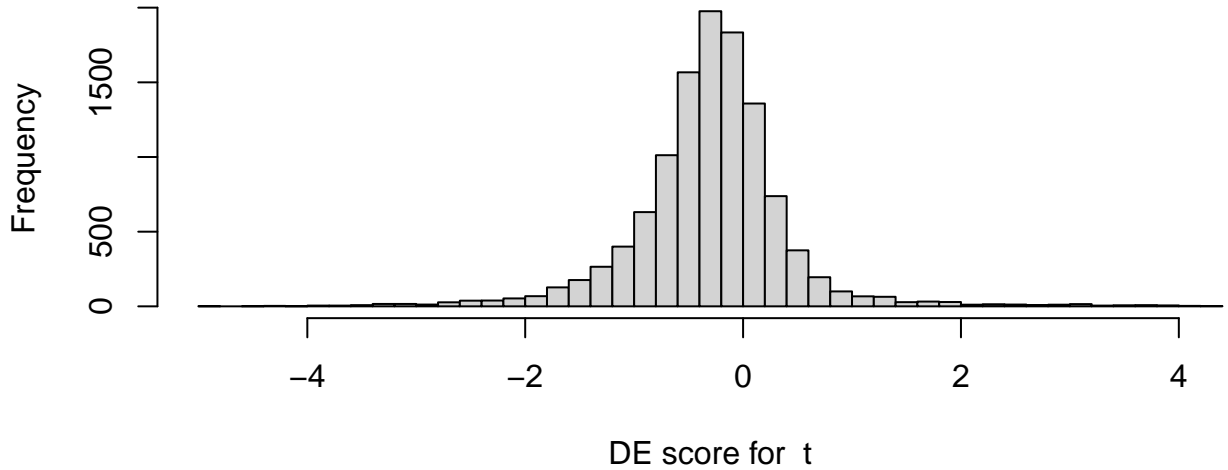
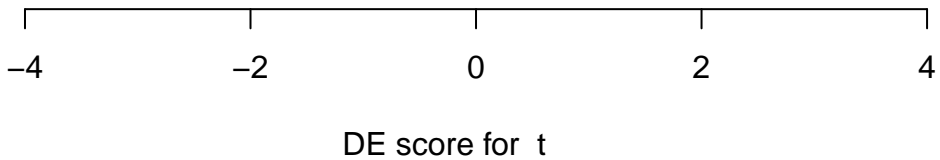


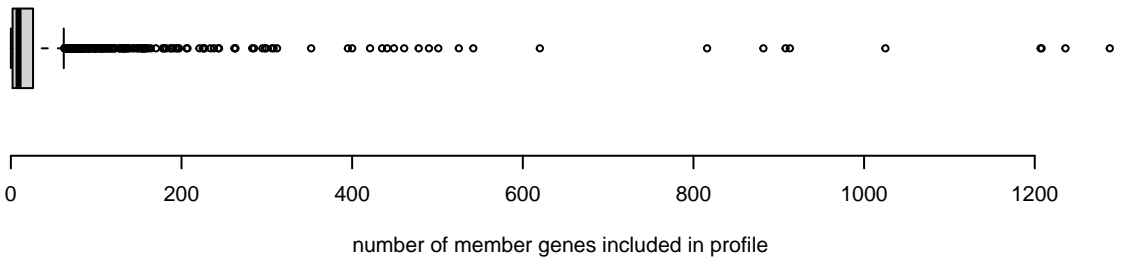
# Distribution of DE scores



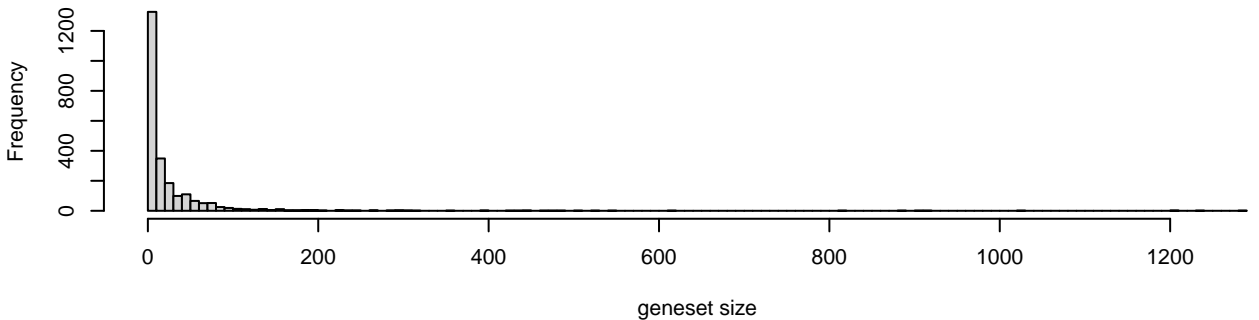
11370 genes in total, 3089 trending up-regulated, 8281 trending down-regulated



