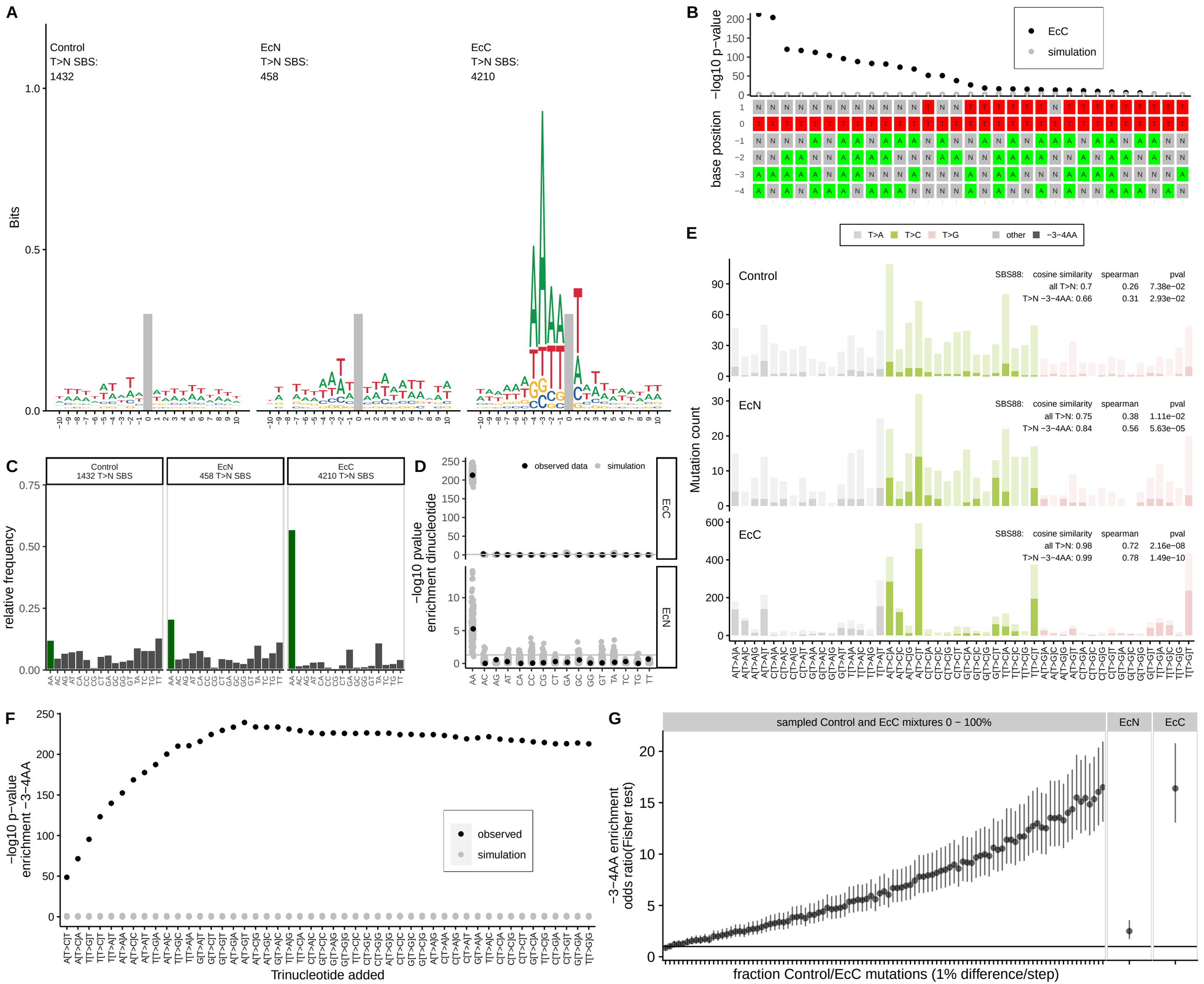
A
Control
T>N SBS:
1432
EcN
T>N SBS:
458
EcC
T>N SBS:
4210
Bits
B
−log10 p−value
base position
EcC
simulation
C
Control
1432 T>N SBS
EcN
458 T>N SBS
EcC
4210 T>N SBS
relative frequency
D
observed data
simulation
−log10 pvalue
enrichment dinucleotide
EcC
EcN
E
T>A
T>C
T>G
other
−3−4AA
Control
SBS88: cosine similarity spearman pval
all T>N: 0.7 0.26 7.38e−02
T>N −3−4AA: 0.66 0.31 2.93e−02
EcN
SBS88: cosine similarity spearman pval
all T>N: 0.75 0.38 1.11e−02
T>N −3−4AA: 0.84 0.56 5.63e−05
EcC
SBS88: cosine similarity spearman pval
all T>N: 0.98 0.72 2.16e−08
T>N −3−4AA: 0.99 0.78 1.49e−10
Mutation count
F
−log10 p−value
enrichment −3−4AA
observed
simulation
Trinucleotide added
G
sampled Control and EcC mixtures 0 − 100%
EcN
EcC
−3−4AA enrichment
odds ratio(Fisher test)
fraction Control/EcC mutations (1% difference/step)