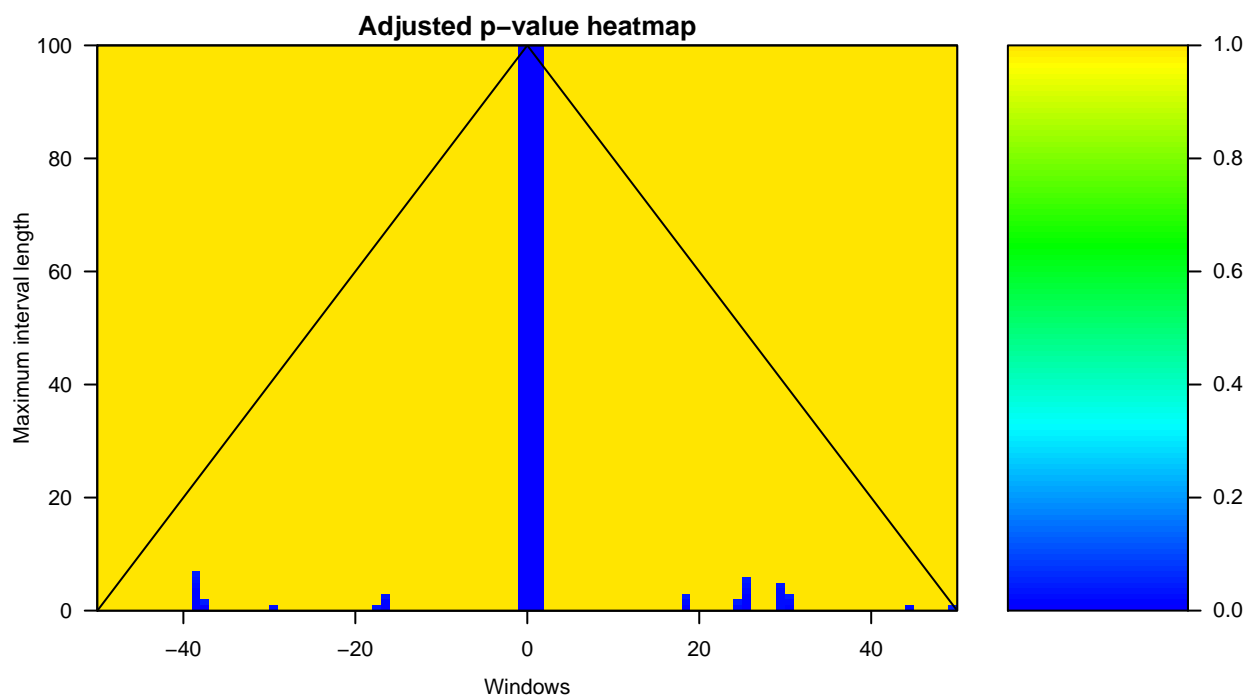




AT content



# Mononucleotides



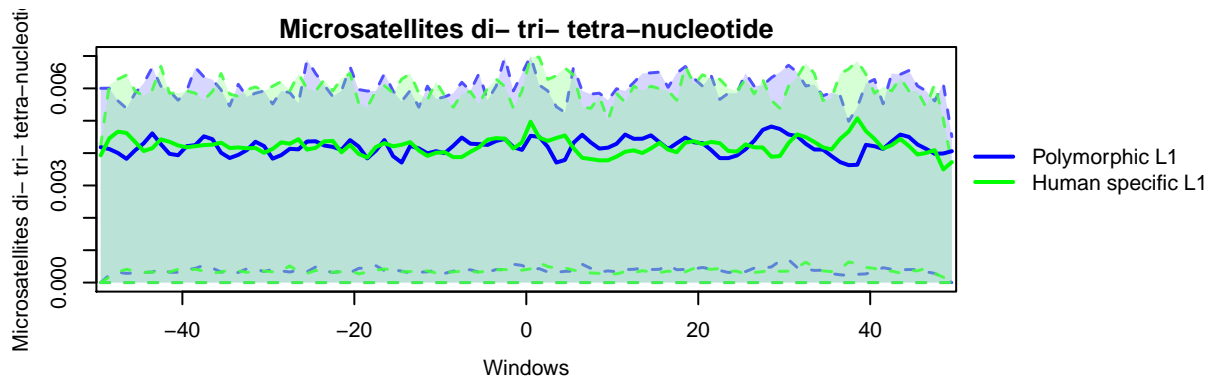
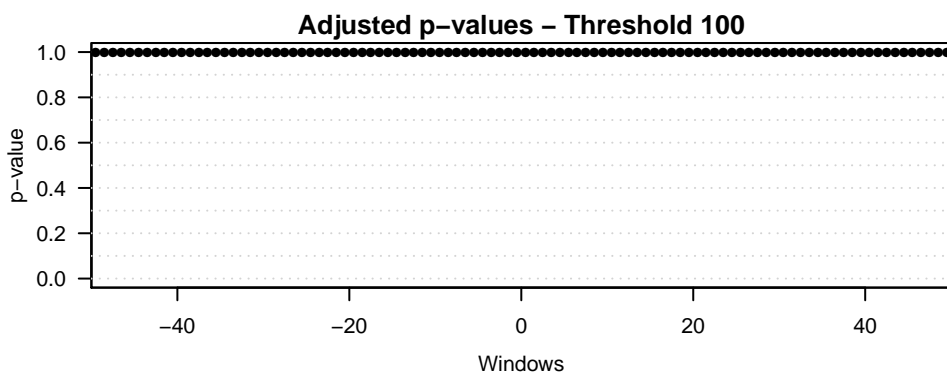
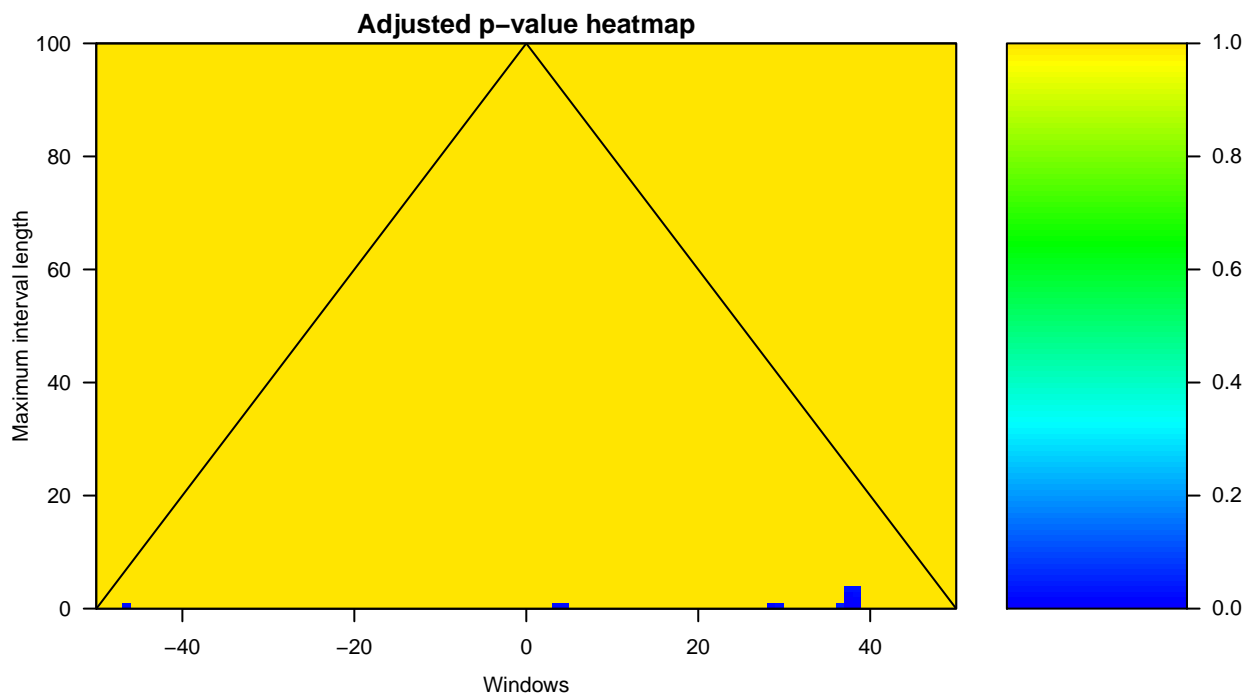
Polymorphic L1

Human specific L1

834 834.5 835 835.5 836

Sample size

# Microsatellites di- tri- tetra-nucleotide



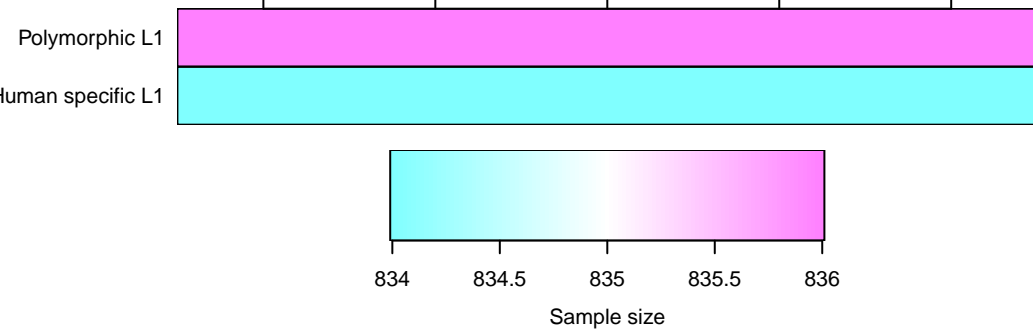
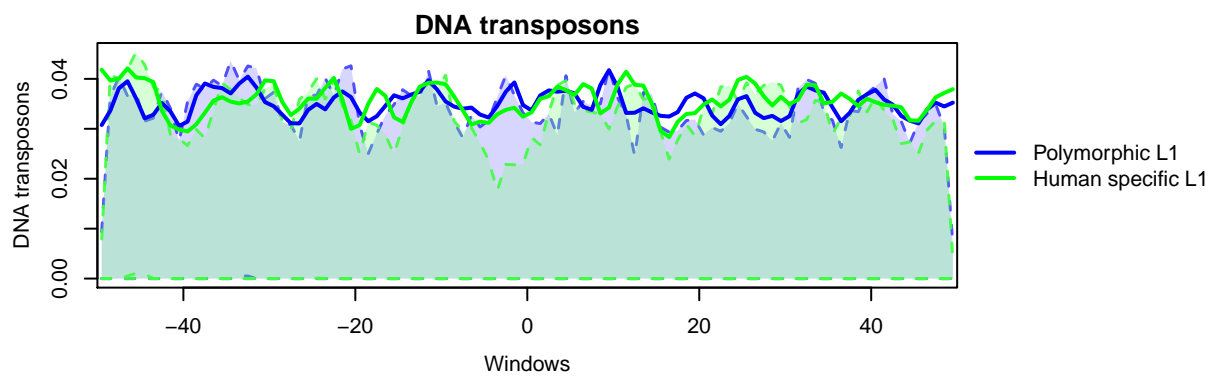
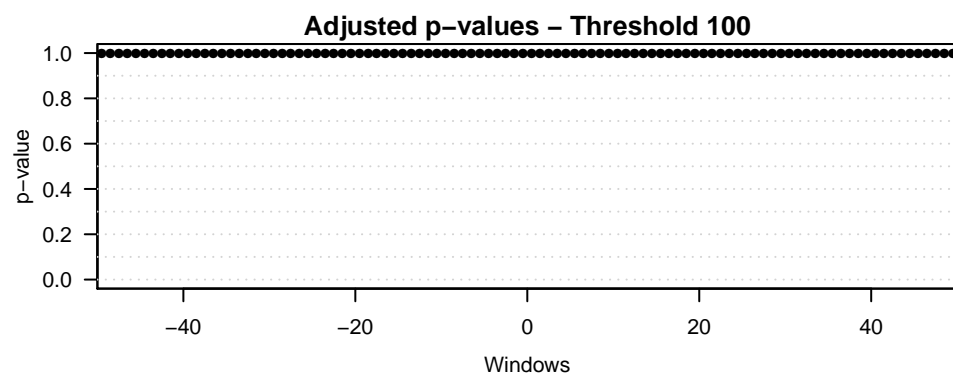
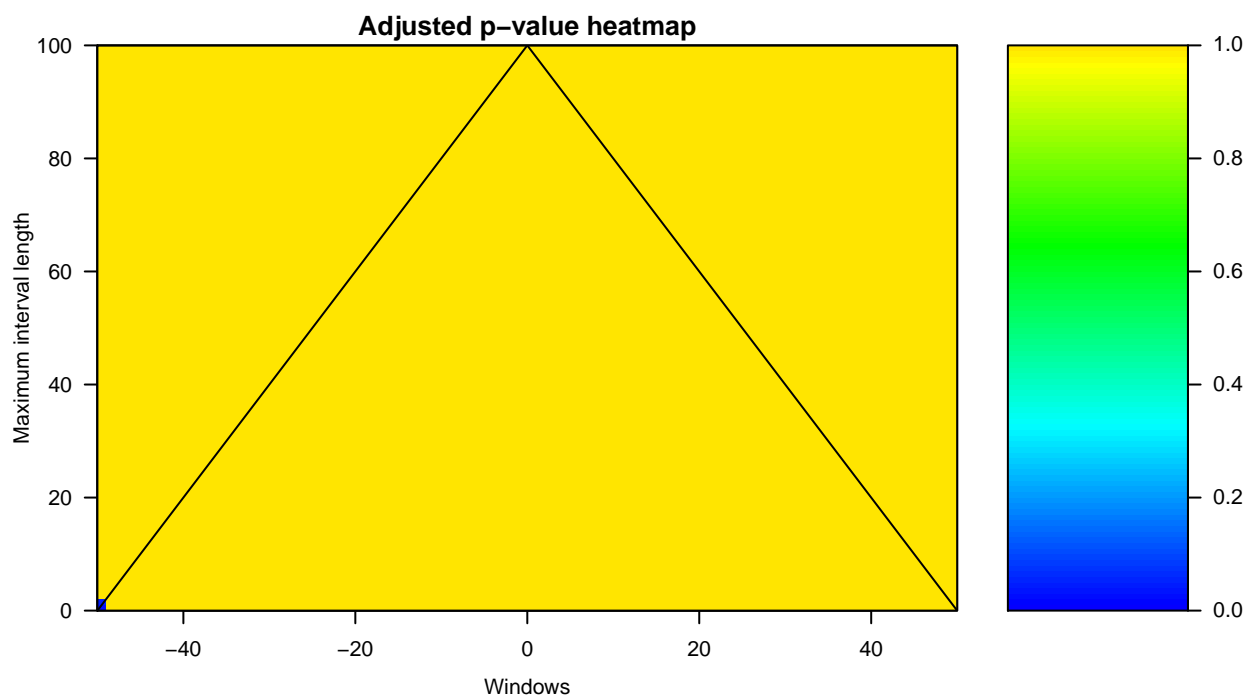
Polymorphic L1