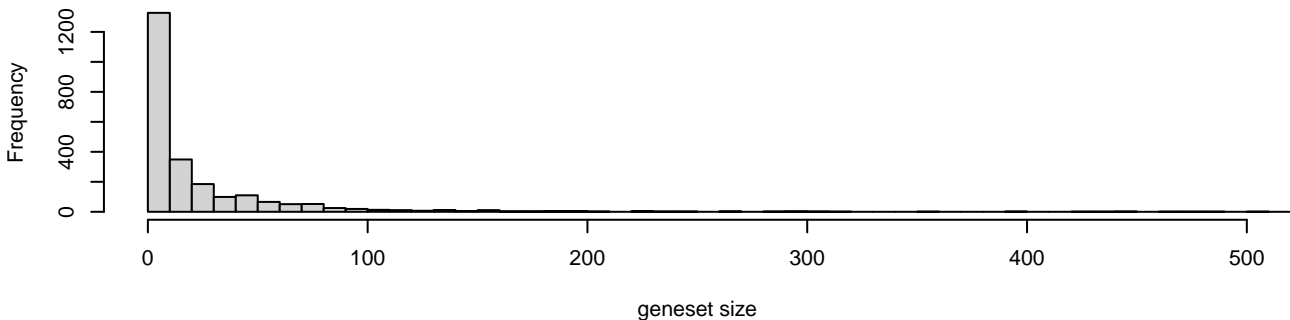
## Gene set size



## Histogram of geneset size

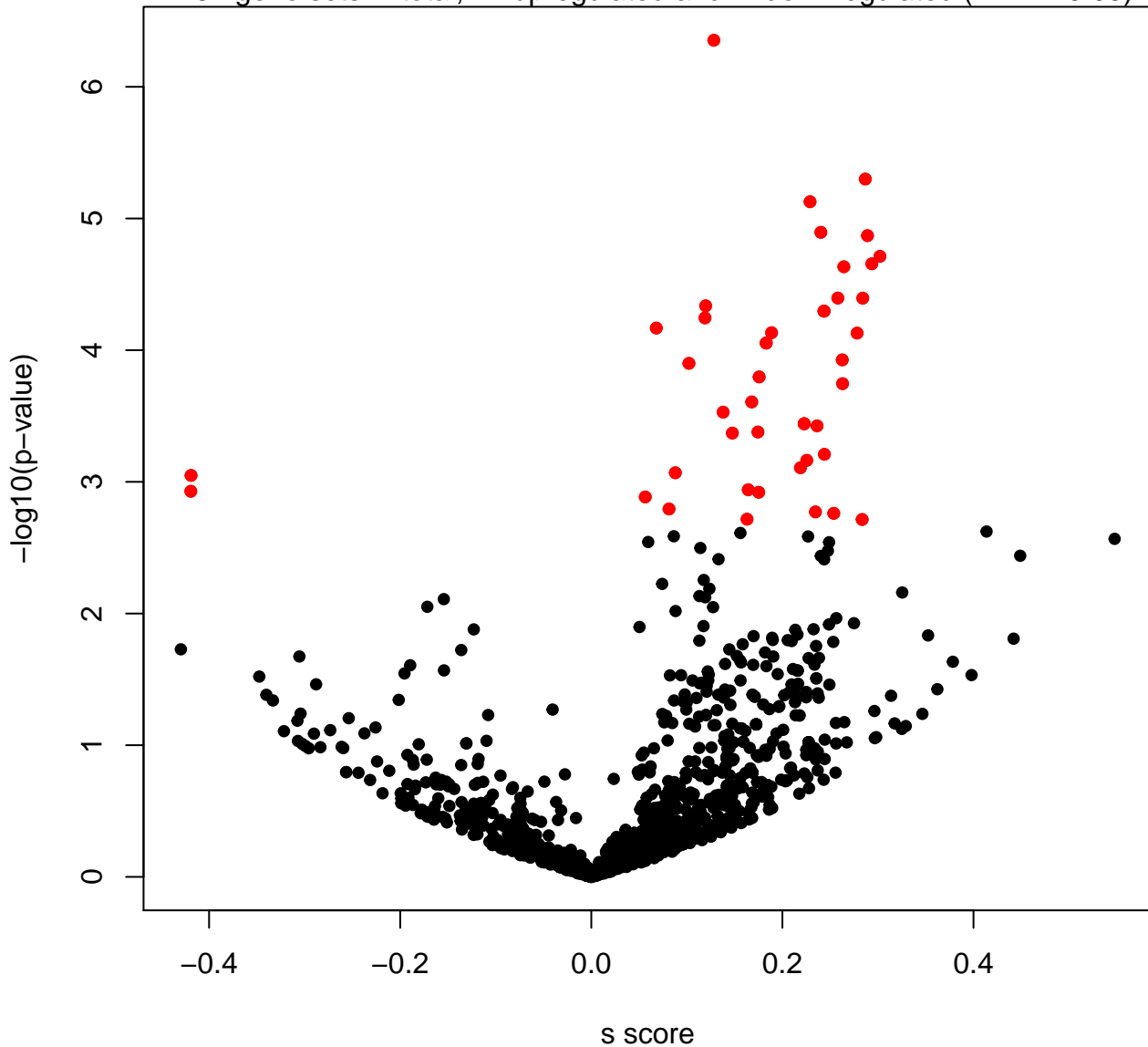


## Trimmed histogram of geneset size



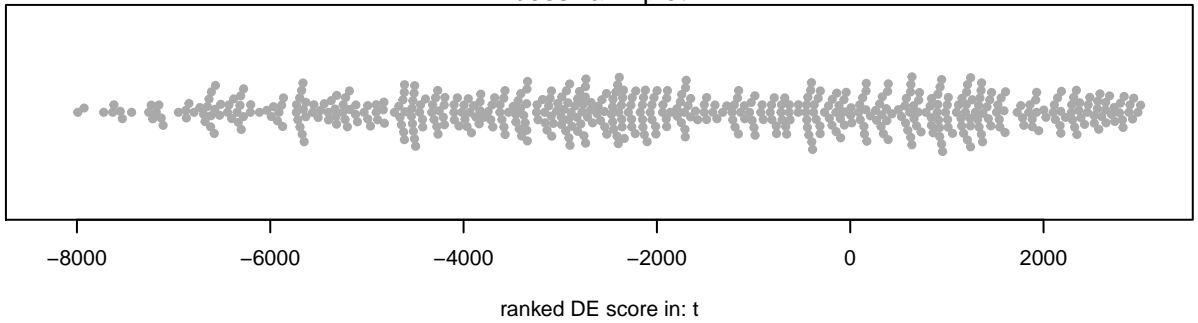
# volcano plot of gene set enrichments

1134 gene sets in total, 42 upregulated and 2 downregulated (FDR $\leq$ 0.05)

