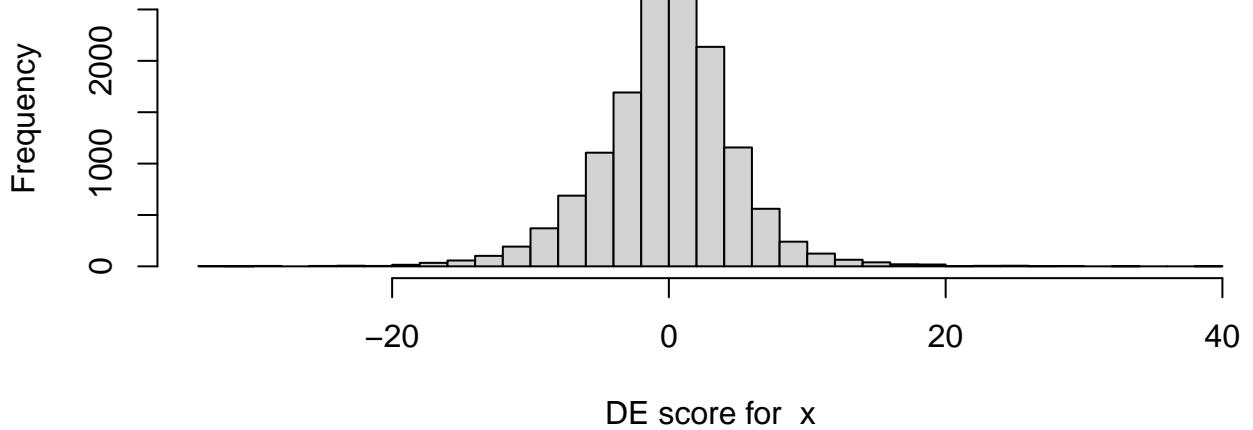
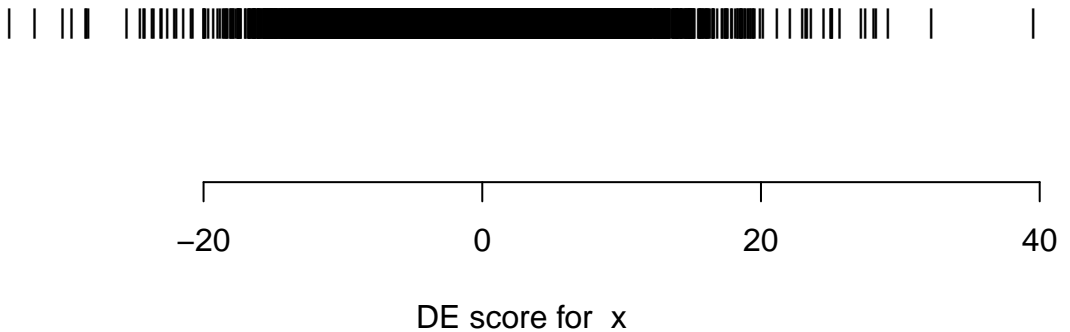


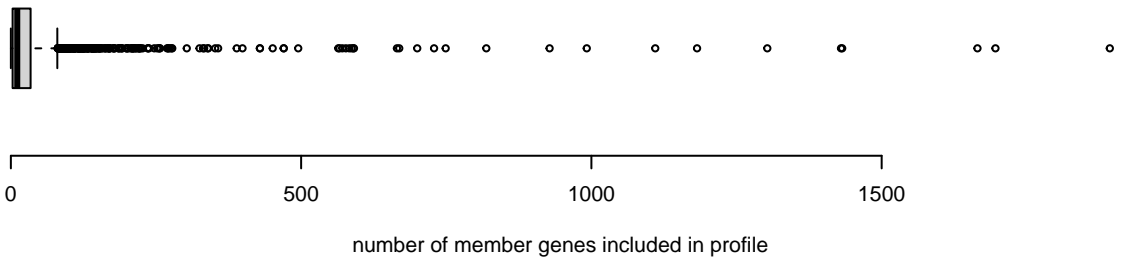
# Distribution of DE scores



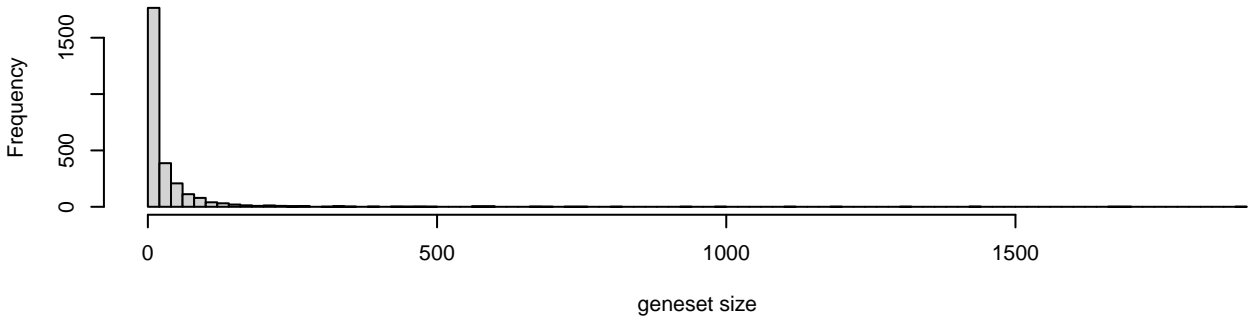
14186 genes in total, 7250 trending up-regulated, 6936 trending down-regulated



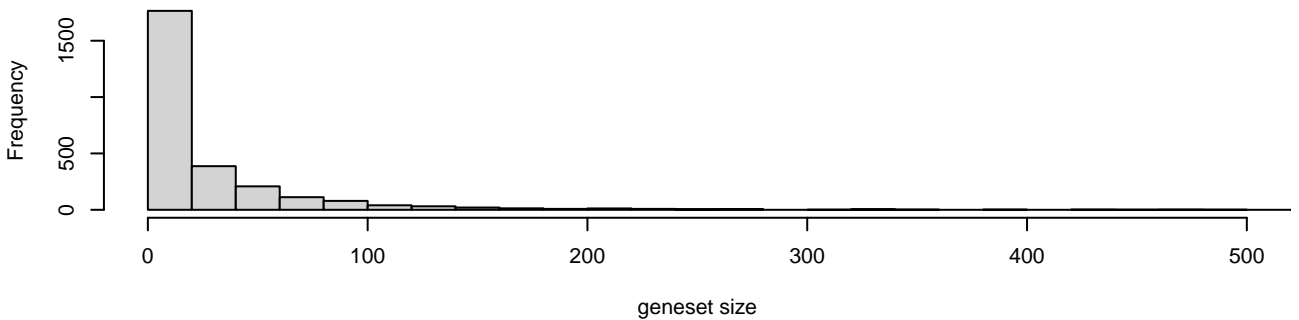
### Gene set size



### Histogram of geneset size

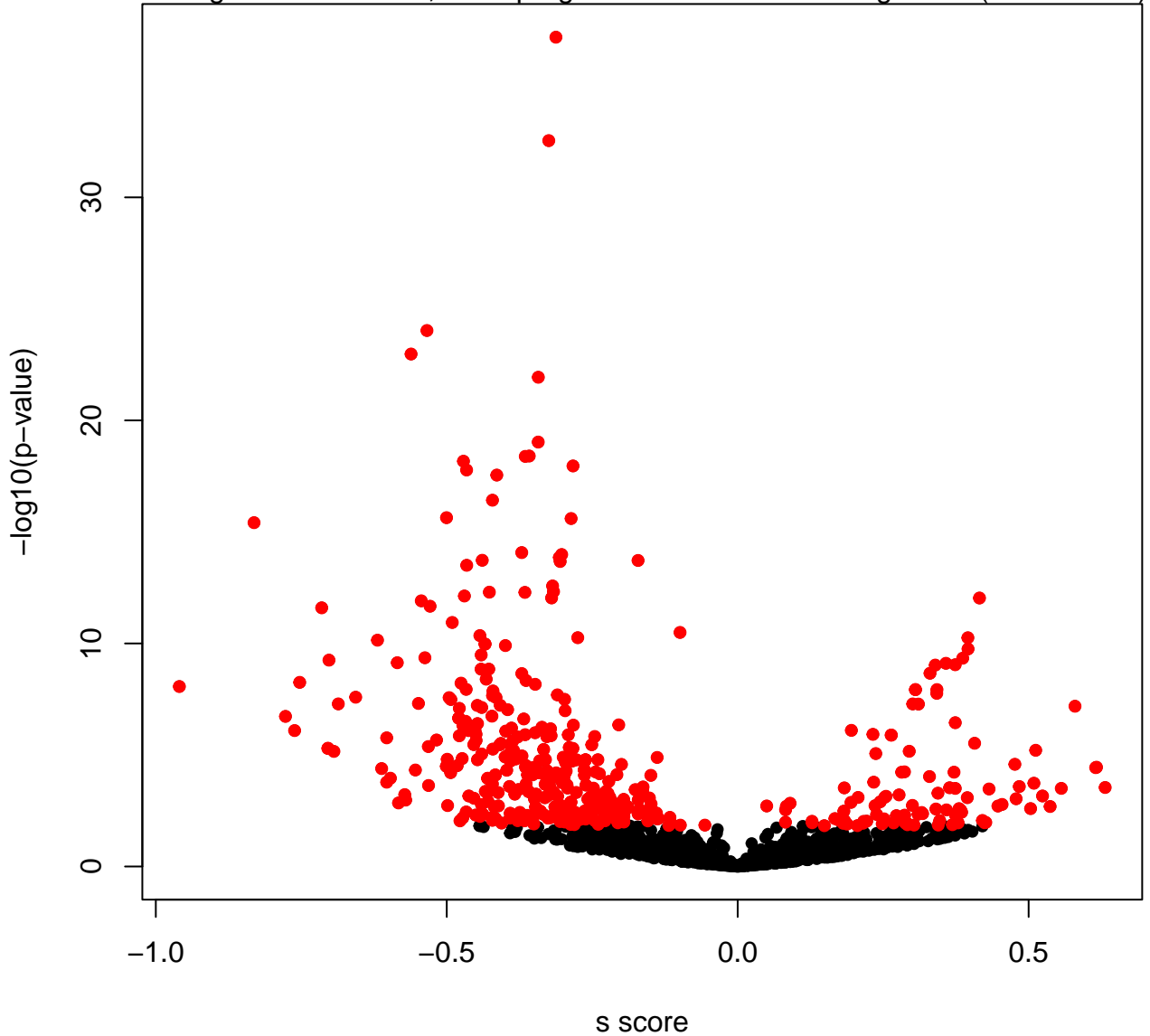


### Trimmed histogram of geneset size



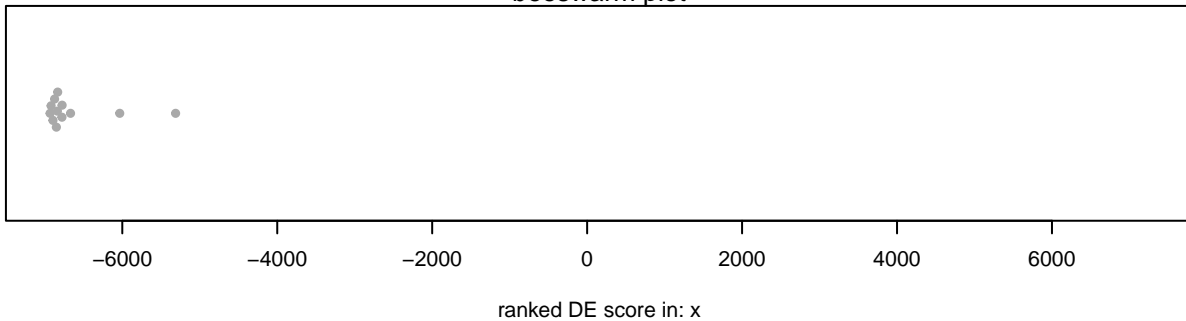
# volcano plot of gene set enrichments

1486 gene sets in total, 101 upregulated and 339 downregulated (FDR $\leq$ 0.05)

