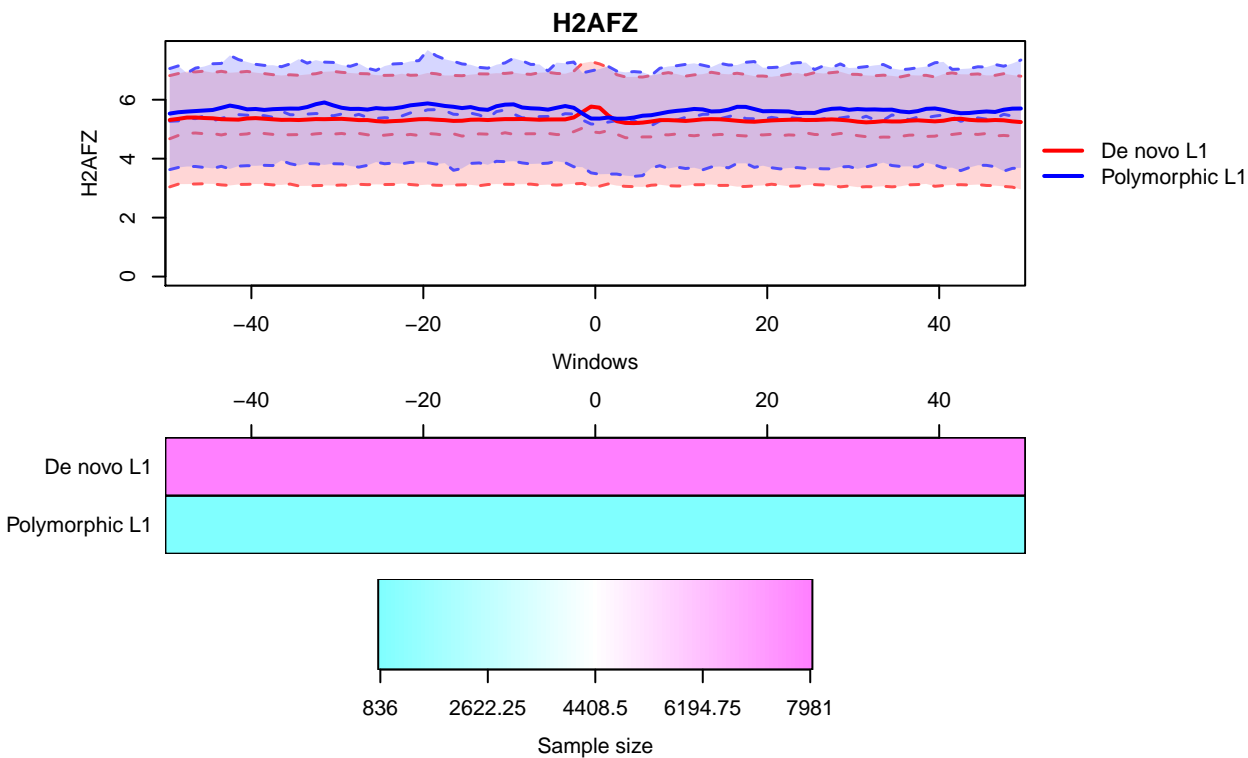
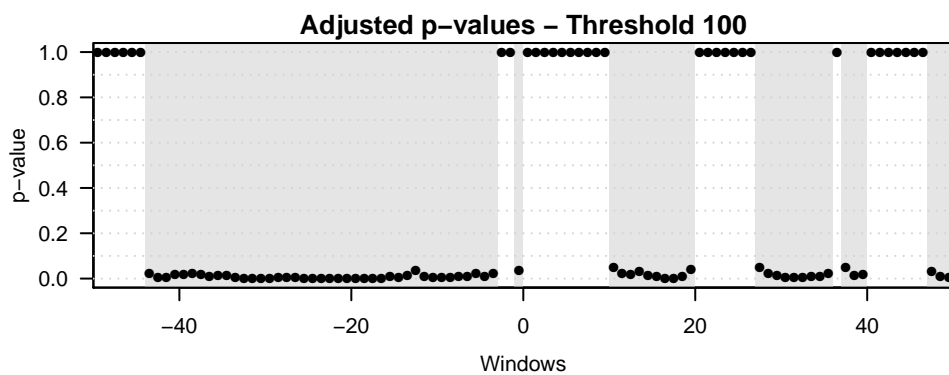
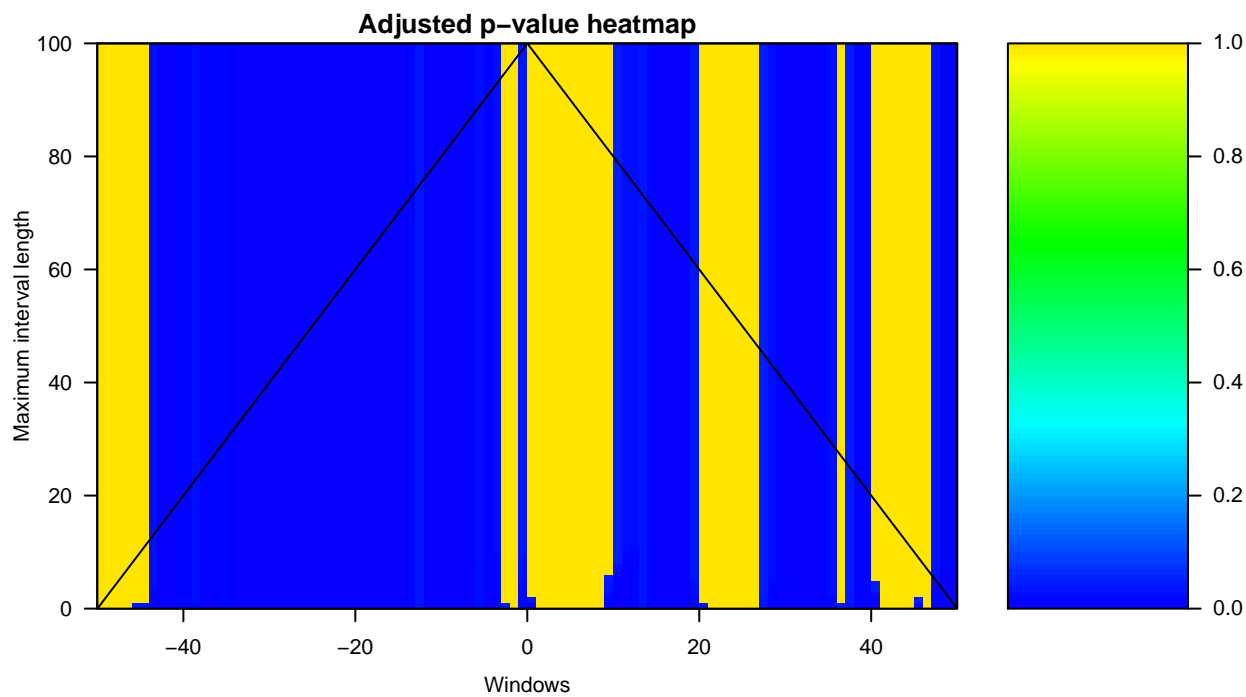
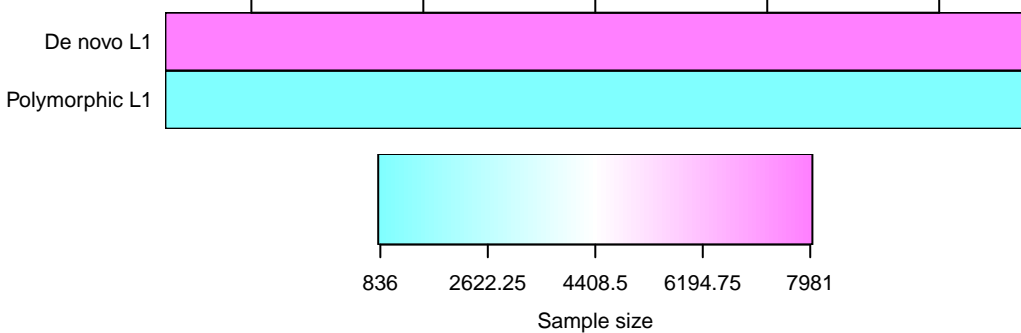
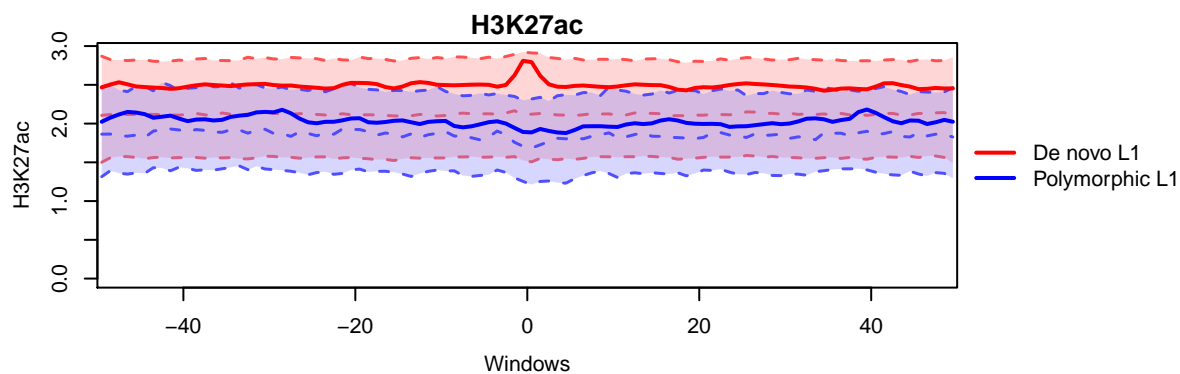
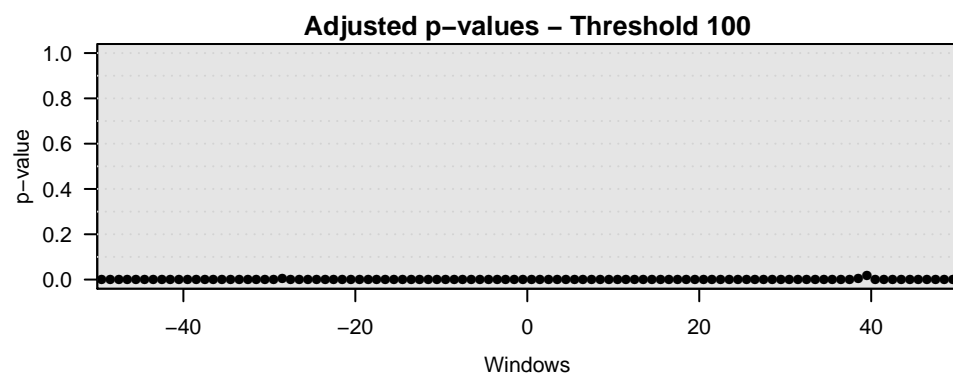
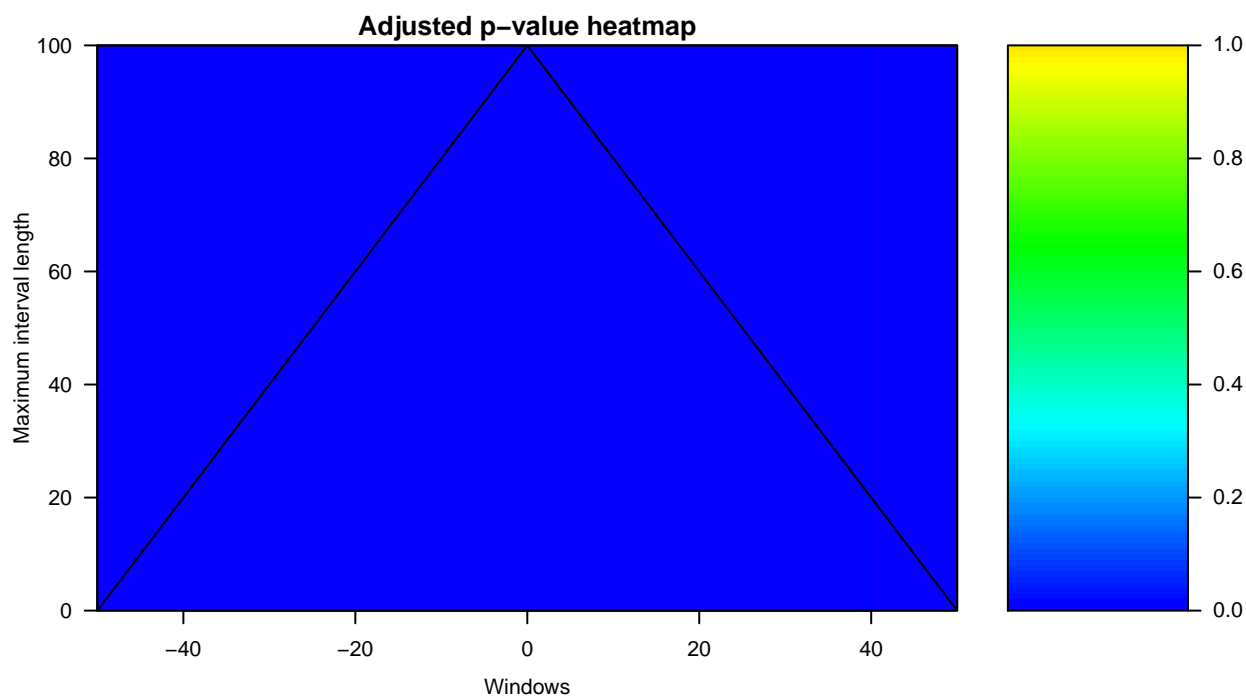


## H2AFZ

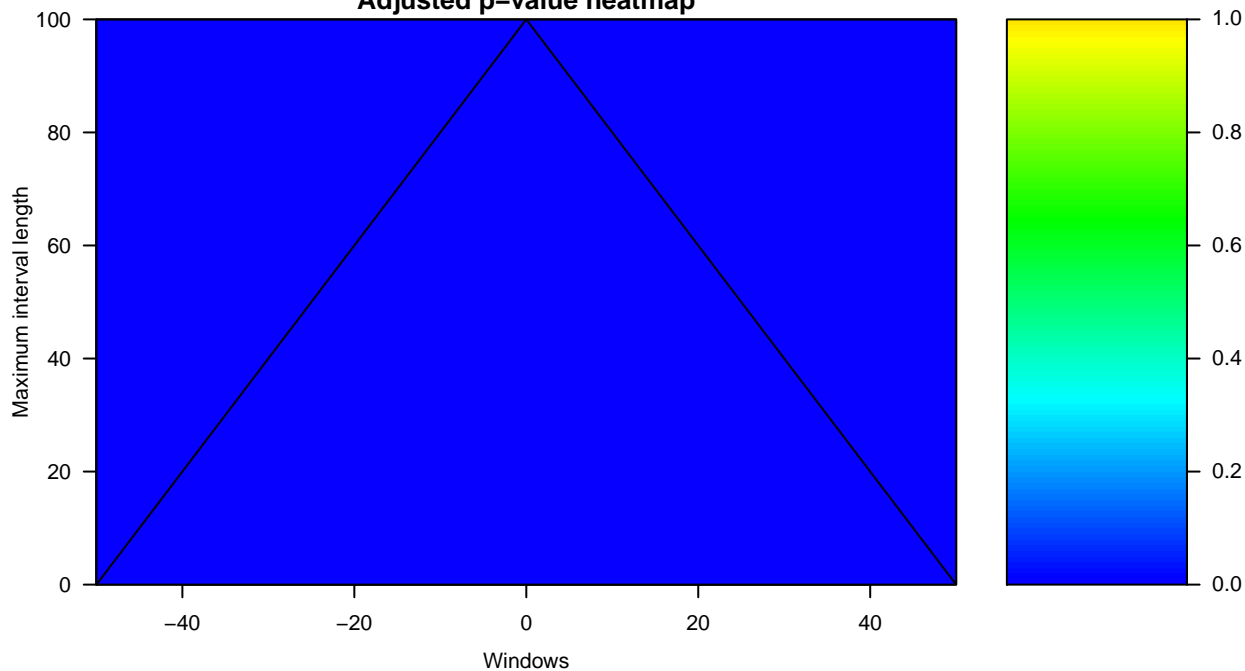


# H3K27ac

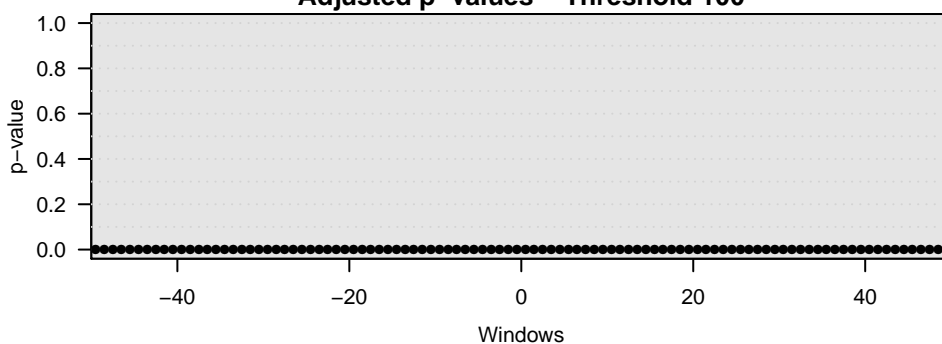


# H4K20me1

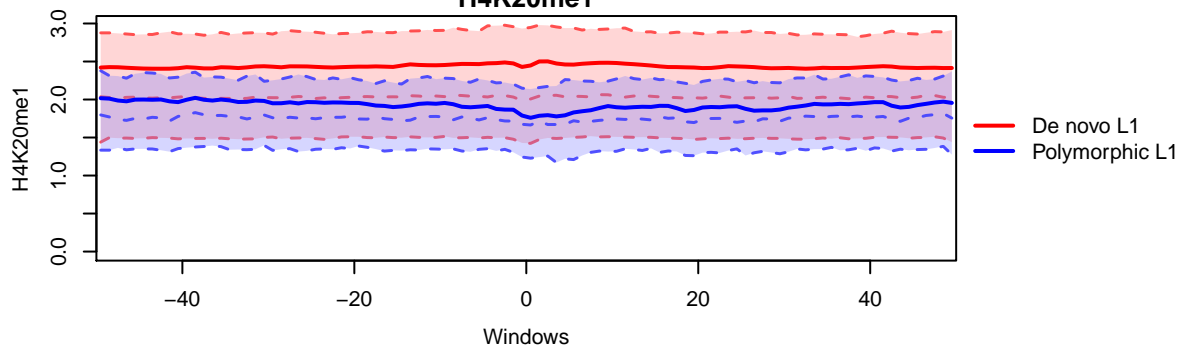
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# H4K20me1



De novo L1

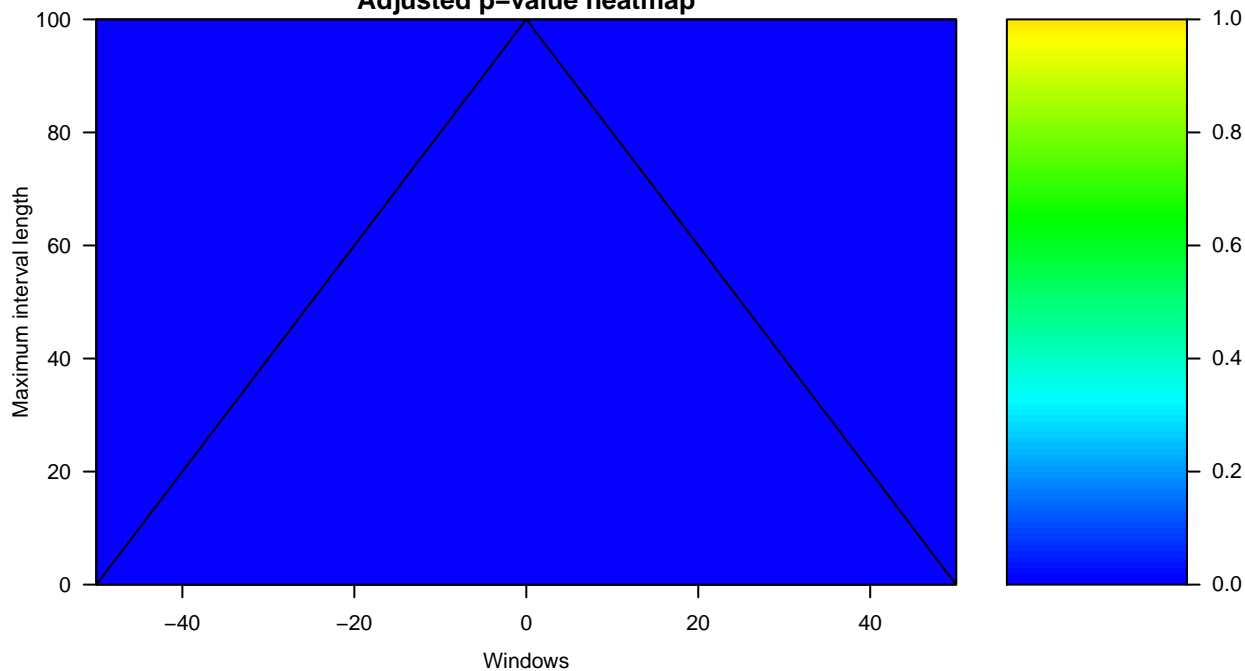
Polymorphic L1

836 2622.25 4408.5 6194.75 7981

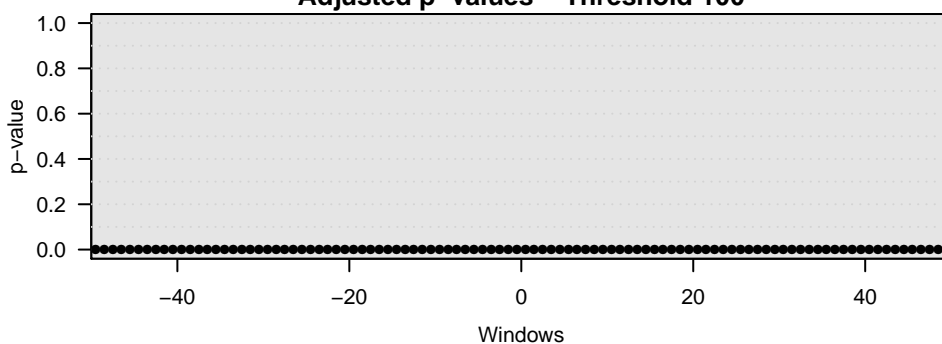
Sample size

# H3K36me3

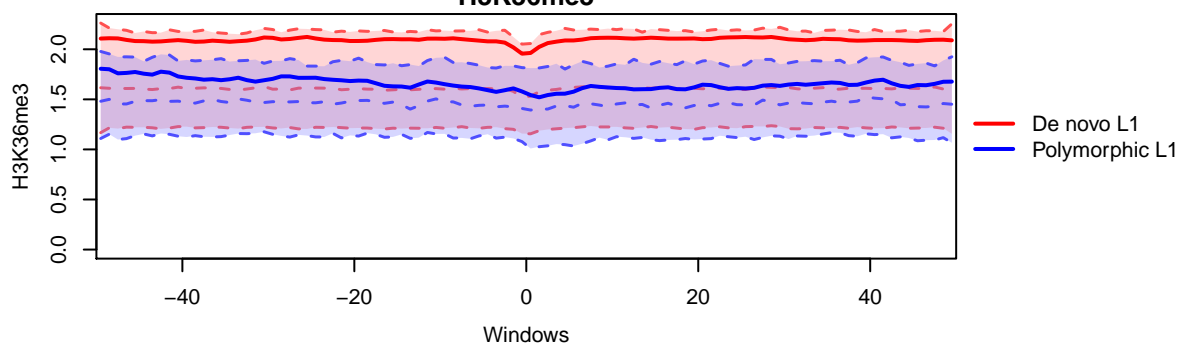
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# H3K36me3



De novo L1

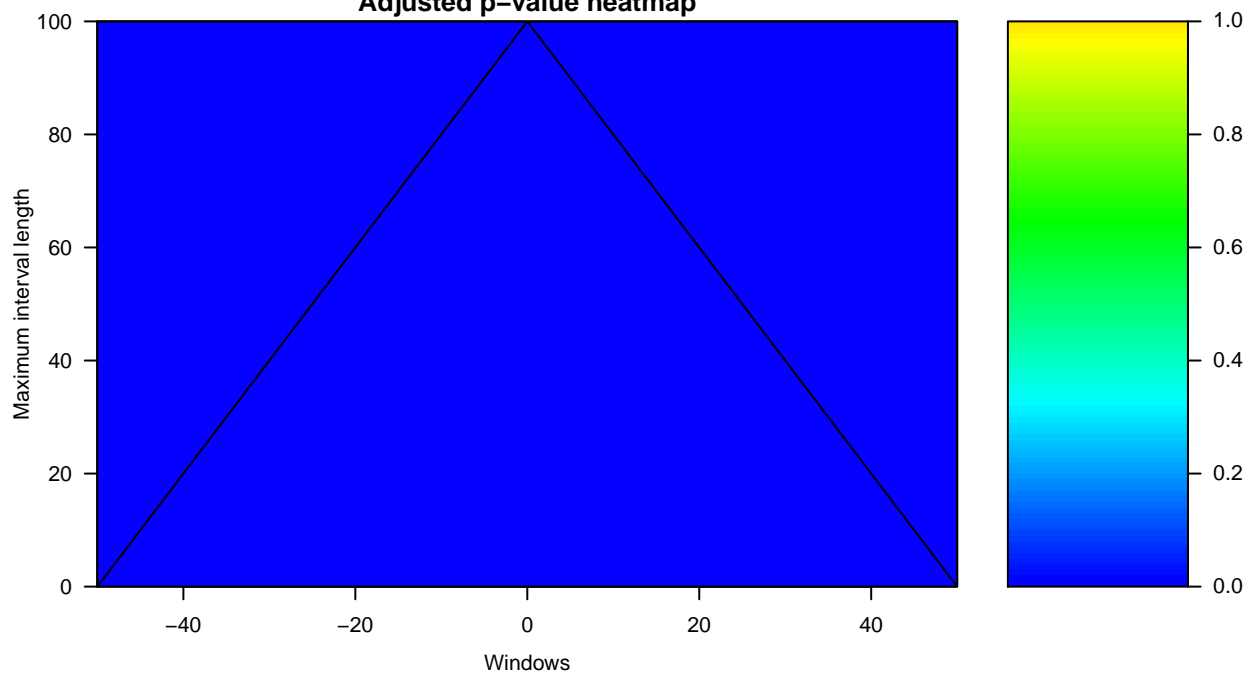
Polymorphic L1

836 2622.25 4408.5 6194.75 7981

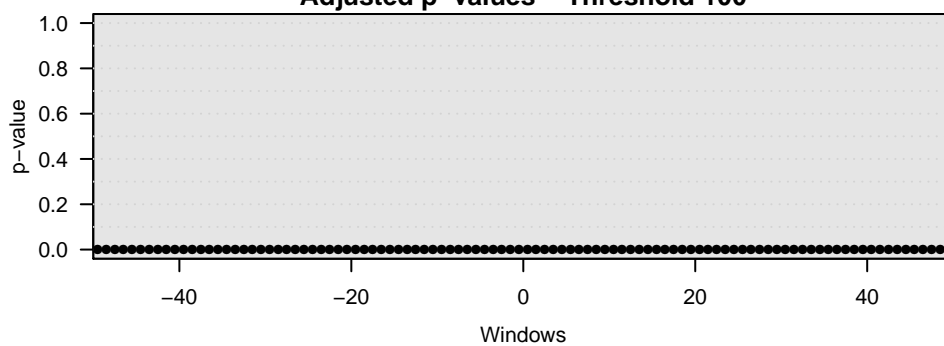
Sample size

# H3K4me1

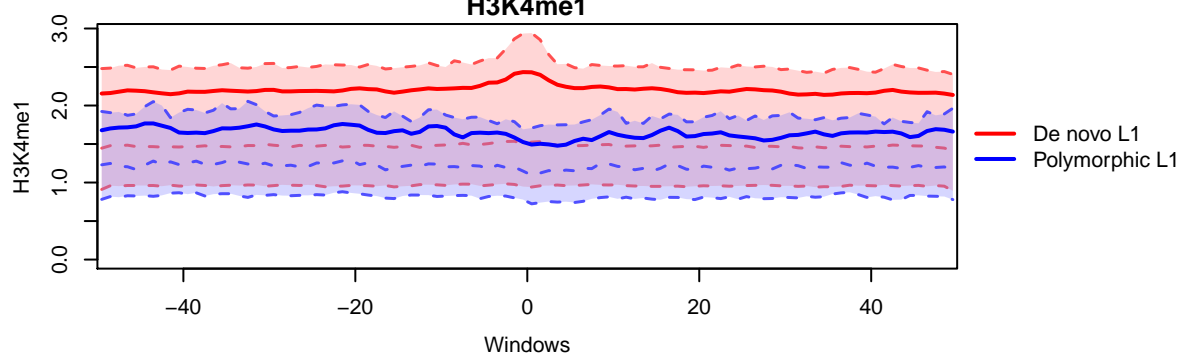
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# H3K4me1



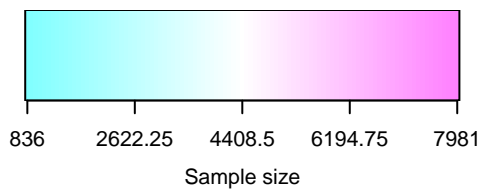
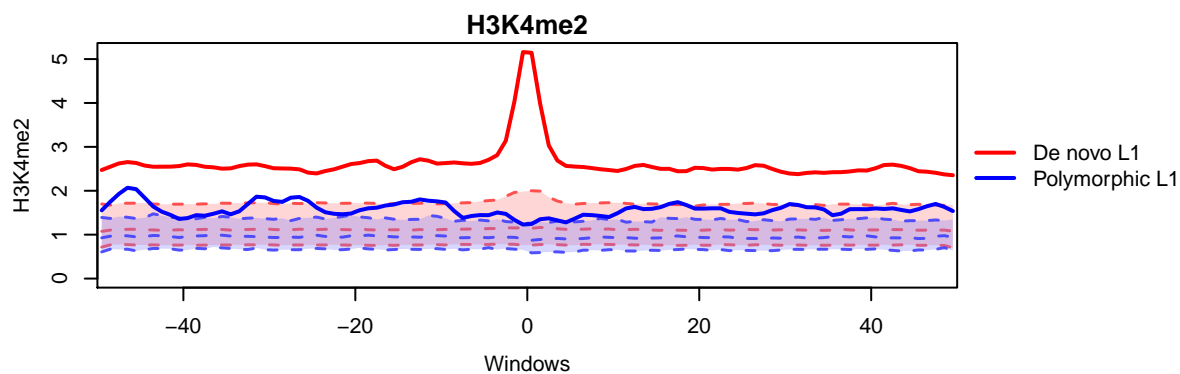
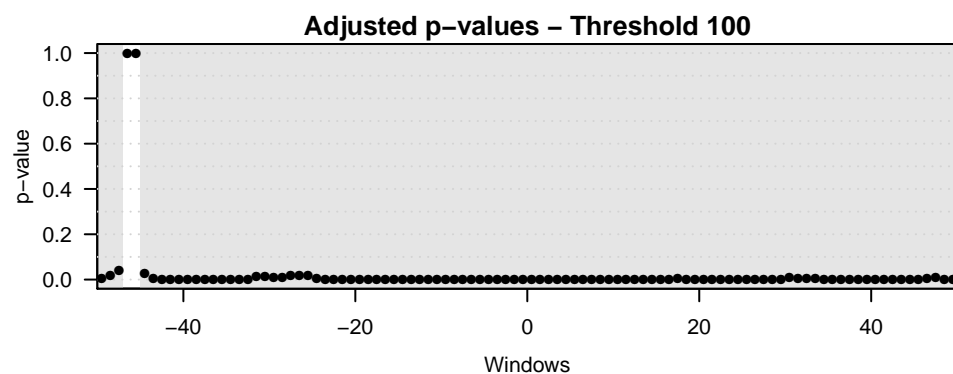
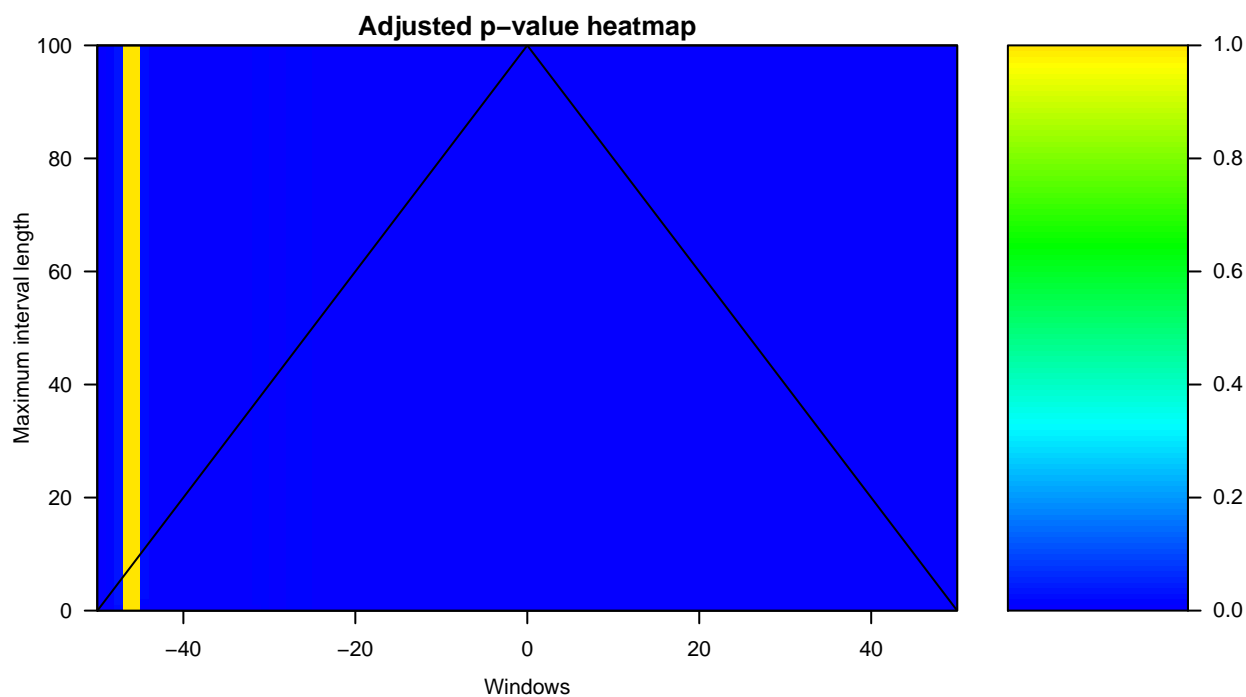
De novo L1