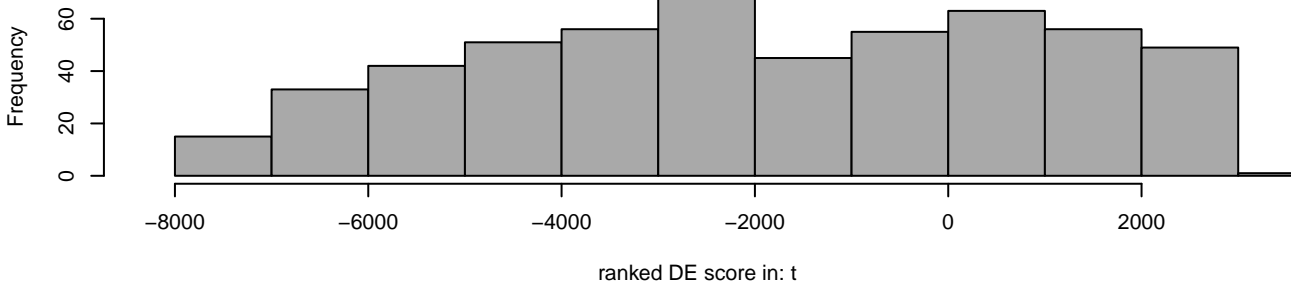


# Metabolism of RNA

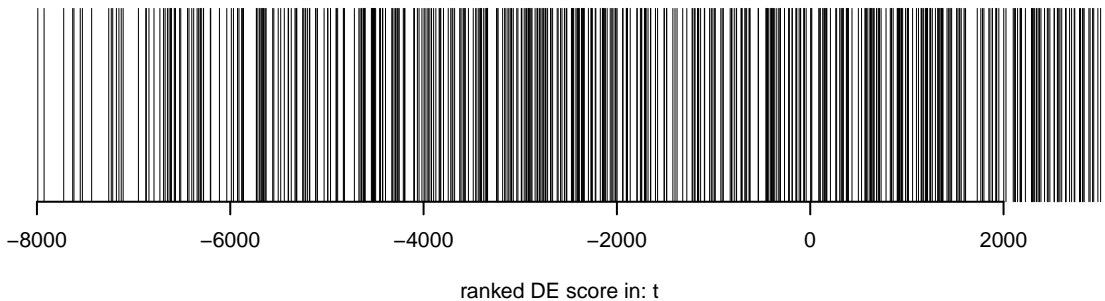
beeswarm plot



histogram

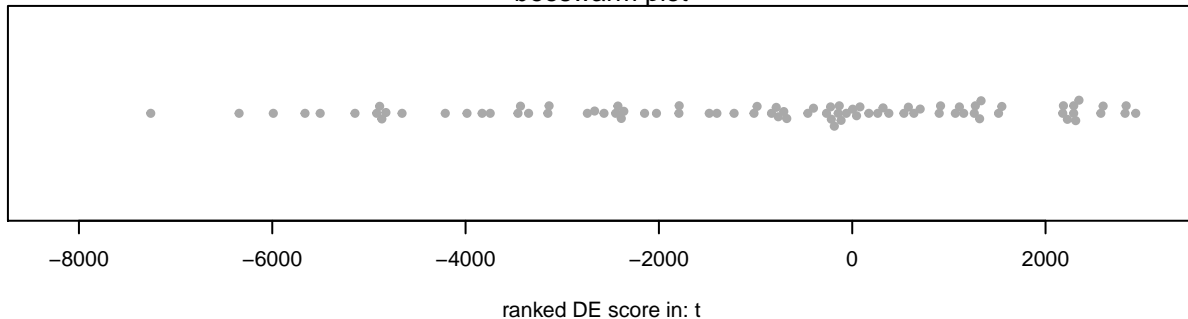


rugplot

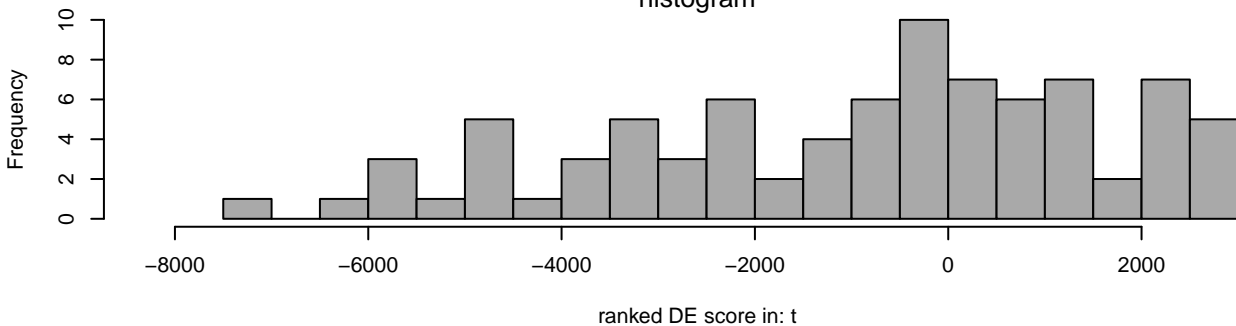


# SRP-dependent cotranslational protein targeting to membrane

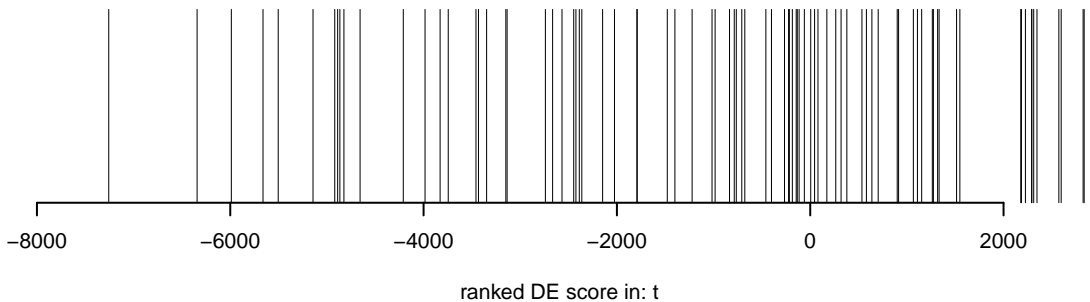
beeswarm plot



histogram

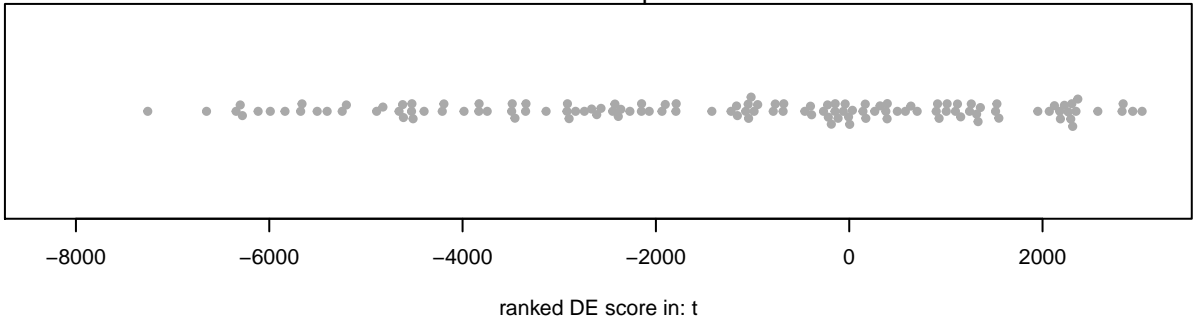


rugplot

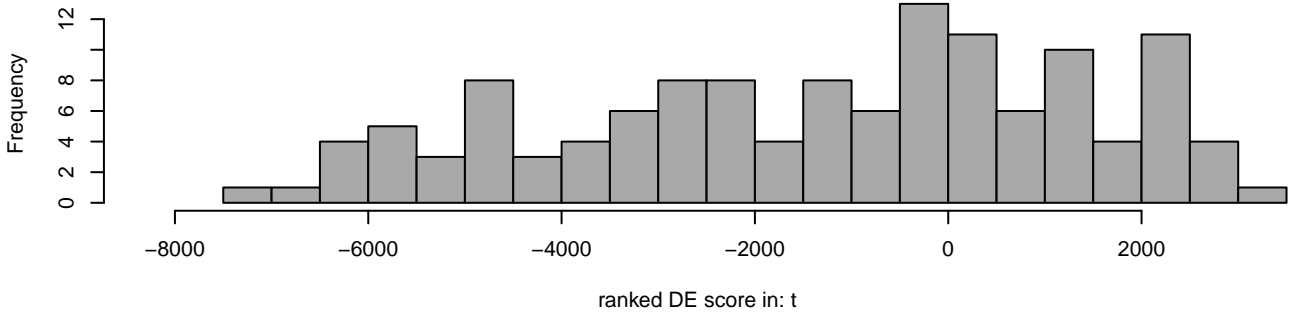


# Influenza Infection

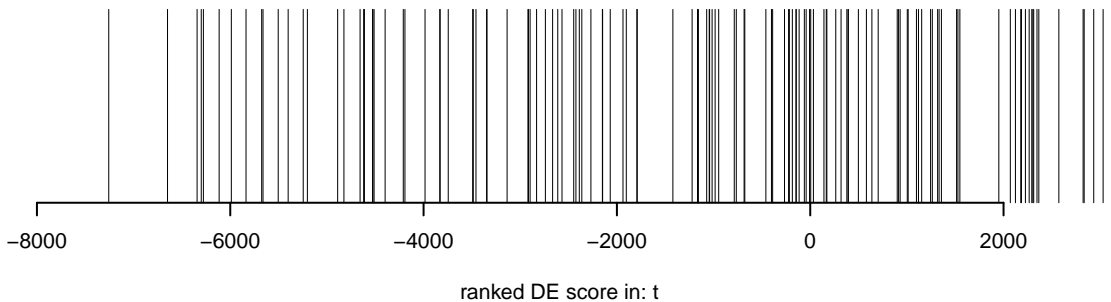
beeswarm plot



histogram

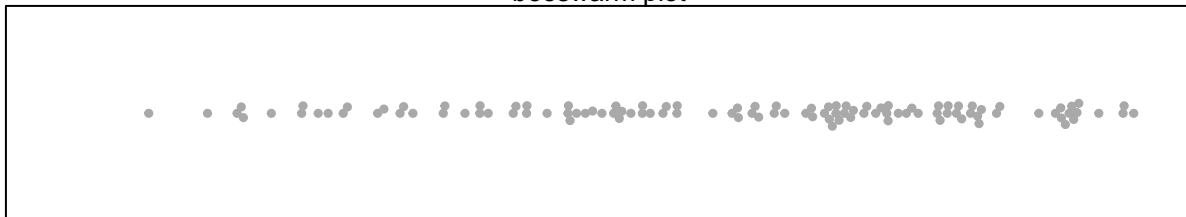


rugplot



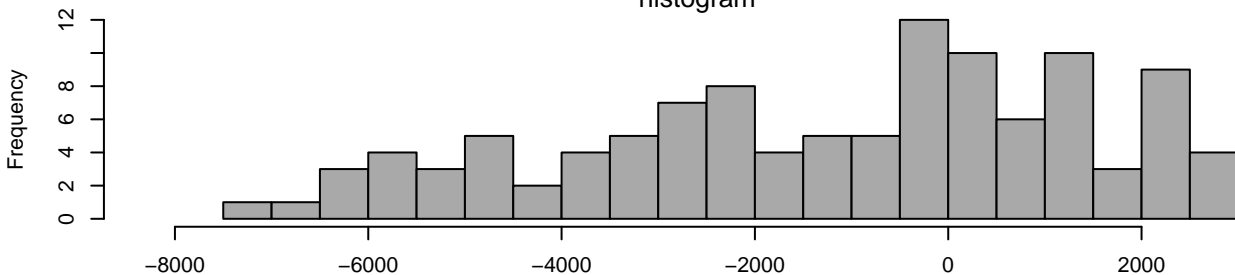
# Influenza Viral RNA Transcription and Replication

beeswarm plot



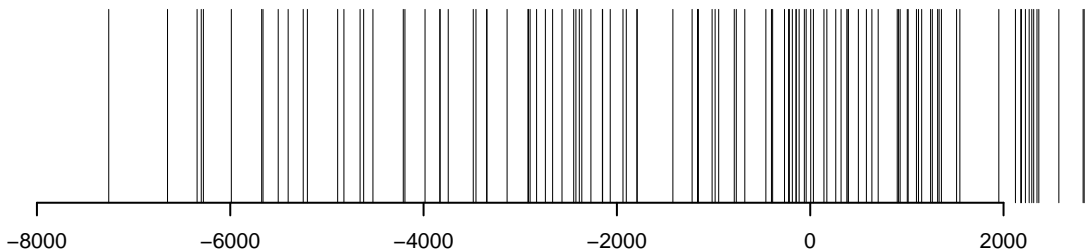
ranked DE score in: t

histogram



ranked DE score in: t

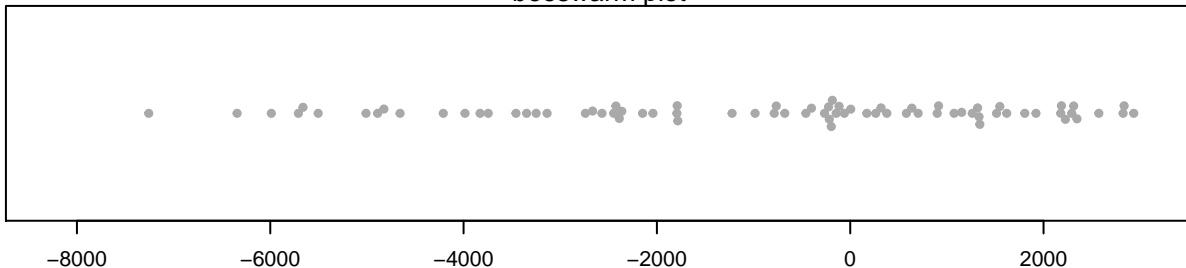
rugplot



ranked DE score in: t

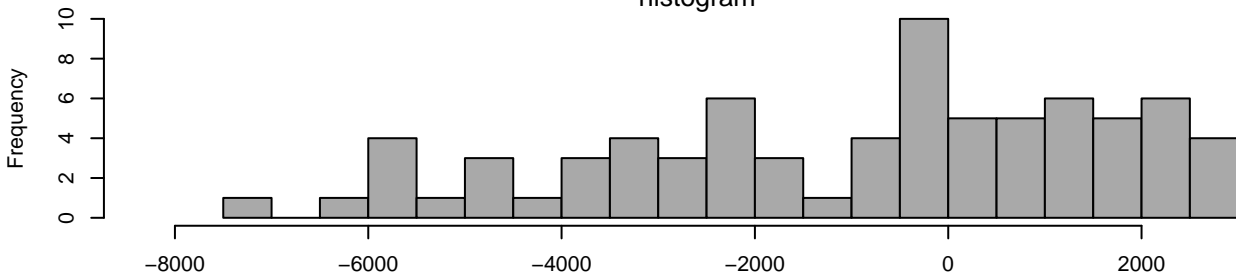
# Formation of a pool of free 40S subunits

