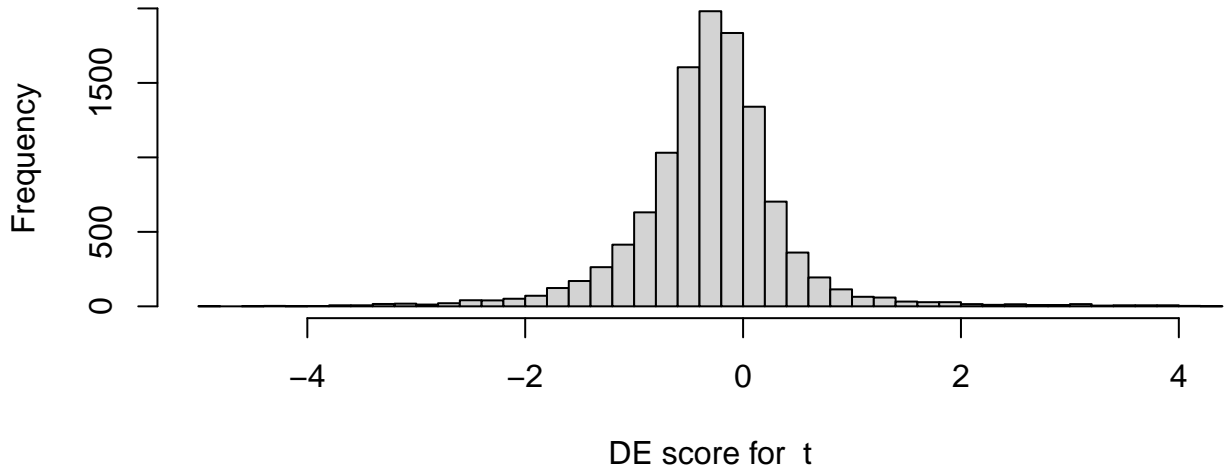
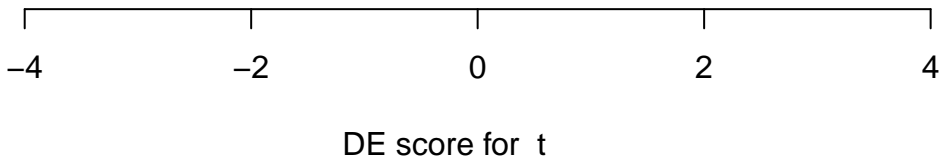


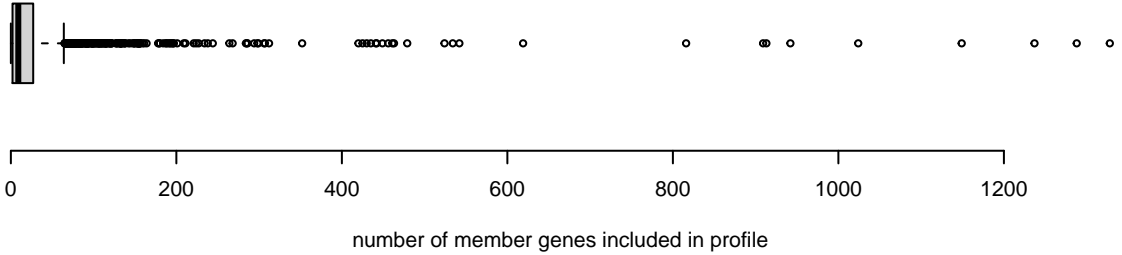
Distribution of DE scores



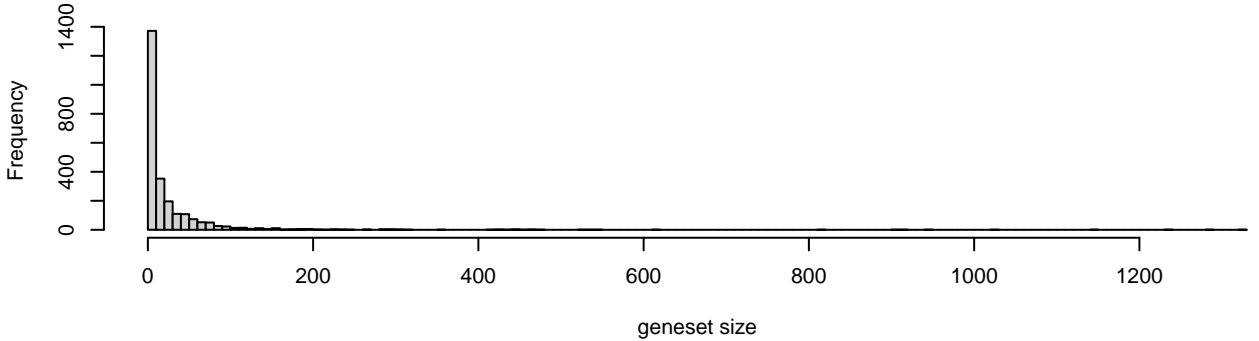
11370 genes in total, 3025 trending up-regulated, 8345 trending down-regulated