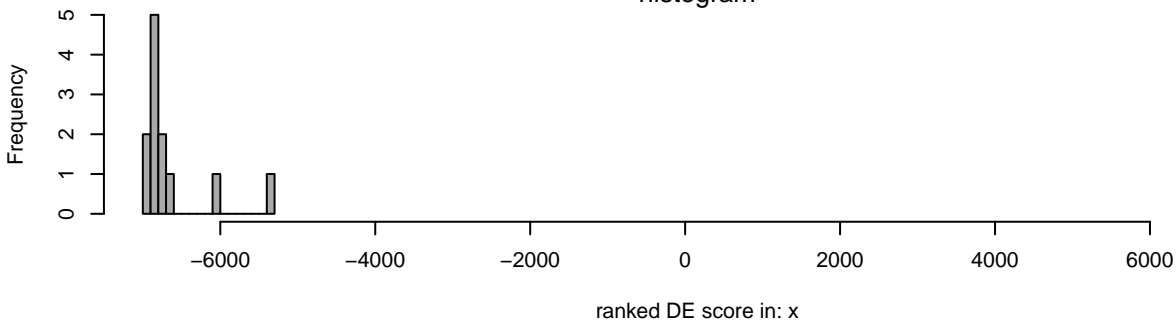


# Unwinding of DNA

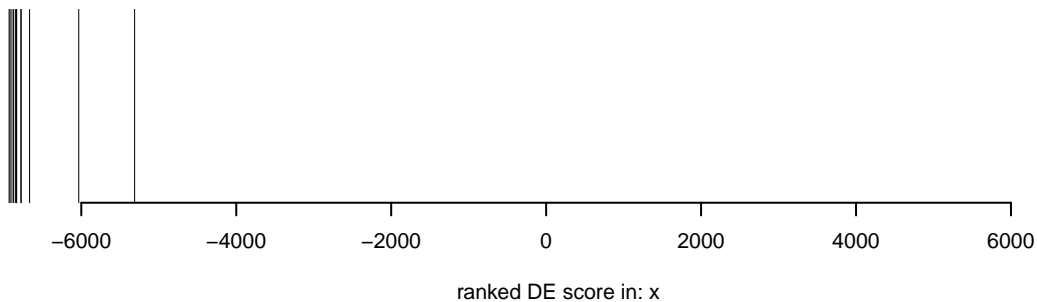
beeswarm plot



histogram

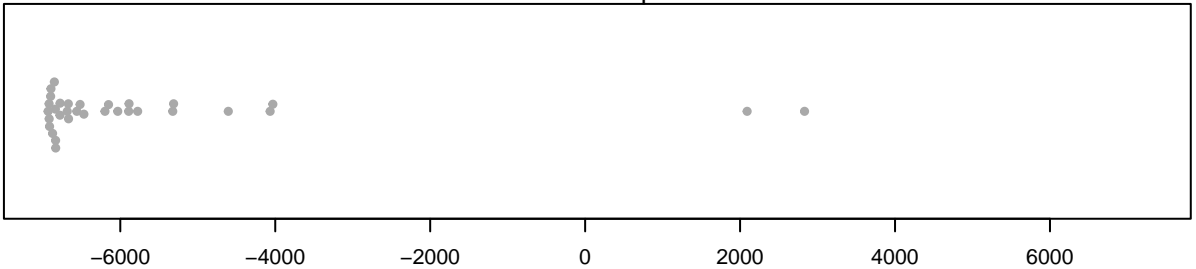


rugplot

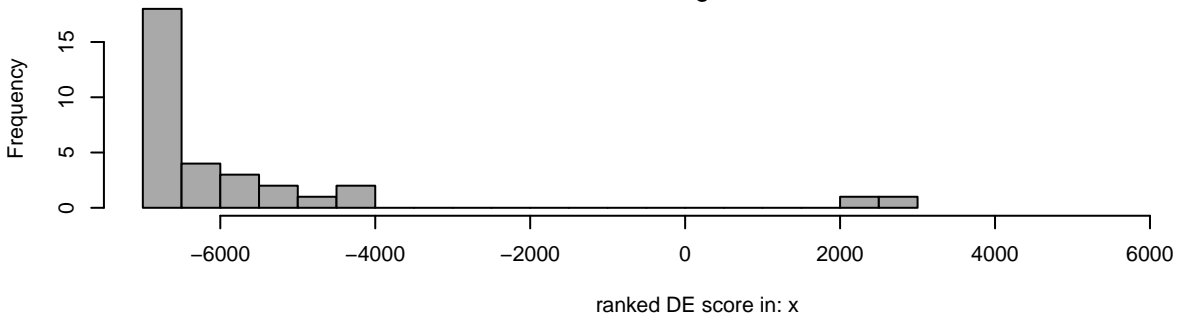


# DNA strand elongation

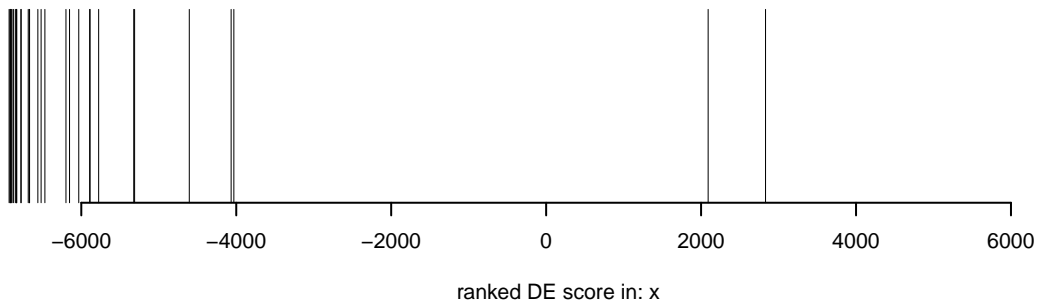
beeswarm plot



histogram

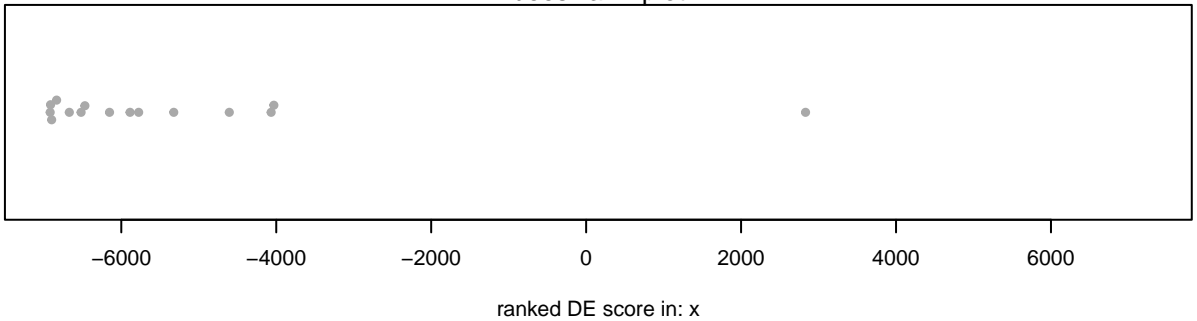


rugplot

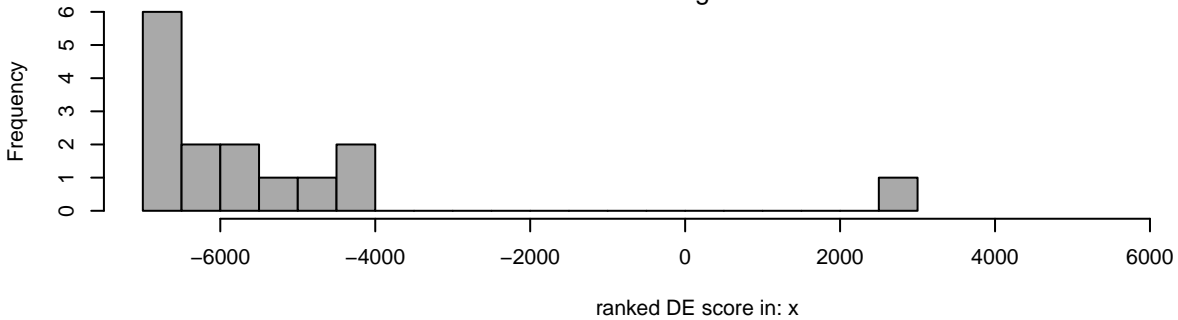


# Processive synthesis on the lagging strand

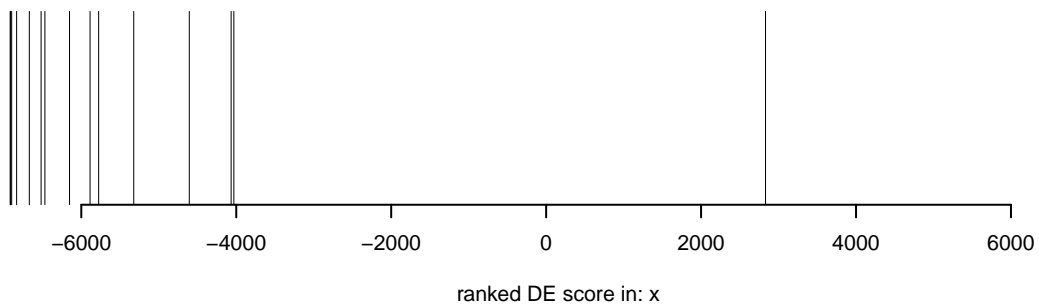
beeswarm plot



histogram

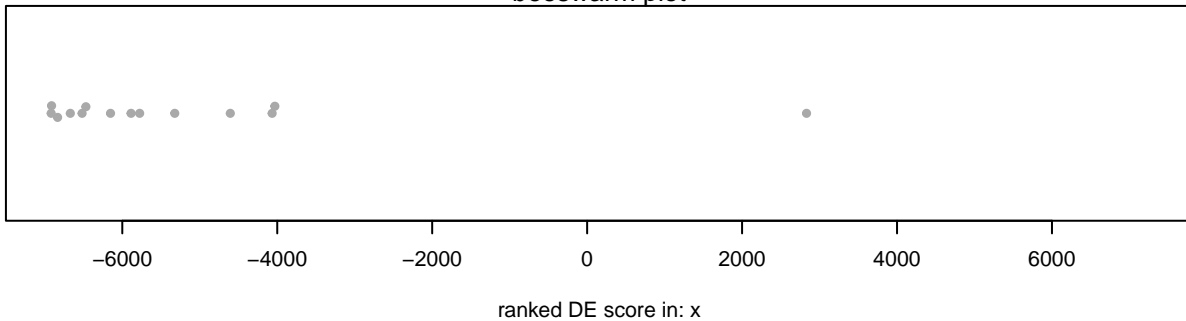


rugplot

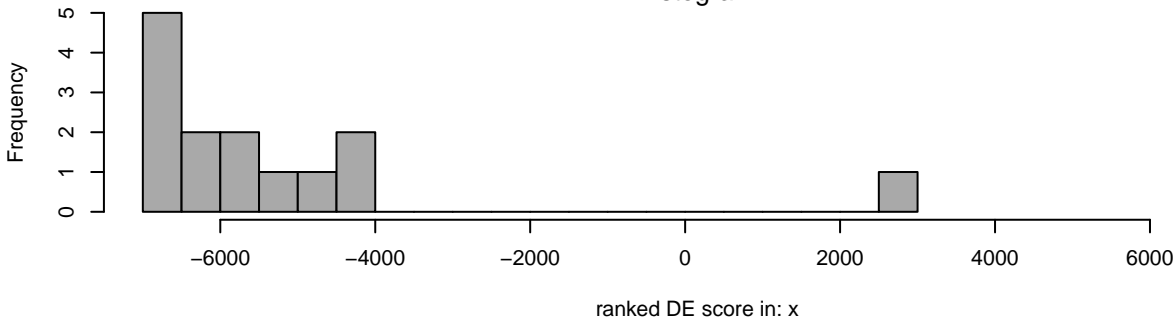


# Removal of the Flap Intermediate

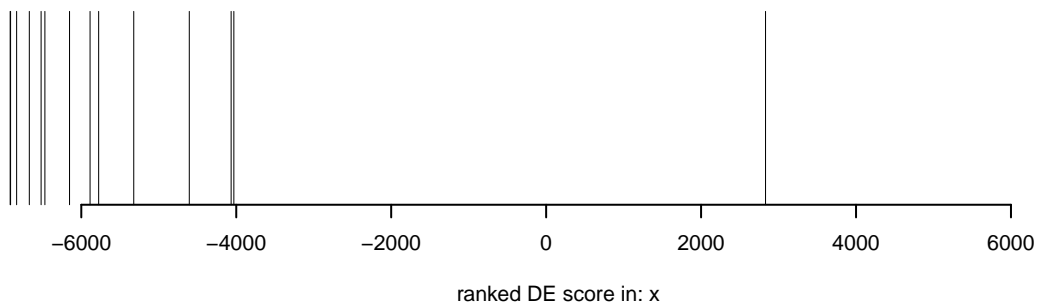
beeswarm plot



histogram

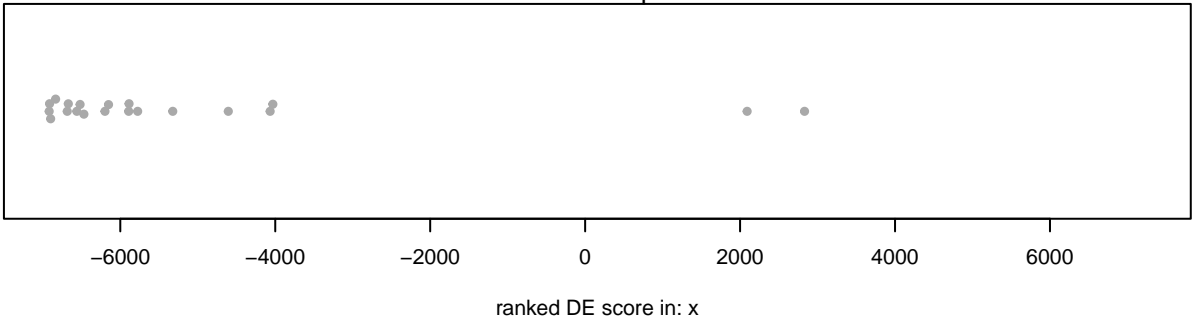


rugplot

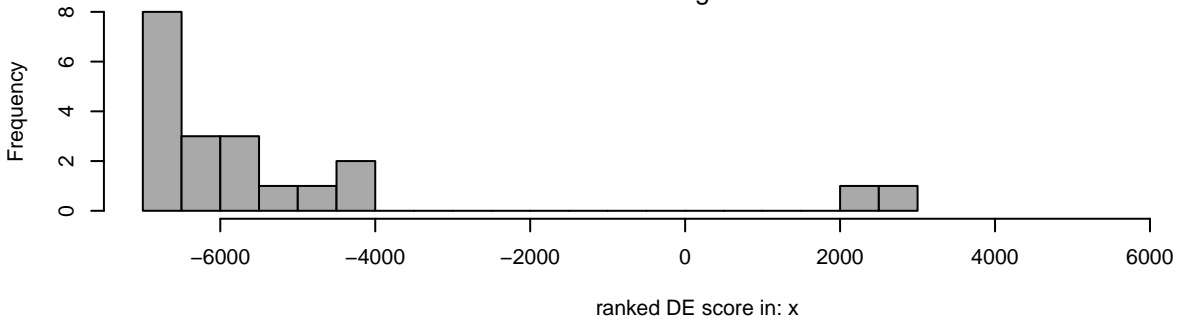


# Lagging Strand Synthesis

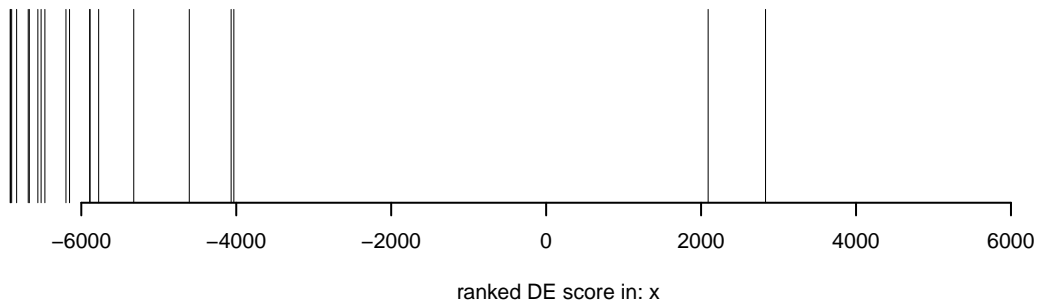
beeswarm plot



histogram



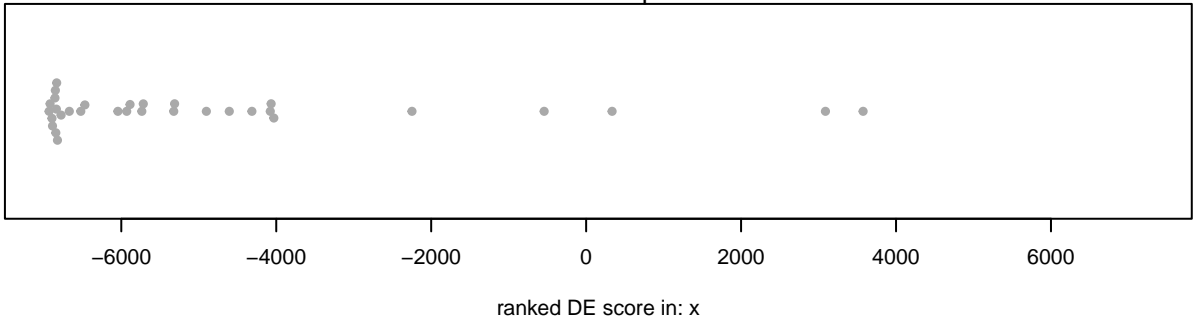
rugplot



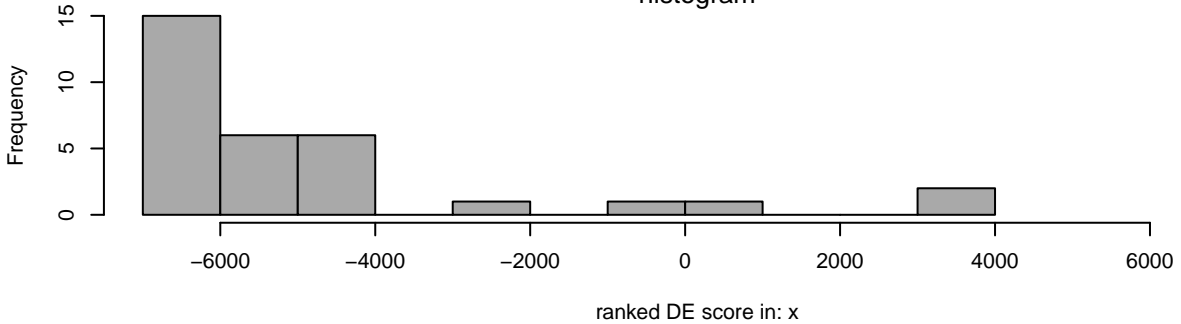


# Activation of the pre-replicative complex

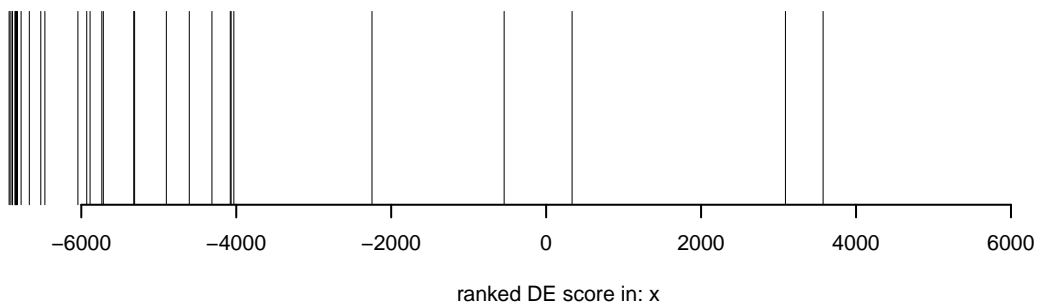
beeswarm plot



histogram

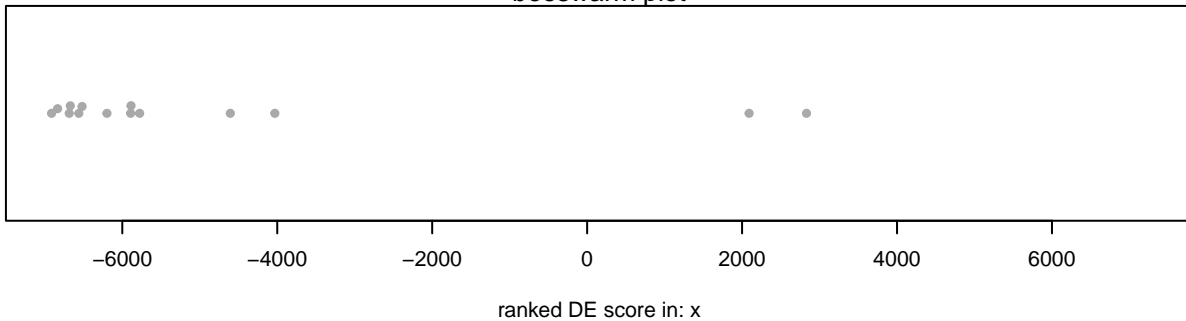


rugplot

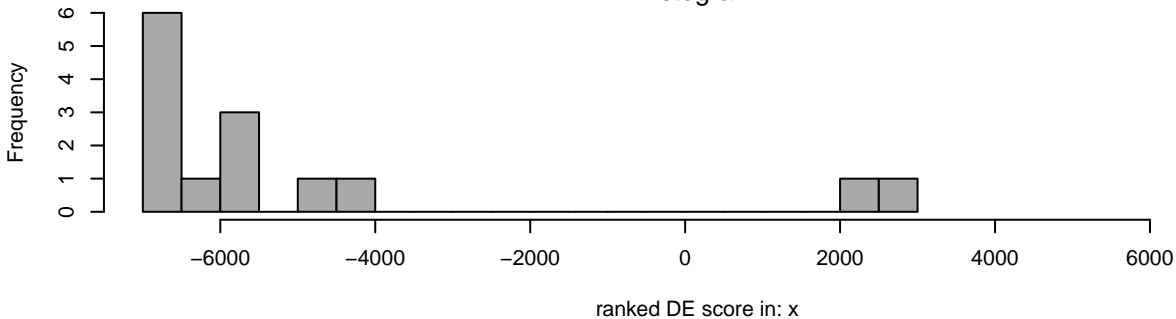


# Leading Strand Synthesis

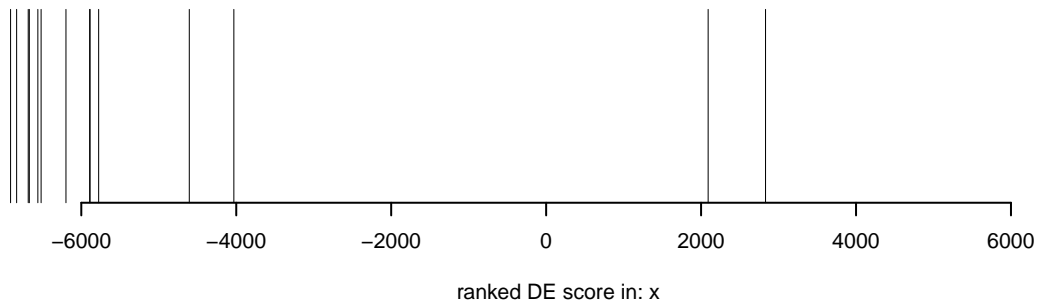
beeswarm plot



histogram

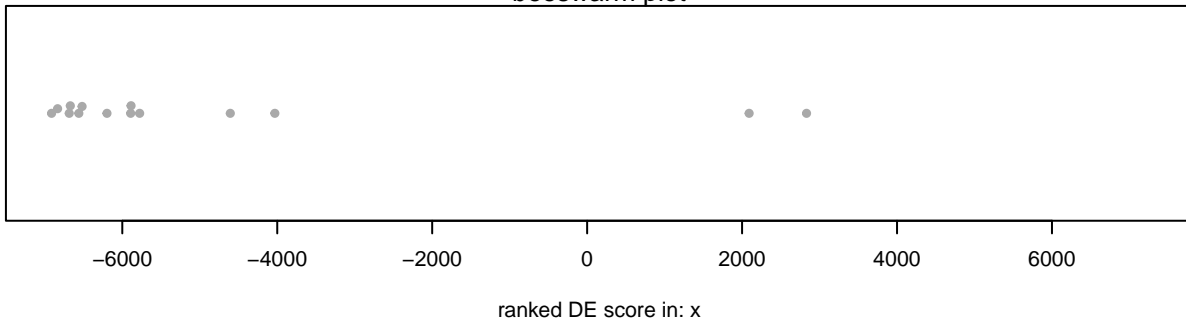


rugplot

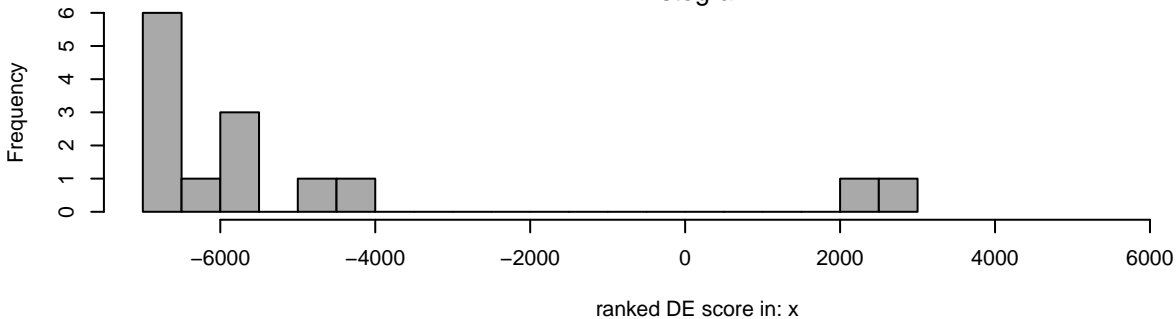


# Polymerase switching

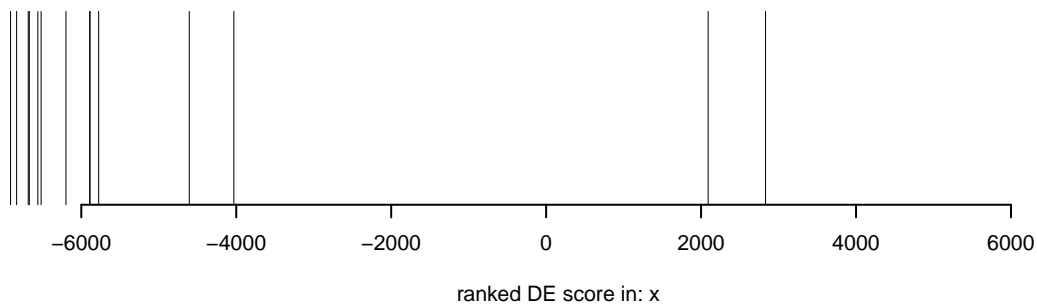
beeswarm plot



histogram

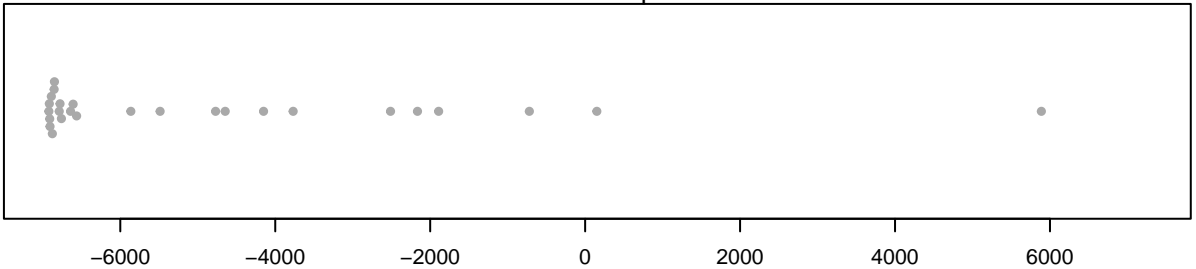


rugplot



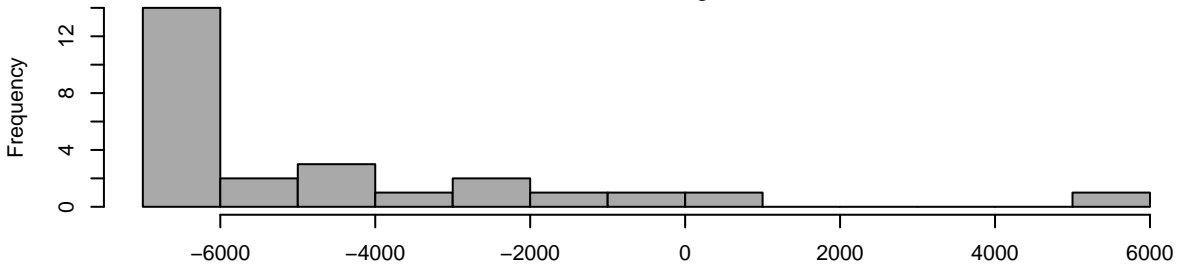
# Cholesterol biosynthesis

beeswarm plot



