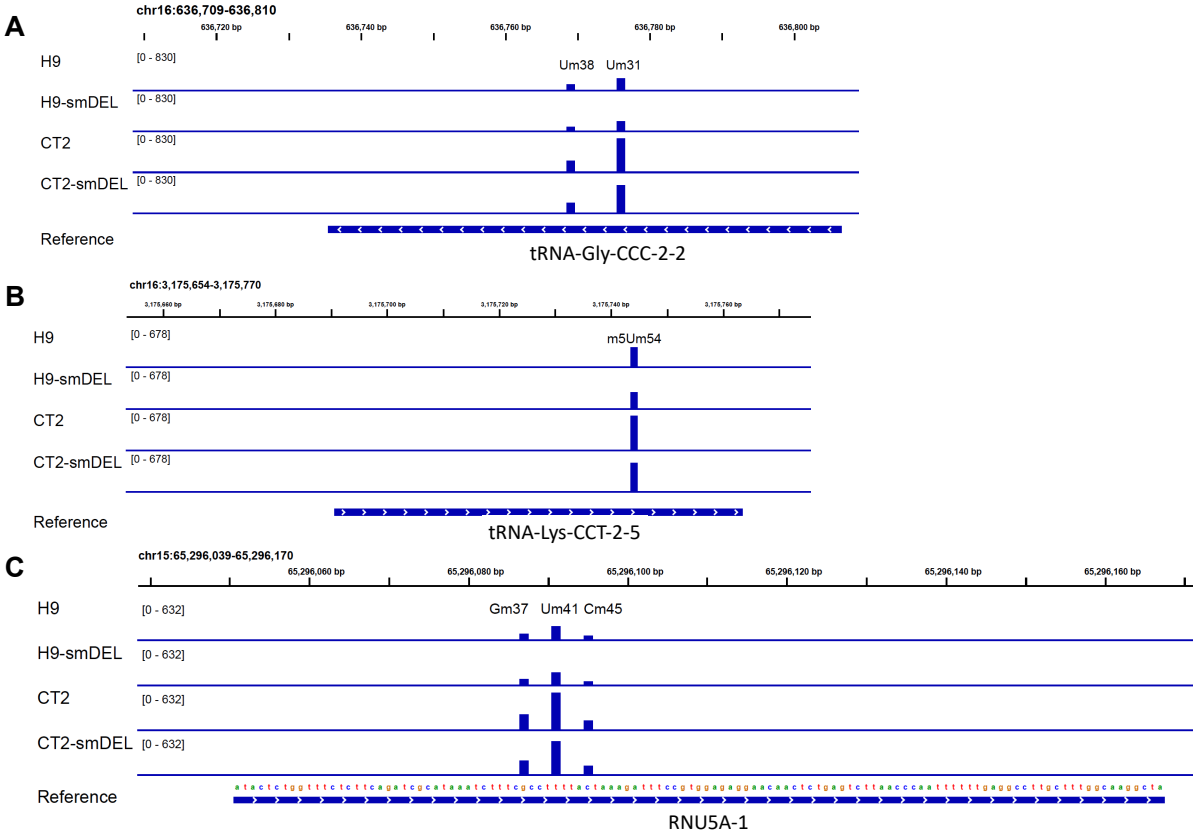
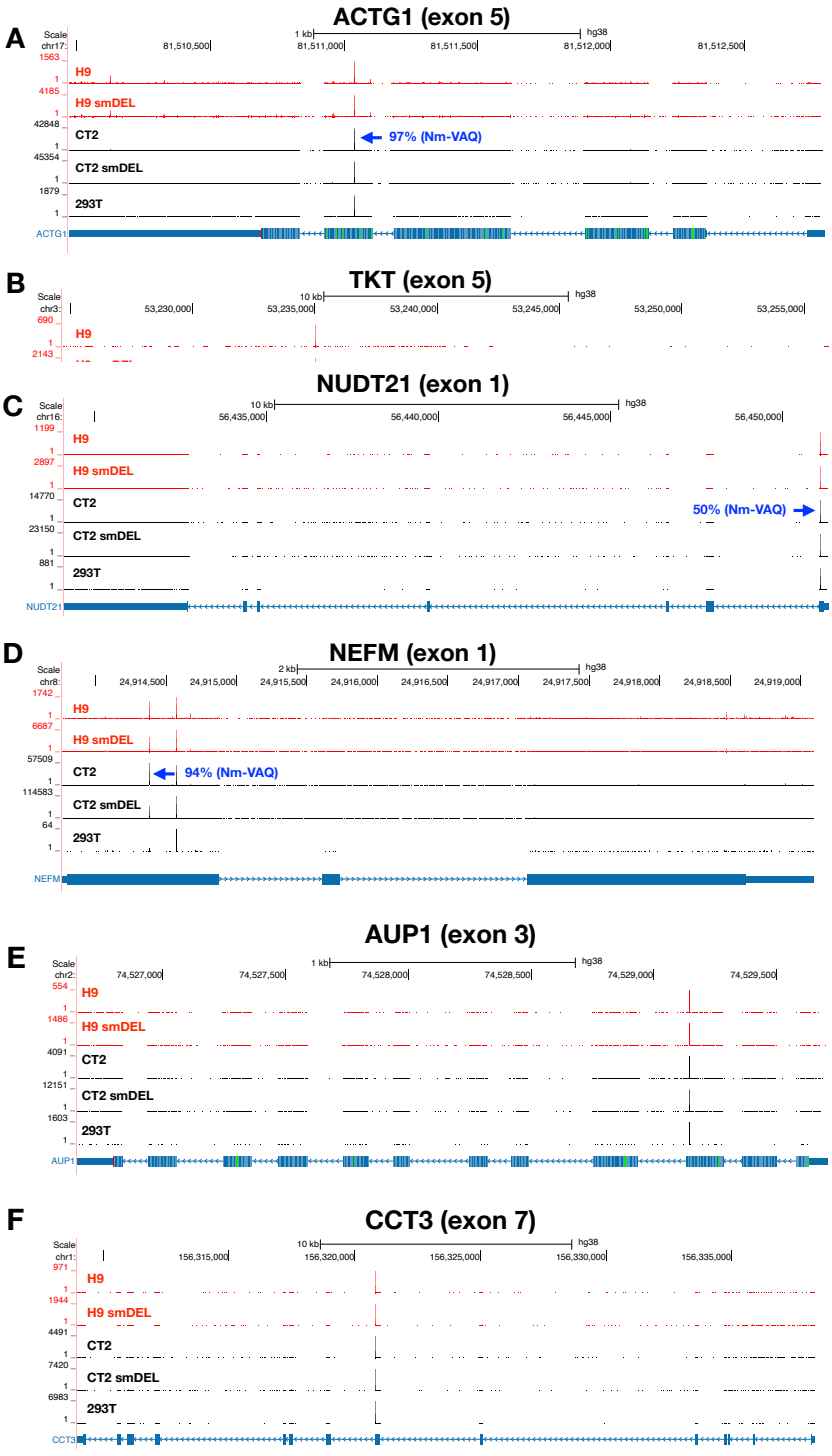
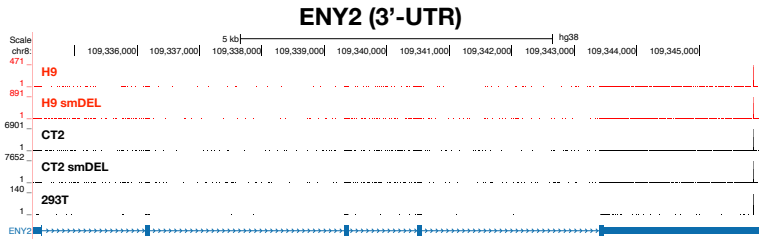