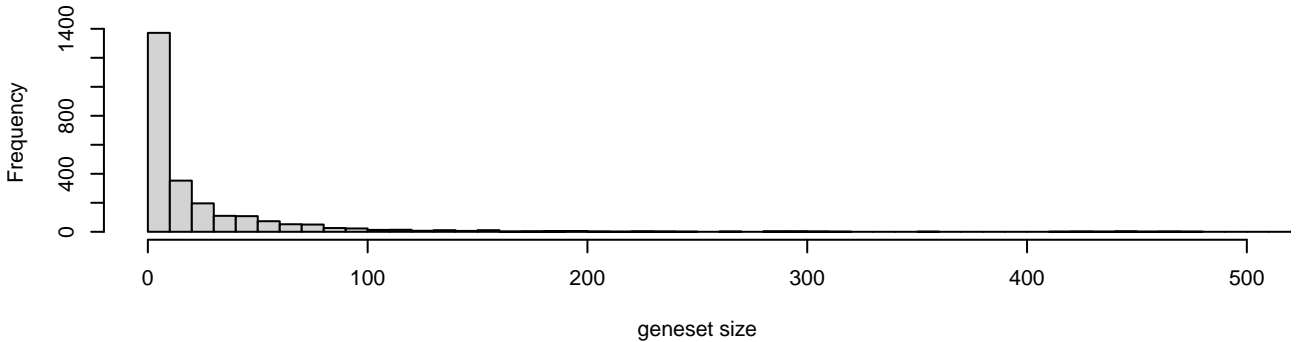
Gene set size



Histogram of geneset size

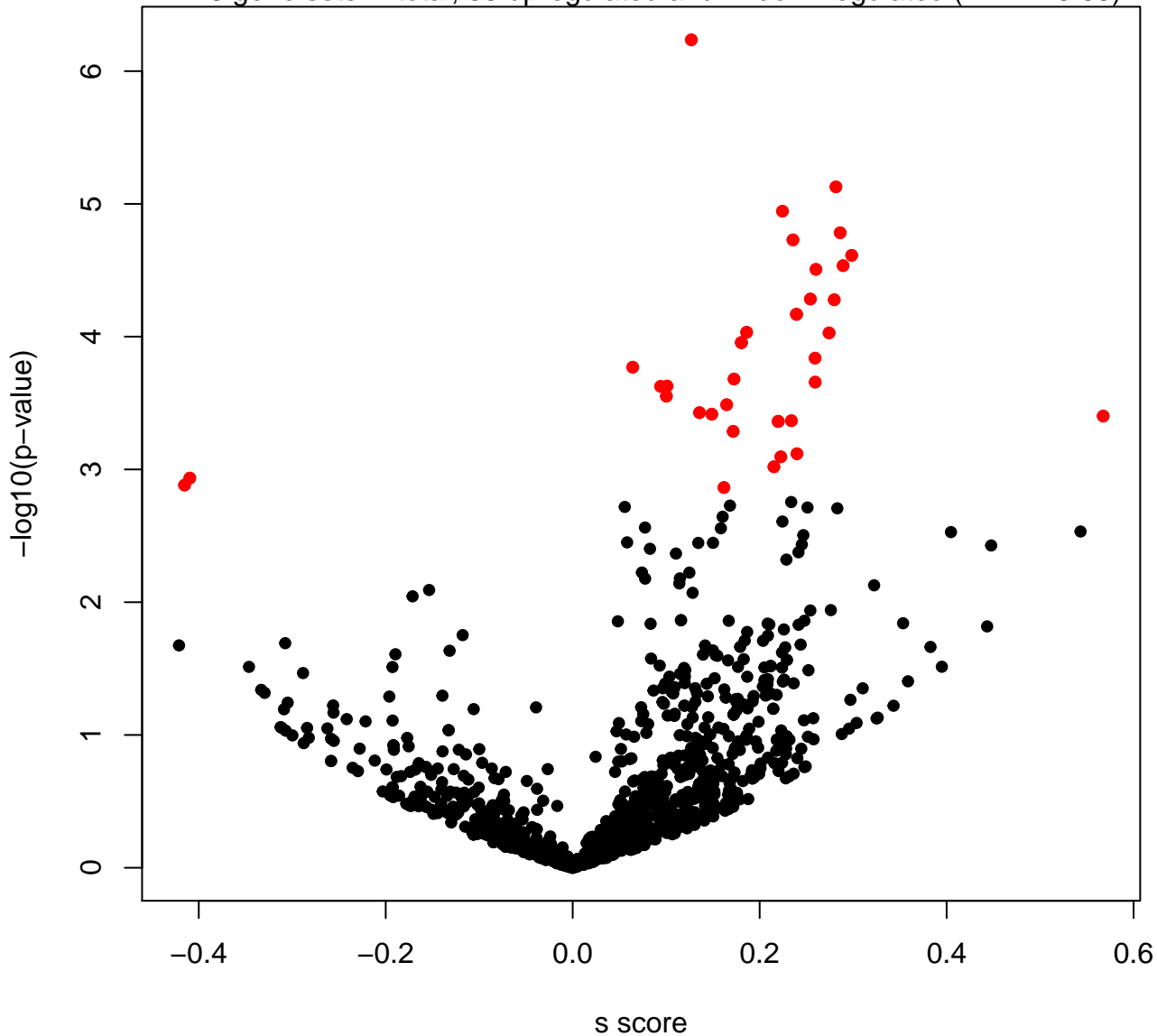


Trimmed histogram of geneset size



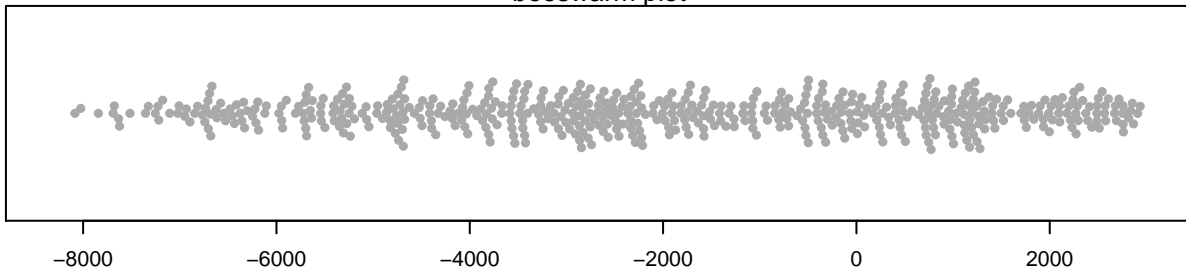
volcano plot of gene set enrichments

1176 gene sets in total, 35 upregulated and 2 downregulated (FDR \leq 0.05)