Human specific L1

834 834.5 835 835.5 836

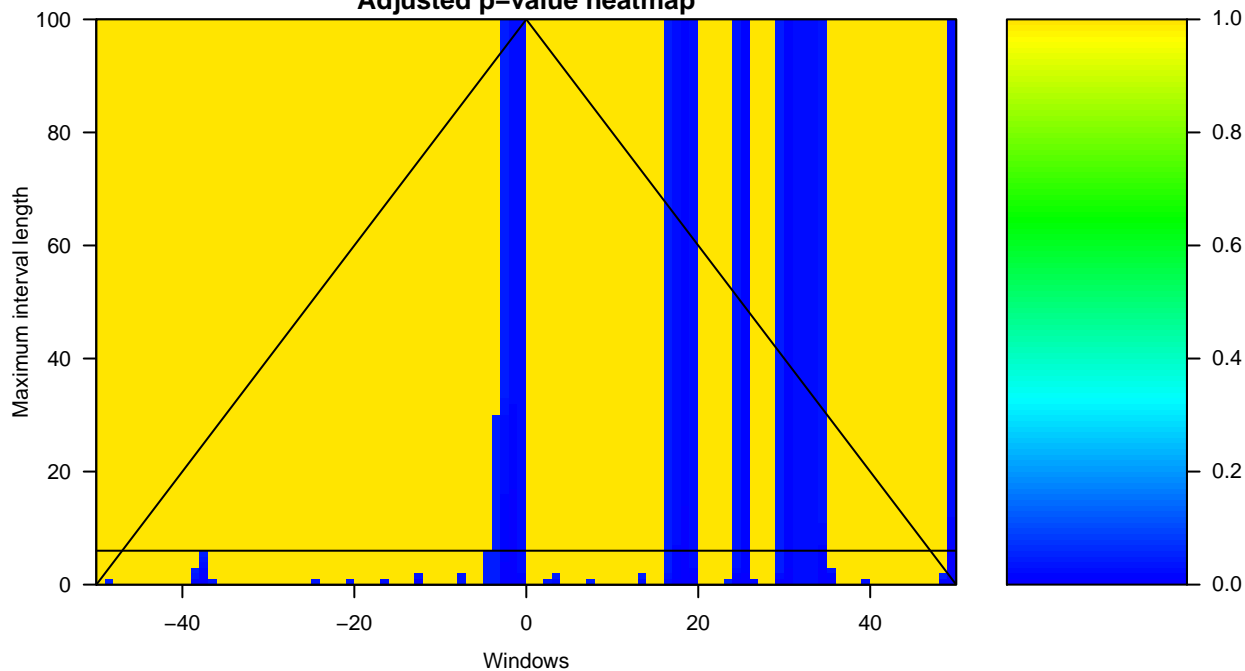
Sample size

# DNA transposons

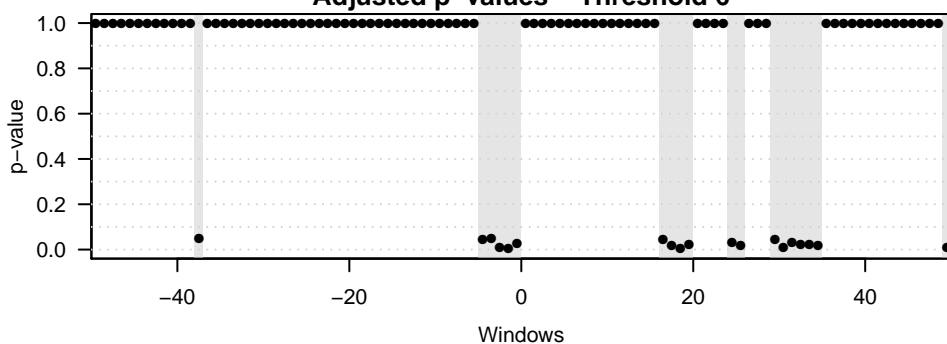


# Alu

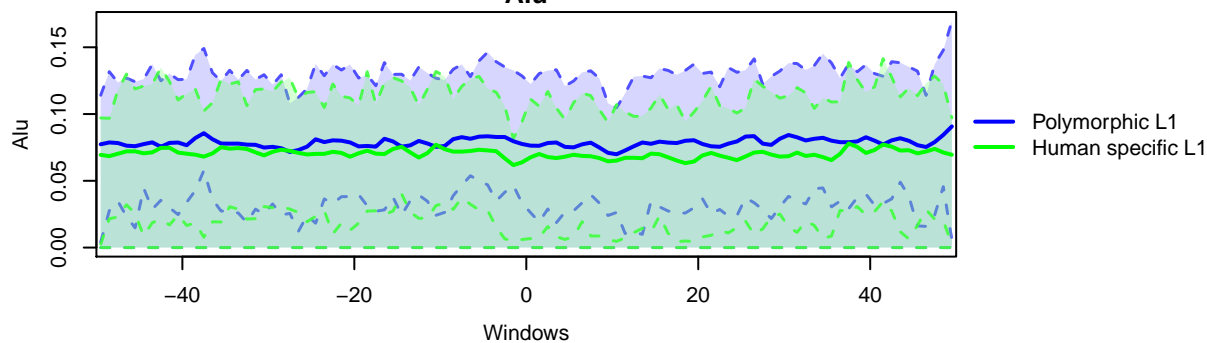
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 6



# Alu



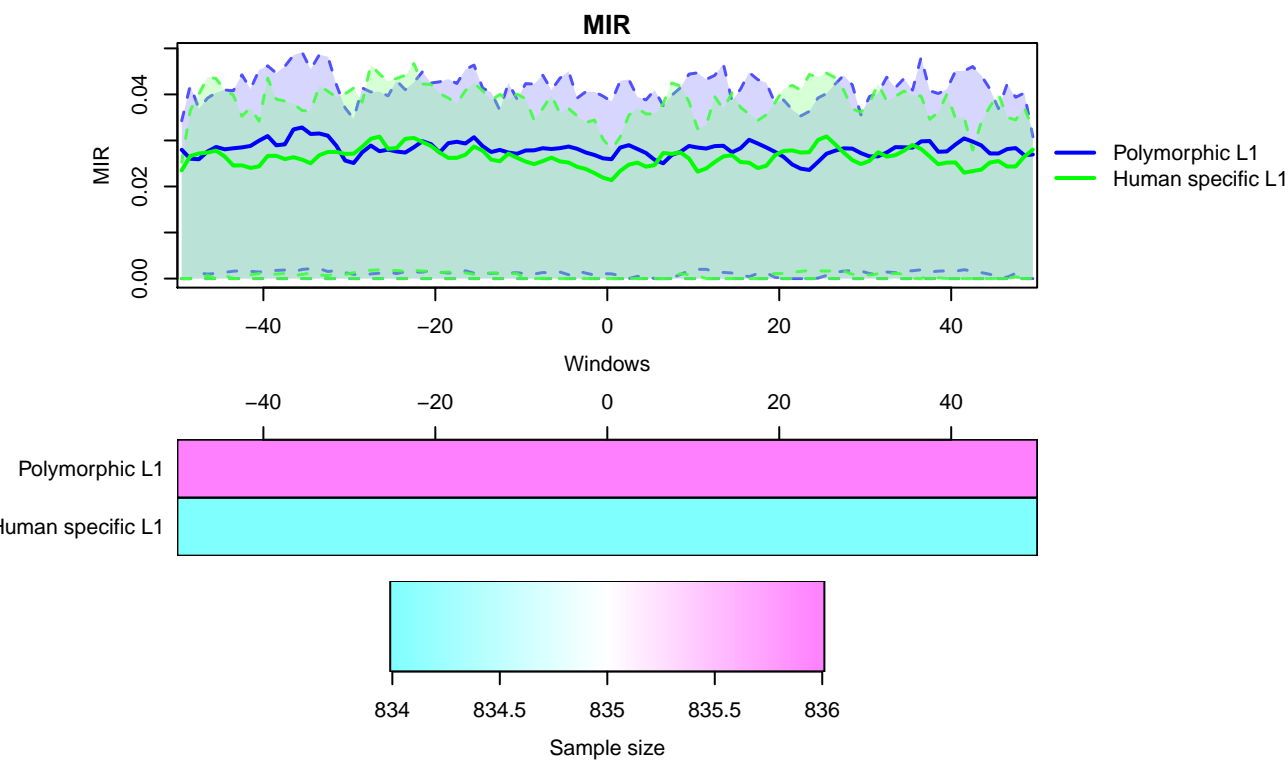
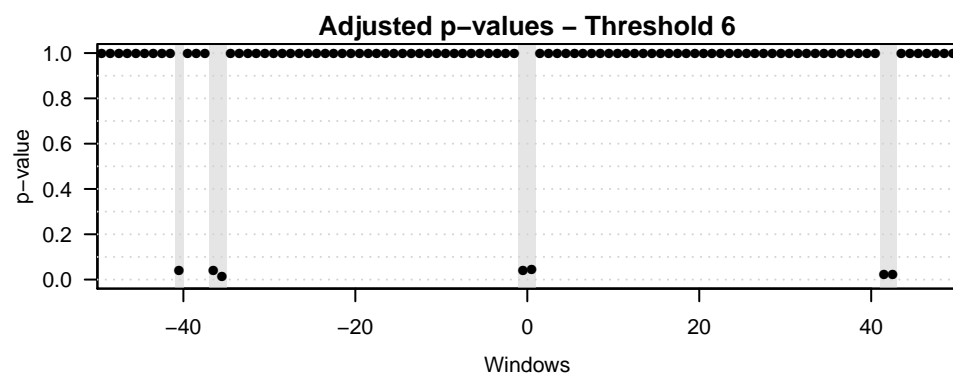
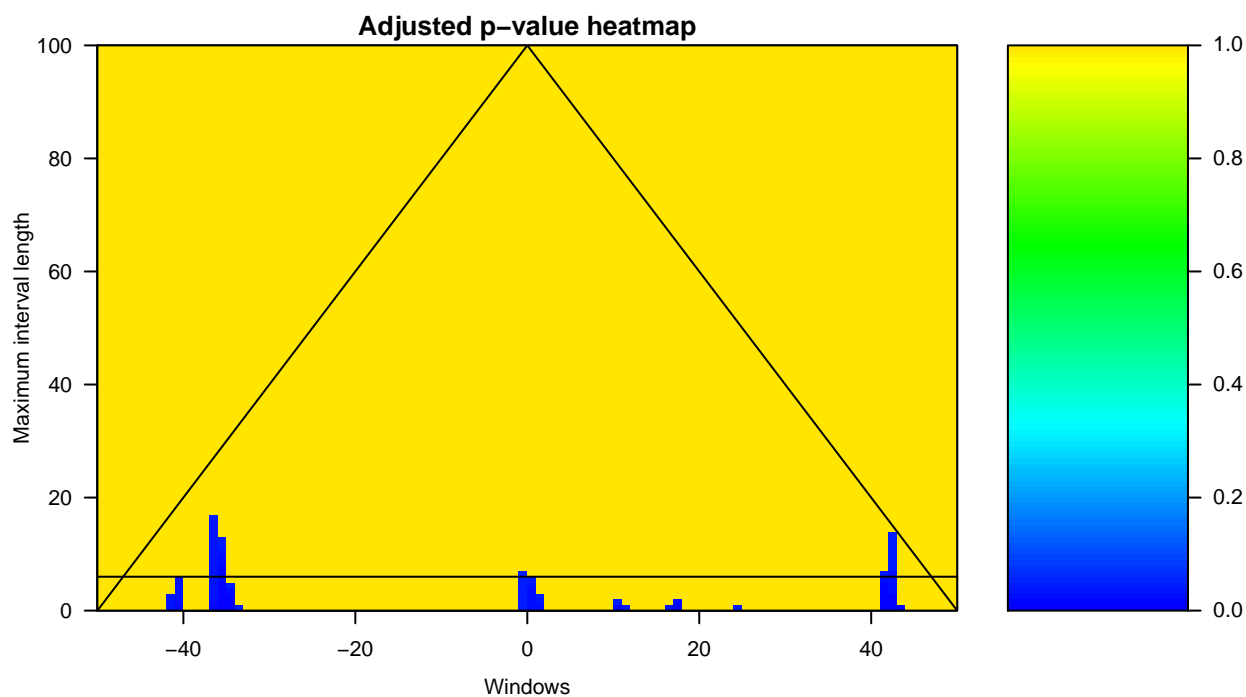
Polymorphic L1

