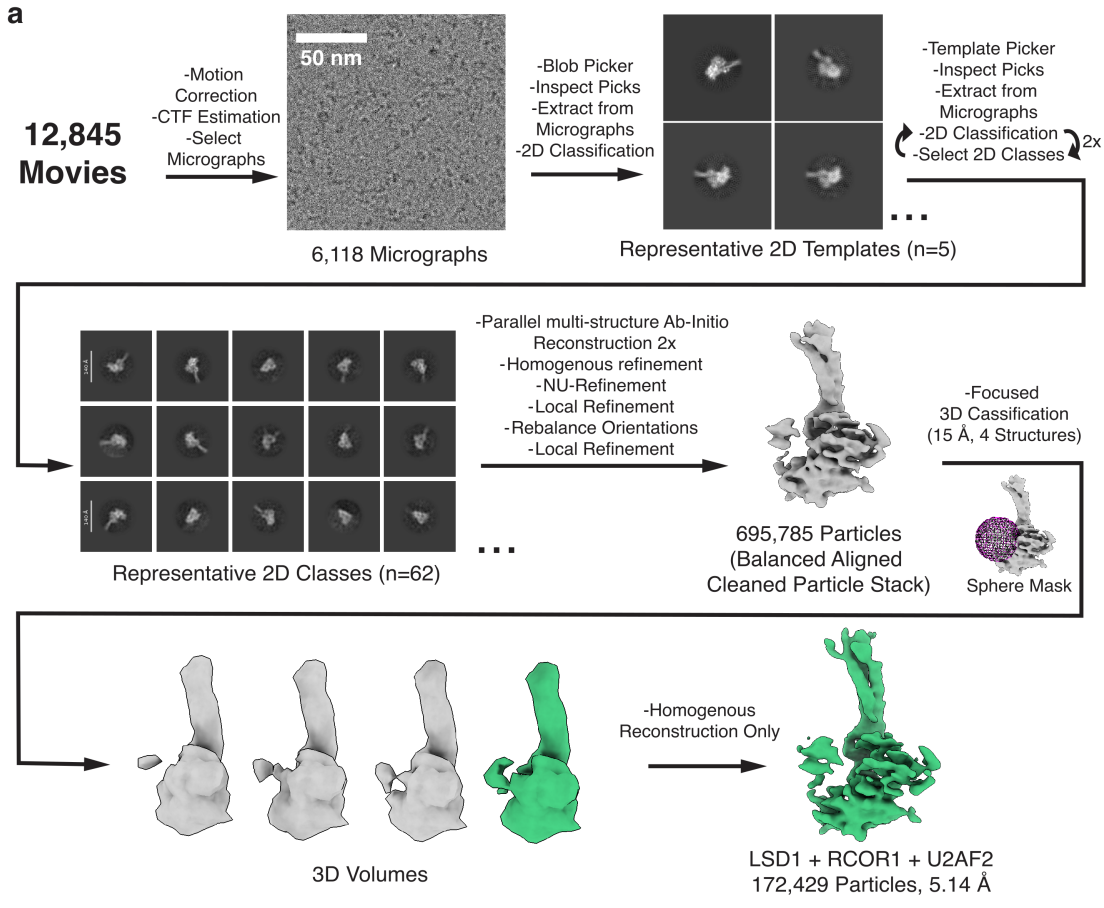
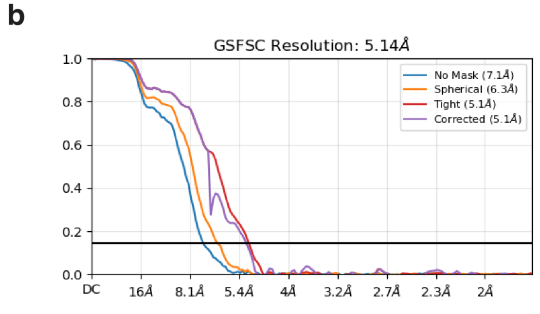
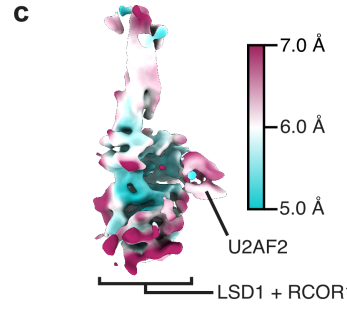
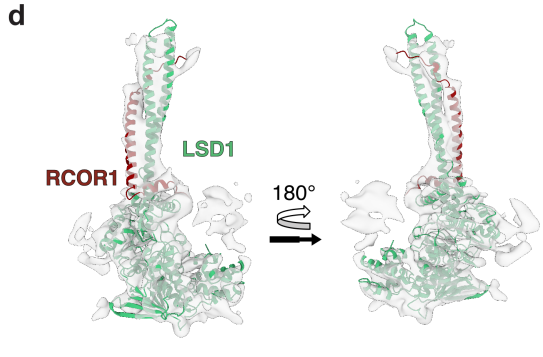
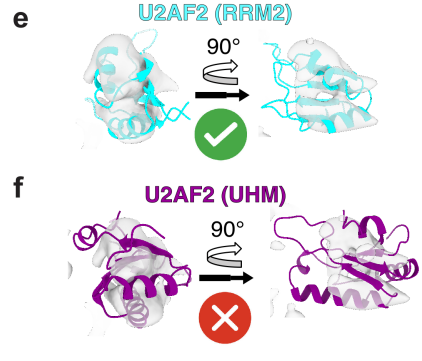
LSD1 + RCOR1 + U2AF2 Glacios 2 Dataset



