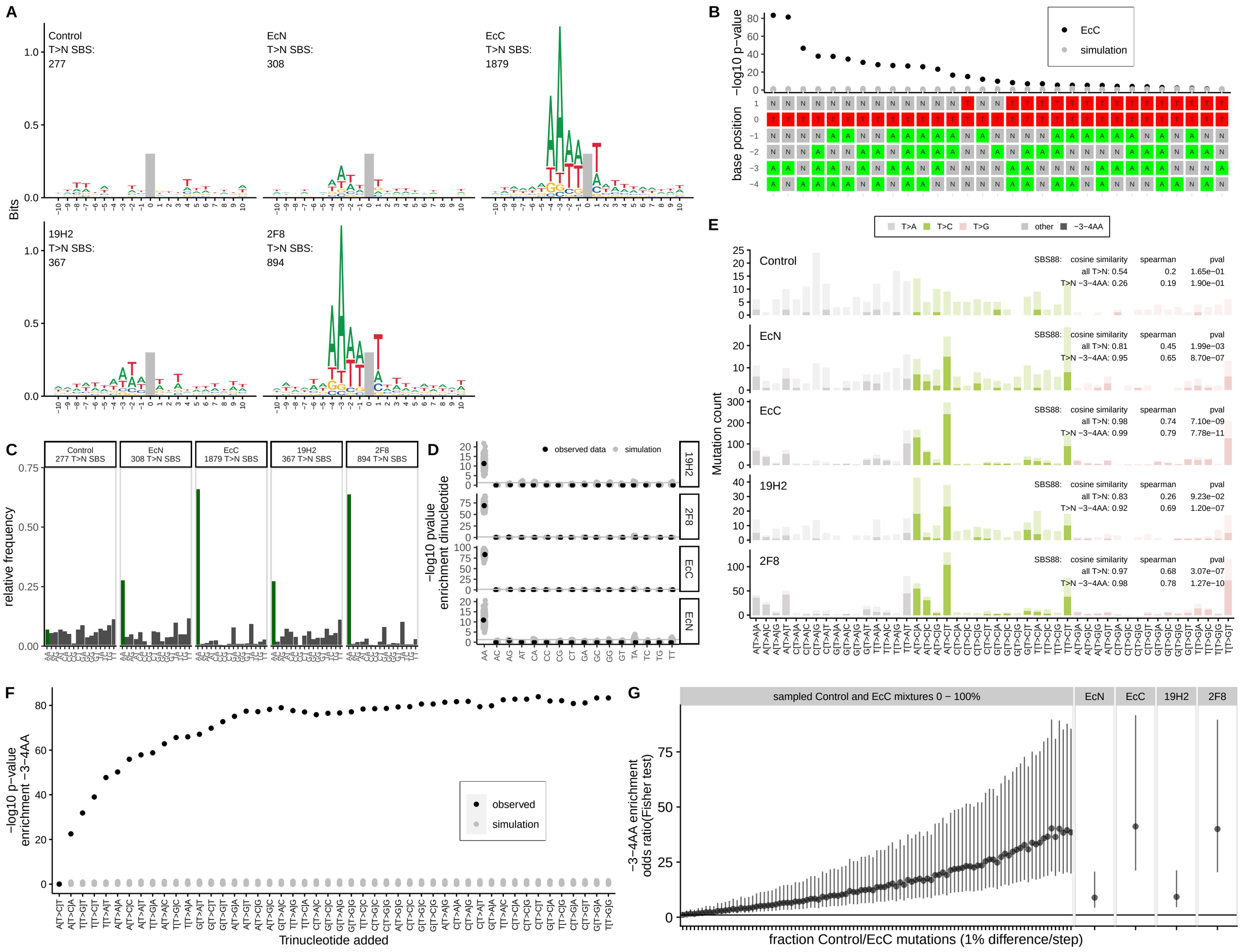
A
Control
T>N SBS:
277
EcN
T>N SBS:
308
EcC
T>N SBS:
1879
19H2
T>N SBS:
367
2F8
T>N SBS:
894
Bits
B
−log10 p−value
base position
EcC
simulation
C
Control
277 T>N SBS
EcN
308 T>N SBS
EcC
1879 T>N SBS
19H2
367 T>N SBS
2F8
894 T>N SBS
relative frequency
D
observed data
simulation
−log10 pvalue
enrichment dinucleotide
19H2
2F8
EcC
EcN
E
T>A
T>C
T>G
other
−3−4AA
Mutation count
Control
EcN
EcC
19H2
2F8
SBS88: cosine similarity spearman pval
all T>N: 0.54 0.2 1.65e−01
T>N −3−4AA: 0.26 0.19 1.90e−01
SBS88: cosine similarity spearman pval
all T>N: 0.81 0.45 1.99e−03
T>N −3−4AA: 0.95 0.65 8.70e−07
SBS88: cosine similarity spearman pval
all T>N: 0.98 0.74 7.10e−09
T>N −3−4AA: 0.99 0.79 7.78e−11
SBS88: cosine similarity spearman pval
all T>N: 0.83 0.26 9.23e−02
T>N −3−4AA: 0.92 0.69 1.20e−07
SBS88: cosine similarity spearman pval
all T>N: 0.97 0.68 3.07e−07
T>N −3−4AA: 0.98 0.78 1.27e−10
F
−log10 p−value
enrichment −3−4AA
observed
simulation
Trinucleotide added
G
sampled Control and EcC mixtures 0 − 100%
EcN
EcC
19H2
2F8
−3−4AA enrichment
odds ratio(Fisher test)
fraction Control/EcC mutations (1% difference/step)