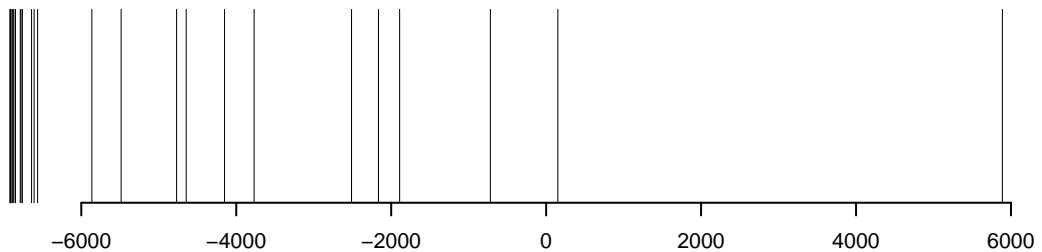
ranked DE score in: x

histogram



ranked DE score in: x

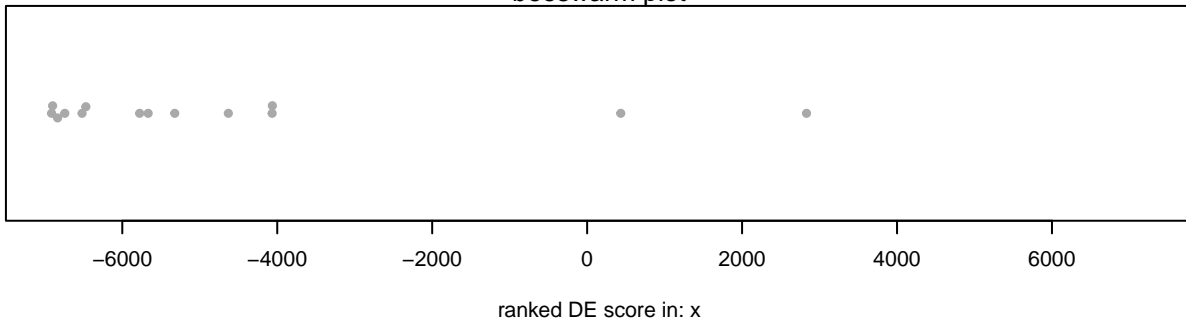
rugplot



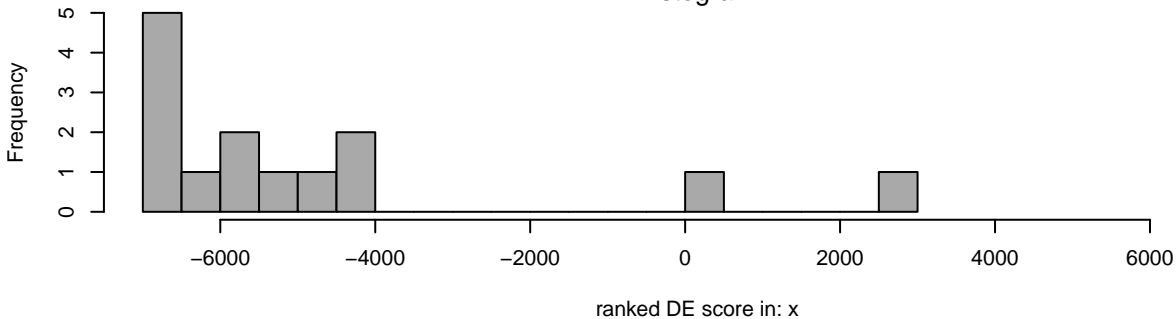
ranked DE score in: x

# Mismatch repair (MMR) directed by MSH2:MSH6 (MutSalpha)

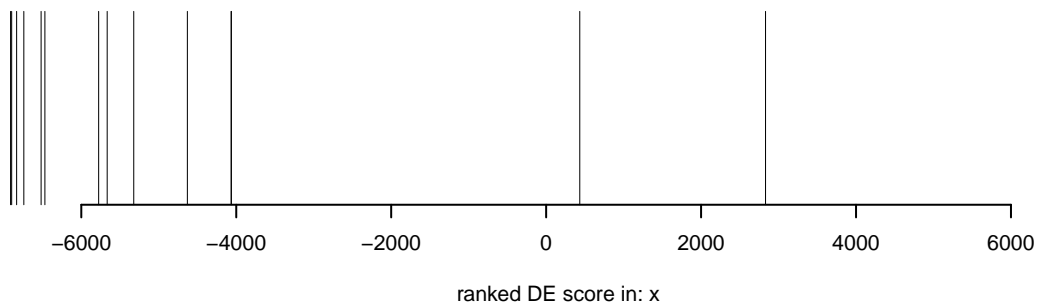
beeswarm plot



histogram

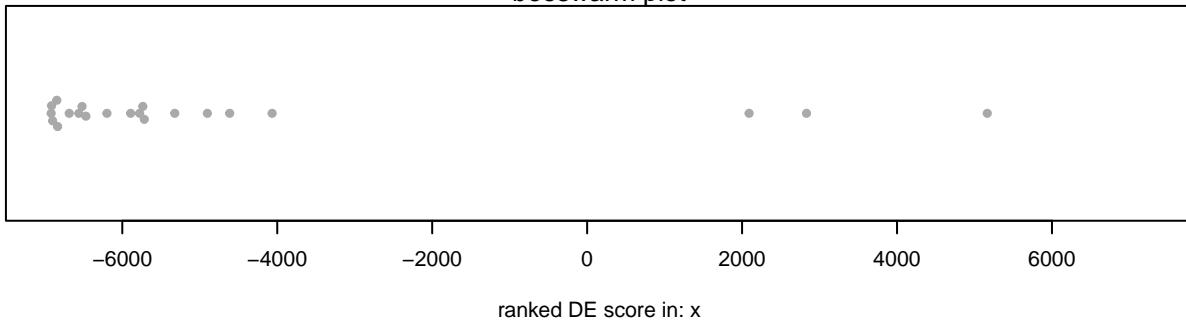


rugplot

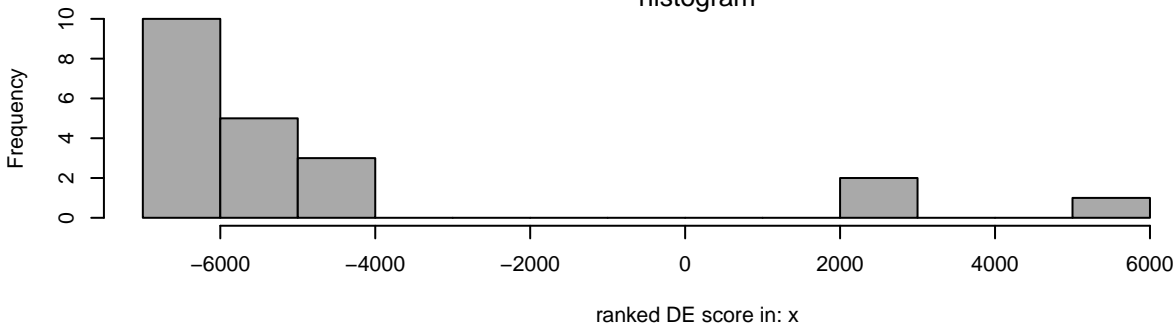


# PCNA-Dependent Long Patch Base Excision Repair

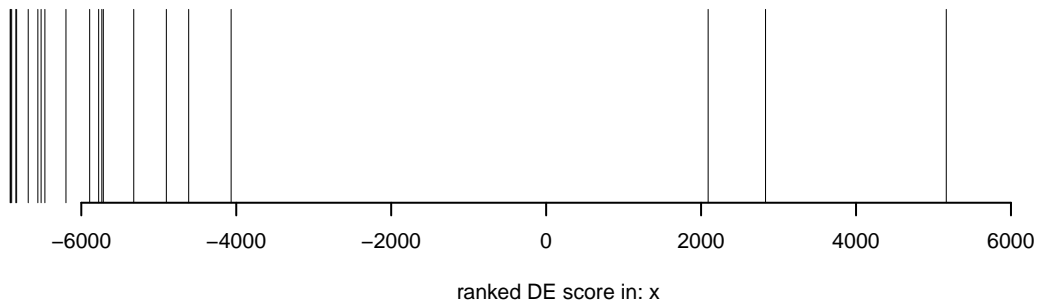
beeswarm plot



histogram

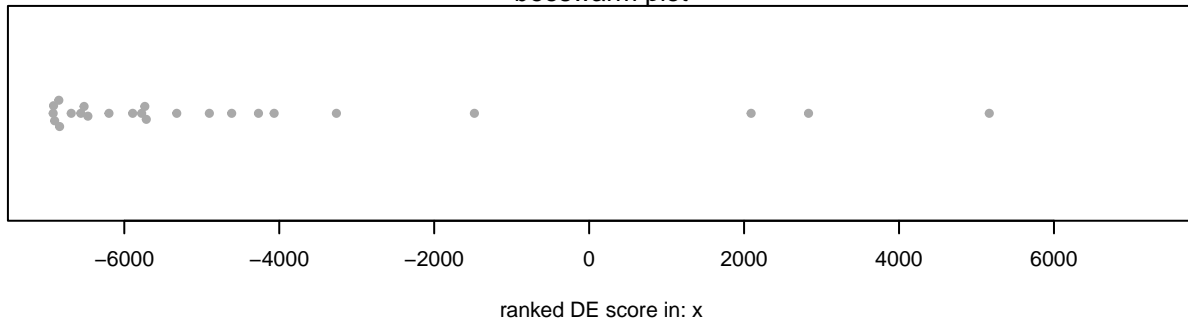


rugplot

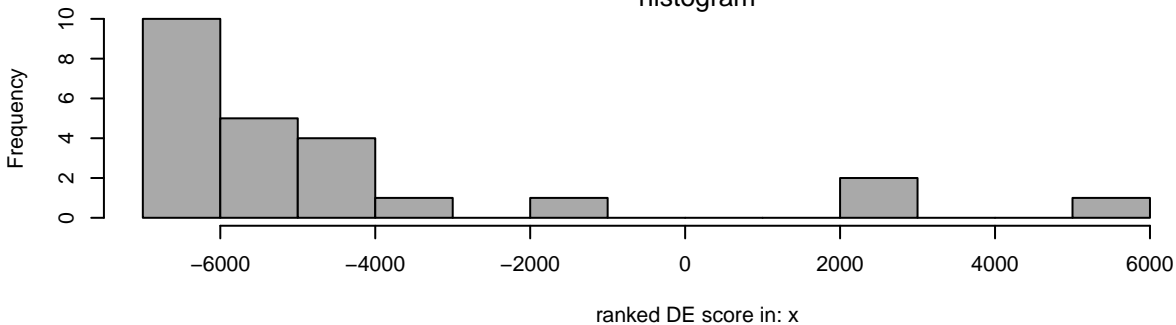


# Resolution of AP sites via the multiple-nucleotide patch replacement pathway

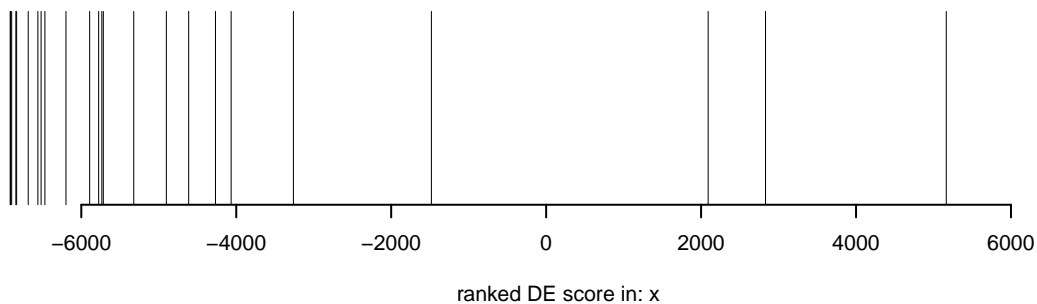
beeswarm plot



histogram

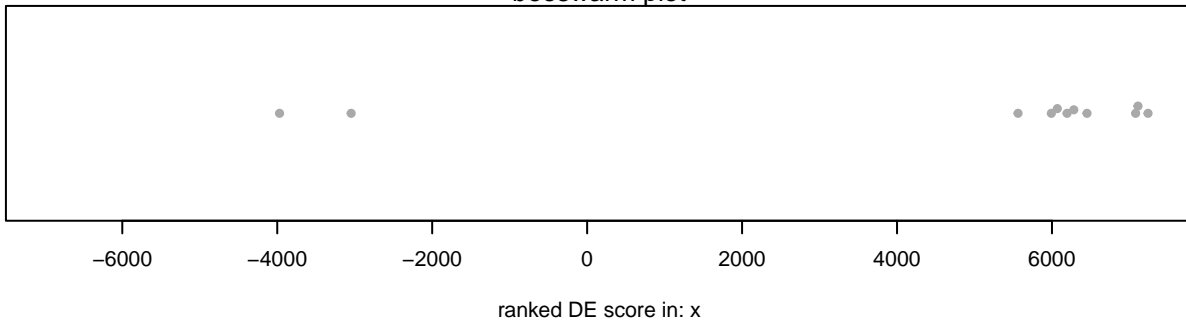


rugplot

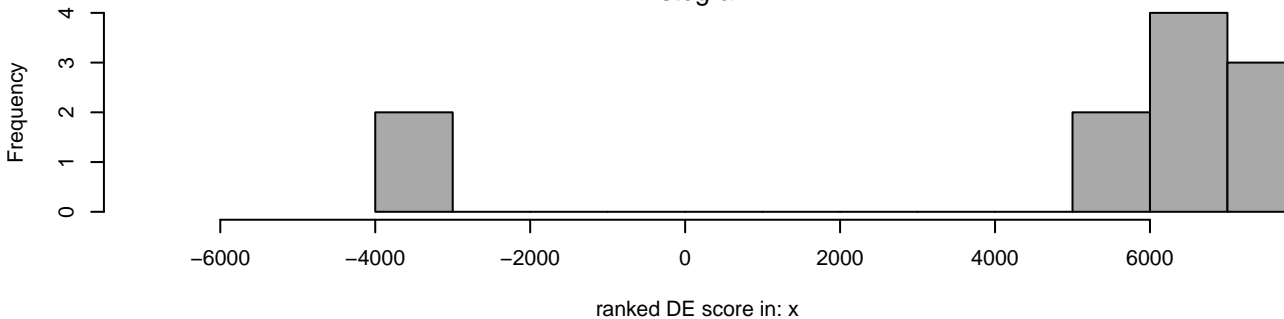


# GRB2 events in EGFR signaling

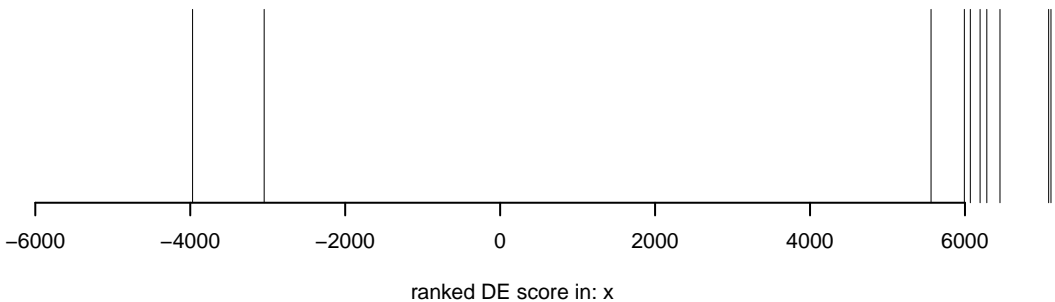
beeswarm plot



histogram



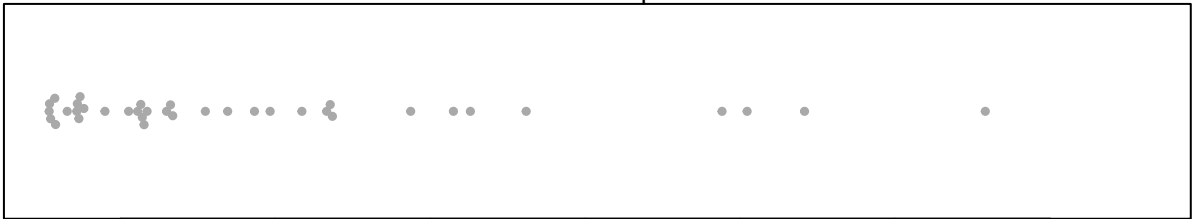
rugplot





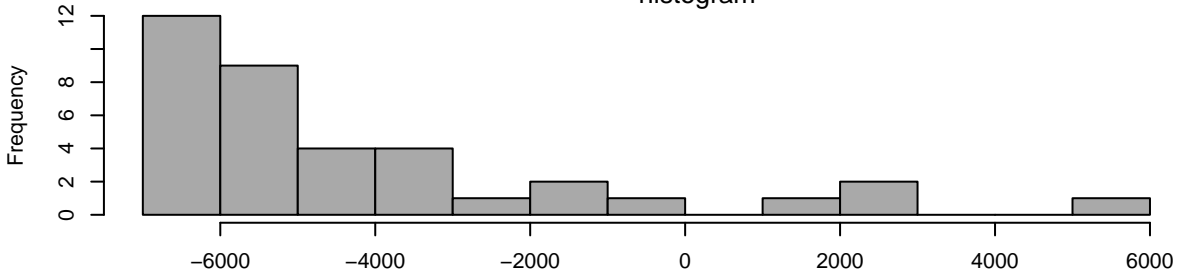
# Resolution of Abasic Sites (AP sites)

beeswarm plot



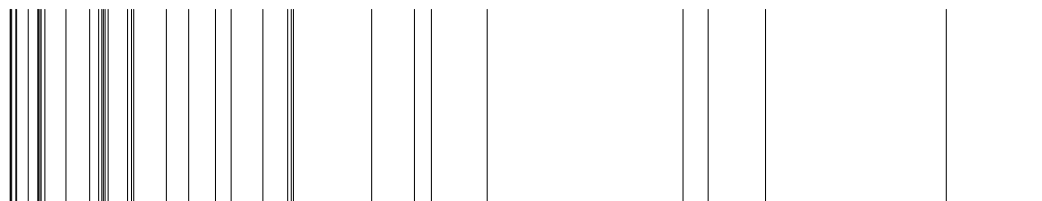
ranked DE score in: x

histogram



ranked DE score in: x

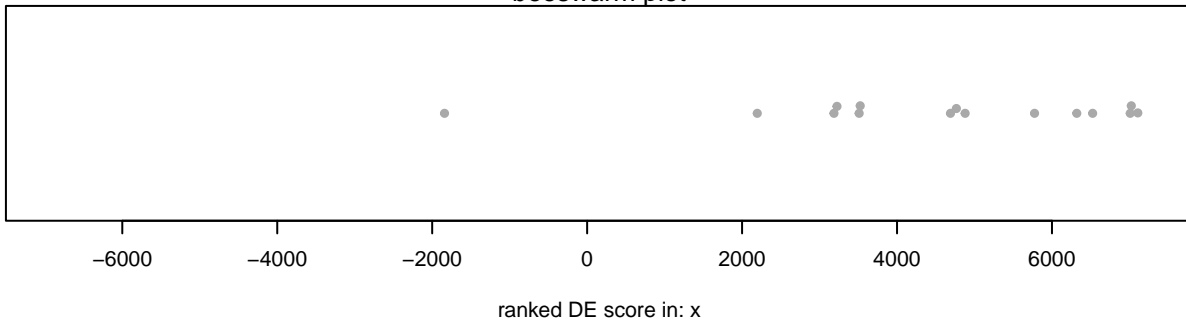
rugplot



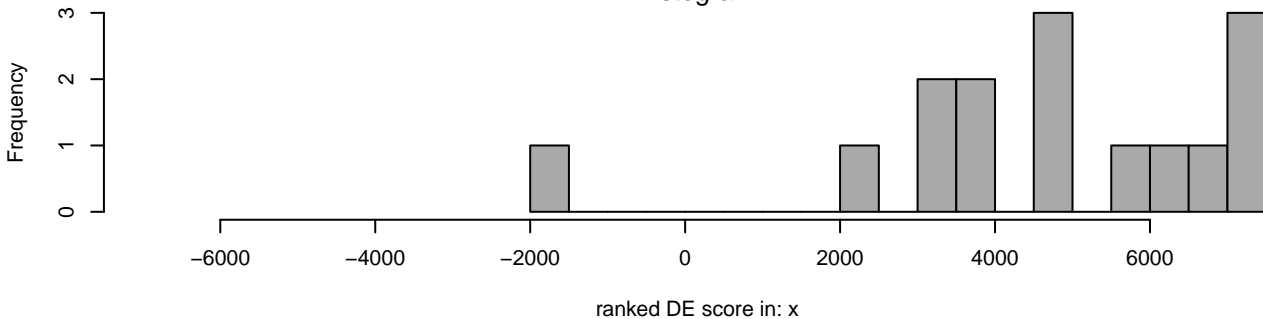
ranked DE score in: x

# FOXO-mediated transcription of cell cycle genes

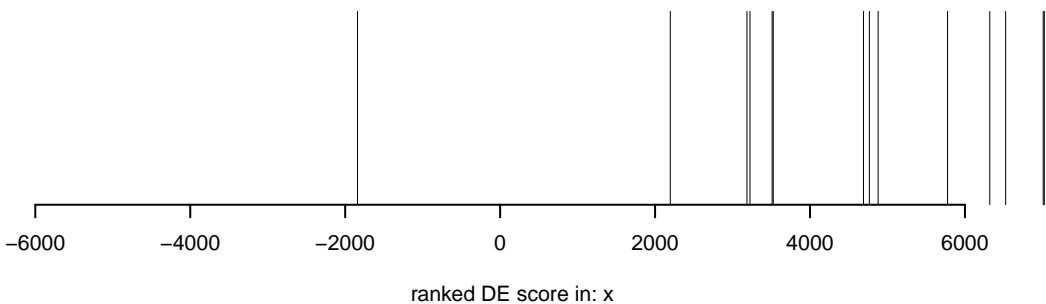
beeswarm plot



histogram

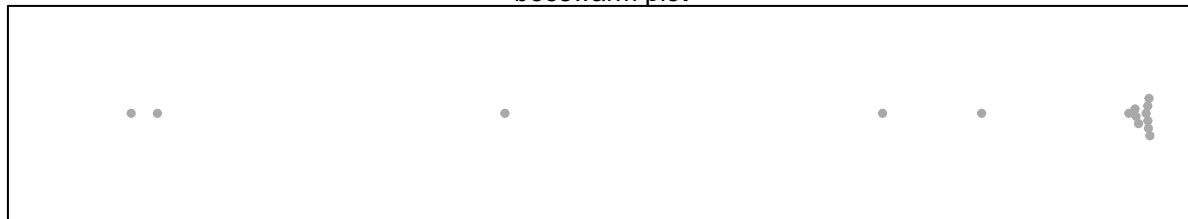


rugplot



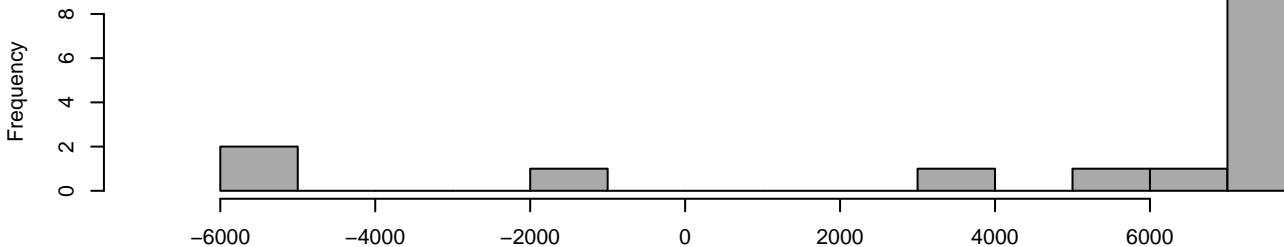
# Response of EIF2AK1 (HRI) to heme deficiency