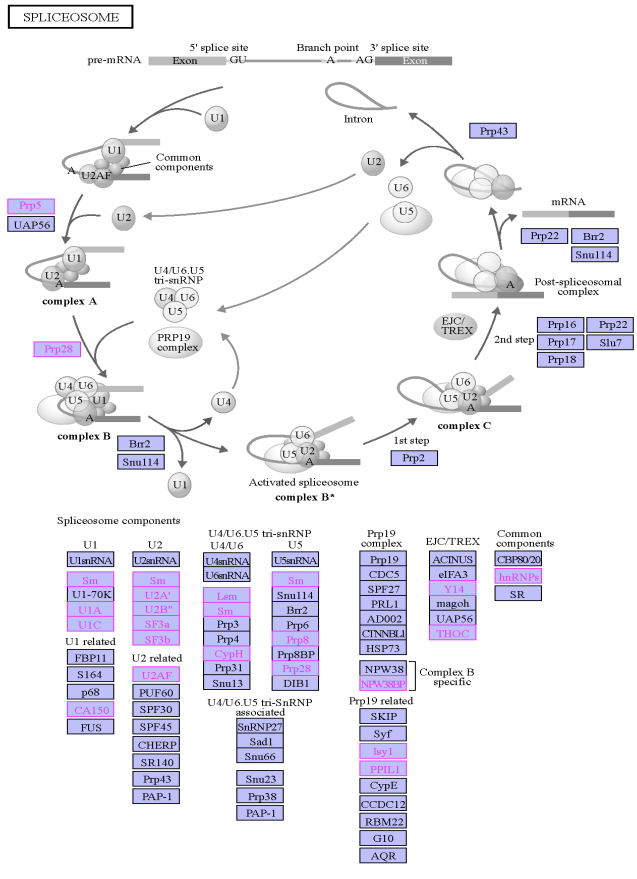




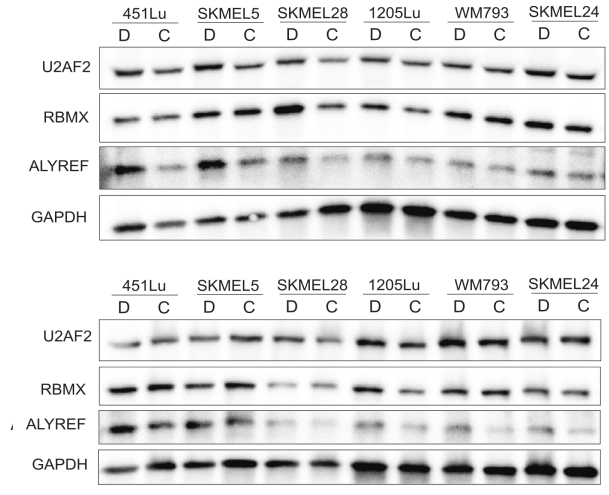




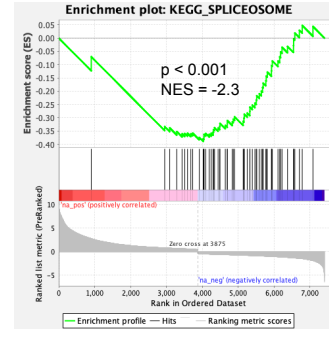
a


SPLICEOSOME
pre-mRNA
5' splice site
Branch point
3' splice site
Exon
GU
A
AG
Exon
Intron
U1
U2AF
Common components
Prp5
UAP56
U2
U6
U5
Prp43
mRNA
Prp22
Brr2
Snu114
complex A
U4/U6.U5 tri-snRNP
U4
U6
U5
PRP19 complex
Post-spliceosomal complex
EJC/ TREX
2nd step
Prp16
Prp22
Prp17
Slu7
Prp18
Prp28
complex B
U4
complex C
Brr2
Snu114
U1
Activated spliceosome
complex B*
1st step
Prp2
Spliceosome components
U1
U1snRNA
Sm
U1-70K
U1A
U1C
U1 related
FBP11
S164
p68
CA150
FUS
U2
U2snRNA
Sm
U2A'
U2B''
SF3a
SF3b
U2 related
U2AF
PUF60
SPF30
SPF45
CHERP
SR140
Prp43
PAP-1
U4/U6.U5 tri-snRNP
U4/U6
U4snRNA
U6snRNA
Lsm
Sm
Prp3
Prp4
CypH
Prp31
Snu13
U4/U6.U5 tri-SnRNP associated
SnRNP27
Sad1
Snu66
Snu23
Prp38
PAP-1
U5
U5snRNA
Sm
Snu114
Brr2
Prp6
Prp8
Prp8BP
Prp28
DIB1
Prp19 complex
Prp19
CDC5
SPF27
PRL1
AD002
CTNNBL1
HSP73
NPW38
NPW38B
Complex B specific
Prp19 related
SKIP
Syf
Iey1
PPIL1
CypE
CCDC12
RBM22
G10
AQR
EJC/TREX
ACINUS
eIFA3
Y14
magoh
UAP56
THOC
Common components
CBP80/20
hnRNPs
SR