Polymorphic L1

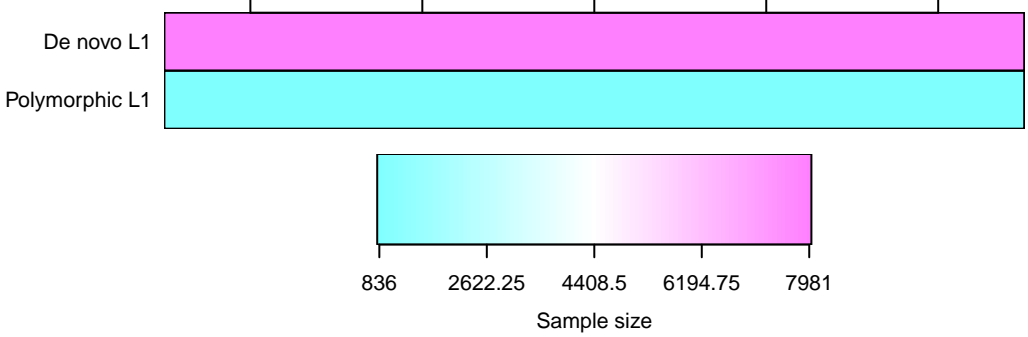
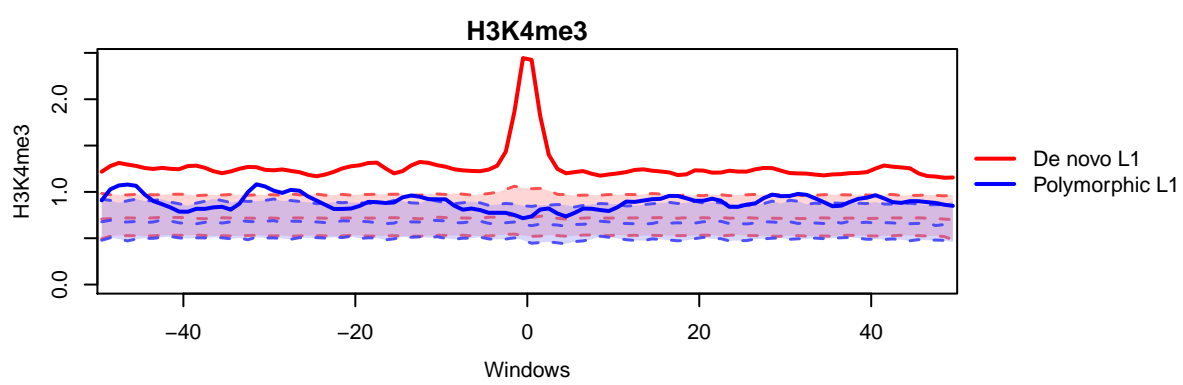
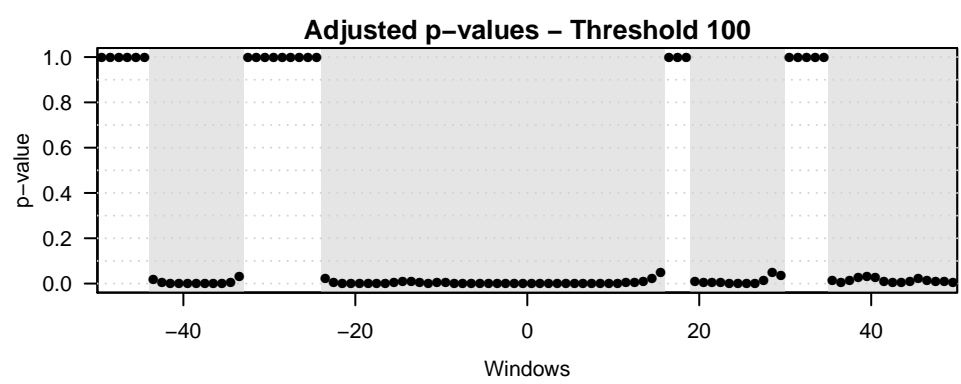
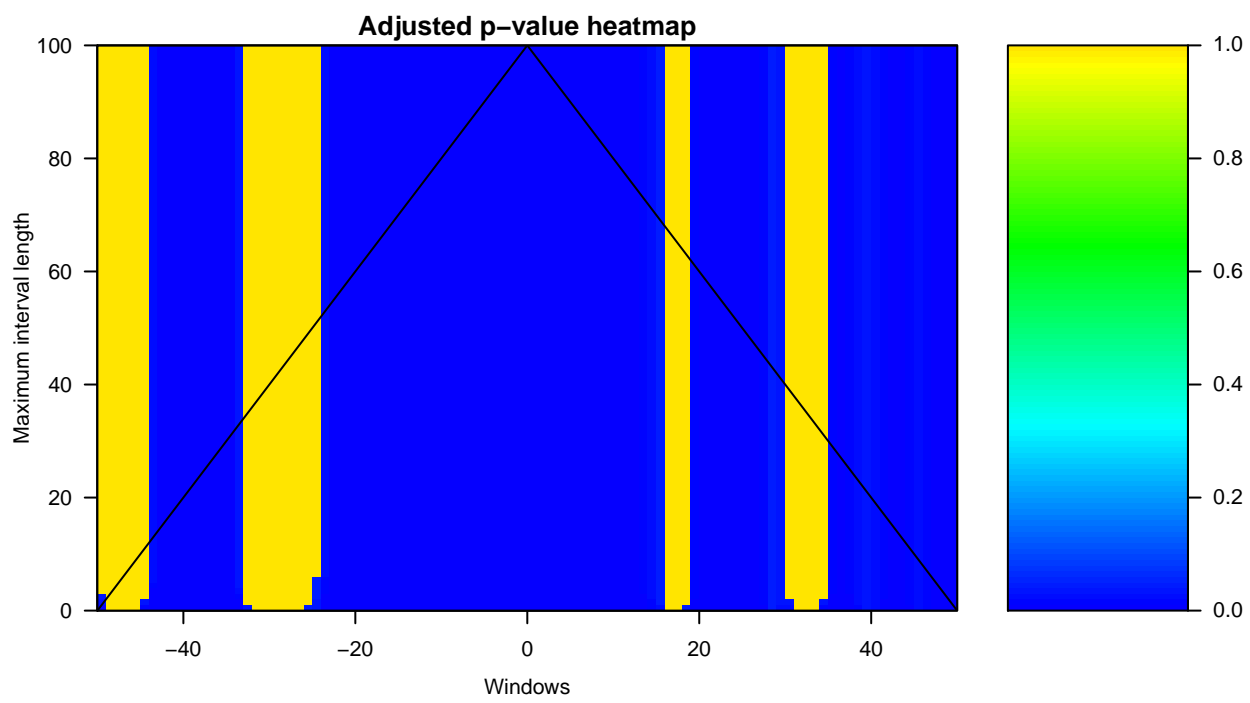
836 2622.25 4408.5 6194.75 7981

Sample size

# H3K4me2

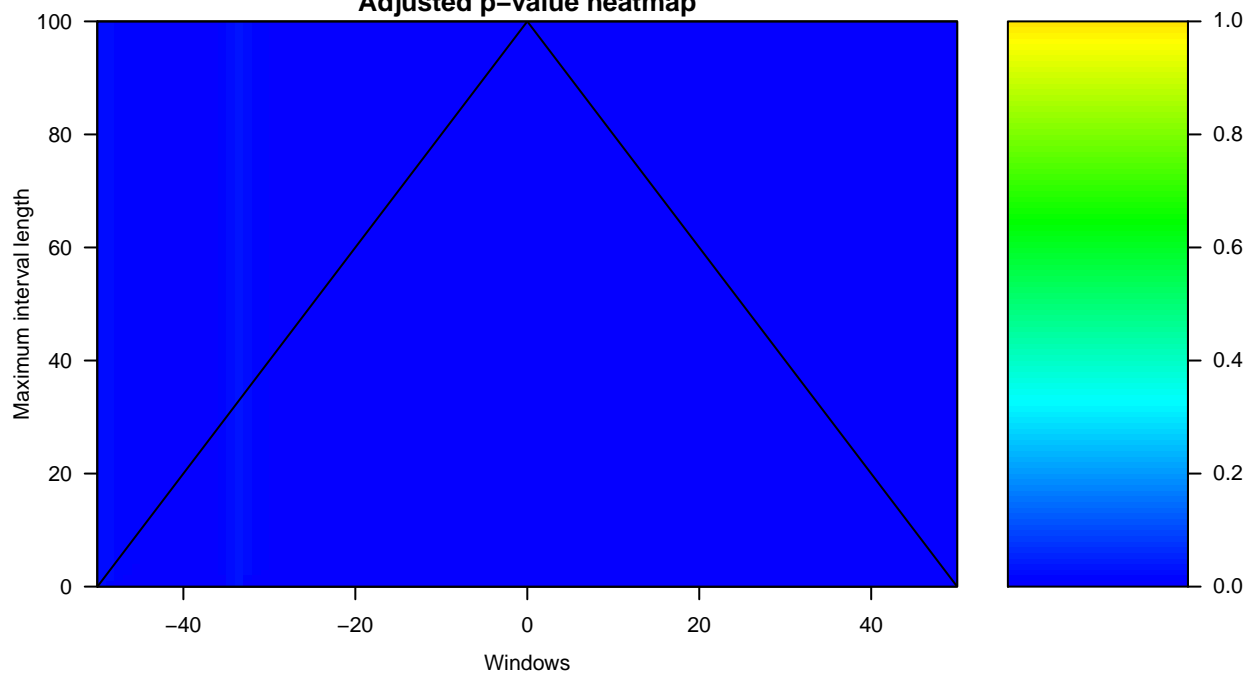


# H3K4me3

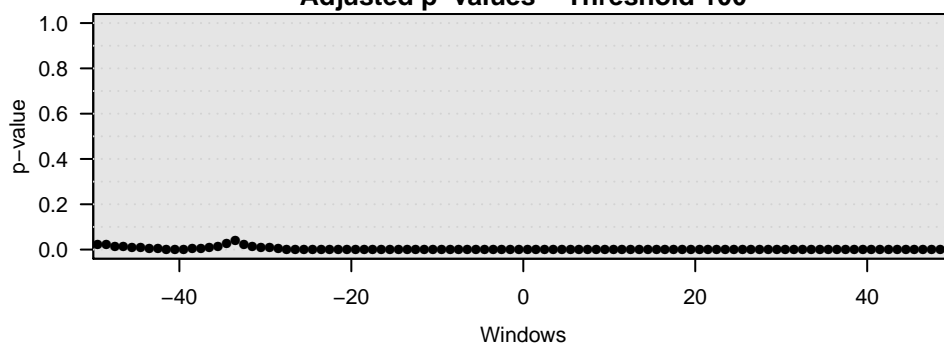


# H3K79me2

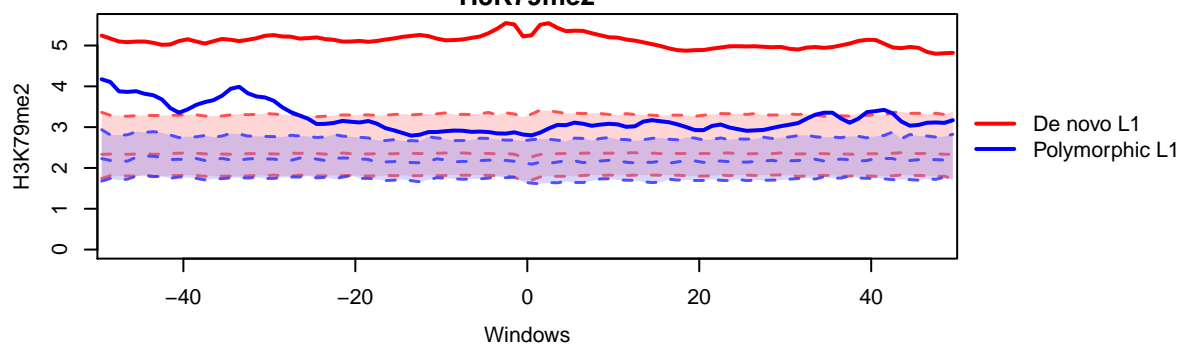
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# H3K79me2



De novo L1

Polymorphic L1

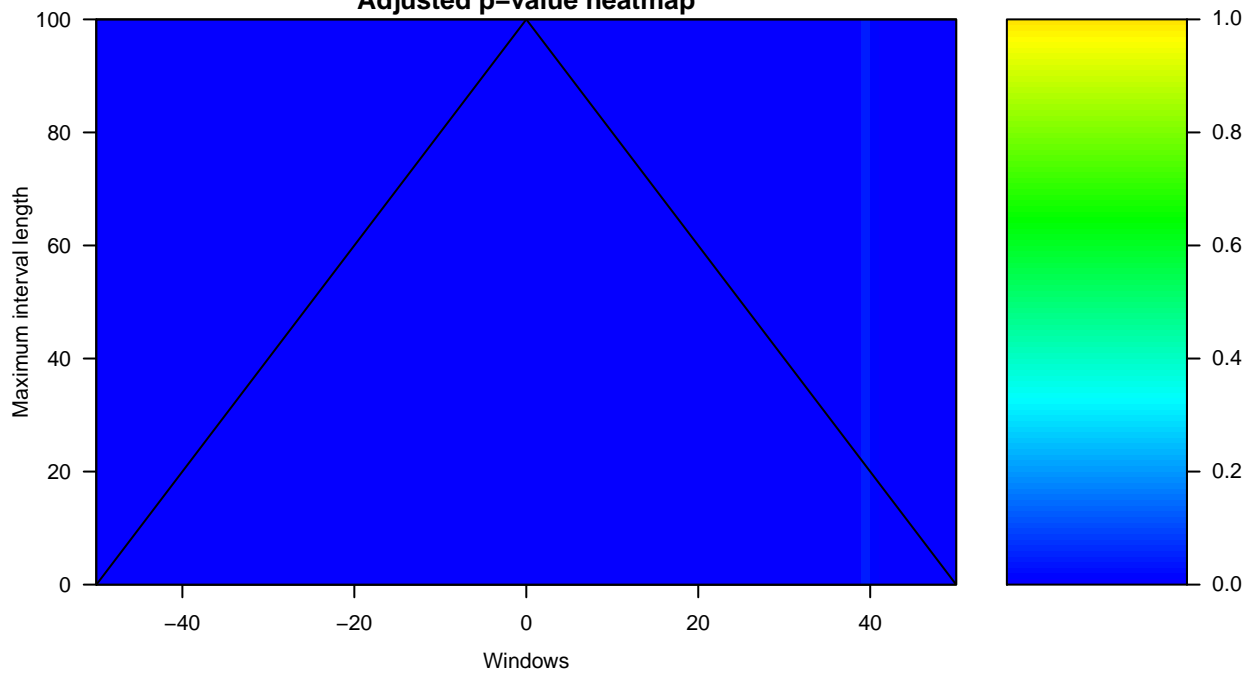
836 2622.25 4408.5 6194.75 7981

Sample size

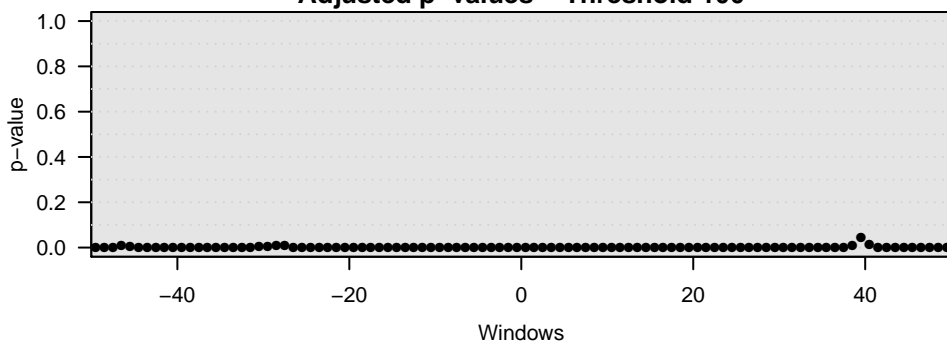


# H3K9ac

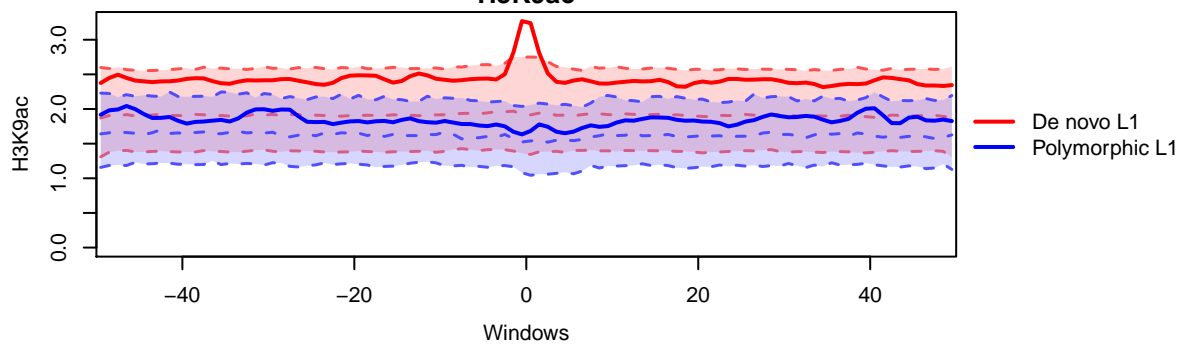
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# H3K9ac



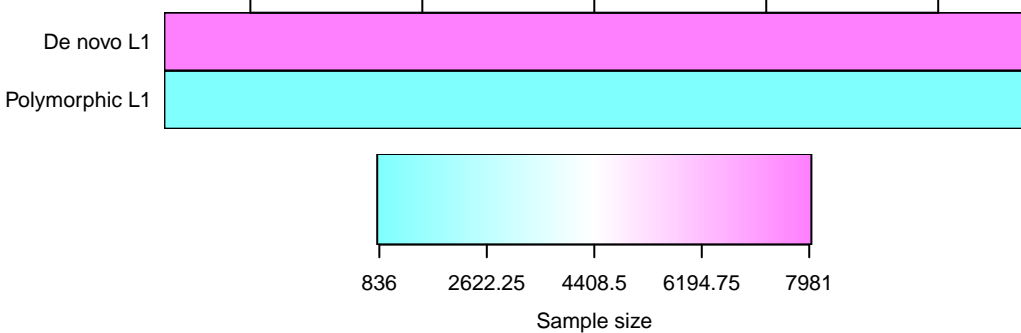
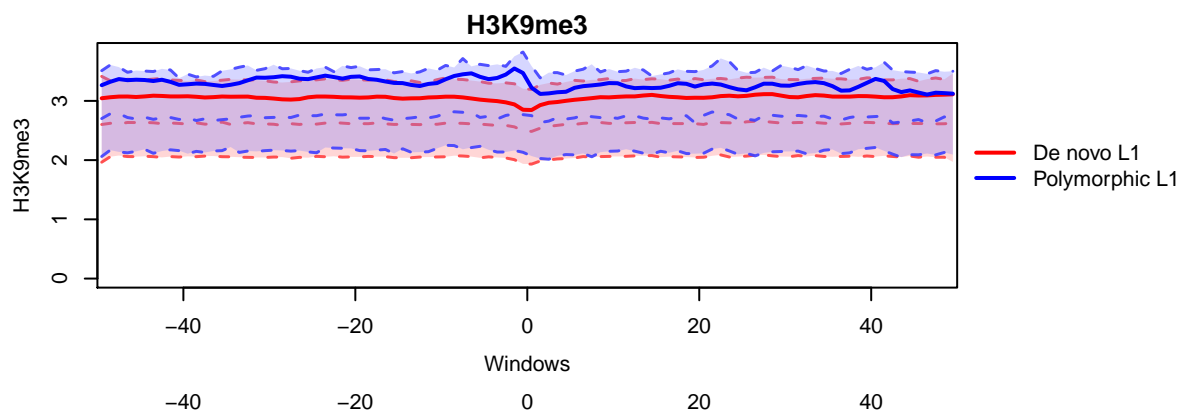
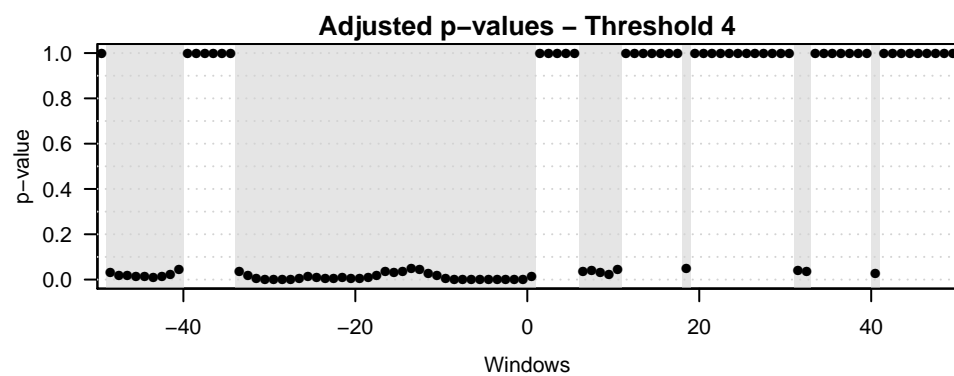
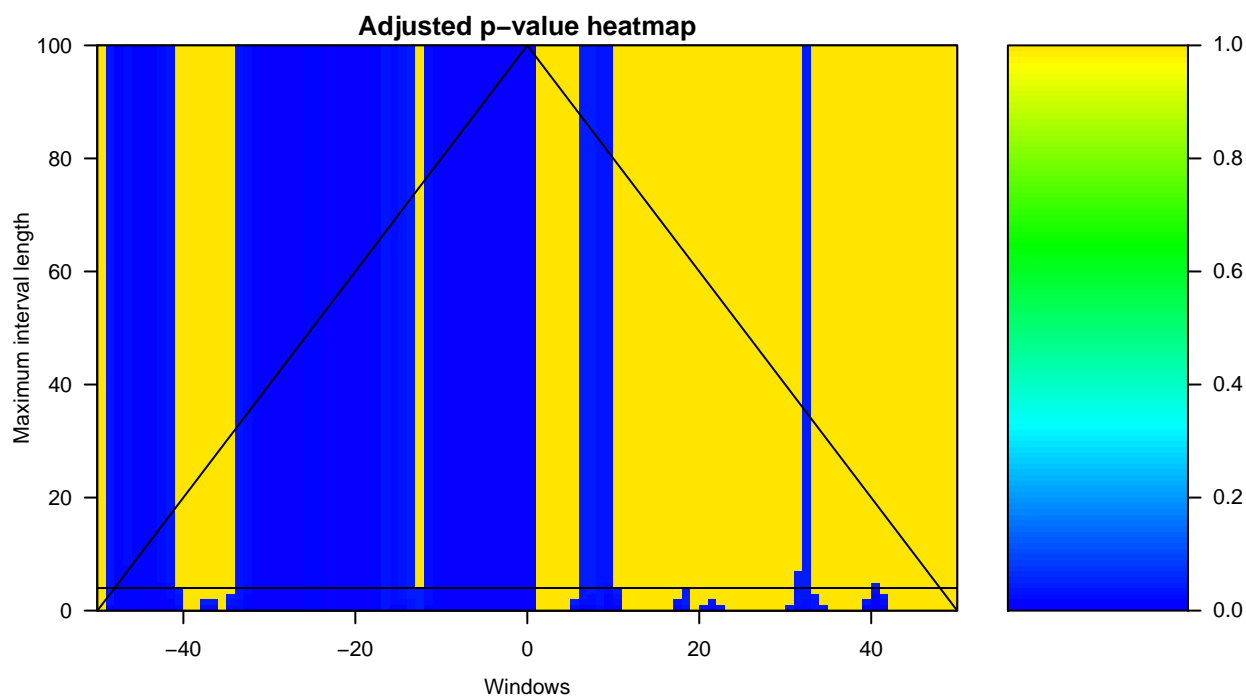
De novo L1

Polymorphic L1

836 2622.25 4408.5 6194.75 7981

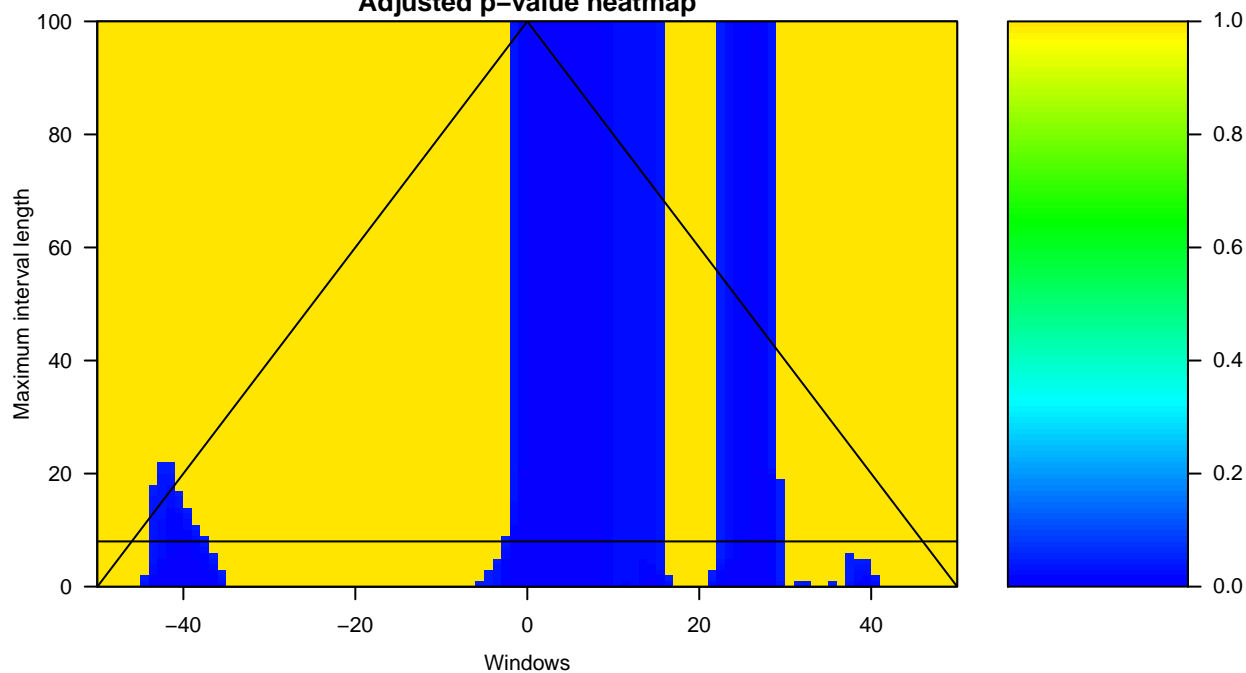
Sample size

# H3K9me3

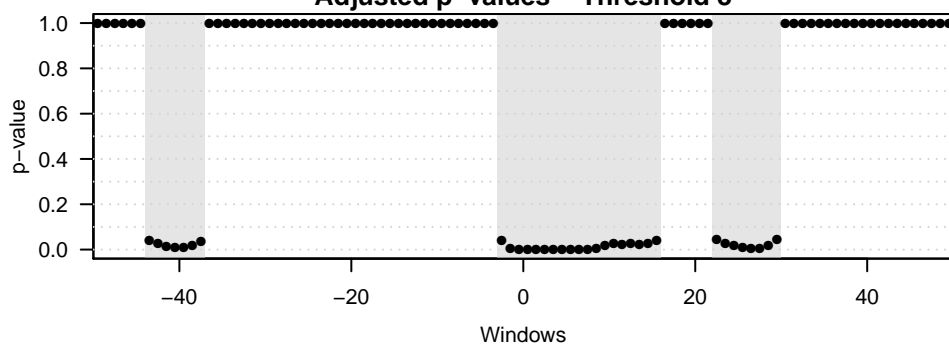


# H3K27me3

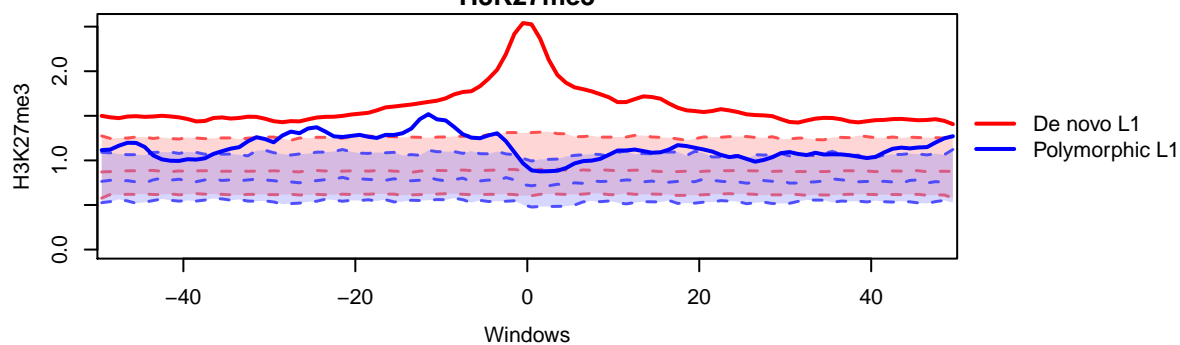
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 8



# H3K27me3



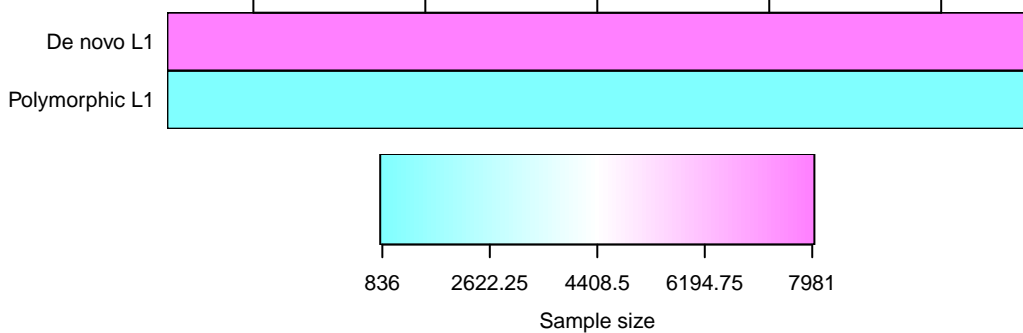
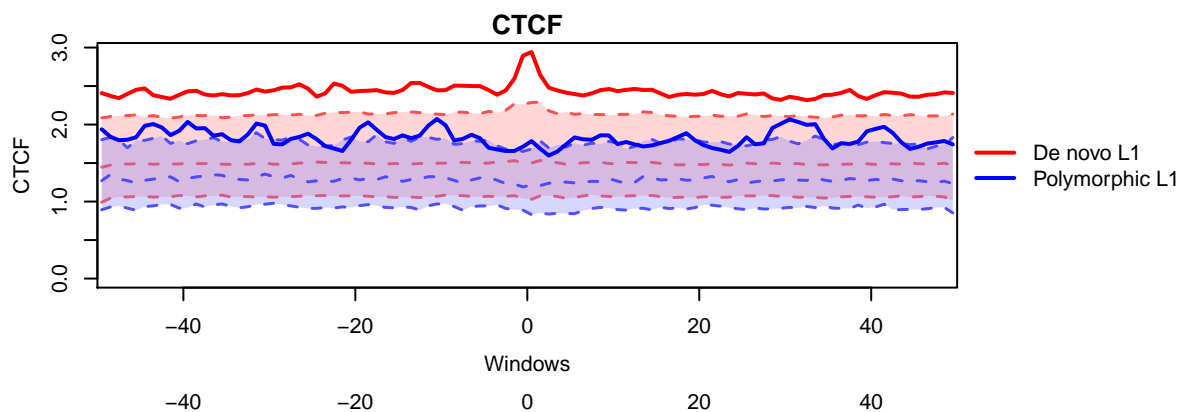
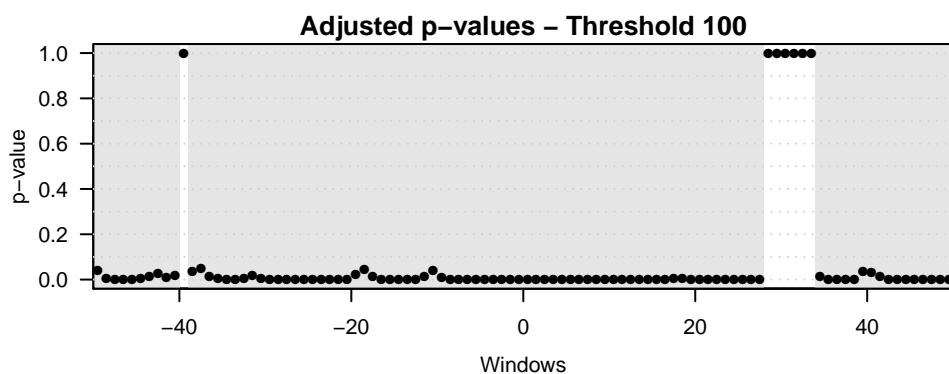
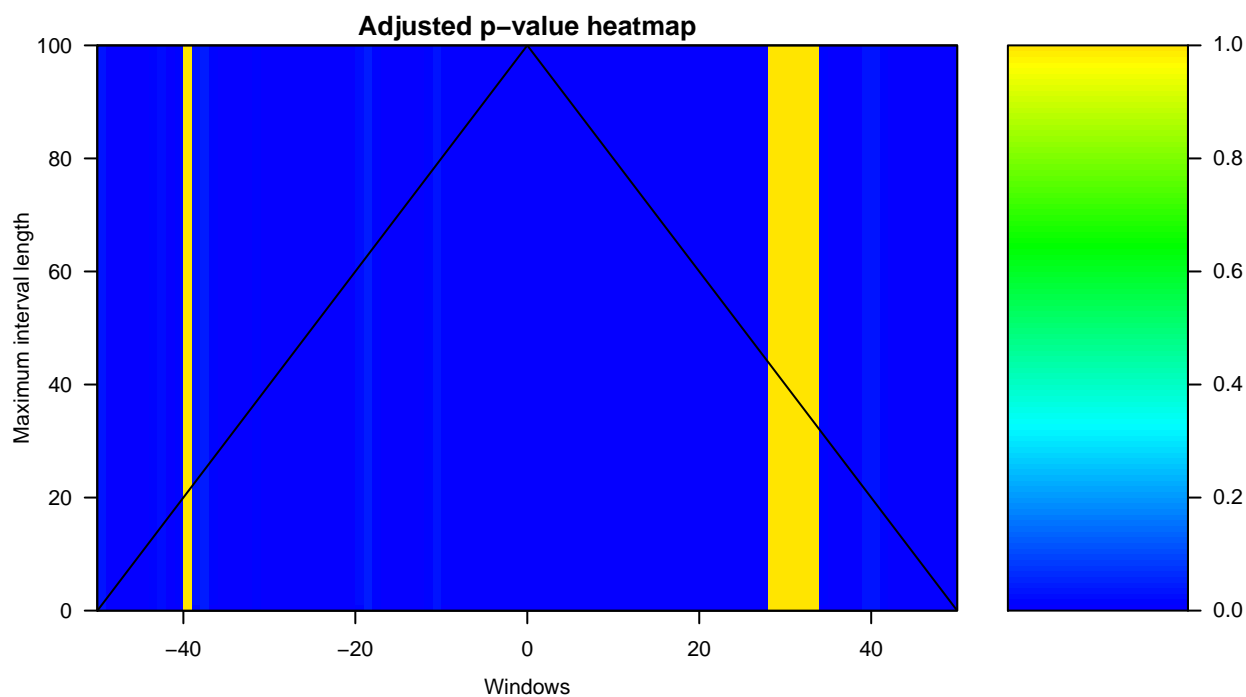
De novo L1

