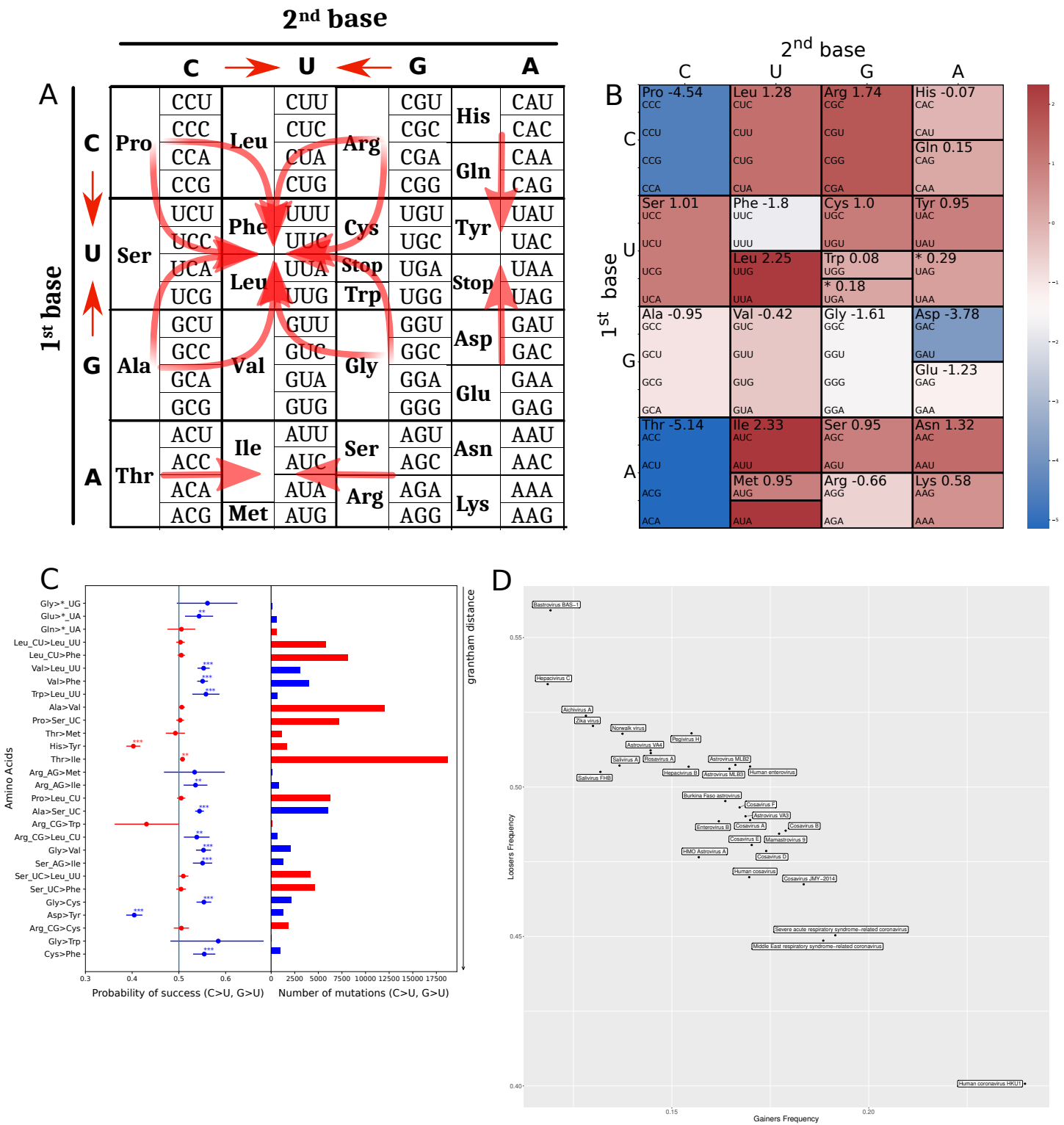
A
2nd base
C
U
G
A
1st base
C
U
G
A
Pro
Leu
Arg
His
Gln
Ser
Phe
Cys
Tyr
Leu
Stop
Stop
Trp
Ala
Val
Gly
Asp
Glu
Thr
Ile
Ser
Asn
Met
Arg
Lys
CCU CCC CCA CCG
CUU CUC CUA CUG
CGU CGC CGA CGG
CAU CAC
CAA CAG
UCU UCC UCA UCG
UUU UUC UUA UUG
UGU UGC UGA UGG
UAU UAC
UAA UAG
GCU GCC GCA GCG
GUU GUC GUA GUG
GGU 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
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
Looseers Frequency
Gainers Frequency

Figure 4