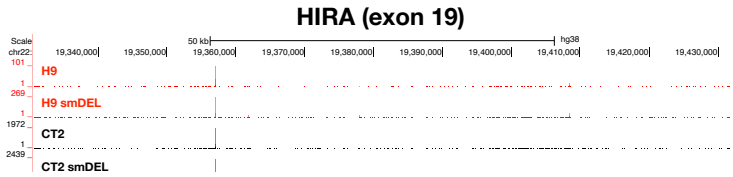
Supplementary Fig. 1. RibOxi-seq2 peaks in tRNA, snRNA, RN7SK from induced neurons. Modified nucleotides annotated in reference are highlighted. The RN7SK Nm site was quantified at 75% using Nm-VAQ.


A
ACTG1 (exon 5)
Scale
chr17:
81,510,500
1 kb
81,511,000
hg38
81,511,500
81,512,000
81,512,500
H9
H9 smDEL
CT2
97% (Nm-VAQ)
CT2 smDEL
293T
ACTG1
B
TKT (exon 5)
chr3:
53,230,000
10 kb
53,235,000
hg38
53,240,000
53,245,000
53,250,000
53,255,000
H9
C
NUDT21 (exon 1)
chr16:
56,435,000
10 kb
56,440,000
hg38
56,445,000
56,450,000
H9
H9 smDEL
CT2
50% (Nm-VAQ)
CT2 smDEL
293T
NUDT21
D
NEFM (exon 1)
chr8:
24,914,500
24,915,000
2 kb
24,915,500
24,916,000
24,916,500
24,917,000
hg38
24,917,500
24,918,000
24,918,500
24,919,000
H9
H9 smDEL
CT2
94% (Nm-VAQ)
CT2 smDEL
293T
NEFM
E
AUP1 (exon 3)
chr2:
74,527,000
74,527,500
1 kb
74,528,000
hg38
74,528,500
74,529,000
74,529,500
H9
H9 smDEL
CT2
CT2 smDEL
293T
AUP1
F
CCT3 (exon 7)
chr1:
156,315,000
10 kb
156,320,000
hg38
156,325,000
156,330,000
156,335,000
H9
H9 smDEL
CT2
CT2 smDEL
293T
CCT3

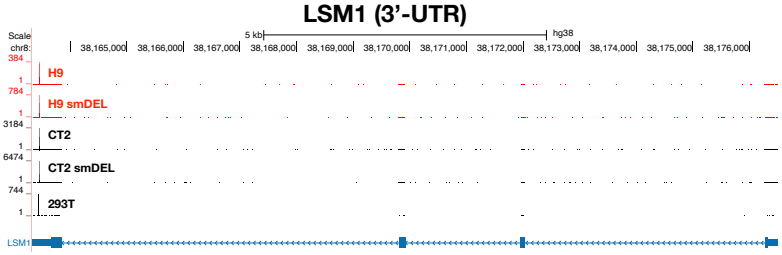
G


ENY2 (3'-UTR)
Scale
chr8:
5 kb
hg38
109,336,000
109,337,000
109,338,000
109,339,000
109,340,000
109,341,000
109,342,000
109,343,000
109,344,000
109,345,000
471
H9
1
891
H9 smDEL
1
6901
CT2
1
7652
CT2 smDEL
1
140
293T
1
ENY2

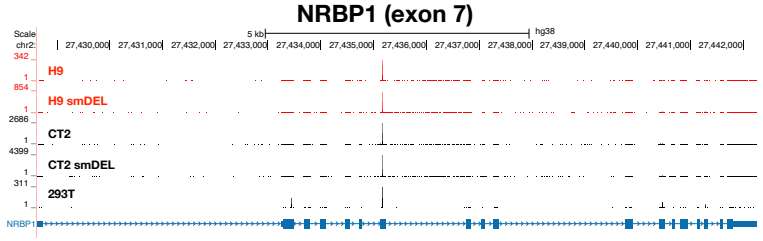
H


HIRA (exon 19)
Scale
chr22:
50 kb
hg38
19,340,000
19,350,000
19,360,000
19,370,000
19,380,000
19,390,000
19,400,000
19,410,000
19,420,000
19,430,000
101
H9
1
269
H9 smDEL
1
1972
CT2
1
2439
CT2 smDEL

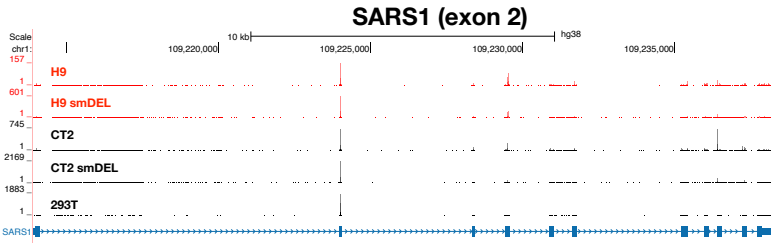
I


LSM1 (3'-UTR)
Scale
chr8:
5 kb
hg38
38,165,000
38,166,000
38,167,000
38,168,000
38,169,000
38,170,000
38,171,000
38,172,000
38,173,000
38,174,000
38,175,000
38,176,000
384
H9
1
784
H9 smDEL
1
3184
CT2
1
6474
CT2 smDEL
1
744
293T
1
LSM1