beeswarm plot



ranked DE score in: x

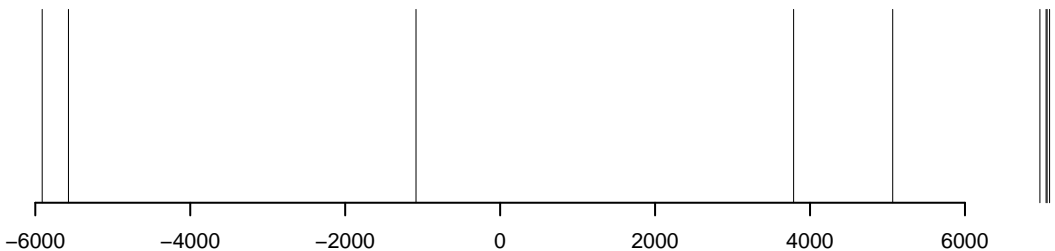
histogram



Frequency

ranked DE score in: x

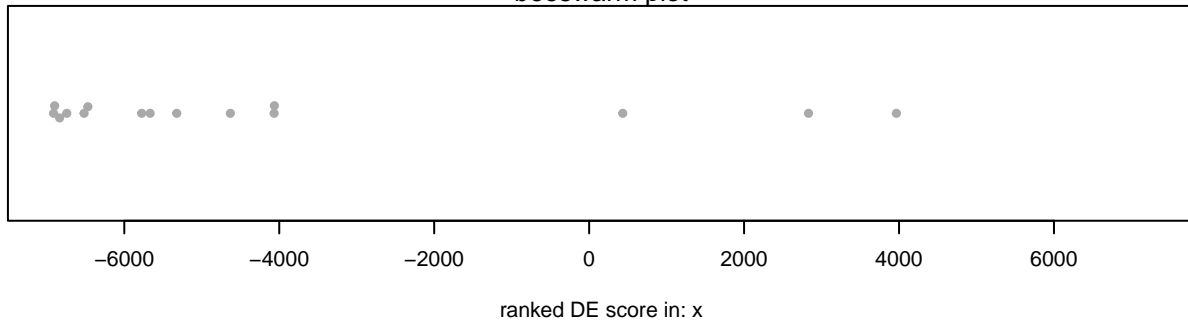
rugplot



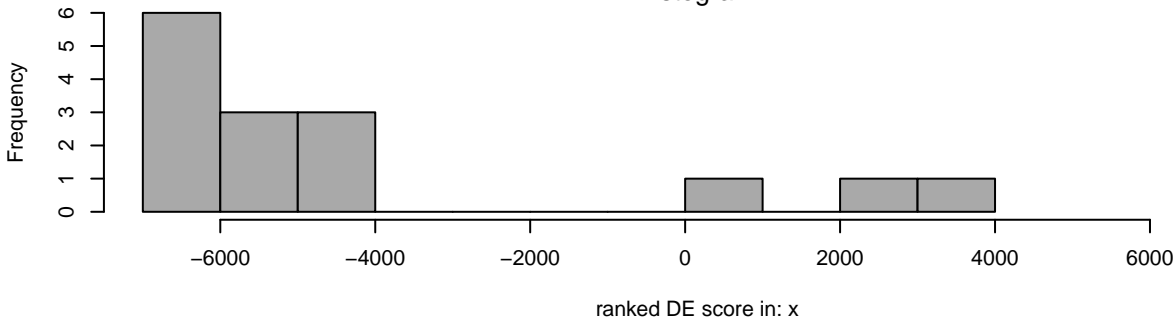
ranked DE score in: x

# Mismatch Repair

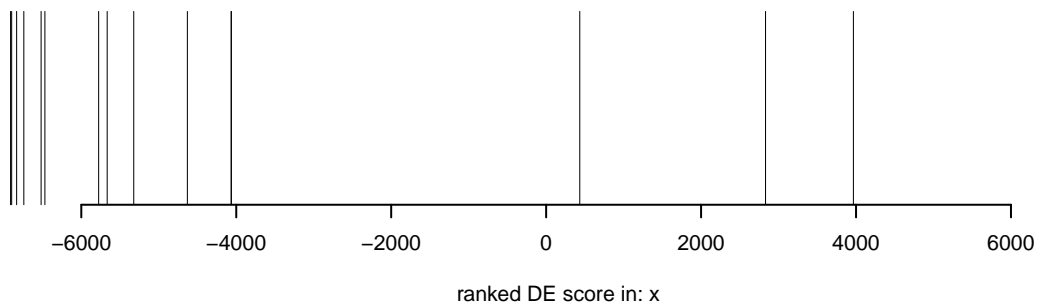
beeswarm plot



histogram

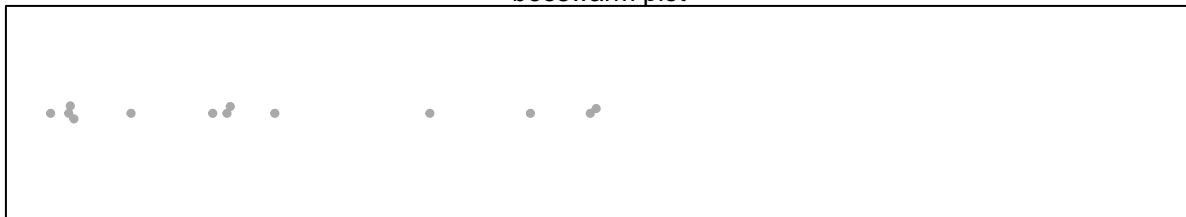


rugplot



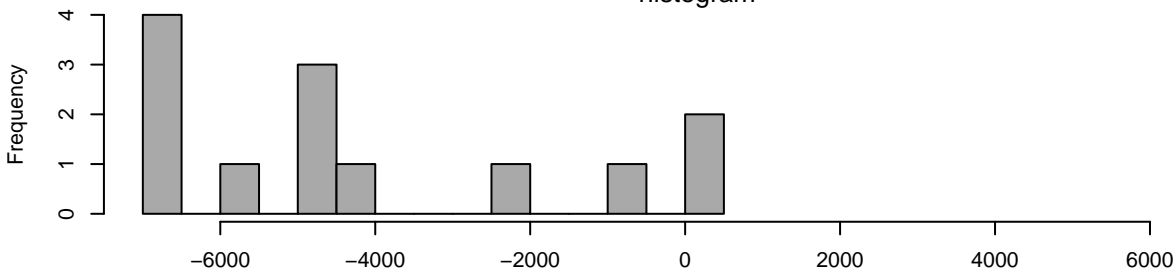
# Defective pyroptosis

beeswarm plot



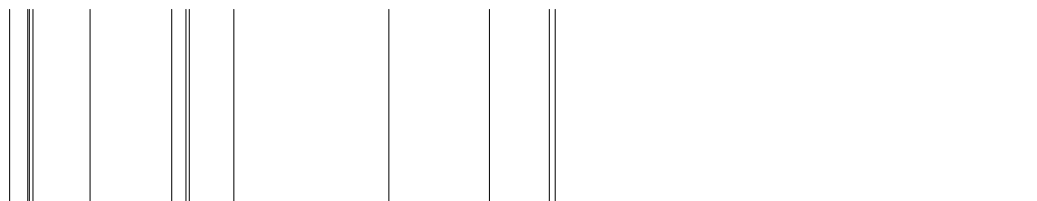
ranked DE score in: x

histogram



ranked DE score in: x

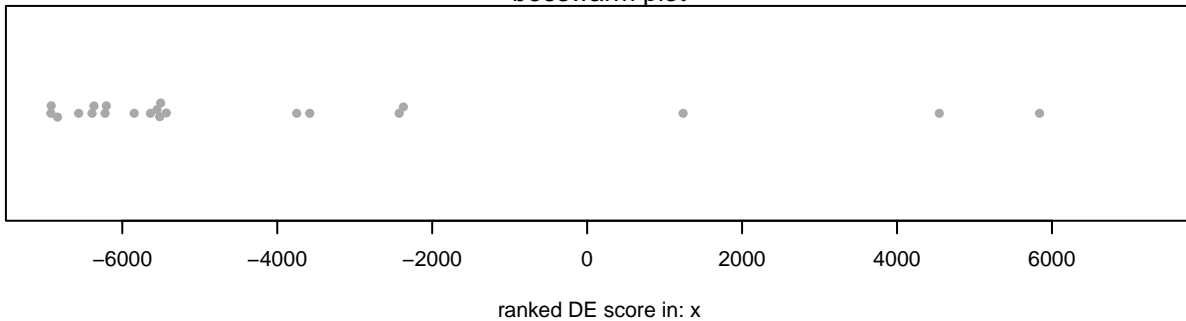
rugplot



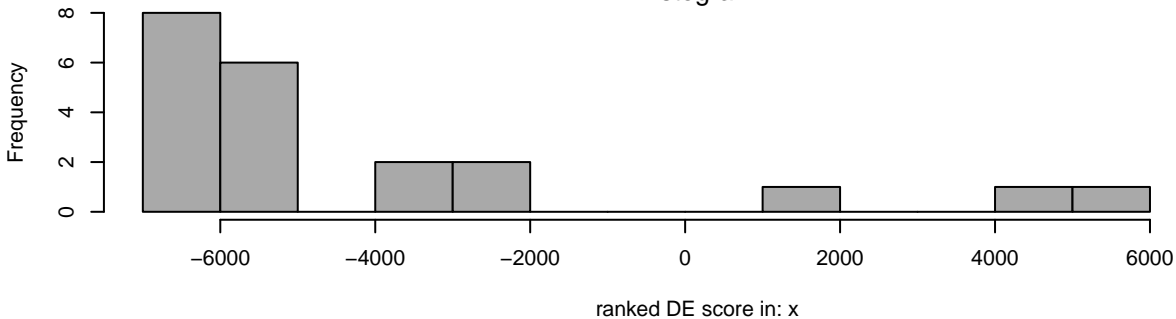
ranked DE score in: x

# Formation of tubulin folding intermediates by CCT/TriC

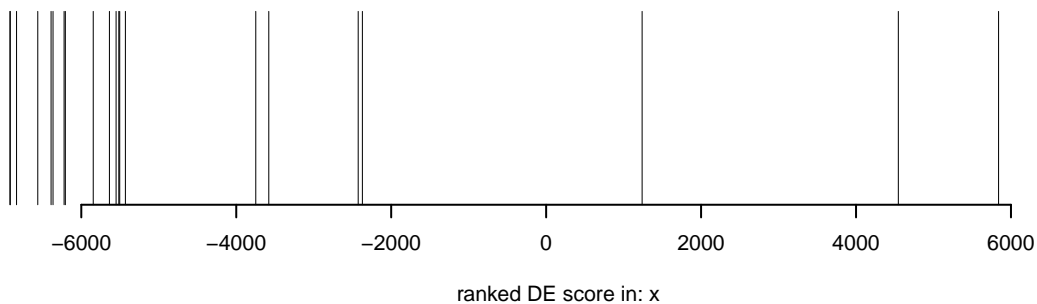
beeswarm plot



histogram

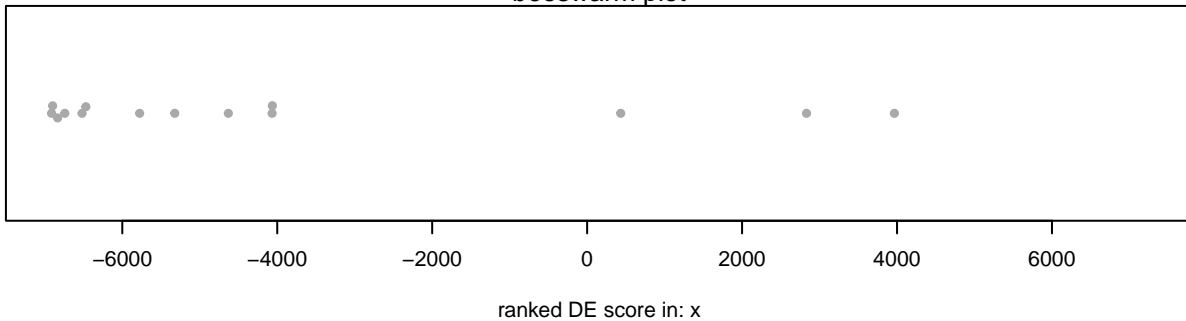


rugplot

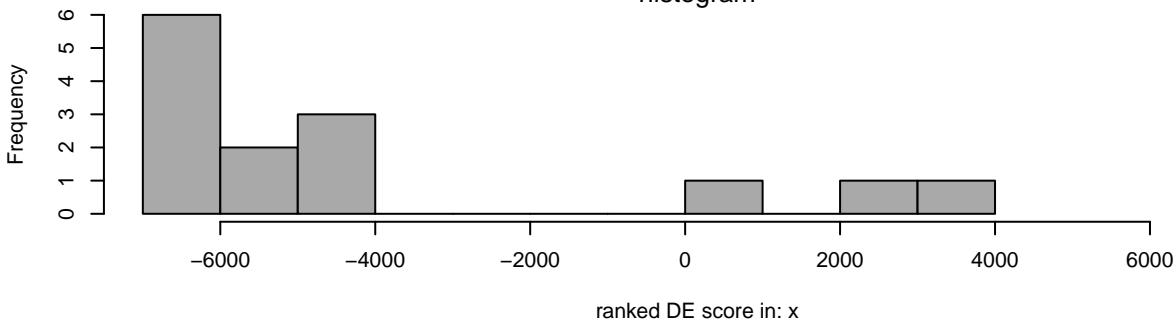


# Mismatch repair (MMR) directed by MSH2:MSH3 (MutSbeta)

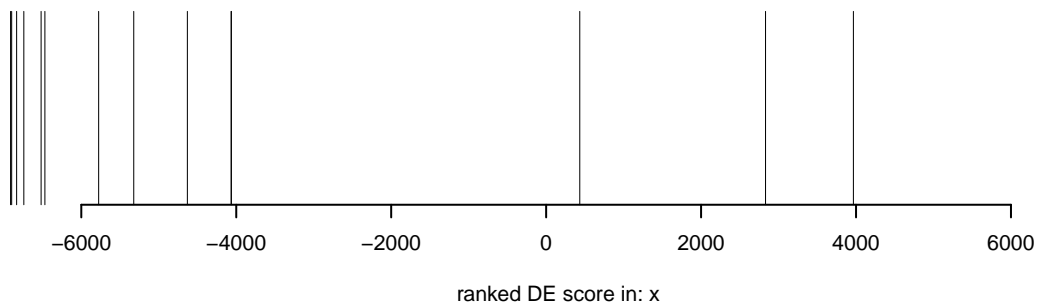
beeswarm plot



histogram

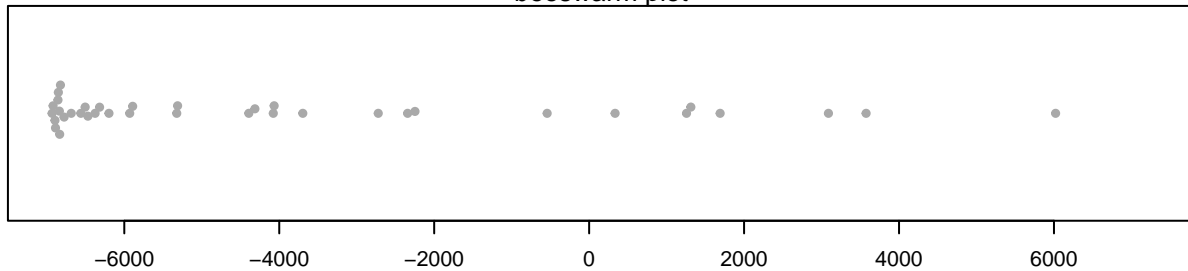


rugplot



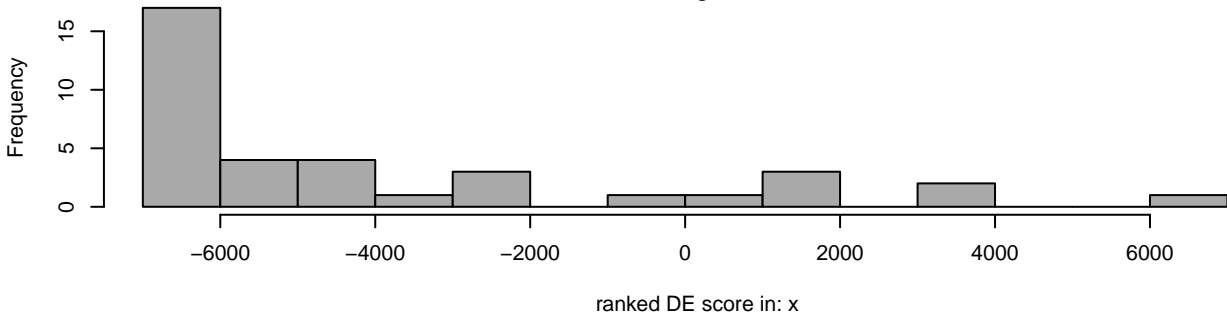
# Activation of ATR in response to replication stress

