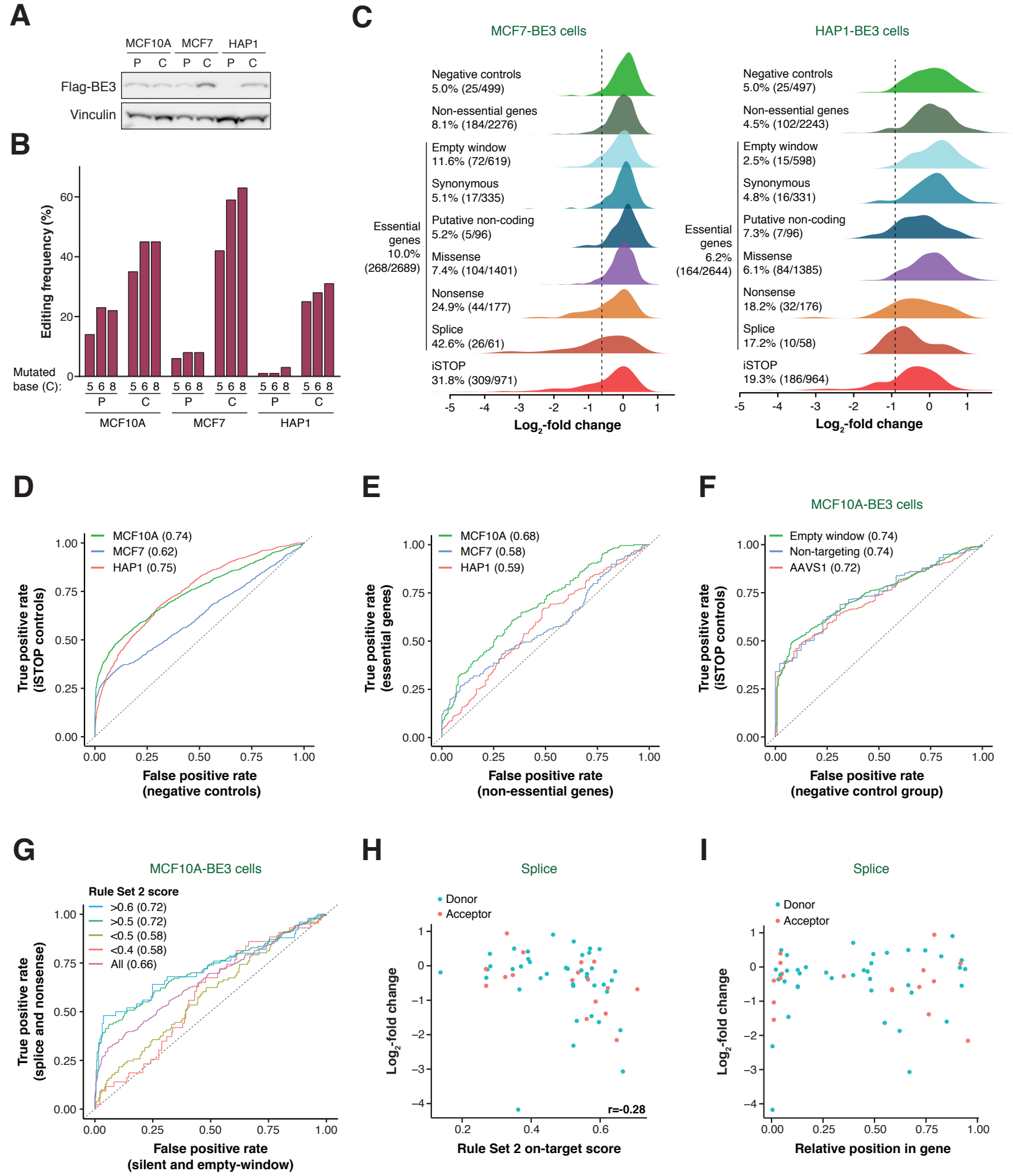
A
MCF10A
MCF7
HAP1
P C P C P C
Flag-BE3
Vinculin
B
Editing frequency (%)
Mutated base (C):
5 6 8
P
C
MCF10A
MCF7
HAP1
C
MCF7-BE3 cells
HAP1-BE3 cells
Negative controls 5.0% (25/499)
Non-essential genes 8.1% (184/2276)
Empty window 11.6% (72/619)
Synonymous 5.1% (17/335)
Putative non-coding 5.2% (5/96)
Missense 7.4% (104/1401)
Nonsense 24.9% (44/177)
Splice 42.6% (26/61)
iSTOP 31.8% (309/971)
Essential genes 10.0% (268/2689)
Negative controls 5.0% (25/497)
Non-essential genes 4.5% (102/2243)
Empty window 2.5% (15/598)
Synonymous 4.8% (16/331)
Putative non-coding 7.3% (7/96)
Missense 6.1% (84/1385)
Nonsense 18.2% (32/176)
Splice 17.2% (10/58)
iSTOP 19.3% (186/964)
Essential genes 6.2% (164/2644)
Log2-fold change
D
MCF10A (0.74)
MCF7 (0.62)
HAP1 (0.75)
True positive rate (iSTOP controls)
False positive rate (negative controls)
E
MCF10A (0.68)
MCF7 (0.58)
HAP1 (0.59)
True positive rate (essential genes)
False positive rate (non-essential genes)
F
MCF10A-BE3 cells
Empty window (0.74)
Non-targeting (0.74)
AAVS1 (0.72)
True positive rate (iSTOP controls)
False positive rate (negative control group)
G
MCF10A-BE3 cells
Rule Set 2 score
>0.6 (0.72)
>0.5 (0.72)
<0.5 (0.58)
<0.4 (0.58)
All (0.66)
True positive rate (splice and nonsense)
False positive rate (silent and empty-window)
H
Splice
Donor
Acceptor
Log2-fold change
r=-0.28
Rule Set 2 on-target score
I
Splice
Donor
Acceptor
Log2-fold change
Relative position in gene

Figure S1