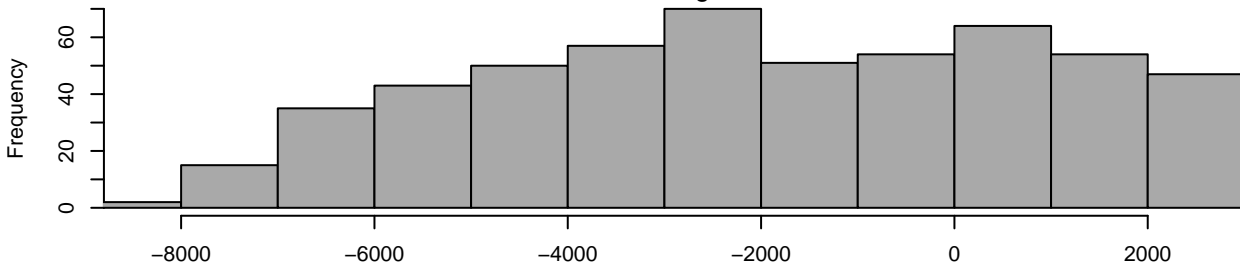
Metabolism of RNA

beeswarm plot



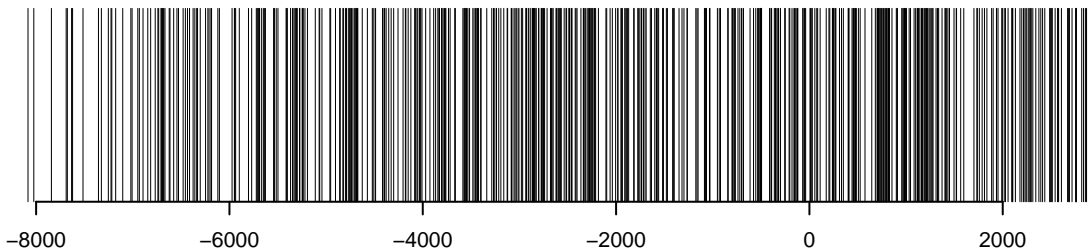
ranked DE score in: t

histogram



ranked DE score in: t

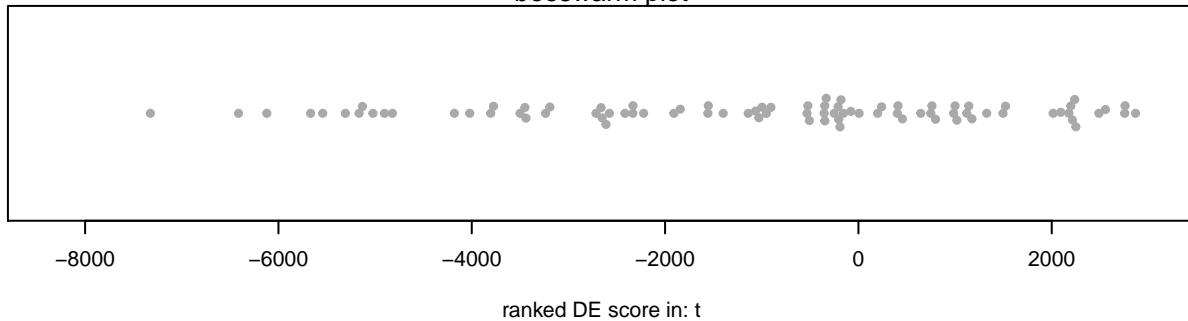
rugplot



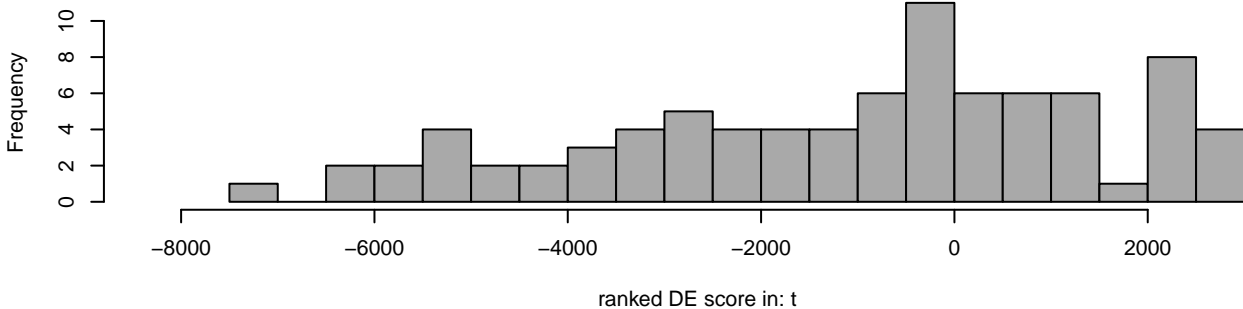
ranked DE score in: t

SRP-dependent cotranslational protein targeting to membrane

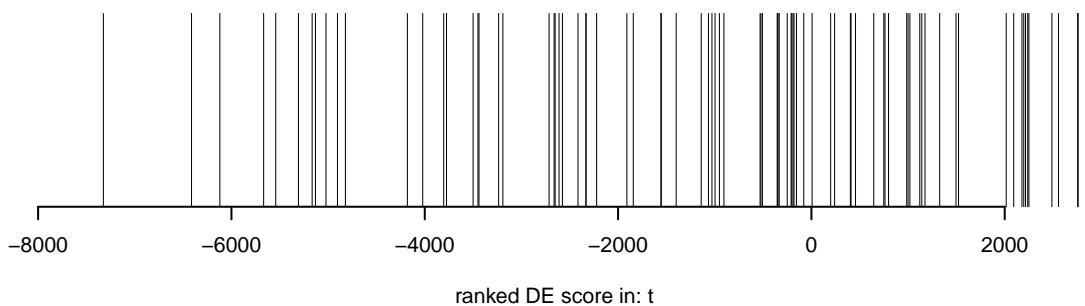
beeswarm plot



histogram

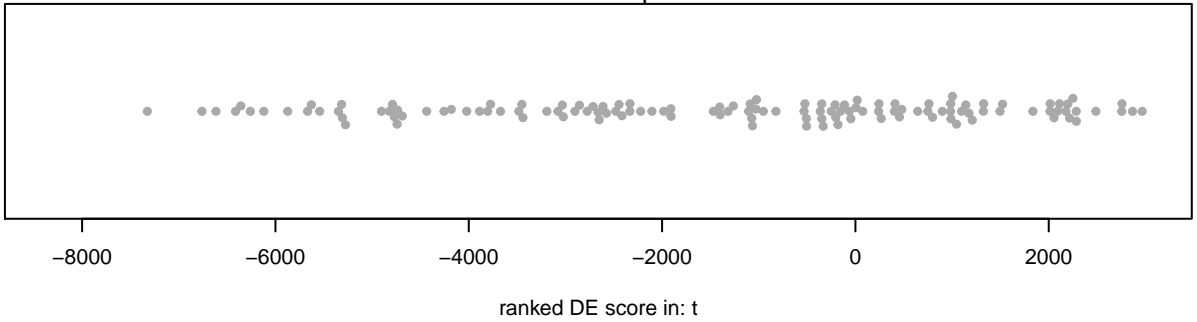


rugplot

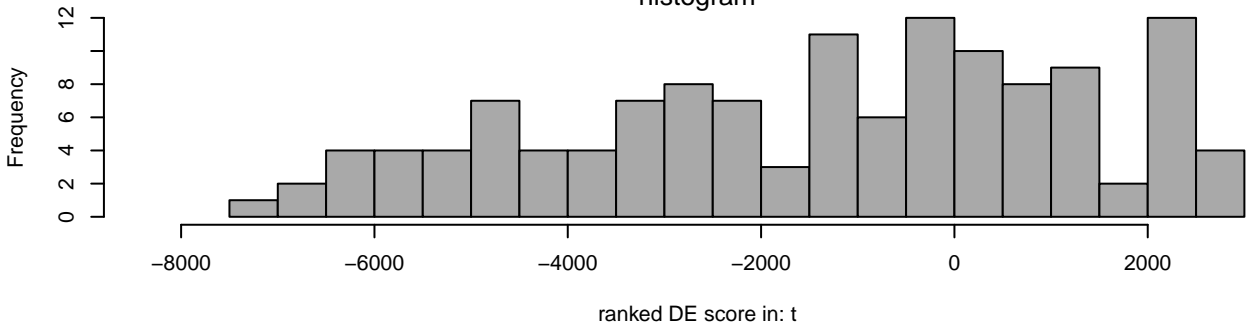


Influenza Infection

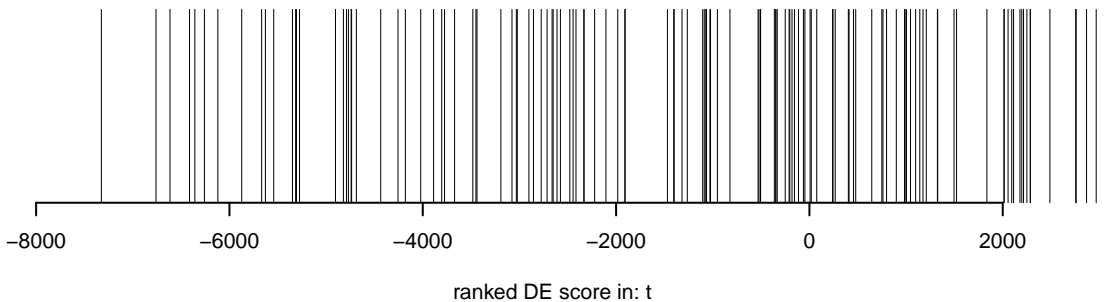
beeswarm plot