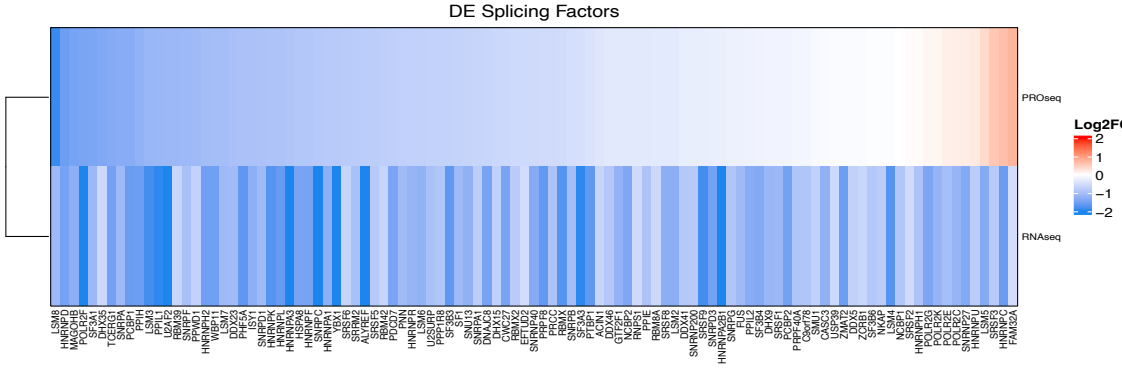
b

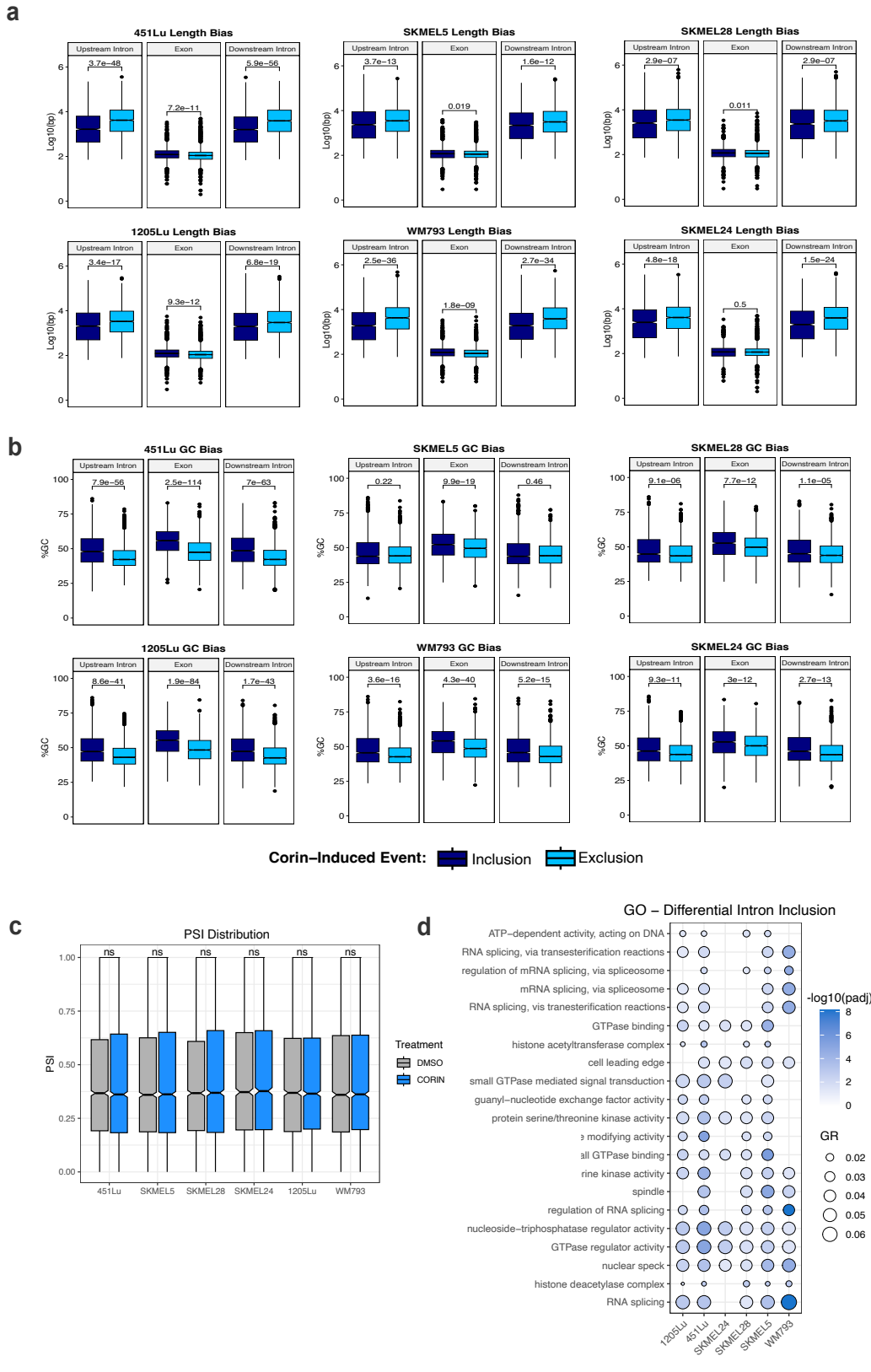

451Lu
SKMEL5
SKMEL28
1205Lu
WM793
SKMEL24
D
C
U2AF2
RBMX
ALYREF
GAPDH

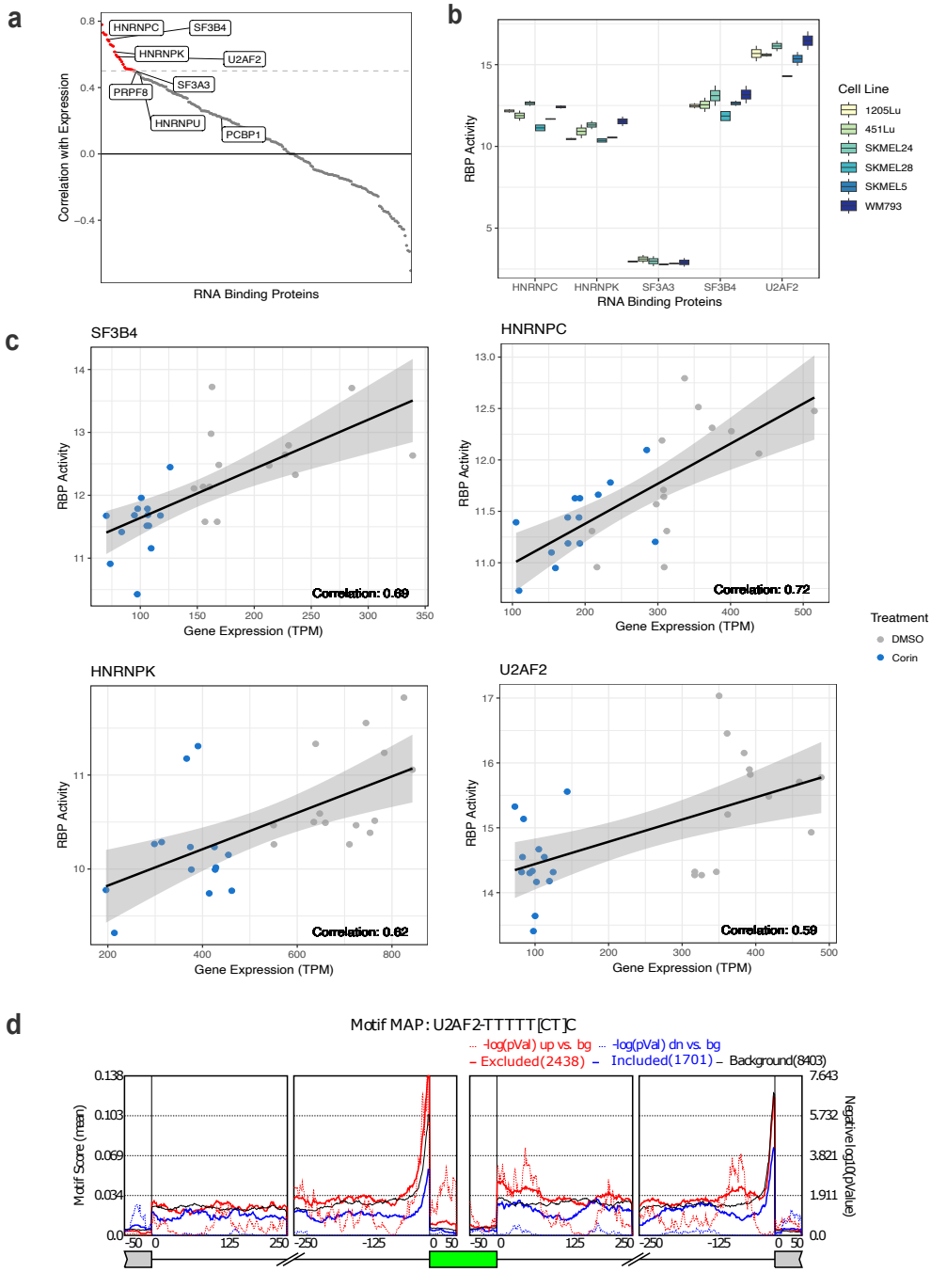
c