beeswarm plot



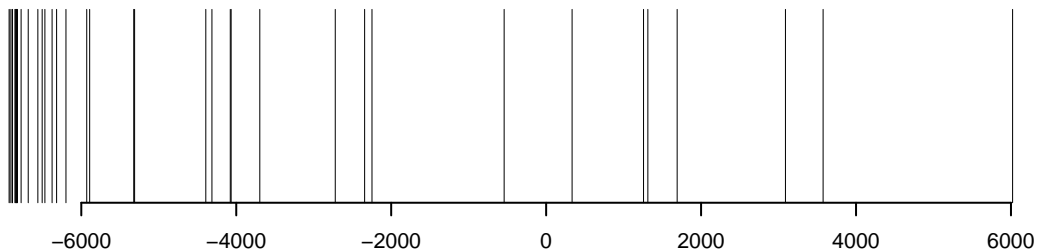
ranked DE score in: x

histogram



ranked DE score in: x

rugplot

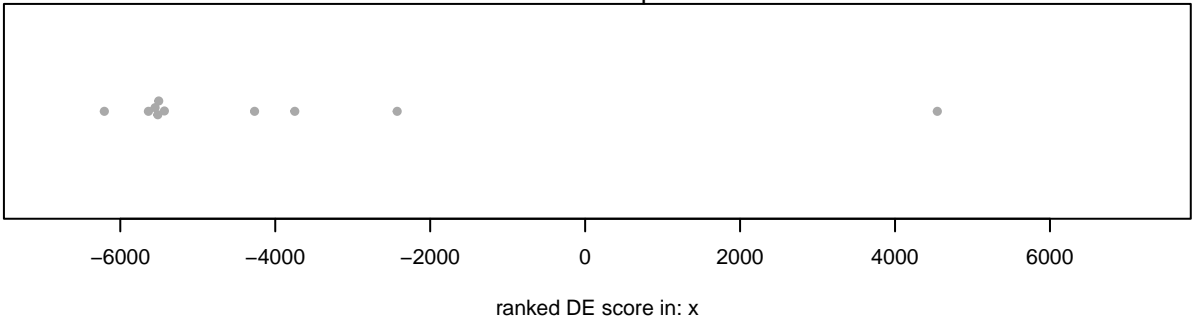


ranked DE score in: x

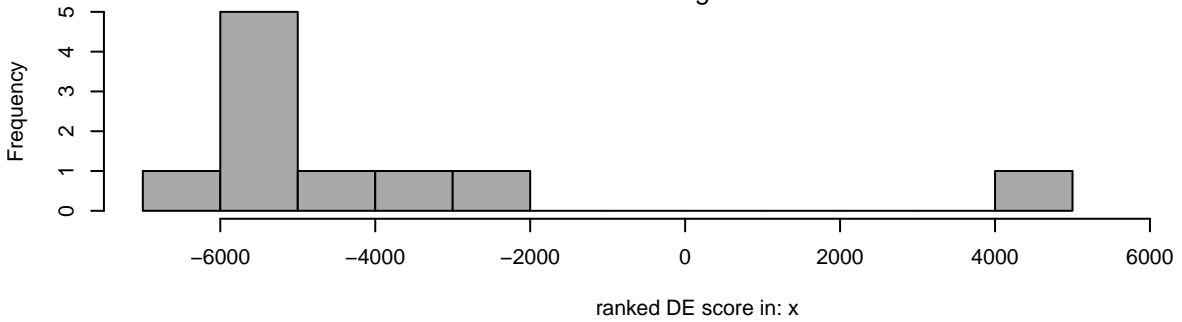


# Folding of actin by CCT/TriC

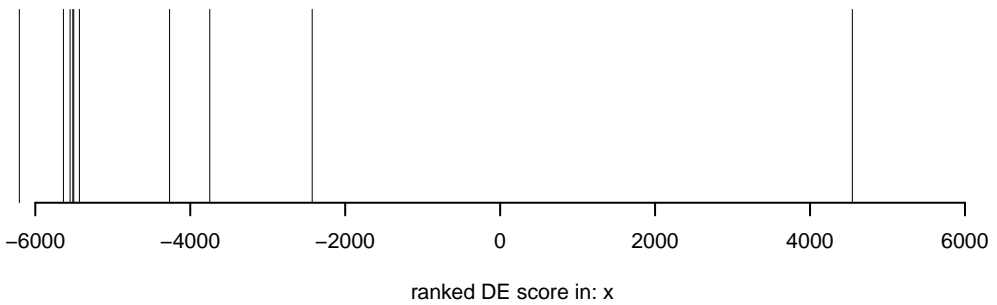
beeswarm plot



histogram

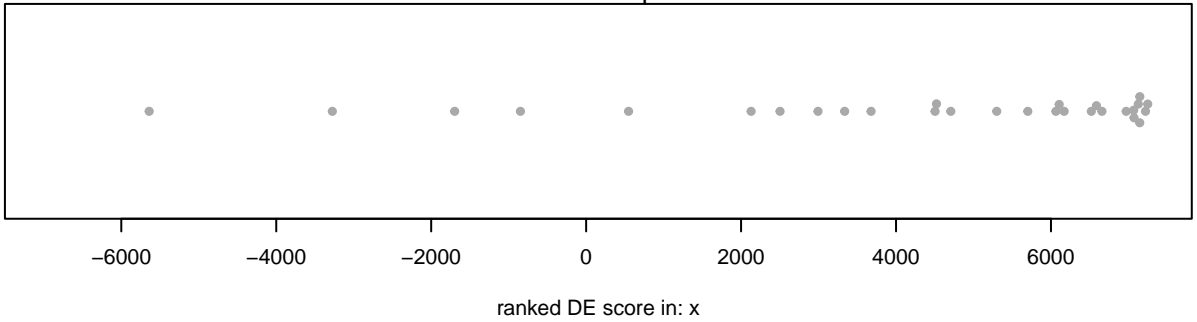


rugplot

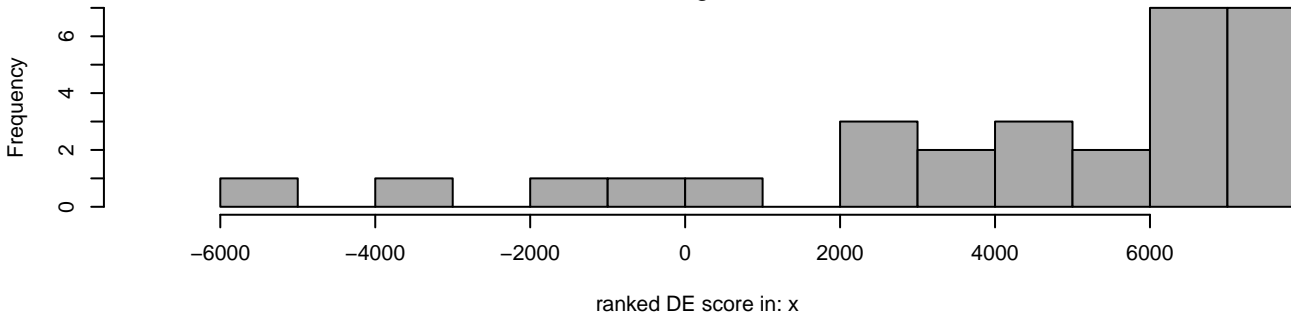


# Laminin interactions

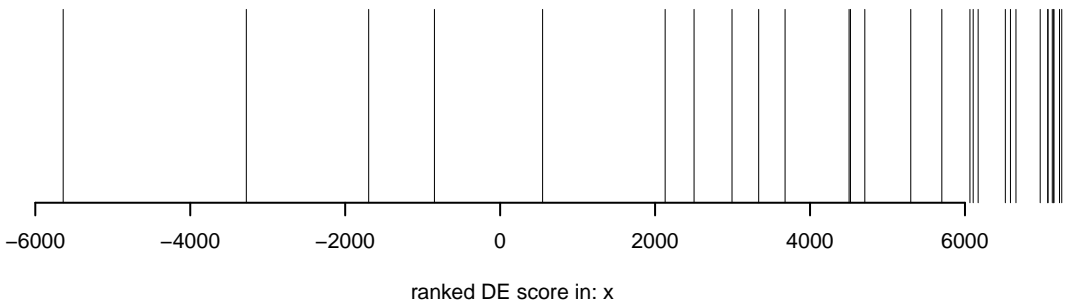
beeswarm plot



histogram

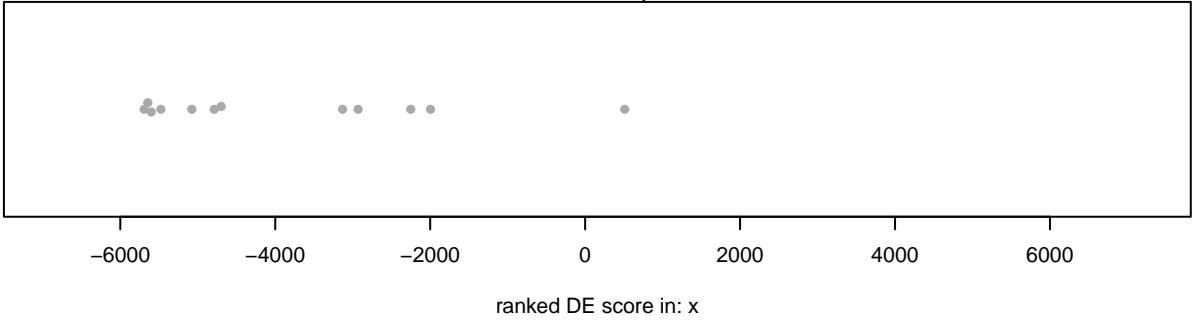


rugplot

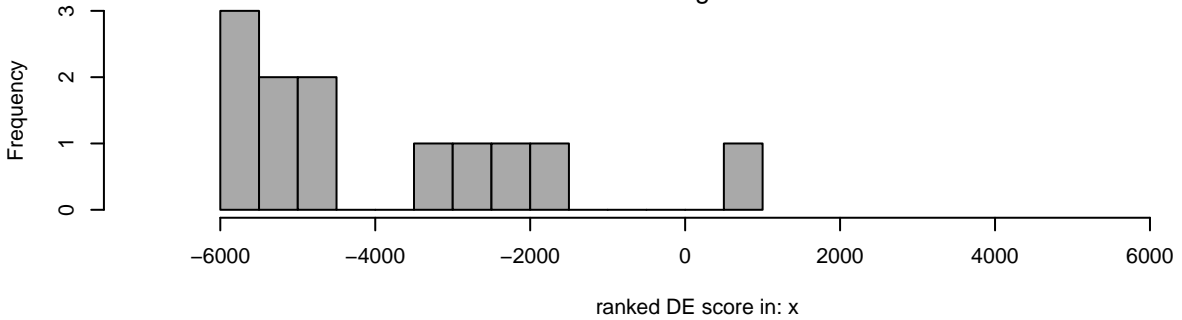


# Heme biosynthesis

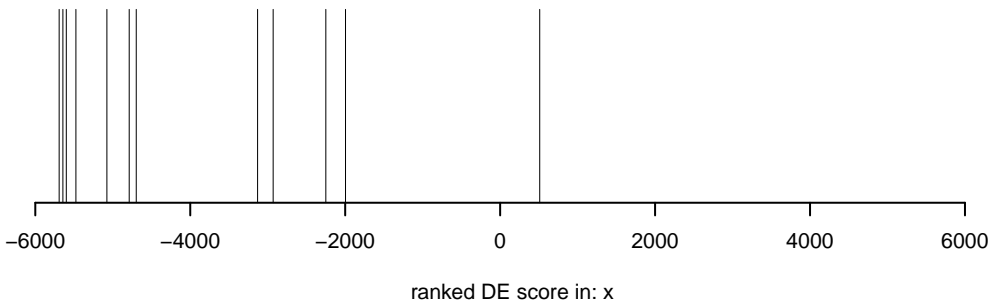
beeswarm plot



histogram

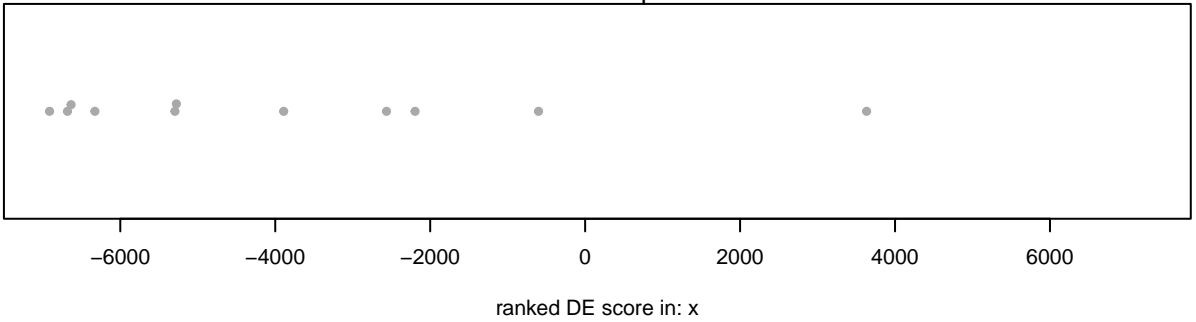


rugplot

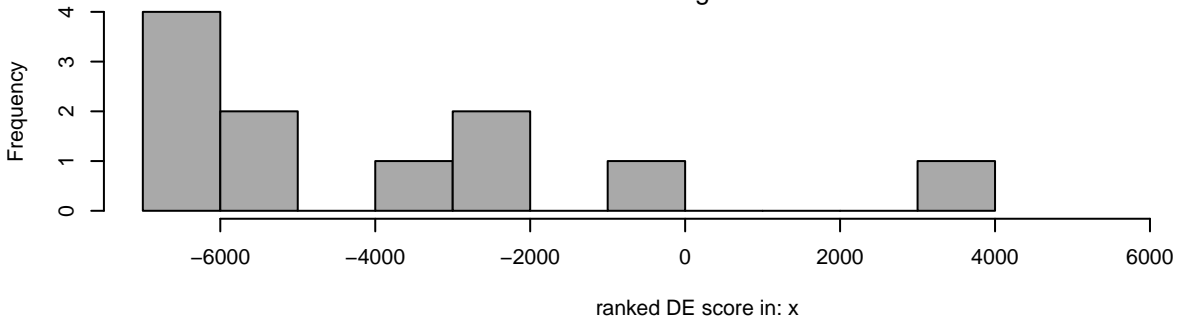


# Cytosolic iron-sulfur cluster assembly

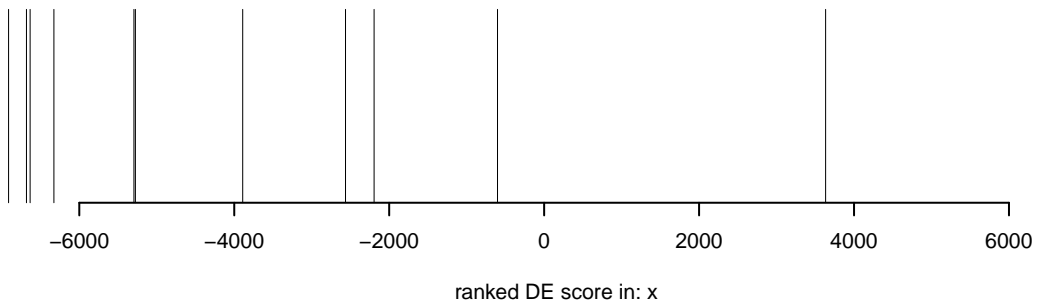
beeswarm plot



histogram

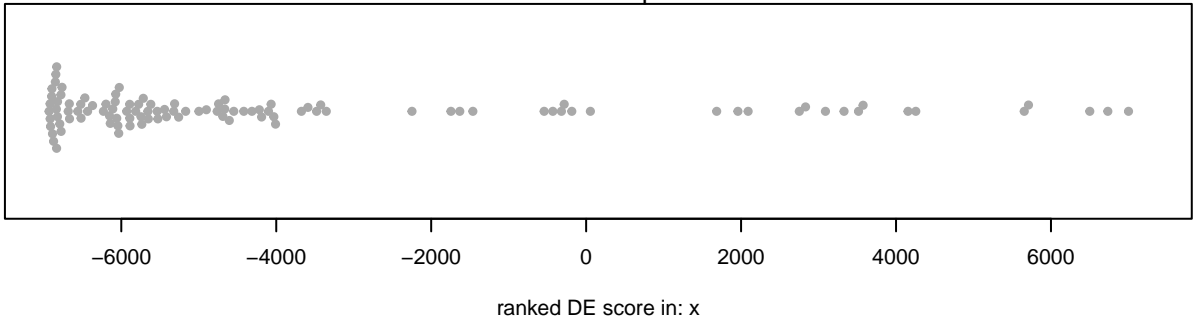


rugplot

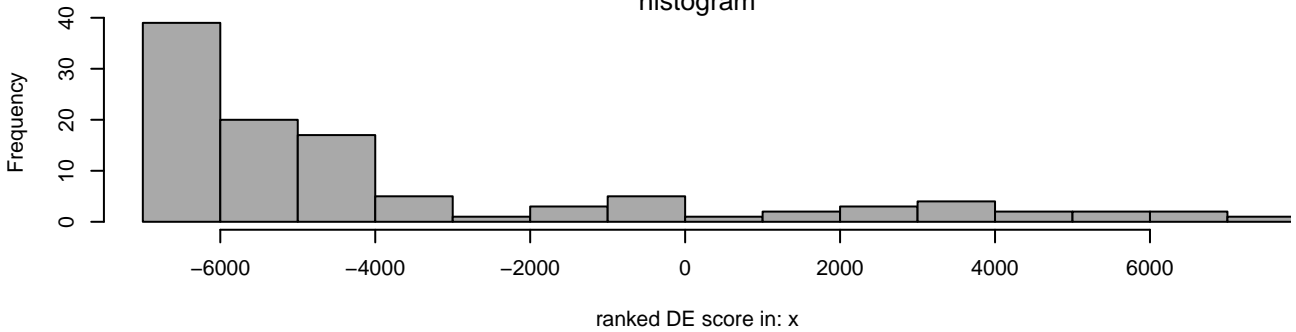


# Synthesis of DNA

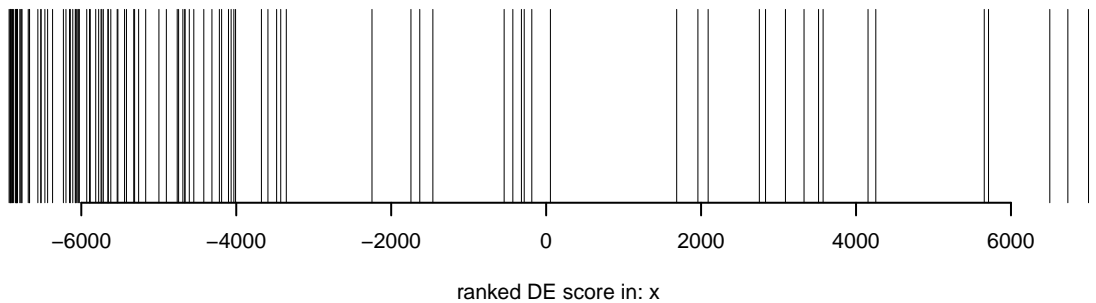
beeswarm plot



histogram

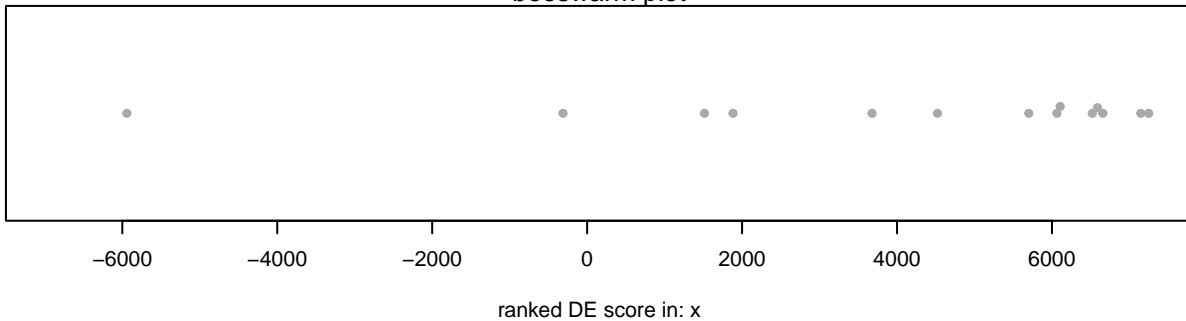


rugplot

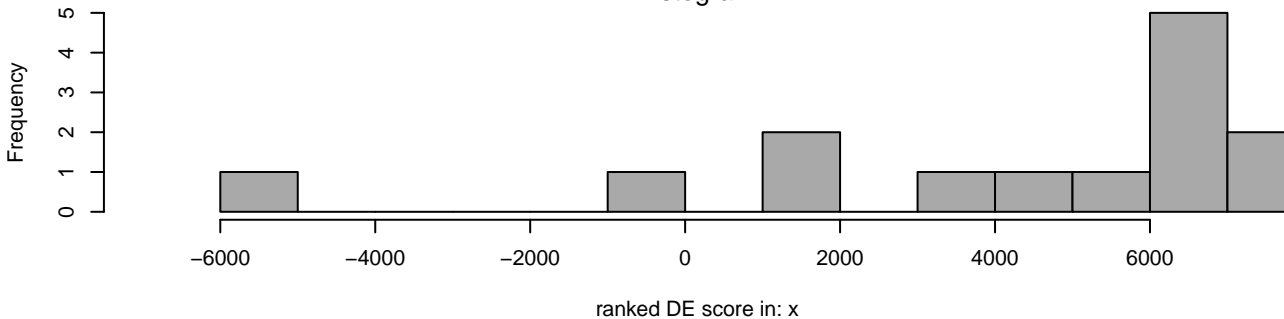


# Anchoring fibril formation

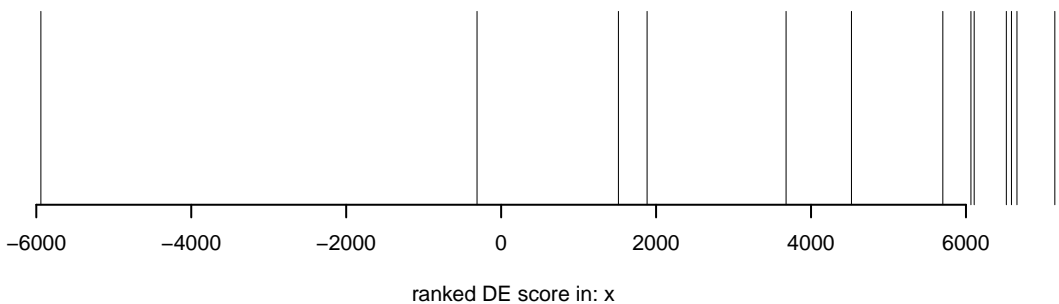
beeswarm plot



histogram

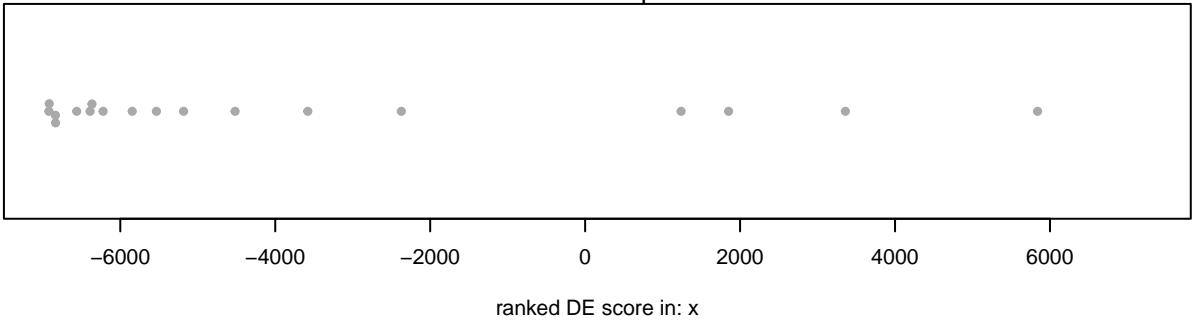


rugplot

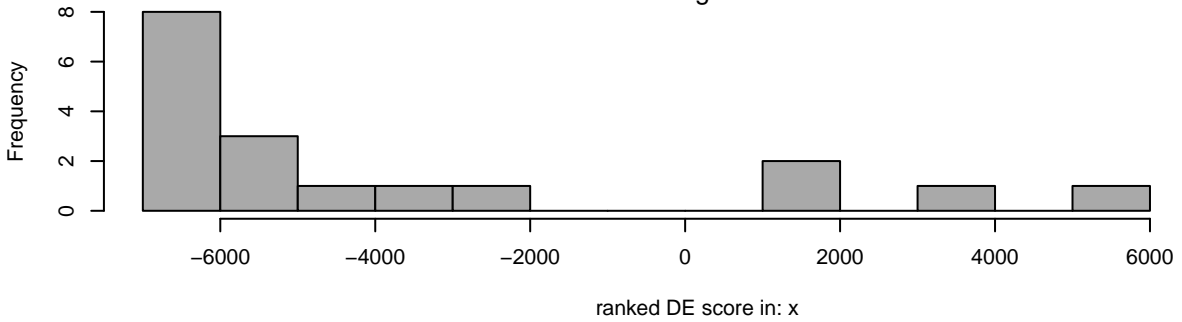


# Post-chaperonin tubulin folding pathway

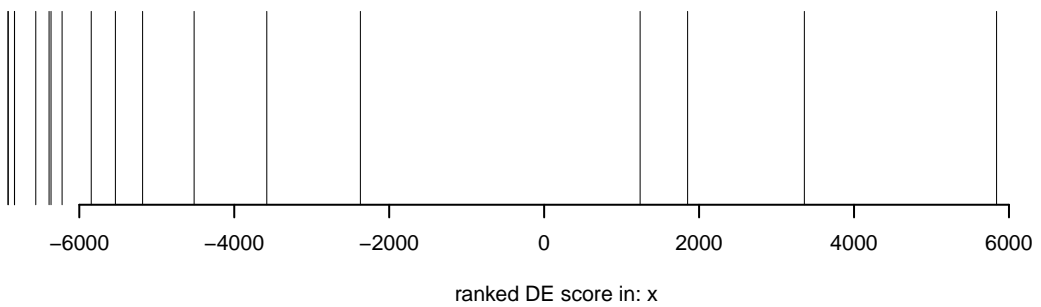
beeswarm plot



histogram

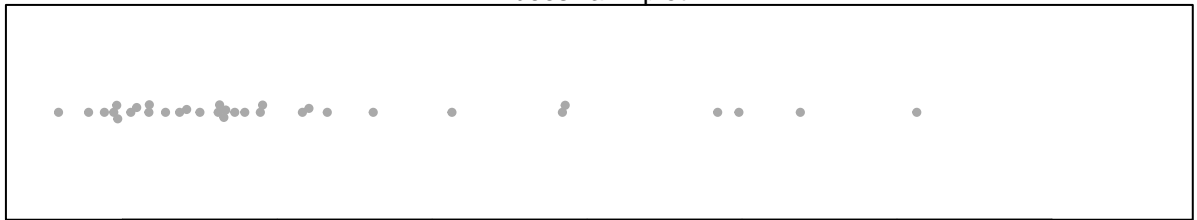


rugplot



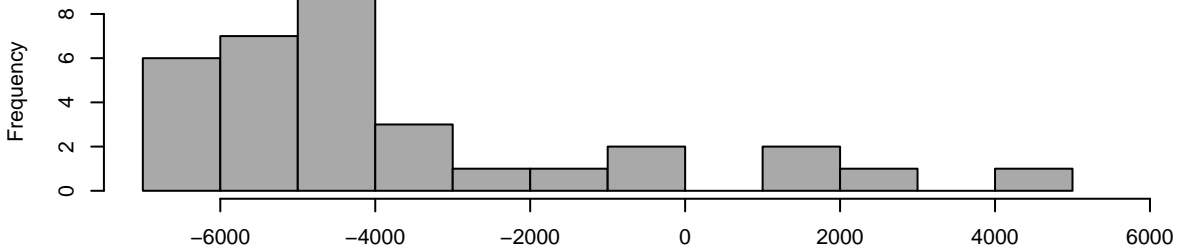
# Cross-presentation of soluble exogenous antigens (endosomes)

