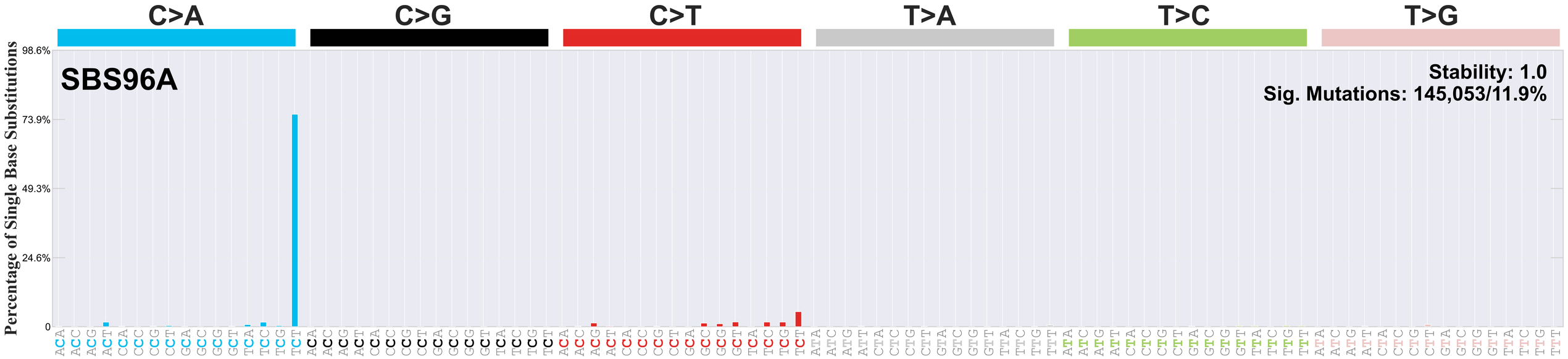
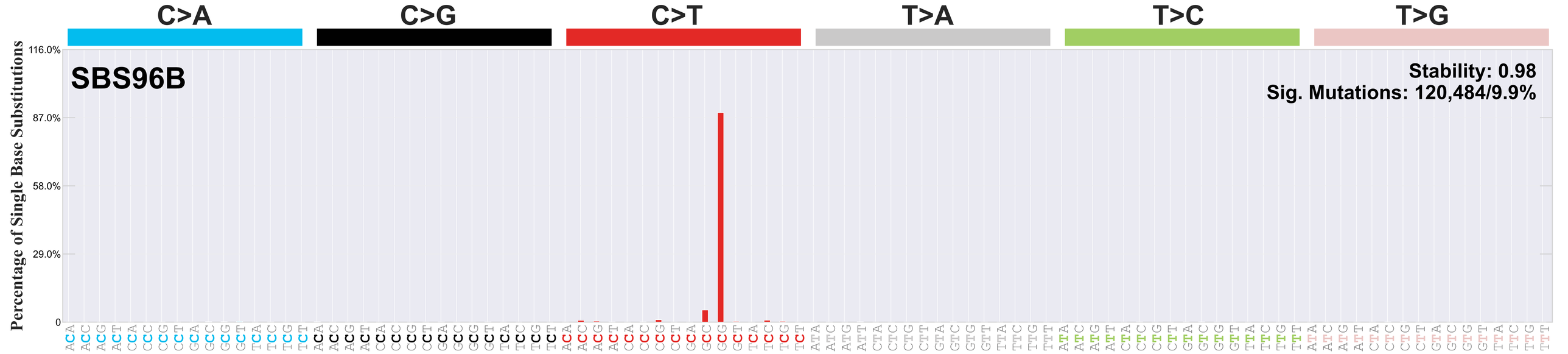
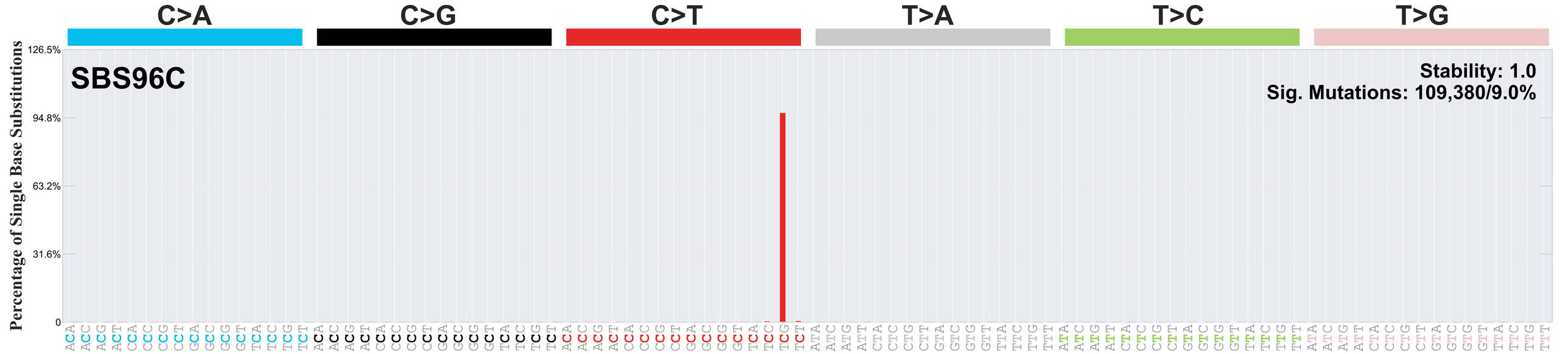
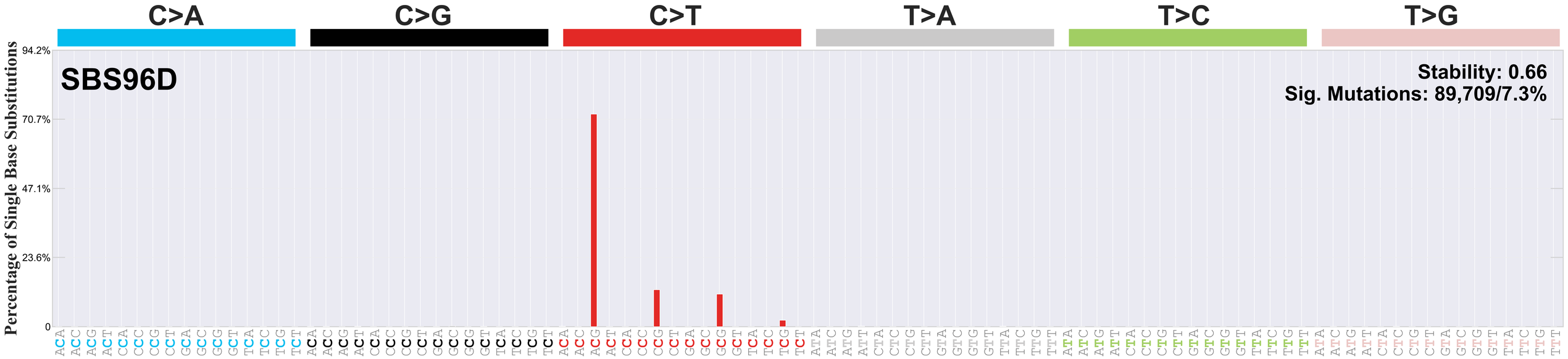
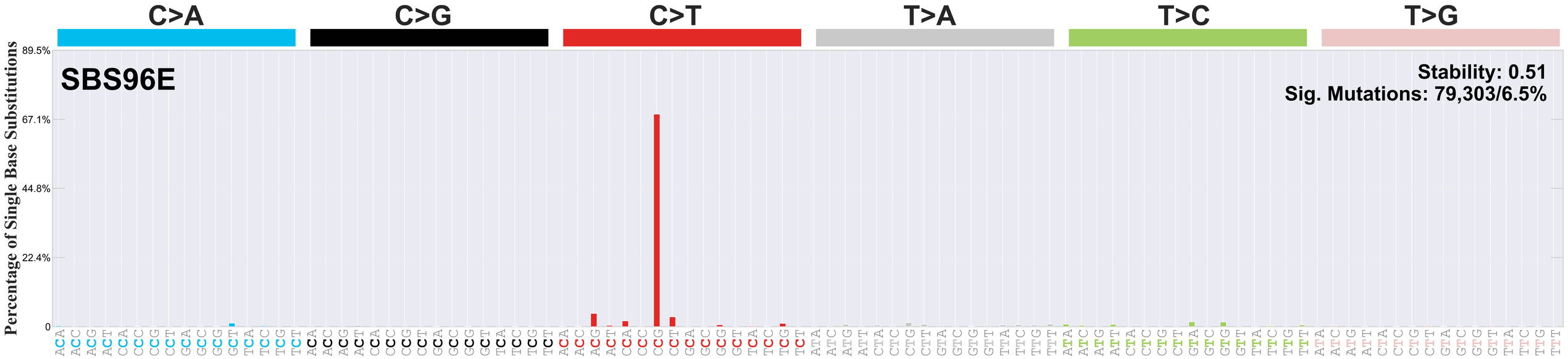
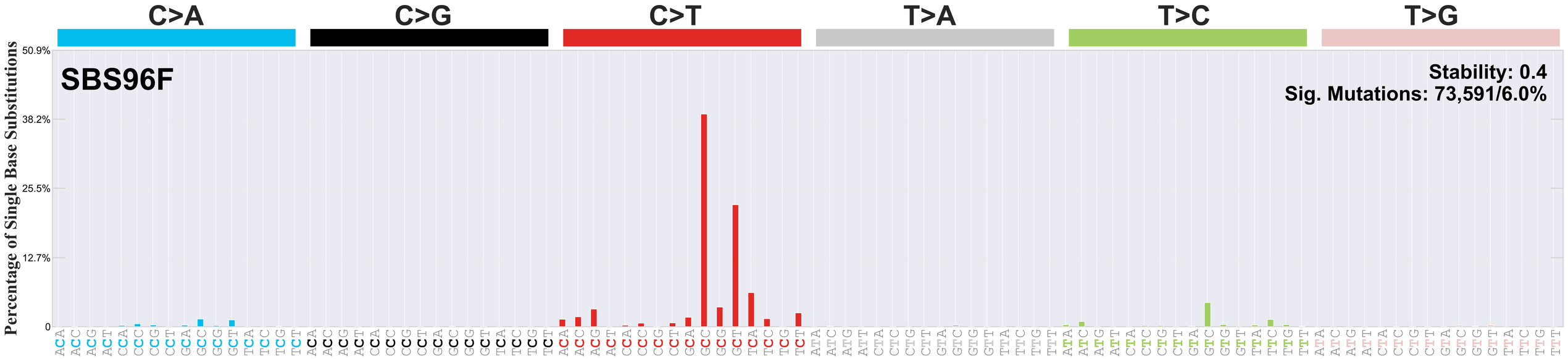