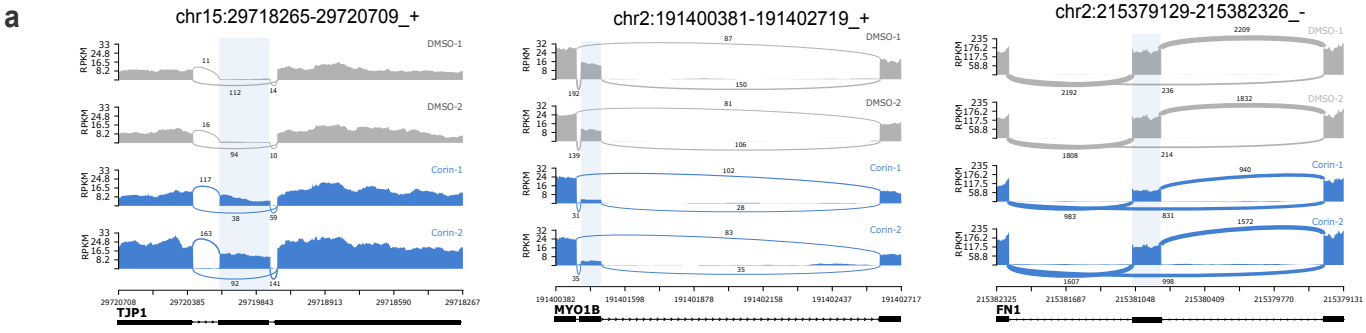

Enrichment plot: KEGG_SPLICEOSOME
p < 0.001
NES = -2.3
Enrichment score (ES)
Ranked list metric (PreRanked)
Zero cross at 3875
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores

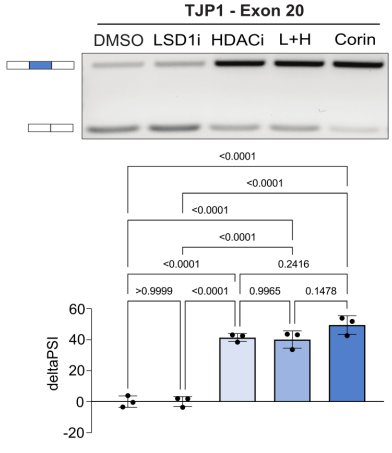
d

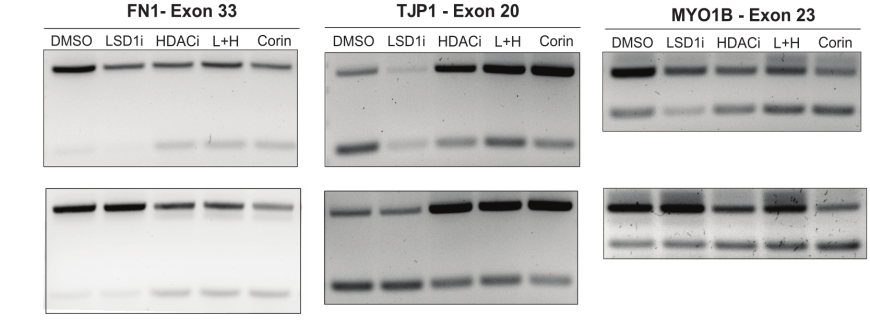

DE Splicing Factors
PROseq
RNAseq
Log2FC
2
1
0
−1
−2

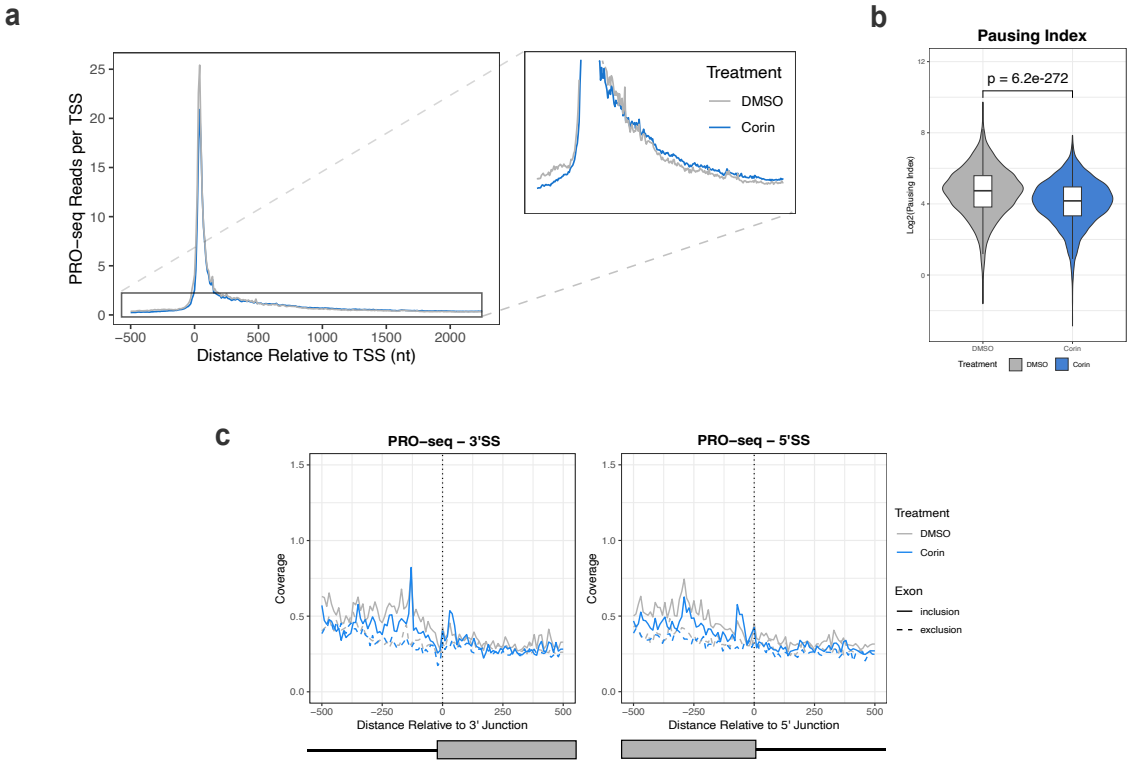

a
451Lu Length Bias
SKMEL5 Length Bias
SKMEL28 Length Bias
1205Lu Length Bias
WM793 Length Bias
SKMEL24 Length Bias
Upstream Intron
Exon
Downstream Intron
Log10(bp)
3.7e−48
7.2e−11
5.9e−56
3.7e−13
0.019
1.6e−12
2.9e−07
0.011
2.9e−07
3.4e−17
9.3e−12
6.8e−19
2.5e−36
1.8e−09
2.7e−34
4.8e−18
0.5
1.5e−24
b
451Lu GC Bias
SKMEL5 GC Bias
SKMEL28 GC Bias
1205Lu GC Bias
WM793 GC Bias
SKMEL24 GC Bias
%GC
7.9e−56
2.5e−114
7e−63
0.22
9.9e−19
0.46
9.1e−06
7.7e−12
1.1e−05
8.6e−41
1.9e−84
1.7e−43
3.6e−16
4.3e−40
5.2e−15
9.3e−11
3e−12
2.7e−13
Corin−Induced Event:
Inclusion
Exclusion
c
PSI Distribution
PSI
ns
451Lu
SKMEL5
SKMEL28
SKMEL24
1205Lu
WM793
Treatment
DMSO
CORIN
d
GO − Differential Intron Inclusion
ATP−dependent activity, acting on DNA
RNA splicing, via transesterification reactions
regulation of mRNA splicing, via spliceosome
mRNA splicing, via spliceosome
RNA splicing, vis tranesterification reactions
GTPase binding
histone acetyltransferase complex
cell leading edge
small GTPase mediated signal transduction
guanyl−nucleotide exchange factor activity
protein serine/threonine kinase activity
modifying activity
all GTPase binding
rine kinase activity
spindle
regulation of RNA splicing
nucleoside−triphosphatase regulator activity
GTPase regulator activity
nuclear speck
histone deacetylase complex
RNA splicing
1205Lu
451Lu
SKMEL24
SKMEL28
SKMEL5
WM793
-log10(padj)
GR

