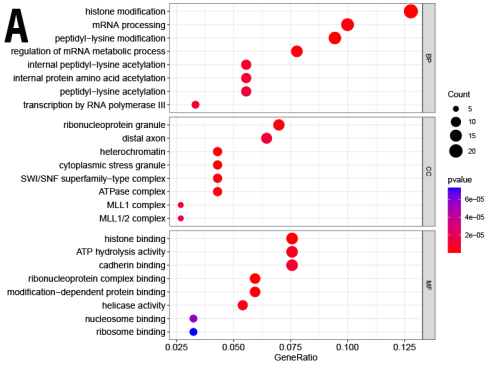
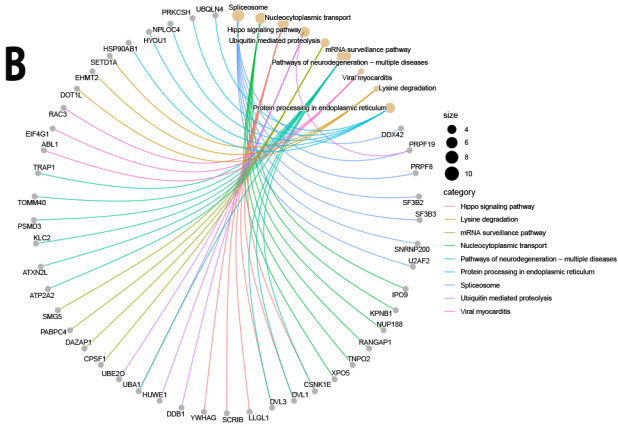
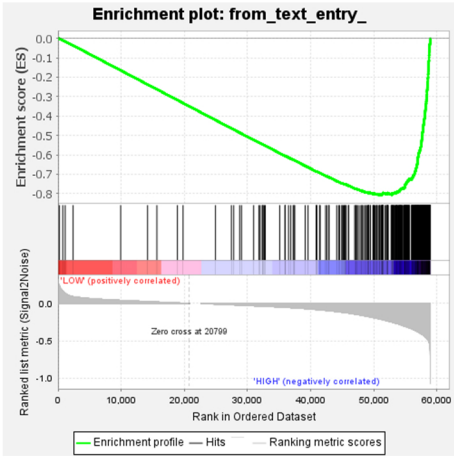
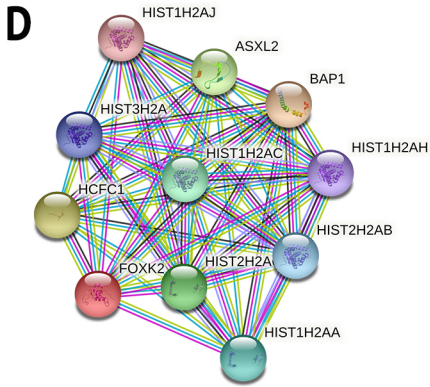

A
histone modification
mRNA processing
peptidyl−lysine modification
regulation of mRNA metabolic process
internal peptidyl−lysine acetylation
internal protein amino acid acetylation
peptidyl−lysine acetylation
transcription by RNA polymerase III
ribonucleoprotein granule
distal axon
heterochromatin
cytoplasmic stress granule
SWI/SNF superfamily−type complex
ATPase complex
MLL1 complex
MLL1/2 complex
histone binding
ATP hydrolysis activity
cadherin binding
ribonucleoprotein complex binding
modification−dependent protein binding
helicase activity
nucleosome binding
ribosome binding
BP
CC
MF
0.025
0.050
0.075
0.100
0.125
GeneRatio
Count
5
10
15
20
pvalue
6e−05
4e−05
2e−05


B
Spliceosome
Nucleocytoplasmic transport
Hippo signaling pathway
Ubiquitin mediated proteolysis
mRNA surveillance pathway
Pathways of neurodegeneration − multiple diseases
Viral myocarditis
Lysine degradation
Protein processing in endoplasmic reticulum
PRKCSH
UBQLN4
NPLOC4
HYOU1
HSP90AB1
SETD1A
EHMT2
DOT1L
RAC3
EIF4G1
ABL1
TRAP1
TOMM40
PSMD3
KLC2
ATXN2L
ATP2A2
SMG5
PABPC4
DAZAP1
CPSF1
UBE2D
UBA1
HUWE1
DDB1
YWHAG
SCRIB
LLGL1
DVL3
DVL1
CSNK1E
XPO5
TNPO2
RANGAP1
NUP188
KPNB1
IPO9
U2AF2
SNRNP200
SF3B3
SF3B2
PRPF8
PRPF19
DDX42
size
4
6
8
10
category
Hippo signaling pathway
Lysine degradation
mRNA surveillance pathway
Nucleocytoplasmic transport
Pathways of neurodegeneration − multiple diseases
Protein processing in endoplasmic reticulum
Spliceosome
Ubiquitin mediated proteolysis
Viral myocarditis


C
Enrichment plot: from_text_entry_
Enrichment score (ES)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
-0.7
-0.8
'LOW' (positively correlated)
Ranked list metric (Signal2Noise)
0.0
-0.5
-1.0
Zero cross at 20799
'HIGH' (negatively correlated)
0
10,000
20,000
30,000
40,000
50,000
60,000
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores


D
HIST1H2AJ
ASXL2
BAP1
HIST3H2A
HIST1H2AC
HIST1H2AH
HCFC1
HIST2H2AB
FOXK2
HIST2H2A
HIST1H2AA