C>A
C>G
C>T
T>A
T>C
T>G
SBS96A
Stability: 1.0
Sig. Mutations: 145,053/11.9%
Percentage of Single Base Substitutions
98.6%
73.9%
49.3%
24.6%
0

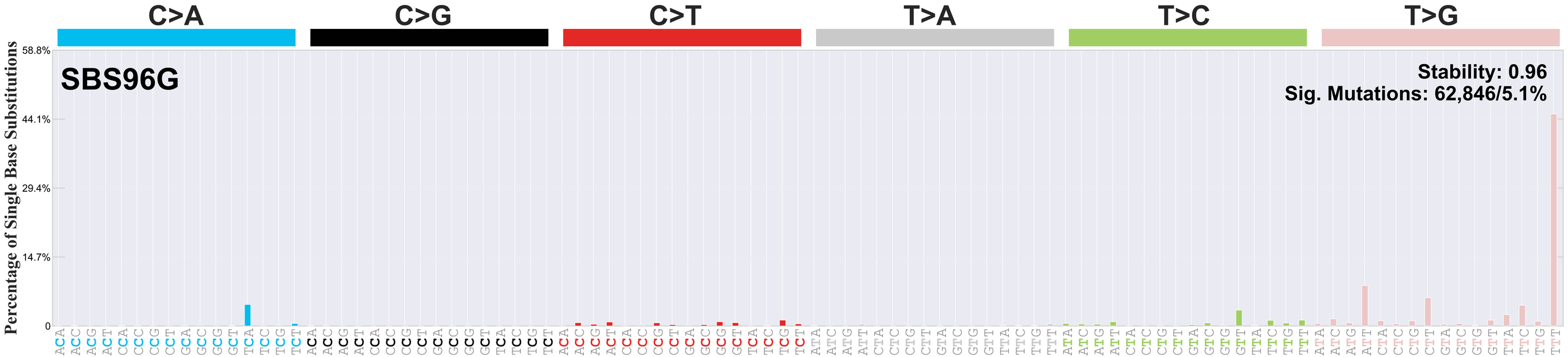

C>A
C>G
C>T
T>A
T>C
T>G
SBS96B
Stability: 0.98
Sig. Mutations: 120,484/9.9%
Percentage of Single Base Substitutions
116.0%
87.0%
58.0%
29.0%
0