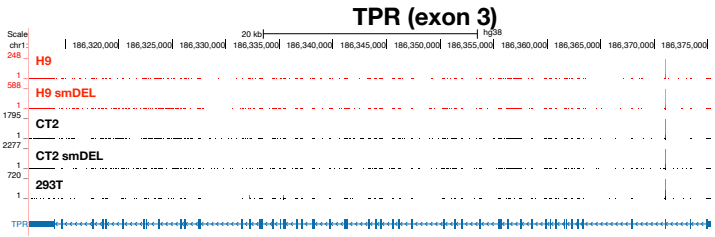
J

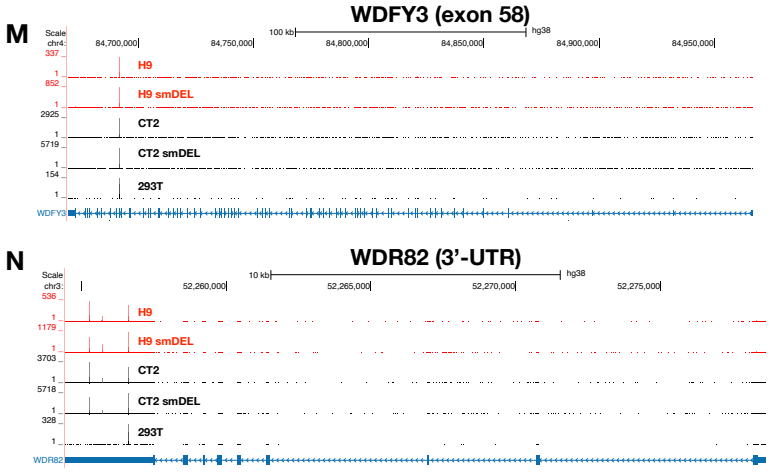

NRBP1 (exon 7)
Scale
chr2:
5 kb
hg38
27,430,000
27,431,000
27,432,000
27,433,000
27,434,000
27,435,000
27,436,000
27,437,000
27,438,000
27,439,000
27,440,000
27,441,000
27,442,000
342
H9
1
854
H9 smDEL
1
2686
CT2
1
4399
CT2 smDEL
1
311
293T
1
NRBP1

K

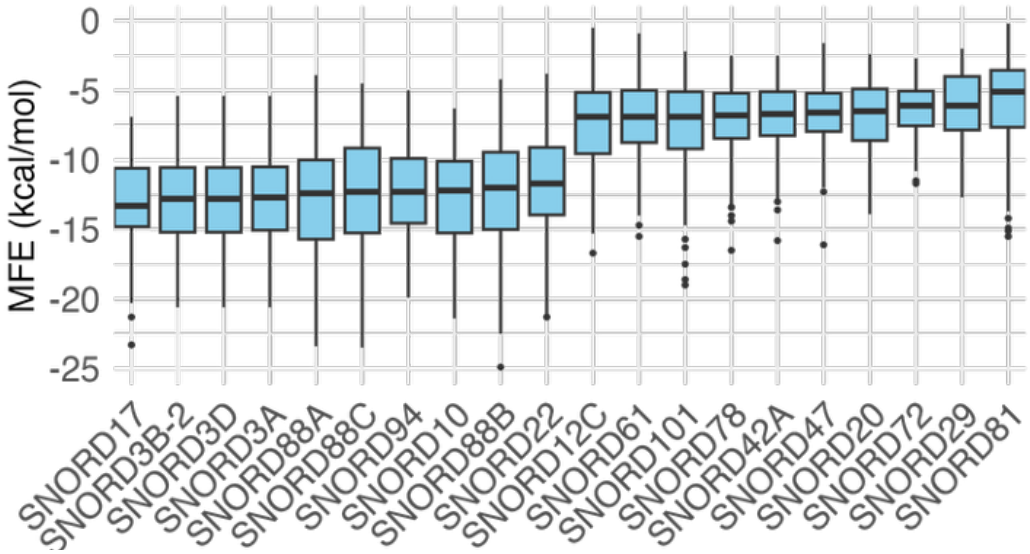

SARS1 (exon 2)
Scale
chr1:
10 kb
hg38
109,220,000
109,225,000
109,230,000
109,235,000
157
H9
1
601
H9 smDEL
1
745
CT2
1
2169
CT2 smDEL
1
1883
293T
1
SARS1