beeswarm plot



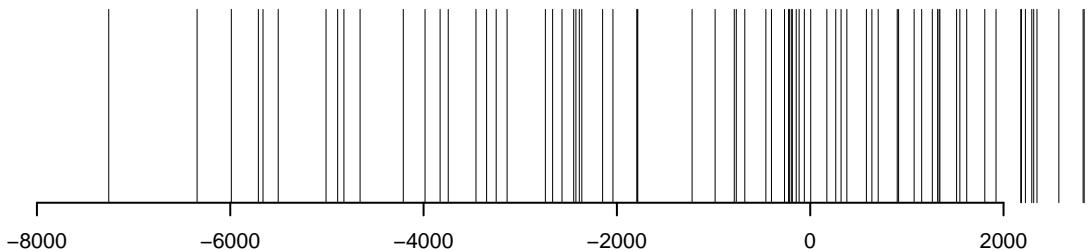
ranked DE score in: t

histogram



ranked DE score in: t

rugplot



ranked DE score in: t



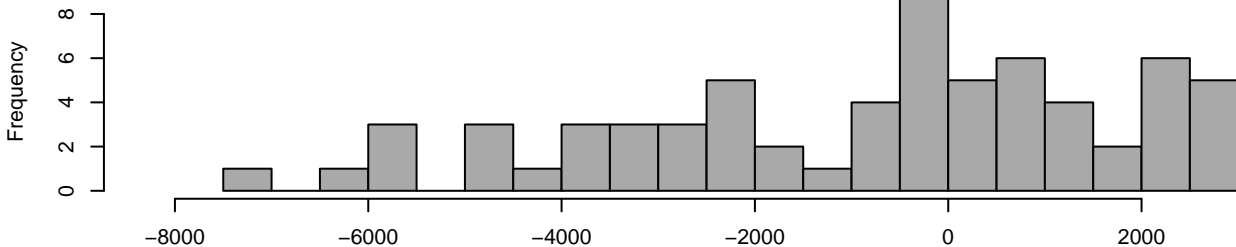
# Peptide chain elongation

beeswarm plot



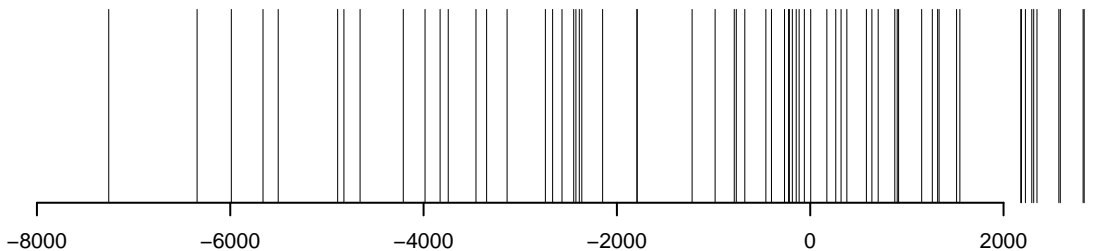
ranked DE score in: t

histogram



ranked DE score in: t

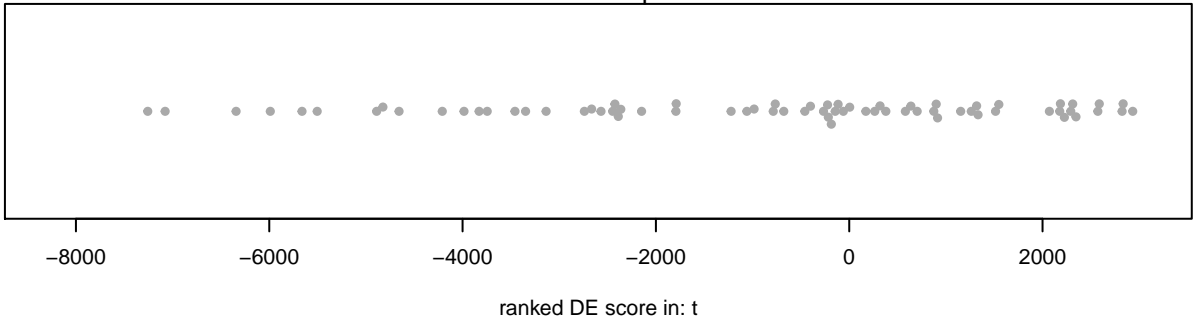
rugplot



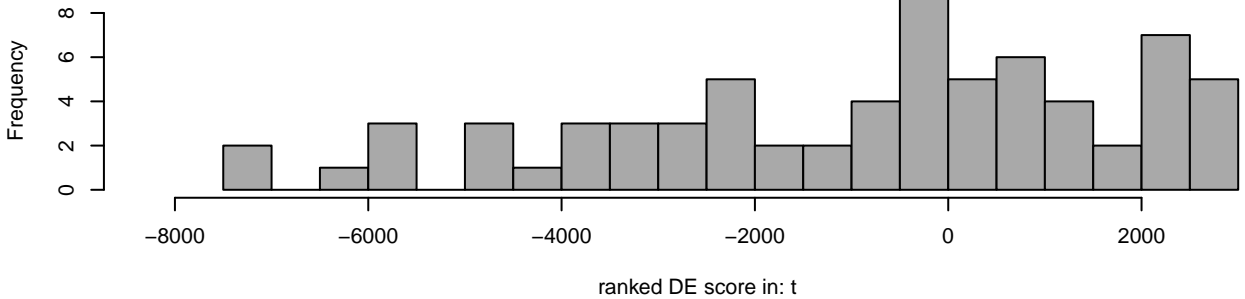
ranked DE score in: t

# Eukaryotic Translation Elongation

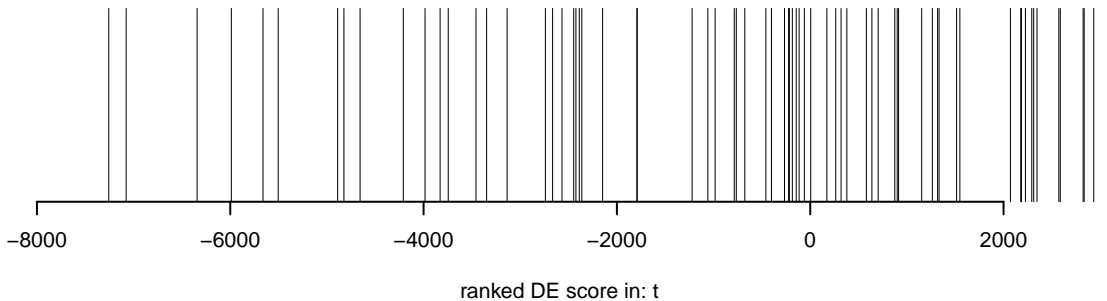
beeswarm plot



histogram

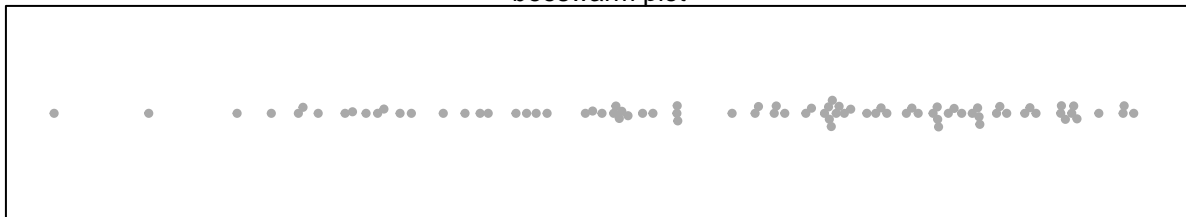


rugplot



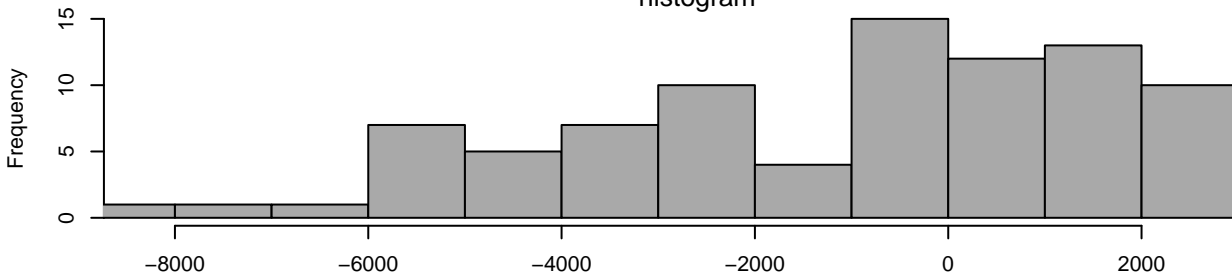
# GTP hydrolysis and joining of the 60S ribosomal subunit

beeswarm plot



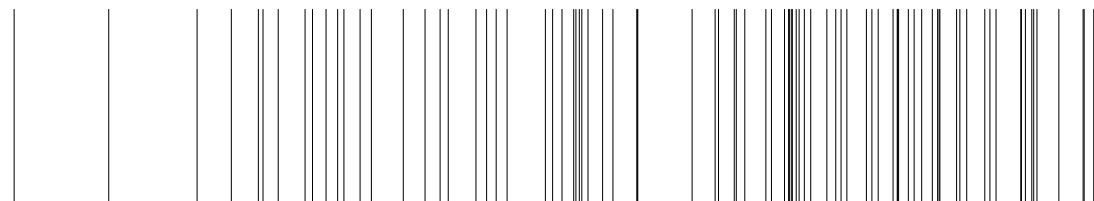
ranked DE score in: t

histogram



ranked DE score in: t

rugplot



ranked DE score in: t

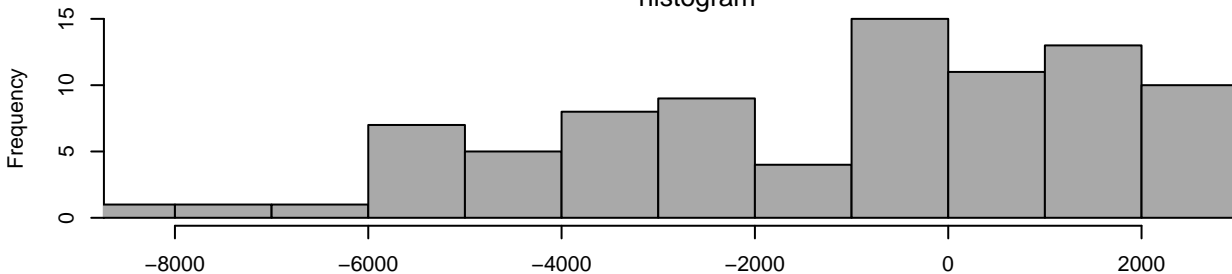
# L13a-mediated translational silencing of Ceruloplasmin expression