Human specific L1

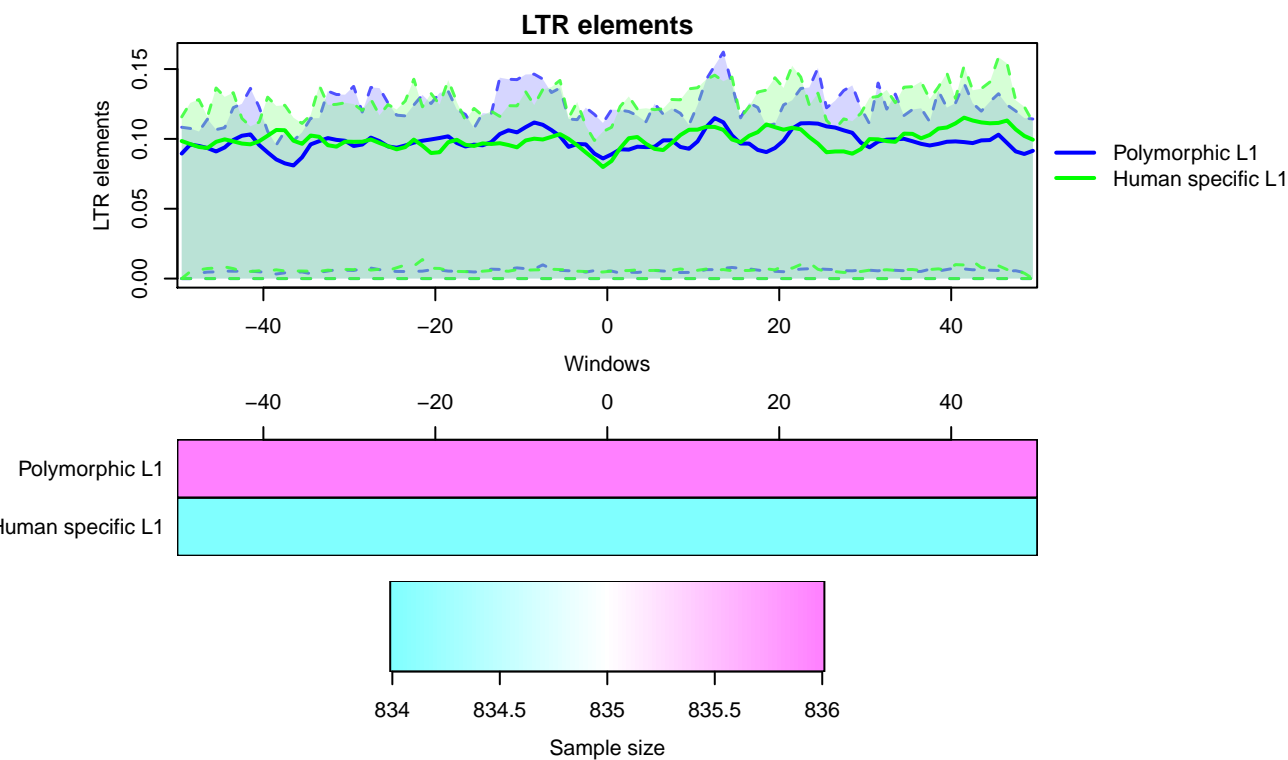
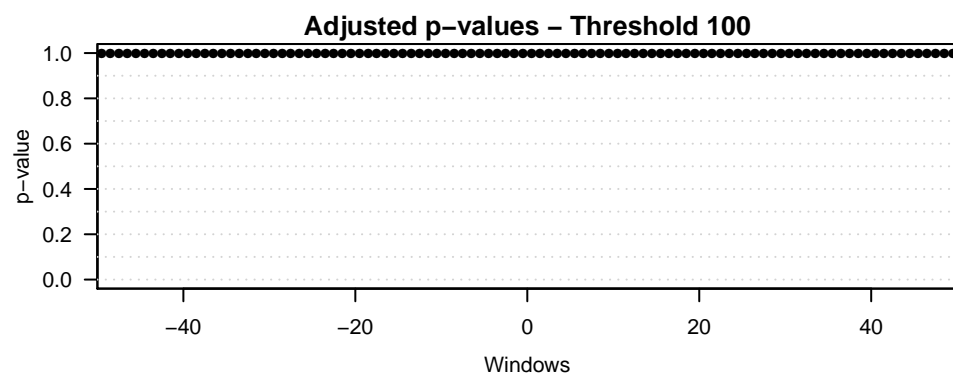
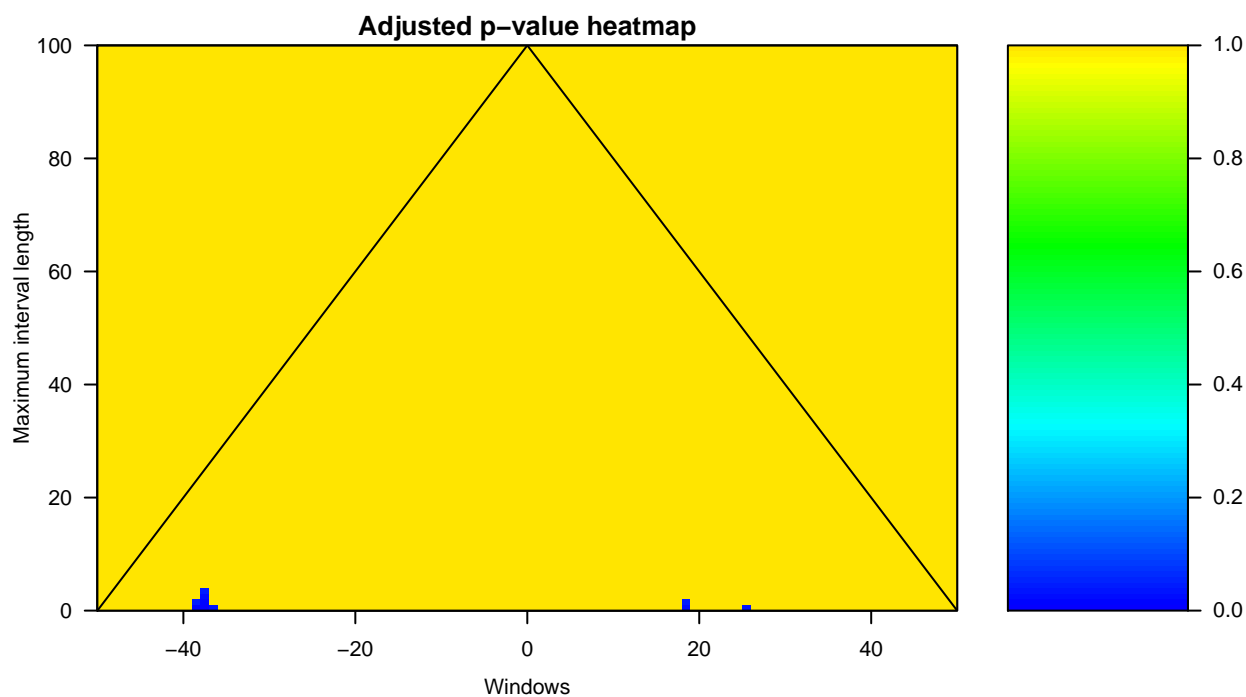
834 834.5 835 835.5 836

Sample size

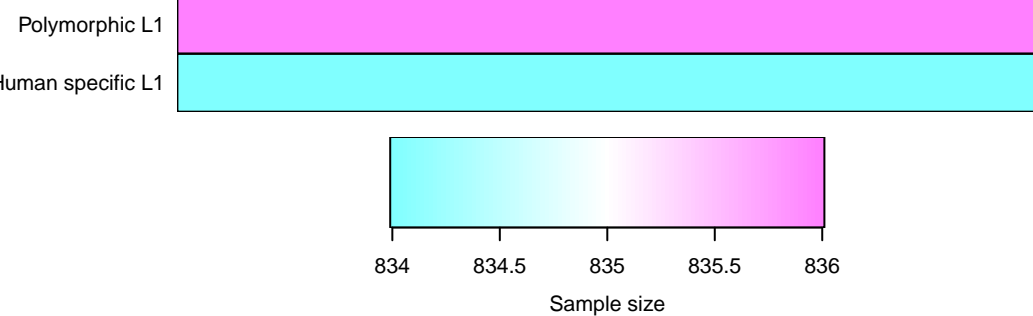
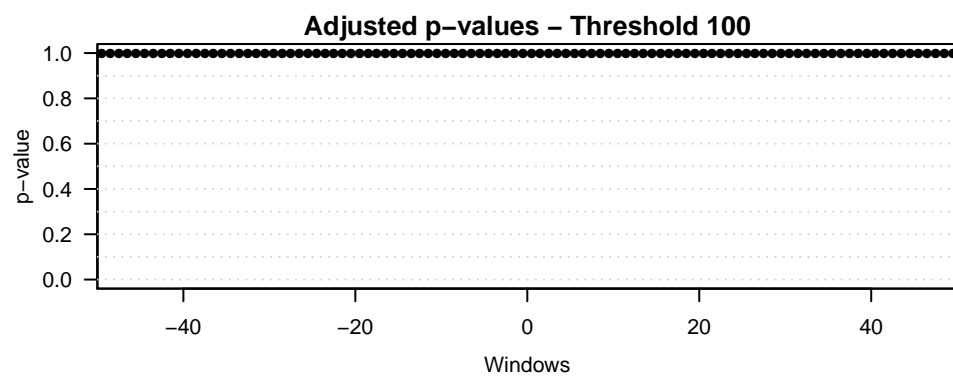
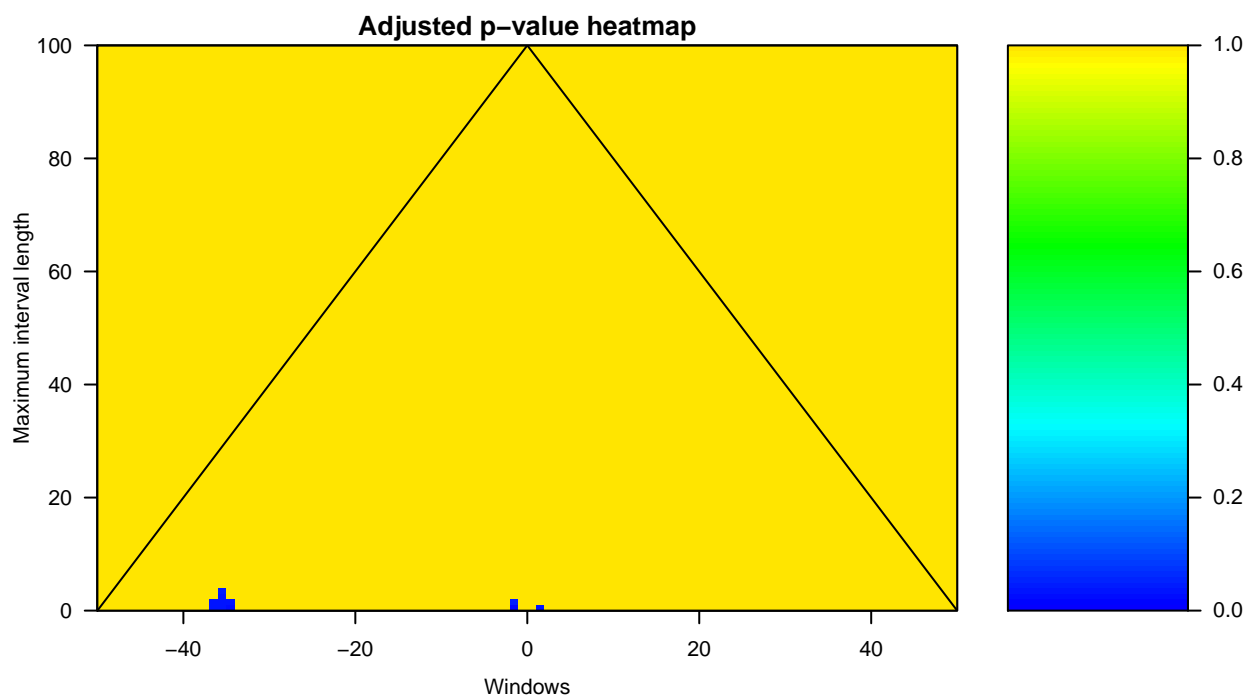
MIR



# LTR elements

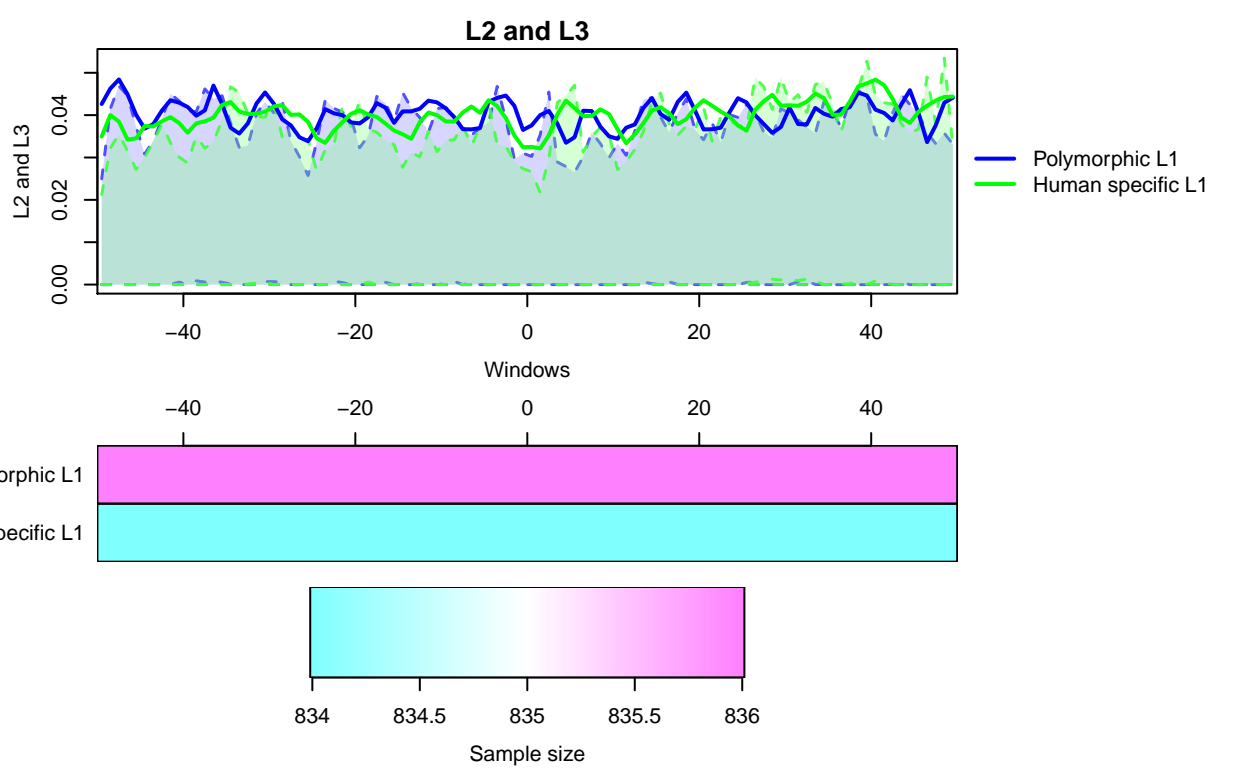
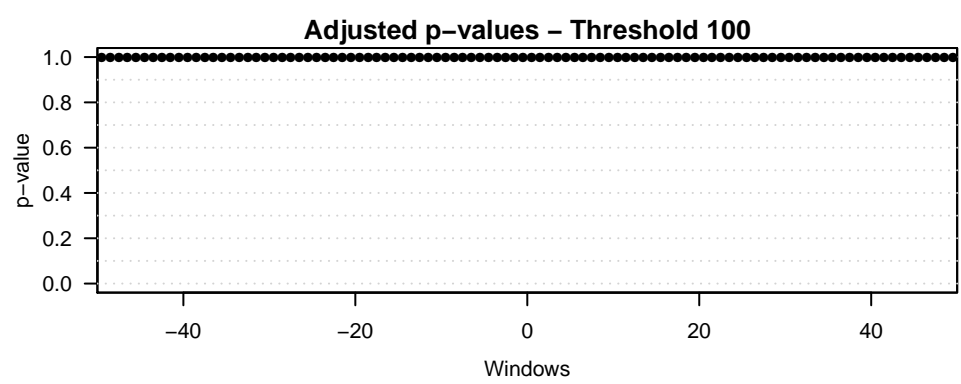
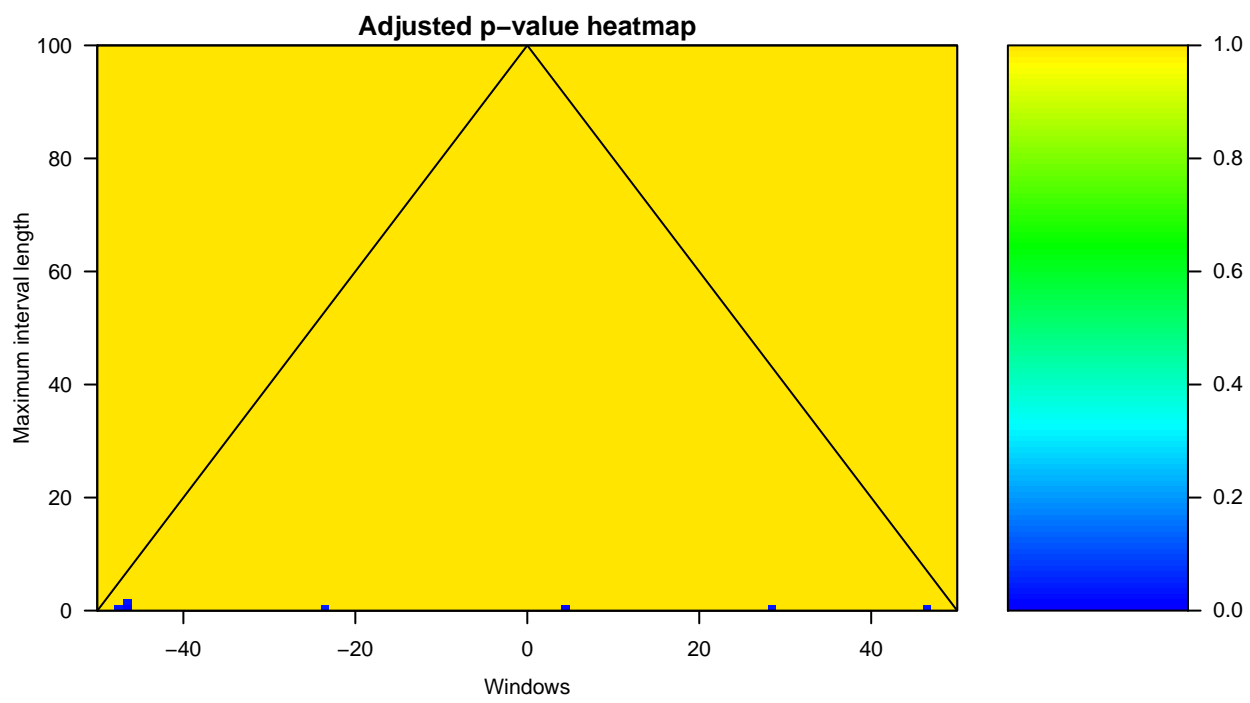