histogram

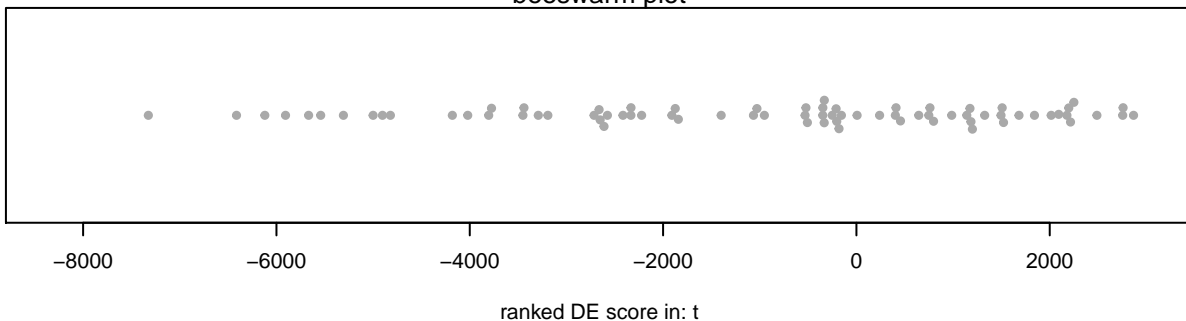


rugplot

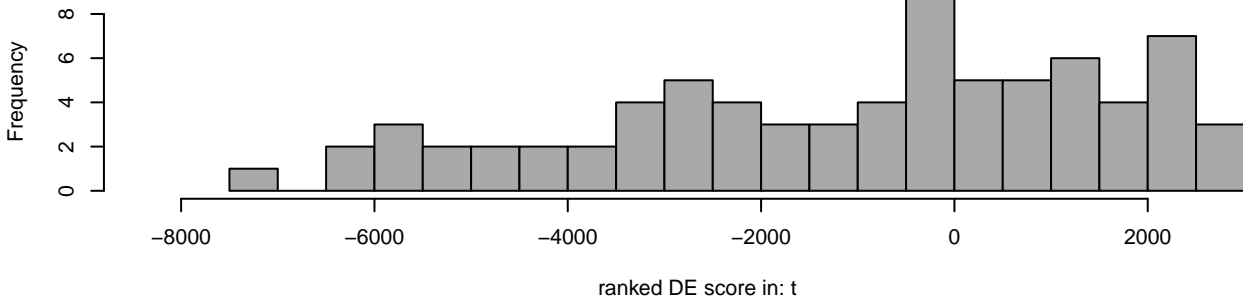


Formation of a pool of free 40S subunits

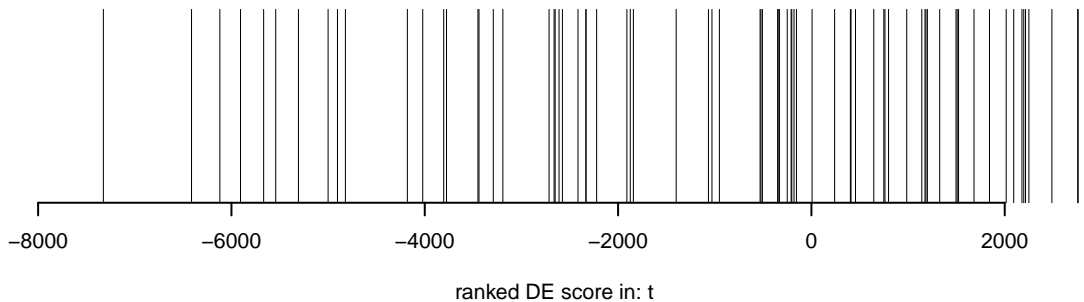
beeswarm plot



histogram

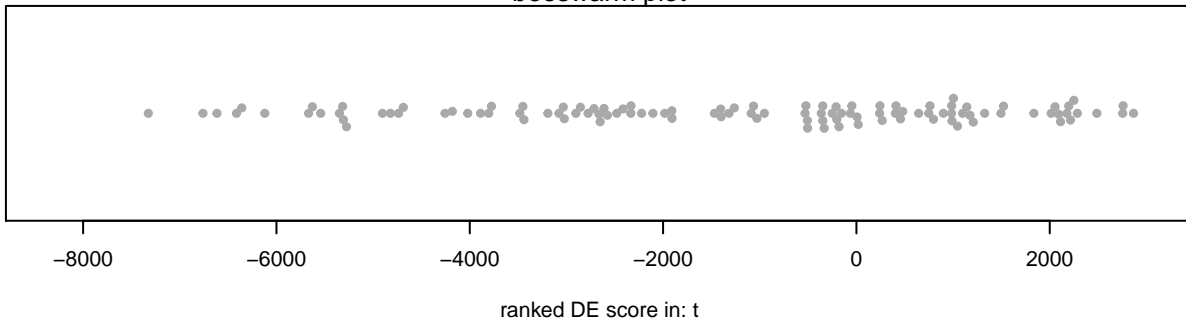


rugplot

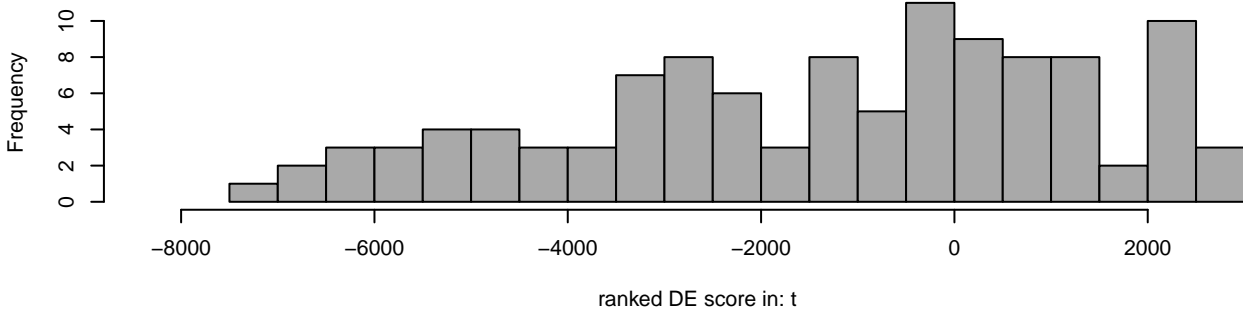


Influenza Viral RNA Transcription and Replication

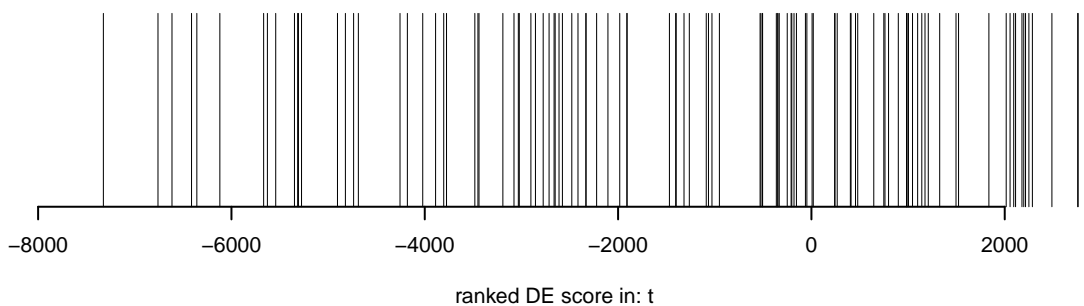
beeswarm plot



histogram

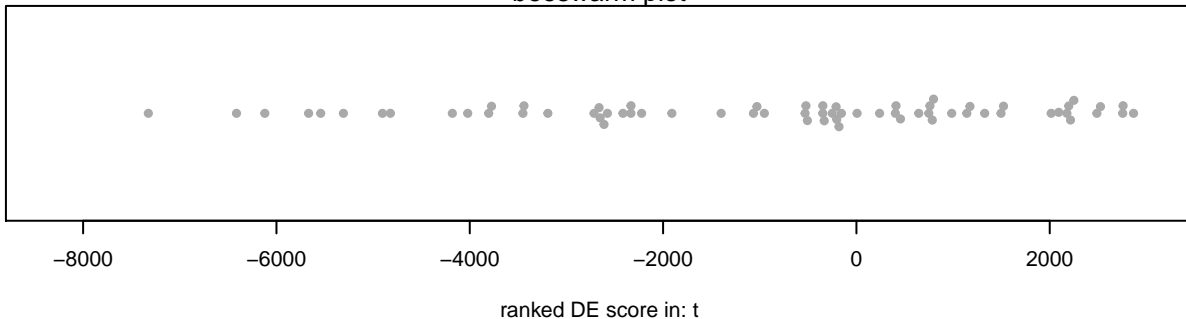


rugplot

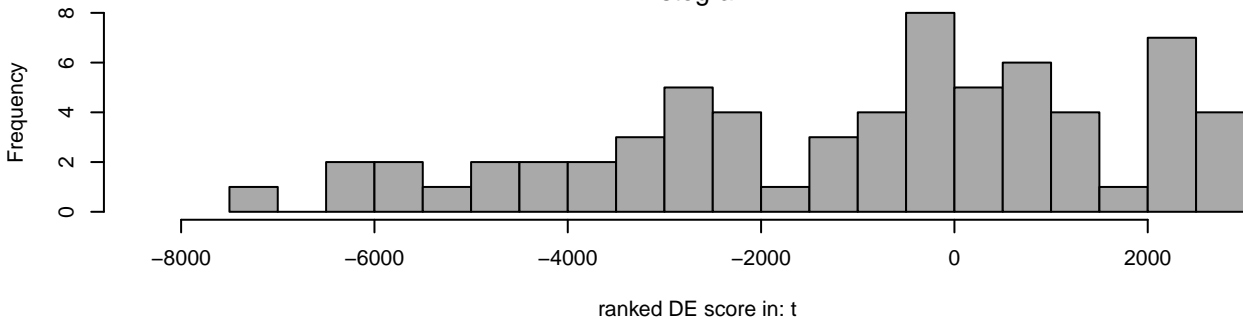


Peptide chain elongation

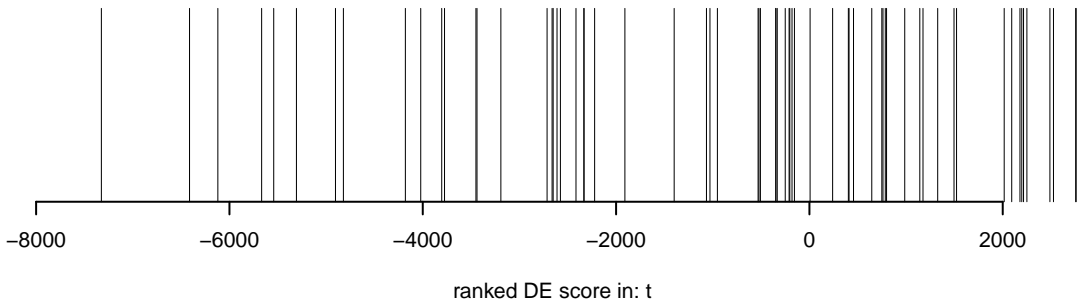
beeswarm plot