L

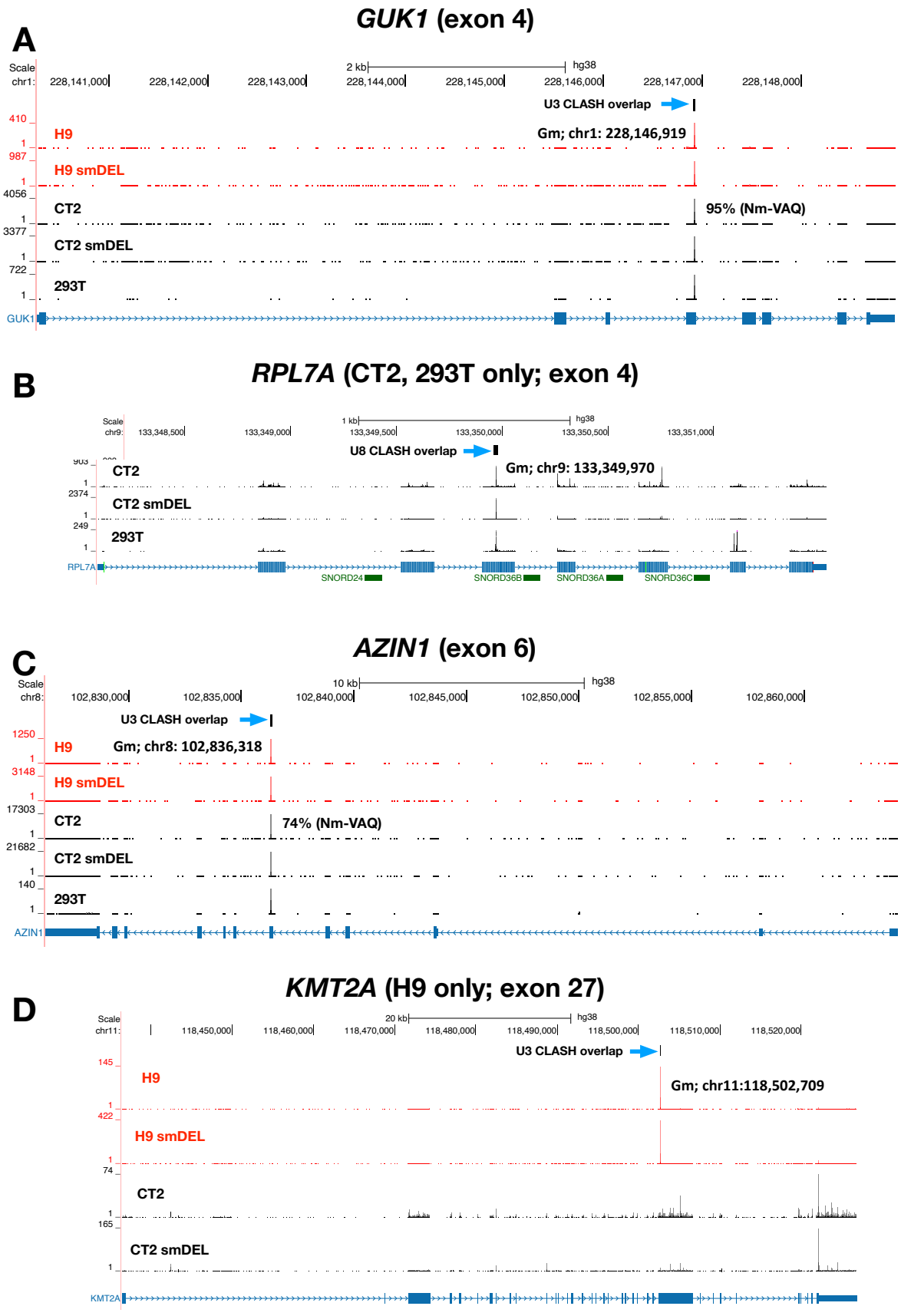

TPR (exon 3)
Scale
chr1:
20 kb
hg38
186,320,000
186,325,000
186,330,000
186,335,000
186,340,000
186,345,000
186,350,000
186,355,000
186,360,000
186,365,000
186,370,000
186,375,000
248
H9
1
588
H9 smDEL
1
1795
CT2
1
2277
CT2 smDEL
1
720
293T
1
TPR