# L1 target motifs

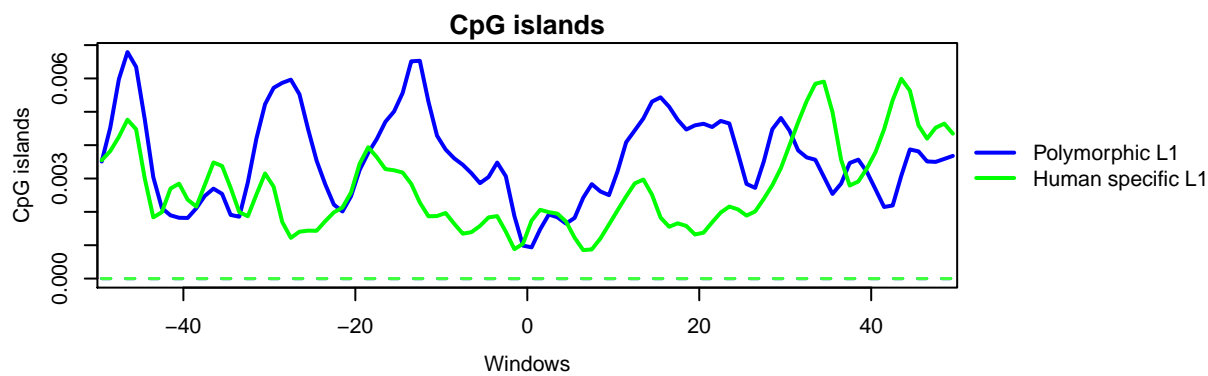
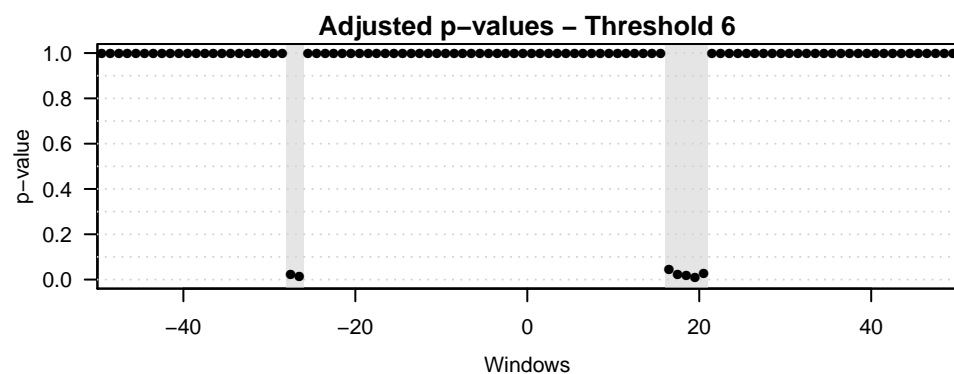
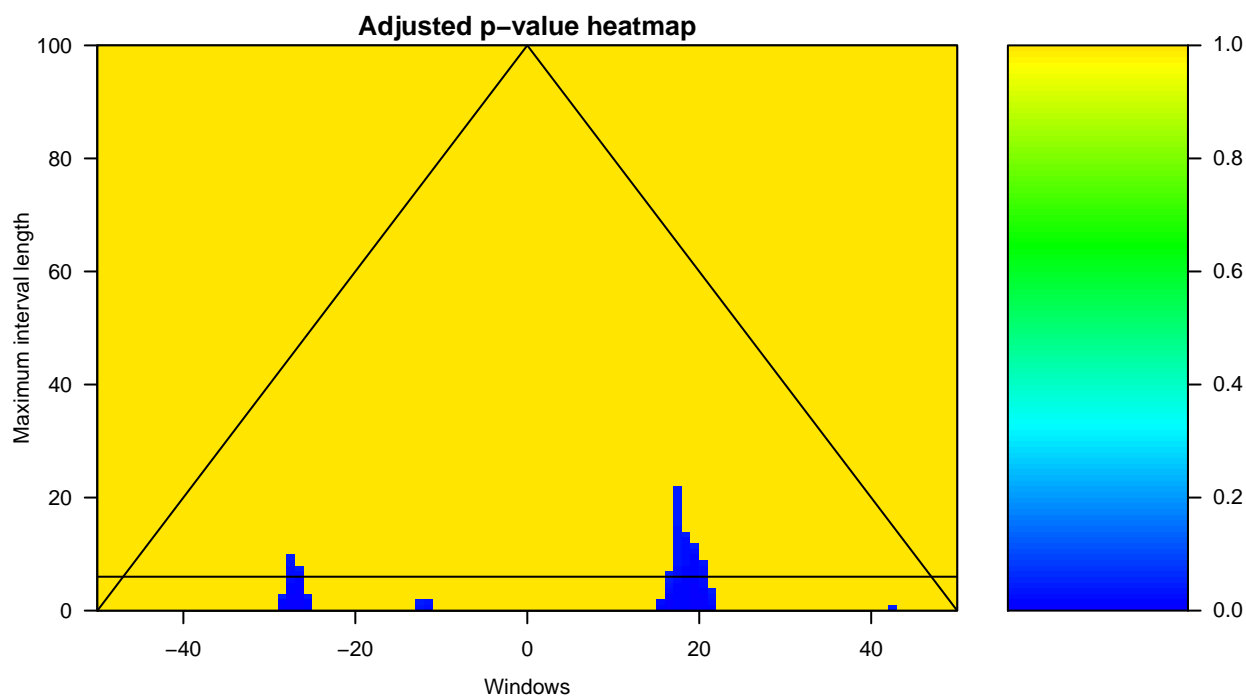




# L2 and L3



# CpG islands



Polymorphic L1

Human specific L1

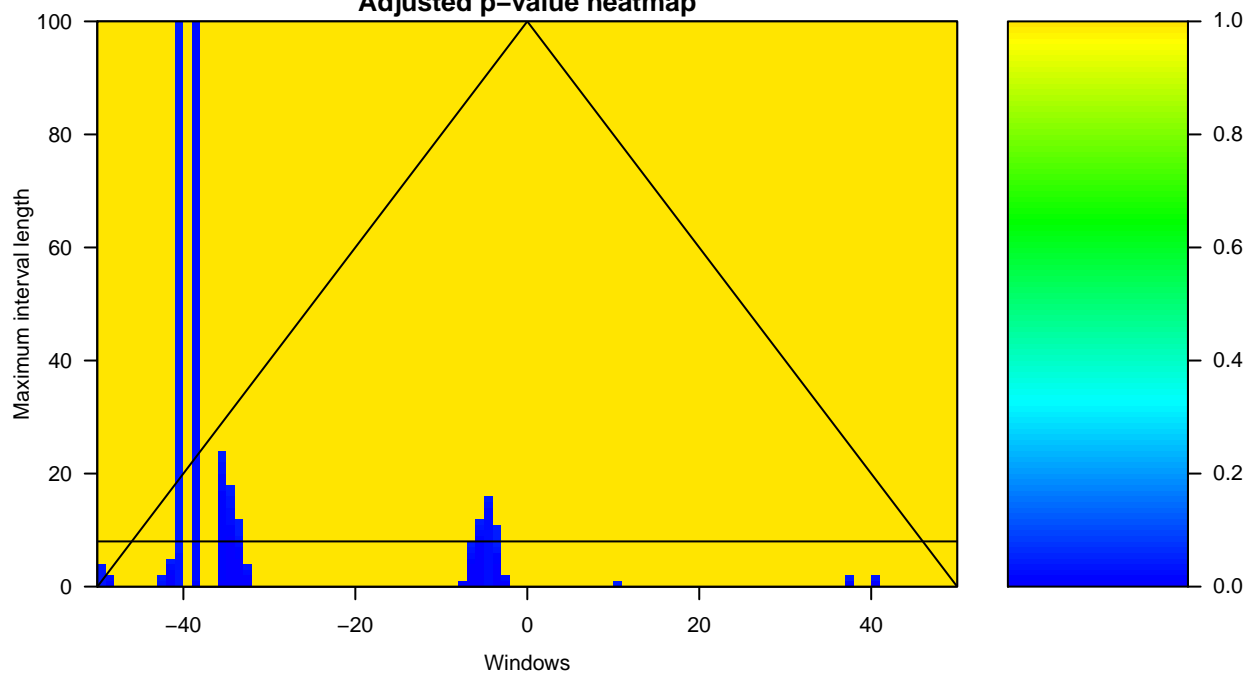


834 834.5 835 835.5 836

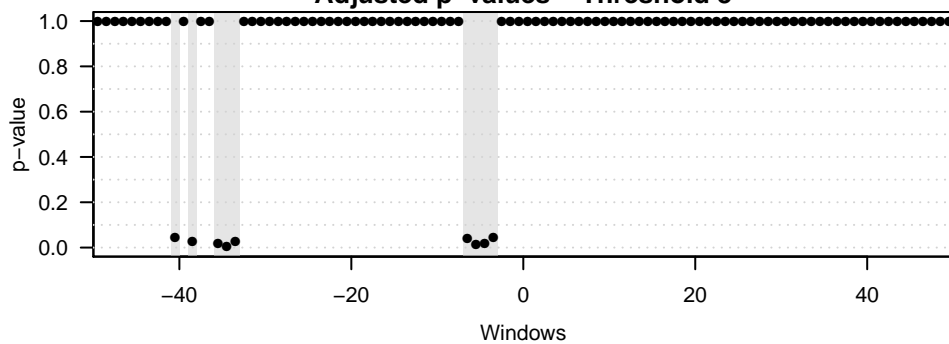
Sample size

# 5-hydroxymethylcytosine

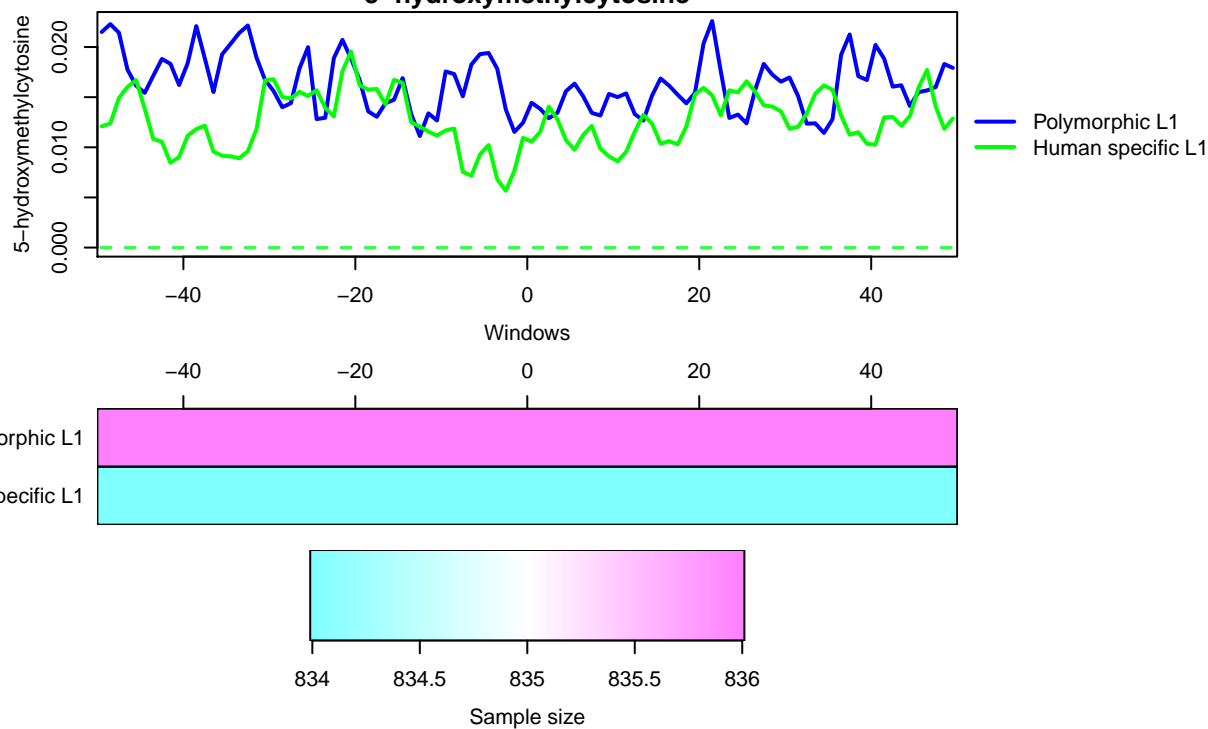
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 8