Polymorphic L1

836 2622.25 4408.5 6194.75 7981

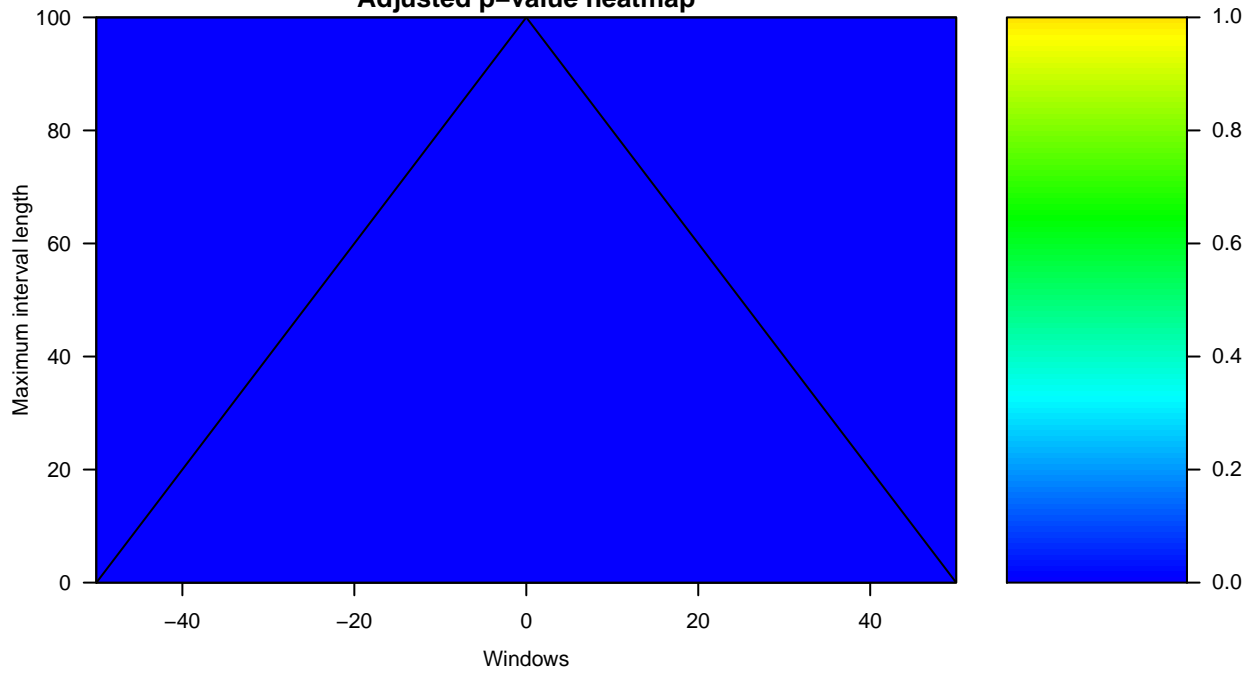
Sample size

# CTCF

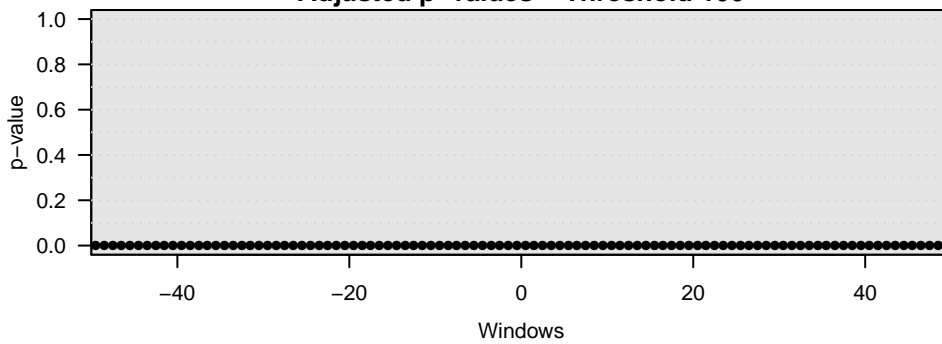


# DNase hypersensitive sites

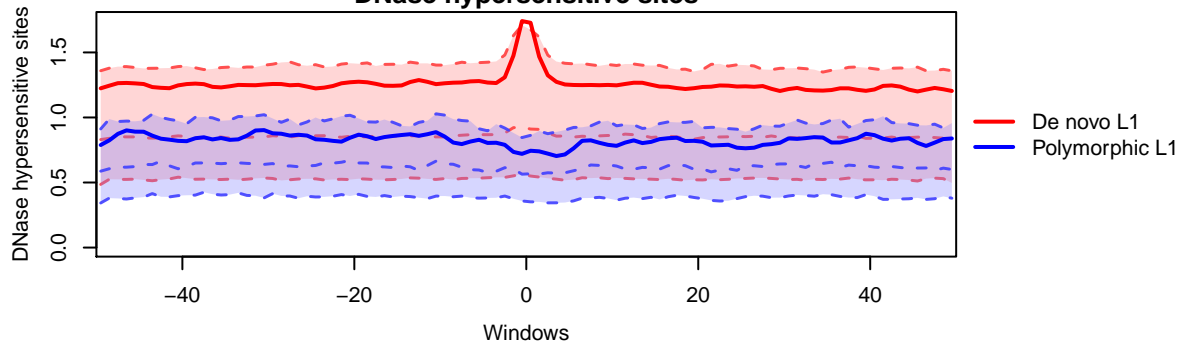
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



## DNase hypersensitive sites



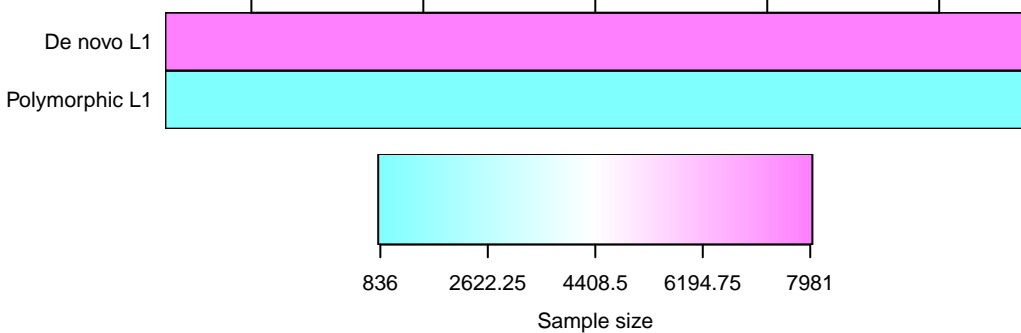
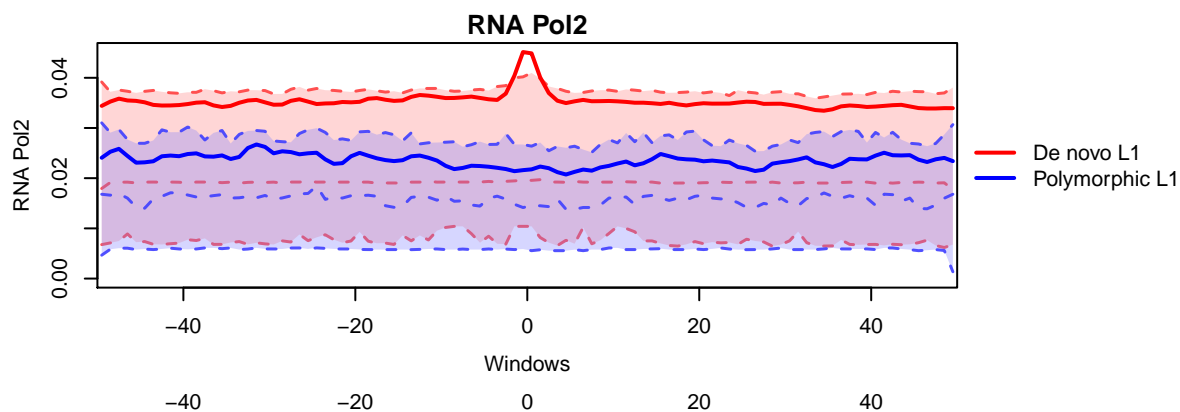
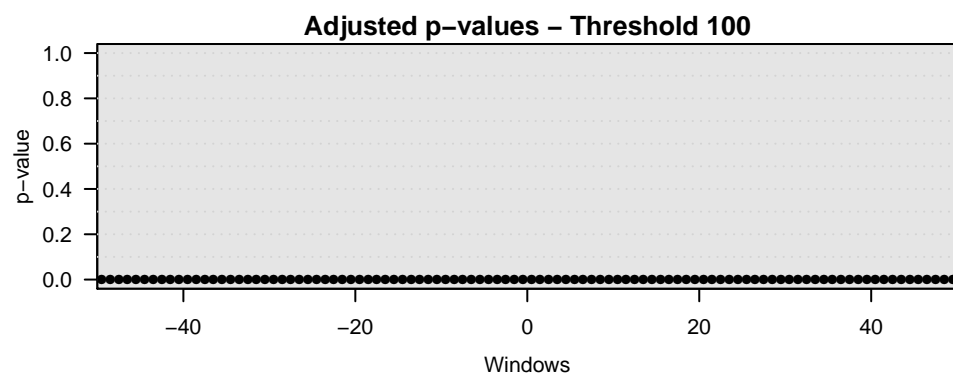
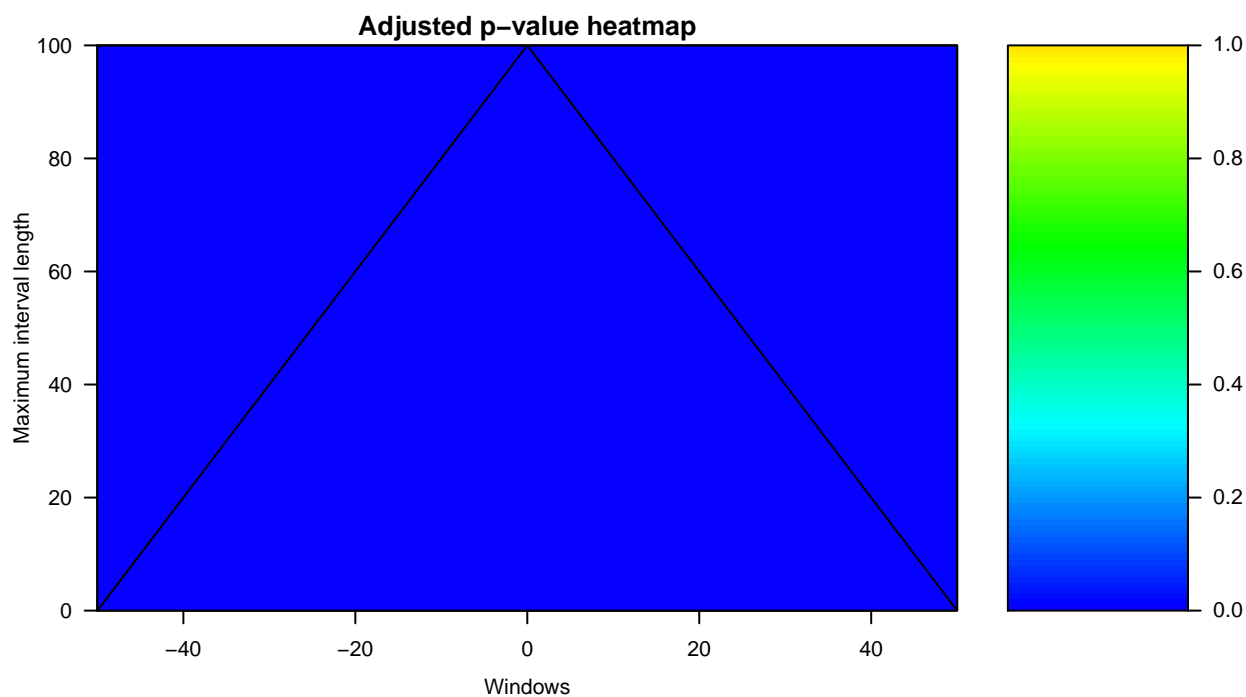
De novo L1

Polymorphic L1

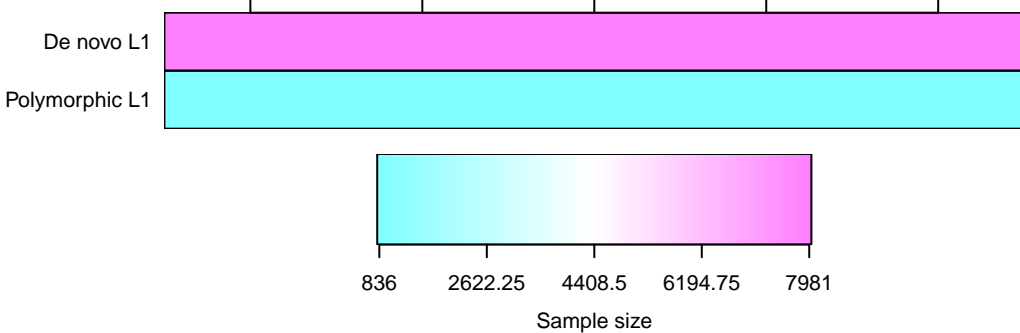
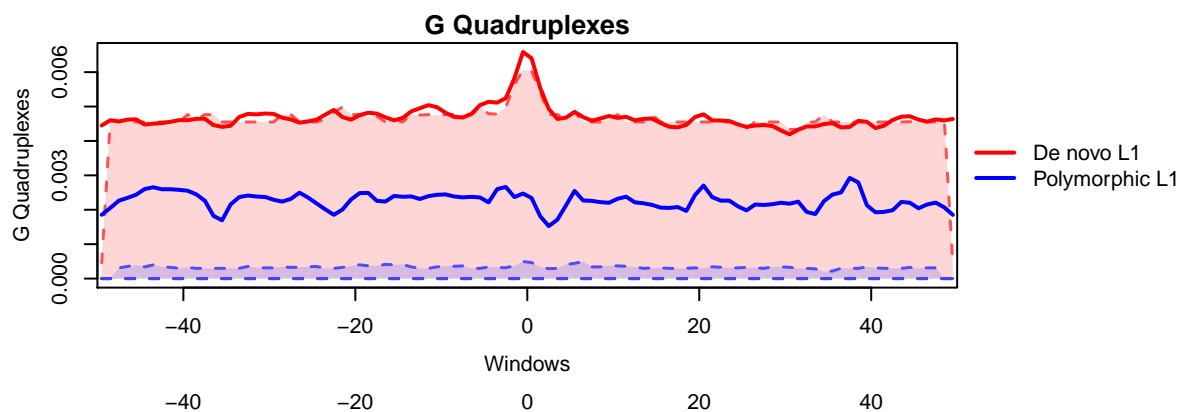
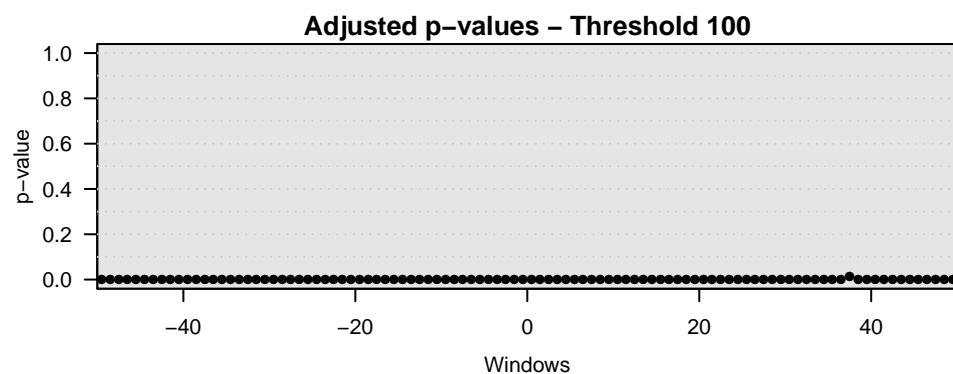
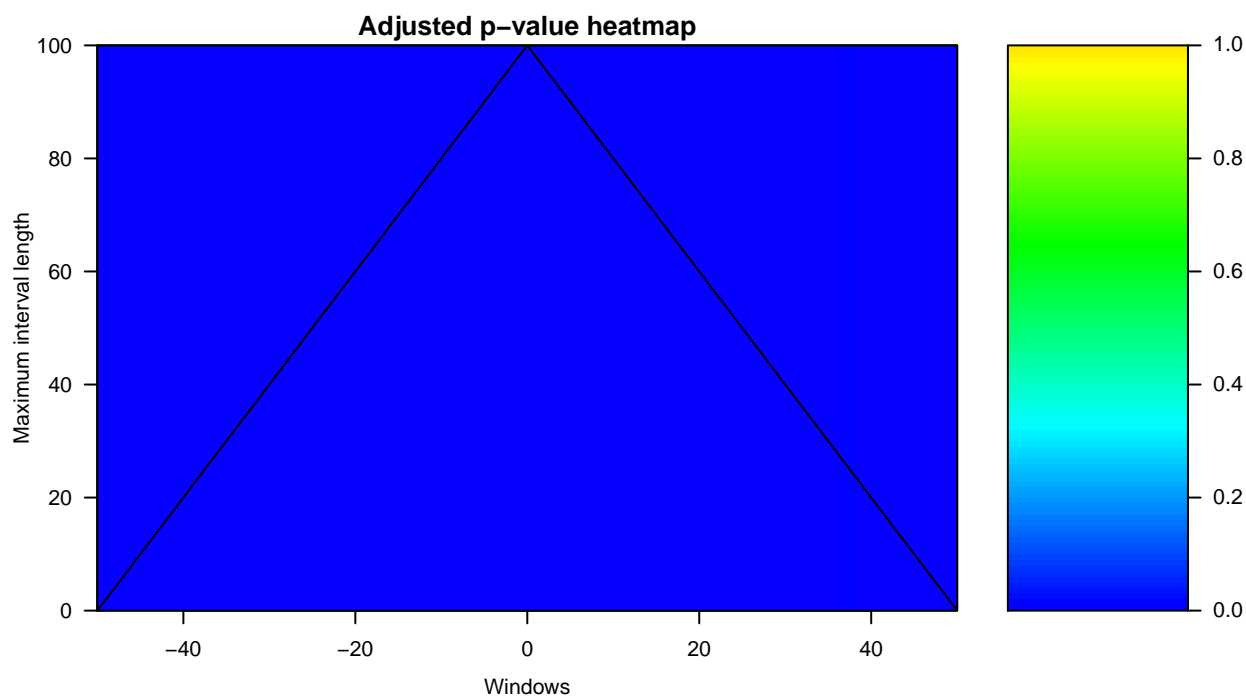
836 2622.25 4408.5 6194.75 7981

Sample size

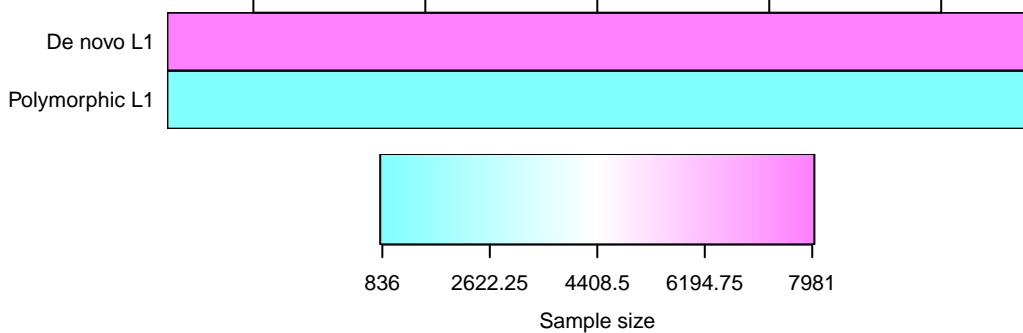
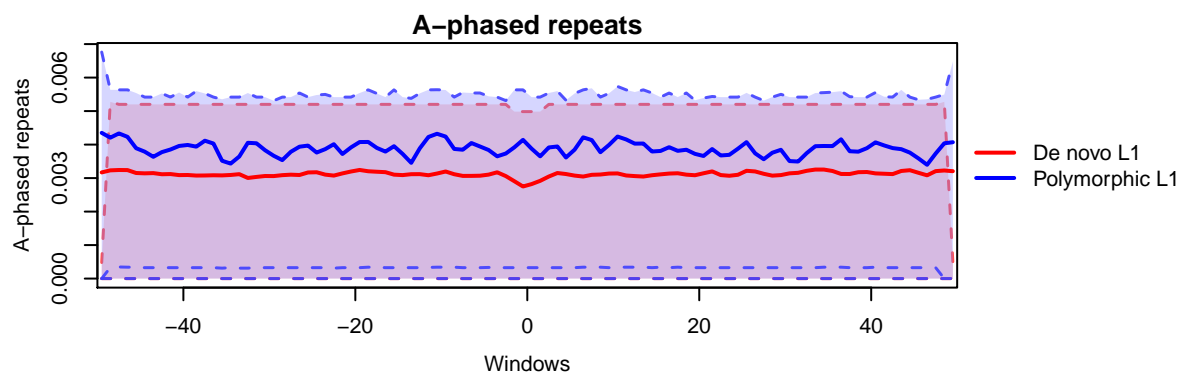
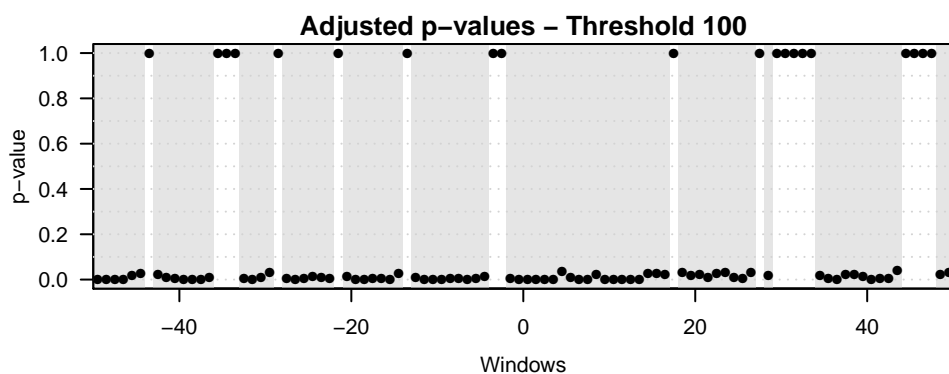
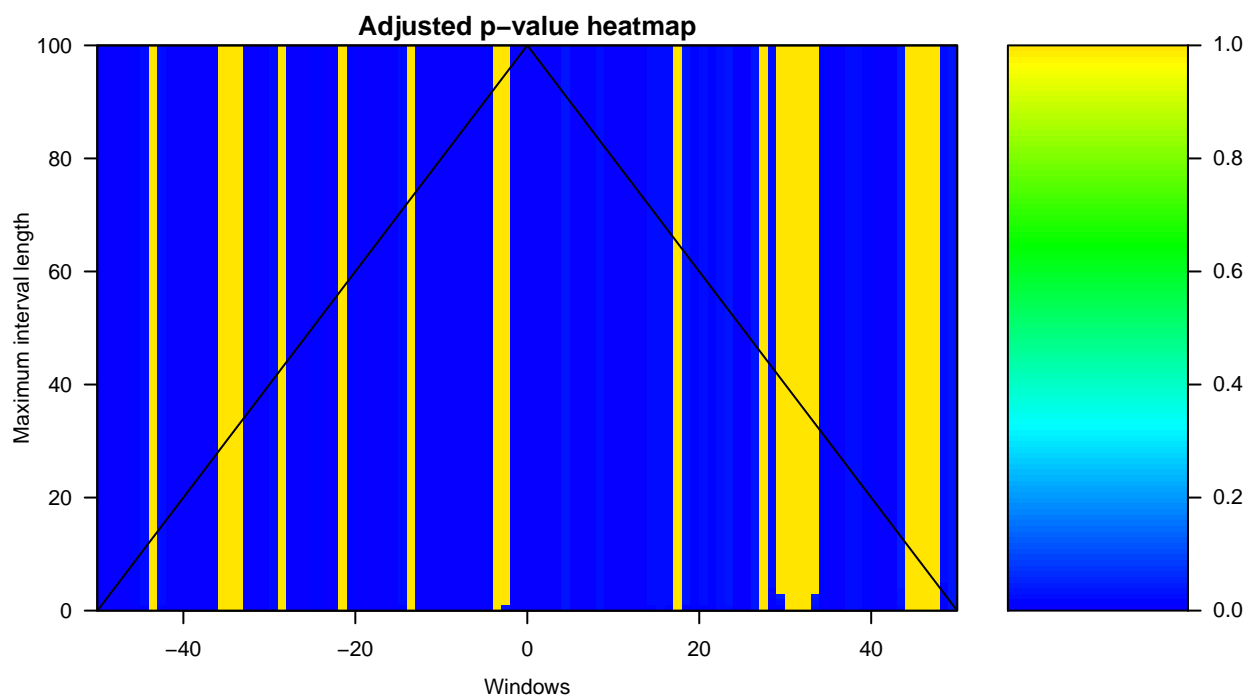
# RNA Pol2



# G Quadruplexes

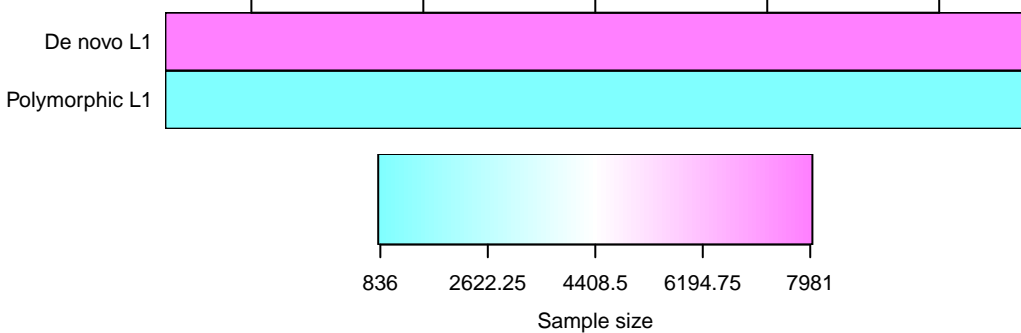
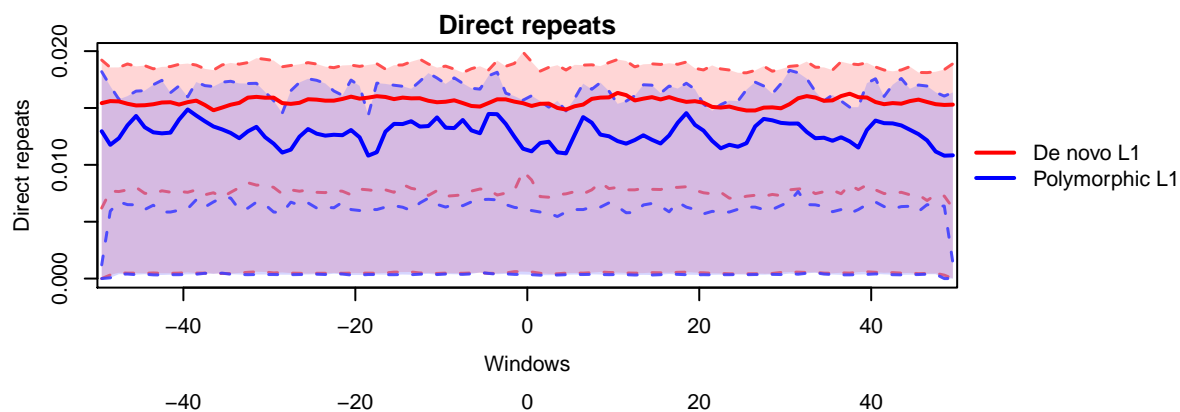
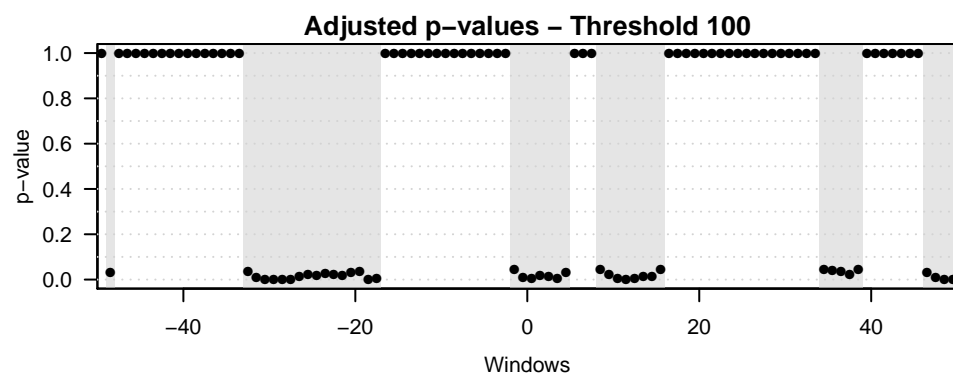
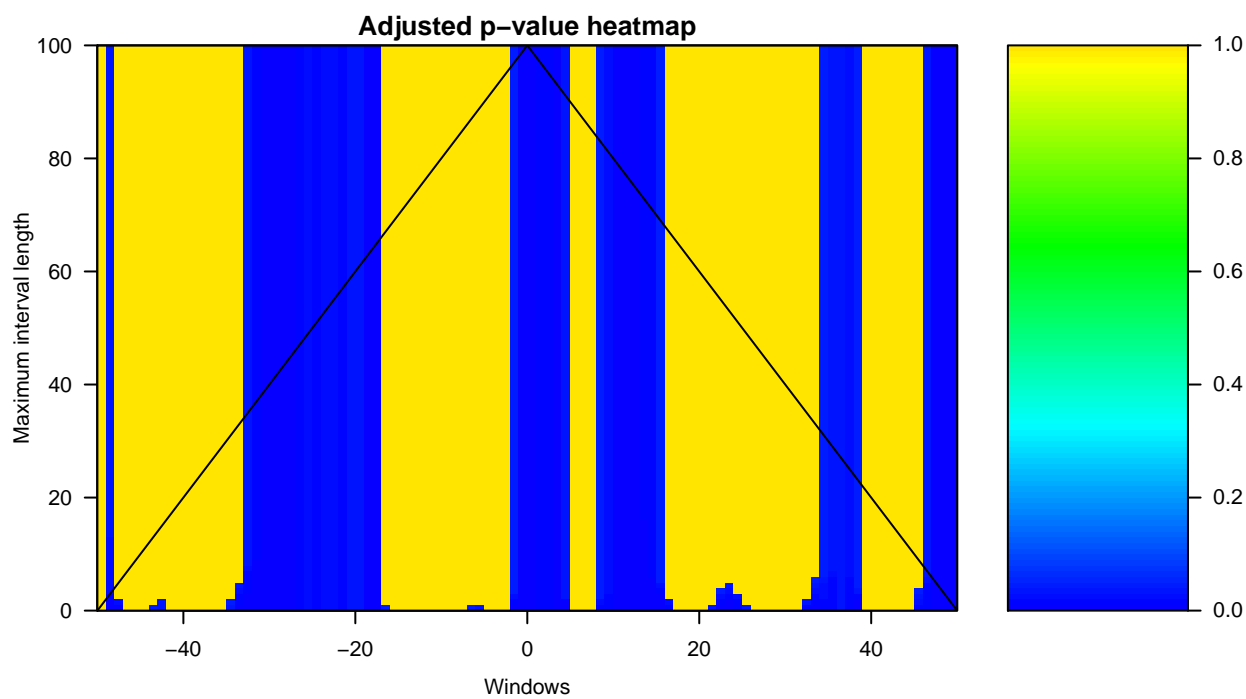