beeswarm plot



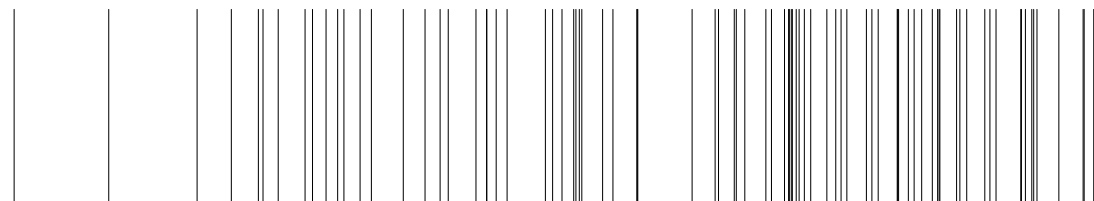
ranked DE score in: t

histogram



ranked DE score in: t

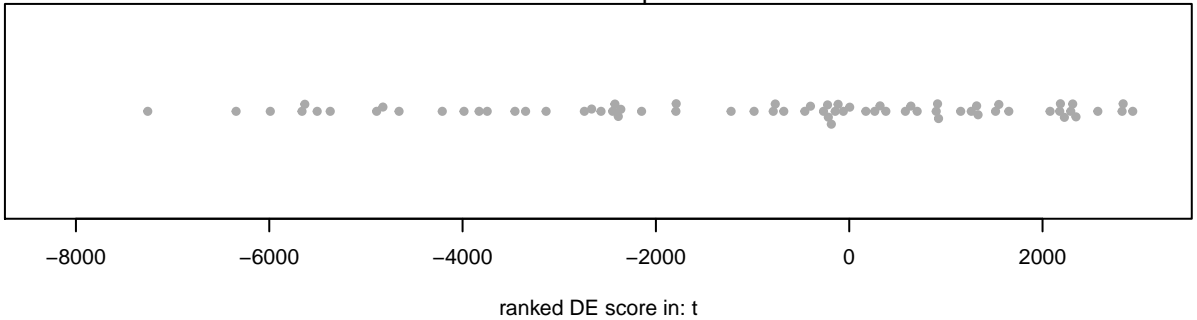
rugplot



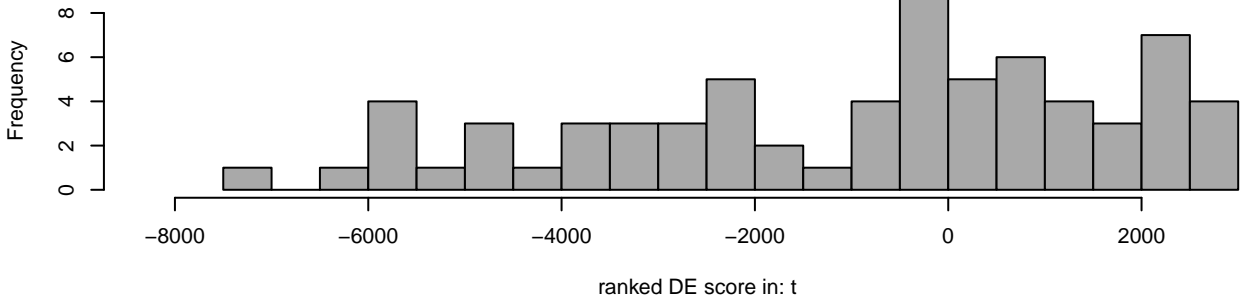
ranked DE score in: t

# Eukaryotic Translation Termination

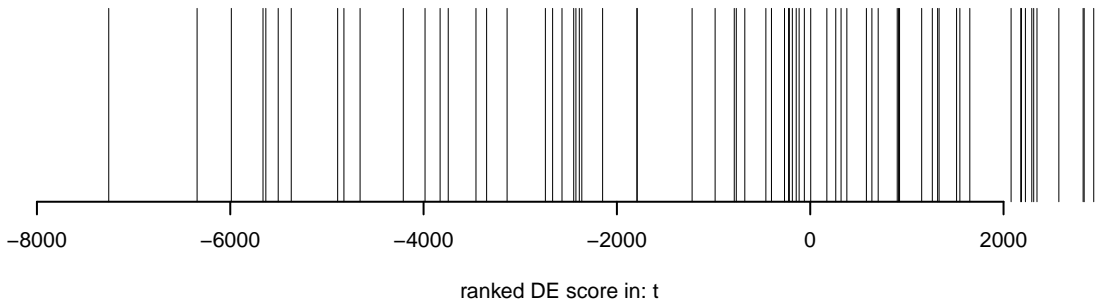
beeswarm plot



histogram

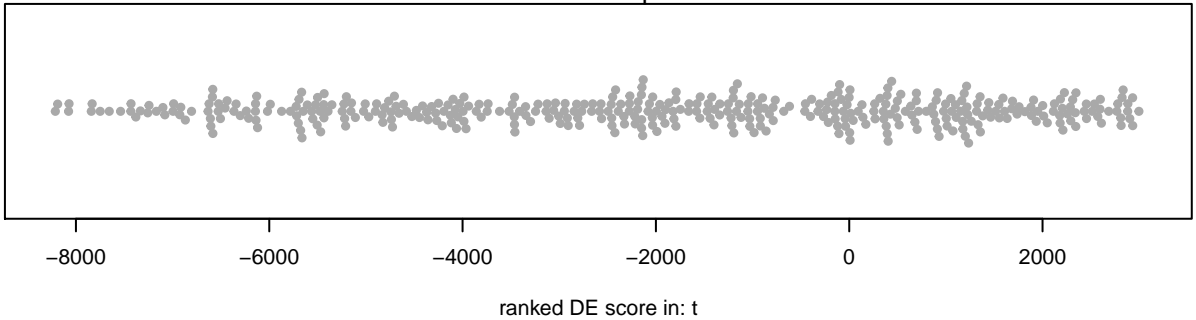


rugplot

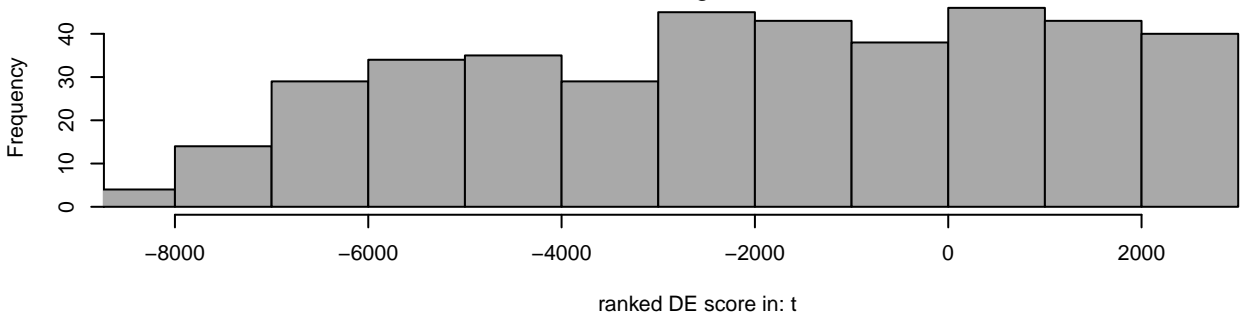


# Cellular responses to external stimuli

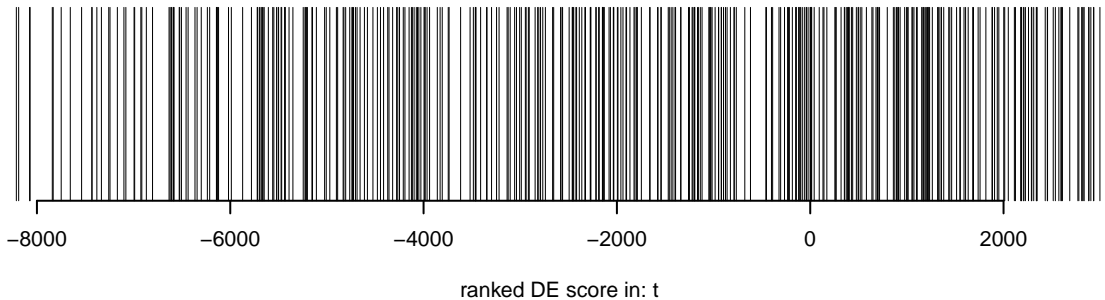
beeswarm plot



histogram

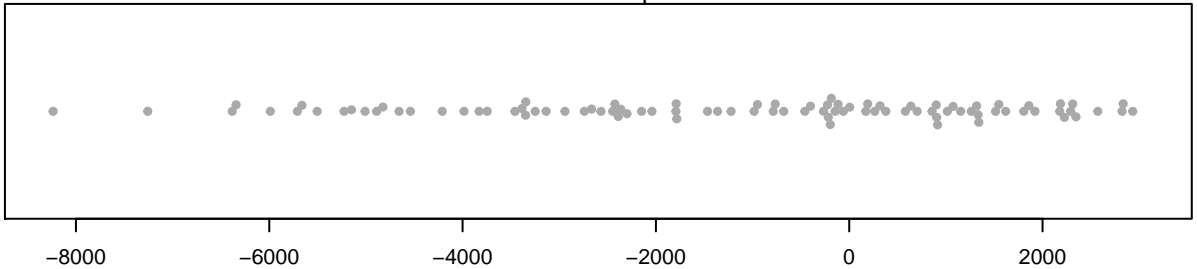


rugplot



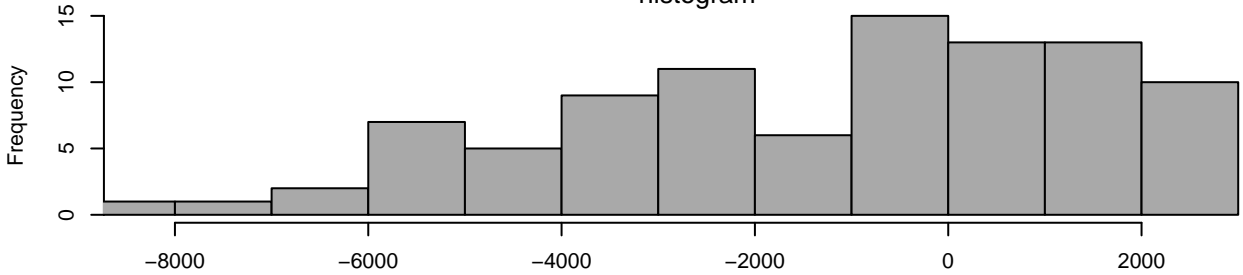
# Cap-dependent Translation Initiation

beeswarm plot



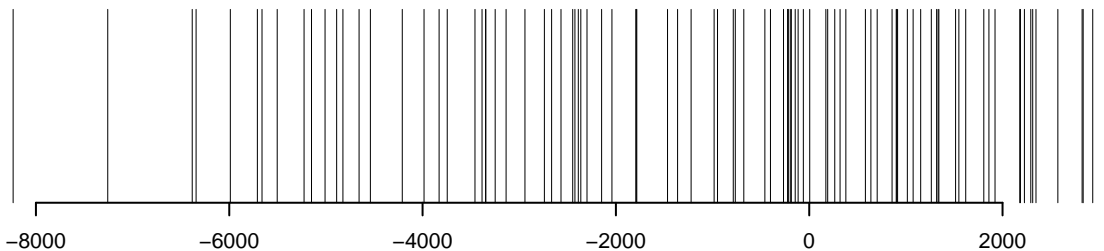
ranked DE score in: t

histogram



ranked DE score in: t

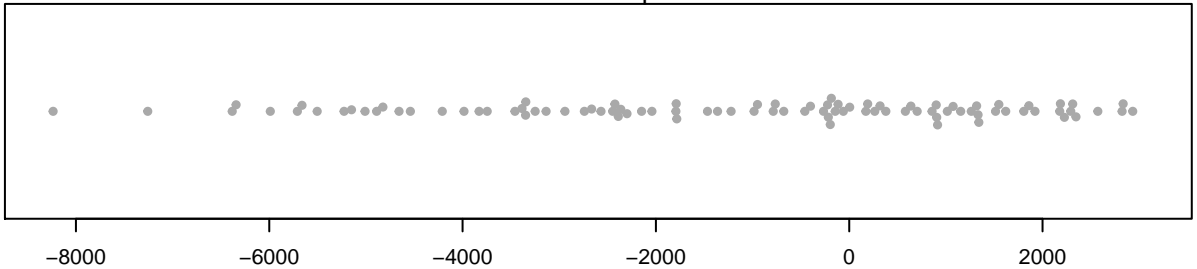
rugplot



ranked DE score in: t

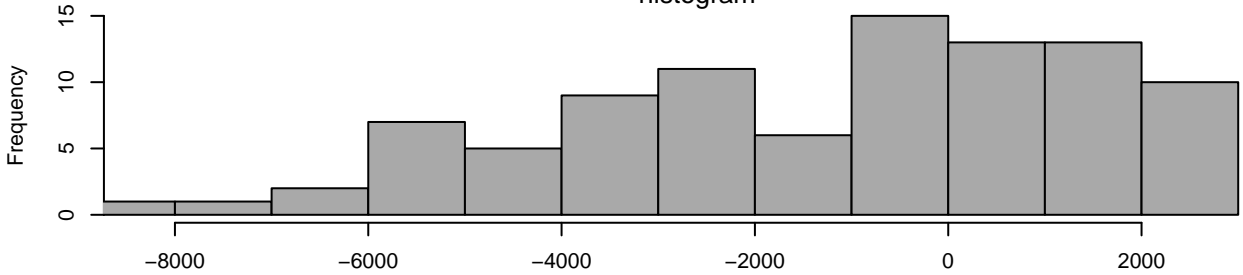