histogram

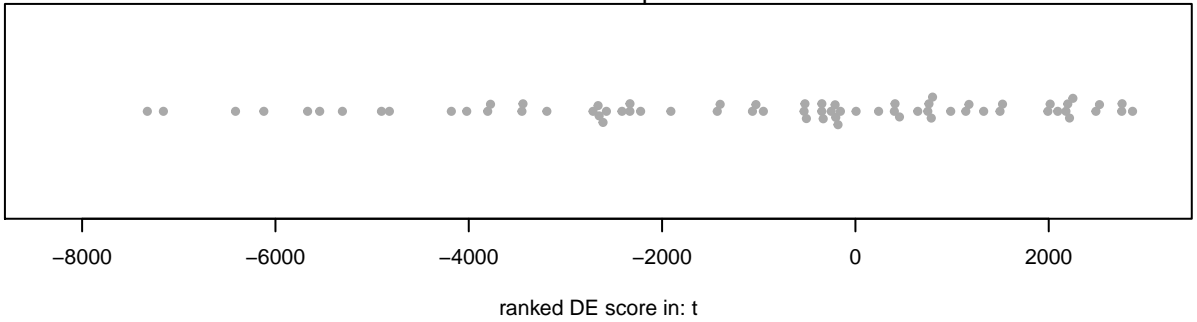


rugplot

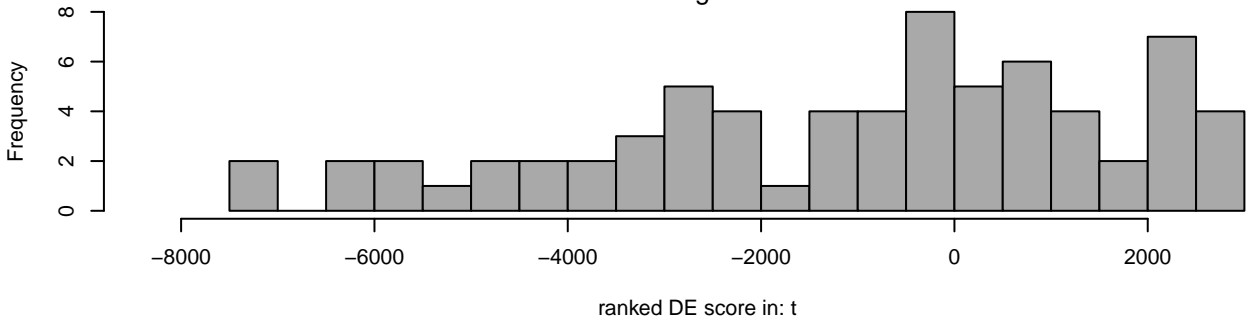


Eukaryotic Translation Elongation

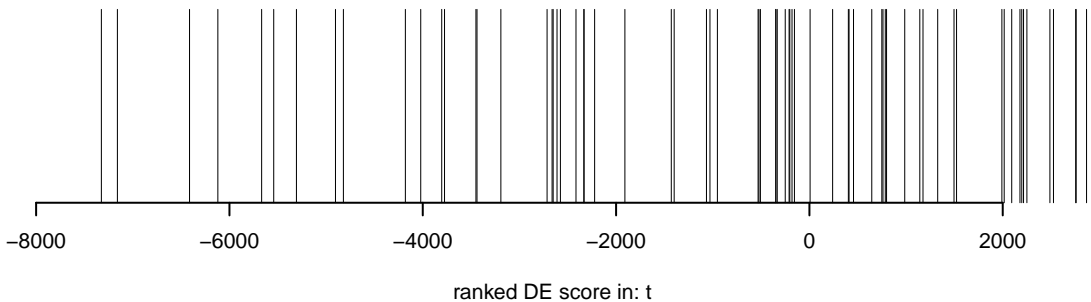
beeswarm plot



histogram

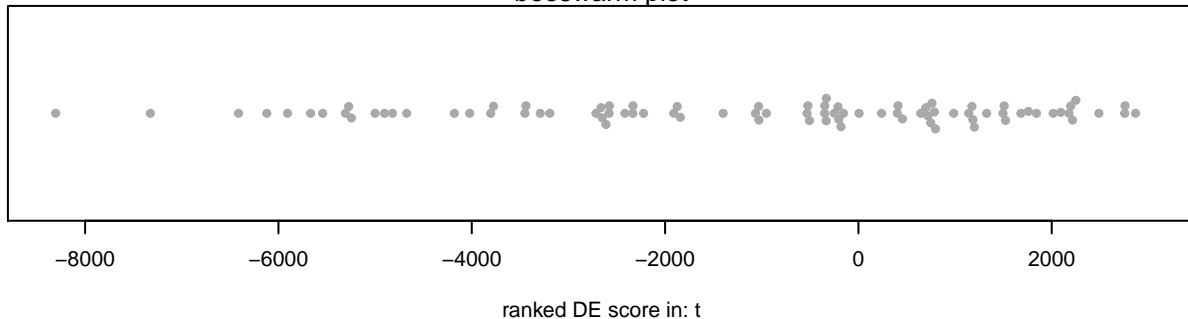


rugplot

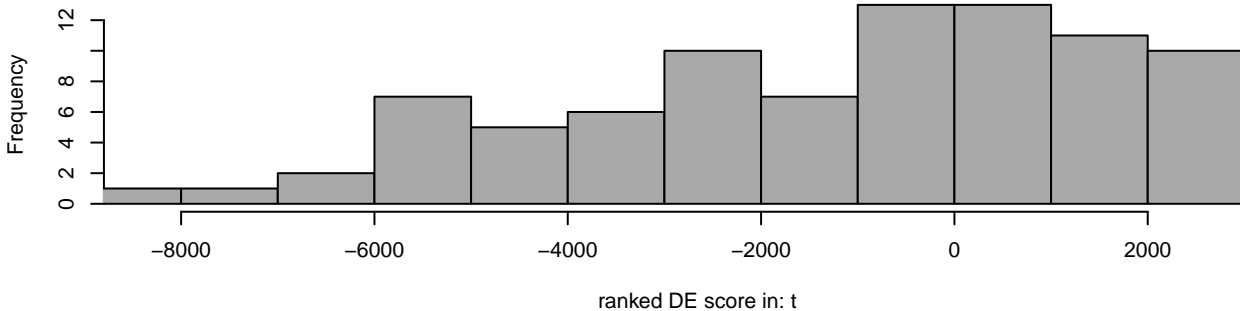


GTP hydrolysis and joining of the 60S ribosomal subunit

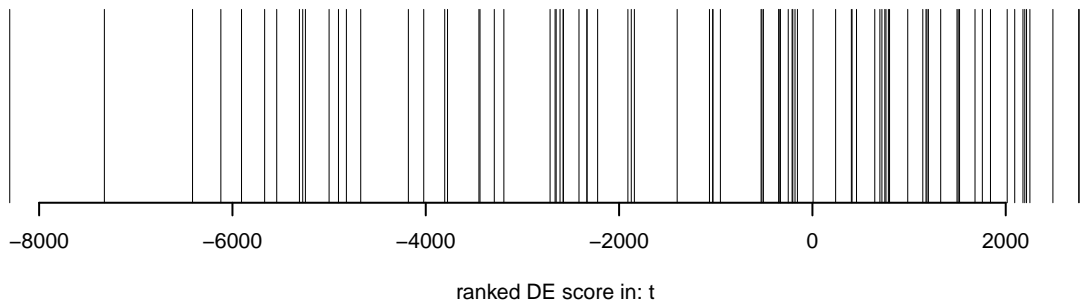
beeswarm plot



histogram

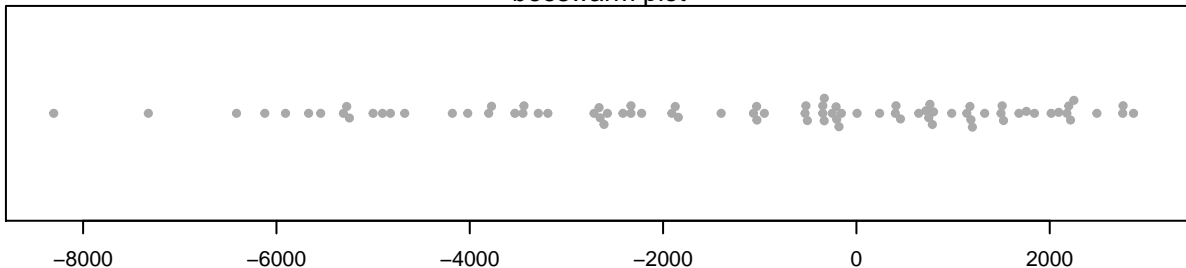


rugplot



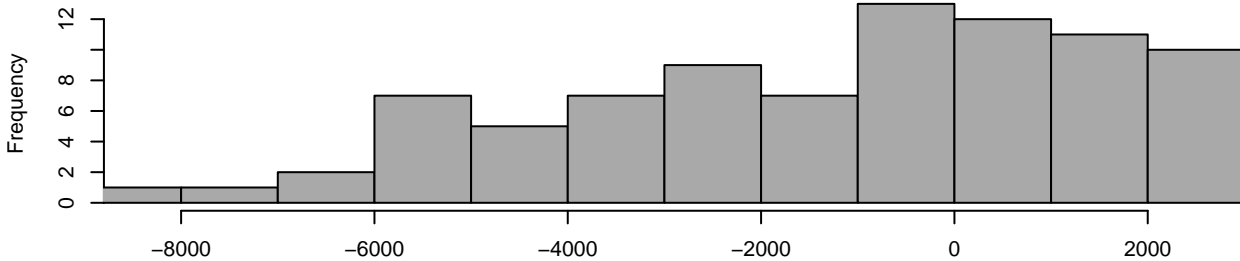
L13a-mediated translational silencing of Ceruloplasmin expression

