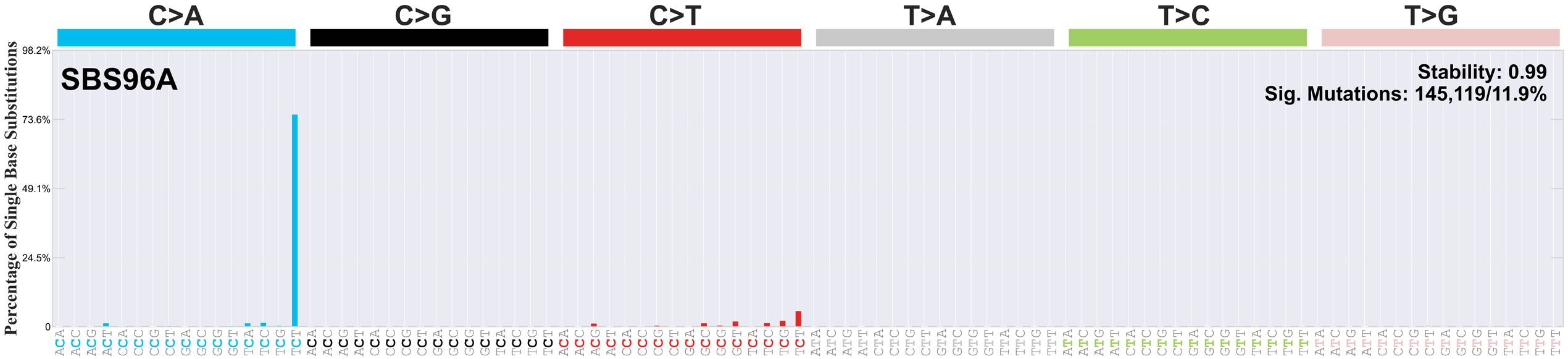
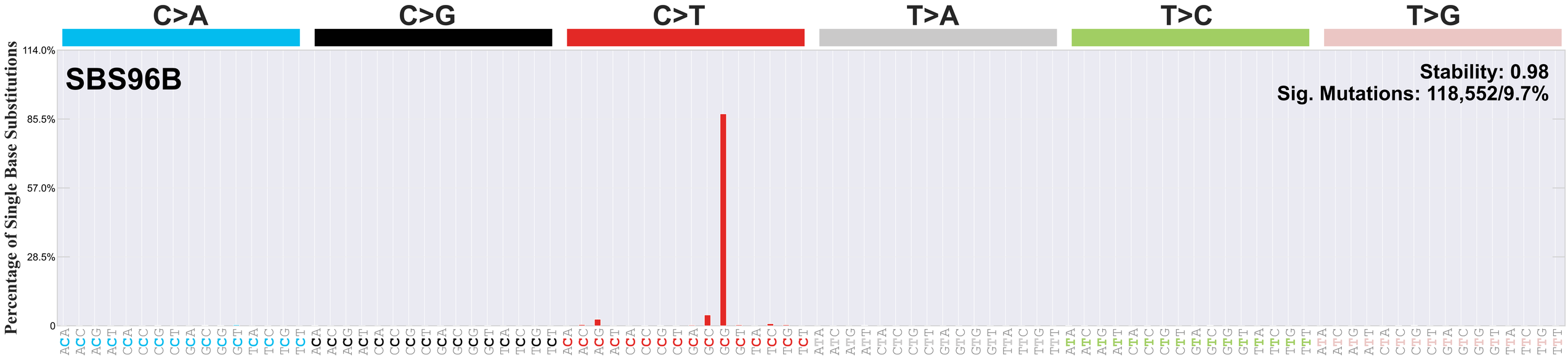
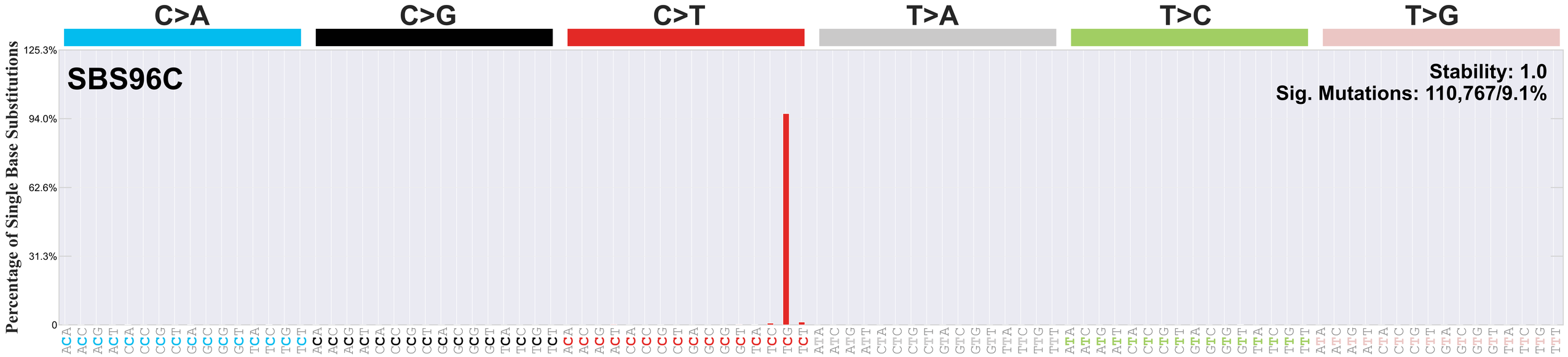