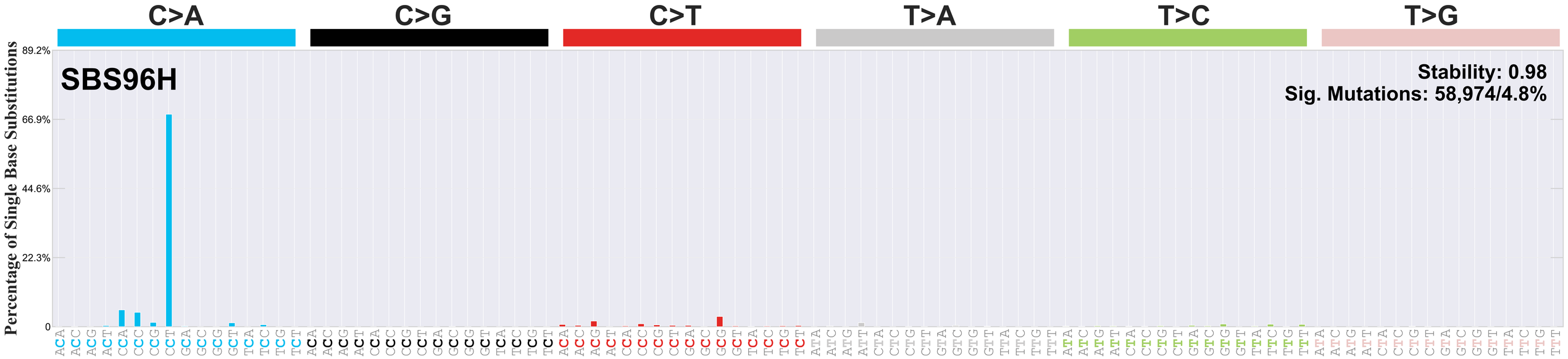

C>A
C>G
C>T
T>A
T>C
T>G
SBS96C
Stability: 1.0
Sig. Mutations: 109,380/9.0%
Percentage of Single Base Substitutions
126.5%
94.8%
63.2%
31.6%
0

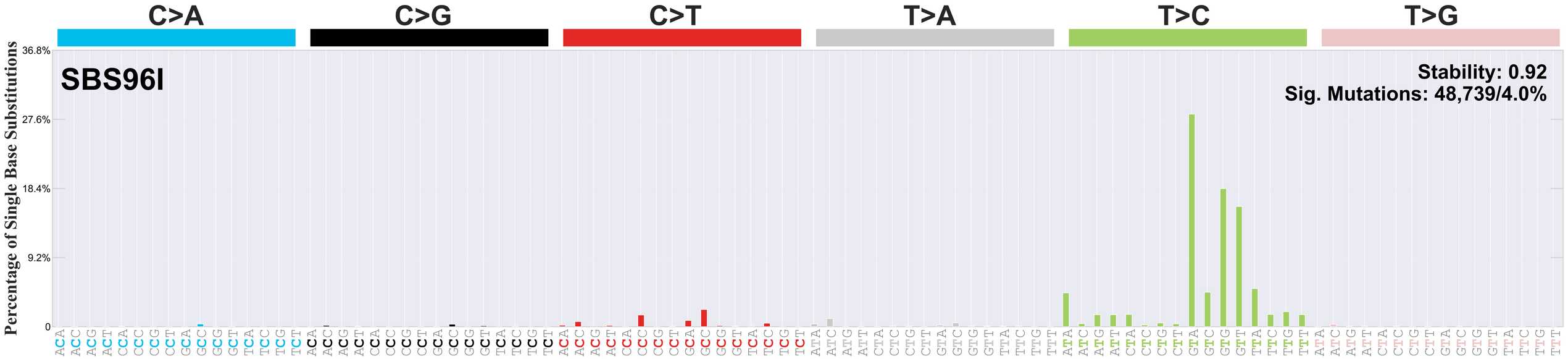

C>A
C>G
C>T
T>A
T>C
T>G
SBS96D
Stability: 0.66
Sig. Mutations: 89,709/7.3%
Percentage of Single Base Substitutions
94.2%
70.7%
47.1%
23.6%
0

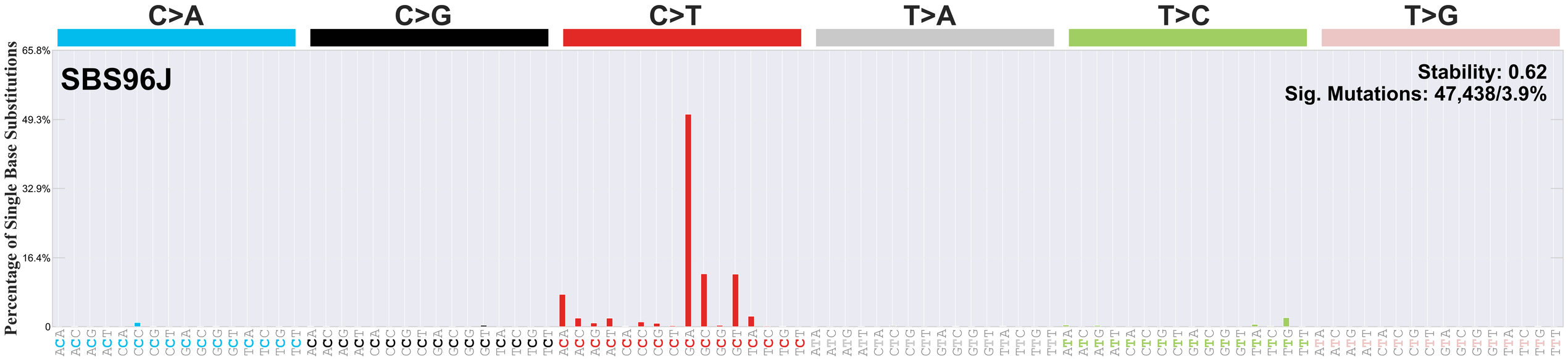

C>A
C>G
C>T
T>A
T>C
T>G
SBS96E
Stability: 0.51
Sig. Mutations: 79,303/6.5%
Percentage of Single Base Substitutions
89.5%
67.1%
44.8%
22.4%
0