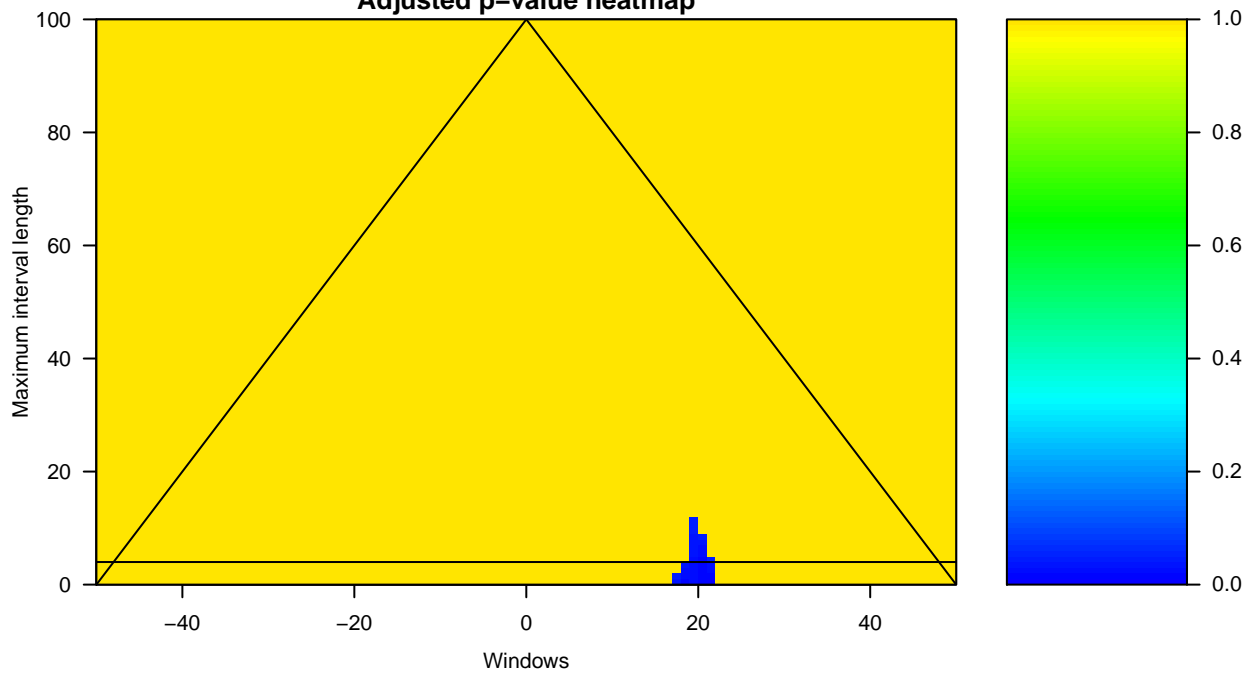


# 5-hydroxymethylcytosine

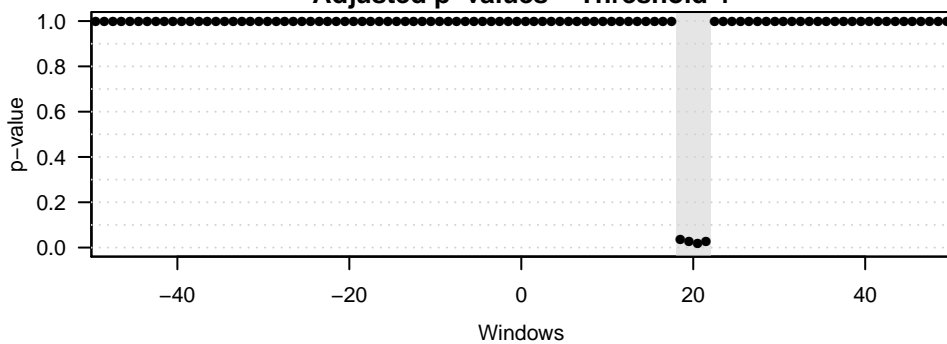


# Sperm hypomethylation

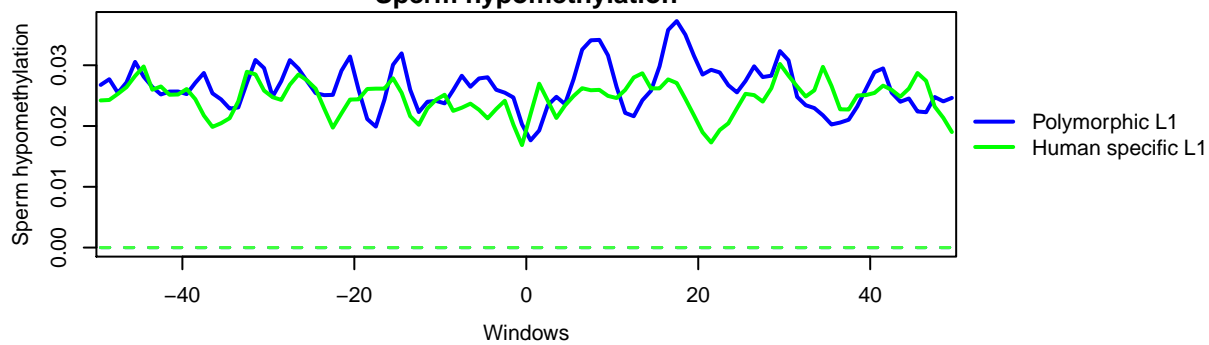
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 4



# Sperm hypomethylation



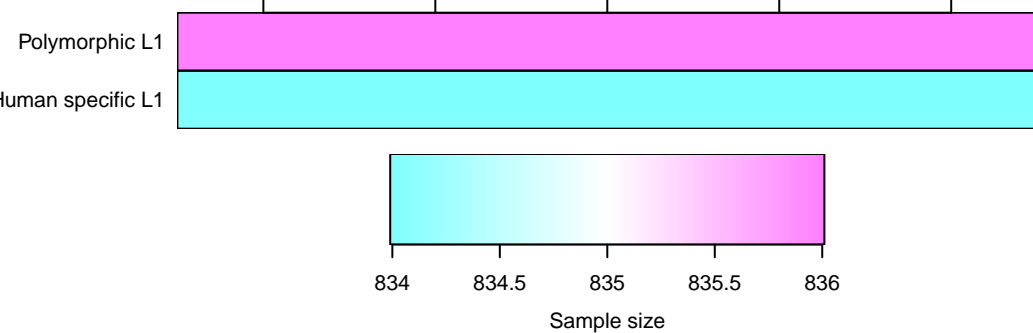
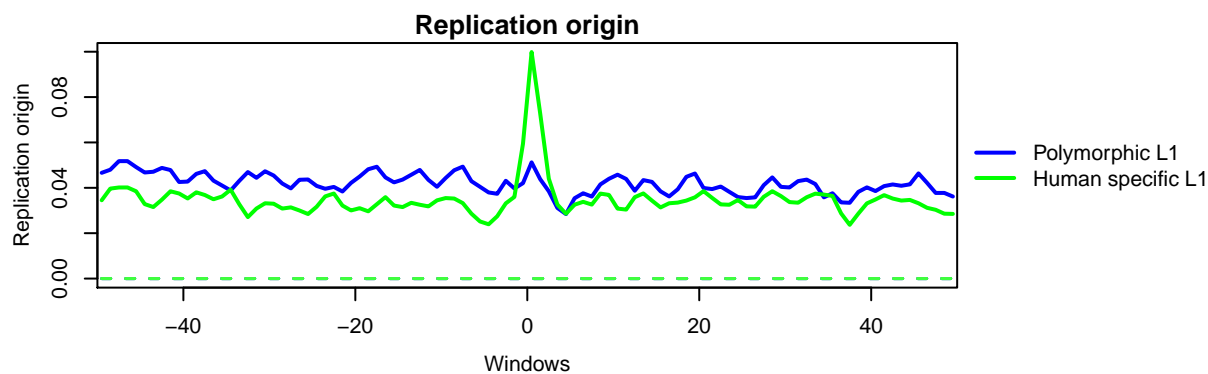
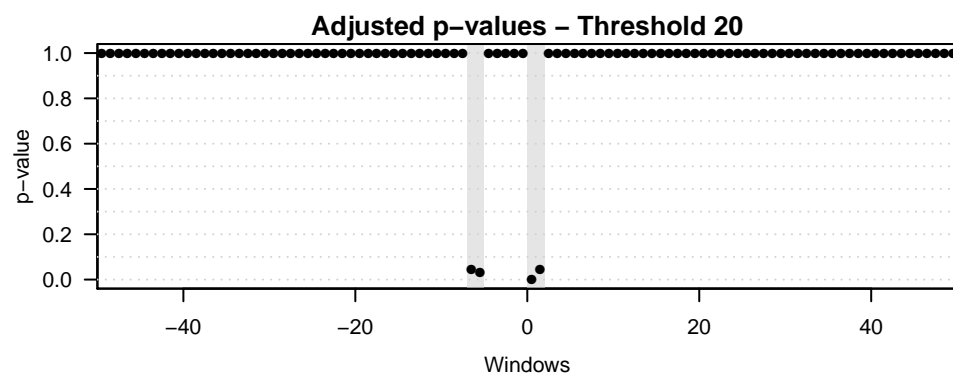
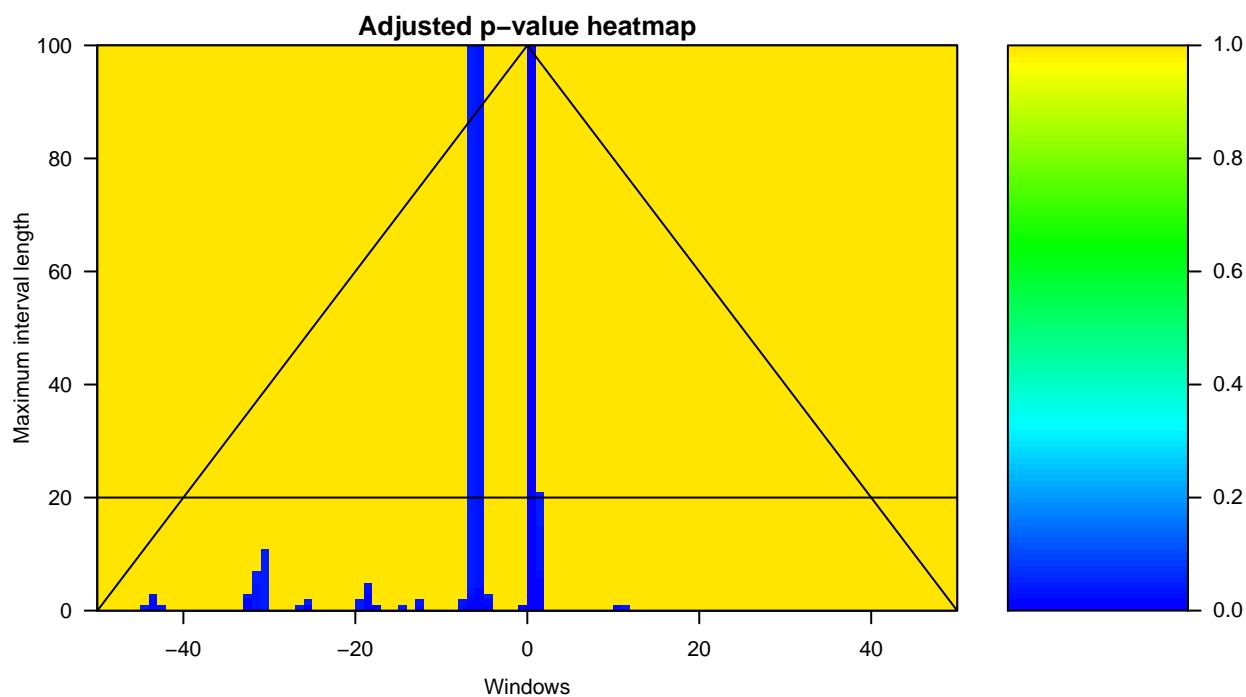
Polymorphic L1

