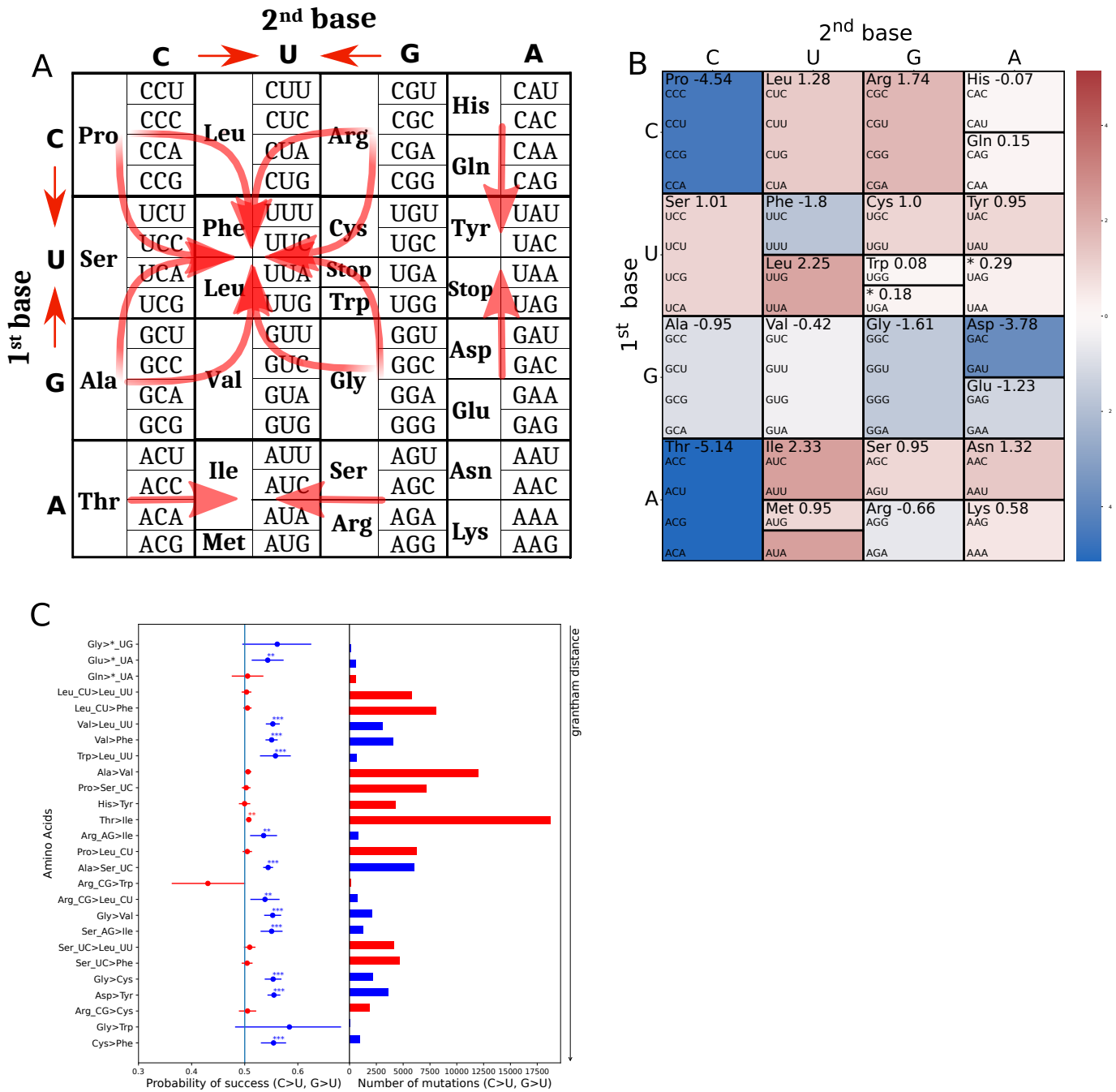
A
2nd base
C
U
G
A
1st base
C
U
G
A
Pro
Leu
Arg
His
Gln
CCU
CCC
CCA
CCG
CUU
CUC
CUA
CUG
CGU
CGC
CGA
CGG
CAU
CAC
CAA
CAG
Ser
Phe
Cys
Tyr
Stop
Trp
UCU
UCC
UCA
UCG
UUU
UUC
UUA
UUG
UGU
UGC
UGA
UGG
UAU
UAC
UAA
UAG
Ala
Val
Gly
Asp
Glu
GCU
GCC
GCA
GCG
GUU
GUC
GUA
GUG
GGU
GGC
GGA
GGG
GAU
GAC
GAA
GAG
Thr
Ile
Met
Ser
Arg
Asn
Lys
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
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
Met 0.95
AUG
AUA
Ser 0.95
AGC
AGU
Arg -0.66
AGG
AGA
Asn 1.32
AAC
AAU
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
His>Tyr
Thr>Ile
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
0.3
0.4
0.5
0.6
Probability of success (C>U, G>U)
0
2500
5000
7500
10000
12500
15000
17500
Number of mutations (C>U, G>U)
grantham distance

Figure 4