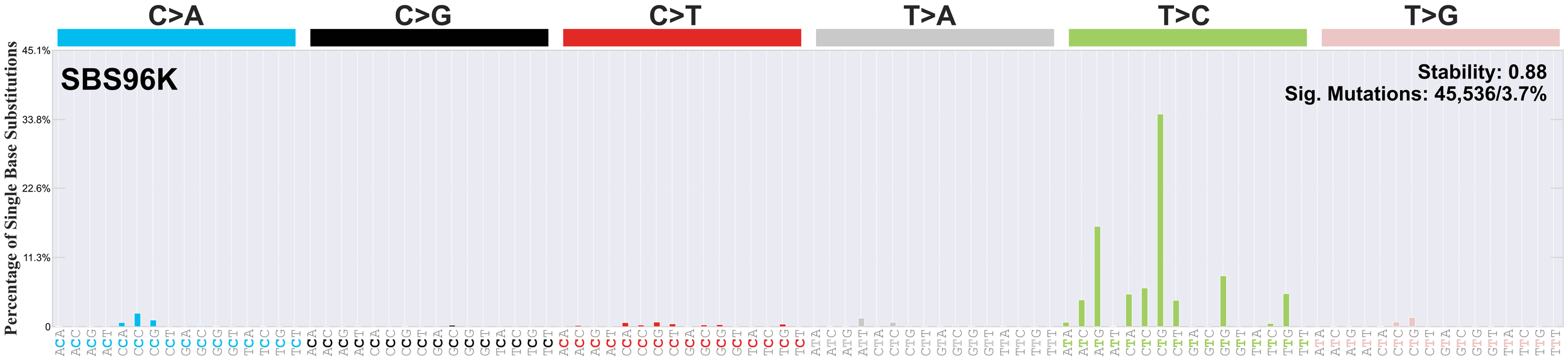

C>A
C>G
C>T
T>A
T>C
T>G
SBS96F
Stability: 0.4
Sig. Mutations: 73,591/6.0%
Percentage of Single Base Substitutions
50.9%
38.2%
25.5%
12.7%
0

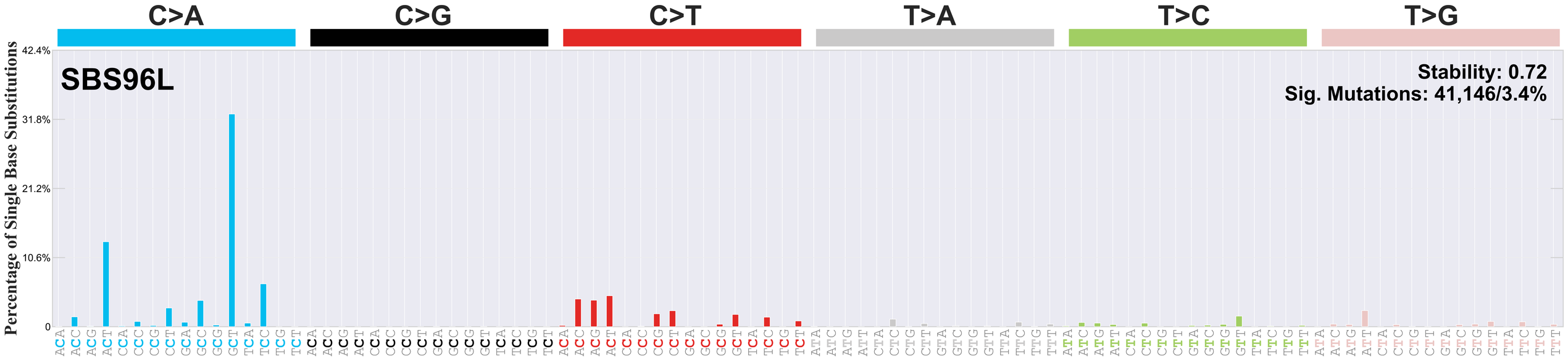

C>A
C>G
C>T
T>A
T>C
T>G
SBS96G
Stability: 0.96
Sig. Mutations: 62,846/5.1%
Percentage of Single Base Substitutions
58.8%
44.1%
29.4%
14.7%
0

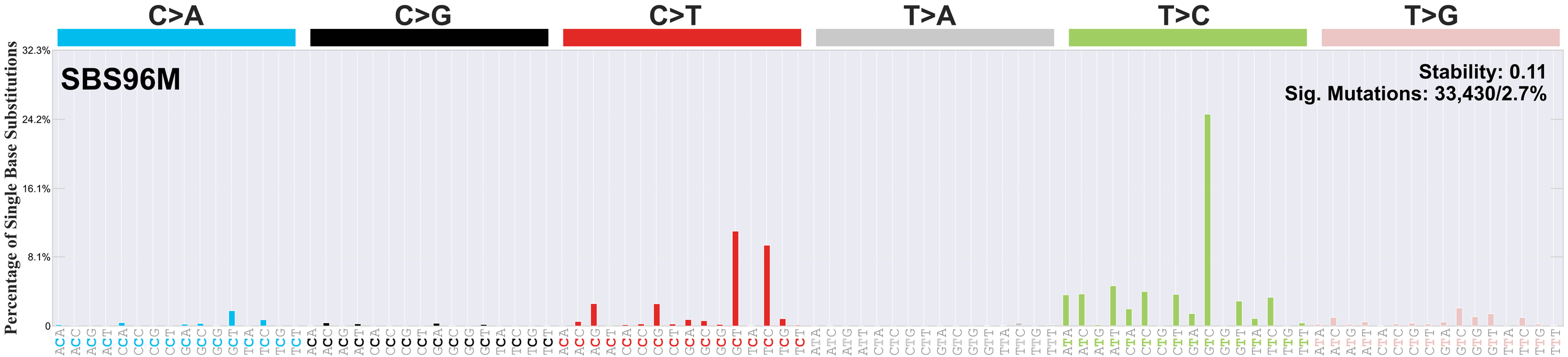

C>A
C>G
C>T
T>A
T>C
T>G
SBS96H
Stability: 0.98
Sig. Mutations: 58,974/4.8%
Percentage of Single Base Substitutions
89.2%
66.9%
44.6%
22.3%
0