beeswarm plot



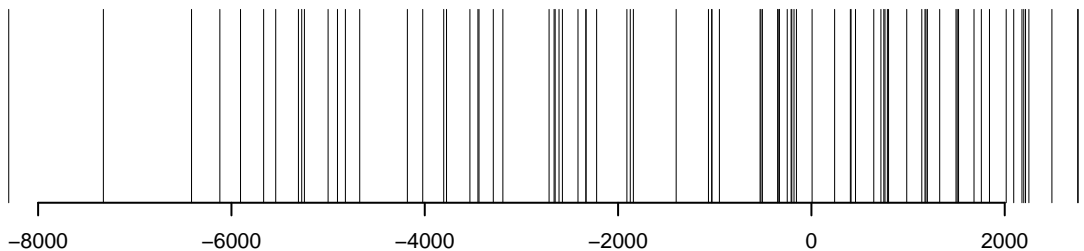
ranked DE score in: t

histogram



ranked DE score in: t

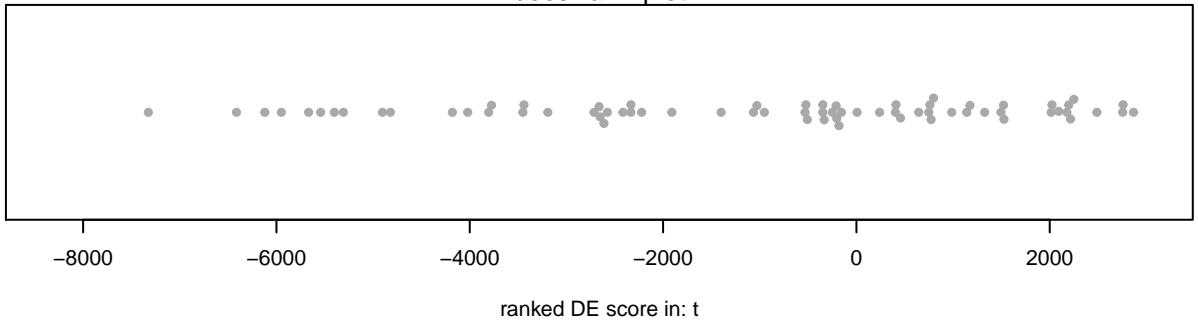
rugplot



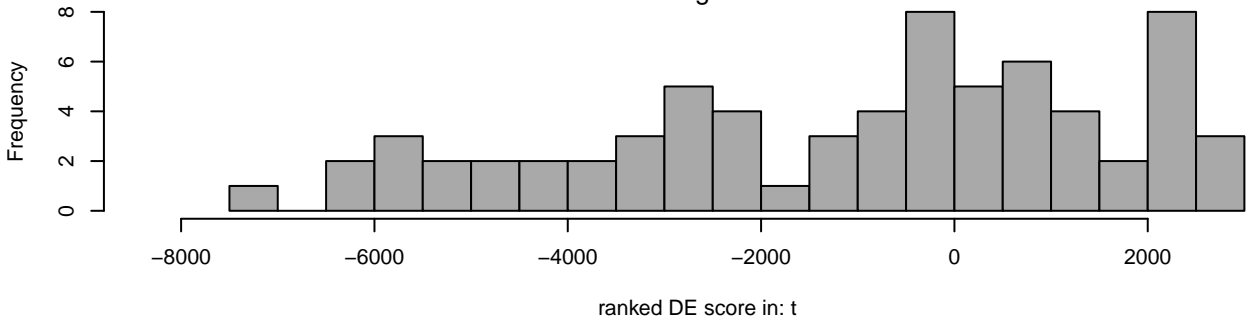
ranked DE score in: t

Eukaryotic Translation Termination

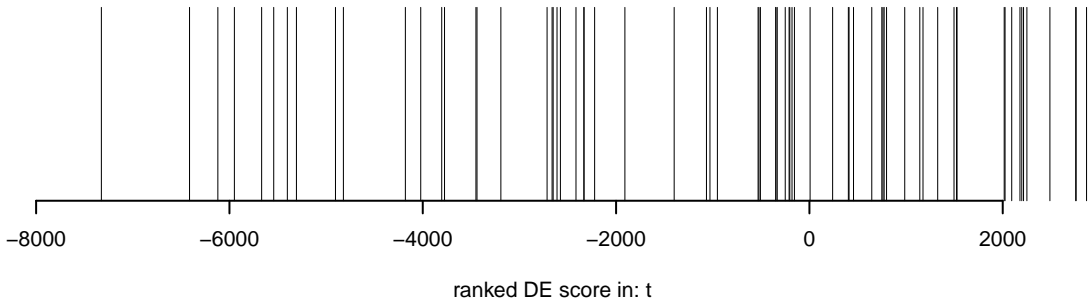
beeswarm plot



histogram

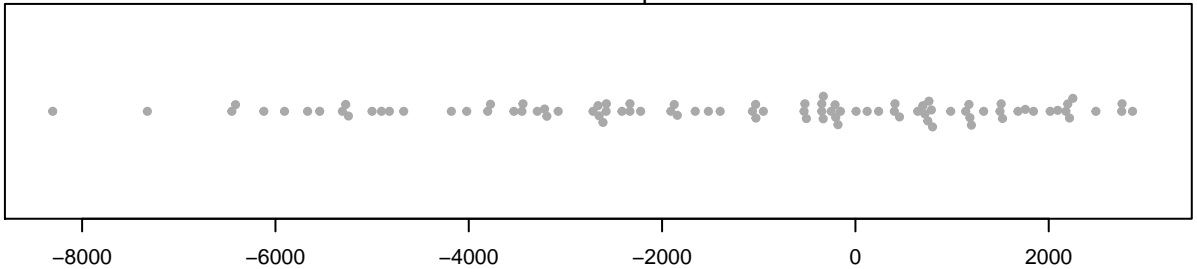


rugplot



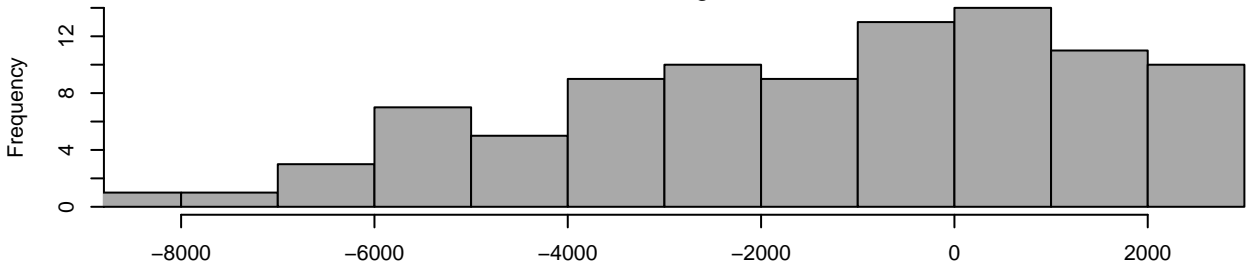
Cap-dependent Translation Initiation

beeswarm plot



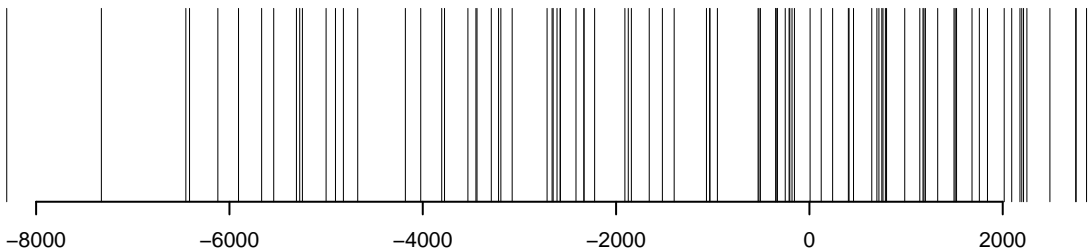
ranked DE score in: t

histogram



ranked DE score in: t

rugplot



ranked DE score in: t

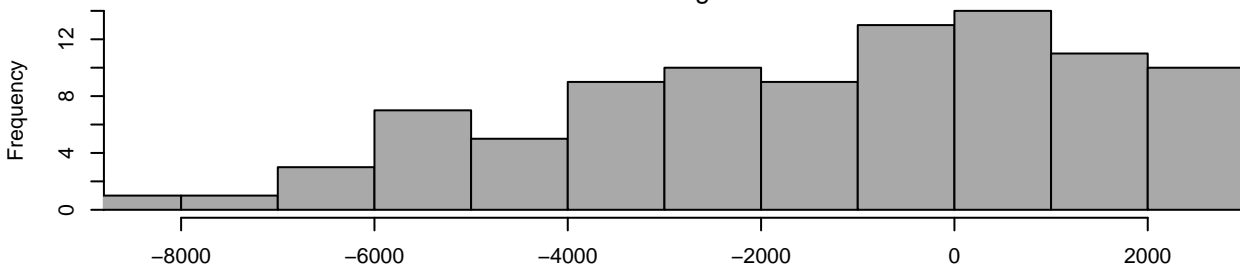
Eukaryotic Translation Initiation

beeswarm plot



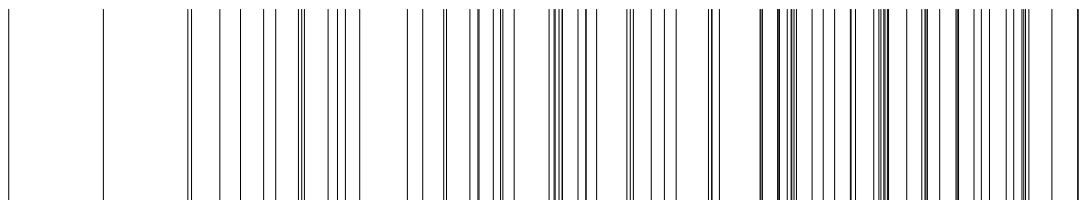
ranked DE score in: t

histogram



ranked DE score in: t

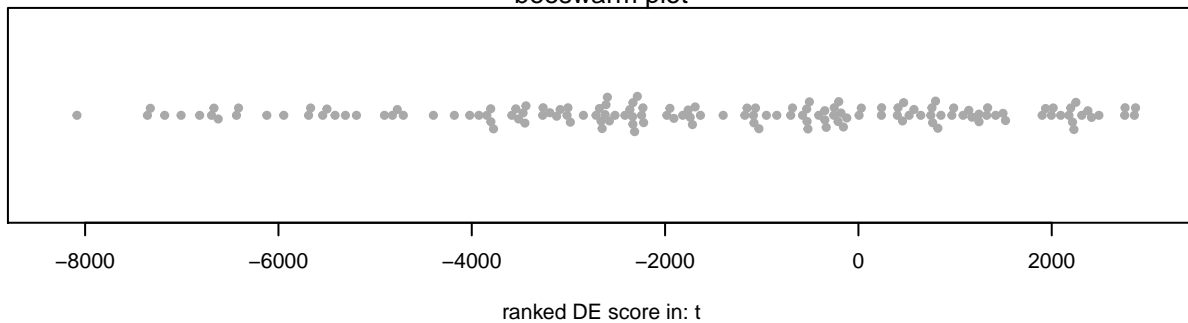
rugplot



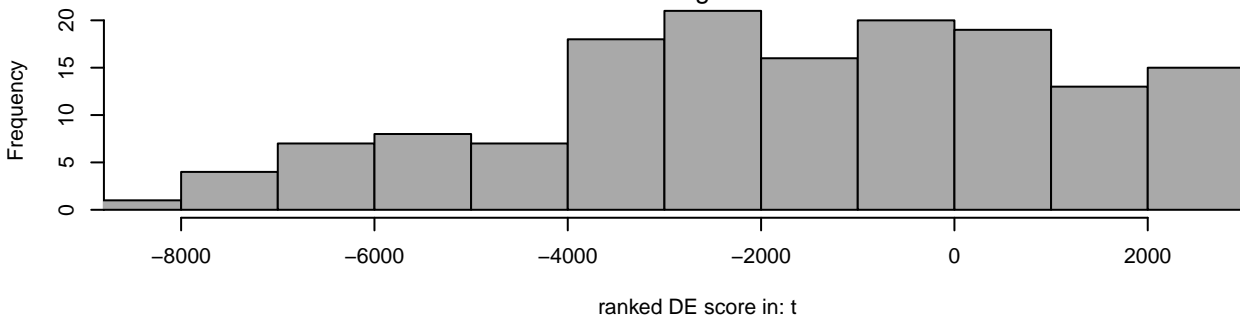
ranked DE score in: t