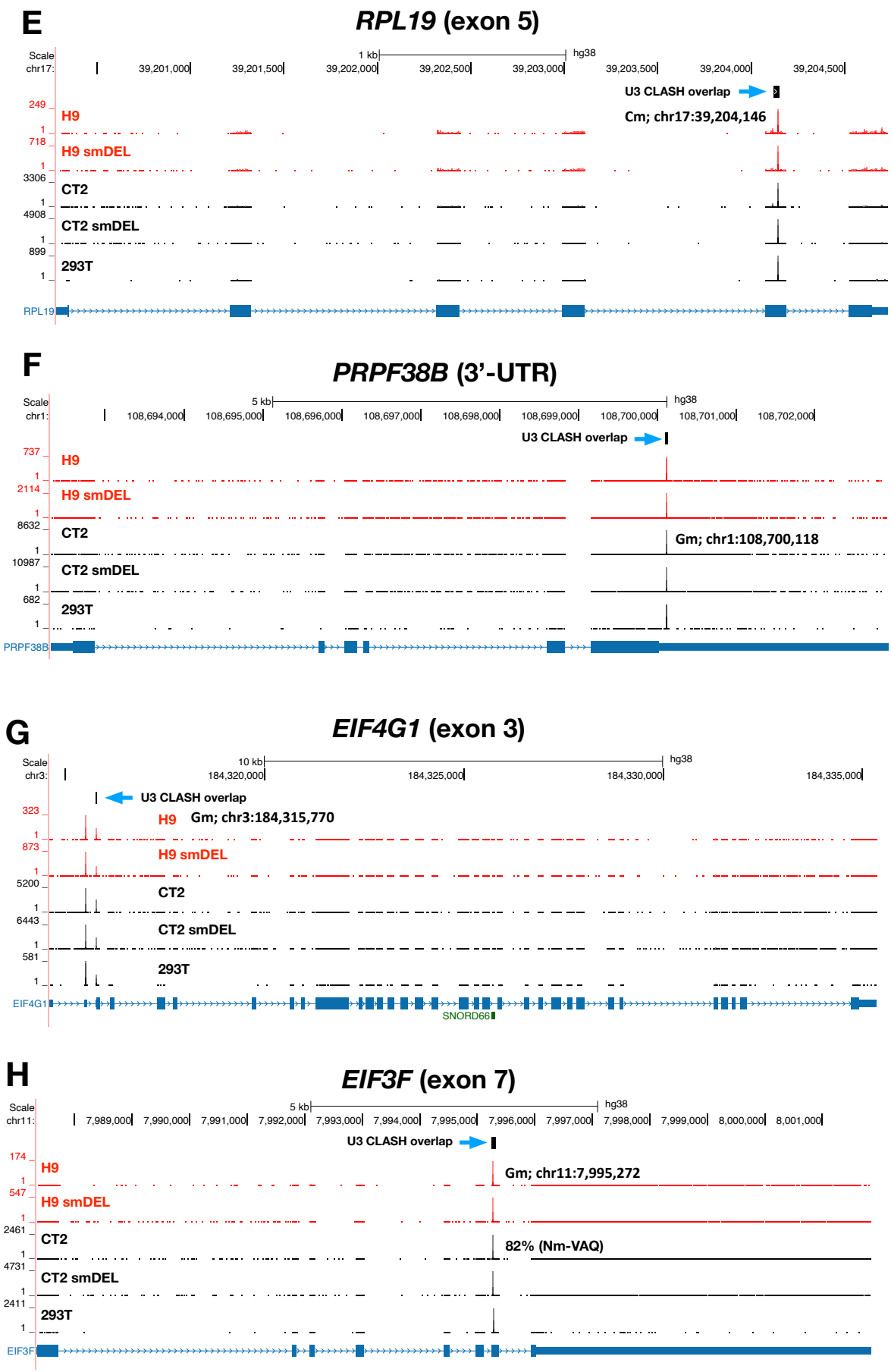


Supplementary Fig. 2. Some additional representative examples of Nm sites in mRNAs, illustrating similar modification profiles between dirrerent cells. Percentages adjacent to some peaks denote modification levels quantified by Nm-VAQ.



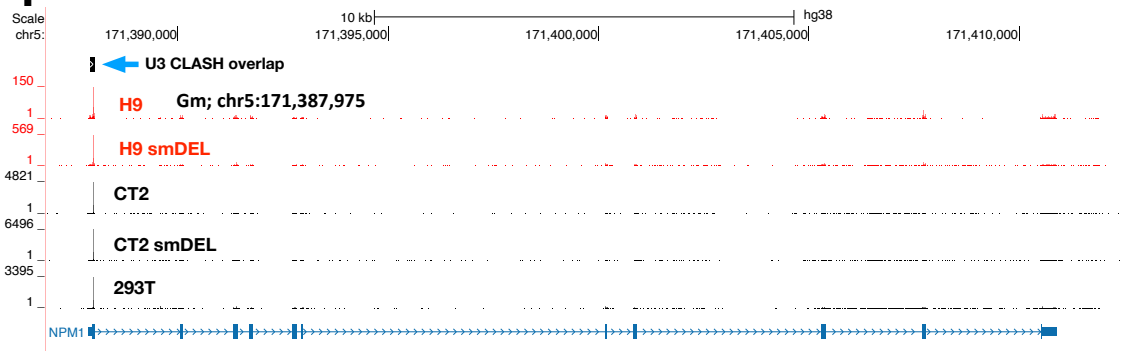
Supplementary Fig. 3. Box plot comparison of minimum folding energy (MFE) across snoRNAs and RNA regions encompassing each Nm site (±7 nt). For each snoRNA species, the potential MFE values are shown; boxes denote the 25th–75th percentiles with a line at the median, and whiskers indicate 1.5× the interquartile range.