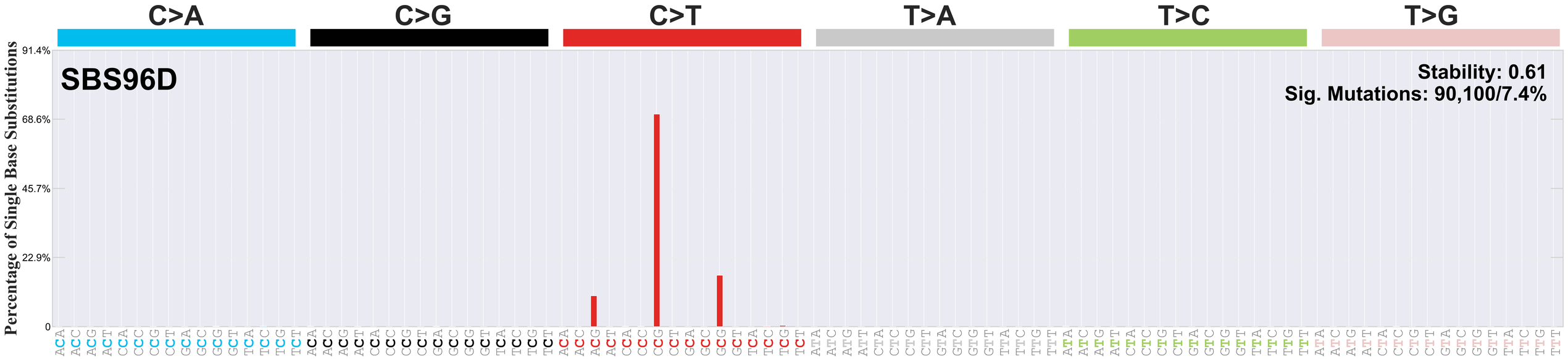
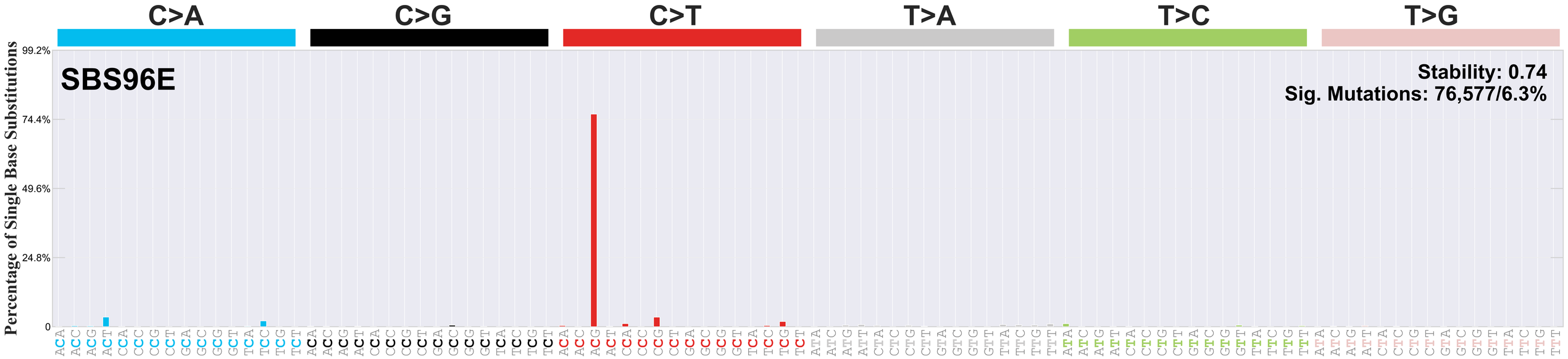
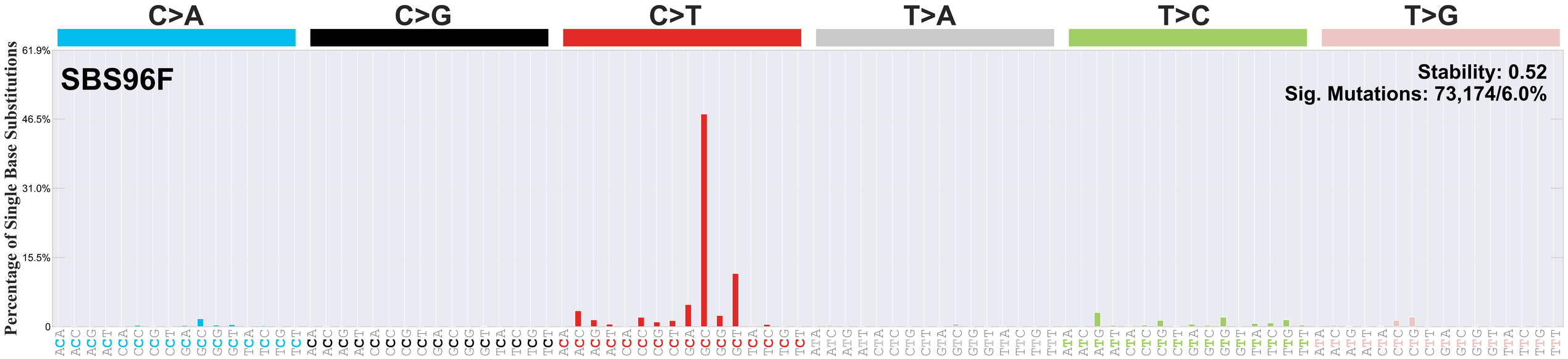