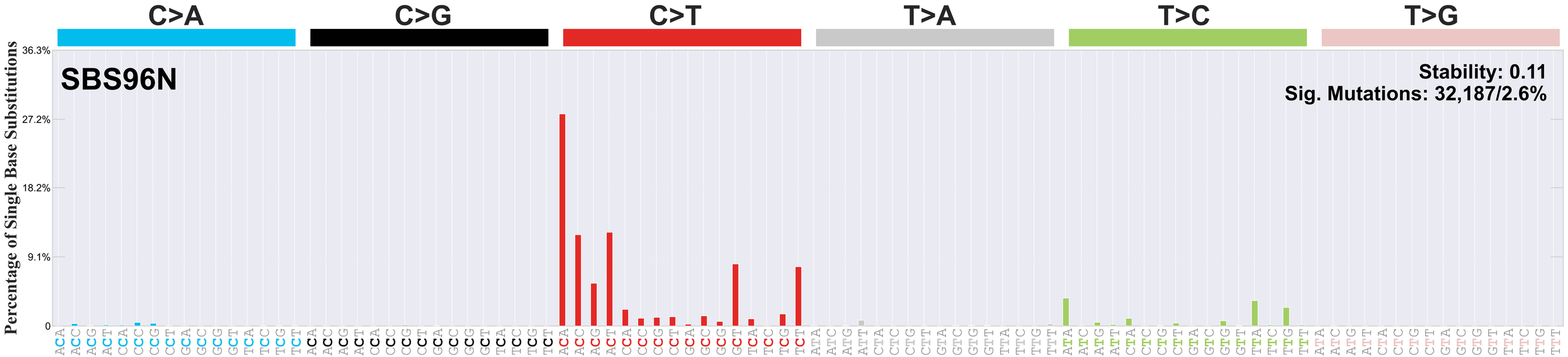

C>A
C>G
C>T
T>A
T>C
T>G
SBS96I
Stability: 0.92
Sig. Mutations: 48,739/4.0%
Percentage of Single Base Substitutions
36.8%
27.6%
18.4%
9.2%
0

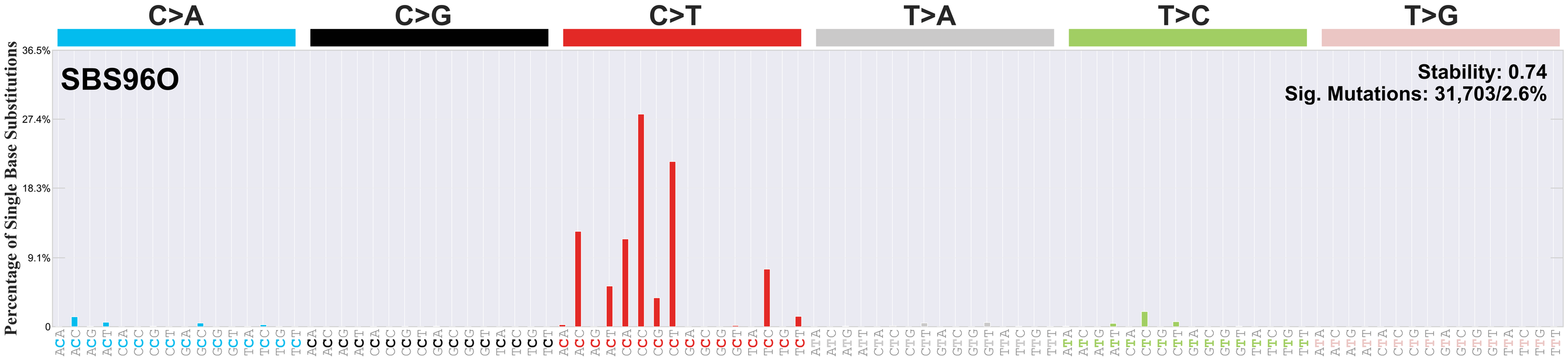

C>A
C>G
C>T
T>A
T>C
T>G
SBS96J
Stability: 0.62
Sig. Mutations: 47,438/3.9%
Percentage of Single Base Substitutions
65.8%
49.3%
32.9%
16.4%
0

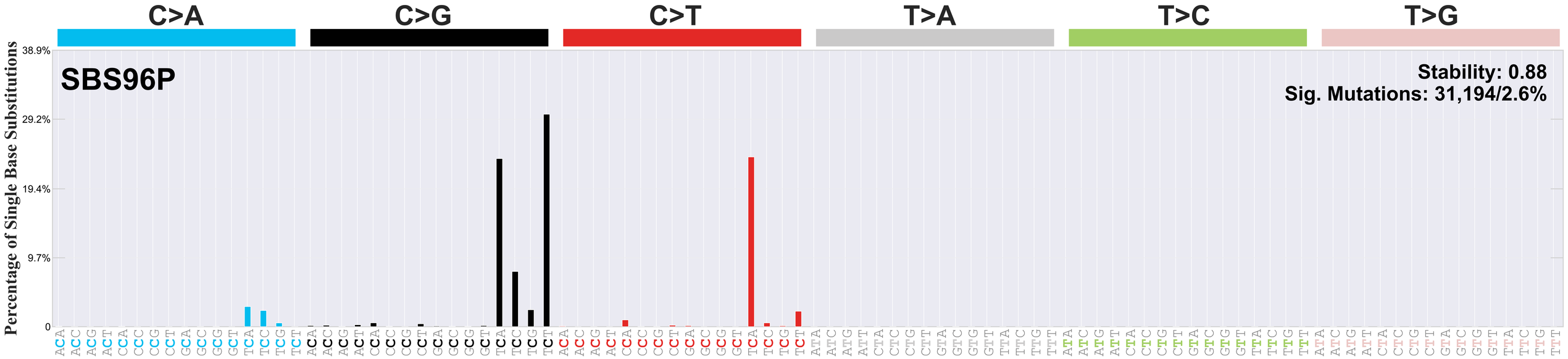

C>A
C>G
C>T
T>A
T>C
T>G
SBS96K
Stability: 0.88
Sig. Mutations: 45,536/3.7%
Percentage of Single Base Substitutions
45.1%
33.8%
22.6%
11.3%
0