A
GUK1 (exon 4)
Scale
chr1:
228,141,000
228,142,000
228,143,000
228,144,000
228,145,000
228,146,000
228,147,000
228,148,000
2 kb
hg38
U3 CLASH overlap
Gm; chr1: 228,146,919
H9
H9 smDEL
CT2
95% (Nm-VAQ)
CT2 smDEL
293T
GUK1
B
RPL7A (CT2, 293T only; exon 4)
Scale
chr9:
133,348,500
133,349,000
133,349,500
133,350,000
133,350,500
133,351,000
1 kb
hg38
U8 CLASH overlap
Gm; chr9: 133,349,970
CT2
CT2 smDEL
293T
RPL7A
SNORD24
SNORD36B
SNORD36A
SNORD36C
C
AZIN1 (exon 6)
Scale
chr8:
102,830,000
102,835,000
102,840,000
102,845,000
102,850,000
102,855,000
102,860,000
10 kb
hg38
U3 CLASH overlap
Gm; chr8: 102,836,318
H9
H9 smDEL
CT2
74% (Nm-VAQ)
CT2 smDEL
293T
AZIN1
D
KMT2A (H9 only; exon 27)
Scale
chr11:
118,450,000
118,460,000
118,470,000
118,480,000
118,490,000
118,500,000
118,510,000
118,520,000
20 kb
hg38
U3 CLASH overlap
Gm; chr11:118,502,709
H9
H9 smDEL
CT2
CT2 smDEL
KMT2A


E
RPL19 (exon 5)
Scale
chr17:
1 kb
hg38
39,201,000
39,201,500
39,202,000
39,202,500
39,203,000
39,203,500
39,204,000
39,204,500
U3 CLASH overlap
Cm; chr17:39,204,146
H9
H9 smDEL
CT2
CT2 smDEL
293T
RPL19
F
PRPF38B (3'-UTR)
Scale
chr1:
5 kb
hg38
108,694,000
108,695,000
108,696,000
108,697,000
108,698,000
108,699,000
108,700,000
108,701,000
108,702,000
U3 CLASH overlap
H9
H9 smDEL
CT2
Gm; chr1:108,700,118
CT2 smDEL
293T
PRPF38B
G
EIF4G1 (exon 3)
Scale
chr3:
10 kb
hg38
184,320,000
184,325,000
184,330,000
184,335,000
U3 CLASH overlap
H9
Gm; chr3:184,315,770
H9 smDEL
CT2
CT2 smDEL
293T
EIF4G1
SNORD66
H
EIF3F (exon 7)
Scale
chr11:
5 kb
hg38
7,989,000
7,990,000
7,991,000
7,992,000
7,993,000
7,994,000
7,995,000
7,996,000
7,997,000
7,998,000
7,999,000
8,000,000
8,001,000
U3 CLASH overlap
H9
Gm; chr11:7,995,272
H9 smDEL
CT2
82% (Nm-VAQ)
CT2 smDEL
293T
EIF3F

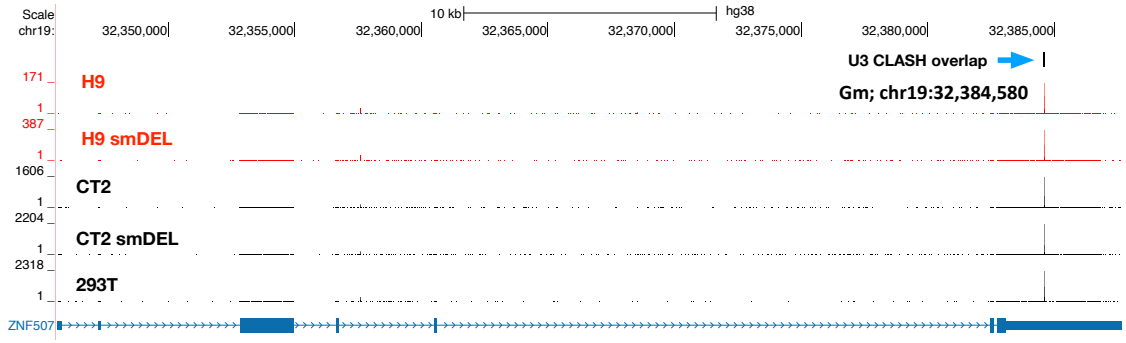
I

NPM1 (5'-UTR)