# A-phased repeats

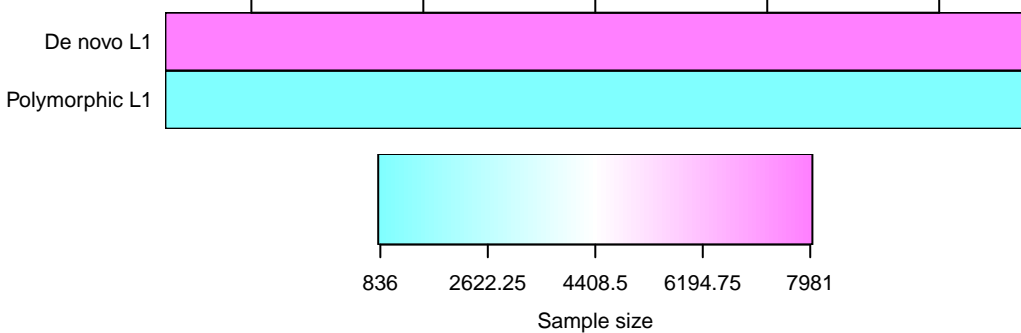
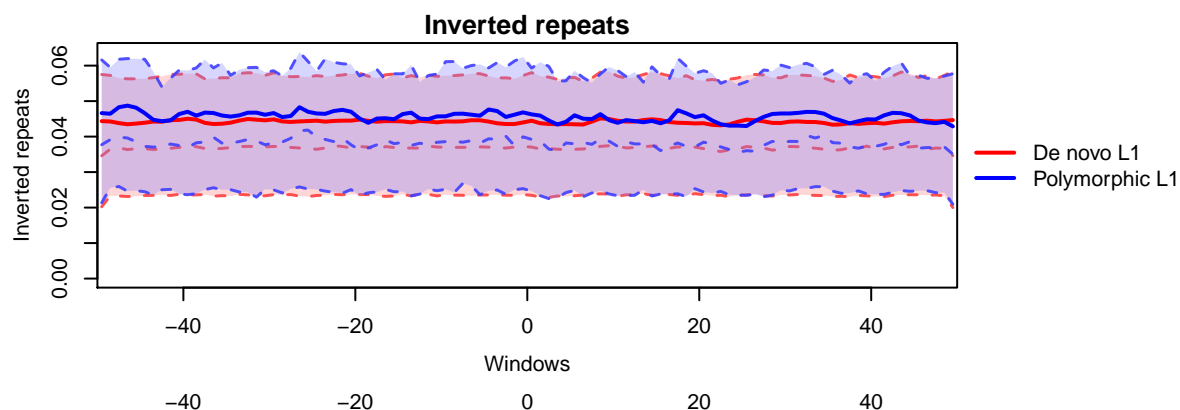
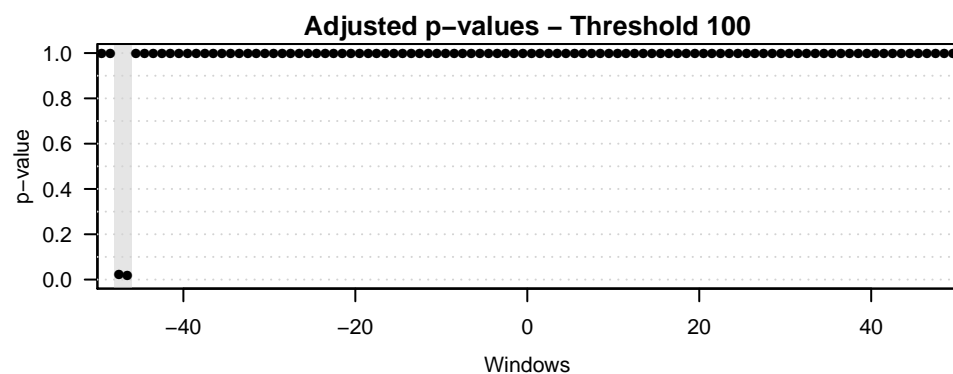
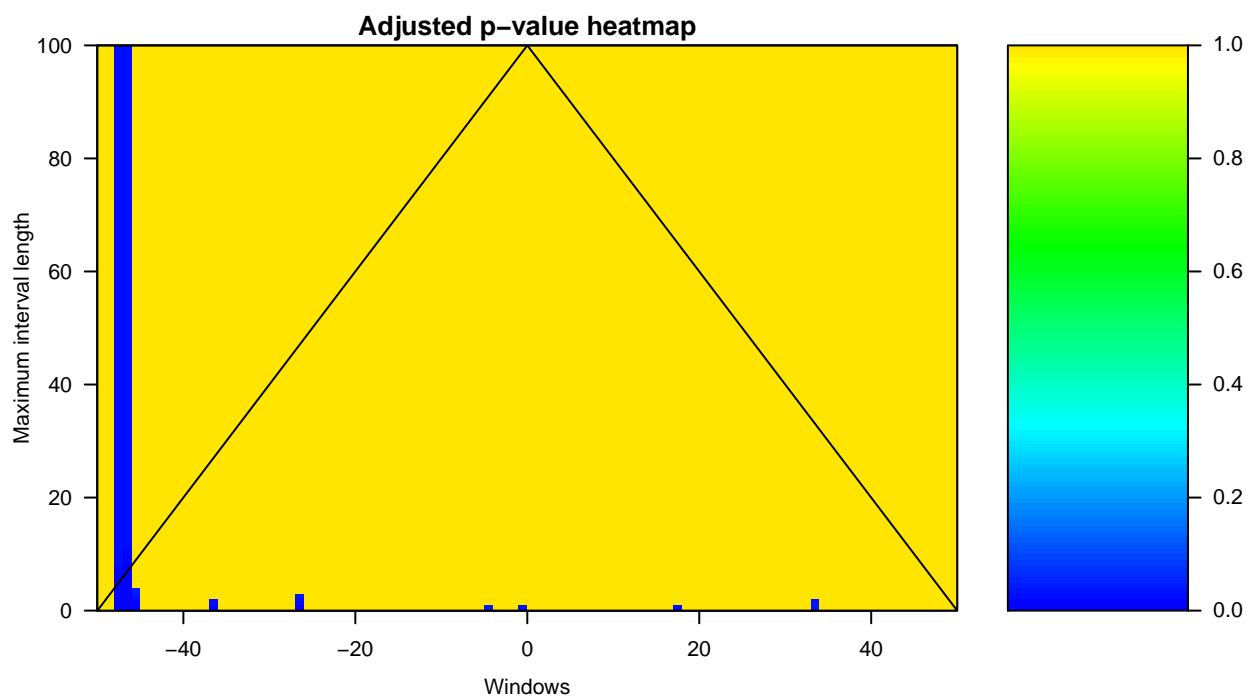




# Direct repeats

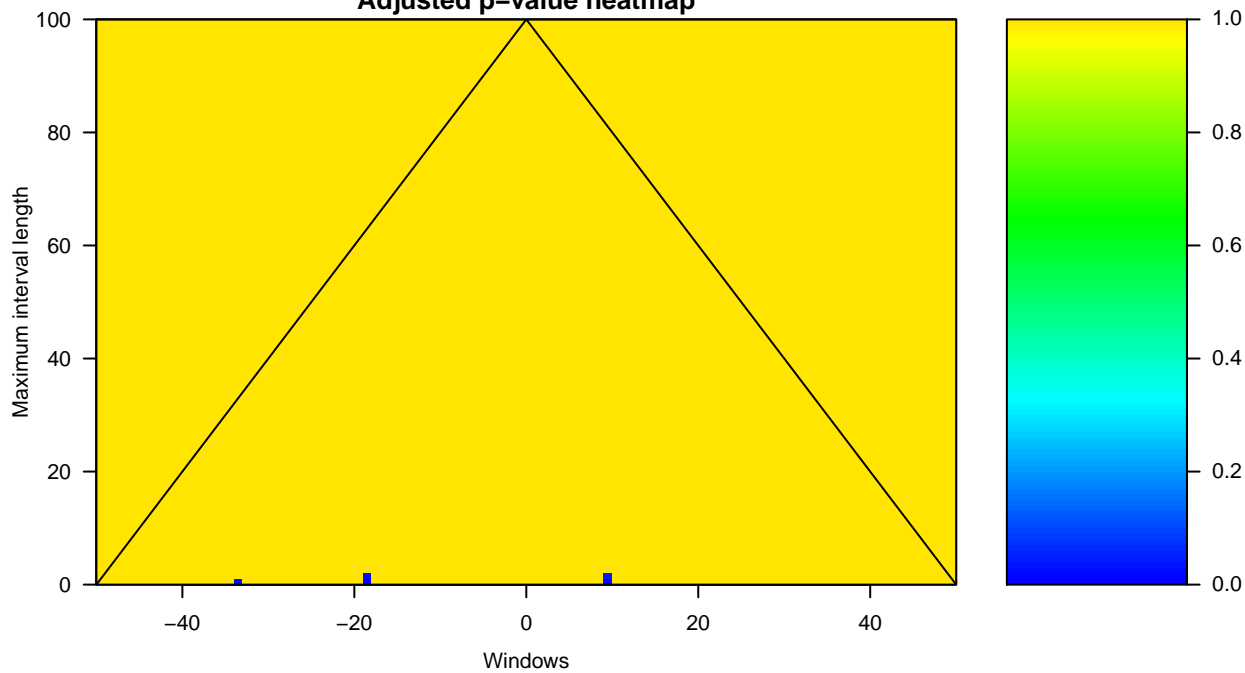


# Inverted repeats

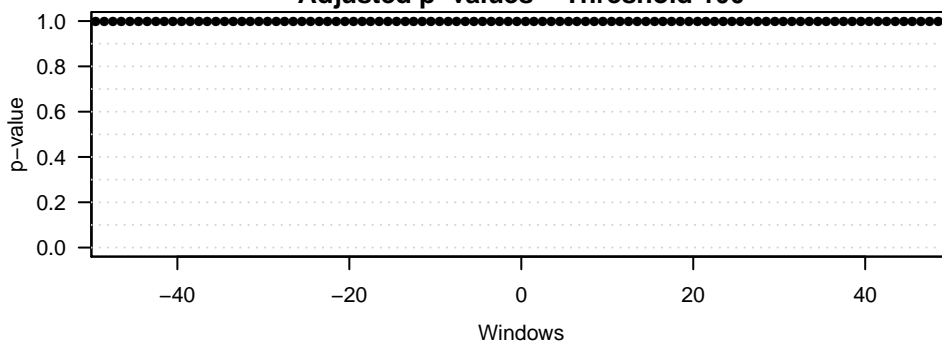


# Mirror repeats

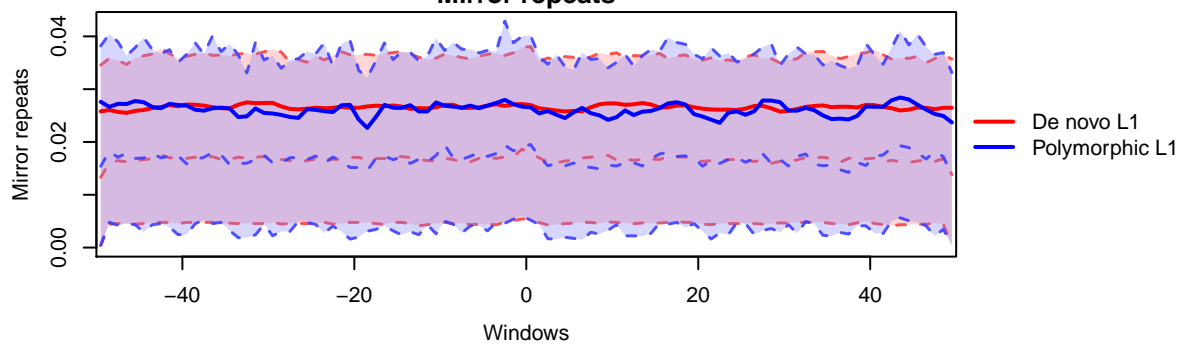
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# Mirror repeats



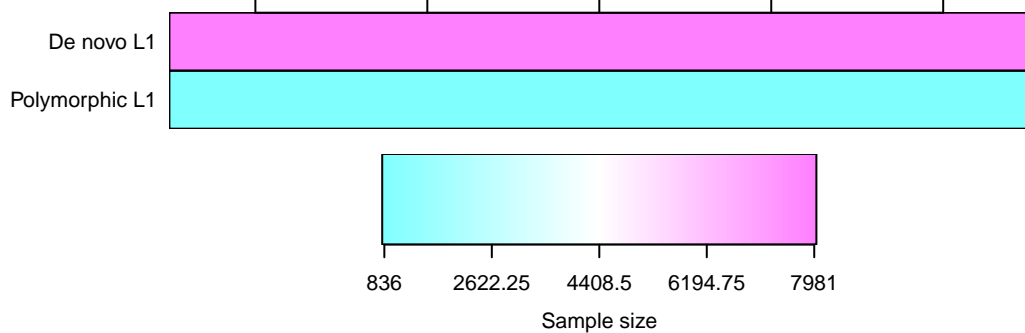
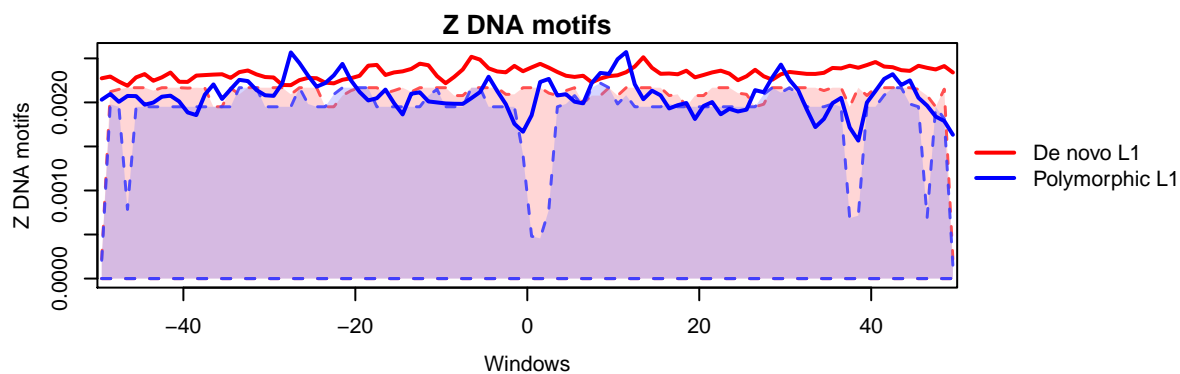
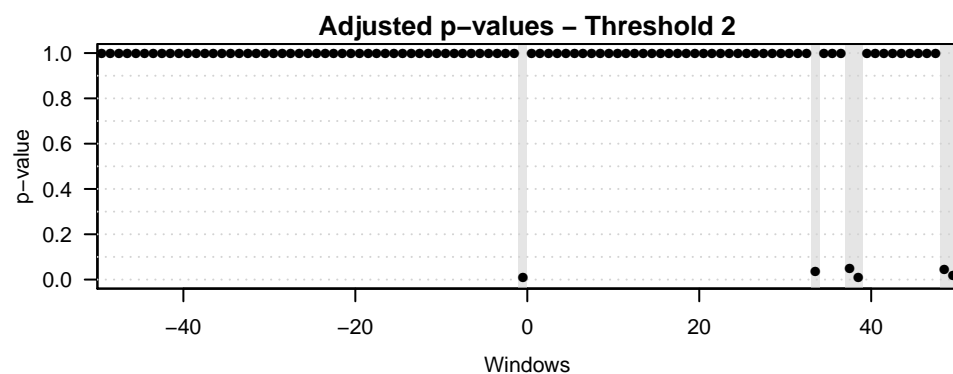
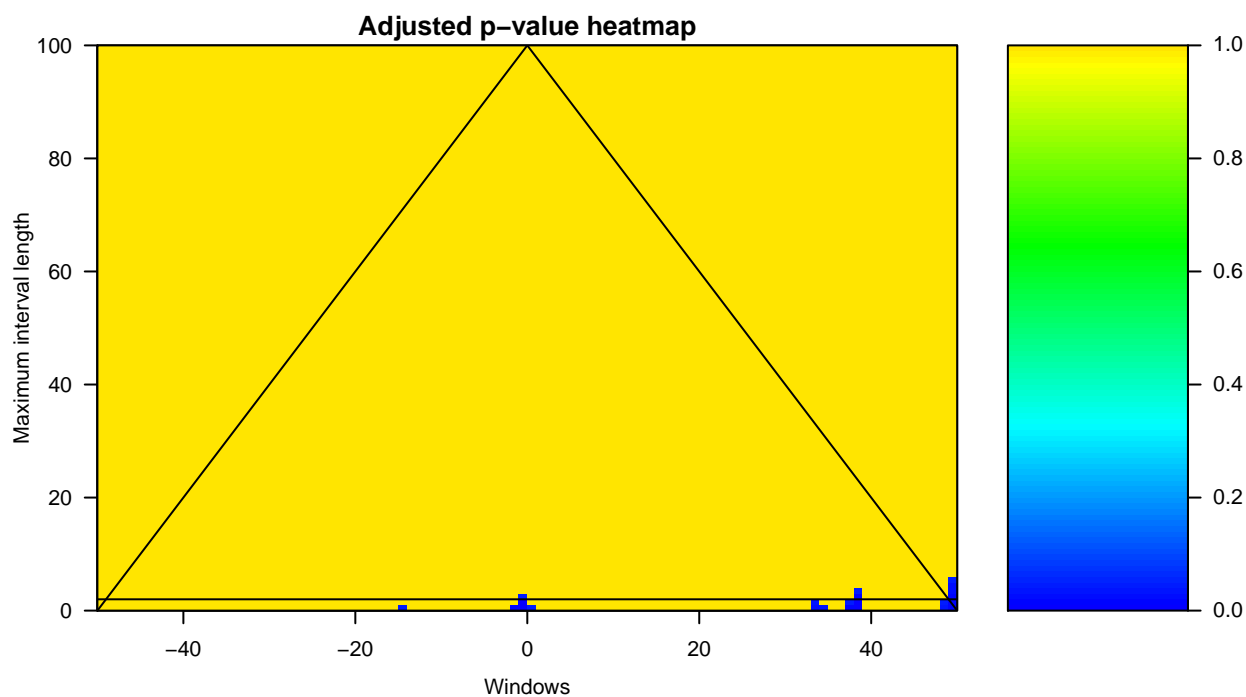
De novo L1

Polymorphic L1

836 2622.25 4408.5 6194.75 7981

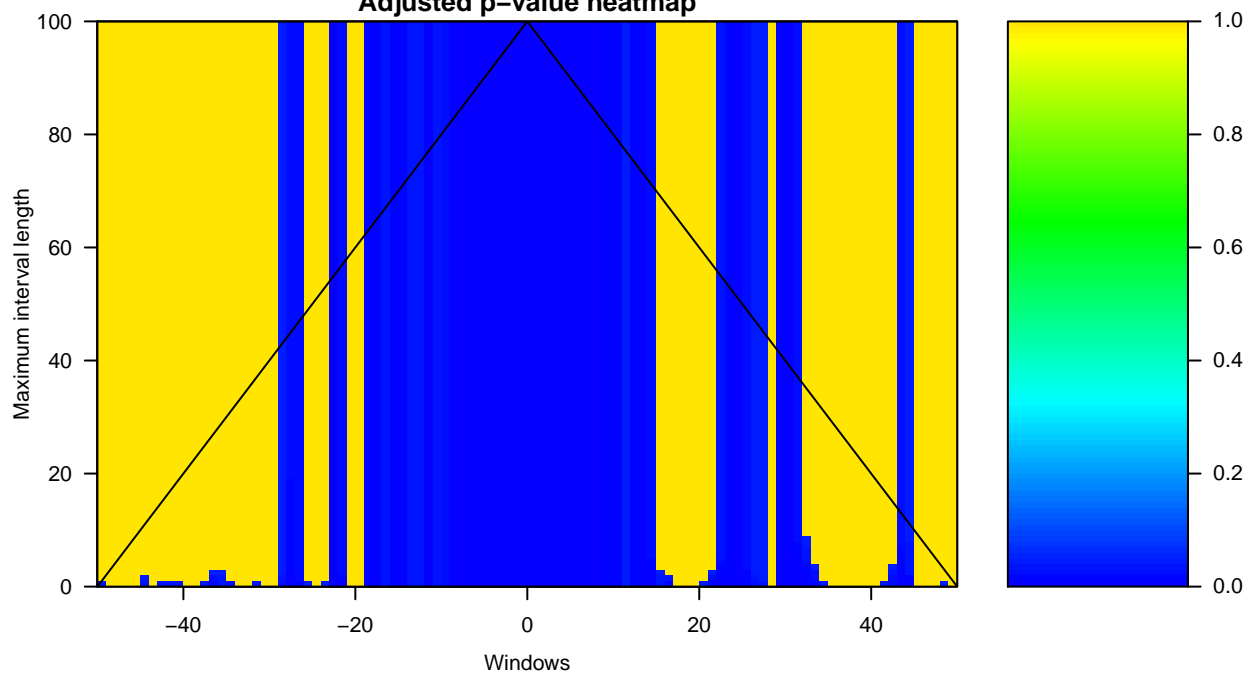
Sample size

# Z DNA motifs

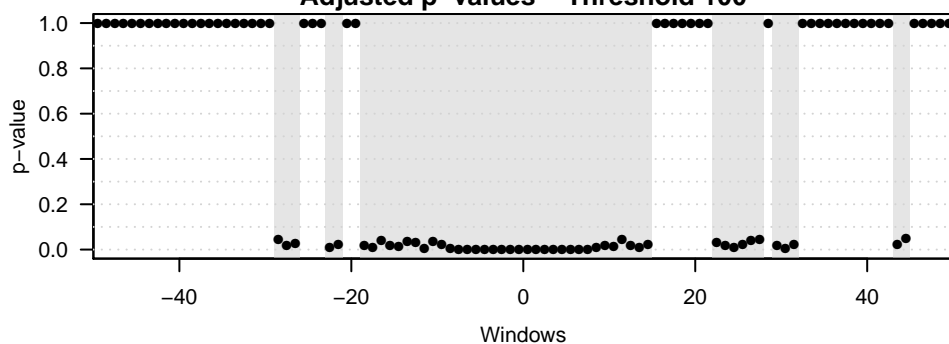


# Most conserved element

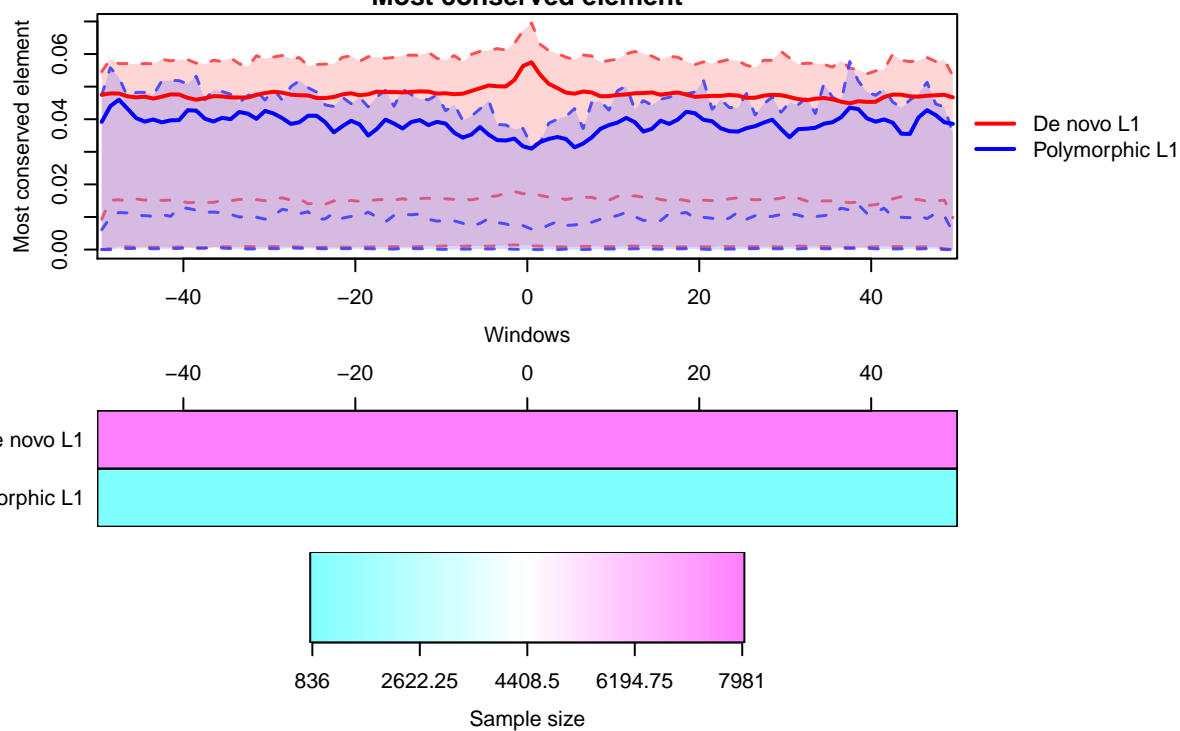
## Adjusted p-value heatmap



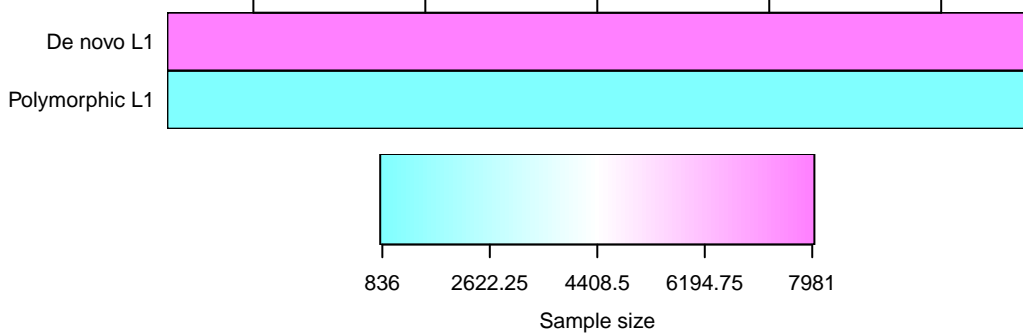
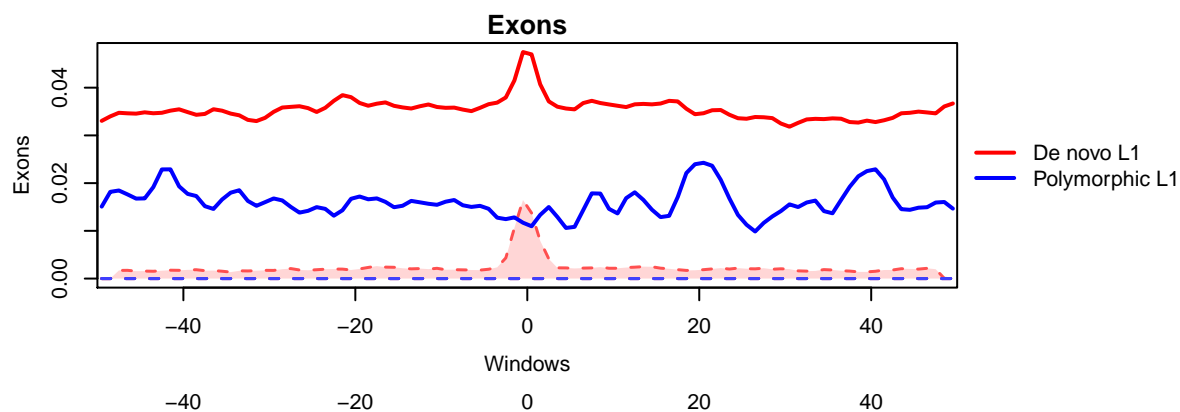
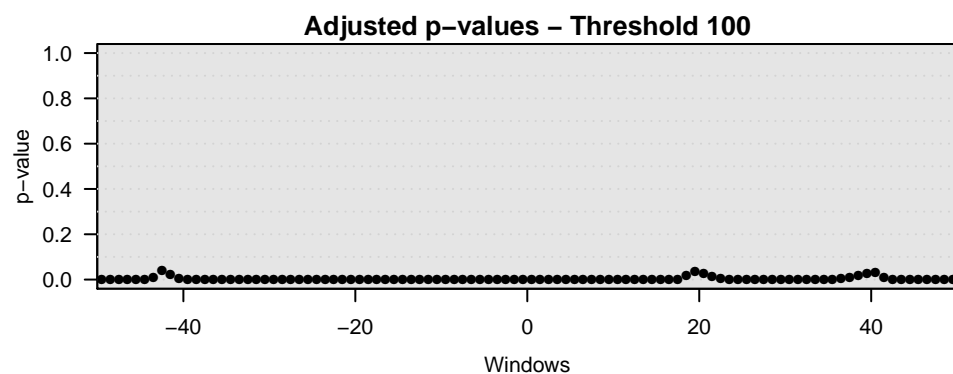
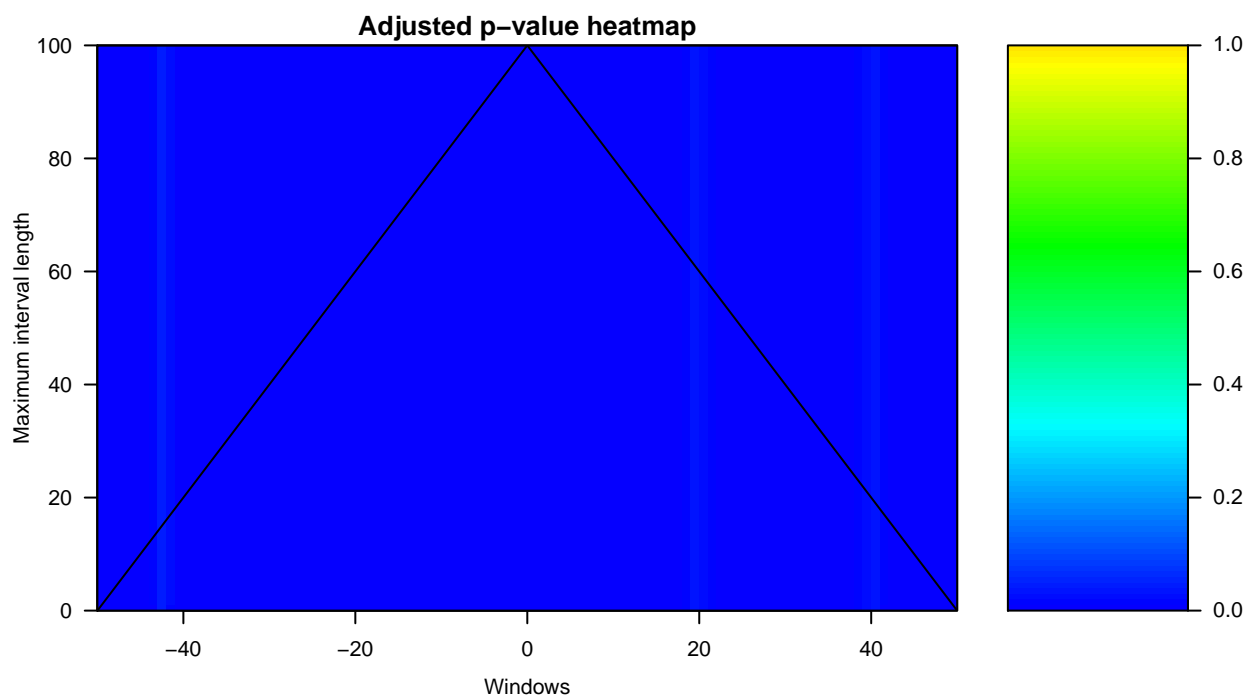
## Adjusted p-values – Threshold 100