Human specific L1

834 834.5 835 835.5 836

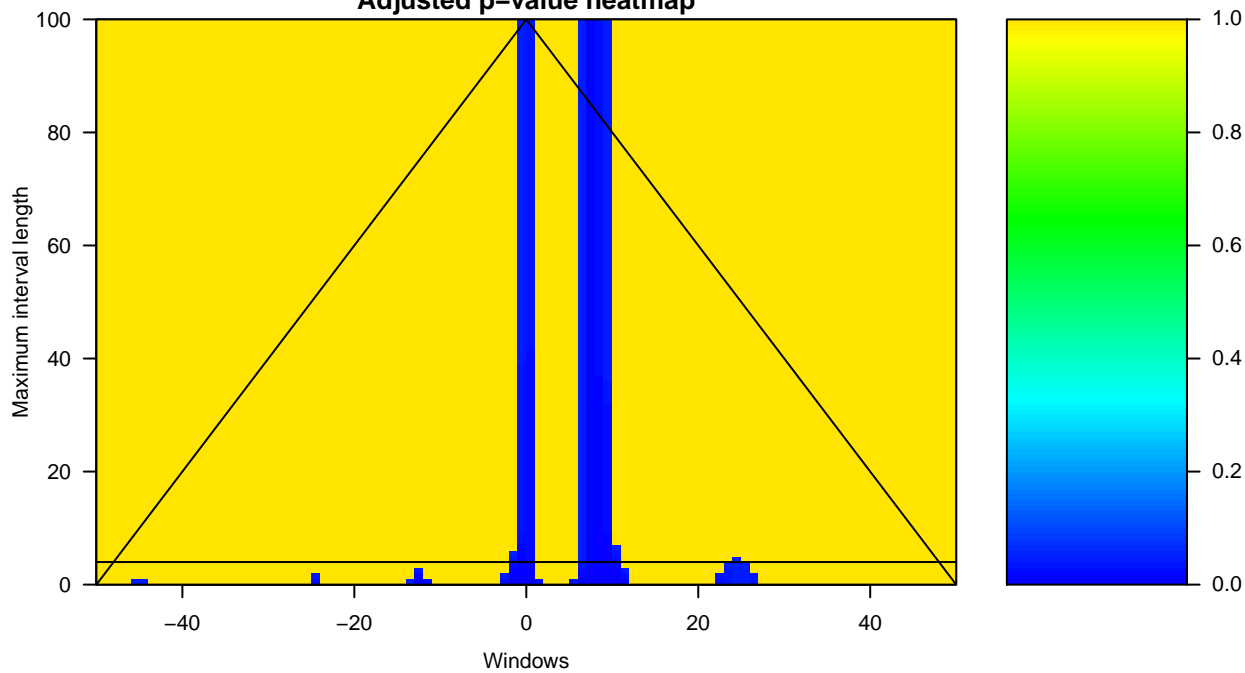
Sample size

# Replication origin

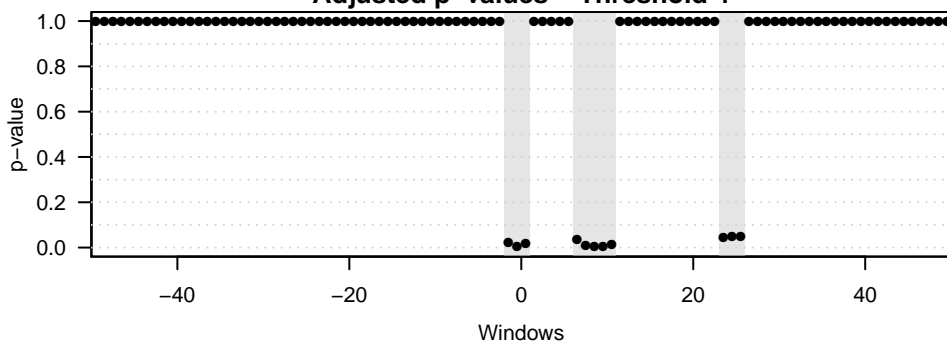


# Sex-averaged recombination hotspots

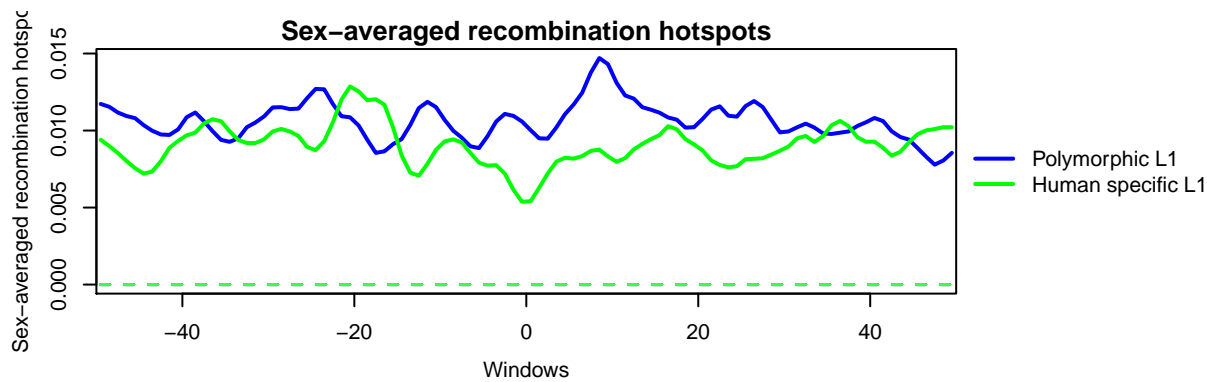
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 4



## Sex-averaged recombination hotspots



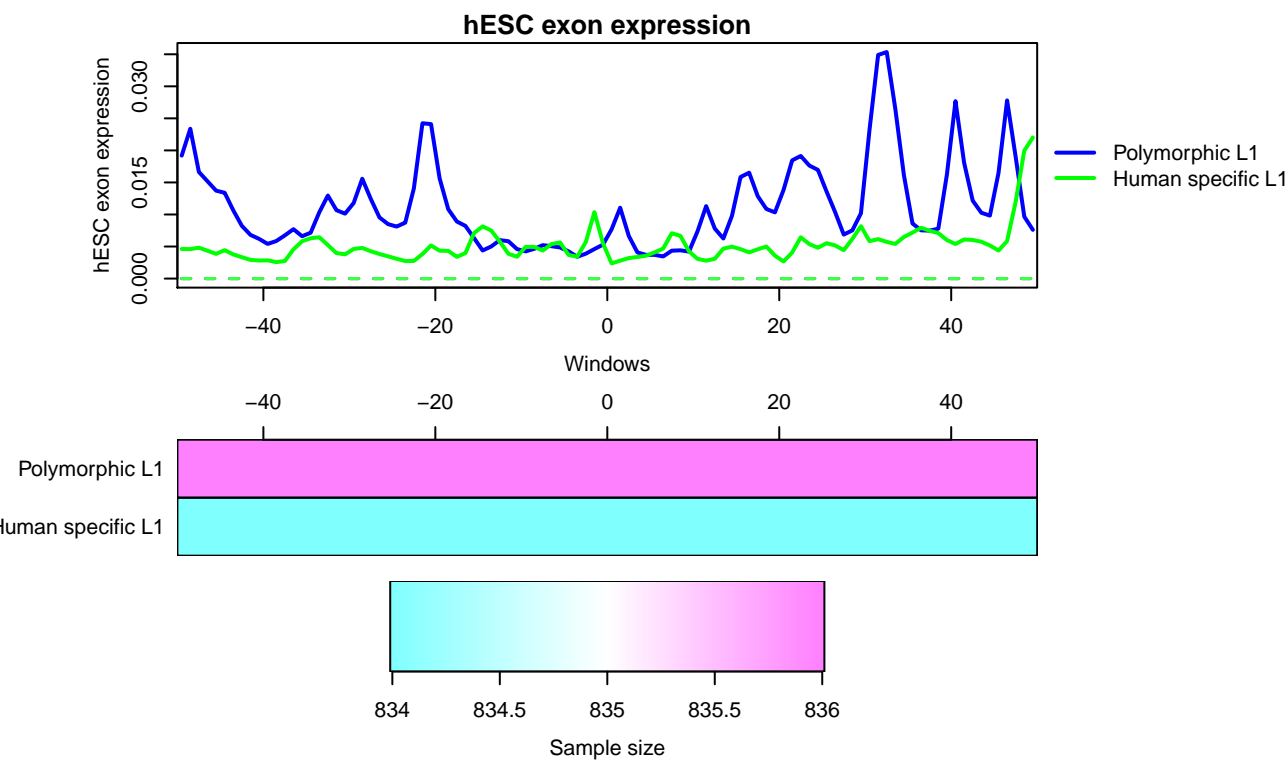
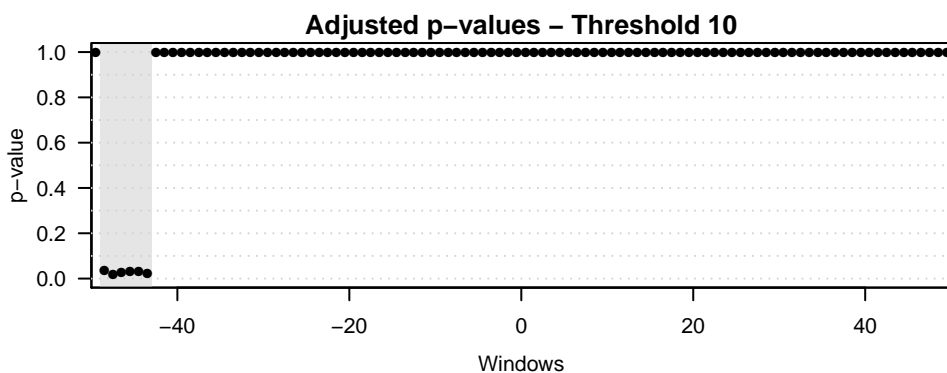
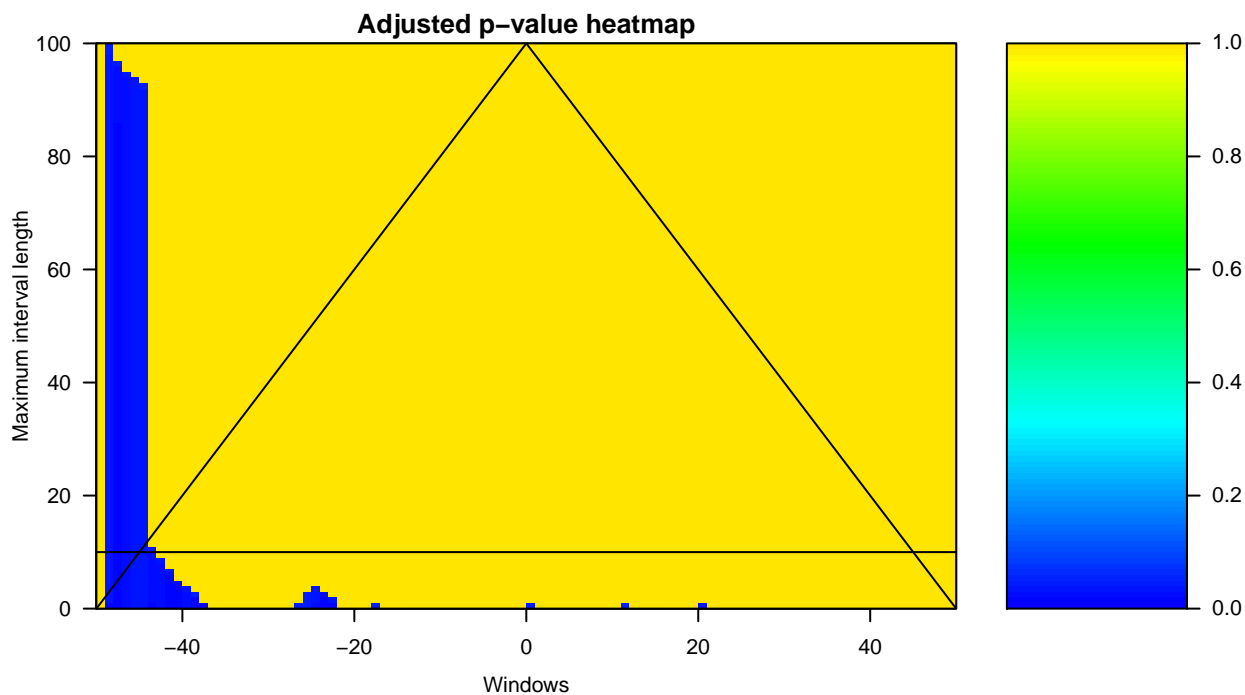
Polymorphic L1