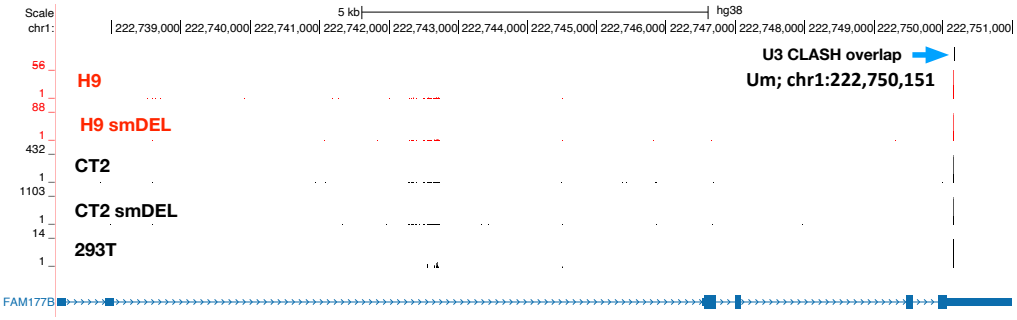
J

ZNF507 (3'-UTR)



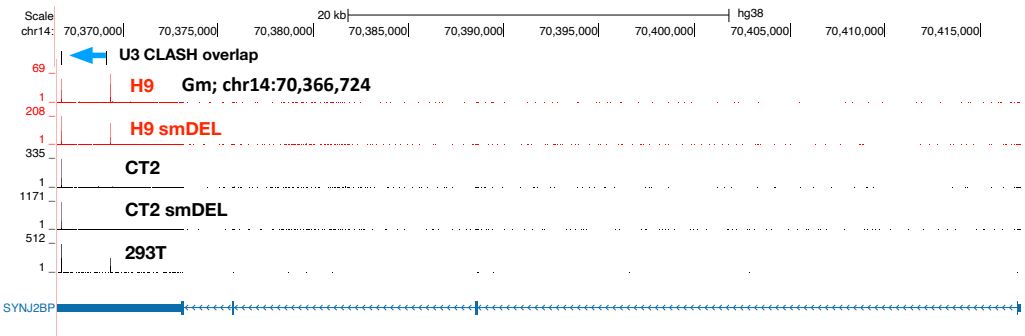
K

FAM177B (3'-UTR)

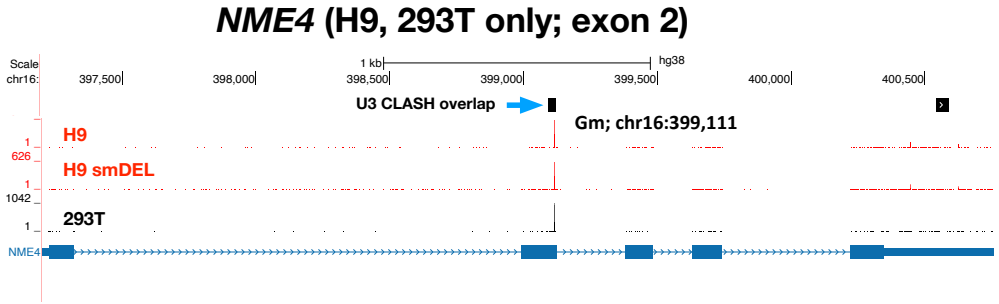


L

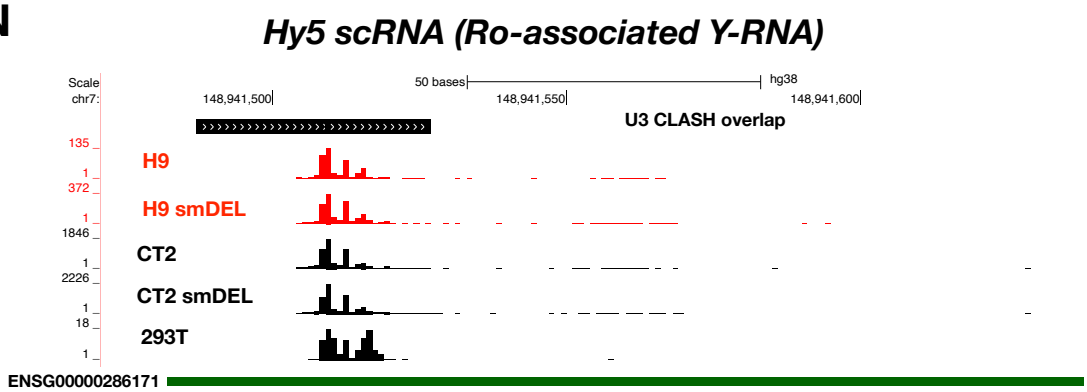
SYNJ2BP (3'-UTR)



M



N



Supplementary Fig. 4. Representative UCSC genome browser images illustrating bigWig tracks from CT2 and H9 induced neurons as well as small-deletion induced neurons and, in almost all cases, 293T cells. Nm positions are denoted by RibOxi-seq peaks, while U3 snoRNA CLASH fragment overlaps from HEK293T cells are shown at the top of each panel.