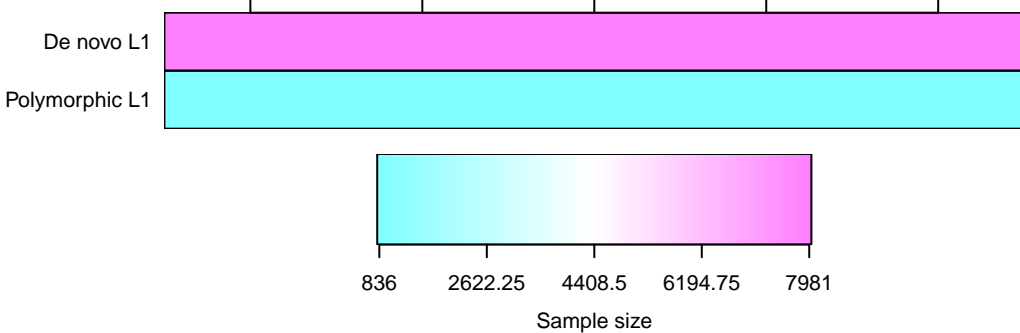
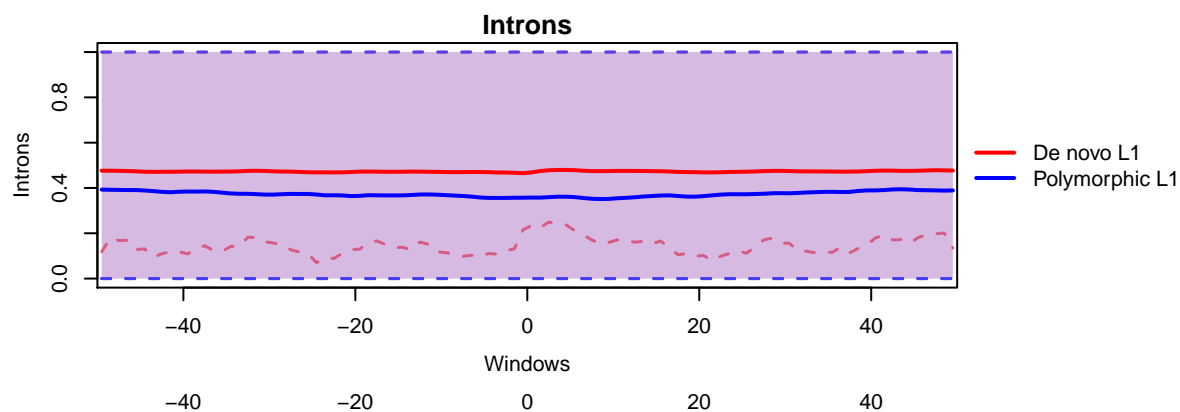
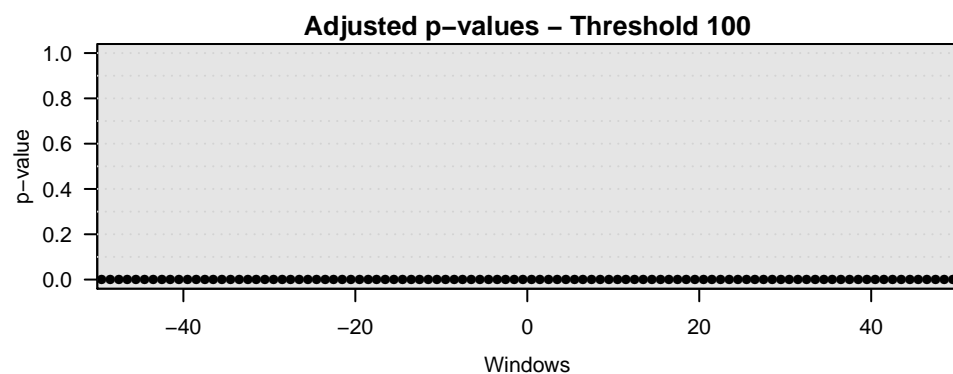
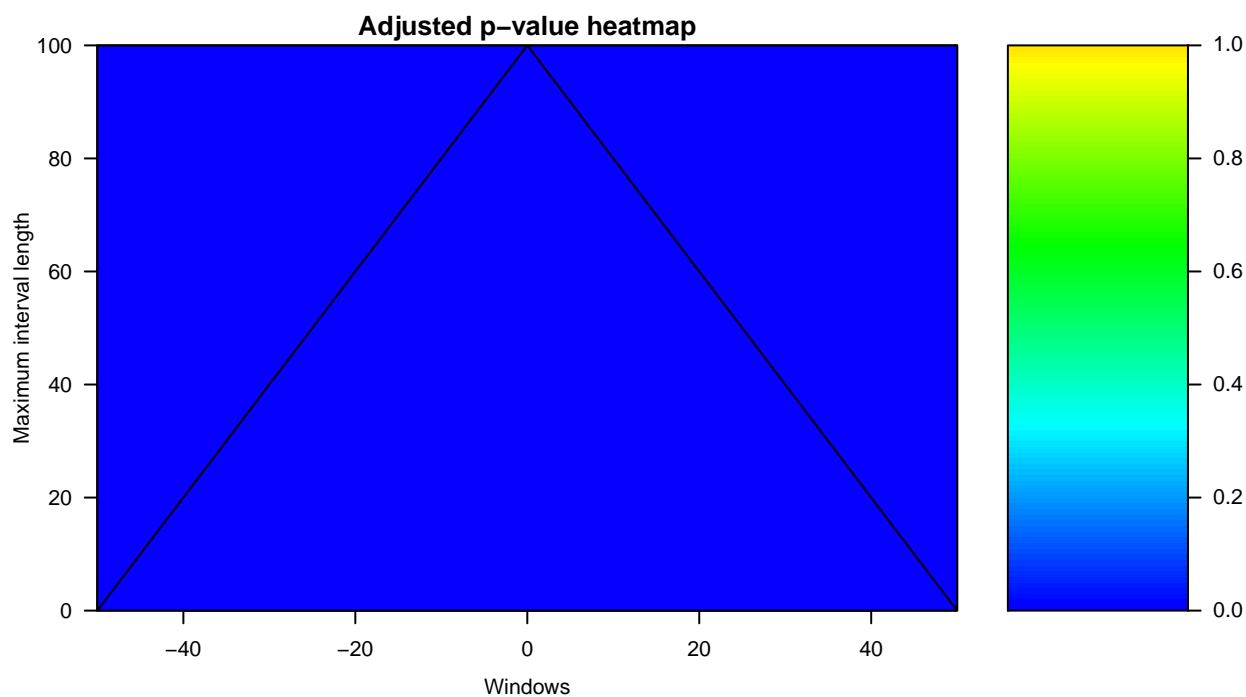
# Most conserved element



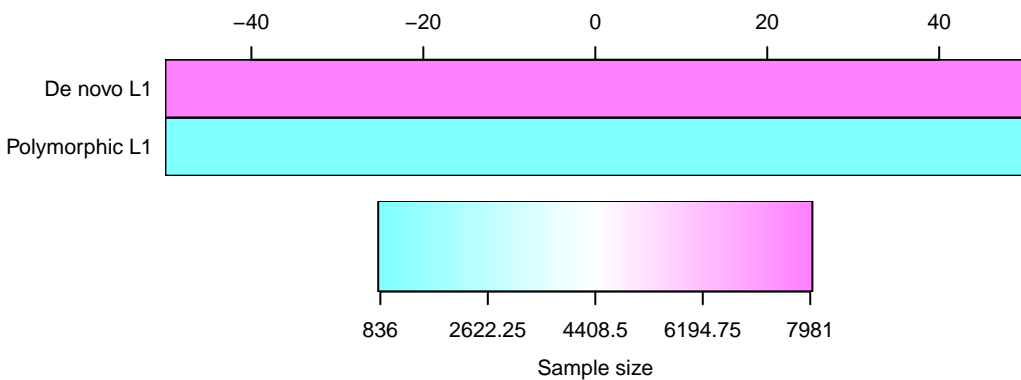
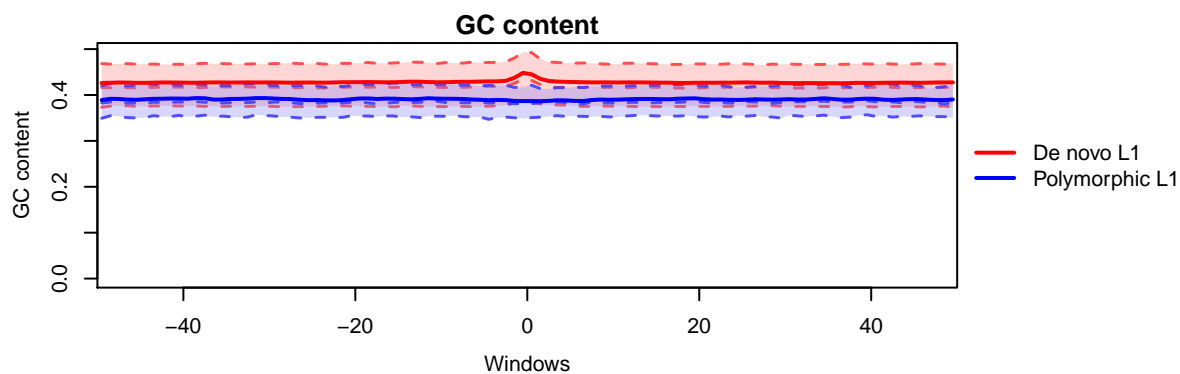
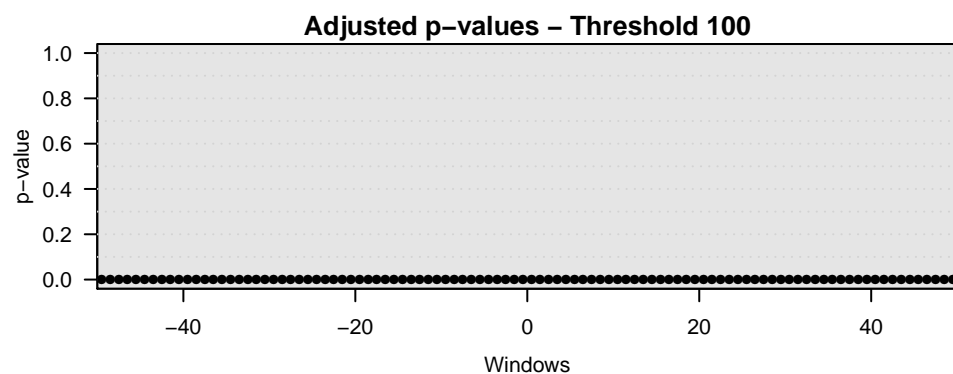
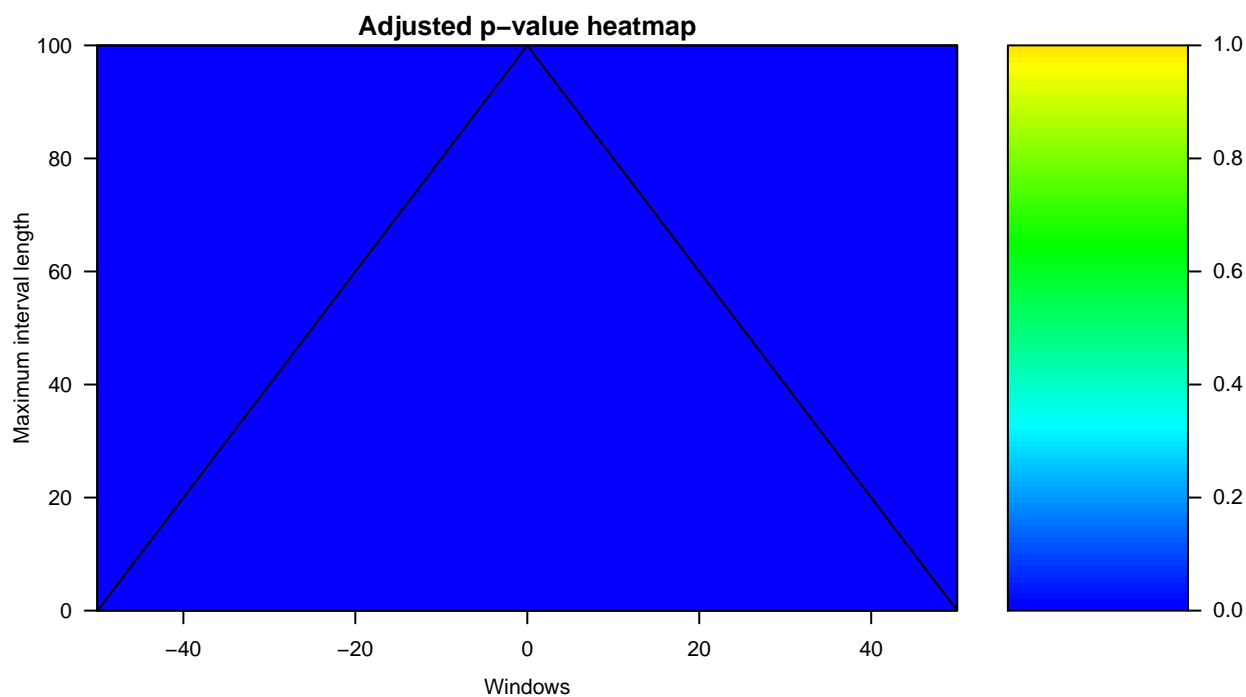
## Exons



# Introns

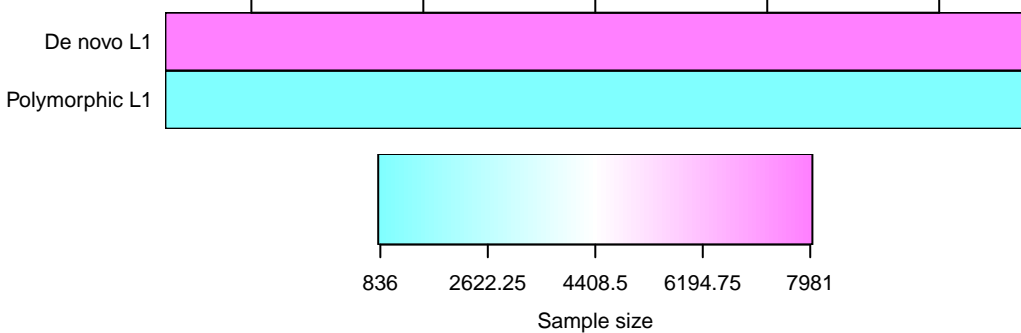
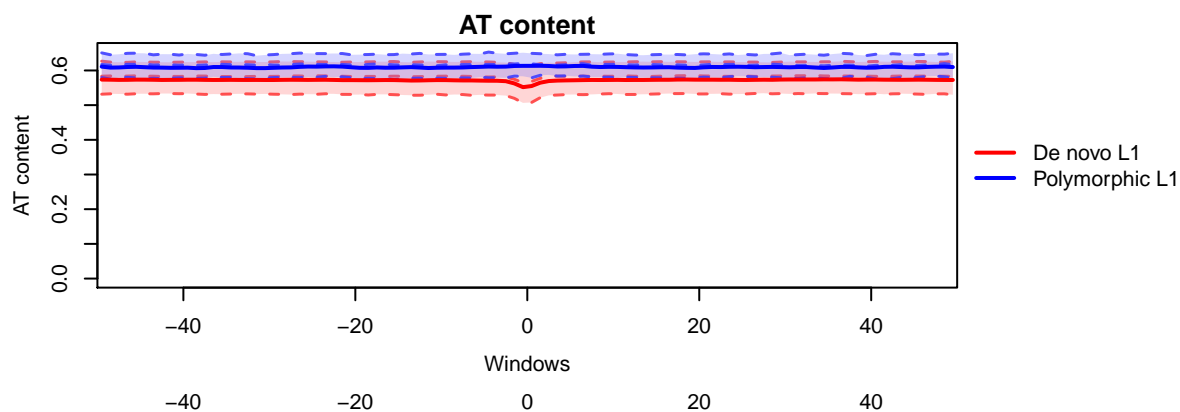
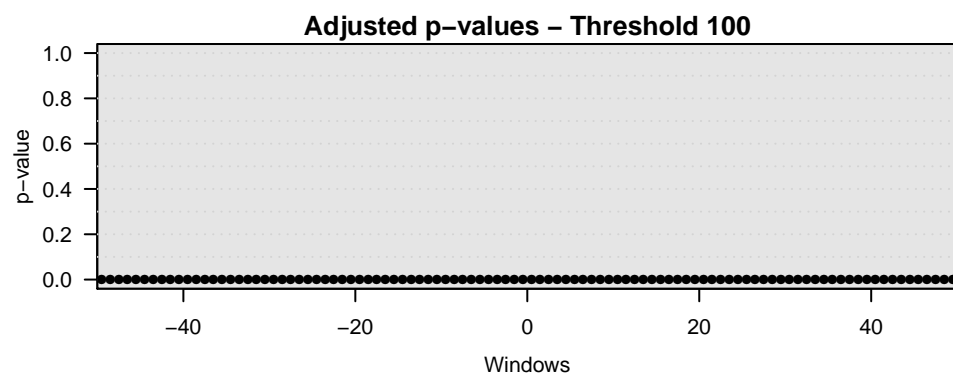
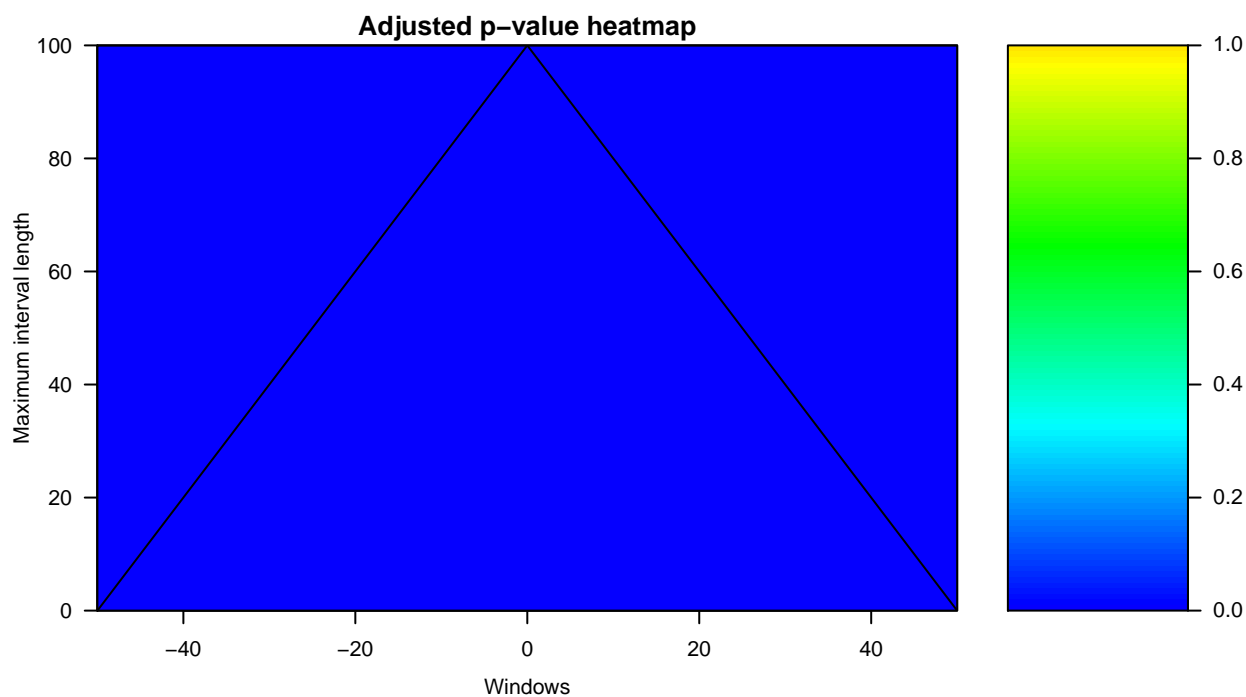


# GC content

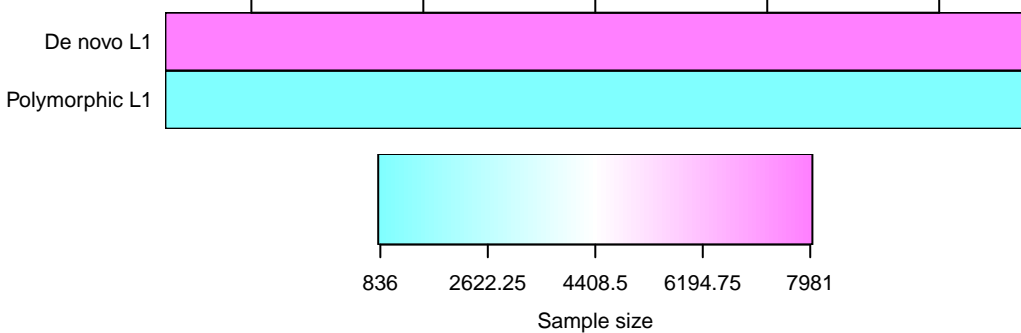
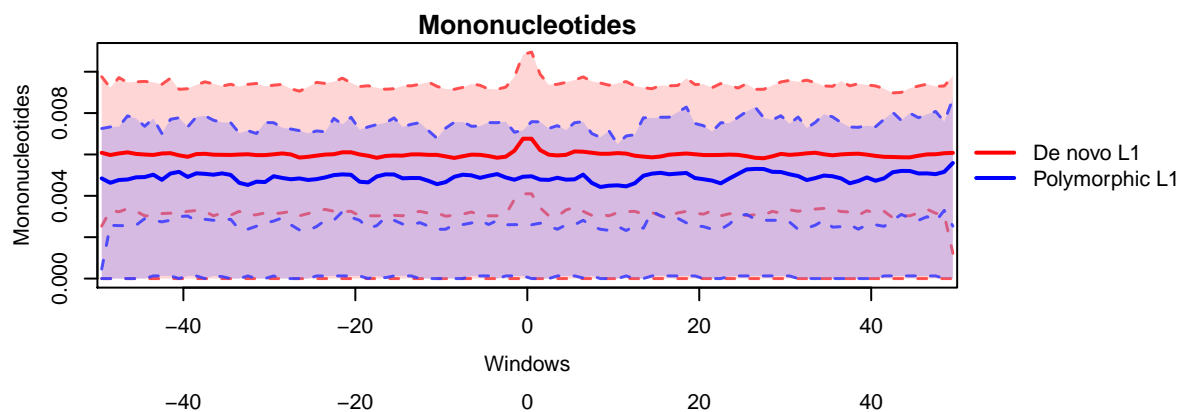
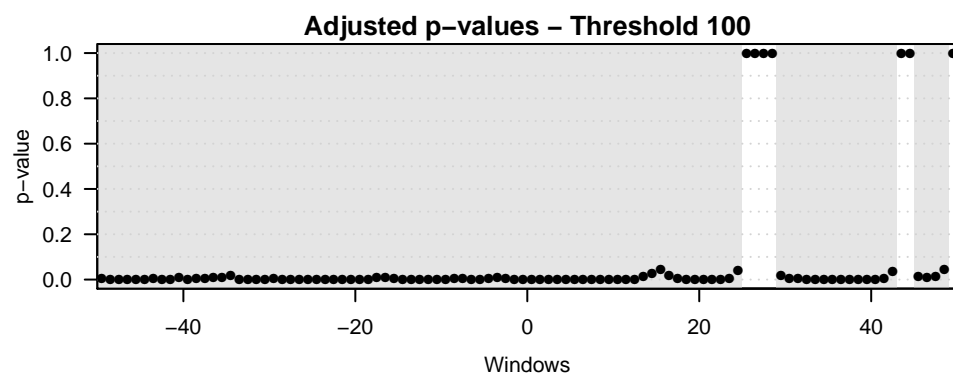
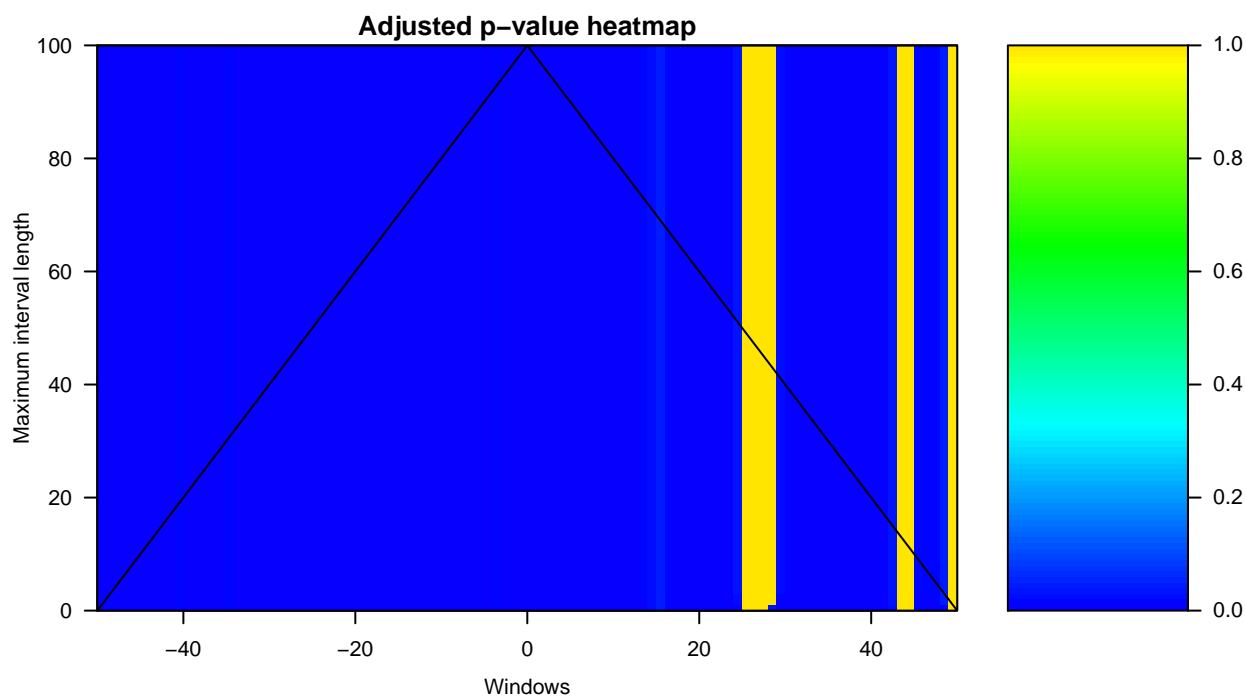




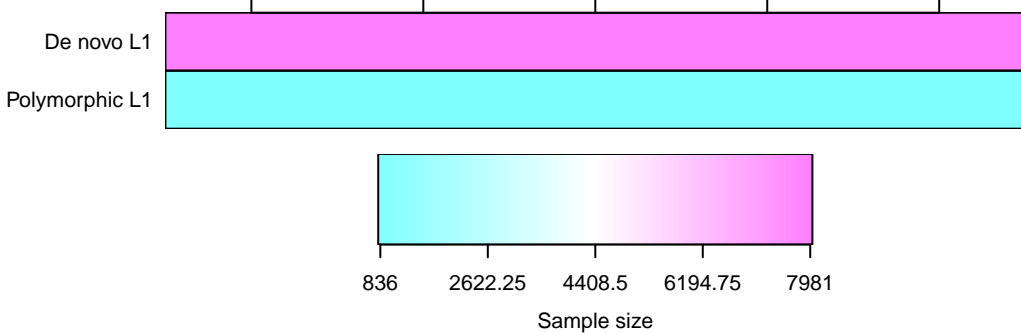
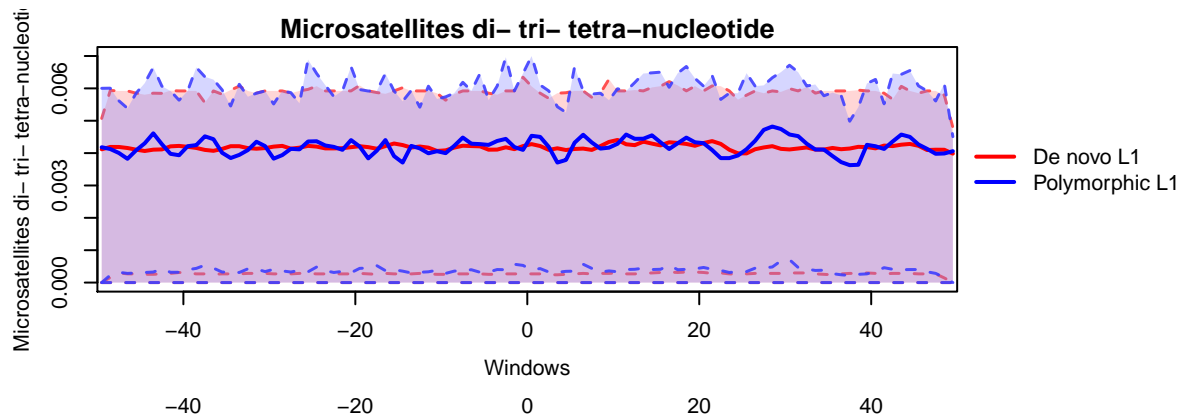
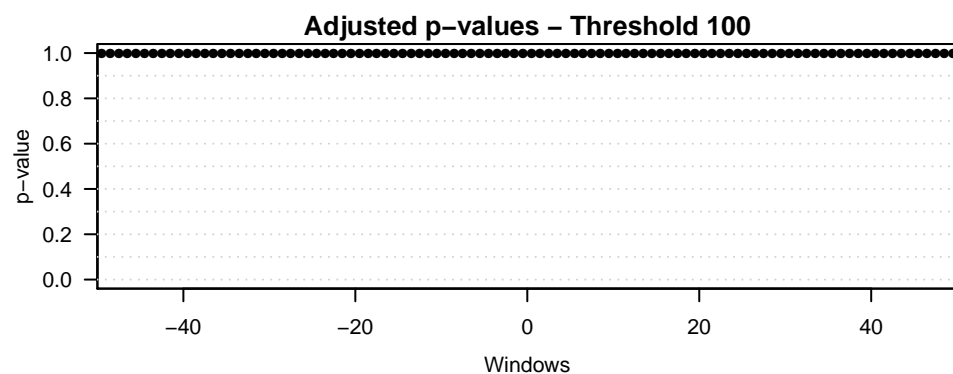
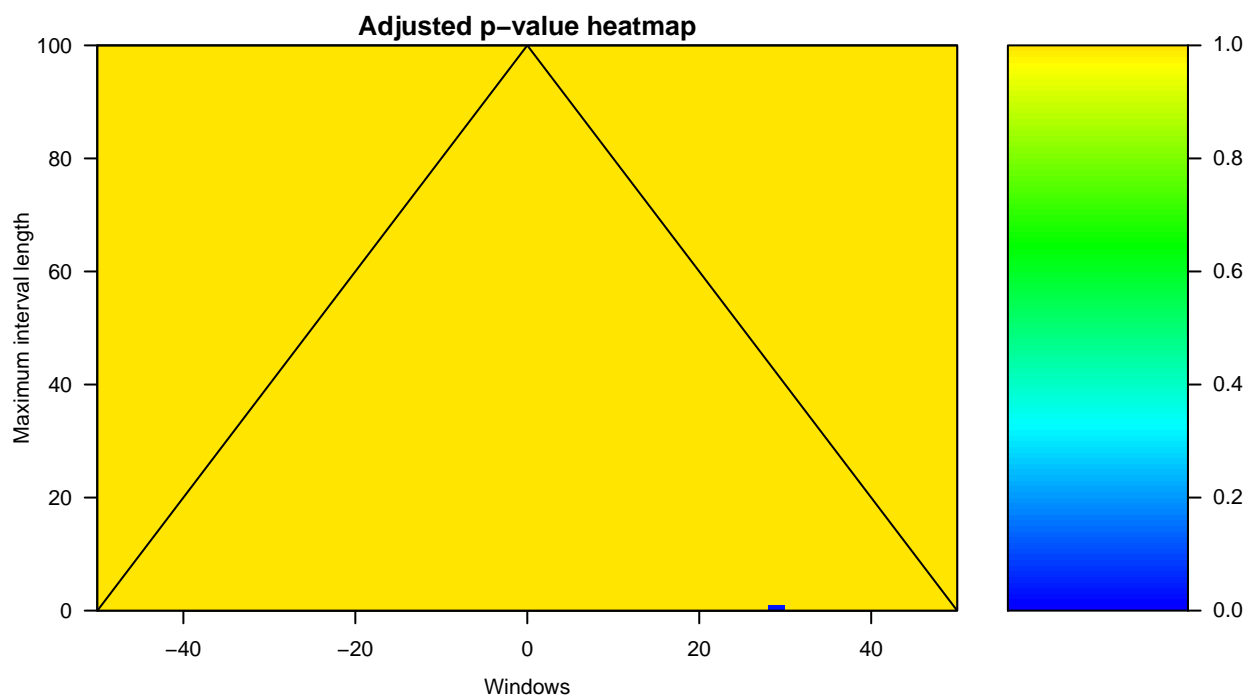
# AT content