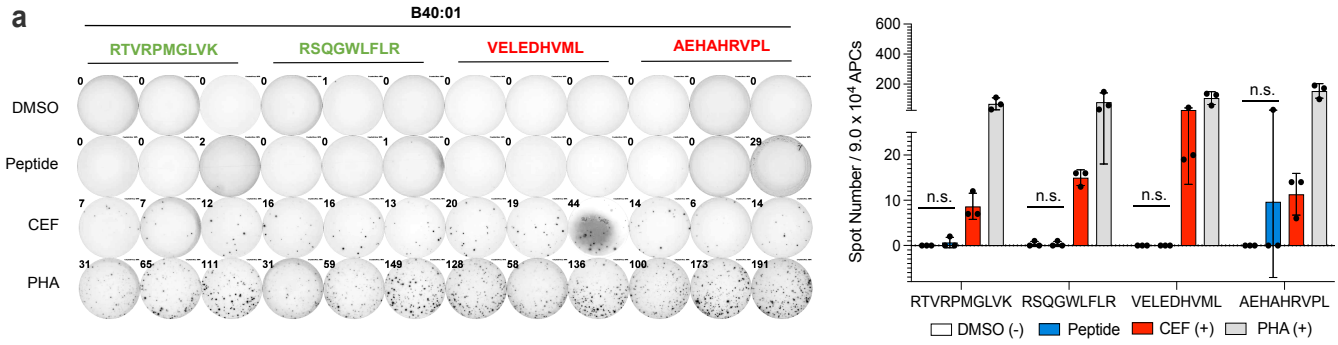

a
HNRNPC
SF3B4
HNRNPK
U2AF2
SF3A3
PRPF8
HNRNPU
PCBP1
Correlation with Expression
RNA Binding Proteins
b
RBP Activity
HNRNPC
HNRNPK
SF3A3
SF3B4
U2AF2
RNA Binding Proteins
Cell Line
1205Lu
451Lu
SKMEL24
SKMEL28
SKMEL5
WM793
c
SF3B4
Correlation: 0.69
HNRNPC
Correlation: 0.72
HNRNPK
Correlation: 0.62
U2AF2
Correlation: 0.59
RBP Activity
Gene Expression (TPM)
Treatment
DMSO
Corin
d
Motif MAP : U2AF2-TTTTTT[CT]C
-log(pVal) up vs. bg
-log(pVal) dn vs. bg
Excluded(2438)
Included(1701)
Background(8403)
Motif Score (mean)
Negative log10(pvalue)

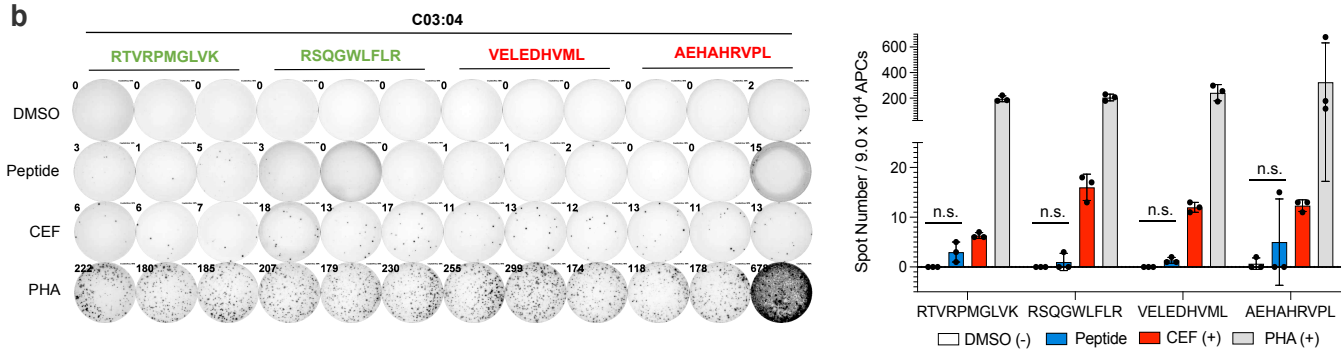

a
chr15:29718265-29720709_+
chr2:191400381-191402719_+
chr2:215379129-215382326_-
DMSO-1
DMSO-2
Corin-1
Corin-2
RPKM
TJP1
MYO1B
FN1