beeswarm plot



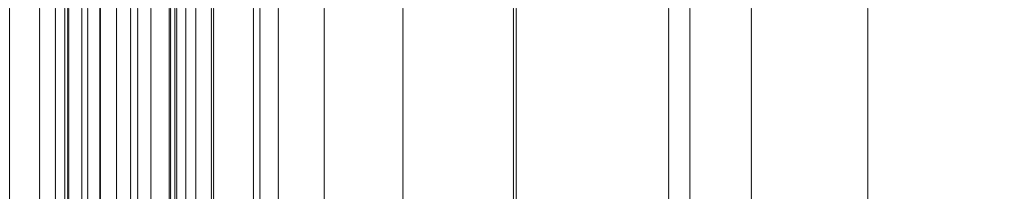
ranked DE score in: x

histogram



ranked DE score in: x

rugplot

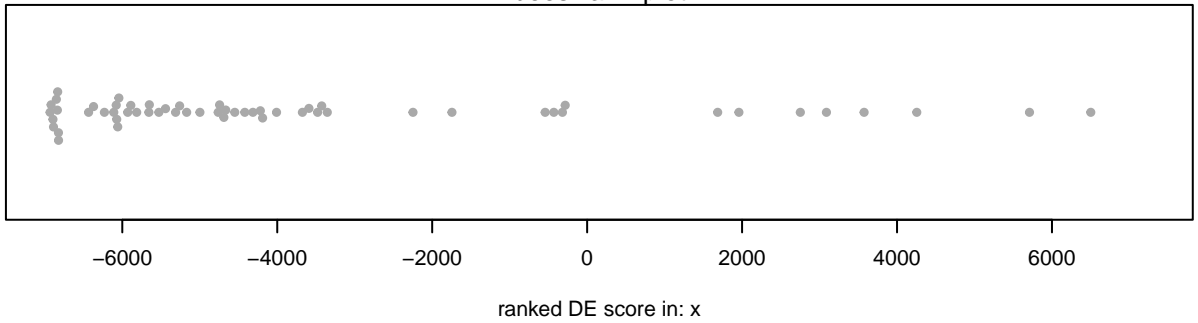


ranked DE score in: x

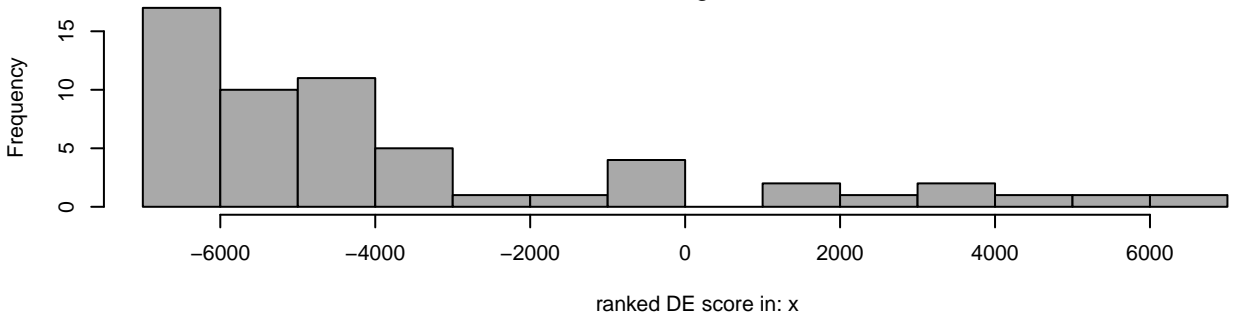


# Orc1 removal from chromatin

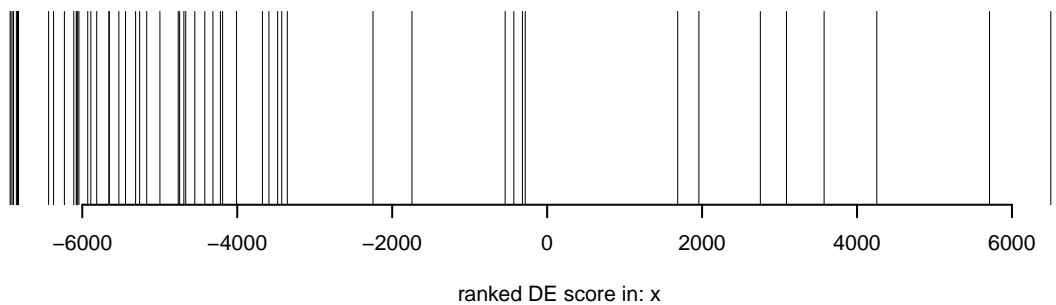
beeswarm plot



histogram

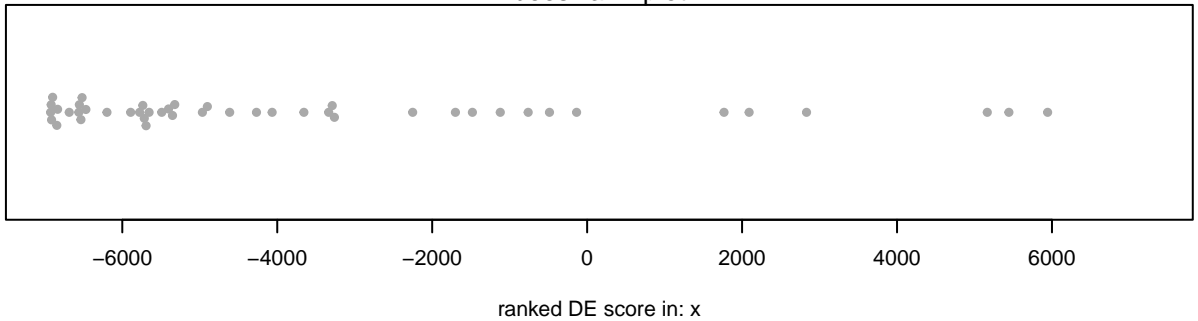


rugplot

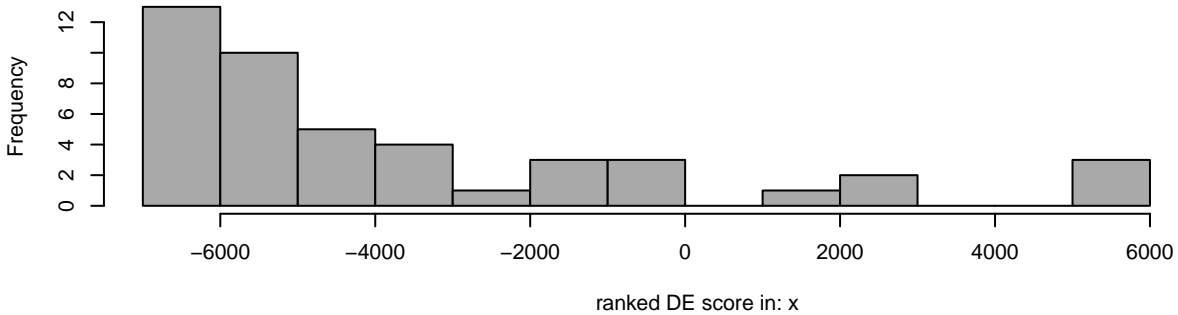


# Base Excision Repair

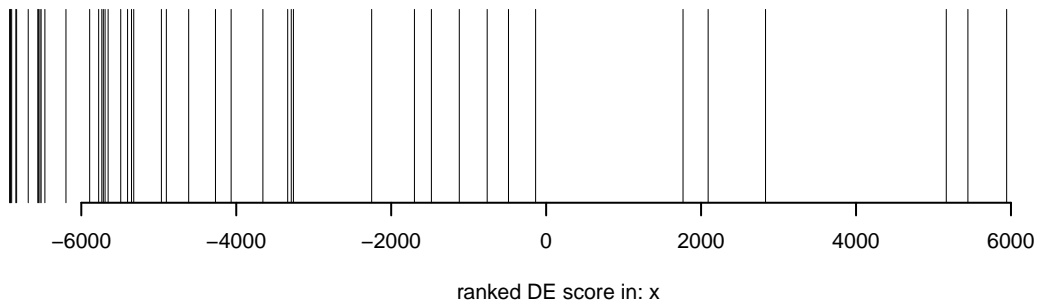
beeswarm plot



histogram

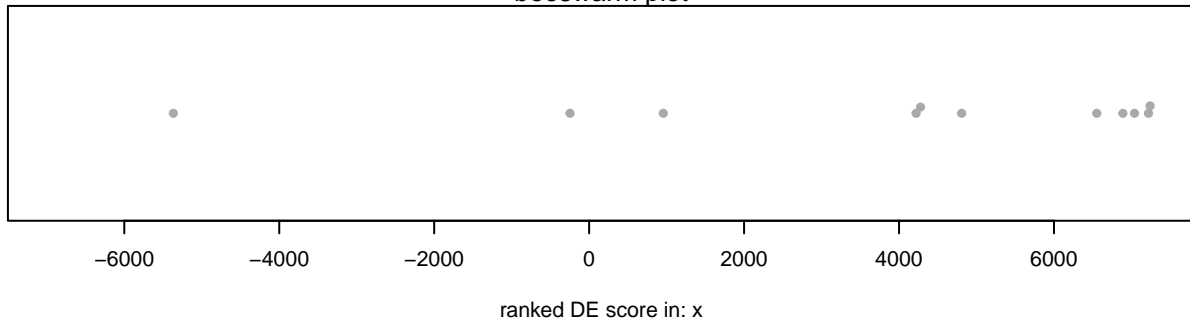


rugplot

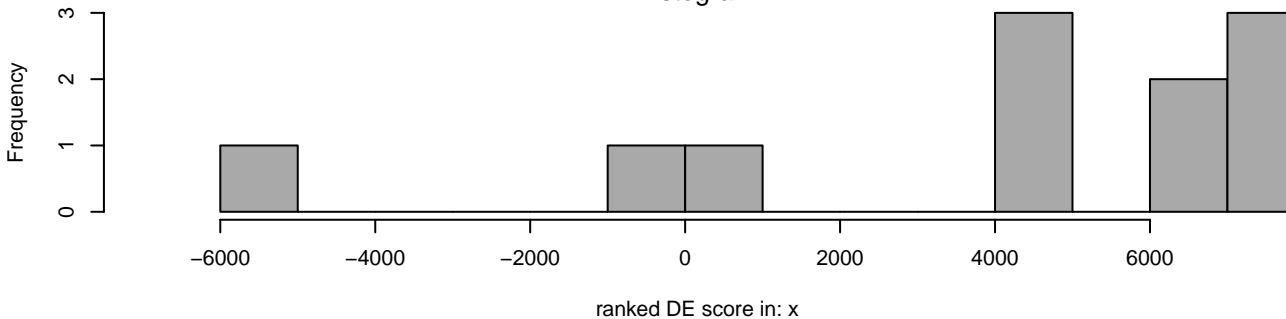


# -M-dependent genes involved in extracellular matrix, focal adhesion and epithelial-to-m

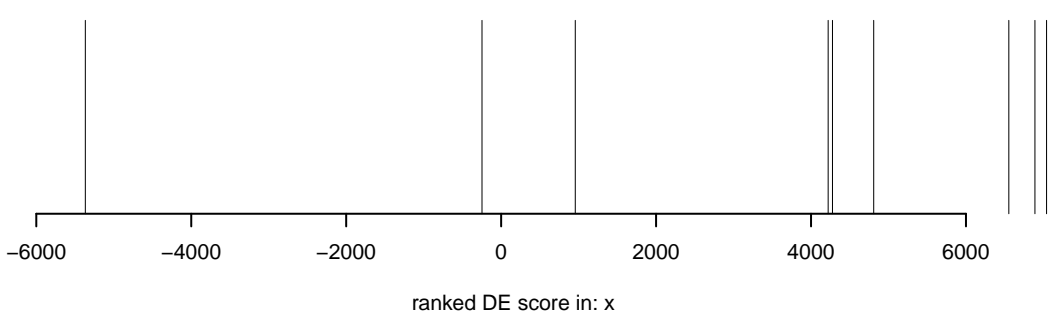
beeswarm plot



histogram

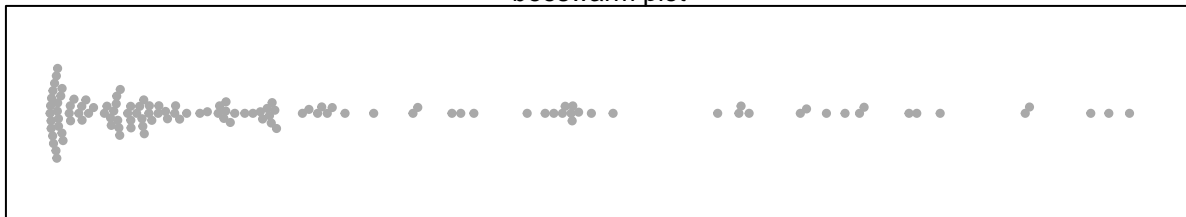


rugplot



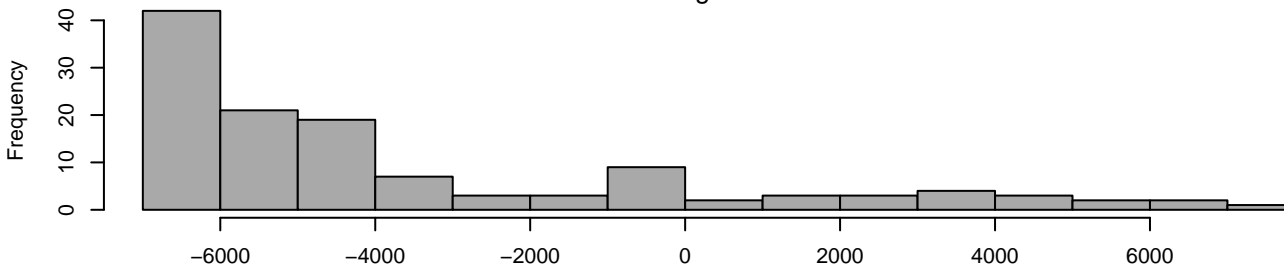
# DNA Replication

beeswarm plot



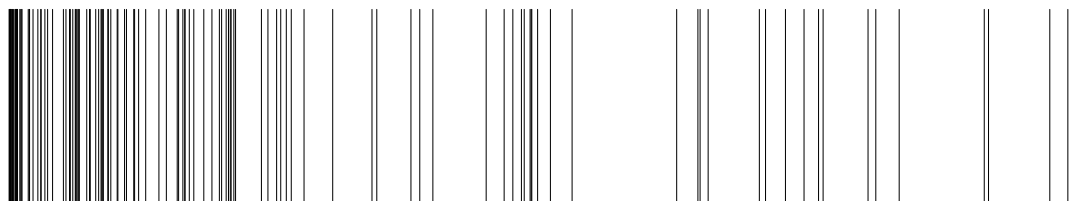
ranked DE score in: x

histogram



ranked DE score in: x

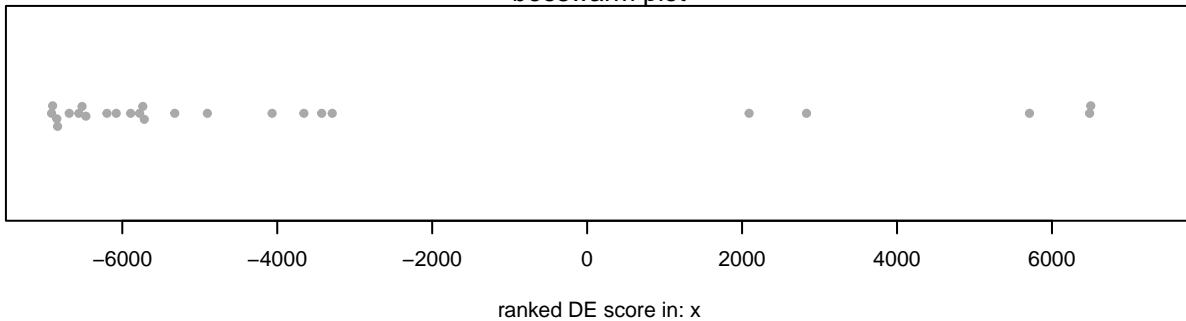
rugplot



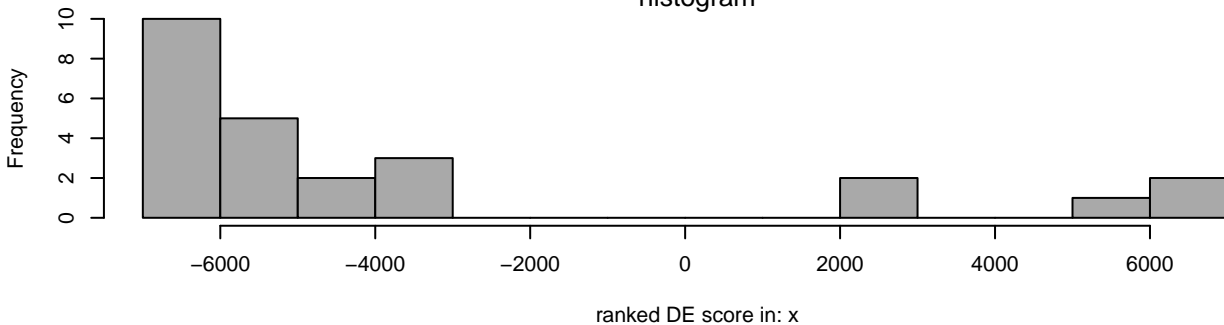
ranked DE score in: x

# Gap-filling DNA repair synthesis and ligation in GG-NER

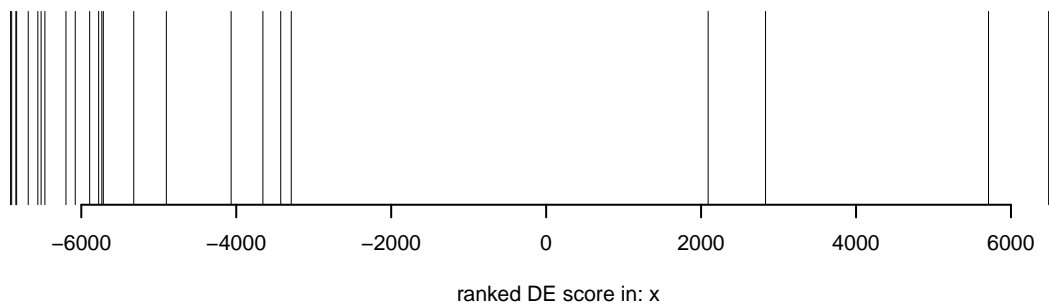
beeswarm plot



histogram

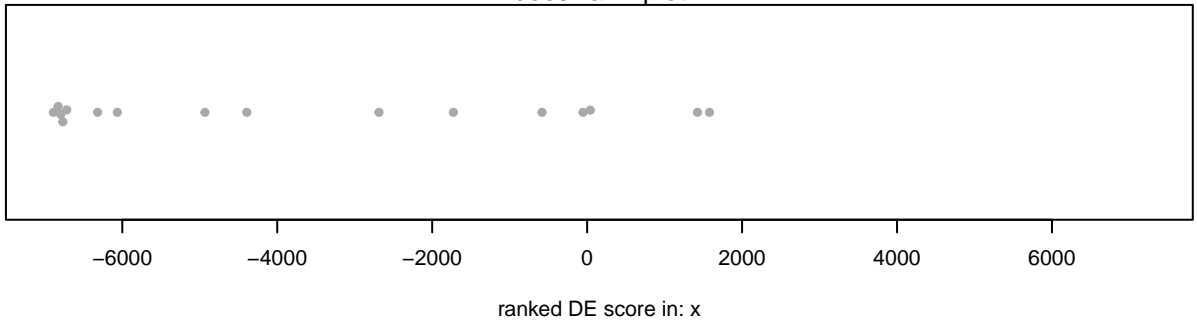


rugplot

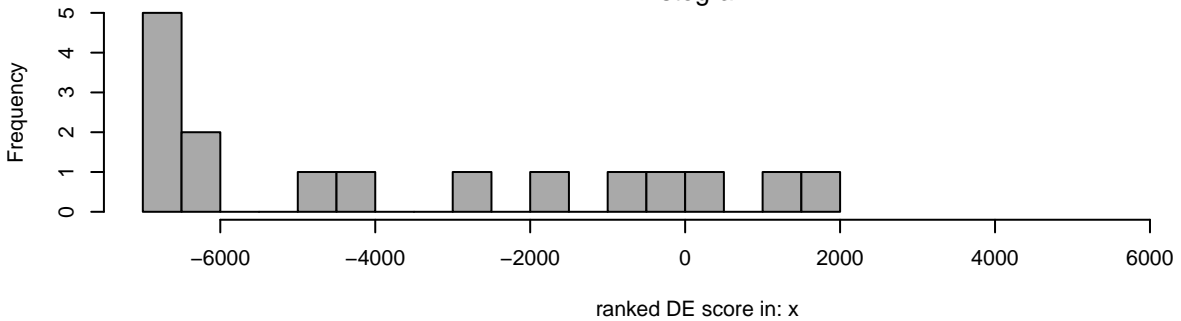


# Polo-like kinase mediated events

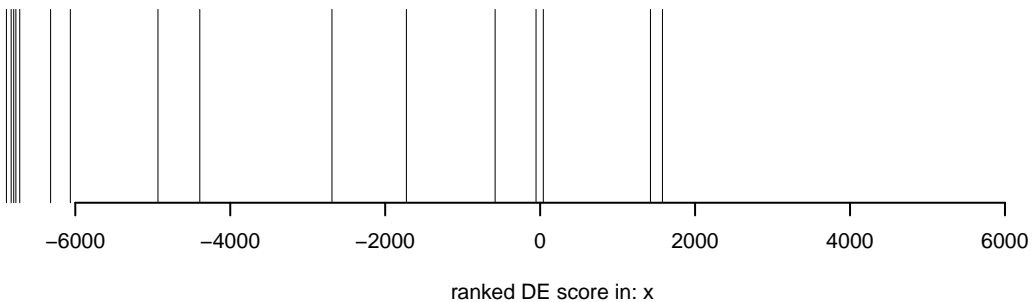
beeswarm plot



histogram

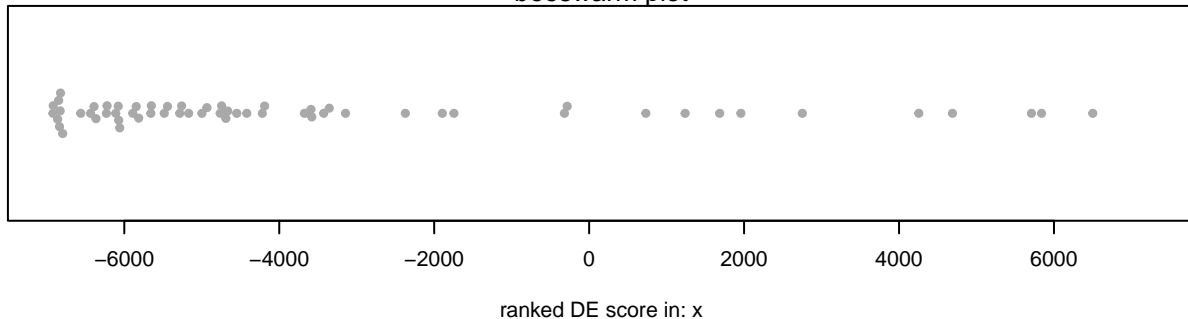


rugplot

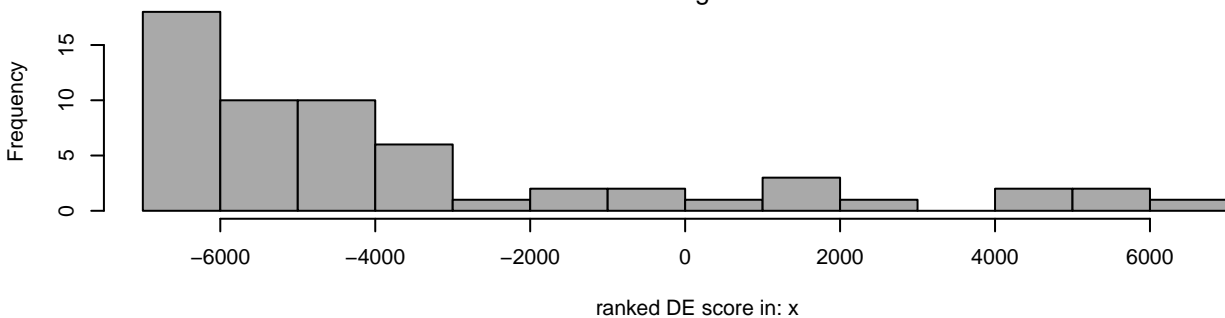