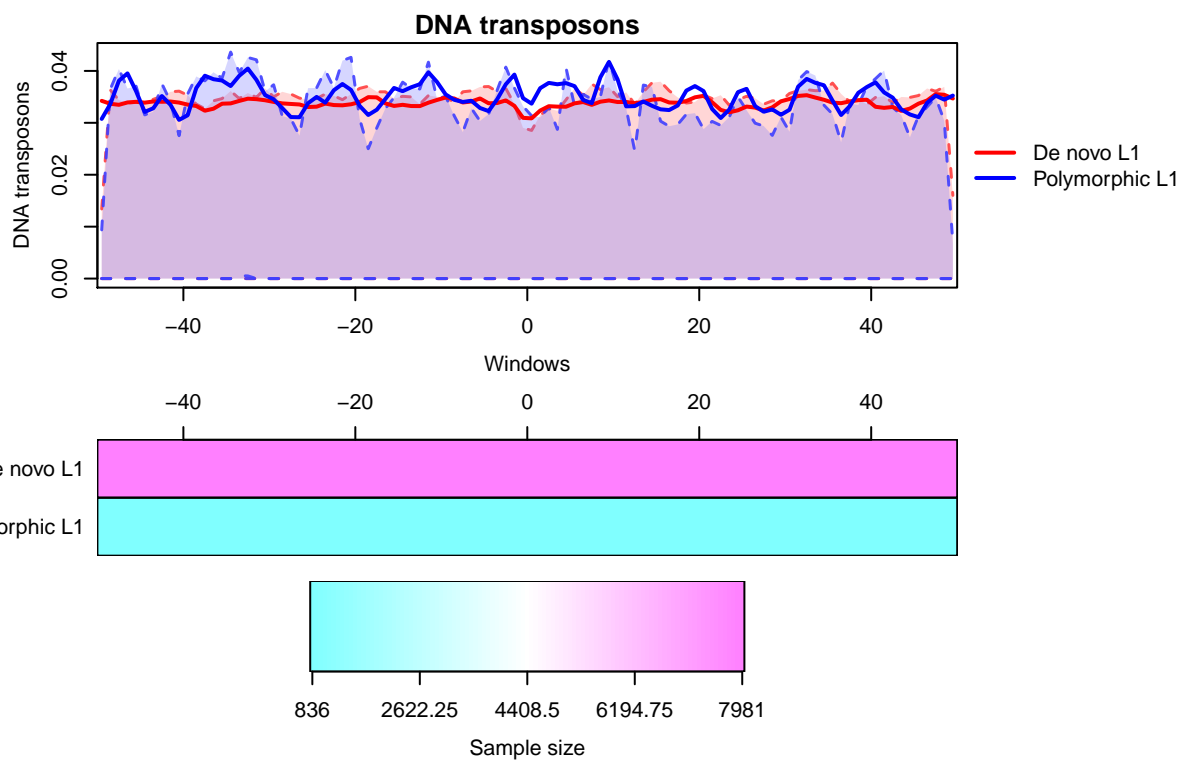
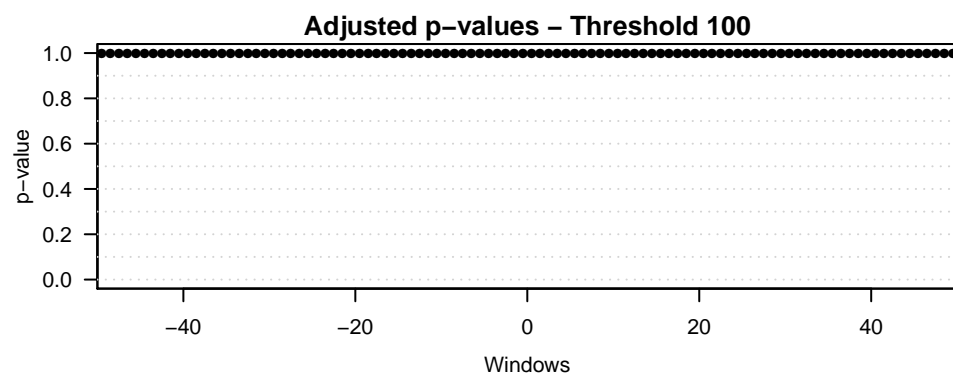
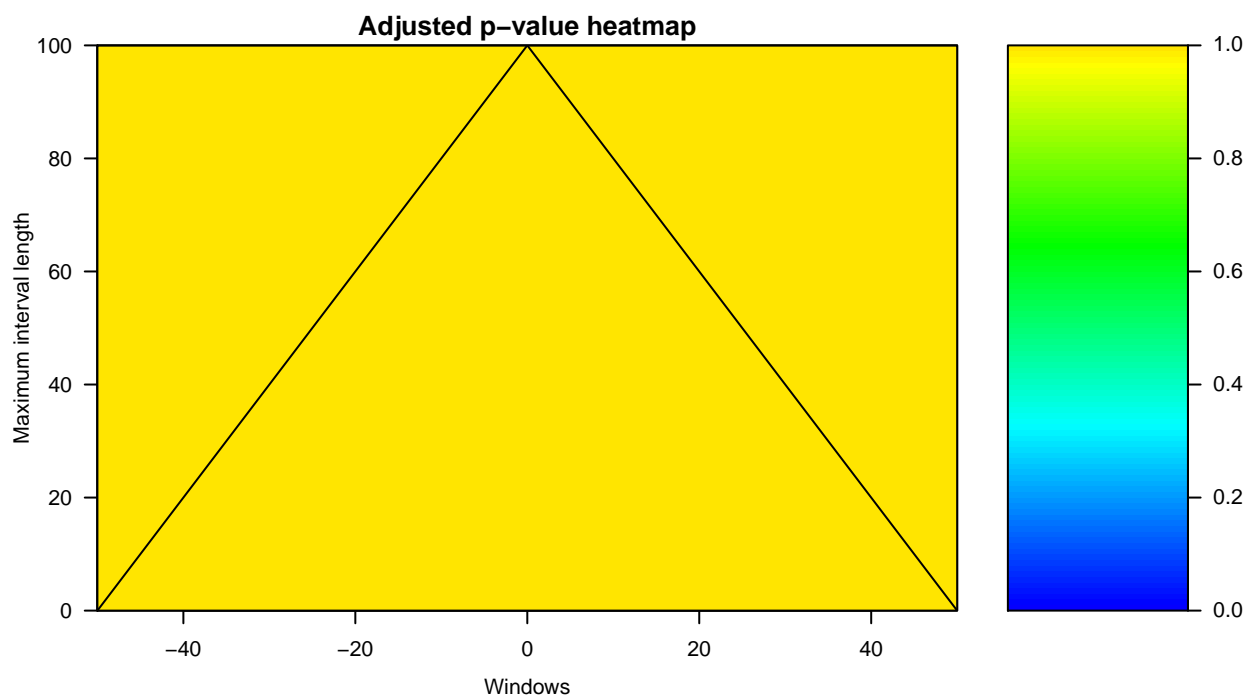
# Mononucleotides



# Microsatellites di- tri- tetra-nucleotide

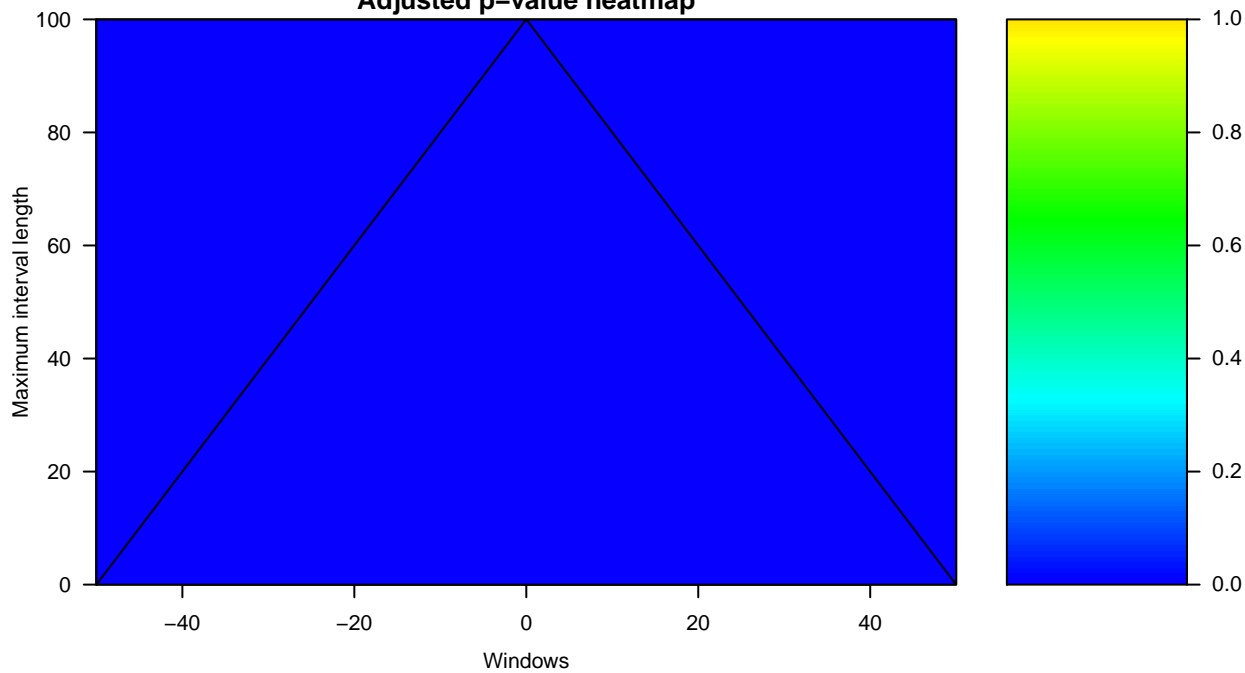


# DNA transposons

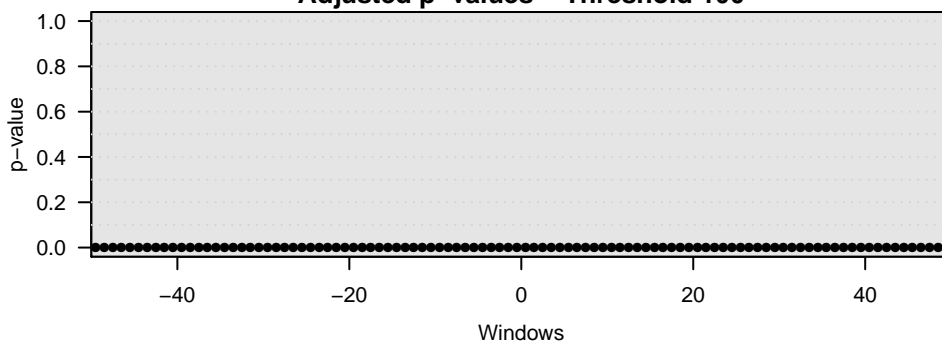


# Alu

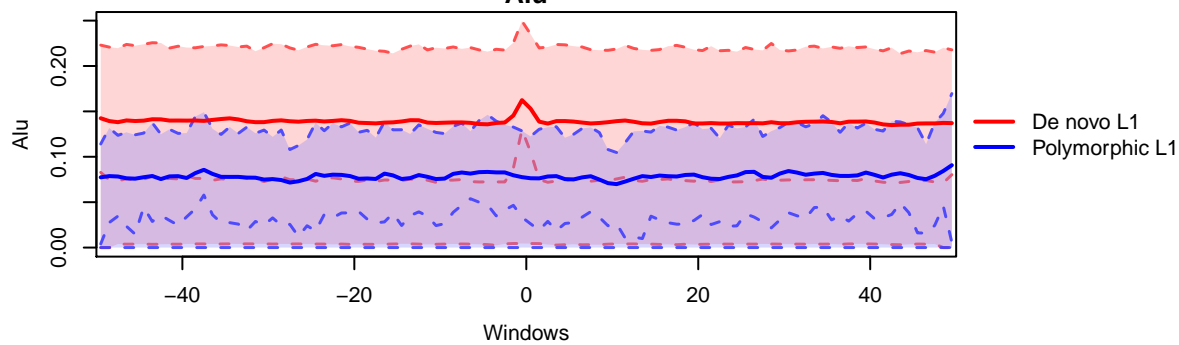
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# Alu



De novo L1

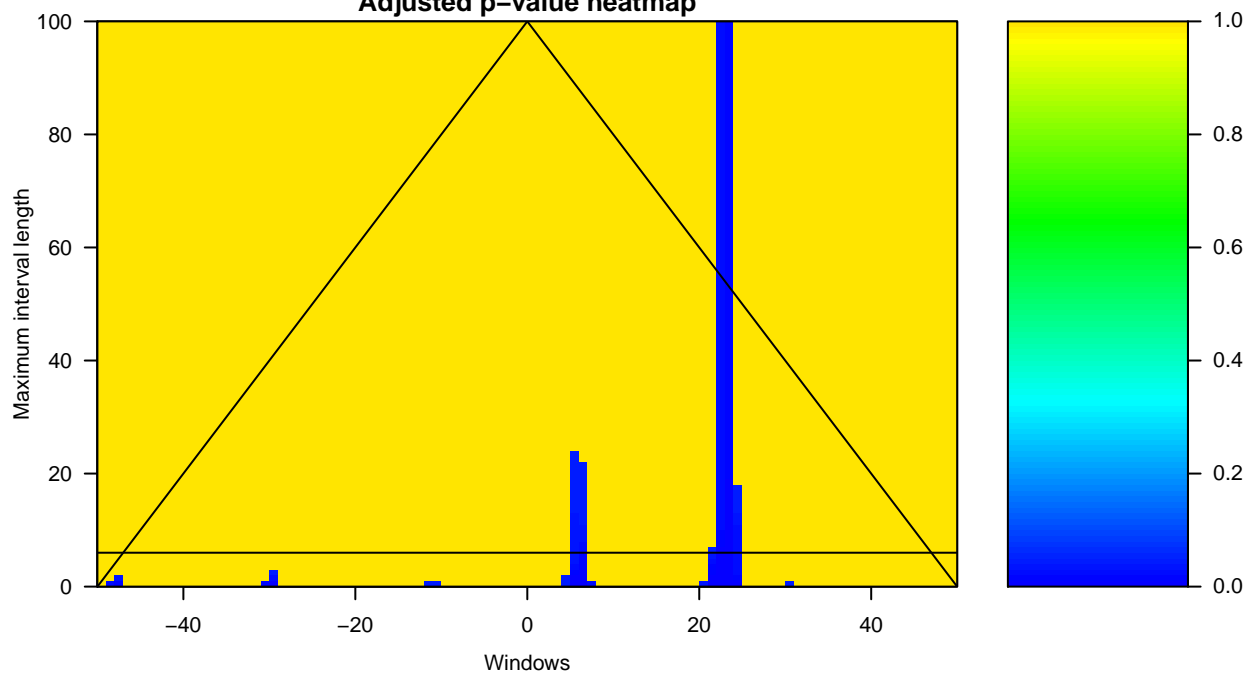
Polymorphic L1

836 2622.25 4408.5 6194.75 7981

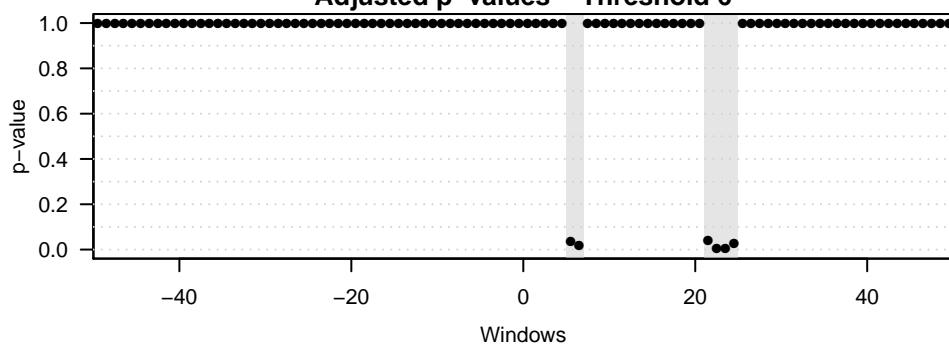
Sample size

MIR

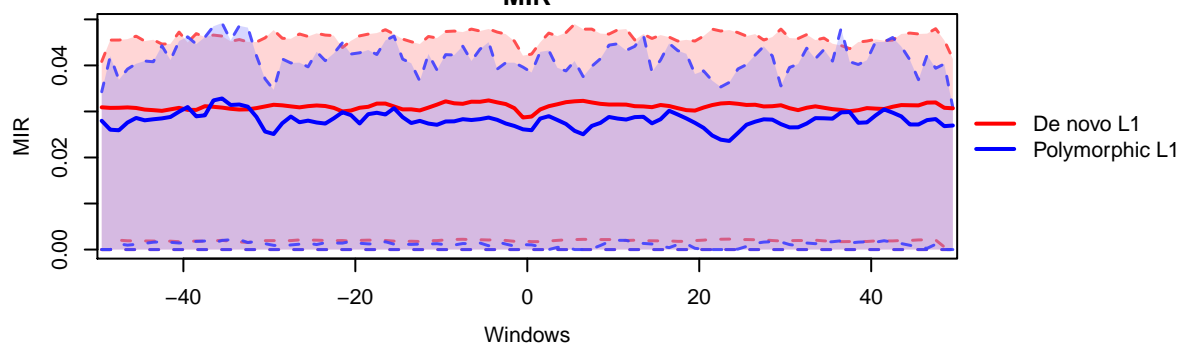
Adjusted p-value heatmap



Adjusted p-values – Threshold 6



MIR



De novo L1

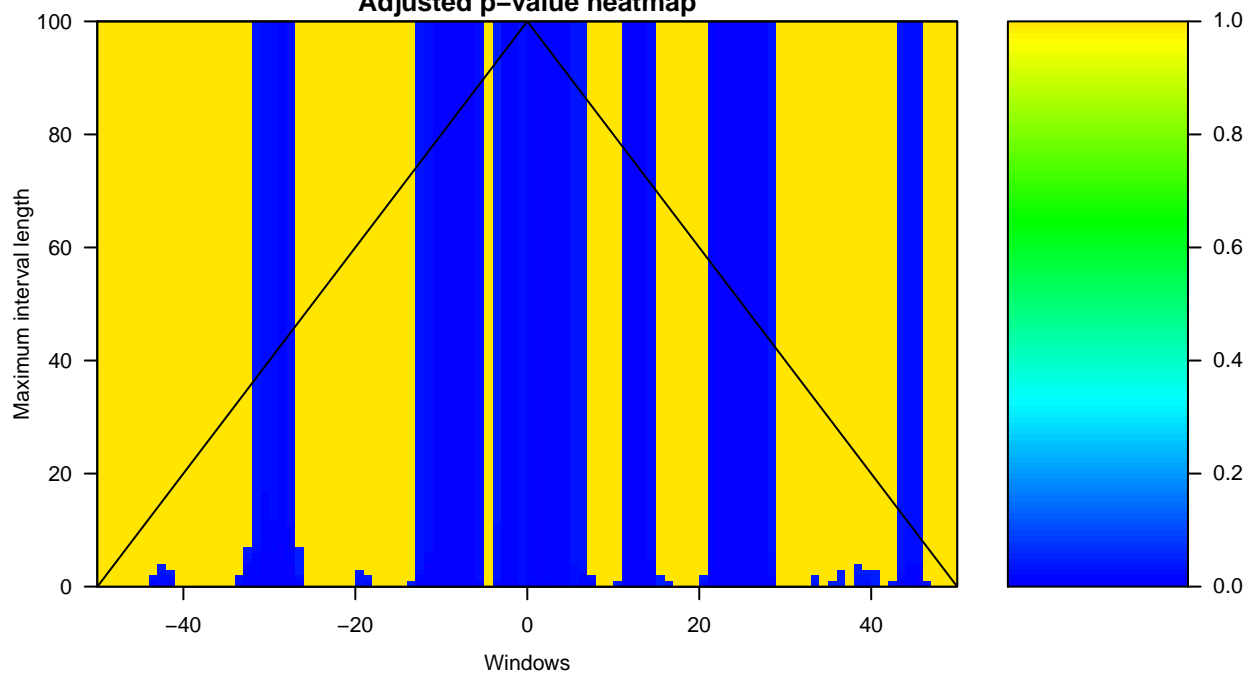
Polymorphic L1

836 2622.25 4408.5 6194.75 7981

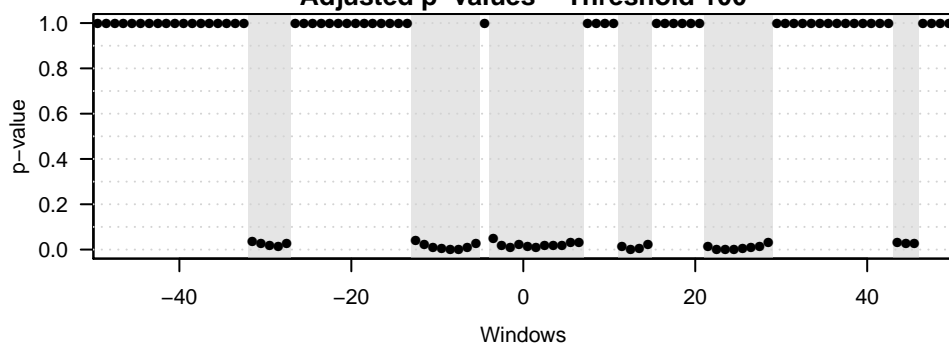
Sample size

# LTR elements

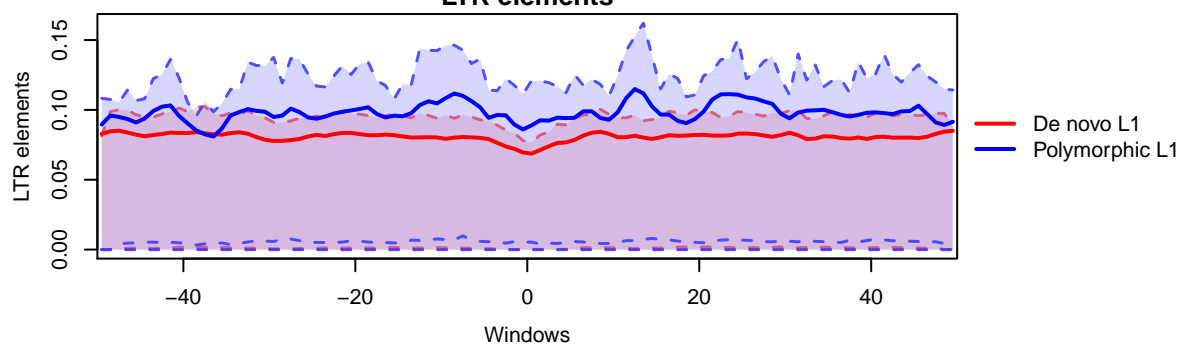
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# LTR elements



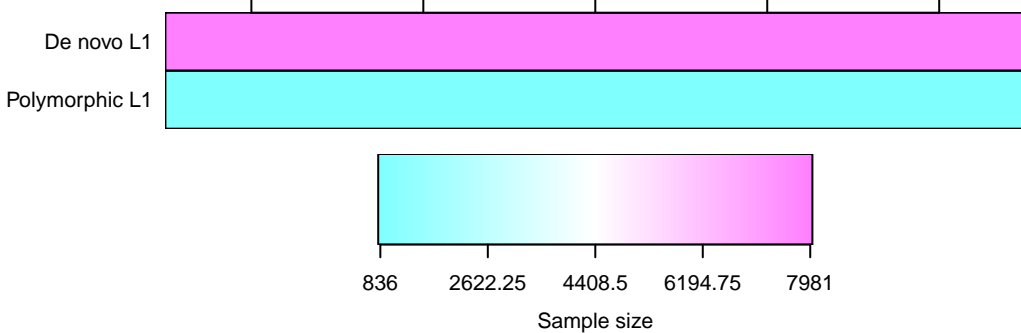
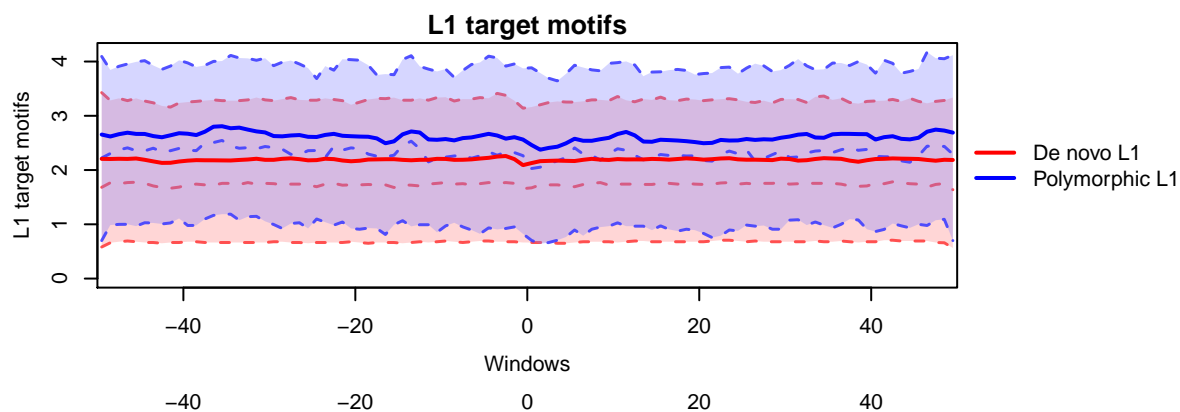
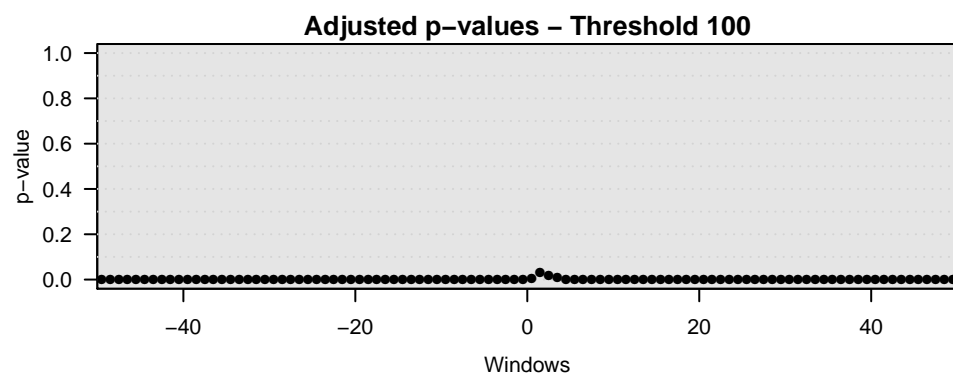
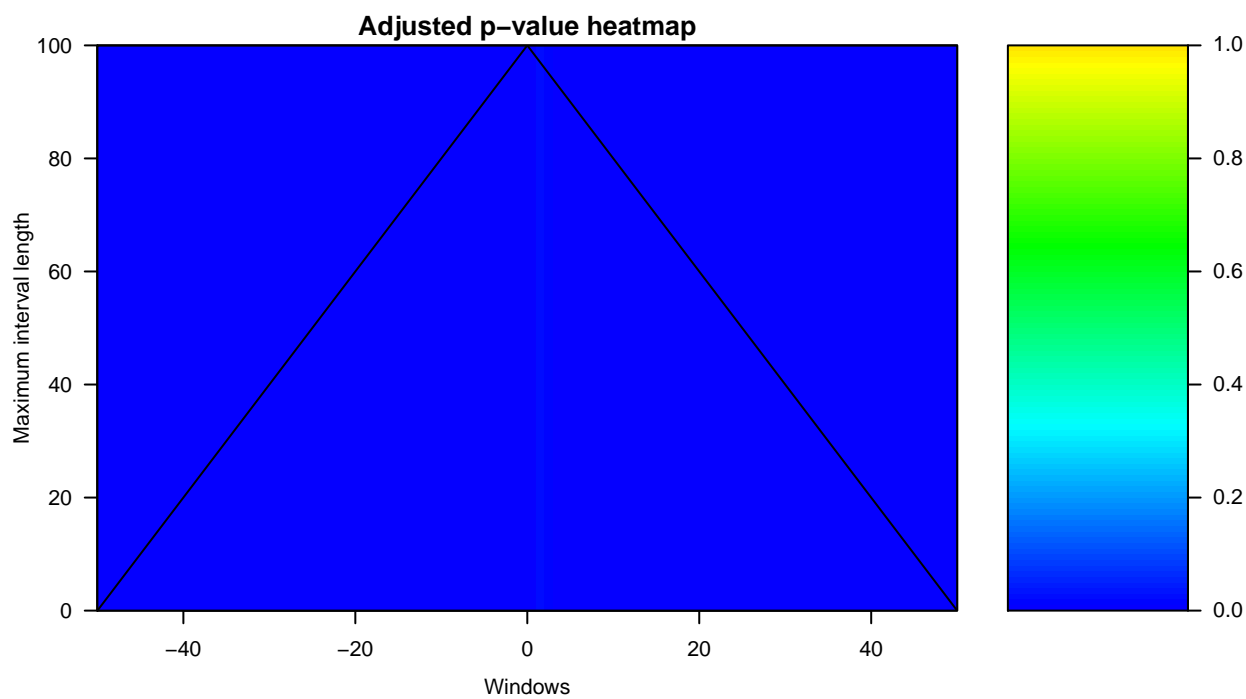
De novo L1

Polymorphic L1

836 2622.25 4408.5 6194.75 7981

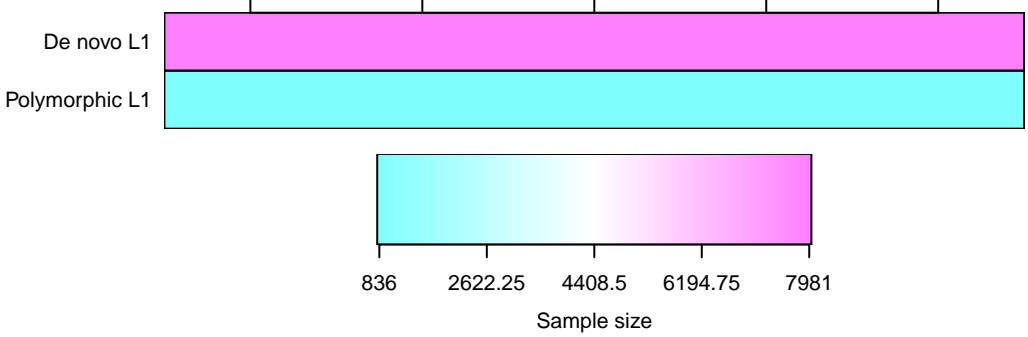
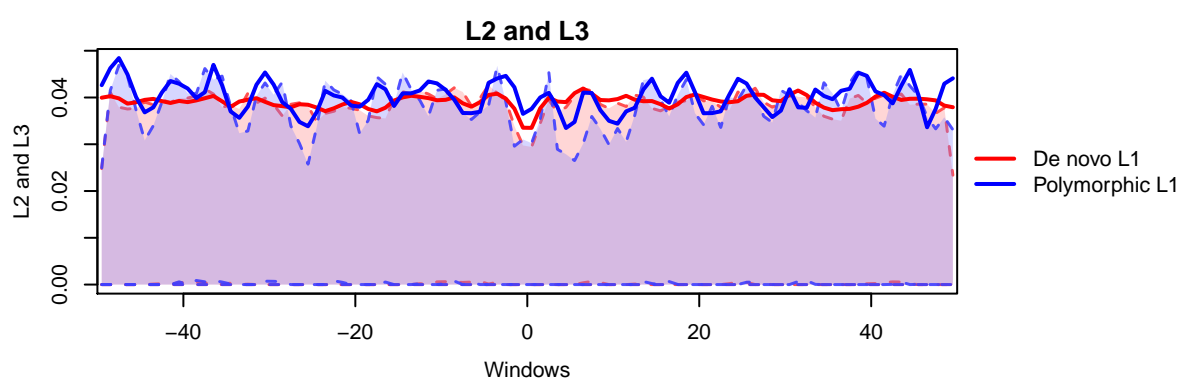
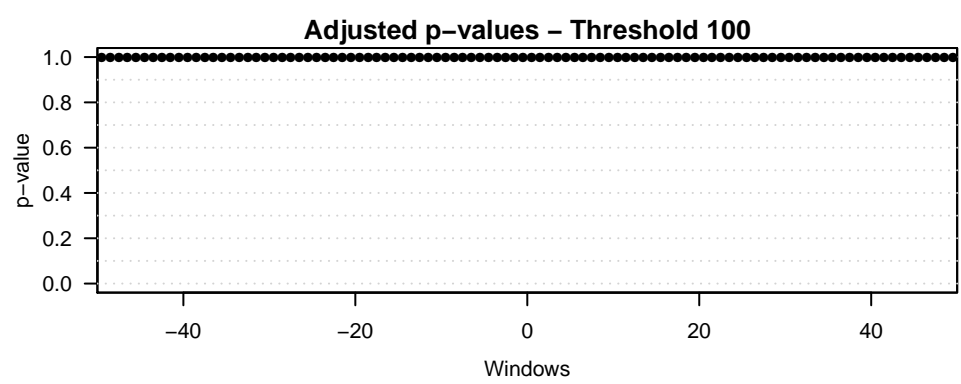
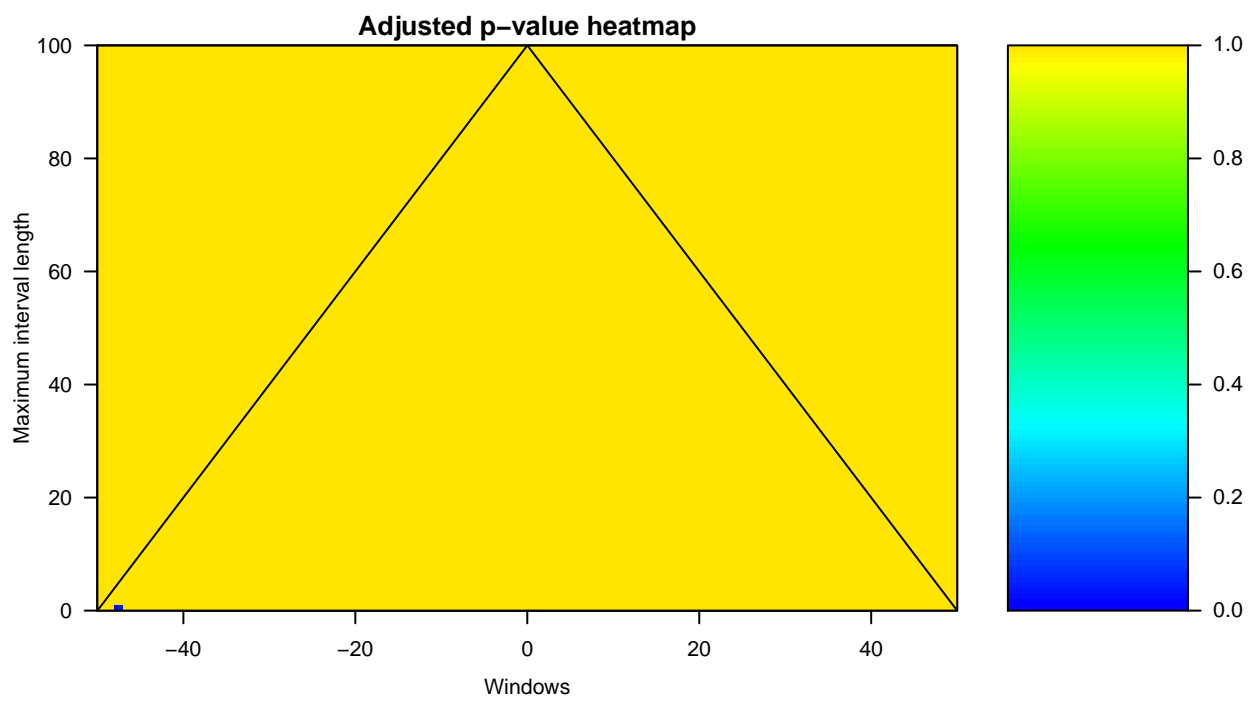
Sample size