Major pathway of rRNA processing in the nucleolus and cytosol

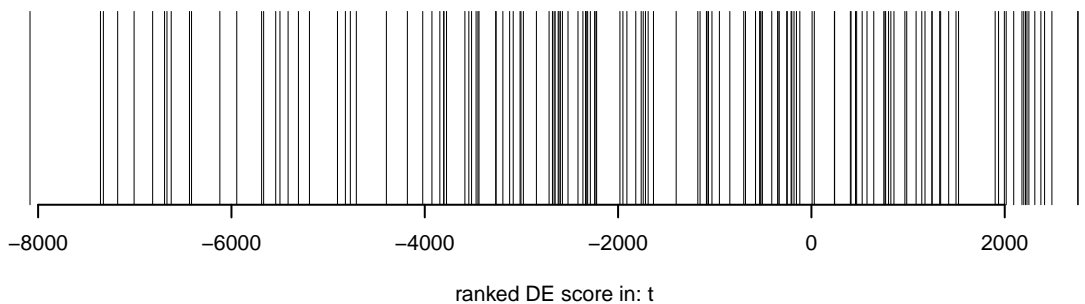
beeswarm plot



histogram

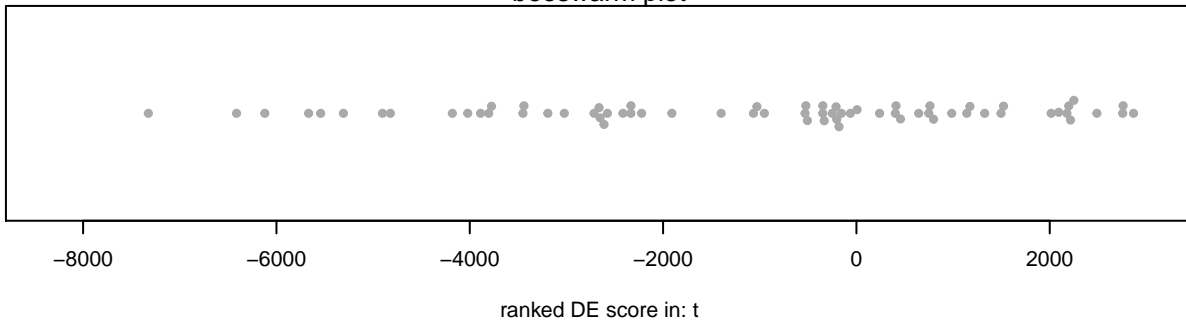


rugplot

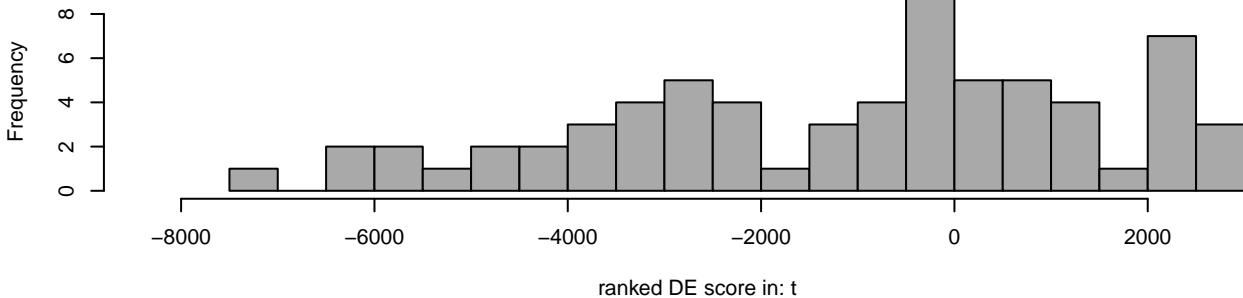


Viral mRNA Translation

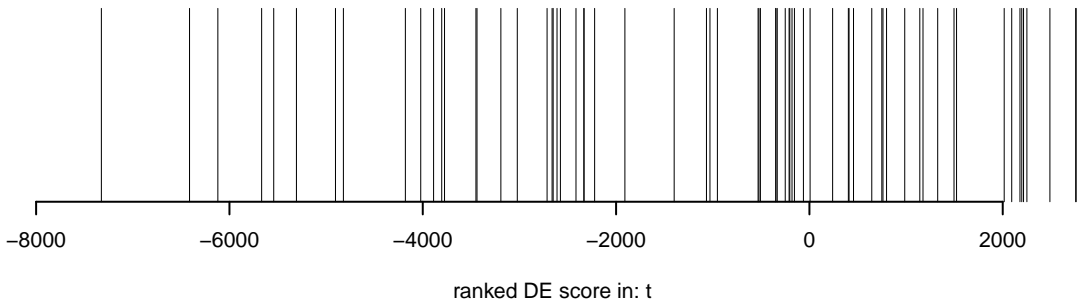
beeswarm plot



histogram

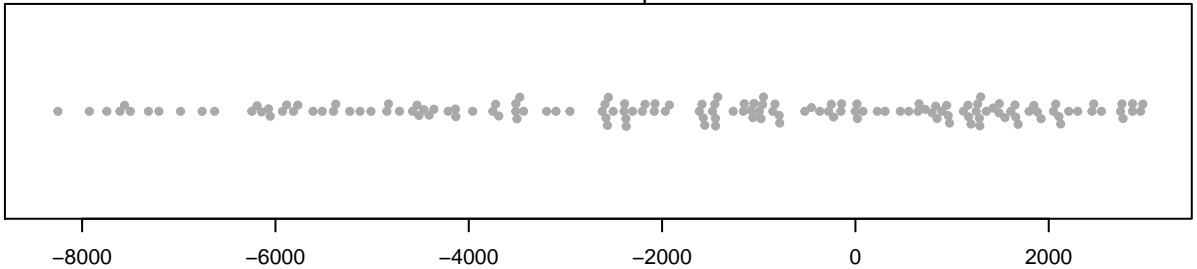


rugplot



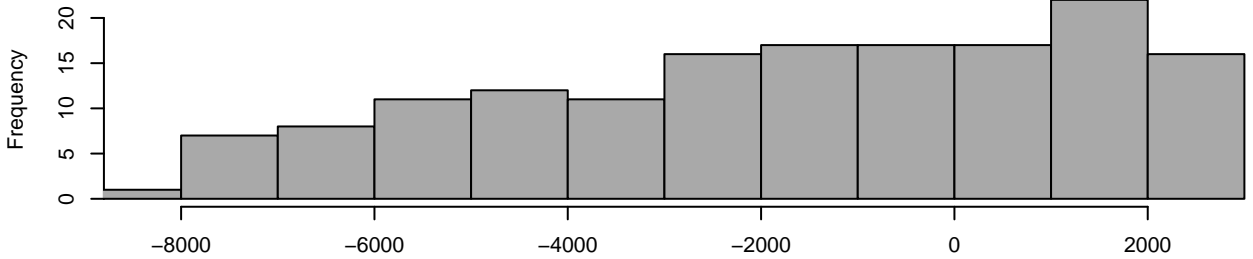
Chromatin modifying enzymes

beeswarm plot



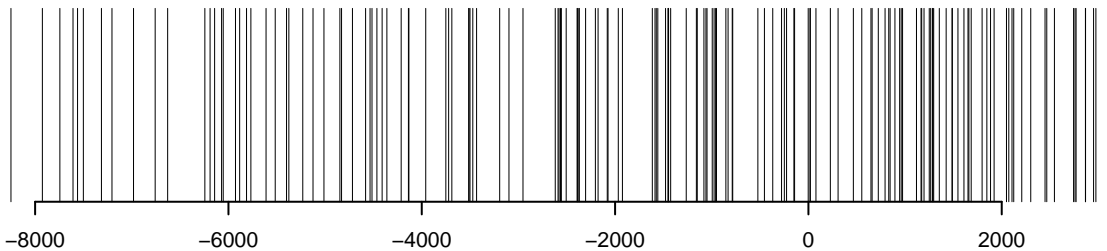
ranked DE score in: t

histogram



ranked DE score in: t

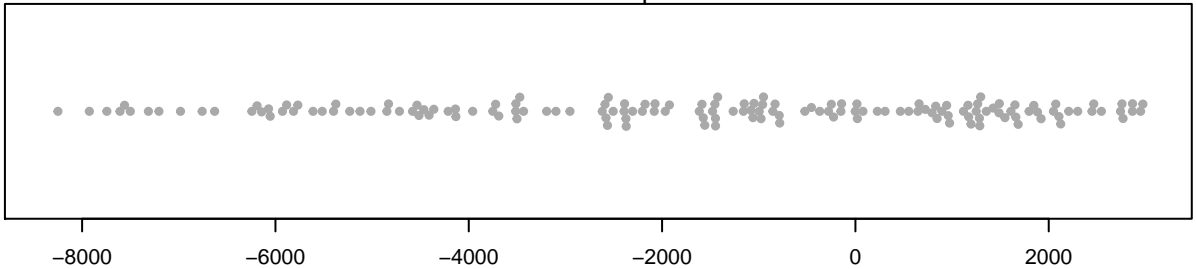
rugplot



ranked DE score in: t

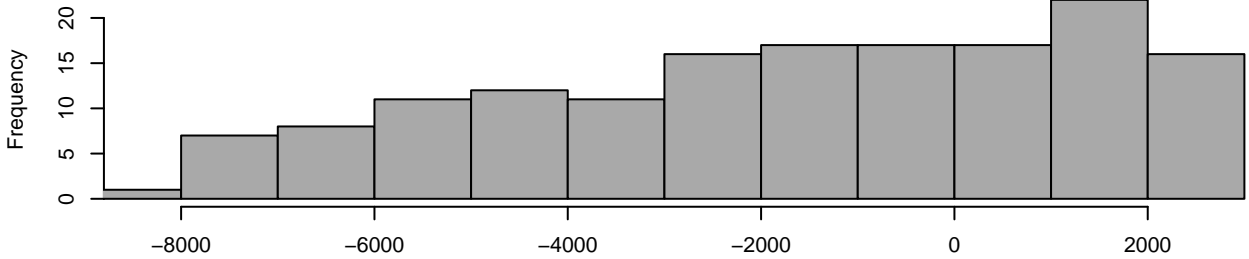
Chromatin organization

beeswarm plot



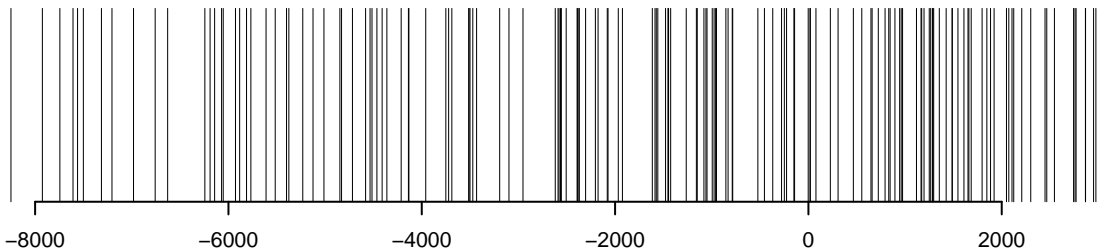
ranked DE score in: t

histogram



ranked DE score in: t

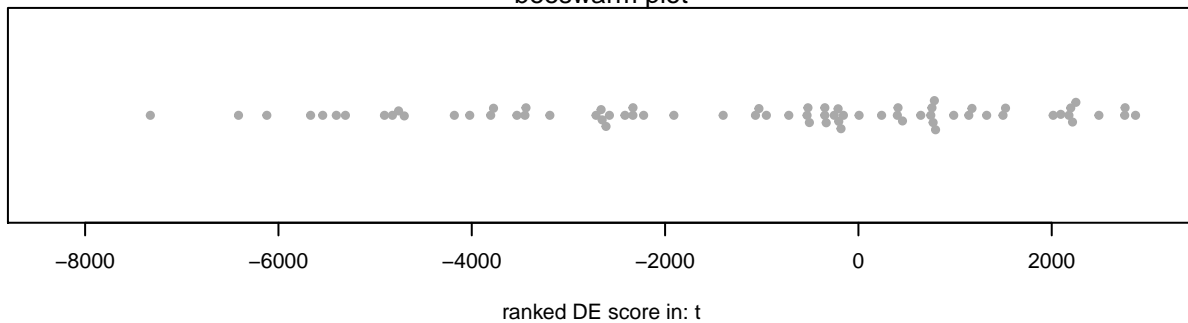
rugplot



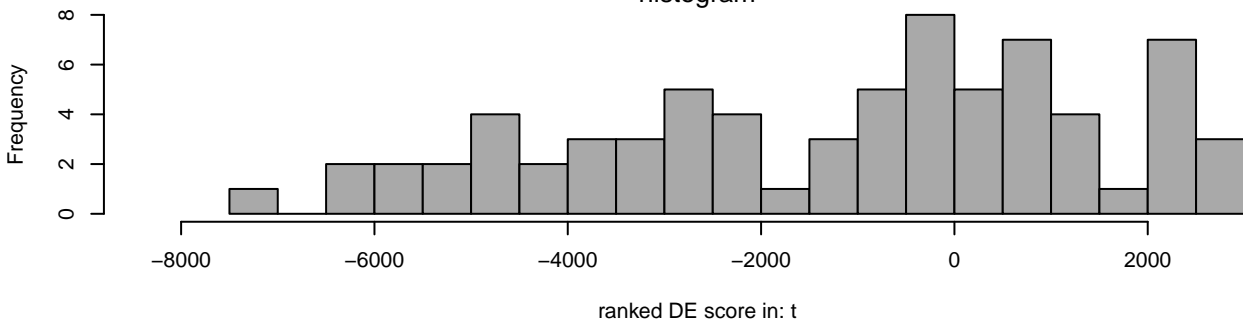
ranked DE score in: t