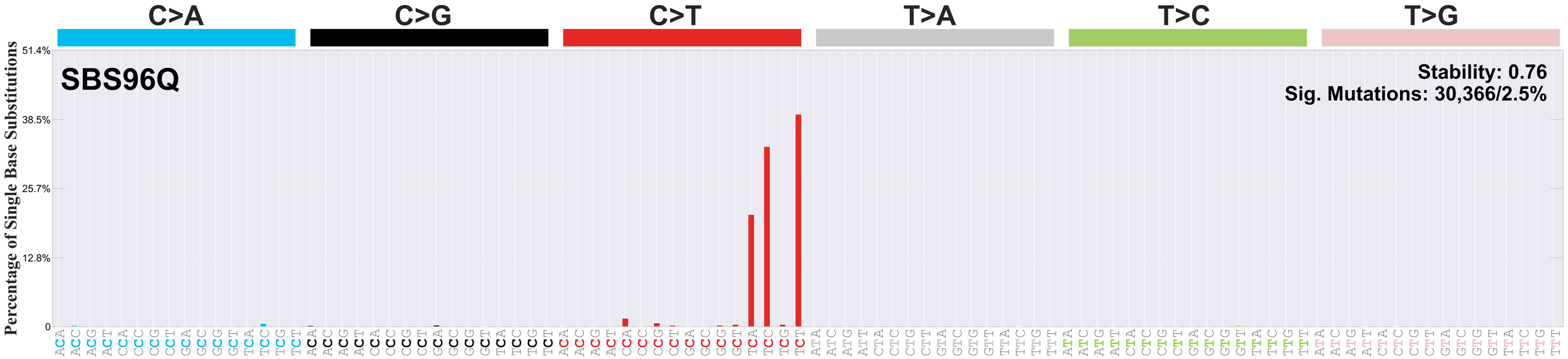

C>A
C>G
C>T
T>A
T>C
T>G
SBS96L
Stability: 0.72
Sig. Mutations: 41,146/3.4%
Percentage of Single Base Substitutions
42.4%
31.8%
21.2%
10.6%
0

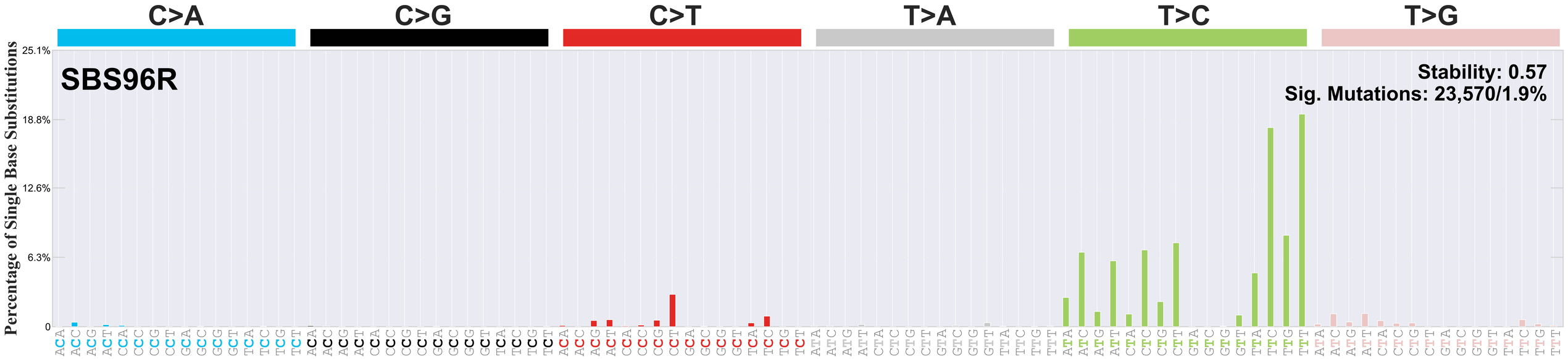

C>A
C>G
C>T
T>A
T>C
T>G
SBS96M
Stability: 0.11
Sig. Mutations: 33,430/2.7%
Percentage of Single Base Substitutions
32.3%
24.2%
16.1%
8.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT

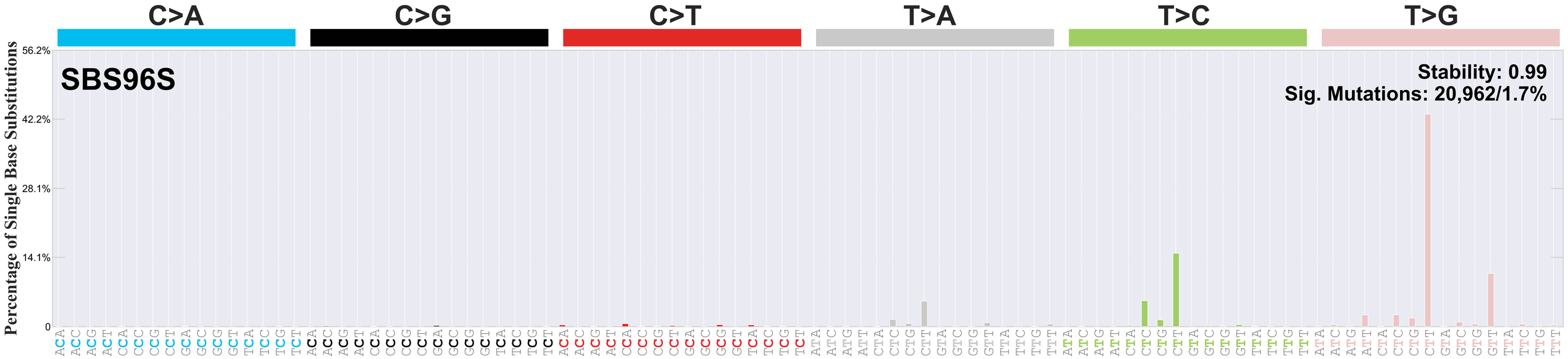

C>A
C>G
C>T
T>A
T>C
T>G
SBS96N
Stability: 0.11
Sig. Mutations: 32,187/2.6%
Percentage of Single Base Substitutions
36.3%
27.2%
18.2%
9.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT

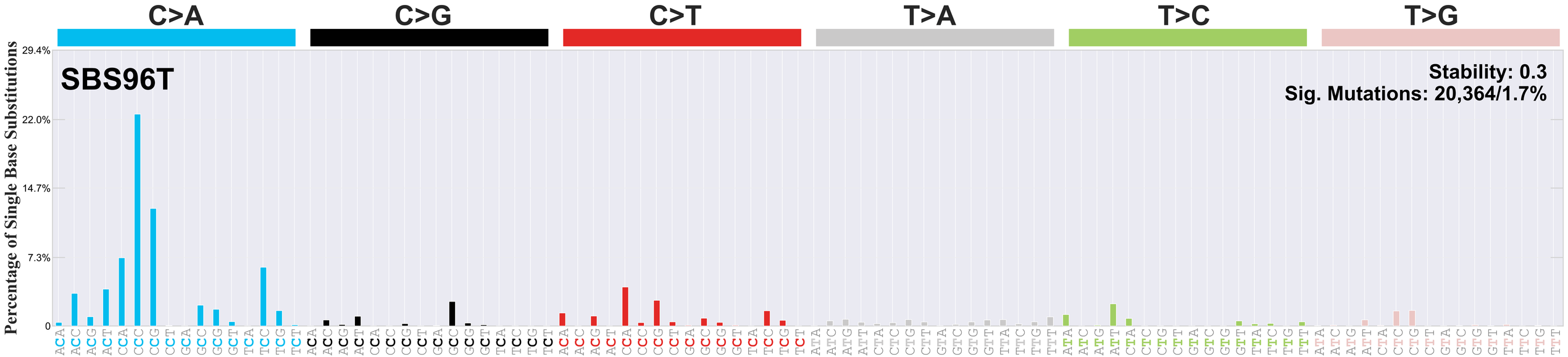

C>A
C>G
C>T
T>A
T>C
T>G
SBS96O
Stability: 0.74
Sig. Mutations: 31,703/2.6%
Percentage of Single Base Substitutions
36.5%
27.4%
18.3%
9.1%
0

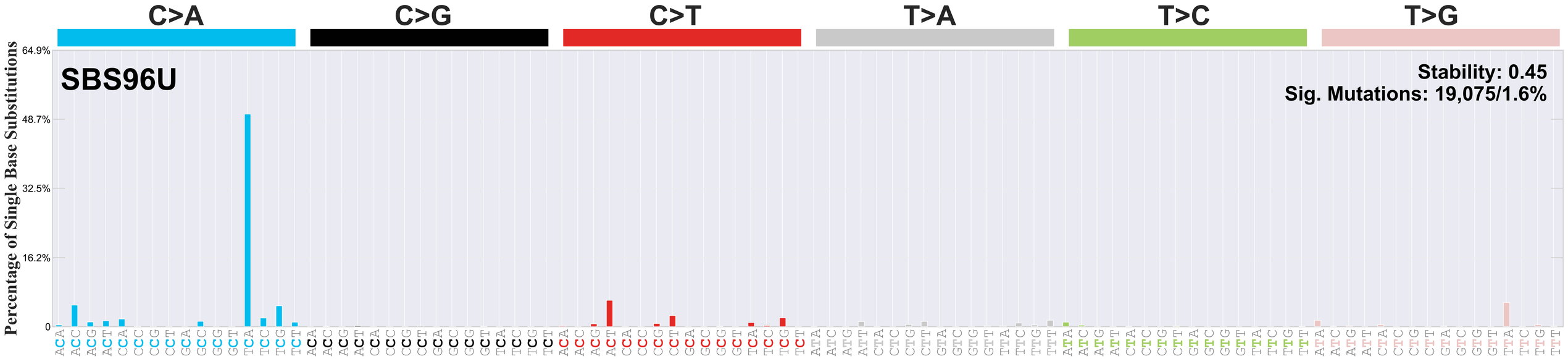

C>A
C>G
C>T
T>A
T>C
T>G
SBS96P
Stability: 0.88
Sig. Mutations: 31,194/2.6%
Percentage of Single Base Substitutions
38.9%
29.2%
19.4%
9.7%
0

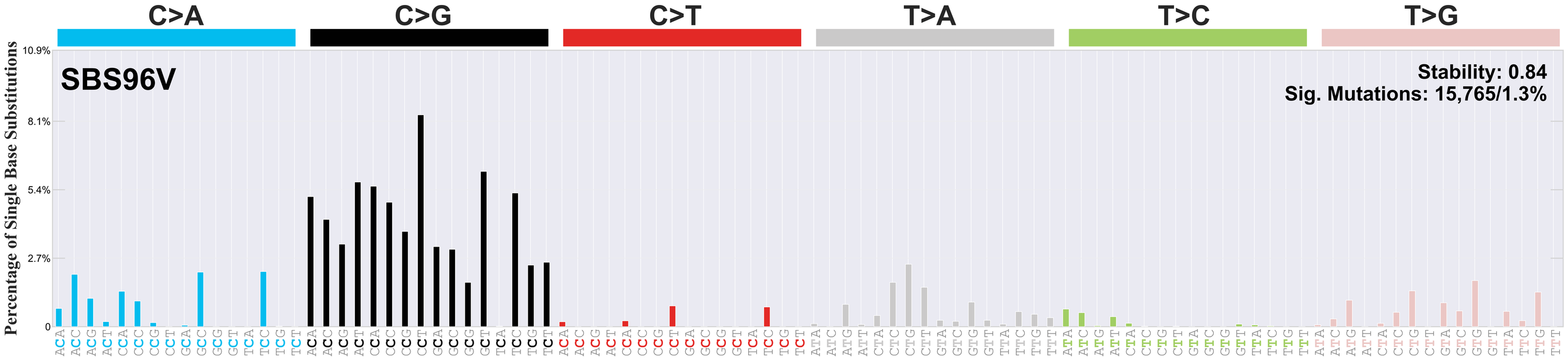

C>A
C>G
C>T
T>A
T>C
T>G
SBS96Q
Stability: 0.76
Sig. Mutations: 30,366/2.5%
Percentage of Single Base Substitutions
51.4%
38.5%
25.7%
12.8%
0