# L1 target motifs

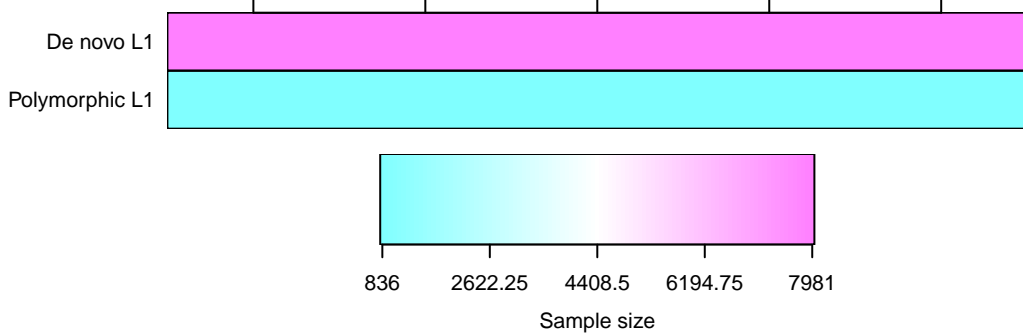
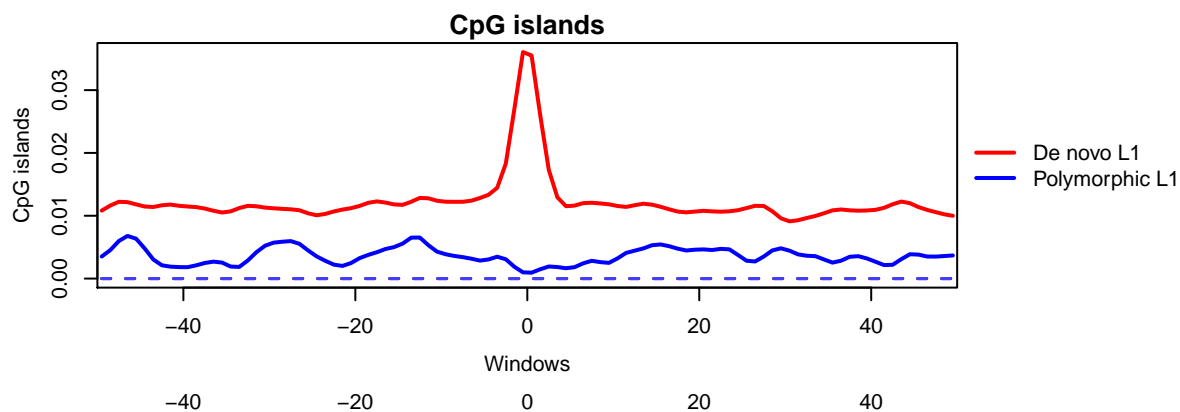
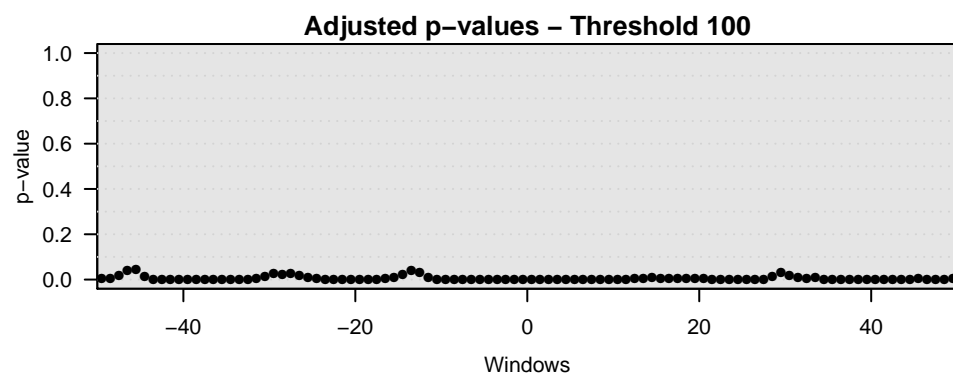
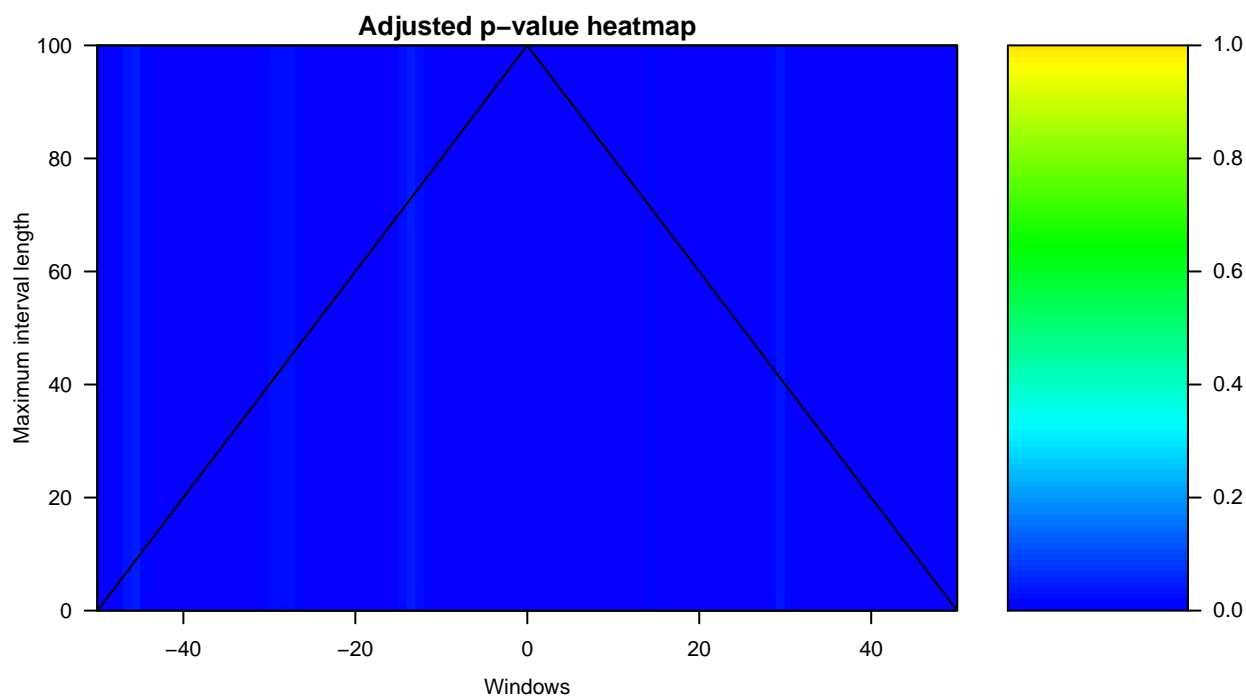




# L2 and L3

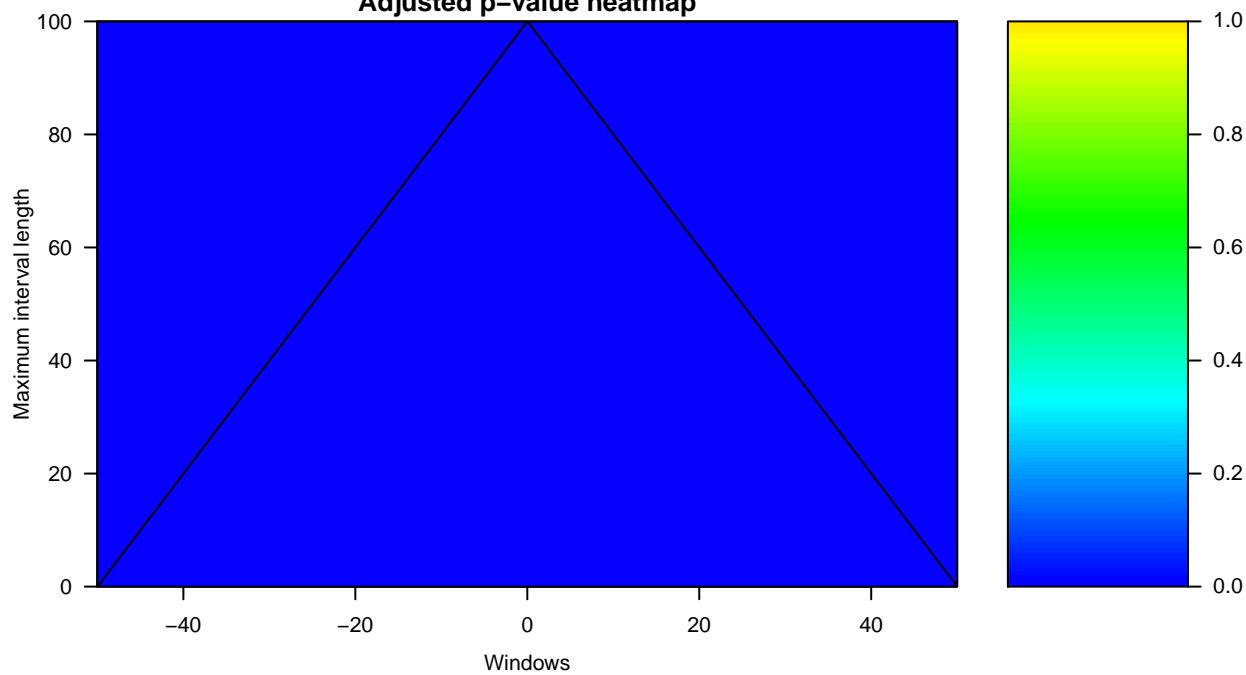


# CpG islands

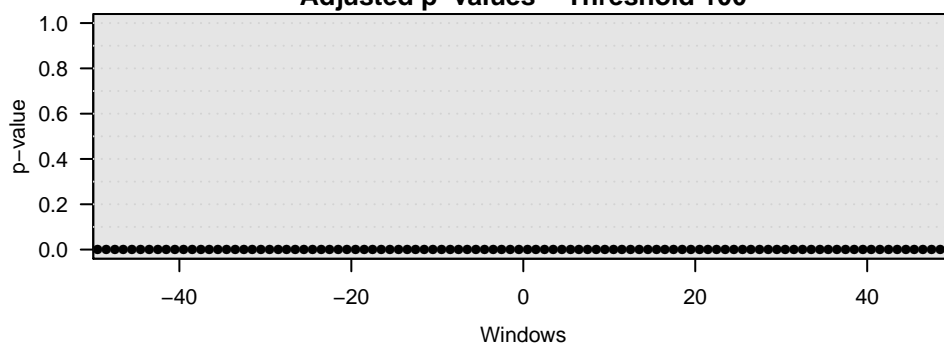


# 5-hydroxymethylcytosine

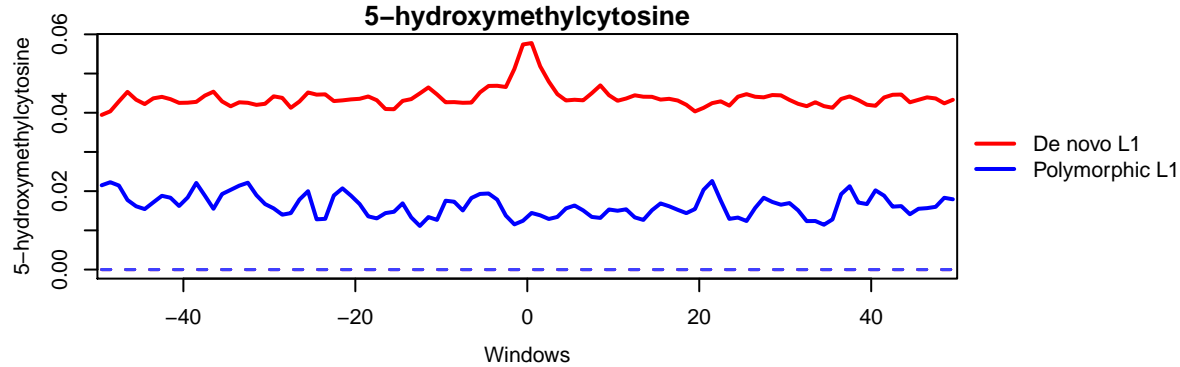
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100



# 5-hydroxymethylcytosine



De novo L1

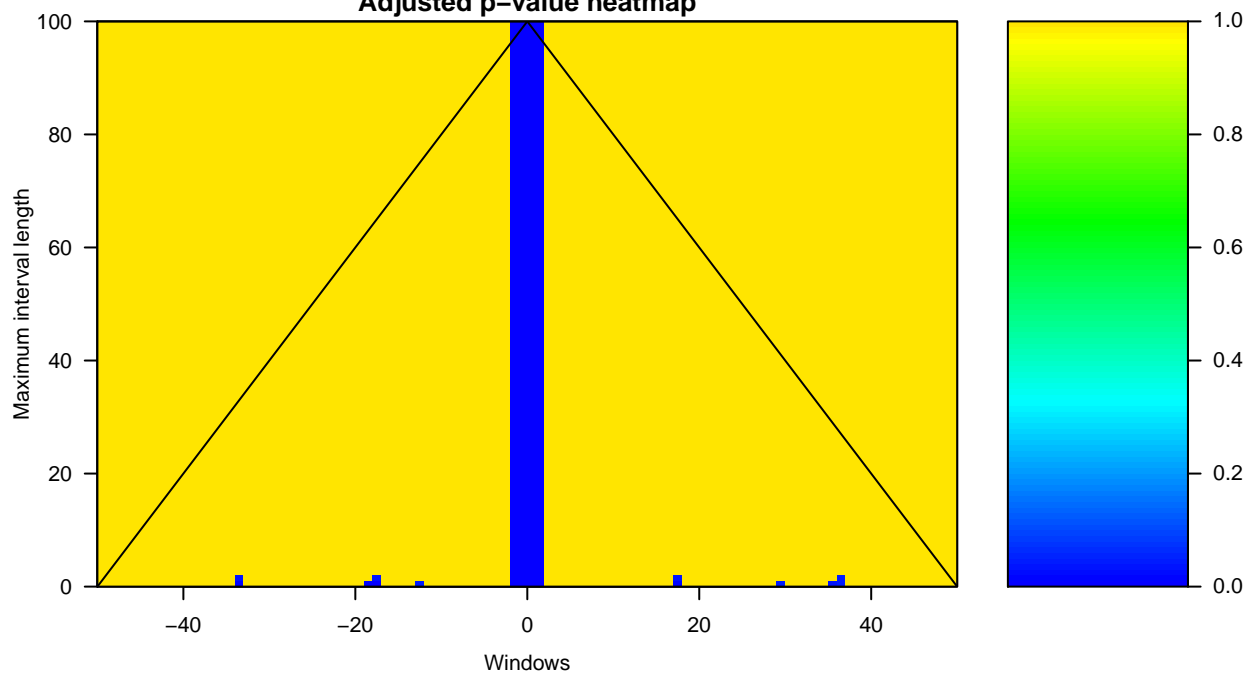
Polymorphic L1

836 2622.25 4408.5 6194.75 7981

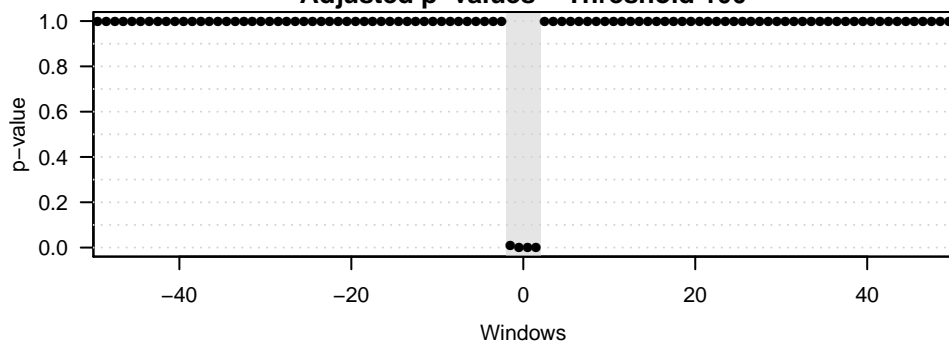
Sample size

# Sperm hypomethylation

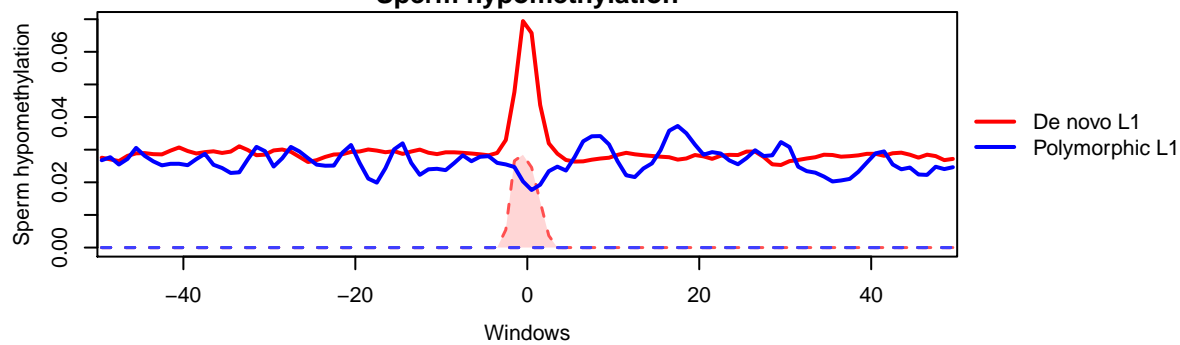
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 100

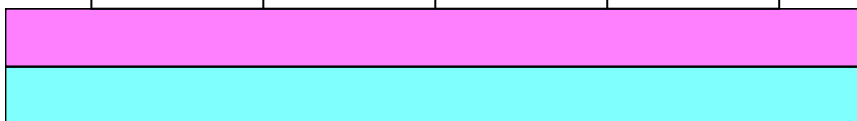


# Sperm hypomethylation



De novo L1

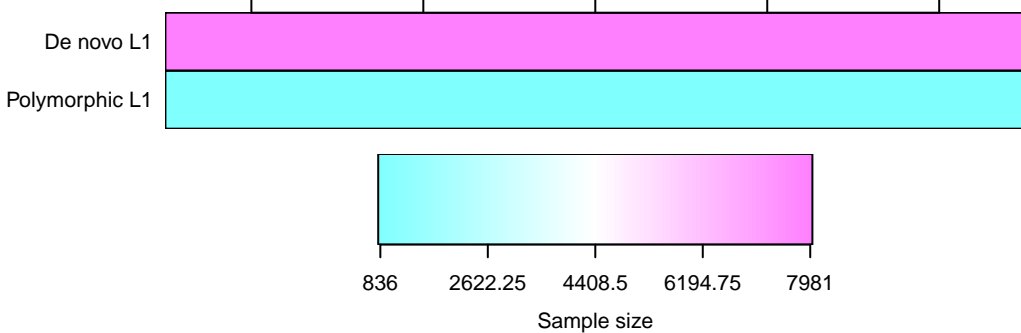
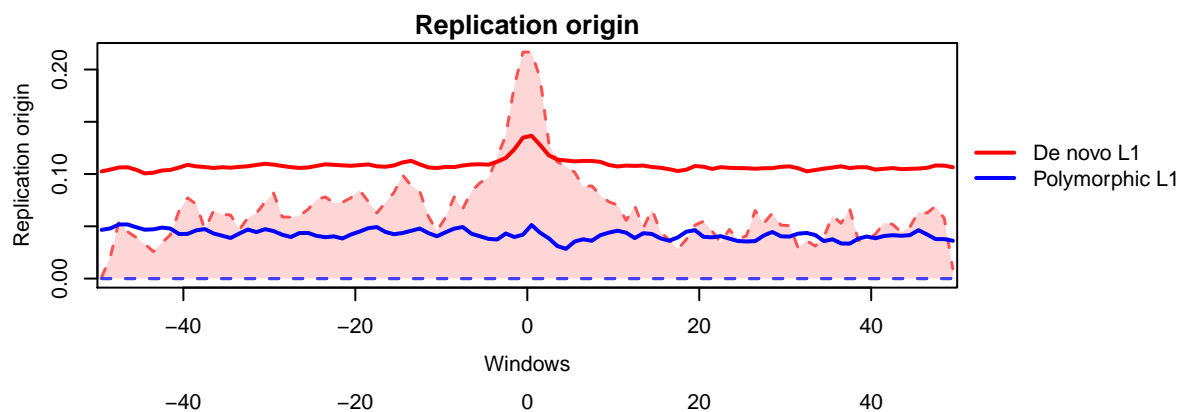
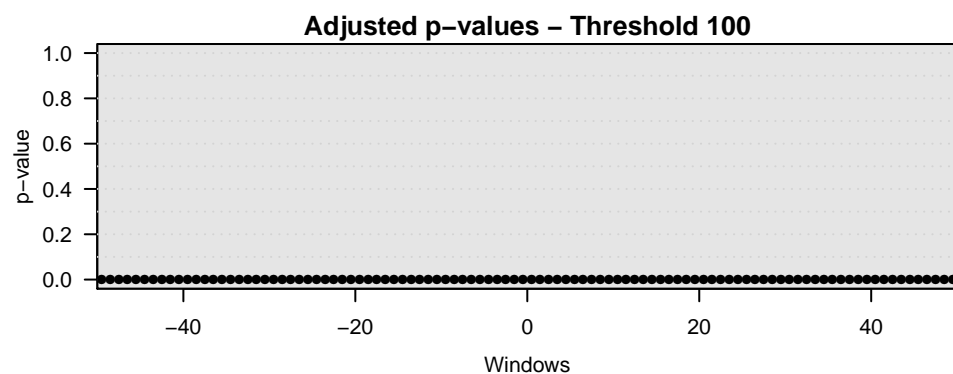
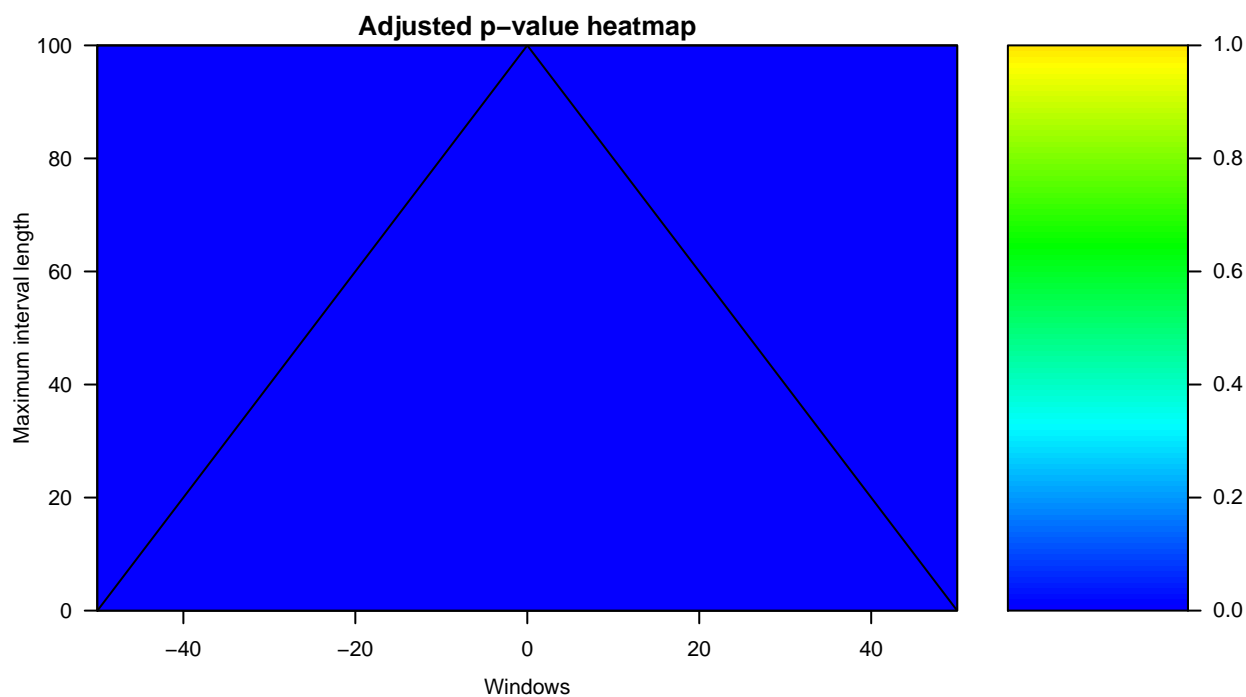
Polymorphic L1



836 2622.25 4408.5 6194.75 7981

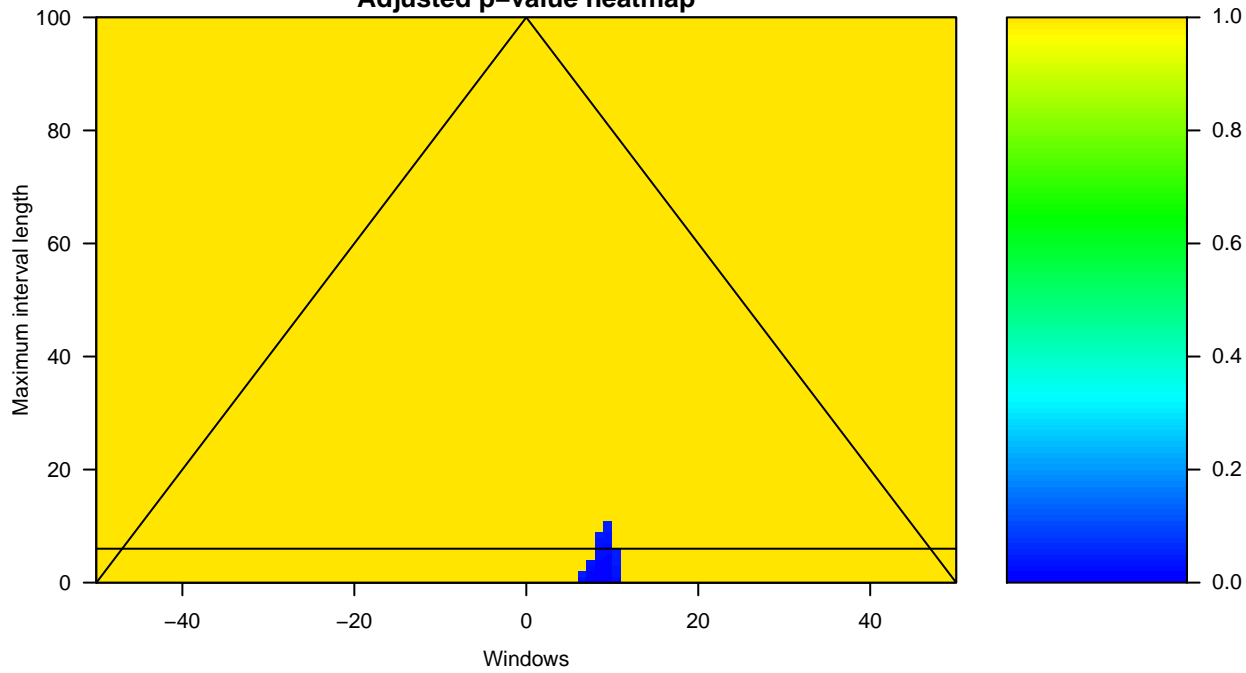
Sample size

# Replication origin

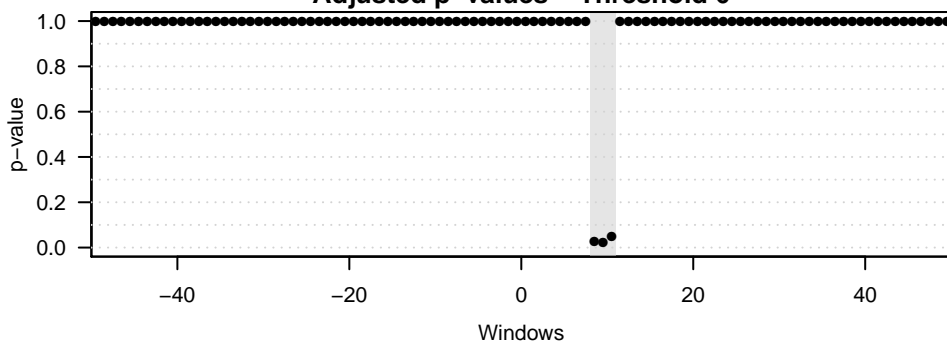


# Sex-averaged recombination hotspots

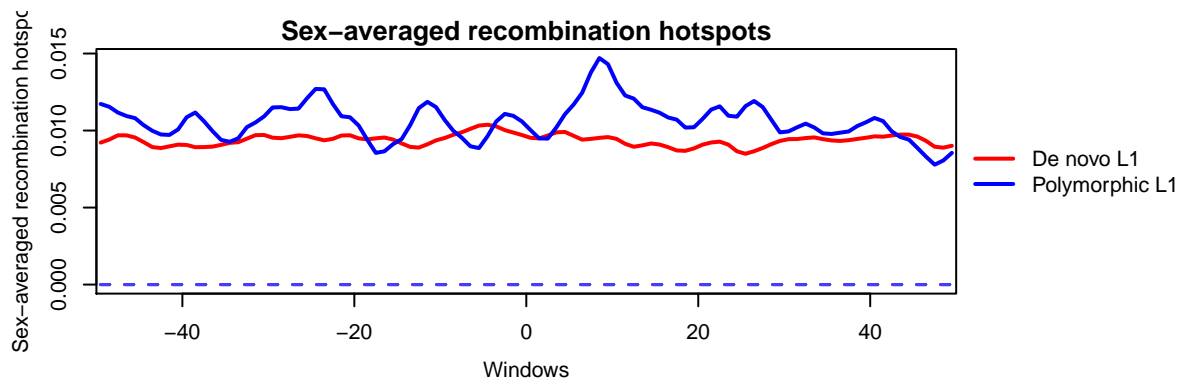
## Adjusted p-value heatmap



## Adjusted p-values – Threshold 6



## Sex-averaged recombination hotspots



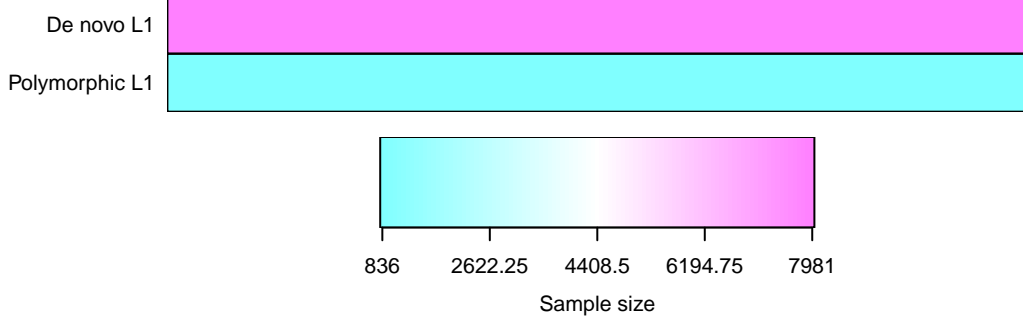
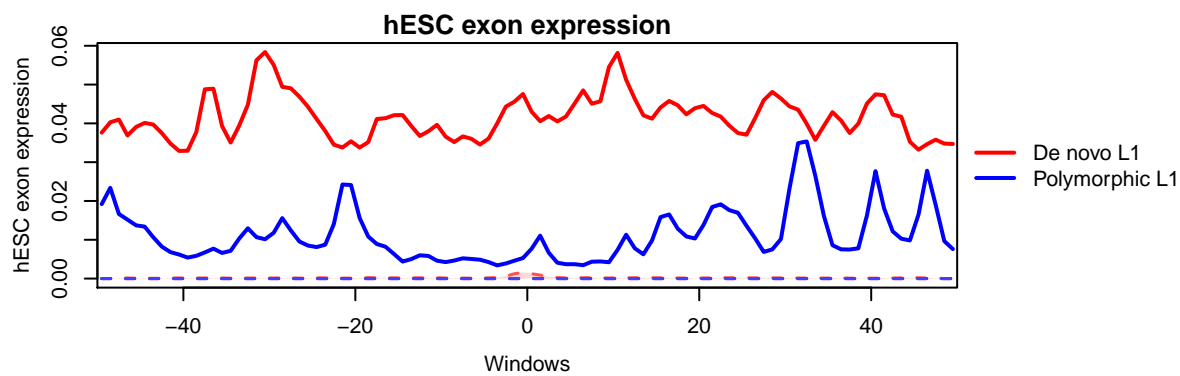
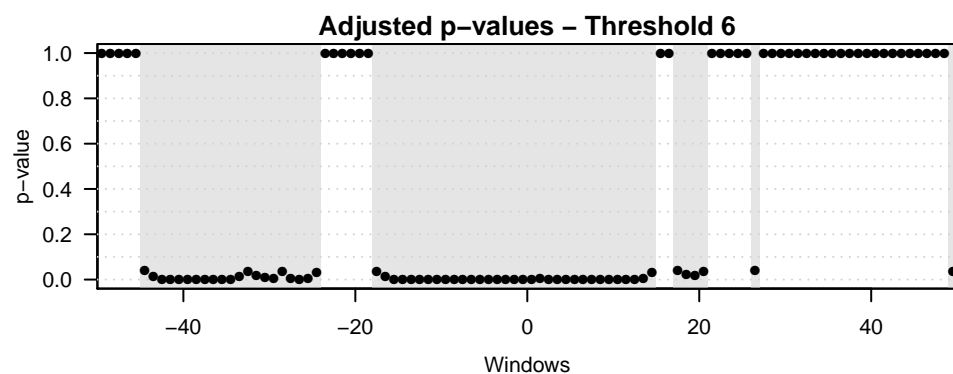
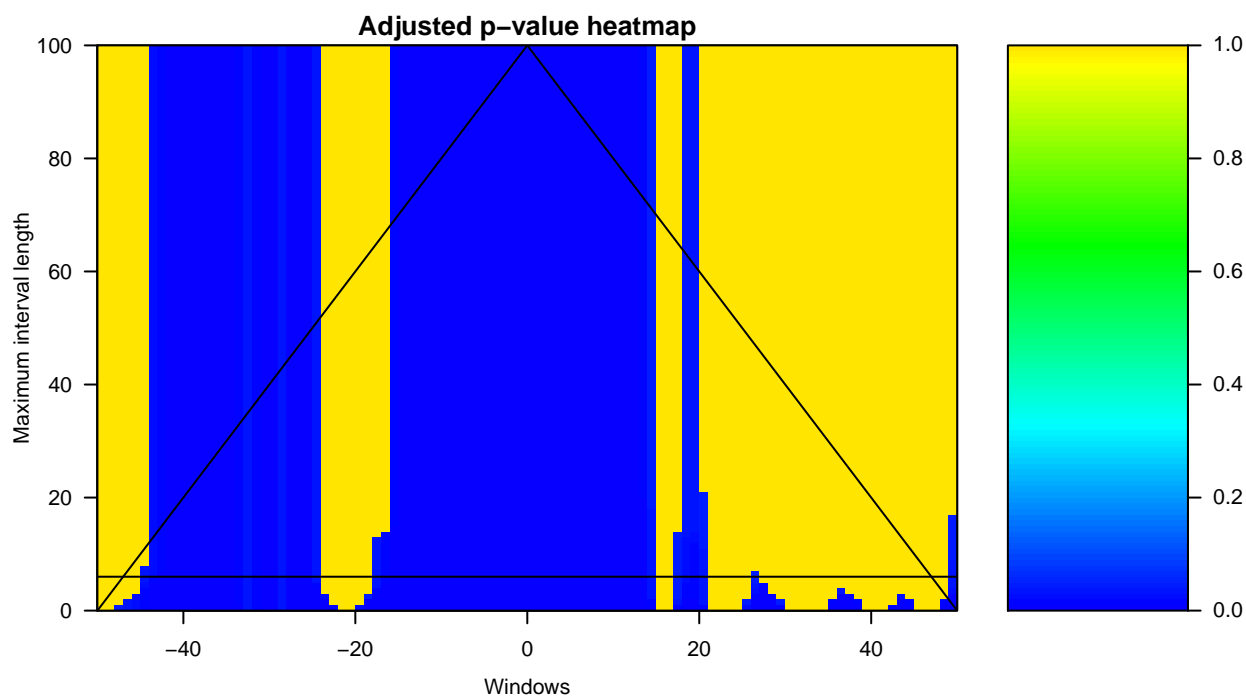
De novo L1