Human specific L1

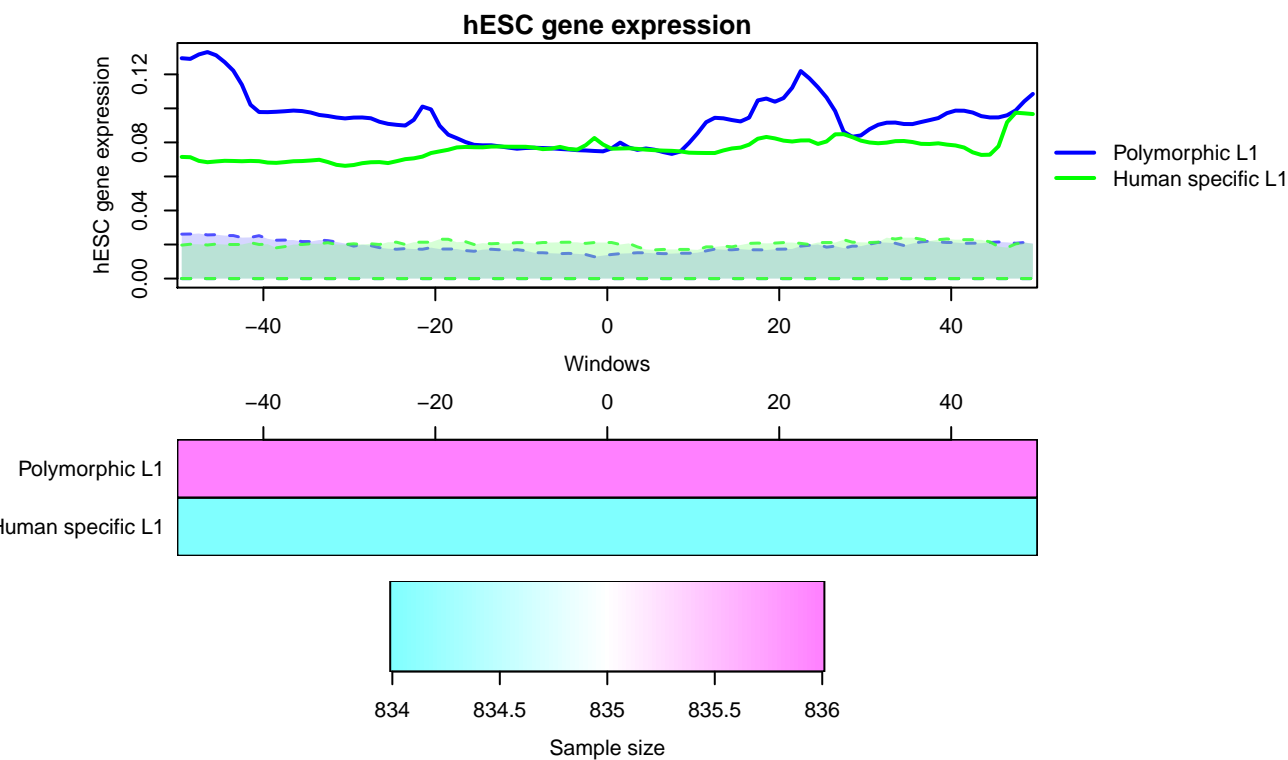
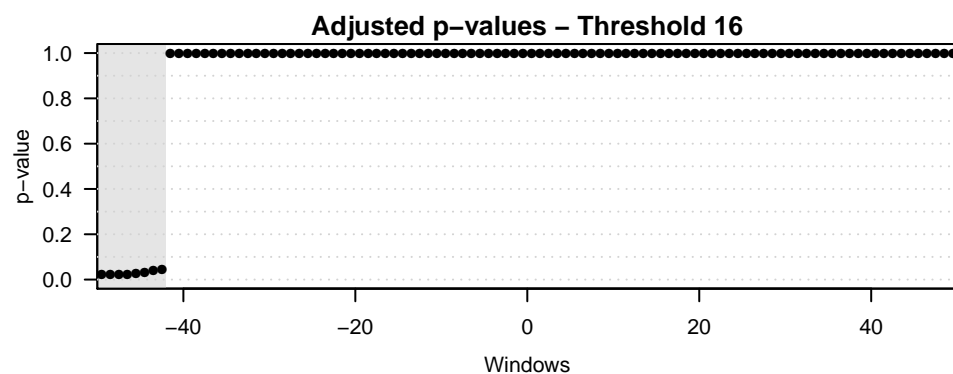
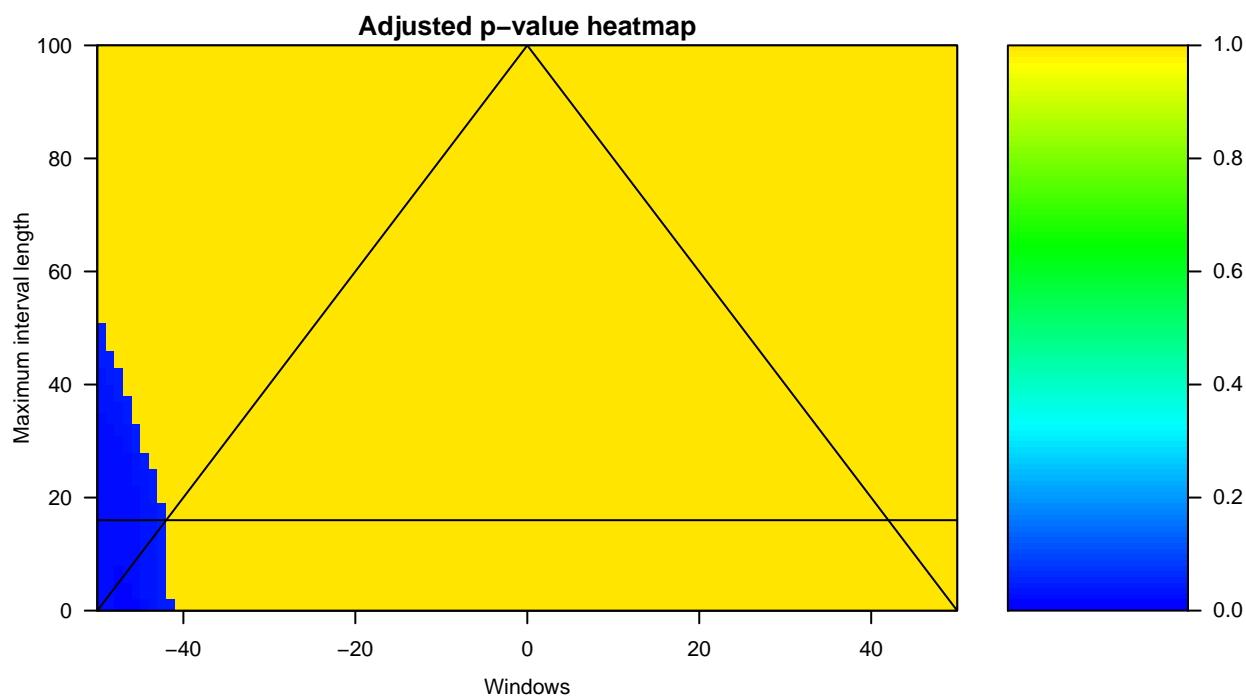
834 834.5 835 835.5 836

Sample size

# hESC exon expression

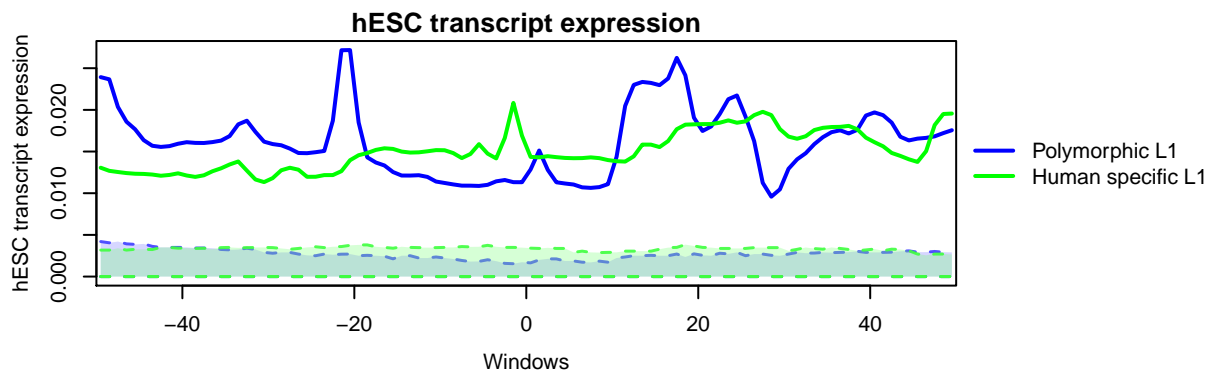
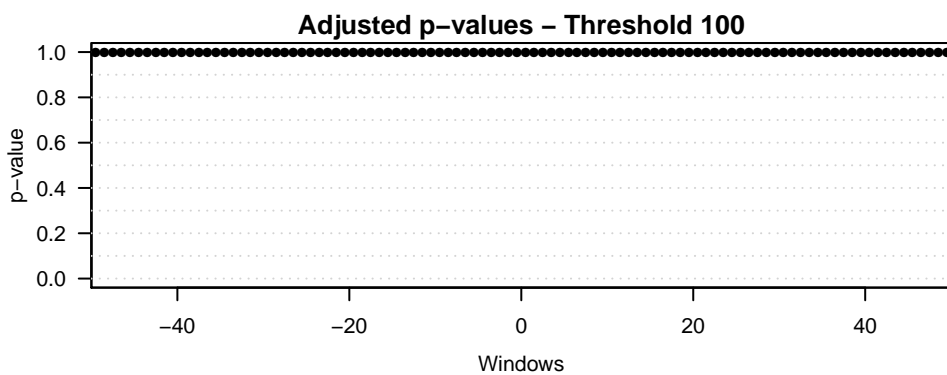
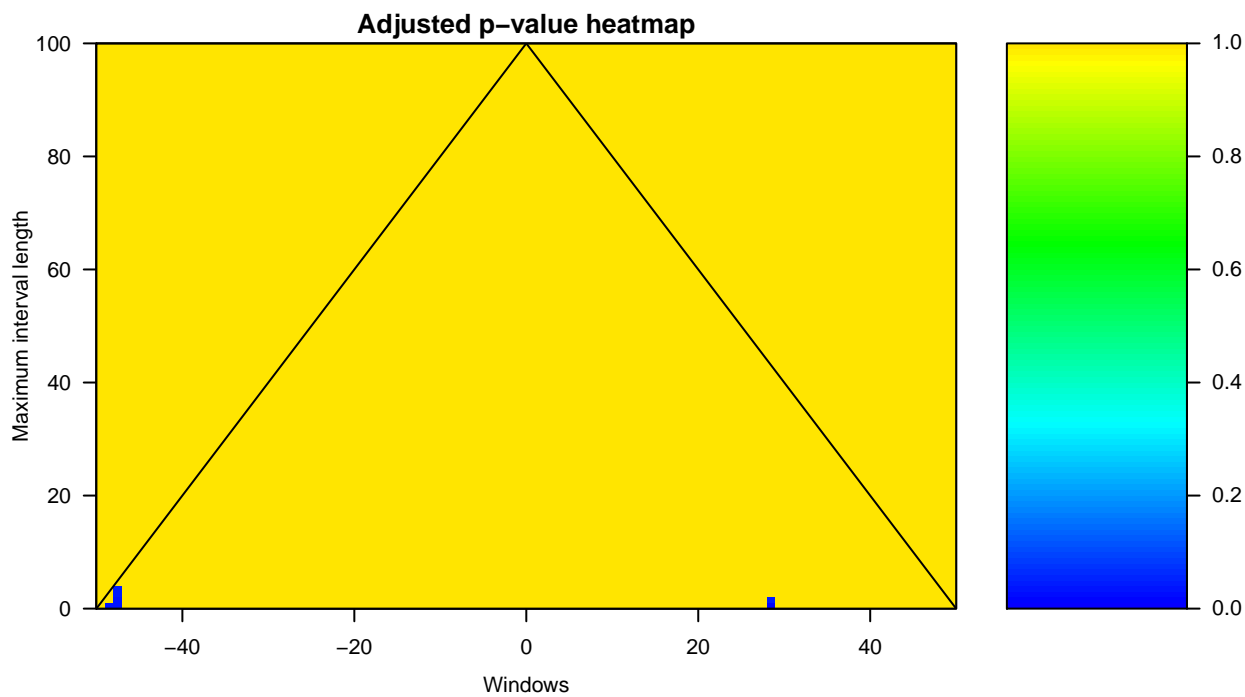


# hESC gene expression





# hESC transcript expression



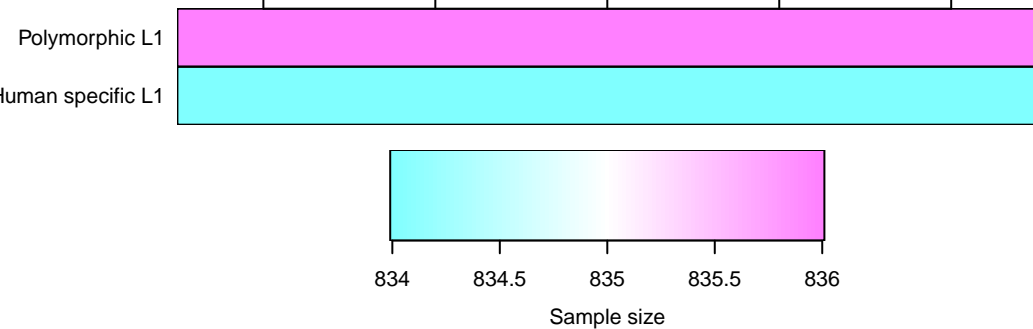
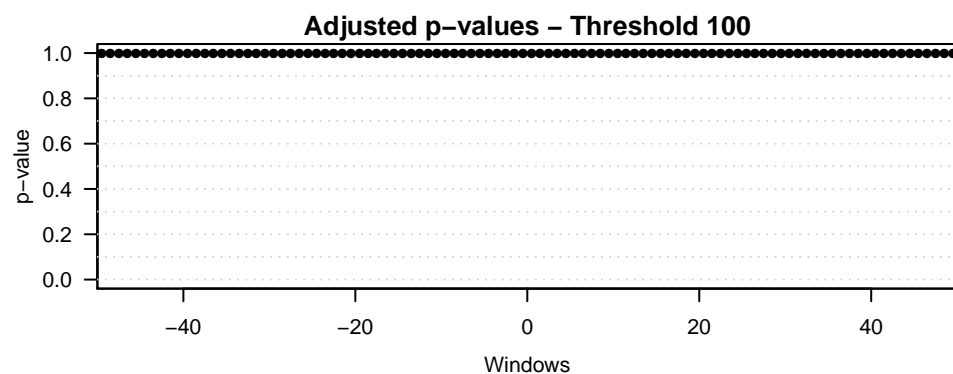
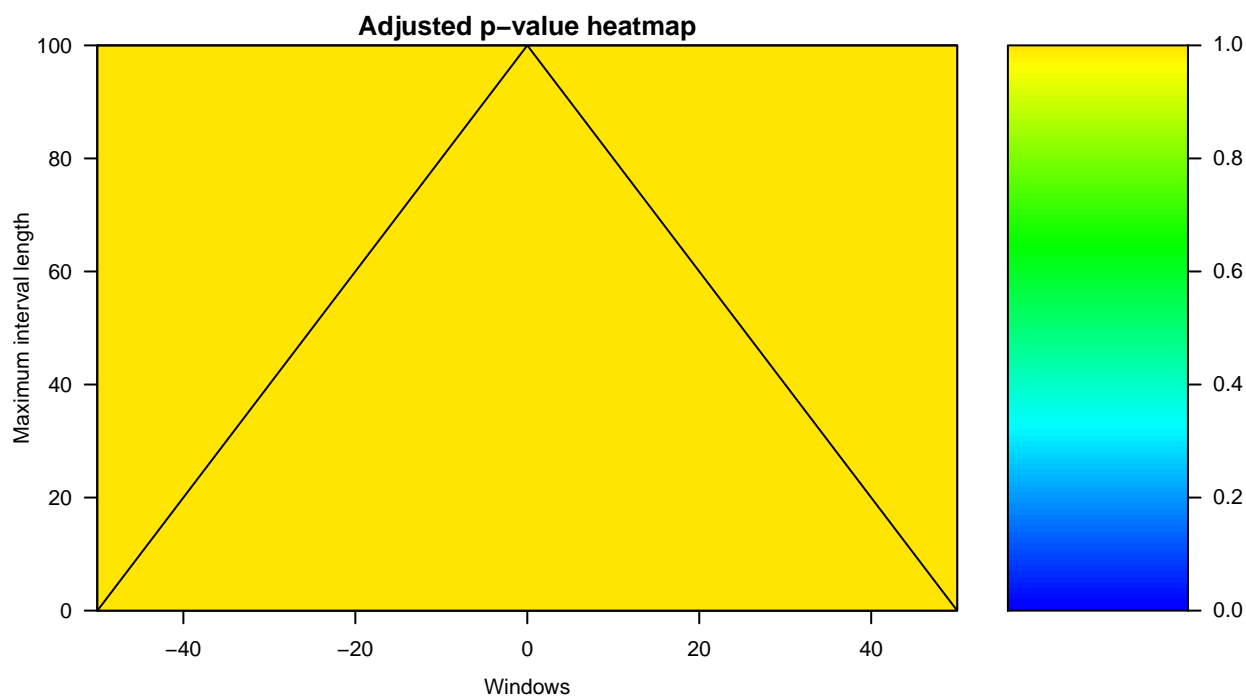
Polymorphic L1