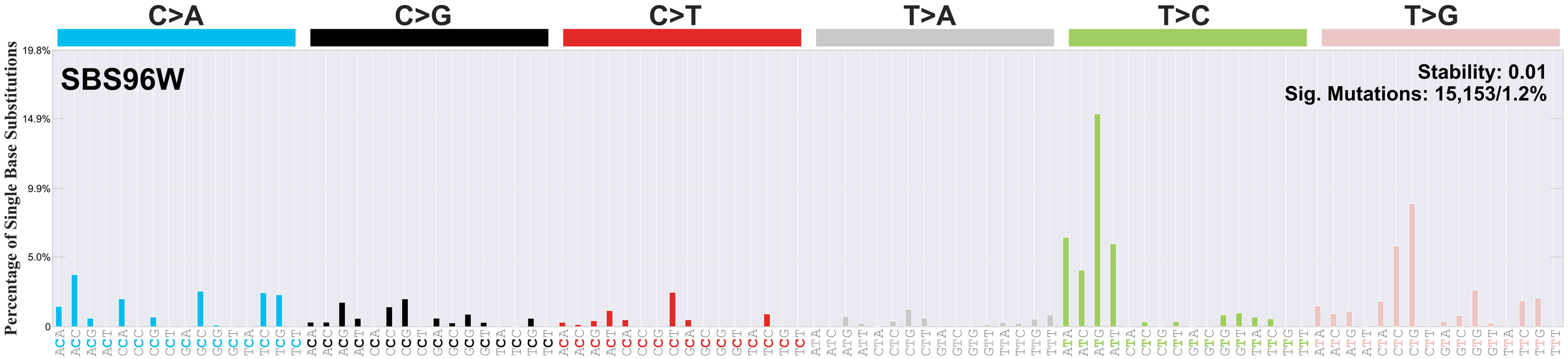

C>A
C>G
C>T
T>A
T>C
T>G
SBS96R
Stability: 0.57
Sig. Mutations: 23,570/1.9%
Percentage of Single Base Substitutions
25.1%
18.8%
12.6%
6.3%
0

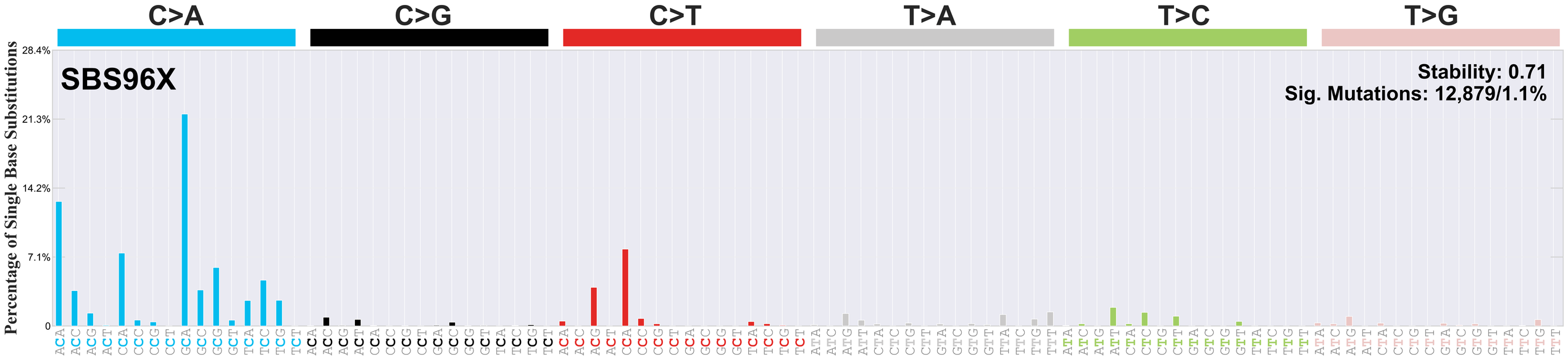

C>A
C>G
C>T
T>A
T>C
T>G
SBS96S
Stability: 0.99
Sig. Mutations: 20,962/1.7%
Percentage of Single Base Substitutions
56.2%
42.2%
28.1%
14.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT

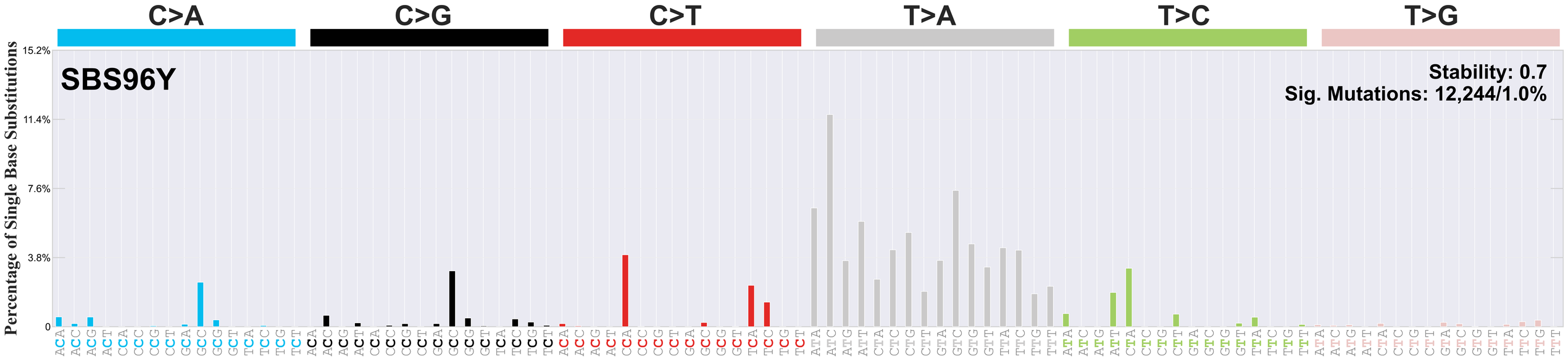

C>A
C>G
C>T
T>A
T>C
T>G
SBS96T
Stability: 0.3
Sig. Mutations: 20,364/1.7%
Percentage of Single Base Substitutions
29.4%
22.0%
14.7%
7.3%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT


C>A
C>G
C>T
T>A
T>C
T>G
SBS96U
Stability: 0.45
Sig. Mutations: 19,075/1.6%
Percentage of Single Base Substitutions
64.9%
48.7%
32.5%
16.2%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS96V
Stability: 0.84
Sig. Mutations: 15,765/1.3%
Percentage of Single Base Substitutions
10.9%
8.1%
5.4%
2.7%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT


C>A
C>G
C>T
T>A
T>C
T>G
SBS96W
Stability: 0.01
Sig. Mutations: 15,153/1.2%
Percentage of Single Base Substitutions
19.8%
14.9%
9.9%
5.0%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT


C>A
C>G
C>T
T>A
T>C
T>G
SBS96X
Stability: 0.71
Sig. Mutations: 12,879/1.1%
Percentage of Single Base Substitutions
28.4%
21.3%
14.2%
7.1%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS96Y
Stability: 0.7
Sig. Mutations: 12,244/1.0%
Percentage of Single Base Substitutions
15.2%
11.4%
7.6%
3.8%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT