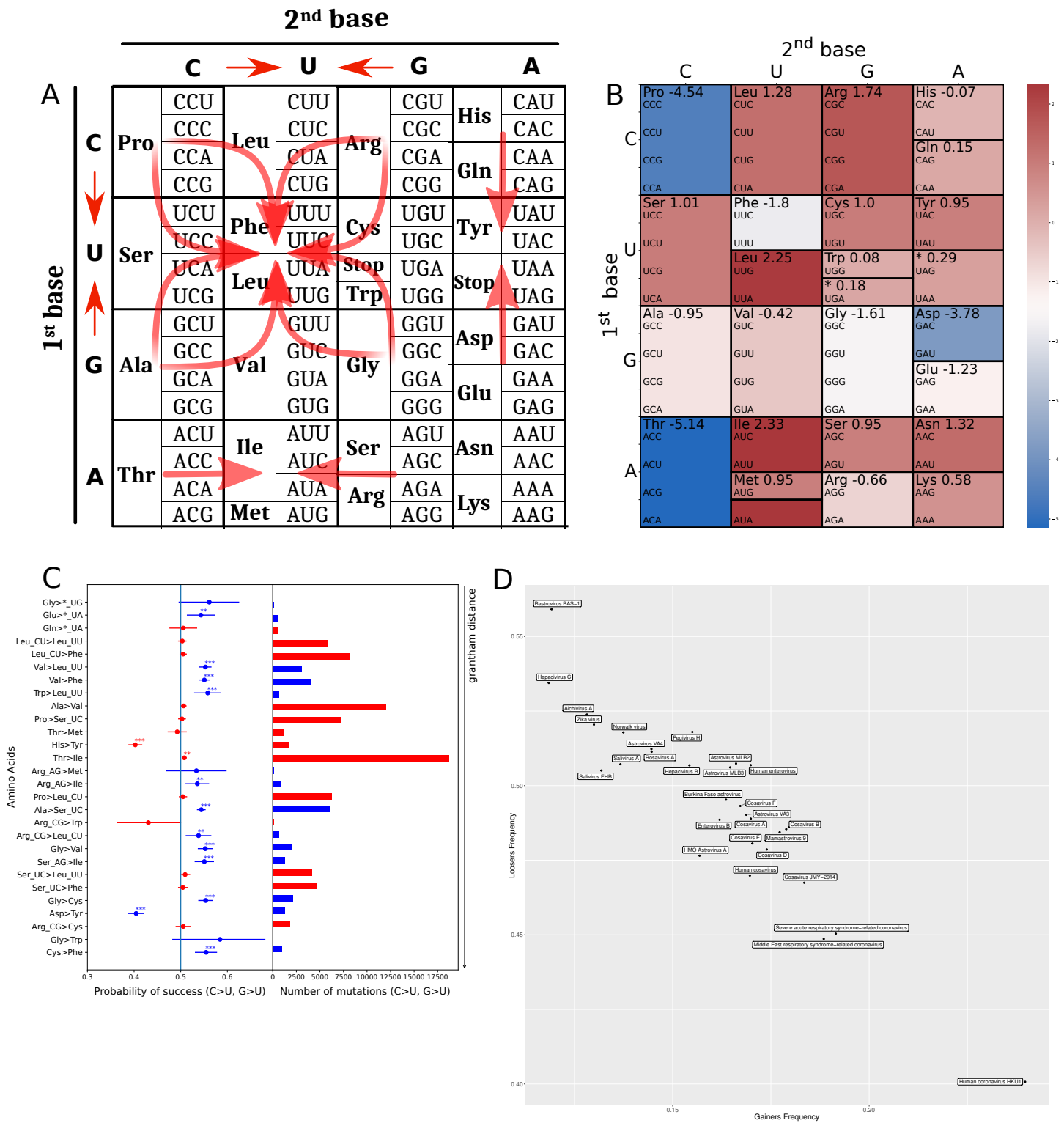
A
2nd base
C
U
G
A
1st base
C
U
G
A
Pro
Leu
Arg
His
Gln
Ser
Phe
Cys
Tyr
Leu
Stop
Stop
Trp
Ala
Val
Gly
Asp
Glu
Thr
Ile
Ser
Asn
Met
Arg
Lys
CCU CCC CCA CCG
CUU CUC CUA CUG
CGU CGC CGA CGG
CAU CAC CAA CAG
UCU UCC UCA UCG
UUU UUC UUA UUG
UGU UGC UGA UGG
UAU UAC UAA UAG
GCU GCC GCA GCG
GUU GUC GUA GUG
GGU GGC GGA GGG
GAU GAC GAA GAG
ACU ACC ACA ACG
AUU AUC AUA AUG
AGU AGC AGA AGG
AAU AAC AAA AAG
B
2nd base
C
U
G
A
1st base
C
U
G
A
Pro -4.54
Leu 1.28
Arg 1.74
His -0.07
Gln 0.15
Ser 1.01
Phe -1.8
Cys 1.0
Tyr 0.95
Leu 2.25
Trp 0.08
* 0.29
* 0.18
Ala -0.95
Val -0.42
Gly -1.61
Asp -3.78
Glu -1.23
Thr -5.14
Ile 2.33
Ser 0.95
Asn 1.32
Met 0.95
Arg -0.66
Lys 0.58
C
Amino Acids
Probability of success (C>U, G>U)
Number of mutations (C>U, G>U)
grantham distance
D
Loosers Frequency
Gainers Frequency
Bastrovirus BAS-1
Hepacivirus C
Aichivirus A
Zika virus
Norwalk virus
Pegivirus H
Astrovirus VA4
Sailvirus A
Rosavirus A
Astrovirus MLB2
Sailvirus FHB
Hepacivirus B
Astrovirus MLB3
Human enterovirus
Burkina Faso astrovirus
Cosavirus F
Astrovirus VA3
Enterovirus B
Cosavirus A
Cosavirus B
Cosavirus E
Mamastrovirus 9
HMO Astrovirus A
Cosavirus D
Human cosavirus
Cosavirus JMY-2014
Severe acute respiratory syndrome-related coronavirus
Middle East respiratory syndrome-related coronavirus
Human coronavirus HKU1

Figure 3