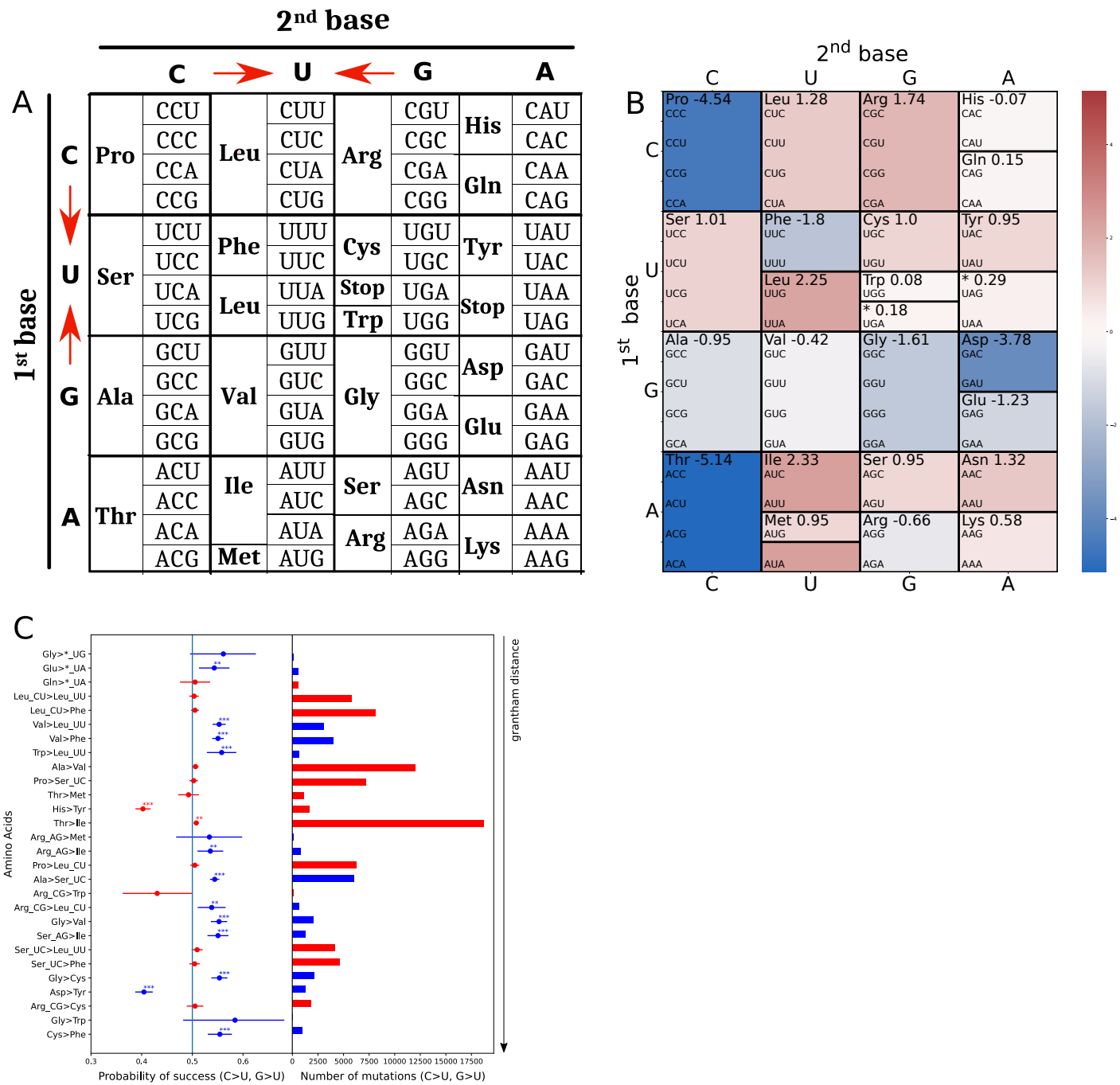
A
2nd base
C
U
G
A
1st base
C
U
G
A
Pro
Leu
Arg
His
Gln
Ser
Phe
Cys
Tyr
Stop
Ala
Val
Gly
Asp
Glu
Thr
Ile
Ser
Asn
Met
Lys
CCU CCC CCA CCG
CUU CUC CUA CUG
CGU CGC CGA CGG
CAU CAC
CAA CAG
UCU UCC UCA UCG
UUU UUC UUA UUG
UGU UGC UGA UGG
UAU UAC
UAA UAG
GCU GCC GCA GCG
GUU GUC GUA GUG
GGU GGC GGA GGG
GAU 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
CCC CCU CCG CCA
Leu 1.28
CUC CUU CUG CUA
Arg 1.74
CGC CGU CGG CGA
His -0.07
CAC CAU
Gln 0.15
CAG CAA
Ser 1.01
UCC UCU UCG UCA
Phe -1.8
UUC UUU
Cys 1.0
UGC UGU
Tyr 0.95
UAC UAU
Leu 2.25
UUG UUA
Trp 0.08
UGG
* 0.18
UGA
* 0.29
UAG UAA
Ala -0.95
GCC GCU GCG GCA
Val -0.42
GUC GUU GUG GUA
Gly -1.61
GGC GGU GGG GGA
Asp -3.78
GAC GAU
Glu -1.23
GAG GAA
Thr -5.14
ACC ACU ACG ACA
Ile 2.33
AUC AUU
Ser 0.95
AGC AGU
Asn 1.32
AAC AAU
Met 0.95
AUG
Arg -0.66
AGG AGA
Lys 0.58
AAG AAA
C
Amino Acids
Gly>*_UG
Glu>*_UA
Gln>*_UA
Leu_CU>Leu_UU
Leu_CU>Phe
Val>Leu_UU
Val>Phe
Trp>Leu_UU
Ala>Val
Pro>Ser_UC
Thr>Met
His>Tyr
Thr>Ile
Arg_AG>Met
Arg_AG>Ile
Pro>Leu_CU
Ala>Ser_UC
Arg_CG>Trp
Arg_CG>Leu_CU
Gly>Val
Ser_AG>Ile
Ser_UC>Leu_UU
Ser_UC>Phe
Gly>Cys
Asp>Tyr
Arg_CG>Cys
Gly>Trp
Cys>Phe
grantham distance
Probability of success (C>U, G>U)
Number of mutations (C>U, G>U)

Figure 4