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

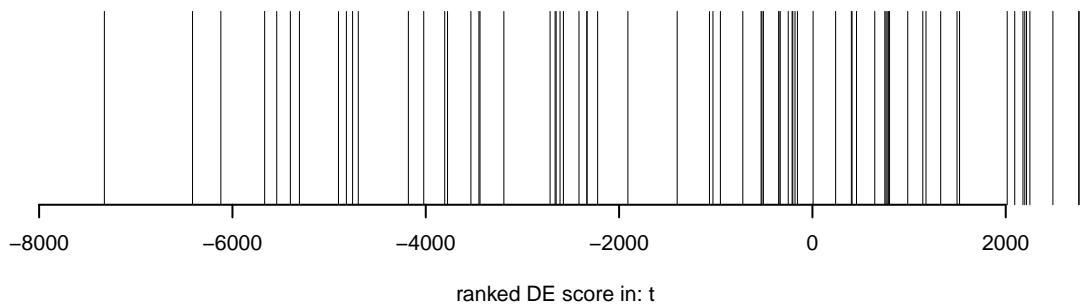
beeswarm plot



histogram

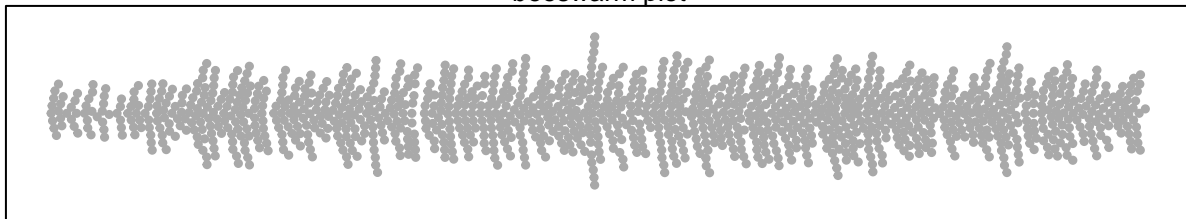


rugplot



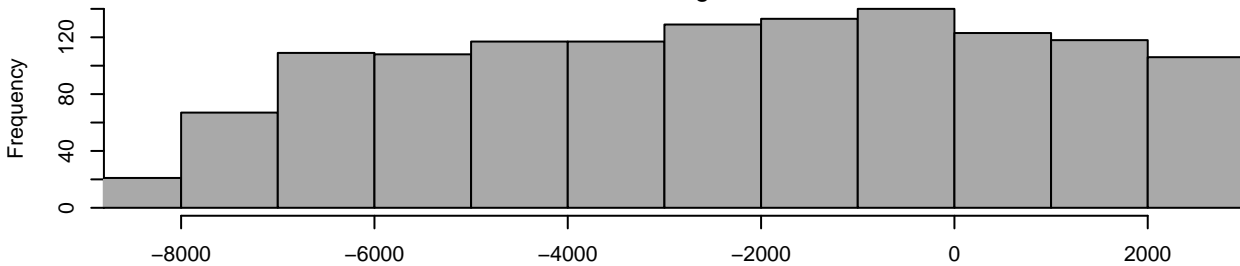
Metabolism of proteins

beeswarm plot



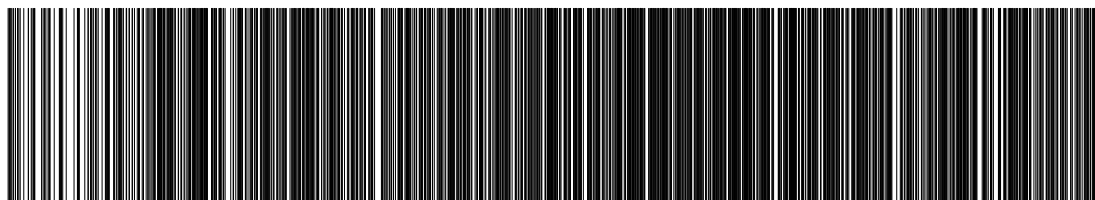
ranked DE score in: t

histogram



ranked DE score in: t

rugplot



-8000

-6000

-4000

-2000

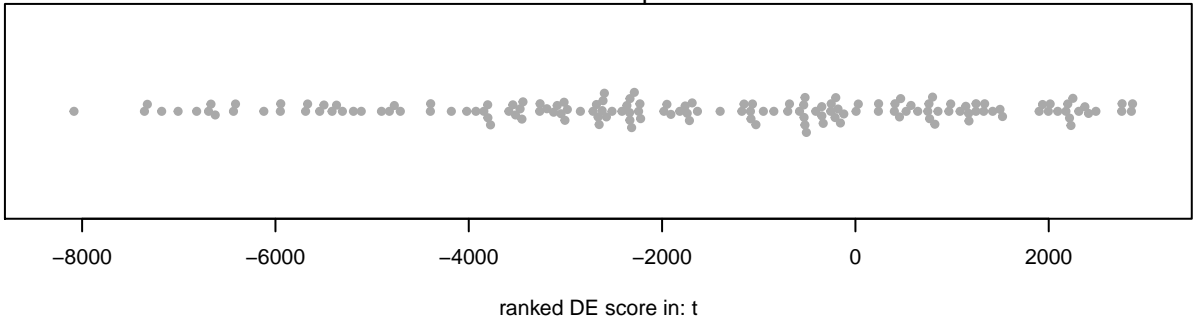
0

2000

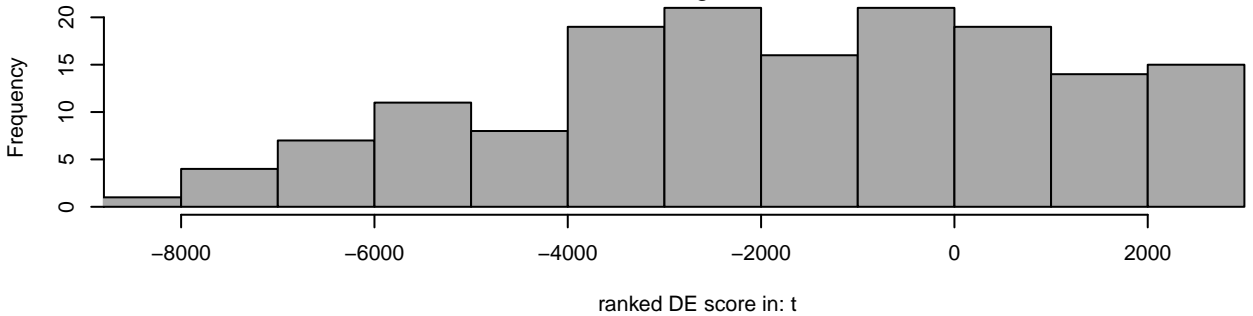
ranked DE score in: t

rRNA processing in the nucleus and cytosol

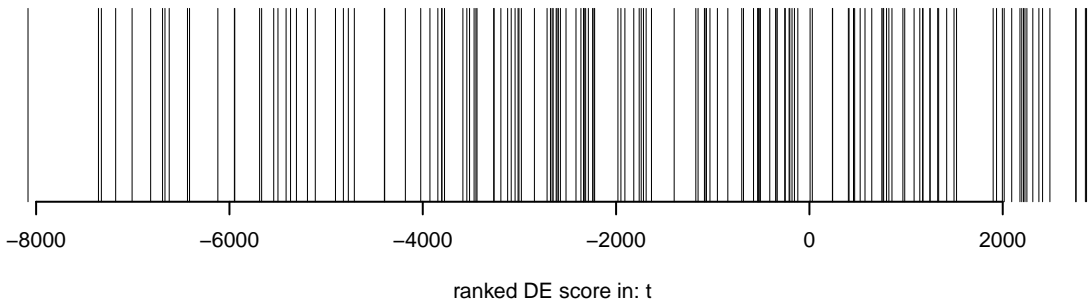
beeswarm plot



histogram

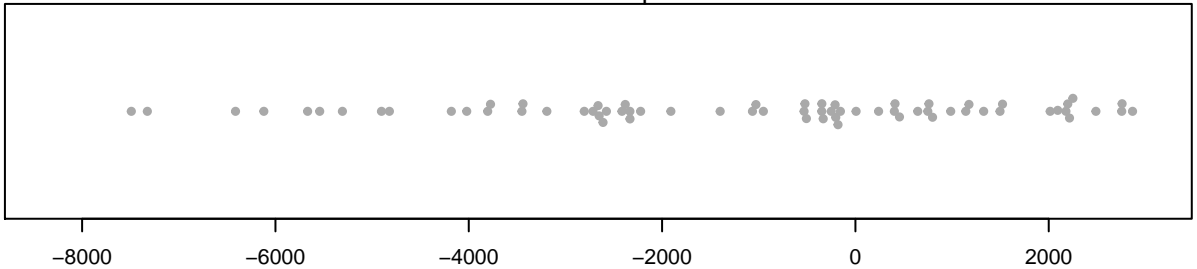


rugplot



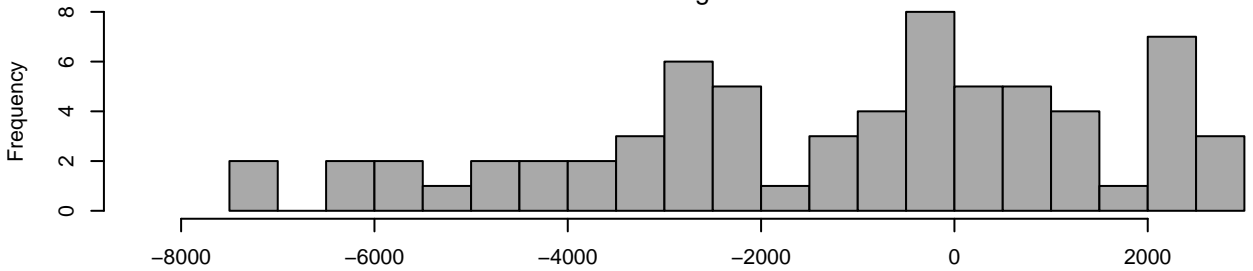
Selenocysteine synthesis

beeswarm plot



ranked DE score in: t

histogram



-8000

-6000

-4000

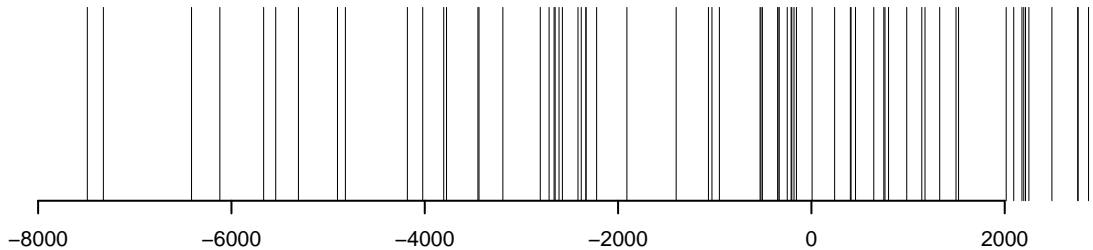
-2000

0

2000

ranked DE score in: t

rugplot



-8000

-6000

-4000

-2000

0

2000

ranked DE score in: t