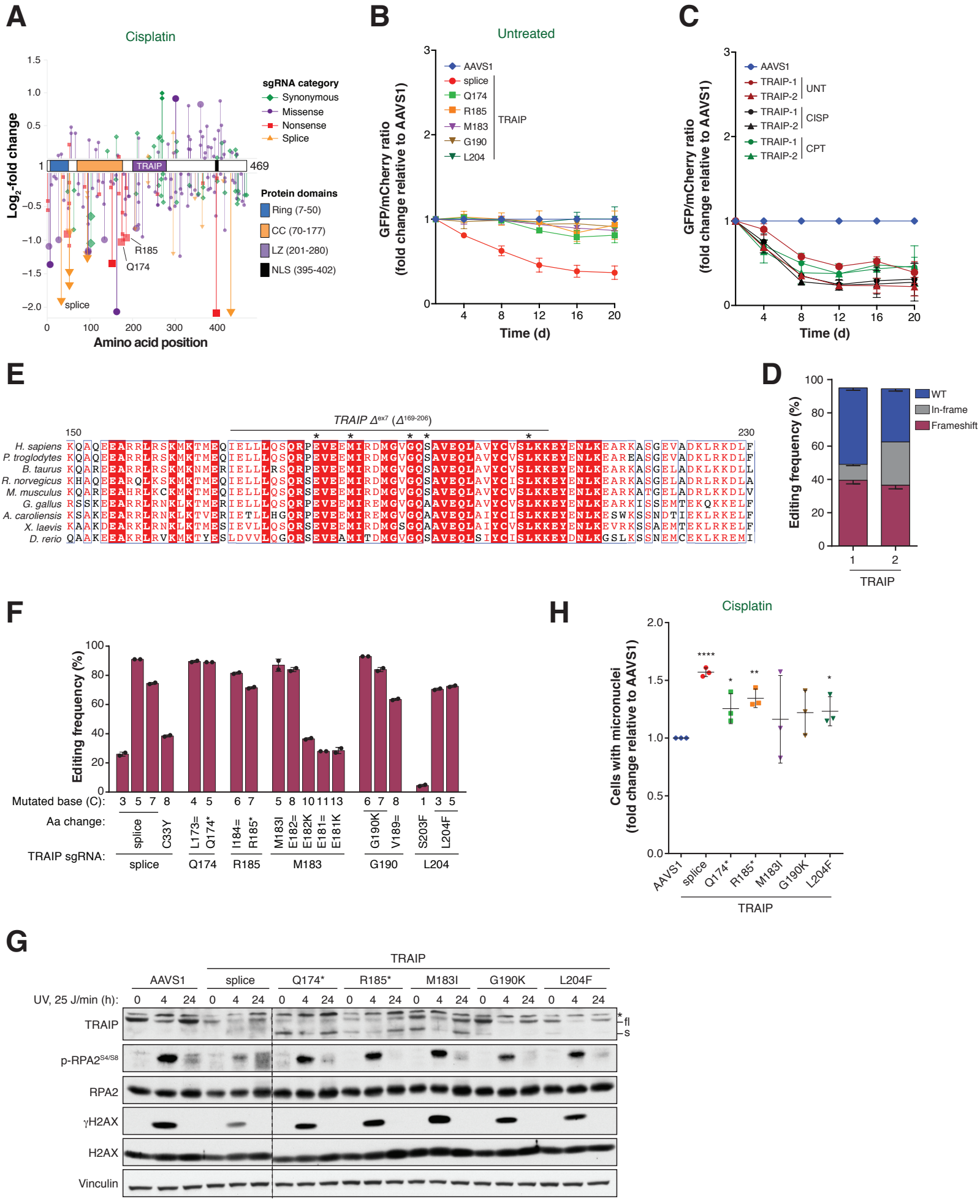
A
Cisplatin
Log2-fold change
Amino acid position
sgRNA category
Synonymous
Missense
Nonsense
Splice
Protein domains
Ring (7-50)
CC (70-177)
LZ (201-280)
NLS (395-402)
TRAIP
469
R185
Q174
splice
B
Untreated
GFP/mCherry ratio (fold change relative to AAVS1)
Time (d)
AAVS1
splice
Q174
R185
M183
G190
L204
TRAIP
C
GFP/mCherry ratio (fold change relative to AAVS1)
Time (d)
AAVS1
TRAIP-1
TRAIP-2
UNT
CISP
CPT
E
TRAIP Δex7 (Δ169-206)
H. sapiens
P. troglodytes
B. taurus
R. norvegicus
M. musculus
G. gallus
A. caroliensis
X. laevis
D. rerio
D
Editing frequency (%)
WT
In-frame
Frameshift
TRAIP
F
Editing frequency (%)
Mutated base (C):
Aa change:
TRAIP sgRNA:
splice
C33Y
L173=
Q174*
I184=
R185*
M183I
E182=
E182K
E181=
E181K
G190K
V189=
S203F
L204F
splice
Q174
R185
M183
G190
L204
H
Cisplatin
Cells with micronuclei (fold change relative to AAVS1)
AAVS1
splice
Q174*
R185*
M183I
G190K
L204F
TRAIP
G
TRAIP
AAVS1
splice
Q174*
R185*
M183I
G190K
L204F
UV, 25 J/min (h):
TRAIP
p-RPA2S4/S8
RPA2
γH2AX
H2AX
Vinculin
fl
s

Figure S4