# Eukaryotic Translation Initiation

beeswarm plot



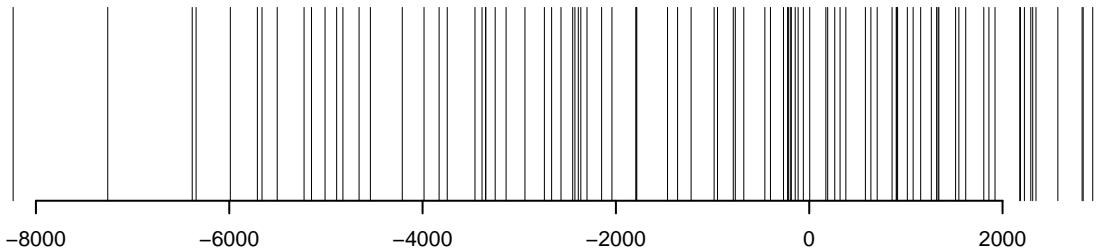
ranked DE score in: t

histogram



ranked DE score in: t

rugplot

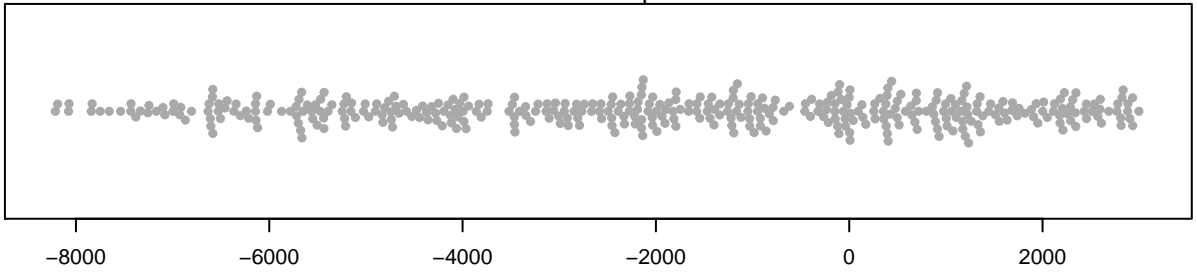


ranked DE score in: t



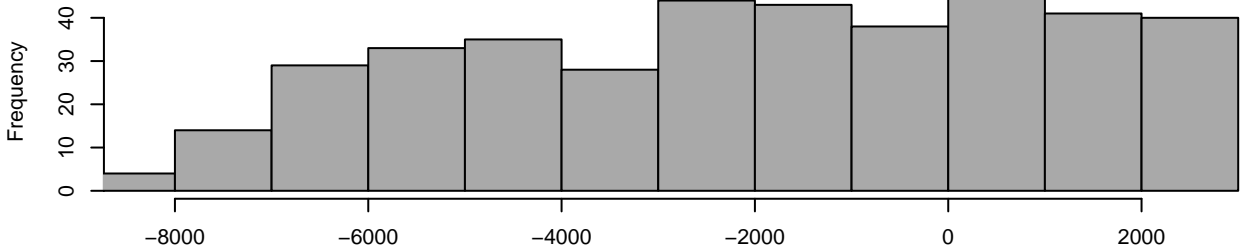
# Cellular responses to stress

beeswarm plot



ranked DE score in: t

histogram



ranked DE score in: t

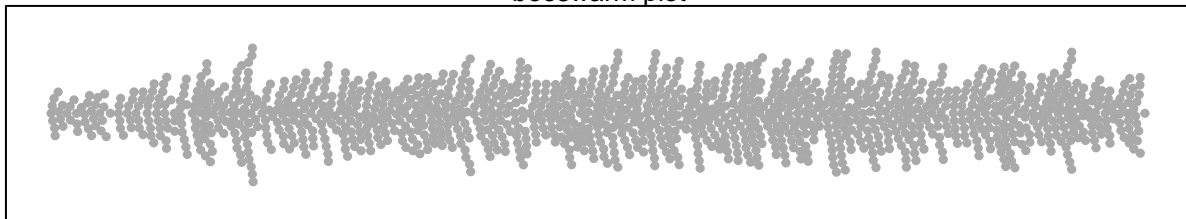
rugplot



ranked DE score in: t

# Metabolism of proteins

beeswarm plot



-8000

-6000

-4000

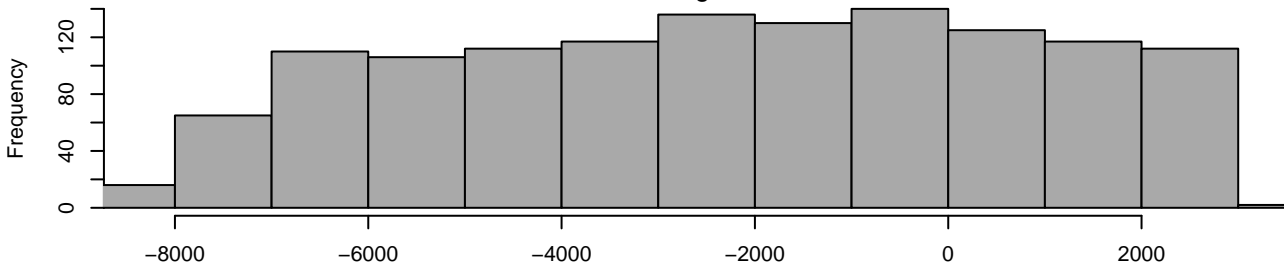
-2000

0

2000

ranked DE score in: t

histogram



Frequency

120

80

40

0

-8000

-6000

-4000

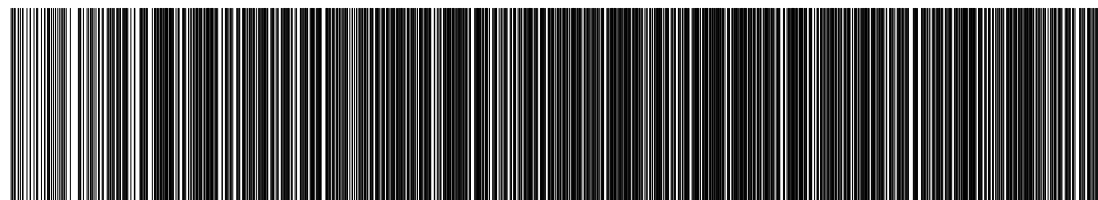
-2000

0

2000

ranked DE score in: t

rugplot



-8000

-6000

-4000

-2000

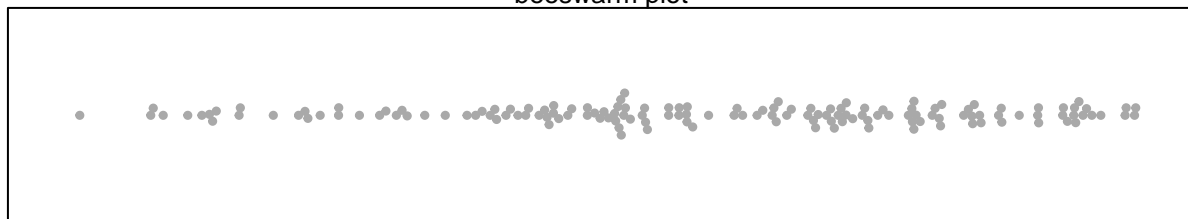
0

2000

ranked DE score in: t

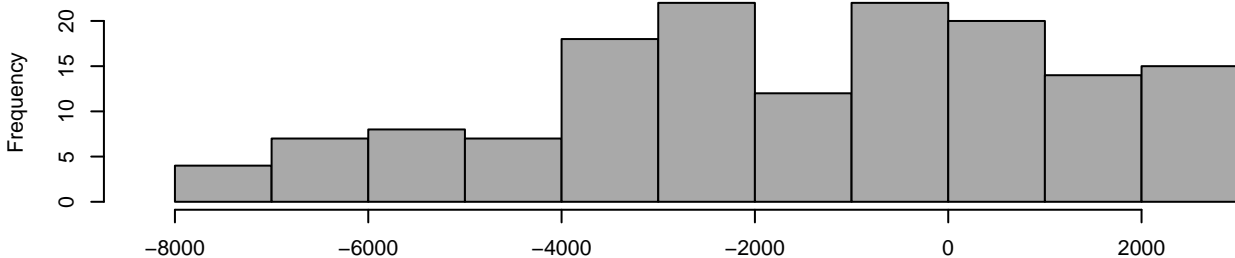
# Major pathway of rRNA processing in the nucleolus and cytosol