Polymorphic L1

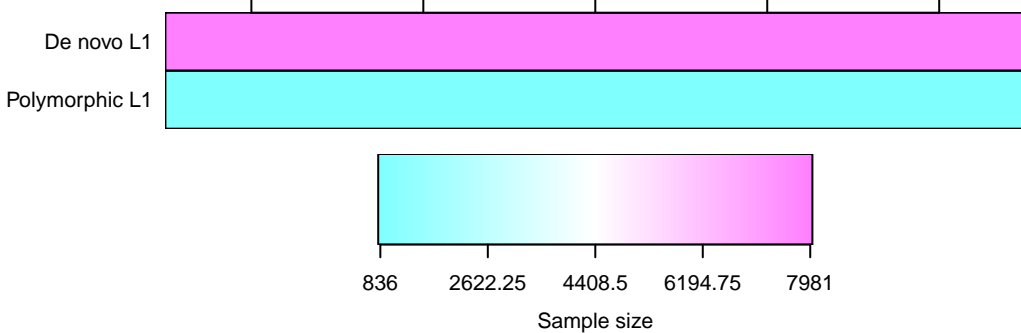
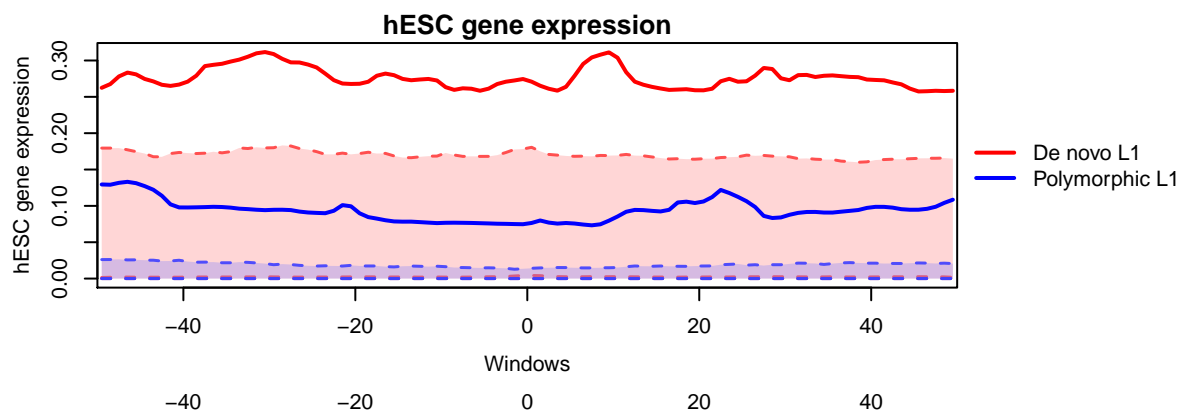
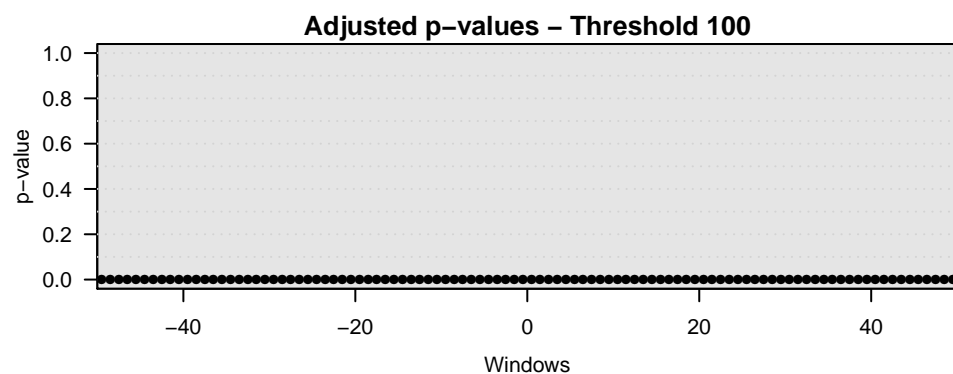
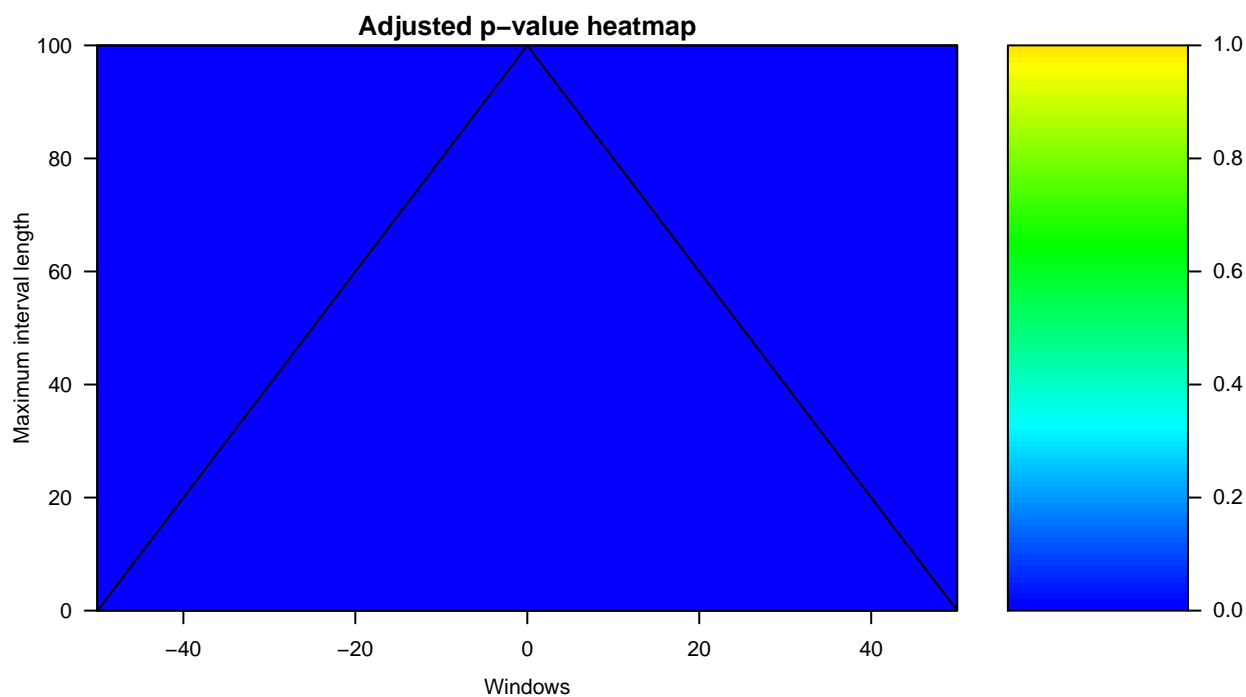
836 2622.25 4408.5 6194.75 7981

Sample size

# hESC exon expression

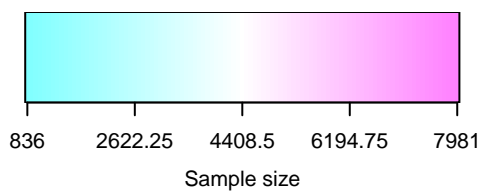
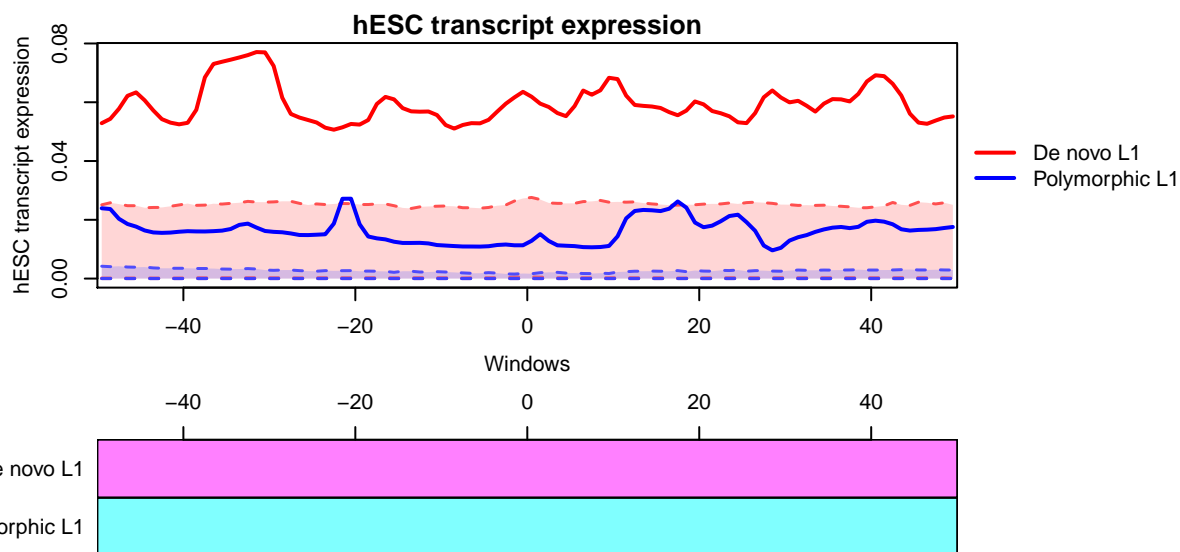
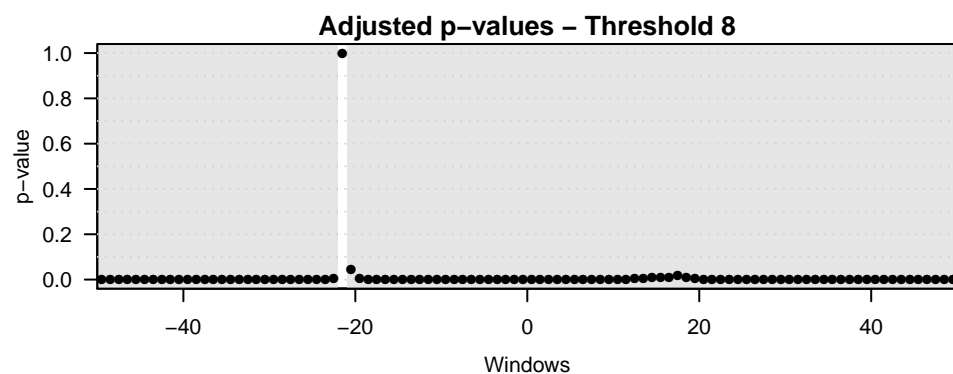
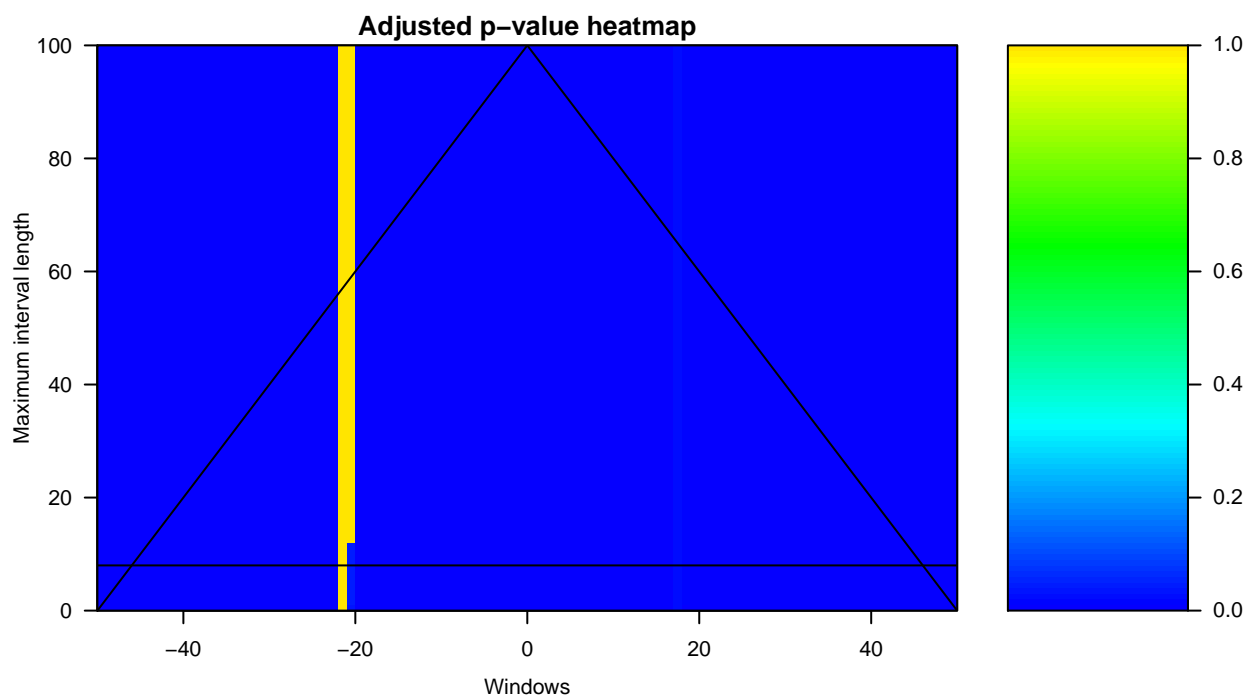


# hESC gene expression

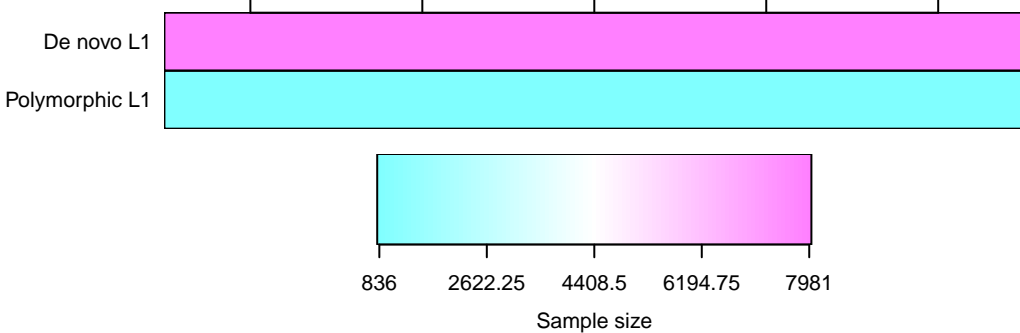
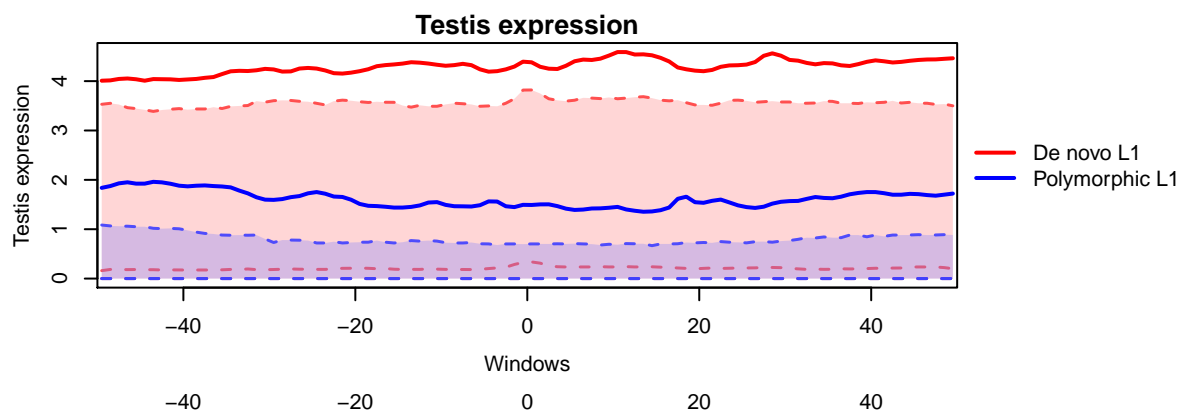
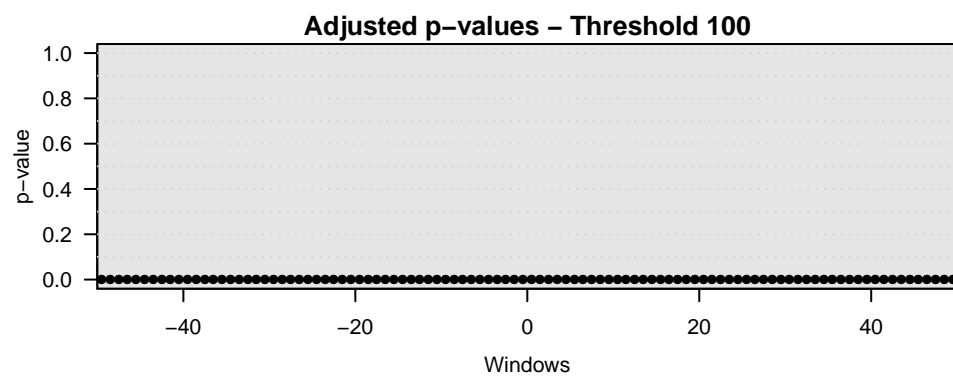
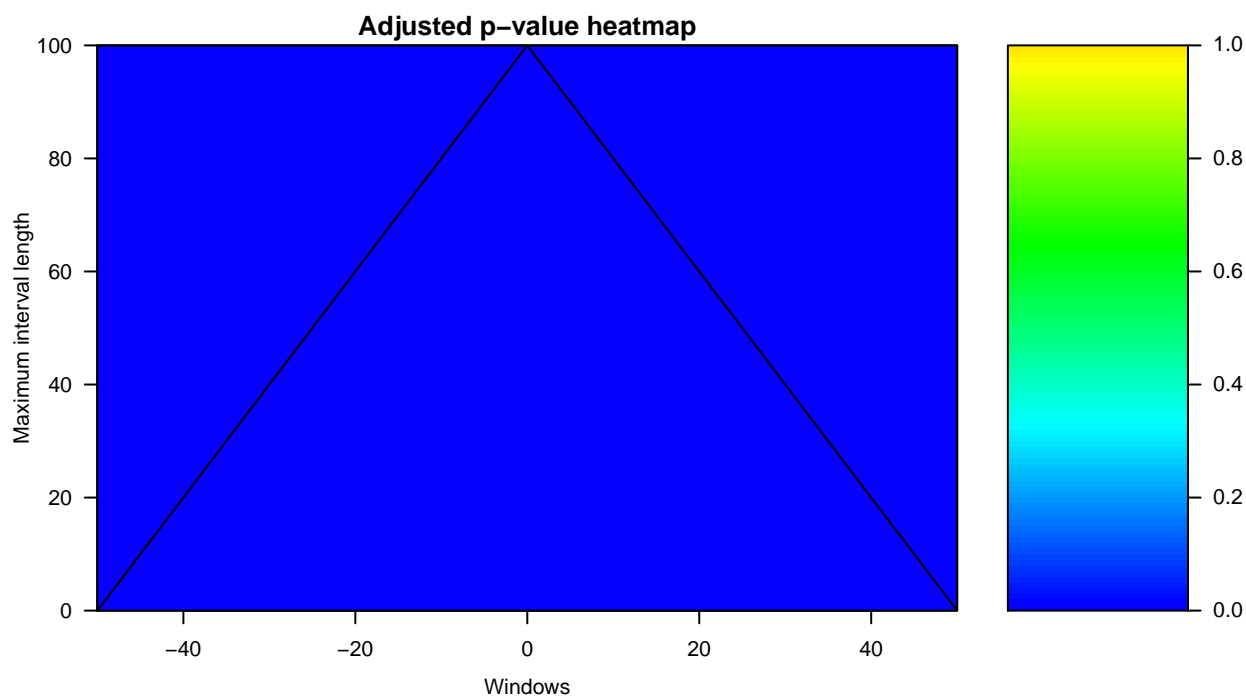




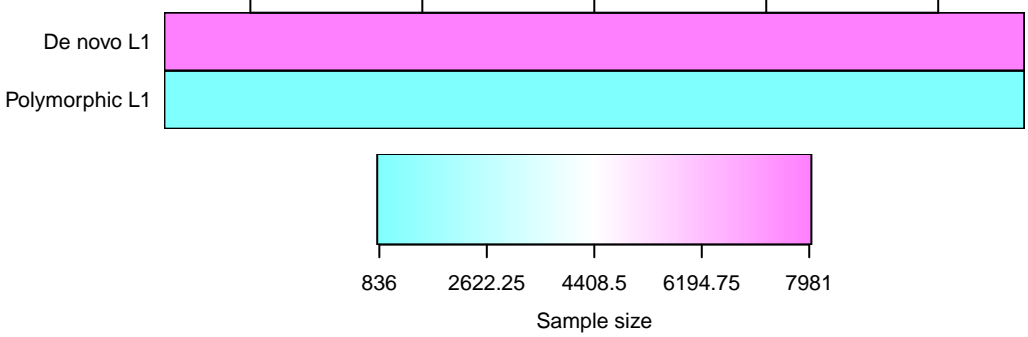
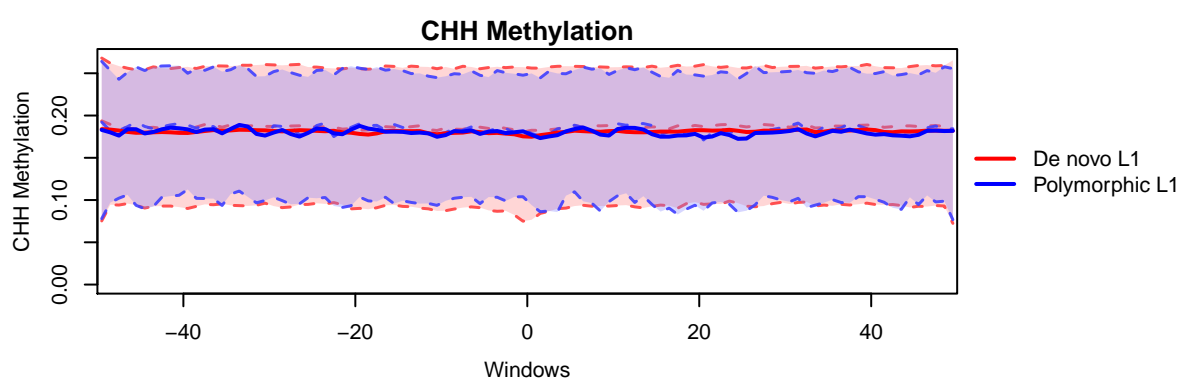
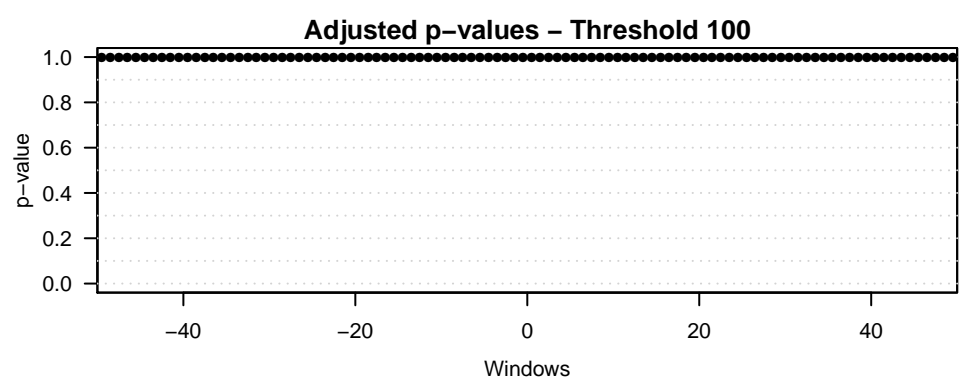
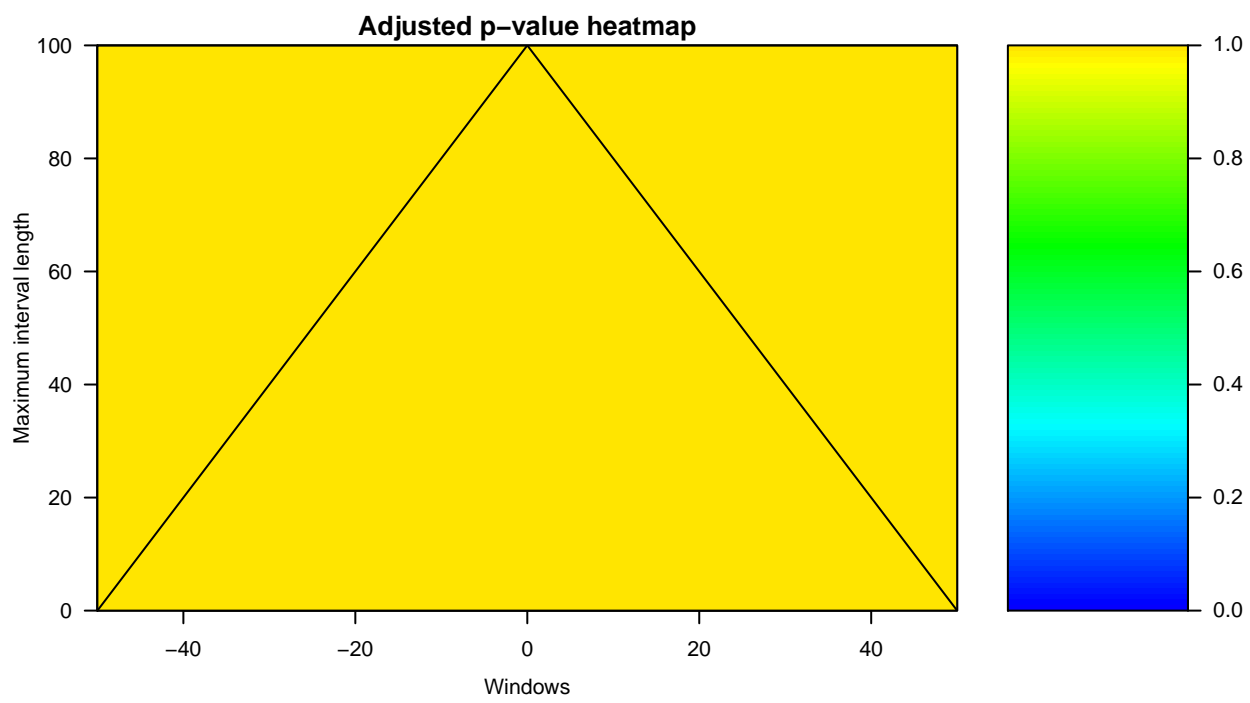
# hESC transcript expression



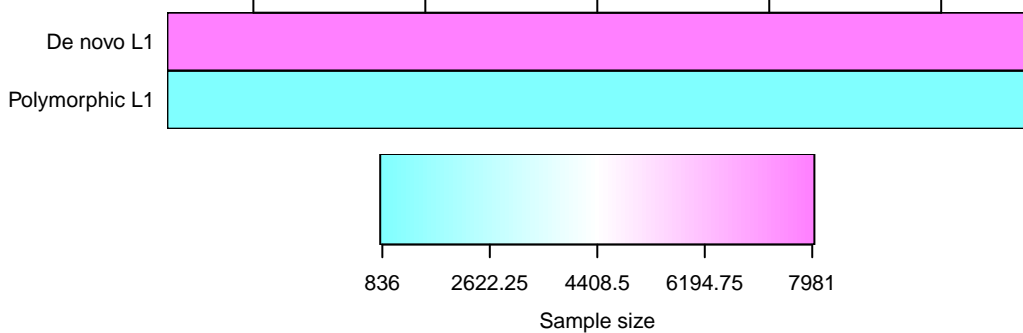
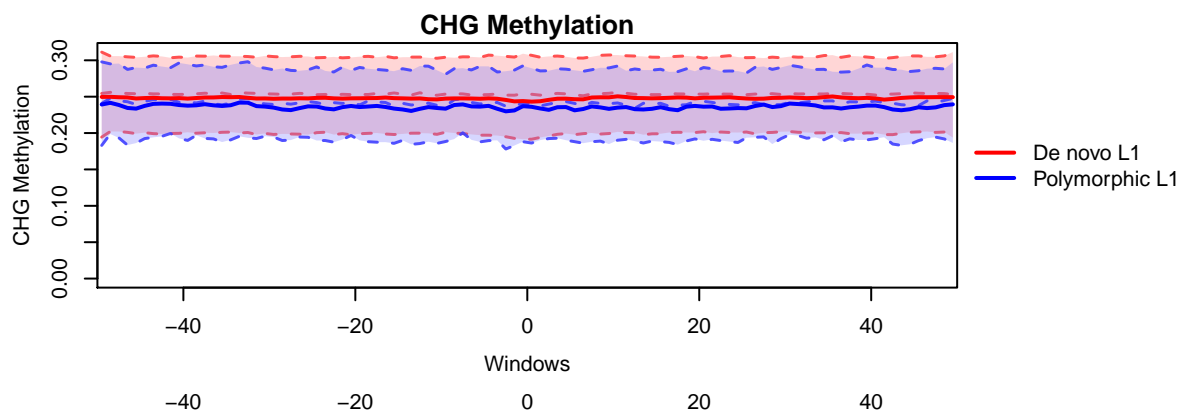
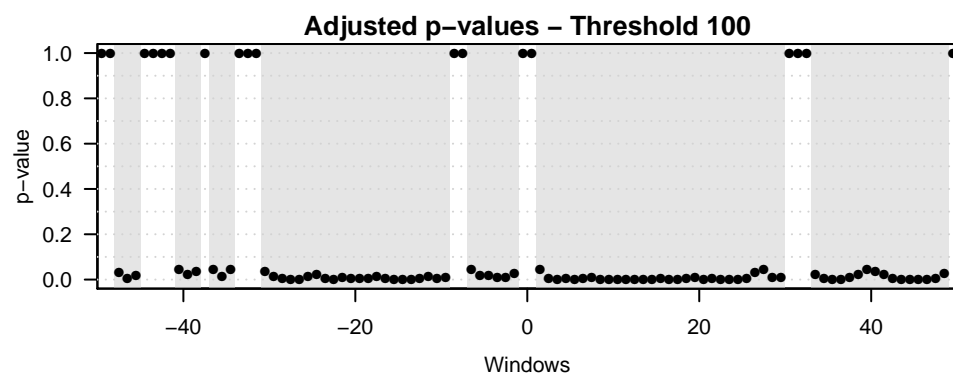
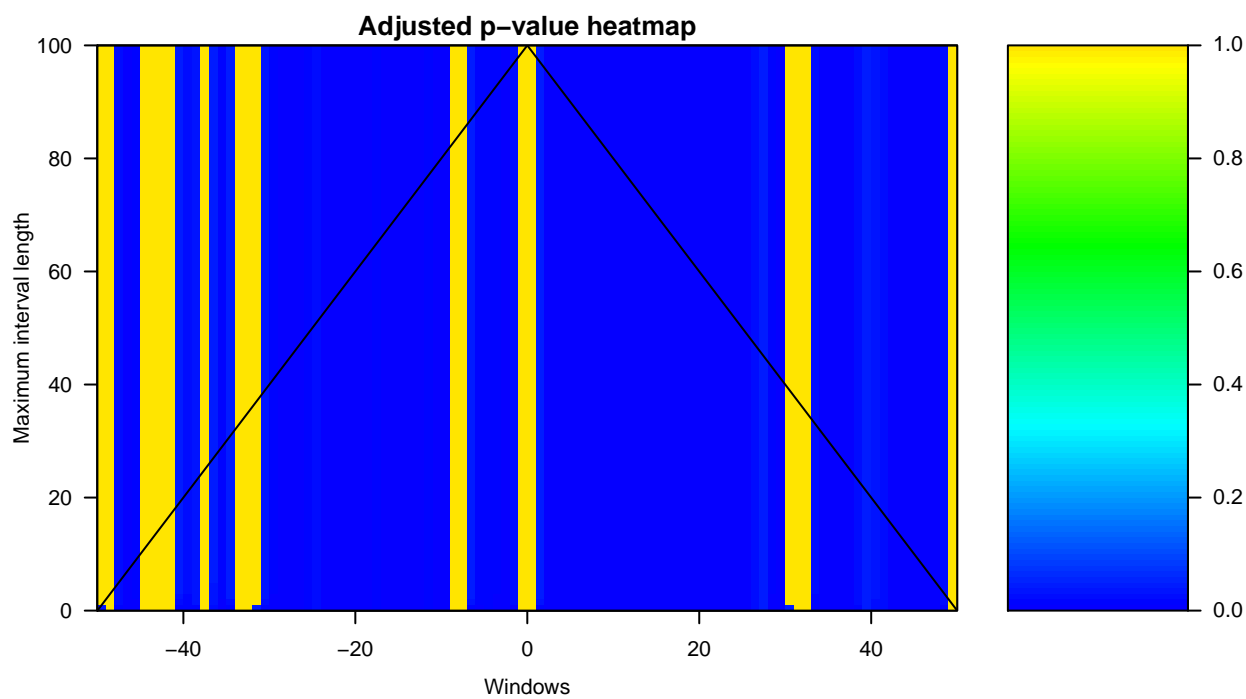
# Testis expression



# CHH Methylation



# CHG Methylation



# CPG Methylation