# The role of GTSE1 in G2/M progression after G2 checkpoint

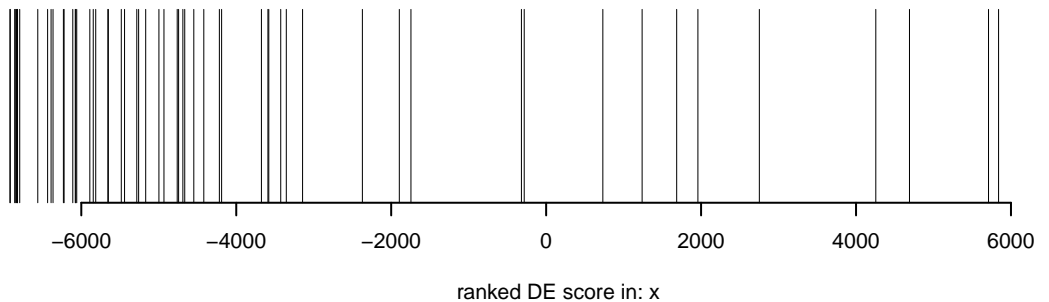
beeswarm plot



histogram

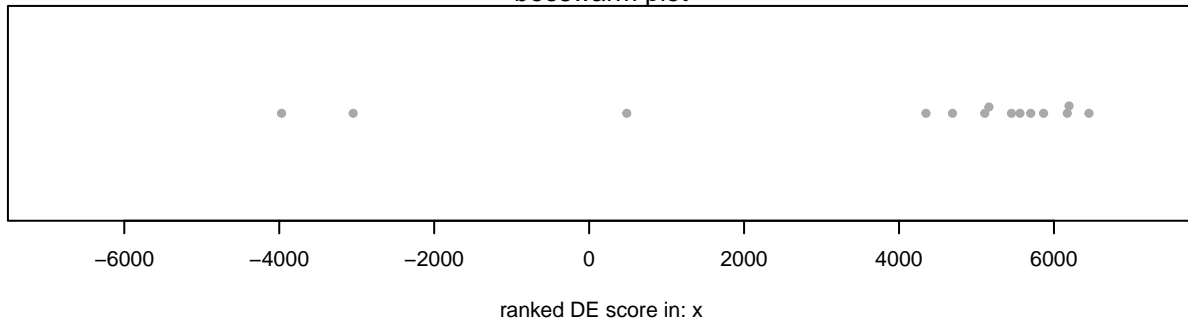


rugplot

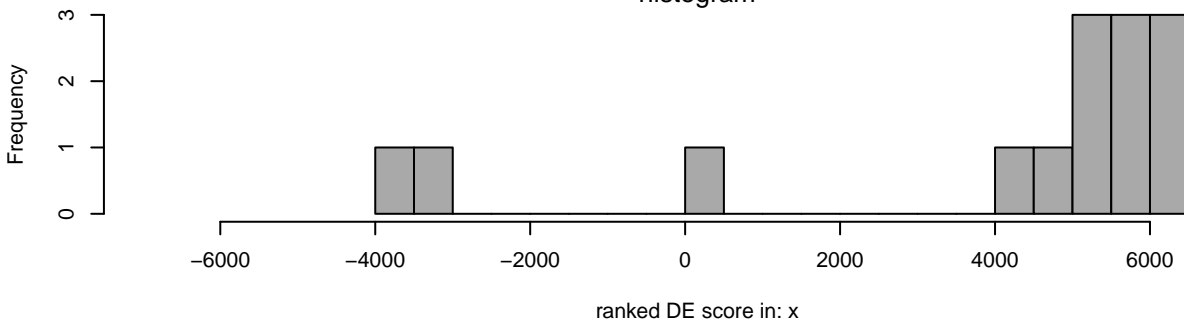


# Signaling by FLT3 ITD and TKD mutants

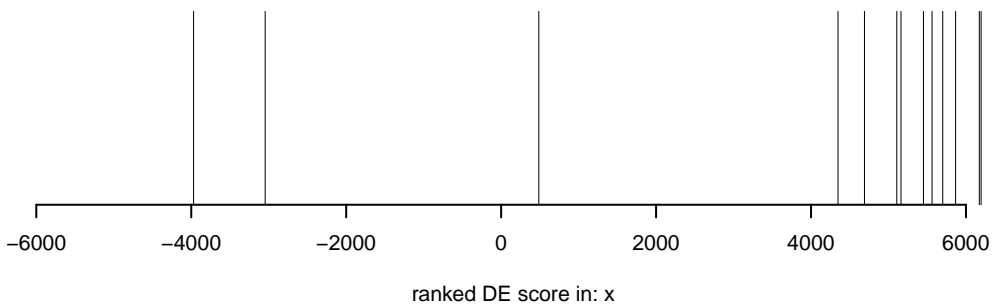
beeswarm plot



histogram



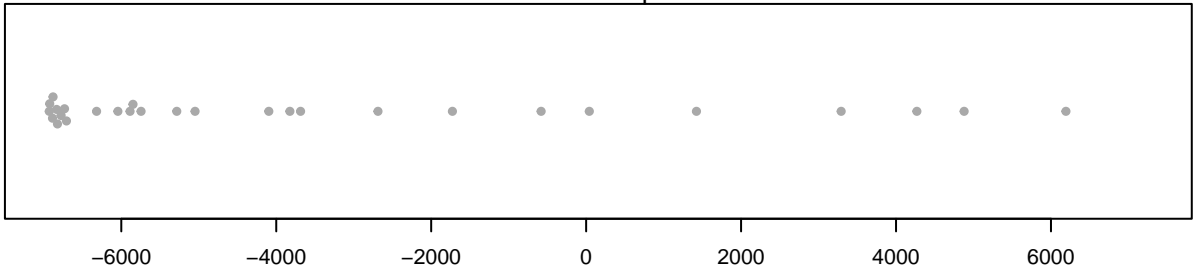
rugplot





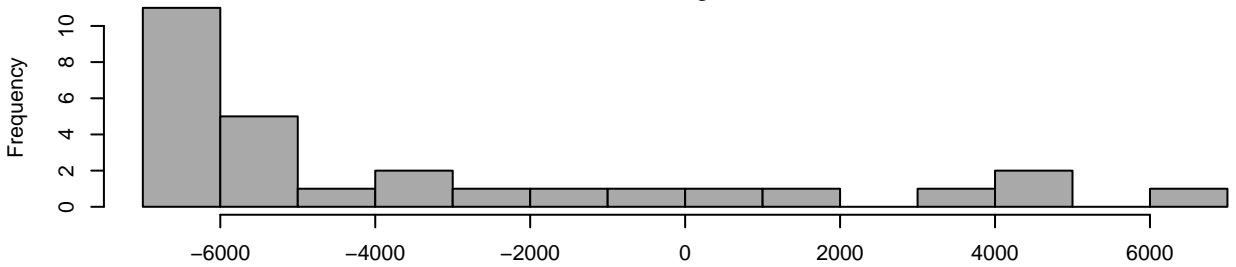
# G1/S-Specific Transcription

beeswarm plot



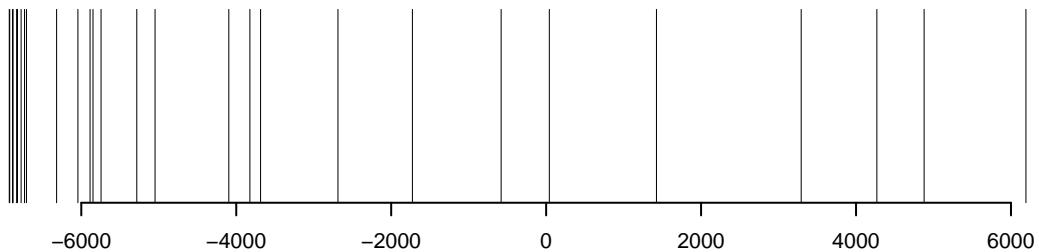
ranked DE score in: x

histogram



ranked DE score in: x

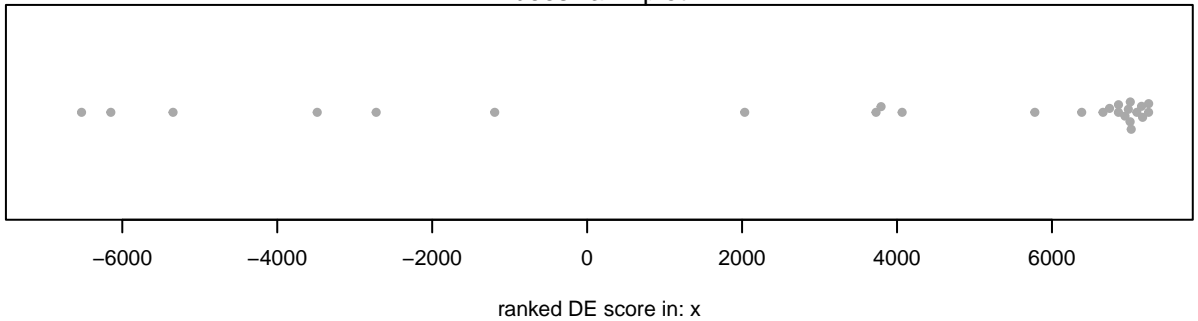
rugplot



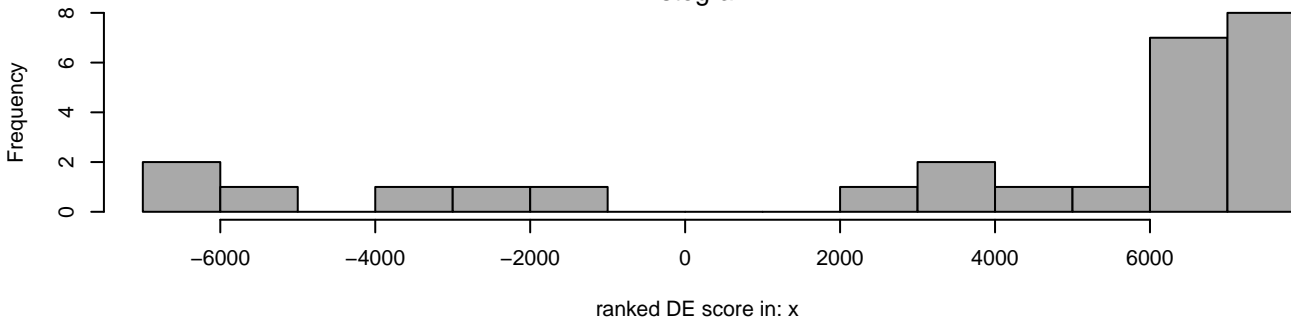
ranked DE score in: x

# Interleukin-10 signaling

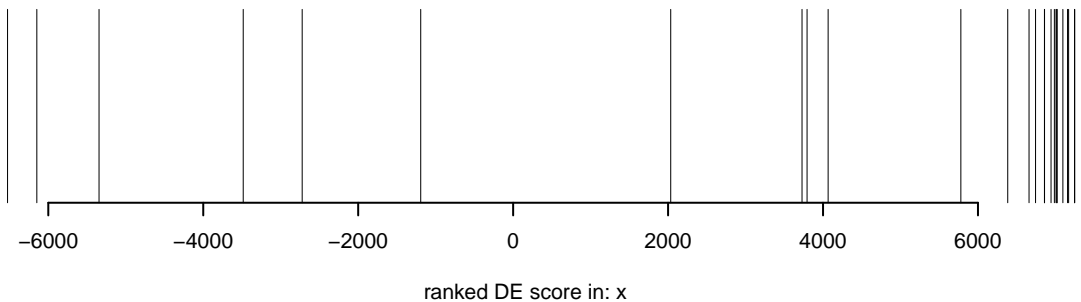
beeswarm plot



histogram

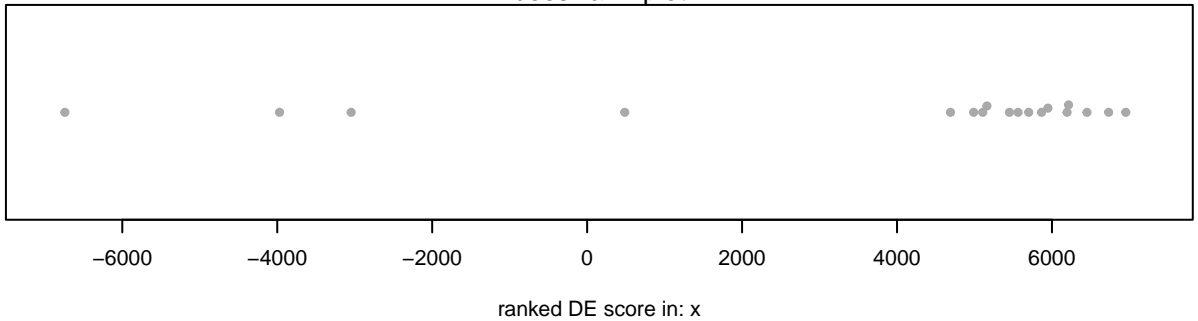


rugplot

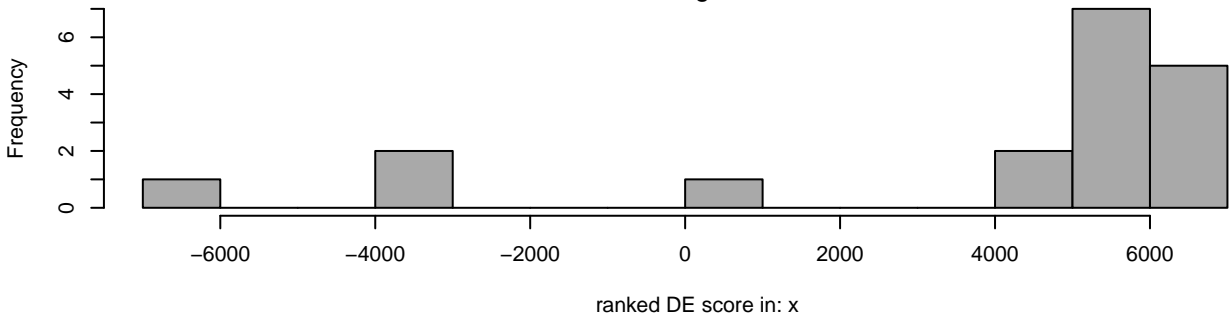


# Signaling by FLT3 fusion proteins

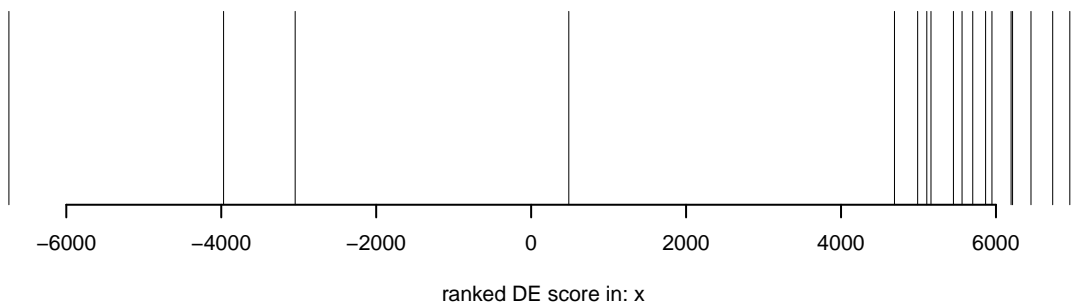
beeswarm plot



histogram

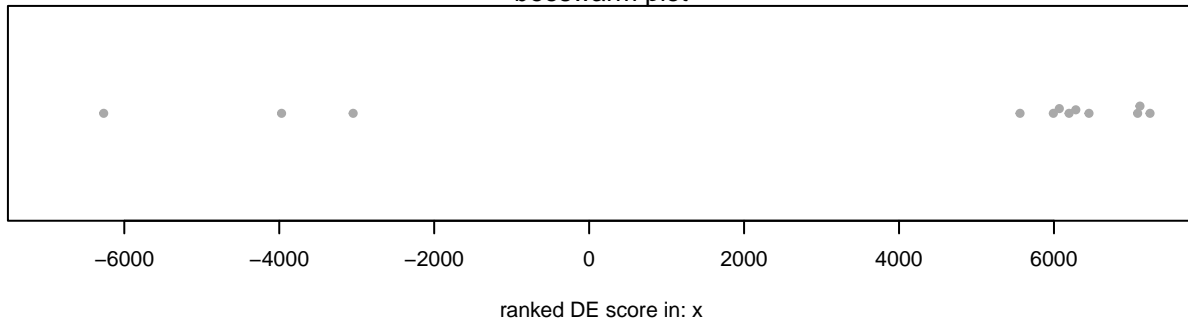


rugplot

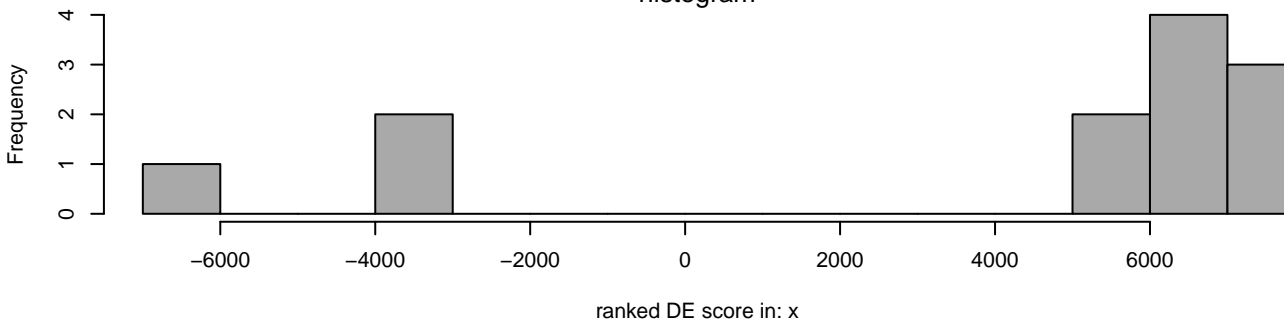


# SHC1 events in EGFR signaling

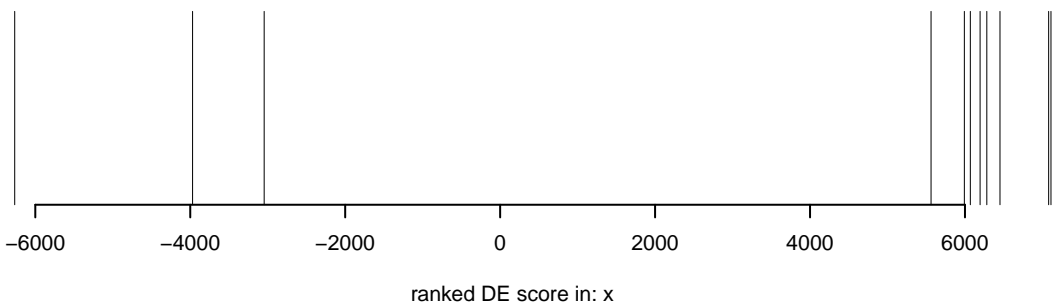
beeswarm plot



histogram

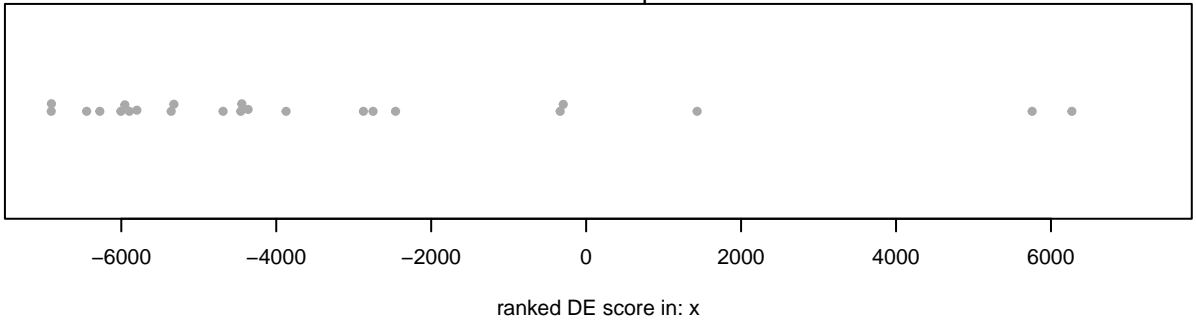


rugplot

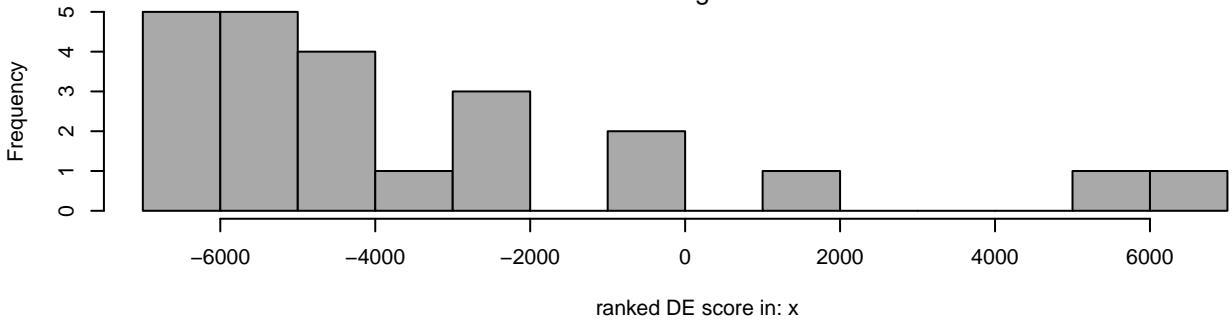


# Abortive elongation of HIV-1 transcript in the absence of Tat

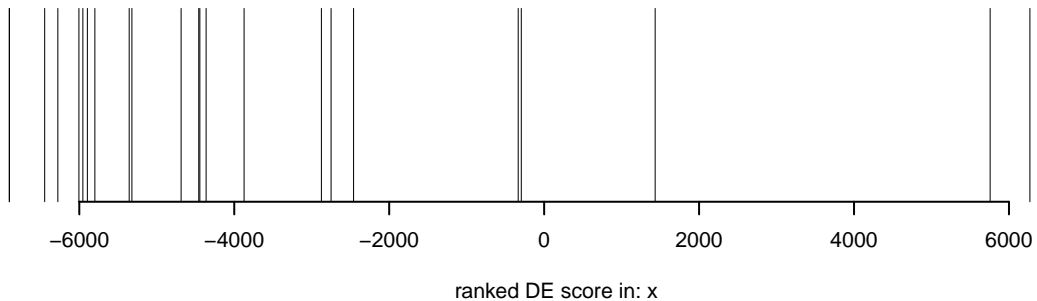
beeswarm plot



histogram

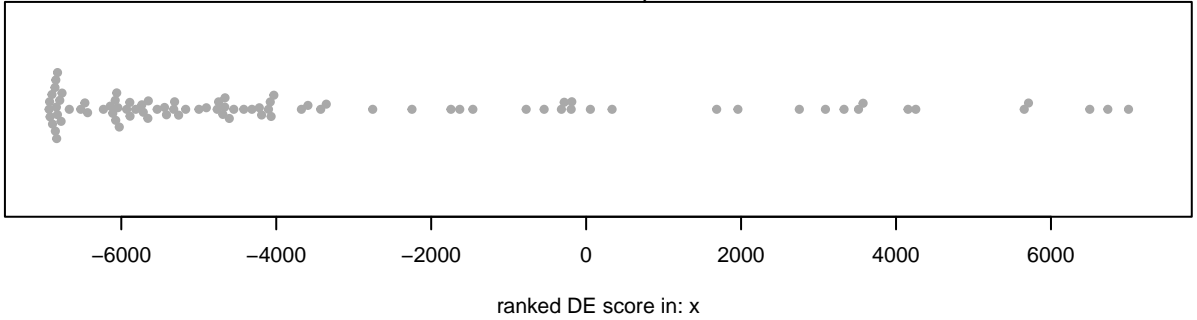


rugplot

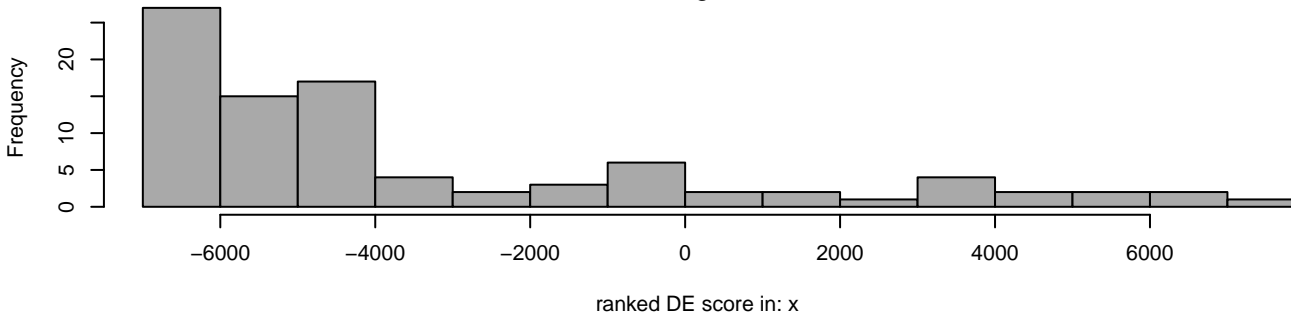


# DNA Replication Pre-Initiation

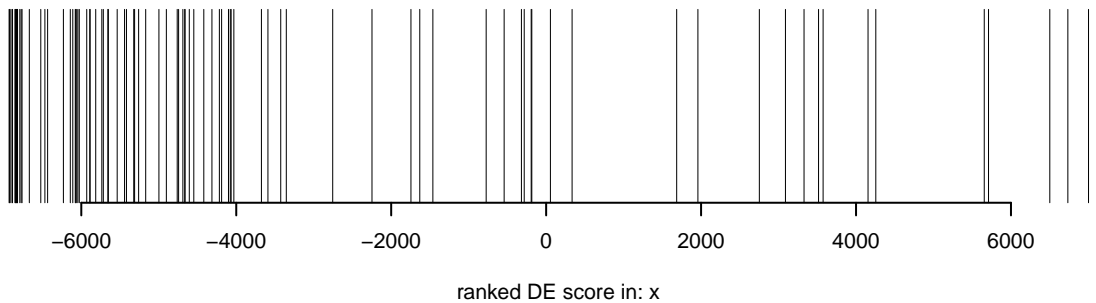
