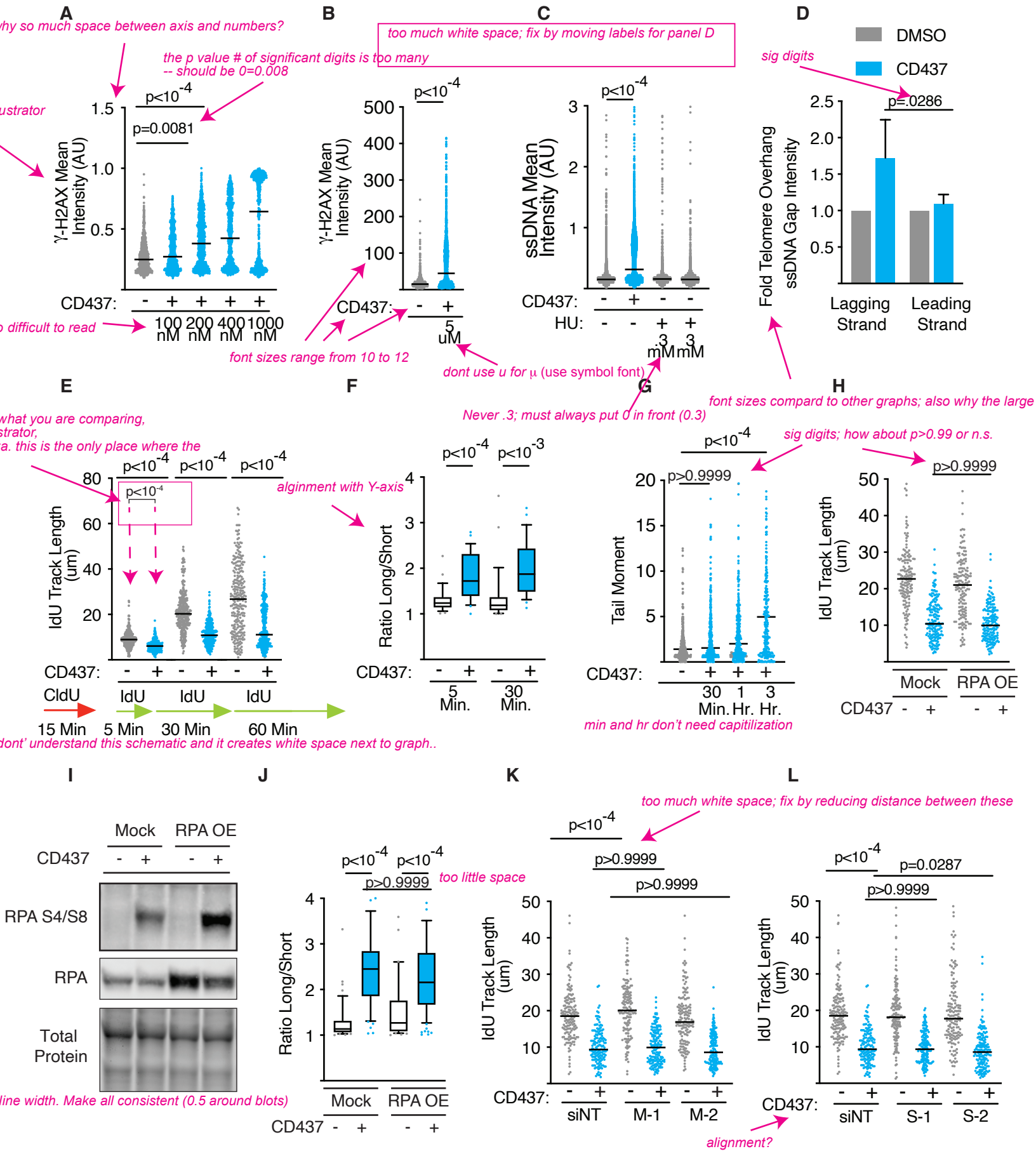
A
why so much space between axis and numbers?
the p value # of significant digits is too many
-- should be 0=0.008
ustrator
p<10-4
p=0.0081
γ-H2AX Mean Intensity (AU)
1.5
1.0
0.5
CD437: - + + + +
100 nM 200 nM 400 nM 1000 nM
o difficult to read
B
too much white space; fix by moving labels for panel D
p<10-4
γ-H2AX Mean Intensity (AU)
500
400
300
200
100
CD437: - +
5 uM
font sizes range from 10 to 12
C
p<10-4
ssDNA Mean Intensity (AU)
3
2
1
CD437: - + - -
HU: - - + +
.3 mM .3 mM
dont use u for μ (use symbol font)
D
DMSO
CD437
sig digits
p=.0286
Fold Telomere Overhang ssDNA Gap Intensity
2.5
2.0
1.5
1.0
0.5
Lagging Strand
Leading Strand
font sizes compard to other graphs; also why the large
E
what you are comparing,
strator,
a. this is the only place where the
p<10-4
p<10-4
p<10-4
p<10-4
IdU Track Length (um)
80
60
40
20
CD437: - + - + - +
CldU
IdU
IdU
IdU
15 Min
5 Min
30 Min
60 Min
dont' understand this schematic and it creates white space next to graph..
F
alginment with Y-axis
p<10-4
p<10-3
Ratio Long/Short
4
3
2
1
CD437: - + - +
5 Min.
30 Min.
Never .3; must always put 0 in front (0.3)
G
sig digits; how about p>0.99 or n.s.
p<10-4
p>0.9999
Tail Moment
20
15
10
5
CD437: - + + +
30 Min.
1 Hr.
3 Hr.
min and hr don't need capitilization
H
p>0.9999
IdU Track Length (um)
50
40
30
20
10
Mock
RPA OE
CD437 - + - +
I
Mock
RPA OE
CD437 - + - +
RPA S4/S8
RPA
Total Protein
line width. Make all consistent (0.5 around blots)
J
p<10-4
p<10-4
too little space
p>0.9999
Ratio Long/Short
4
3
2
1
Mock
RPA OE
CD437 - + - +
K
too much white space; fix by reducing distance between these
p<10-4
p>0.9999
p>0.9999
IdU Track Length (um)
50
40
30
20
10
CD437: - + - + - +
siNT
M-1
M-2
L
p<10-4
p=0.0287
p>0.9999
IdU Track Length (um)
50
40
30
20
10
CD437: - + - + - +
siNT
S-1
S-2
alignment?
JOurnals have standard width sizes for their figures based on column widths. Need to at least have margins on your figure pages