C>A
C>G
C>T
T>A
T>C
T>G
SBS96A
Stability: 0.99
Sig. Mutations: 145,119/11.9%
Percentage of Single Base Substitutions
98.2%
73.6%
49.1%
24.5%
0

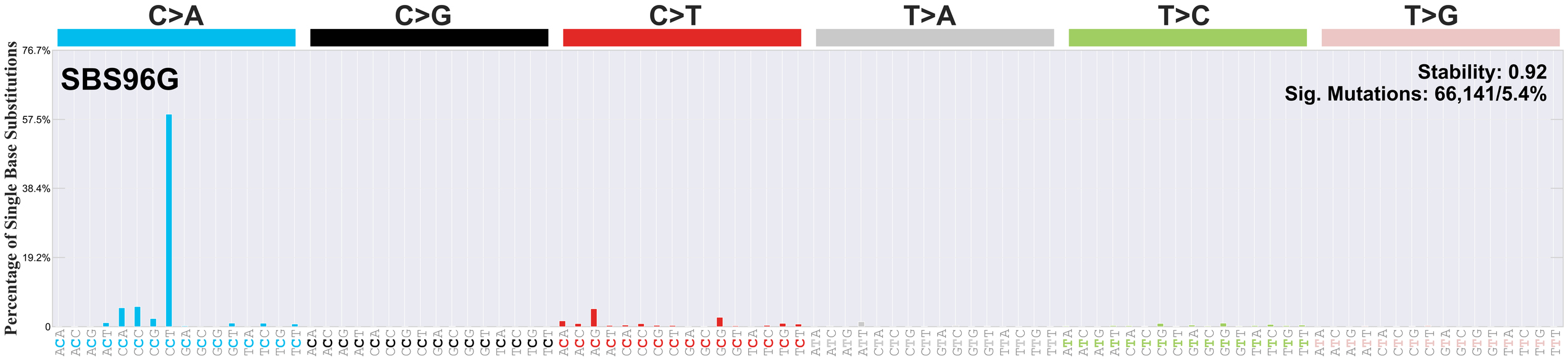

C>A
C>G
C>T
T>A
T>C
T>G
SBS96B
Stability: 0.98
Sig. Mutations: 118,552/9.7%
Percentage of Single Base Substitutions
114.0%
85.5%
57.0%
28.5%
0