beeswarm plot



histogram

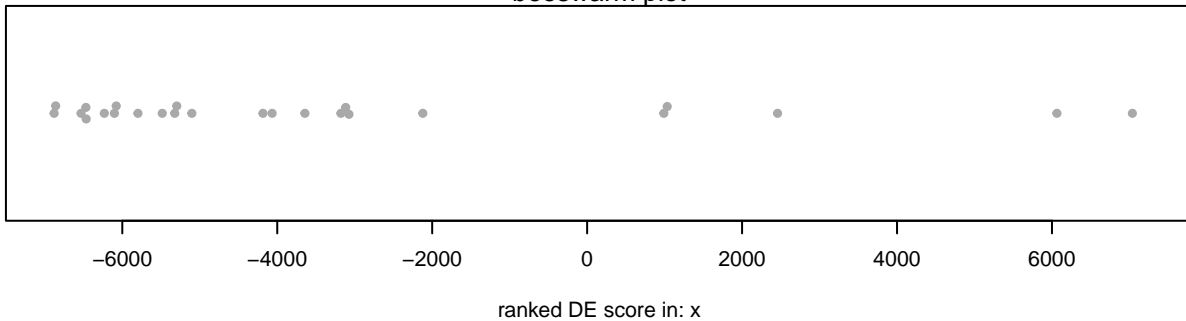


rugplot

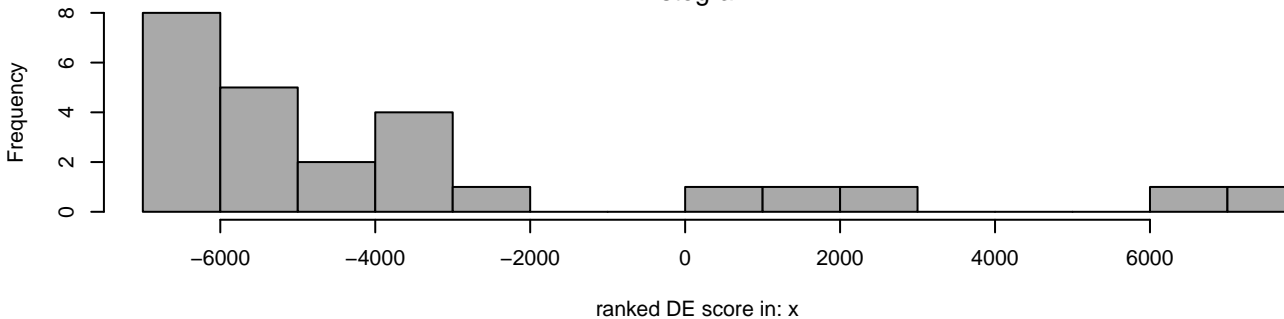


# HSF1 activation

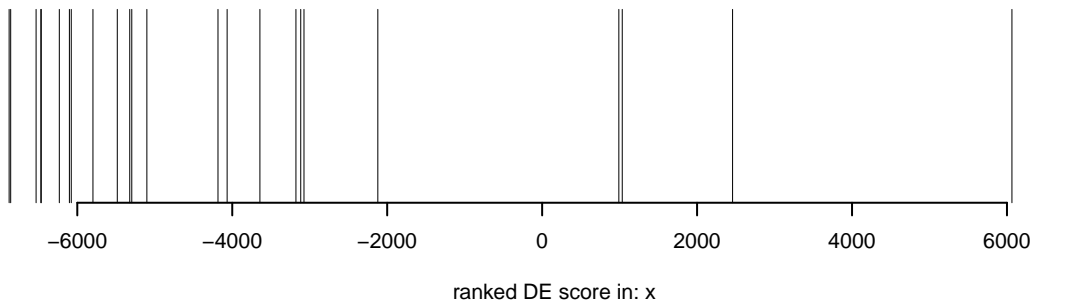
beeswarm plot



histogram

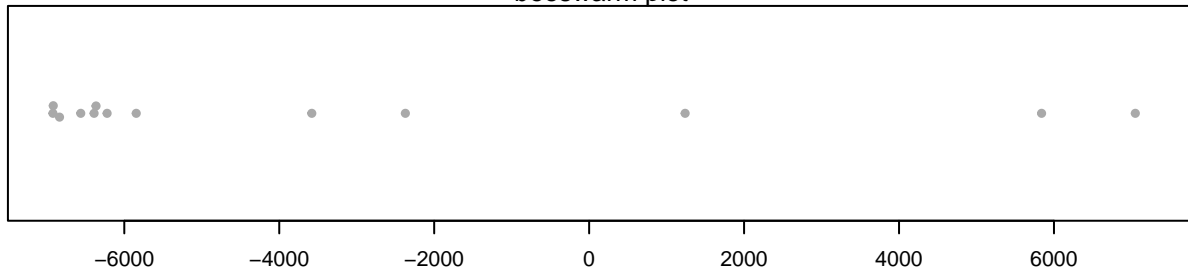


rugplot



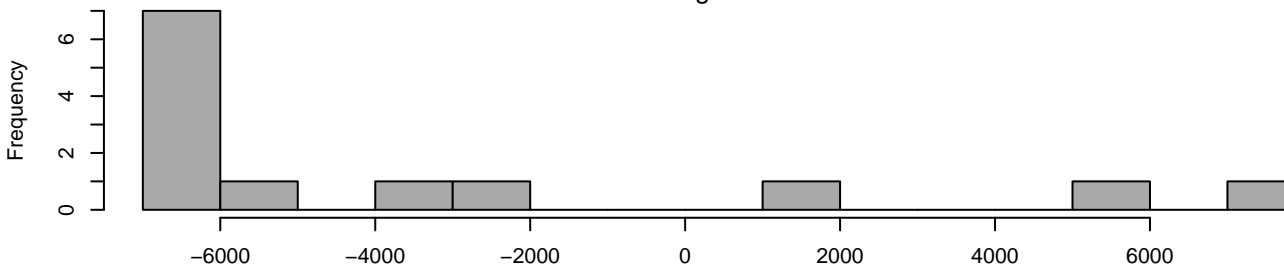
# Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane

beeswarm plot



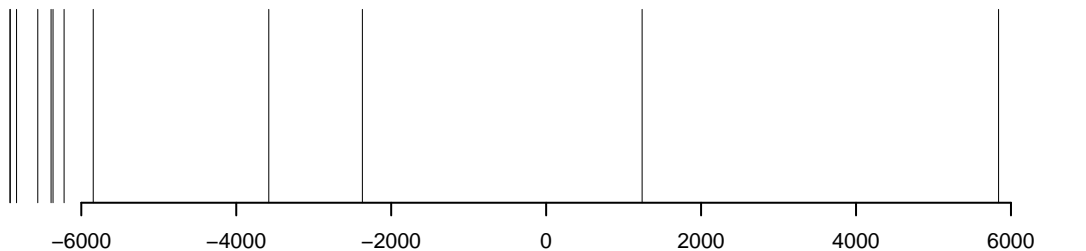
ranked DE score in: x

histogram



ranked DE score in: x

rugplot

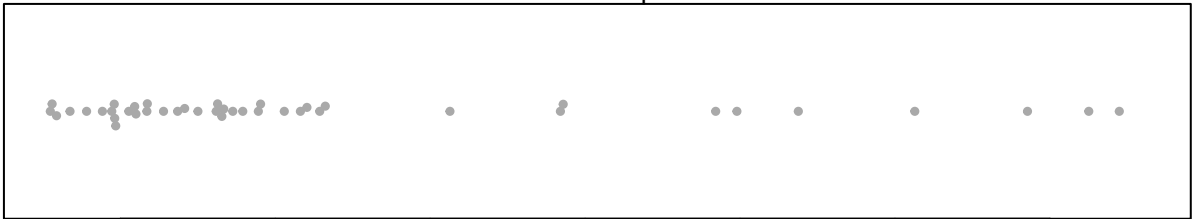


ranked DE score in: x



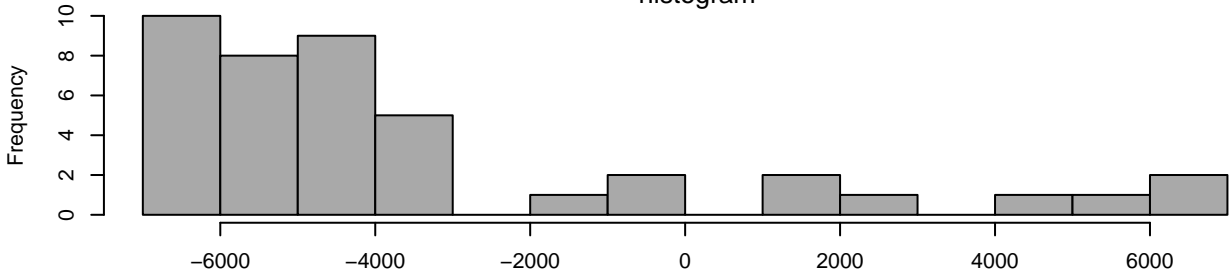
# AUF1 (hnRNP D0) binds and destabilizes mRNA

beeswarm plot



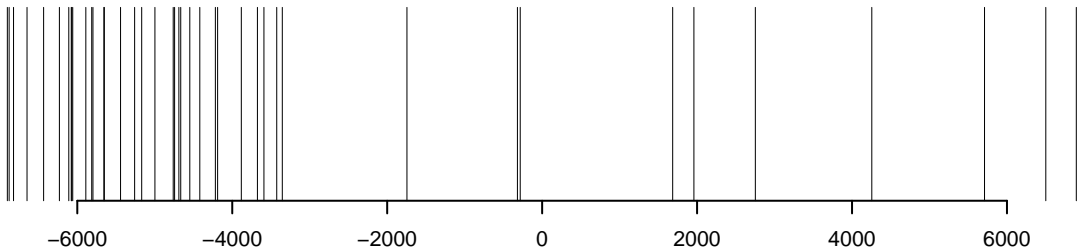
ranked DE score in: x

histogram



ranked DE score in: x

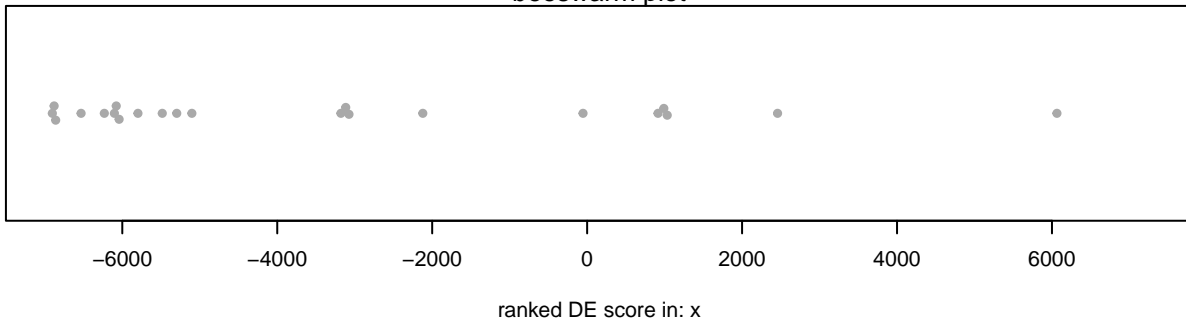
rugplot



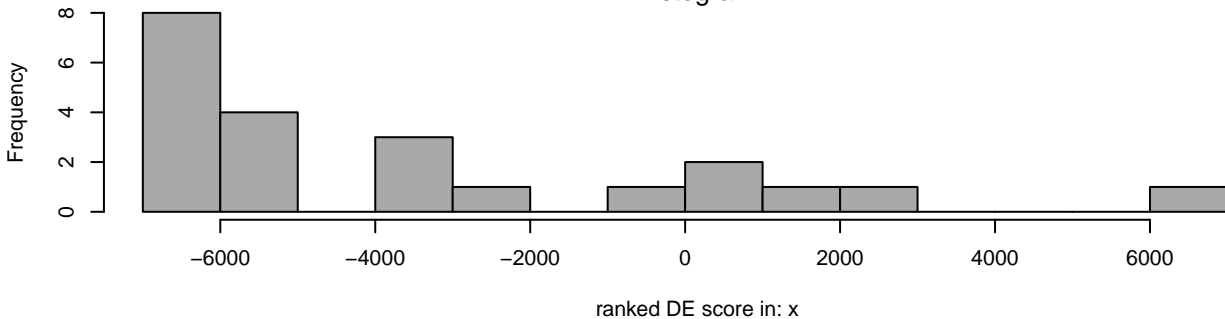
ranked DE score in: x

# Attenuation phase

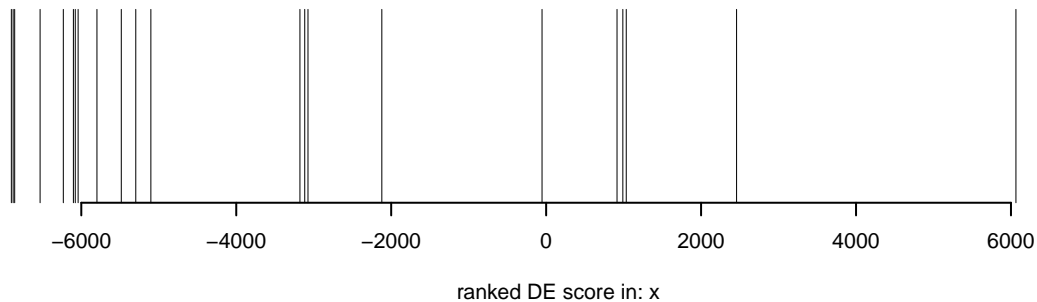
beeswarm plot



histogram

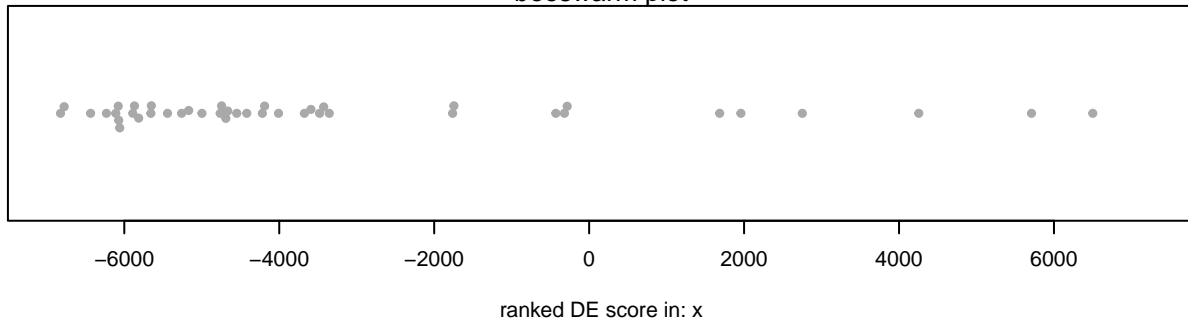


rugplot

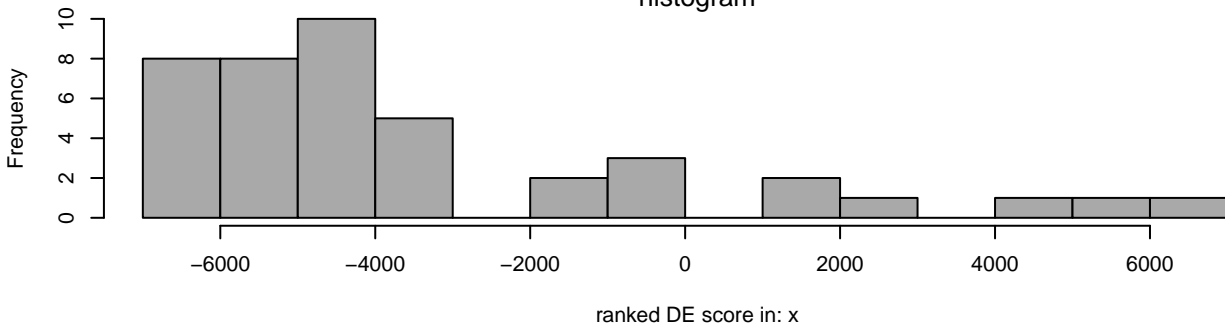


# FBXL7 down-regulates AURKA during mitotic entry and in early mitosis

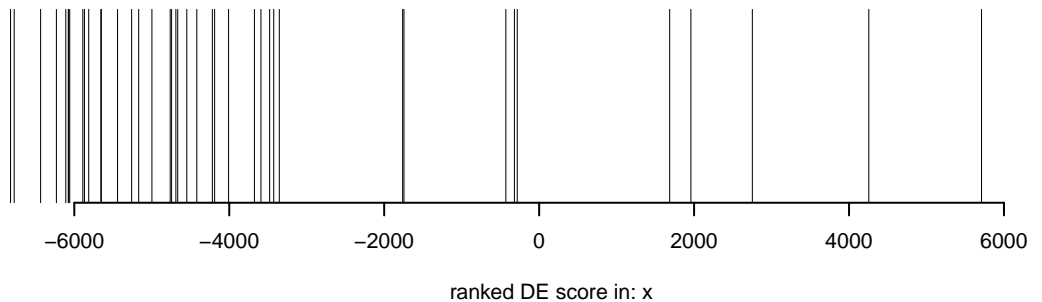
beeswarm plot



histogram

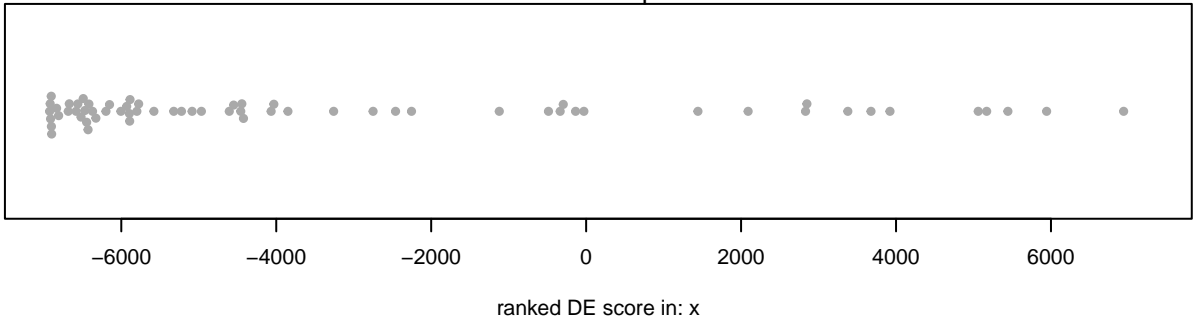


rugplot

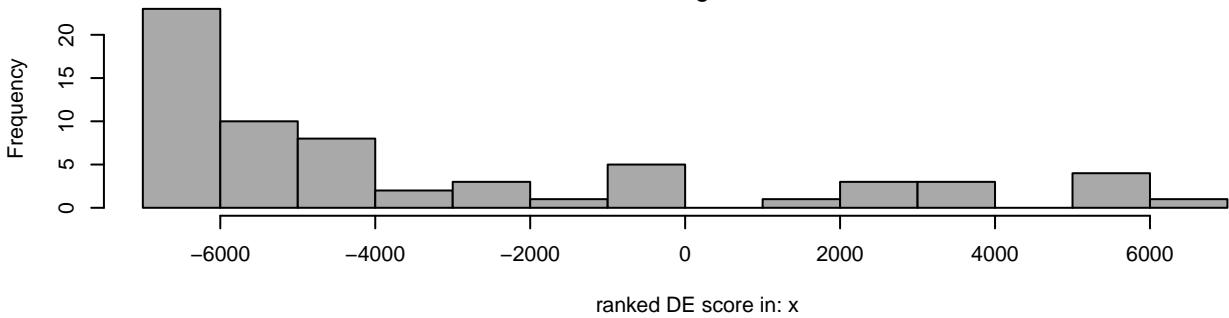


# Telomere Maintenance

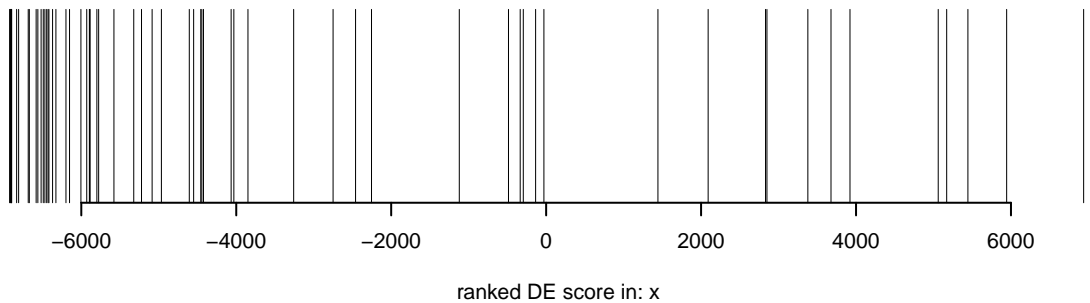
beeswarm plot



histogram

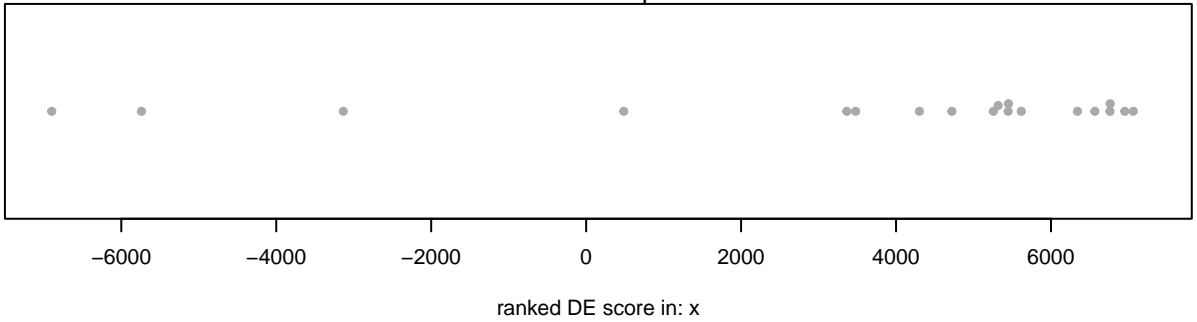


rugplot

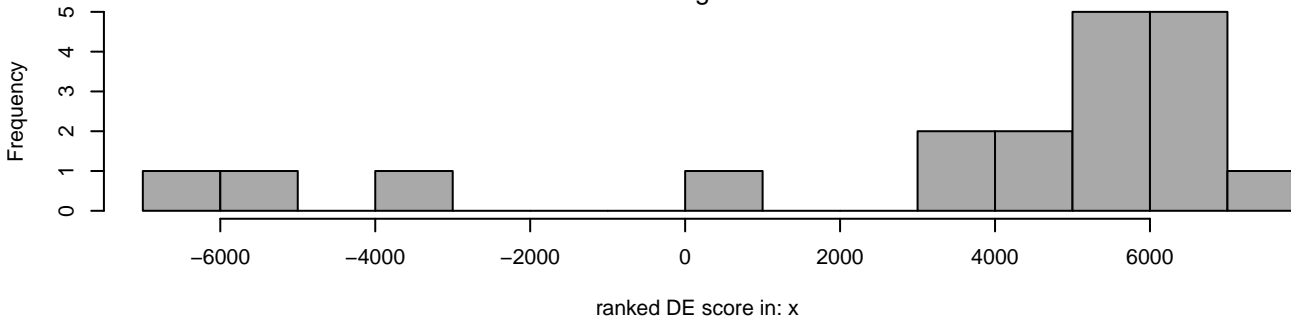


# Nephrin family interactions

beeswarm plot



histogram



rugplot