beeswarm plot



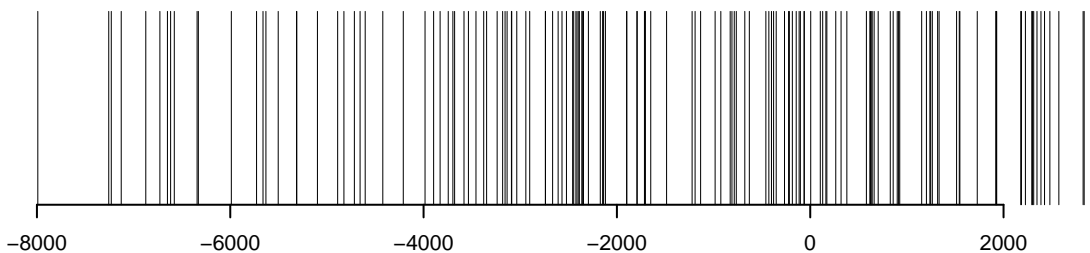
ranked DE score in: t

histogram



ranked DE score in: t

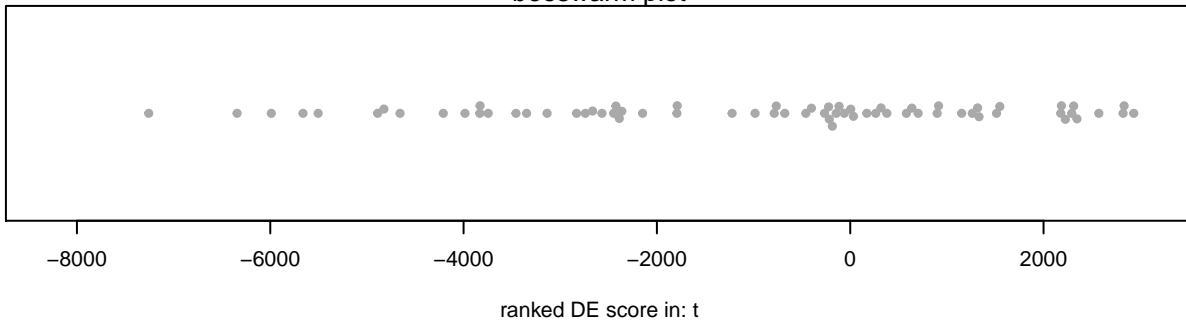
rugplot



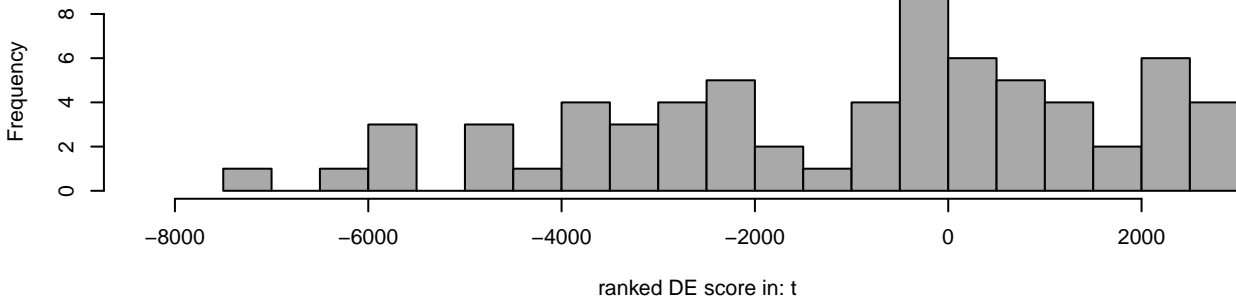
ranked DE score in: t

# Viral mRNA Translation

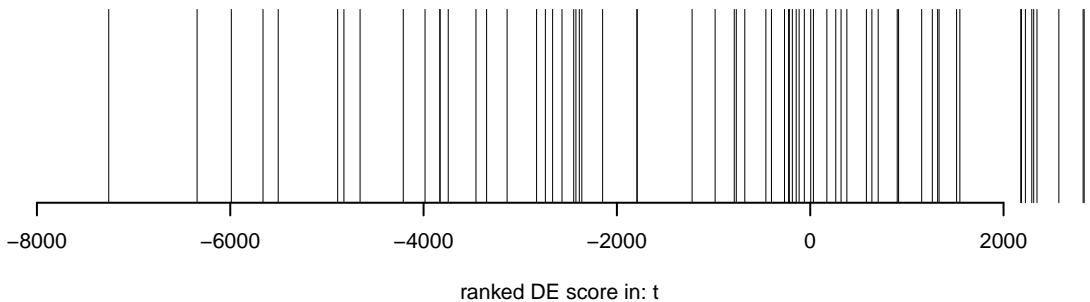
beeswarm plot



histogram

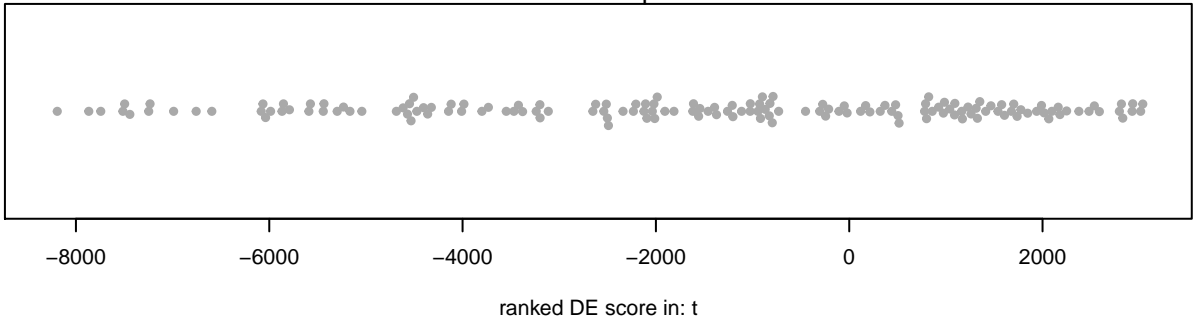


rugplot

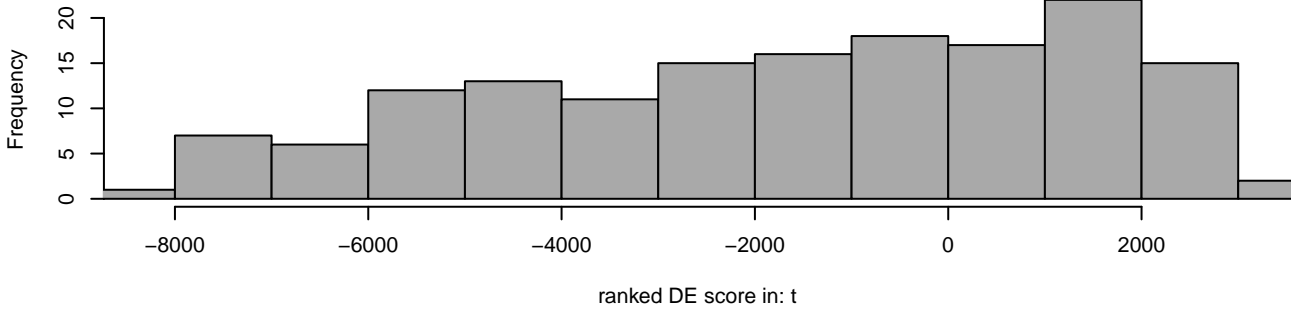


# Chromatin modifying enzymes

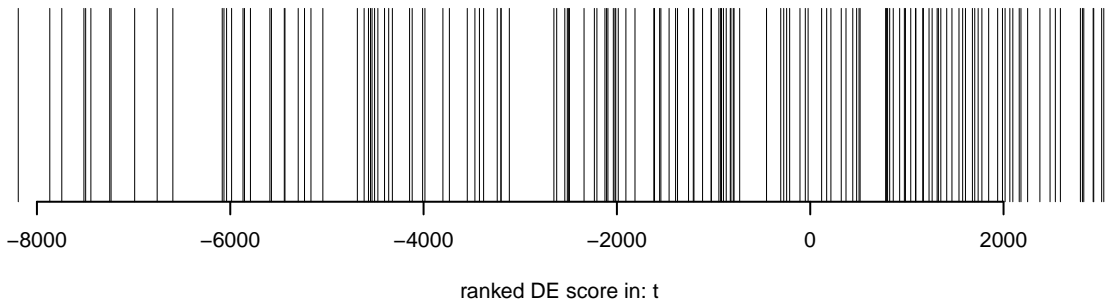
beeswarm plot