Human specific L1

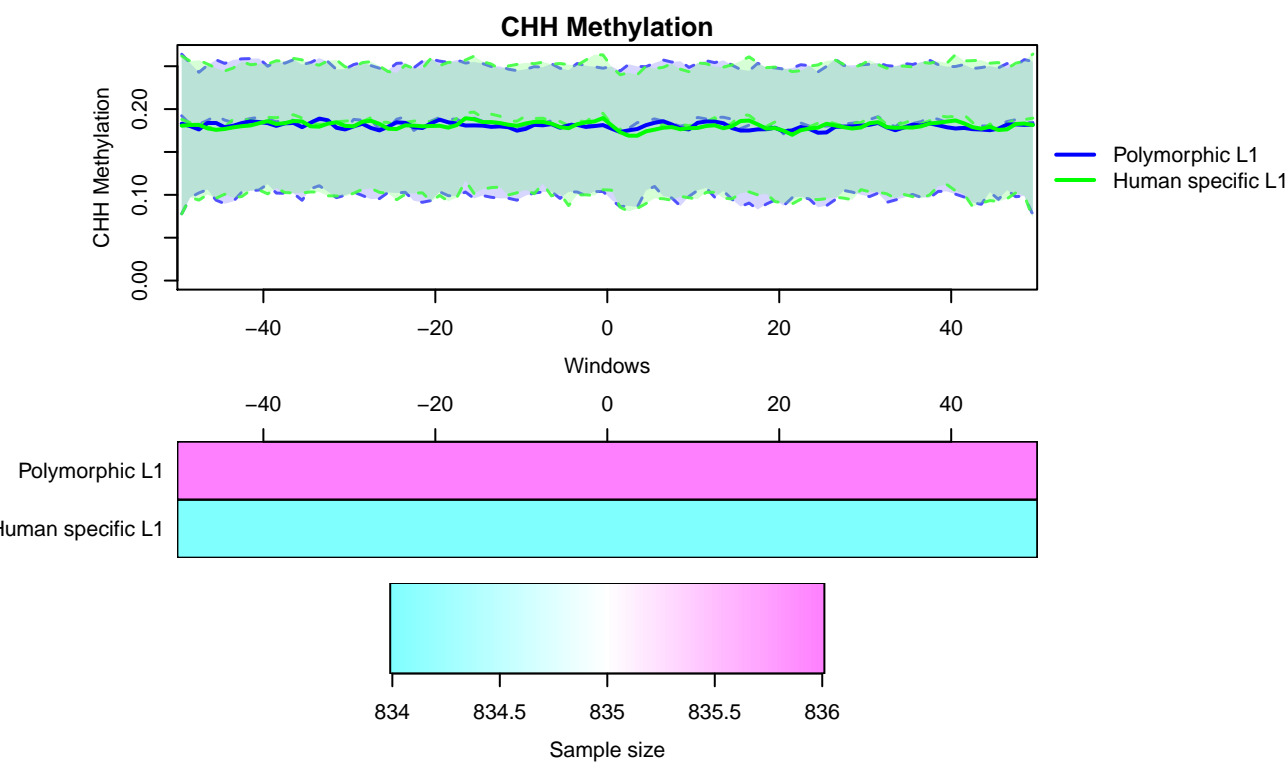
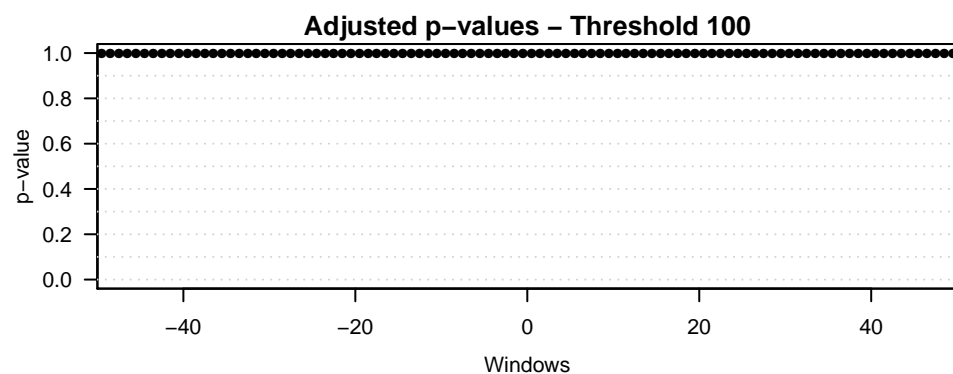
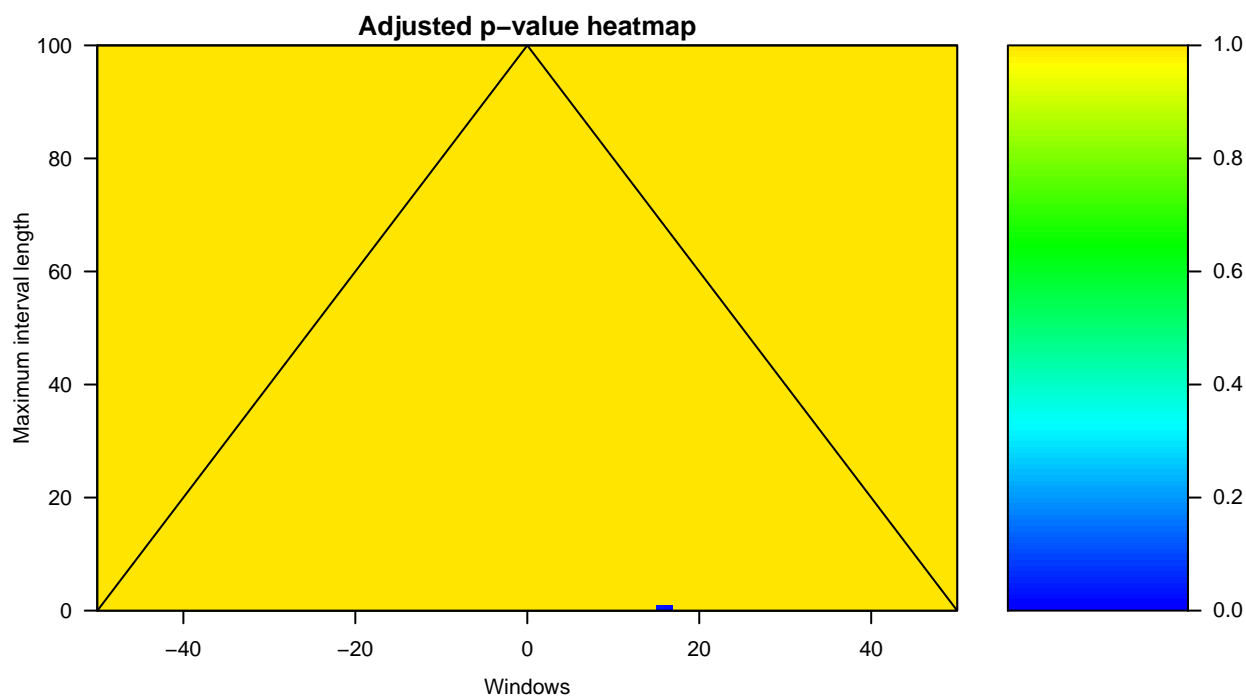
834 834.5 835 835.5 836

Sample size

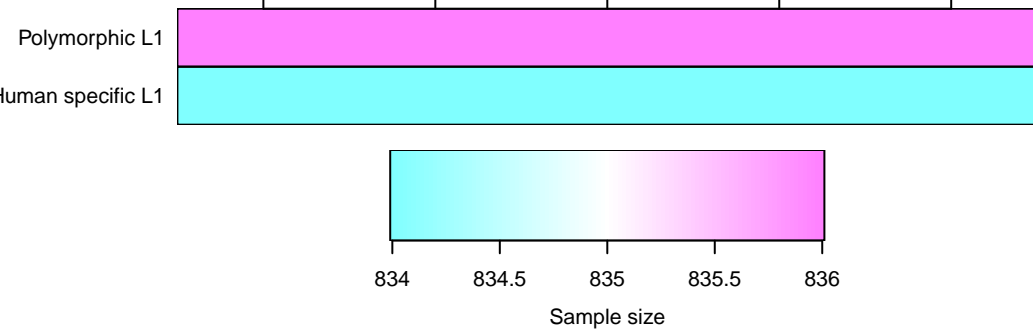
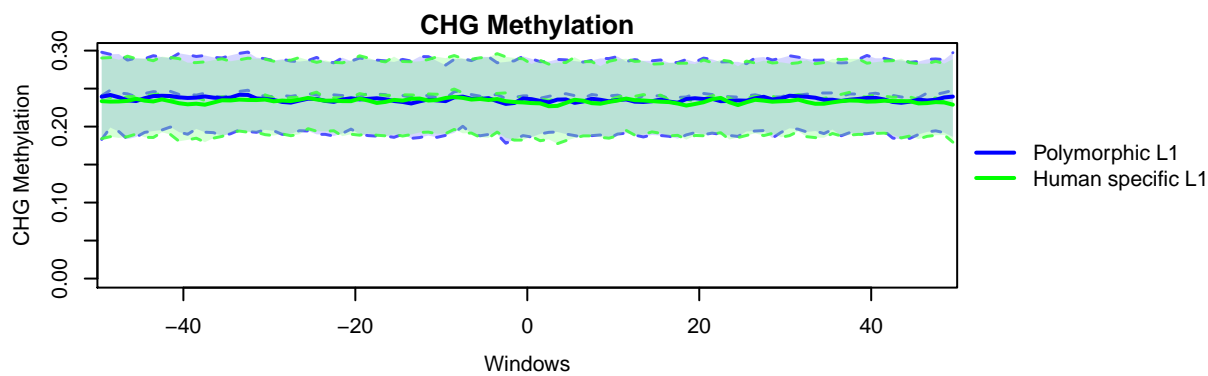
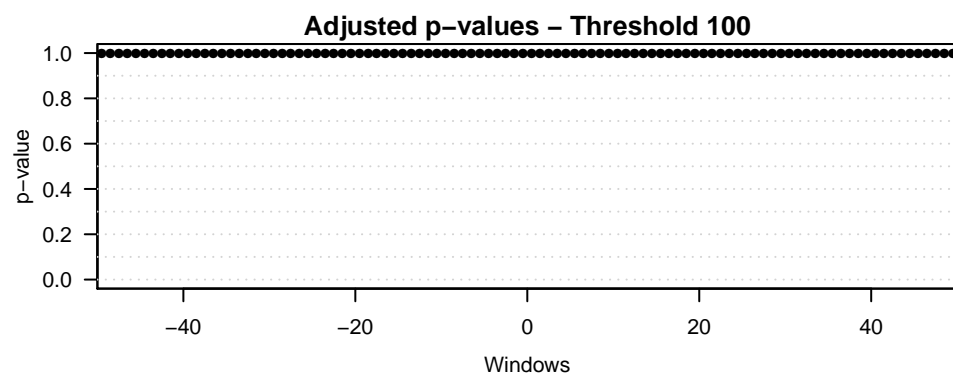
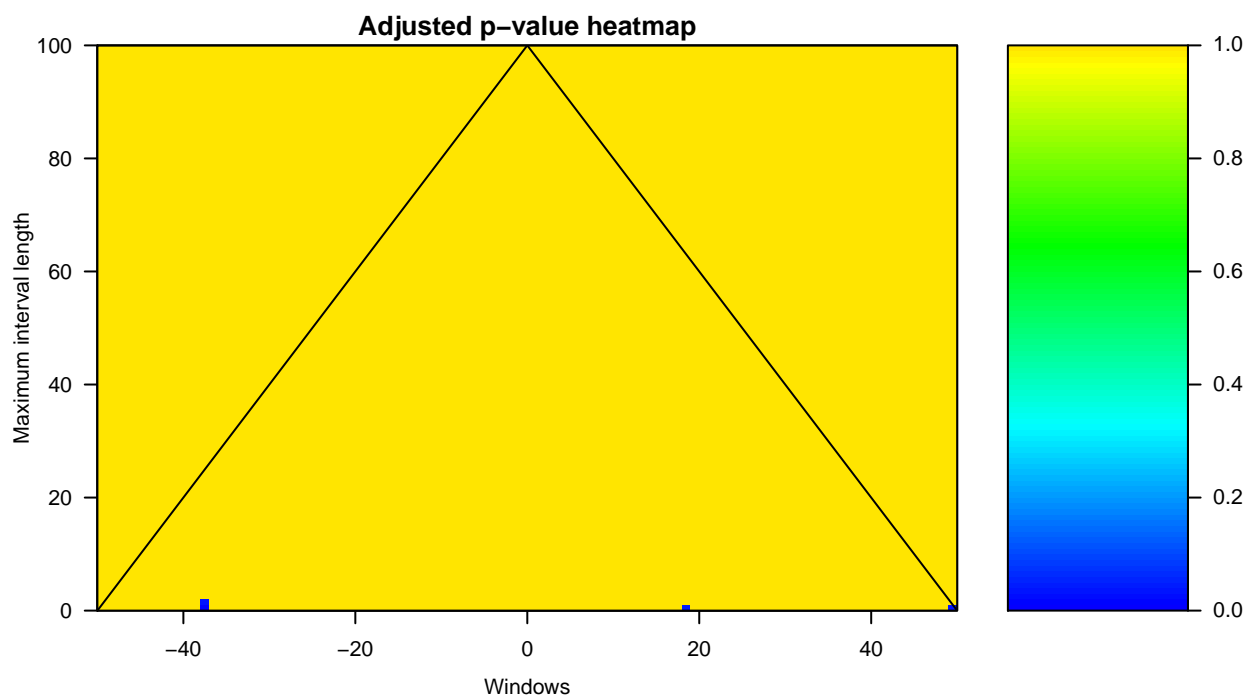
# Testis expression



# CHH Methylation



# CHG Methylation



# CPG Methylation