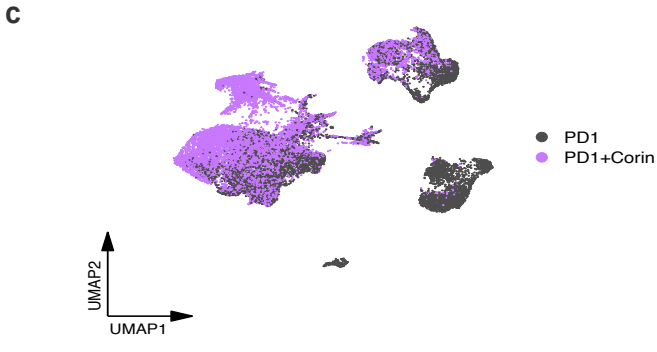

b
TJP1 - Exon 20
DMSO
LSD1i
HDACi
L+H
Corin
<0.0001
0.2416
>0.9999
0.9965
0.1478
deltaPSI

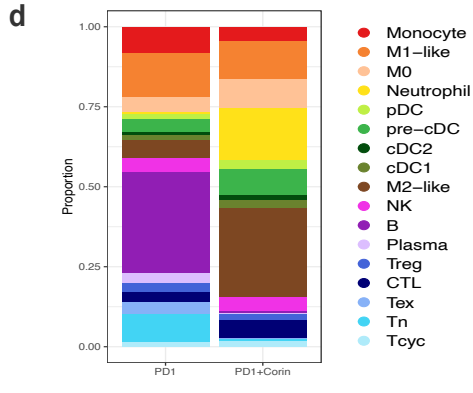

c
FN1- Exon 33
TJP1 - Exon 20
MYO1B - Exon 23
DMSO
LSD1i
HDACi
L+H
Corin

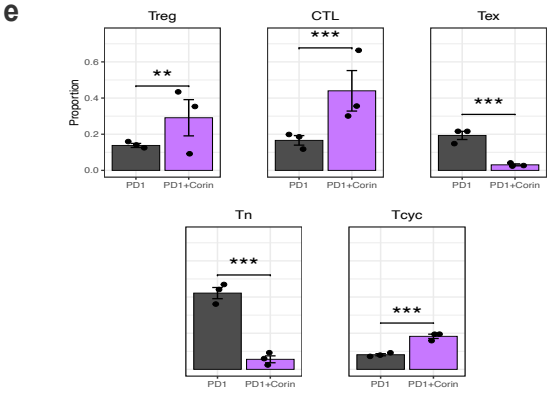

a
PRO−seq Reads per TSS
Distance Relative to TSS (nt)
Treatment
DMSO
Corin
b
Pausing Index
p = 6.2e-272
Log2(Pausing Index)
DMSO
Corin
Treatment
c
PRO−seq − 3'SS
PRO−seq − 5'SS
Coverage
Distance Relative to 3' Junction
Distance Relative to 5' Junction
Treatment
DMSO
Corin
Exon
inclusion
exclusion

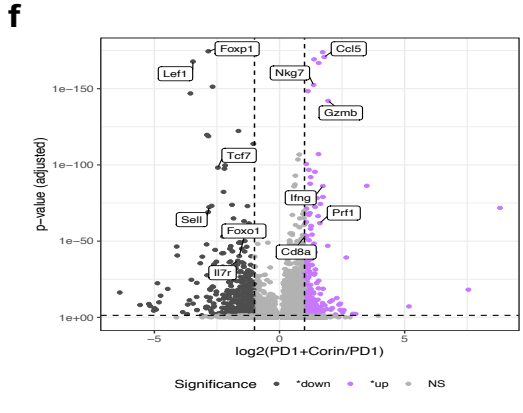

a
B40:01
RTVRPMGLVK
RSQGWLFLR
VELEDHVML
AEHAHRVPL
DMSO
Peptide
CEF
PHA
Spot Number / 9.0 x 10^4 APCs
n.s.
DMSO (-)
Peptide
CEF (+)
PHA (+)


b
C03:04
RTVRPMGLVK
RSQGWLFLR
VELEDHVML
AEHAHRVPL
DMSO
Peptide
CEF
PHA
Spot Number / 9.0 x 10^4 APCs
n.s.
DMSO (-)
Peptide
CEF (+)
PHA (+)


c
PD1
PD1+Corin
UMAP2
UMAP1


d
Proportion
PD1
PD1+Corin
Monocyte
M1−like
M0
Neutrophil
pDC
pre−cDC
cDC2
cDC1
M2−like
NK
B
Plasma
Treg
CTL
Tex
Tn
Tcyc


e
Treg
CTL
Tex
Tn
Tcyc
Proportion
PD1
PD1+Corin


f
Foxp1
Ccl5
Lef1
Nkg7
Gzmb
Tcf7
Ifng
Prf1
Sell
Foxo1
Cd8a
Il7r
p−value (adjusted)
log2(PD1+Corin/PD1)
Significance
*down
*up
NS