histogram

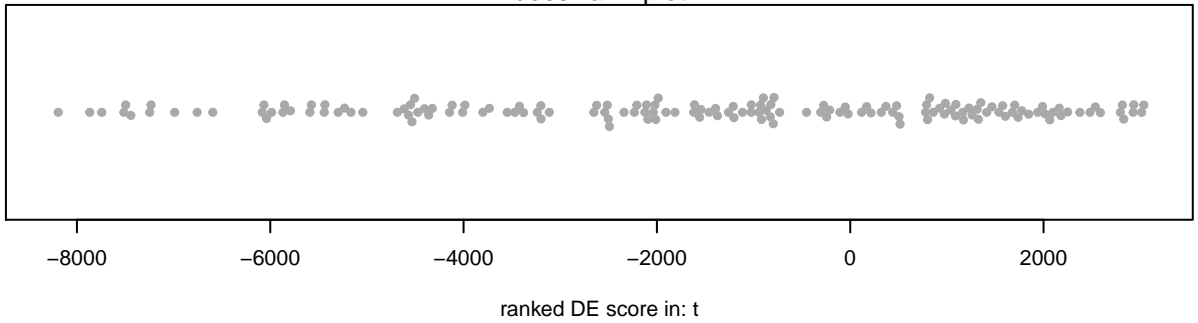


rugplot

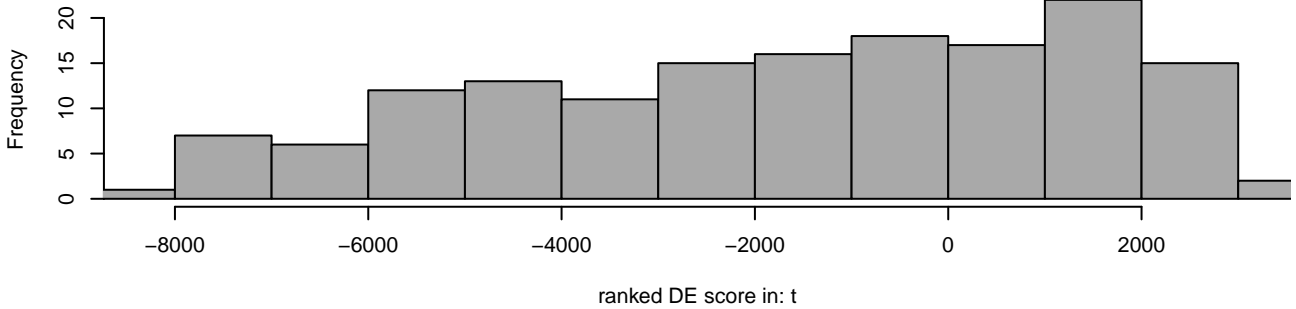


# Chromatin organization

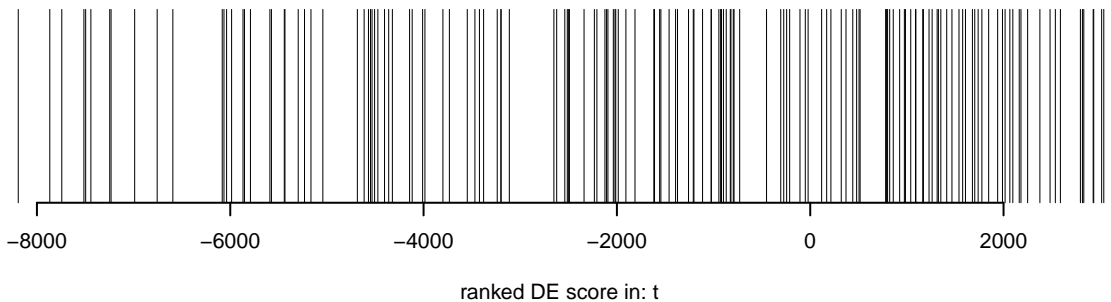
beeswarm plot



histogram

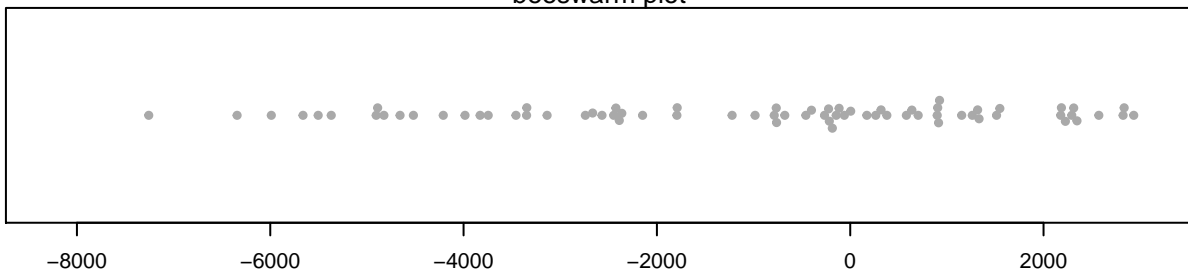


rugplot



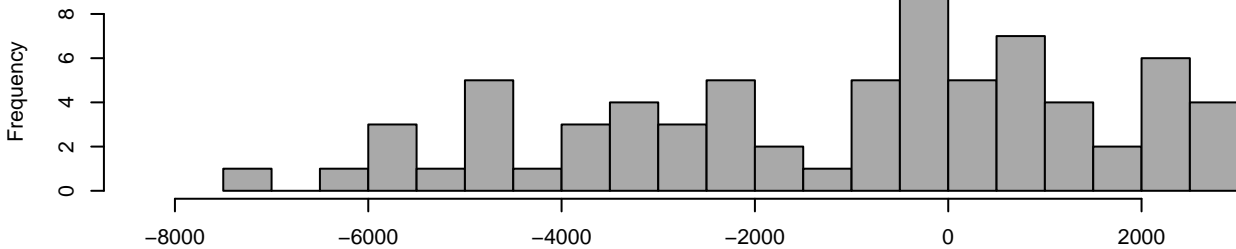
# Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)

beeswarm plot



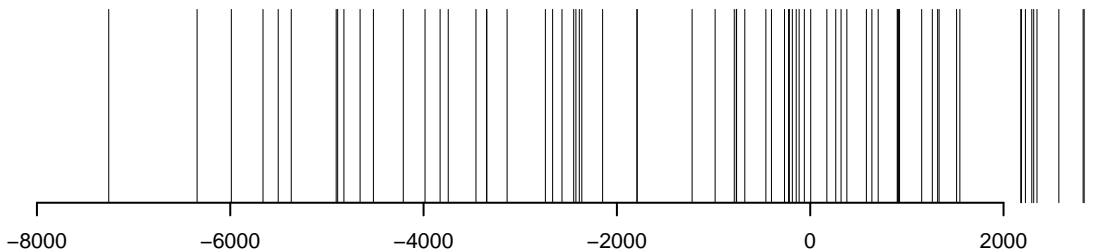
ranked DE score in: t

histogram



ranked DE score in: t

rugplot



ranked DE score in: t