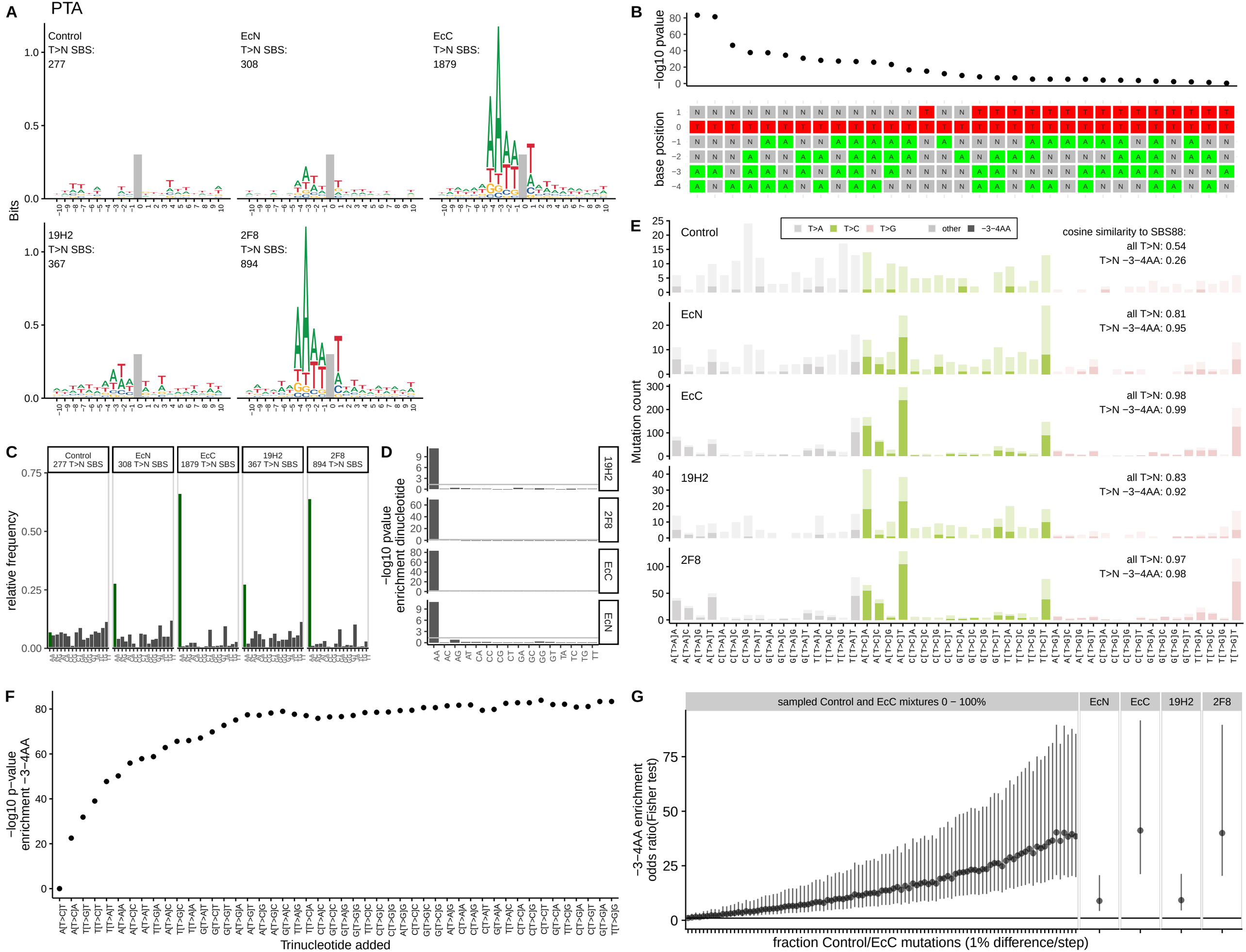
A
PTA
Control
T>N SBS:
277
EcN
T>N SBS:
308
EcC
T>N SBS:
1879
19H2
T>N SBS:
367
2F8
T>N SBS:
894
Bits
B
−log10 pvalue
base position
C
Control
277 T>N SBS
EcN
308 T>N SBS
EcC
1879 T>N SBS
19H2
367 T>N SBS
2F8
894 T>N SBS
relative frequency
D
−log10 pvalue
enrichment dinucleotide
19H2
2F8
EcC
EcN
E
Control
T>A
T>C
T>G
other
−3−4AA
cosine similarity to SBS88:
all T>N: 0.54
T>N −3−4AA: 0.26
EcN
all T>N: 0.81
T>N −3−4AA: 0.95
EcC
all T>N: 0.98
T>N −3−4AA: 0.99
19H2
all T>N: 0.83
T>N −3−4AA: 0.92
2F8
all T>N: 0.97
T>N −3−4AA: 0.98
Mutation count
F
−log10 p−value
enrichment −3−4AA
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)