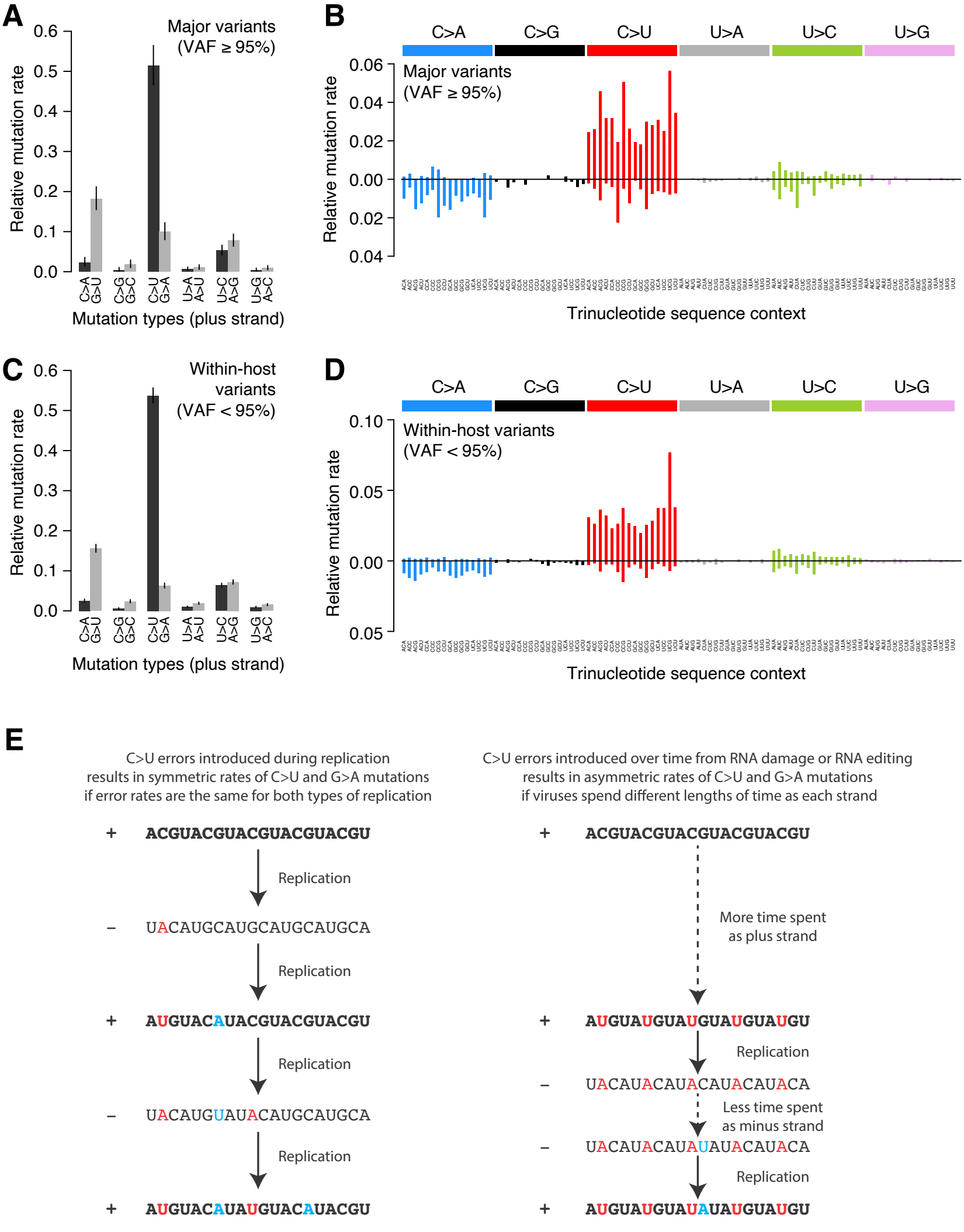
A
Major variants
(VAF ≥ 95%)
Relative mutation rate
0.6
0.5
0.4
0.3
0.2
0.1
0.0
C>A G>U
C>G G>C
C>U G>A
U>A A>U
U>C A>G
U>G A>C
Mutation types (plus strand)
B
C>A
C>G
C>U
U>A
U>C
U>G
Major variants
(VAF ≥ 95%)
Relative mutation rate
0.06
0.04
0.02
0.00
0.02
0.04
Trinucleotide sequence context
C
Within-host
variants
(VAF < 95%)
Relative mutation rate
0.6
0.5
0.4
0.3
0.2
0.1
0.0
C>A G>U
C>G G>C
C>U G>A
U>A A>U
U>C A>G
U>G A>C
Mutation types (plus strand)
D
C>A
C>G
C>U
U>A
U>C
U>G
Within-host variants
(VAF < 95%)
Relative mutation rate
0.10
0.05
0.00
0.05
Trinucleotide sequence context
E
C>U errors introduced during replication
results in symmetric rates of C>U and G>A mutations
if error rates are the same for both types of replication
+ ACGUACGUACGUACGUACGU
Replication
– UACAUGCAUGCAUGCAUGCA
Replication
+ AUGUACAUACGUACGUACGU
Replication
– UACAUGUAUACAUGCAUGCA
Replication
+ AUGUACAUAUGUACAUACGU
C>U errors introduced over time from RNA damage or RNA editing
results in asymmetric rates of C>U and G>A mutations
if viruses spend different lengths of time as each strand
+ ACGUACGUACGUACGUACGU
More time spent
as plus strand
+ AUGUAUGUAUGUAUGUAUGU
Replication
– UACAUACAUACAUACAUACA
Less time spent
as minus strand
– UACAUACAUAUAUACAUACA
Replication
+ AUGUAUGUAUAUAUGUAUGU