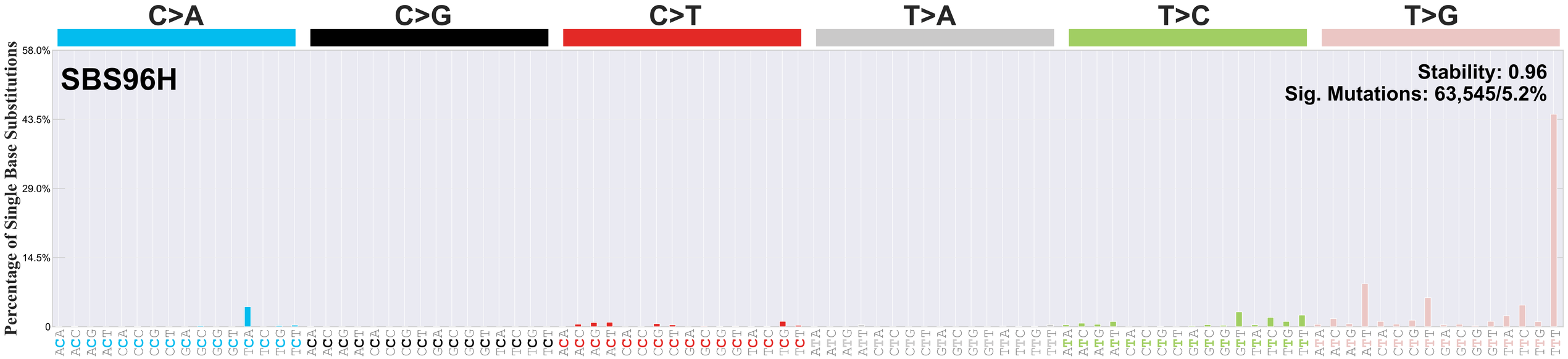

C>A
C>G
C>T
T>A
T>C
T>G
SBS96C
Stability: 1.0
Sig. Mutations: 110,767/9.1%
Percentage of Single Base Substitutions
125.3%
94.0%
62.6%
31.3%
0

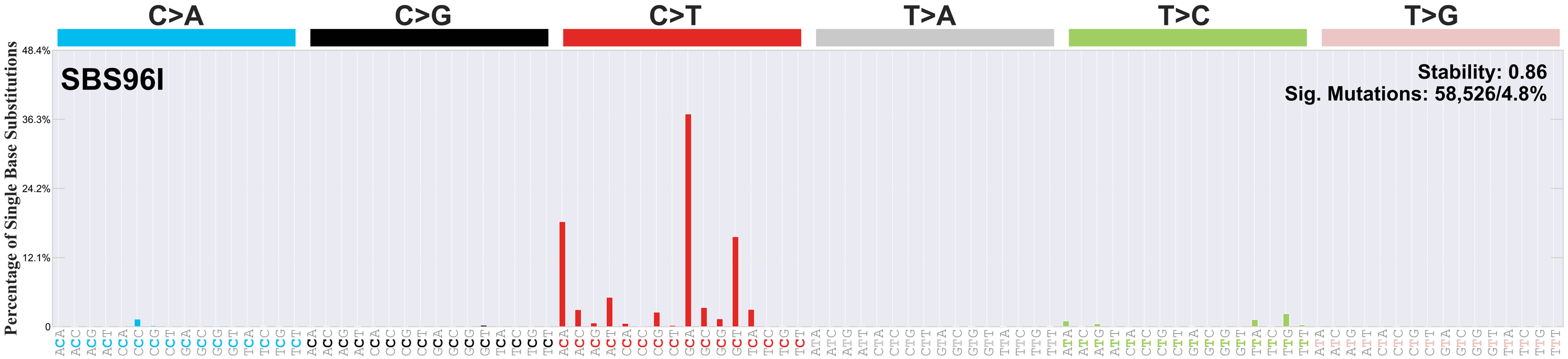

C>A
C>G
C>T
T>A
T>C
T>G
SBS96D
Stability: 0.61
Sig. Mutations: 90,100/7.4%
Percentage of Single Base Substitutions
91.4%
68.6%
45.7%
22.9%
0

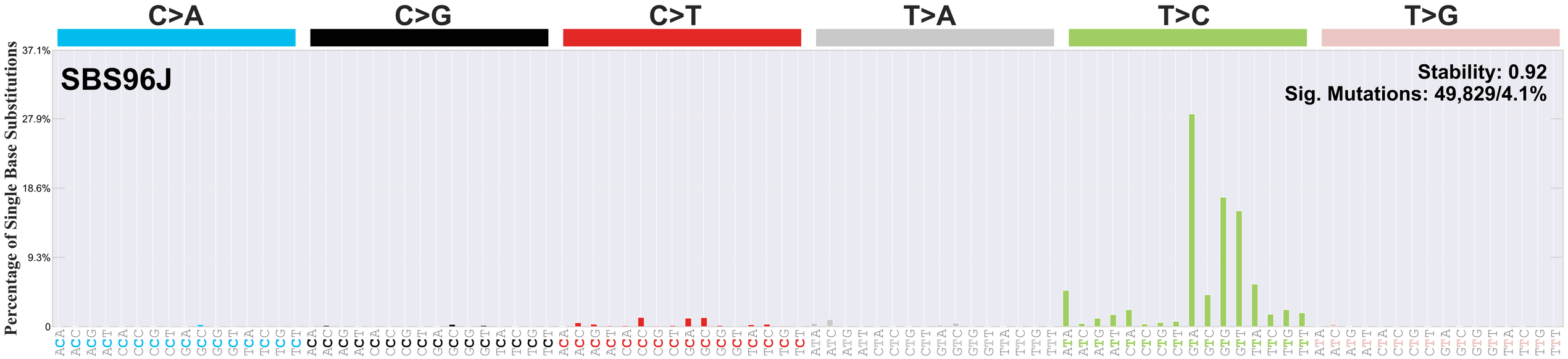

C>A
C>G
C>T
T>A
T>C
T>G
SBS96E
Stability: 0.74
Sig. Mutations: 76,577/6.3%
Percentage of Single Base Substitutions
99.2%
74.4%
49.6%
24.8%
0

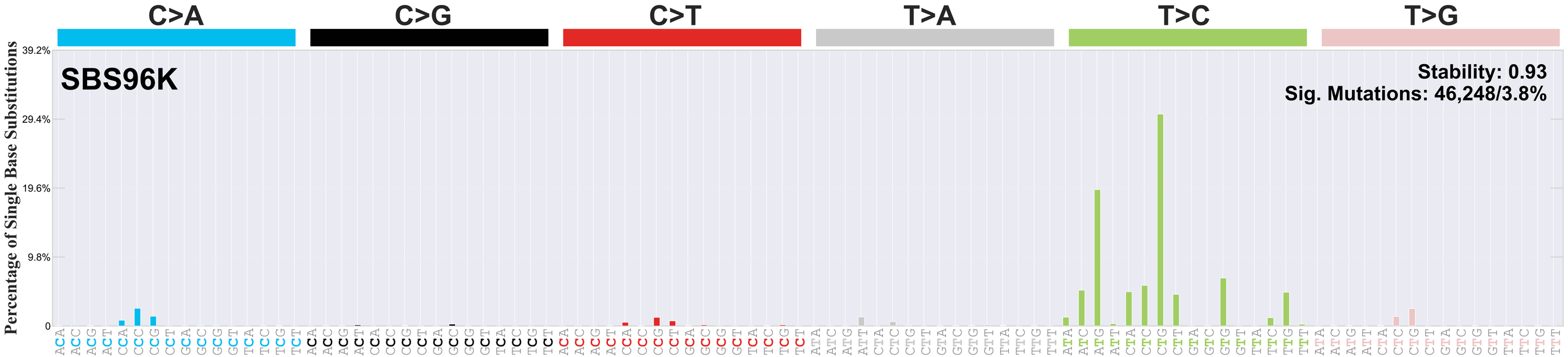

C>A
C>G
C>T
T>A
T>C
T>G
SBS96F
Stability: 0.52
Sig. Mutations: 73,174/6.0%
Percentage of Single Base Substitutions
61.9%
46.5%
31.0%
15.5%
0

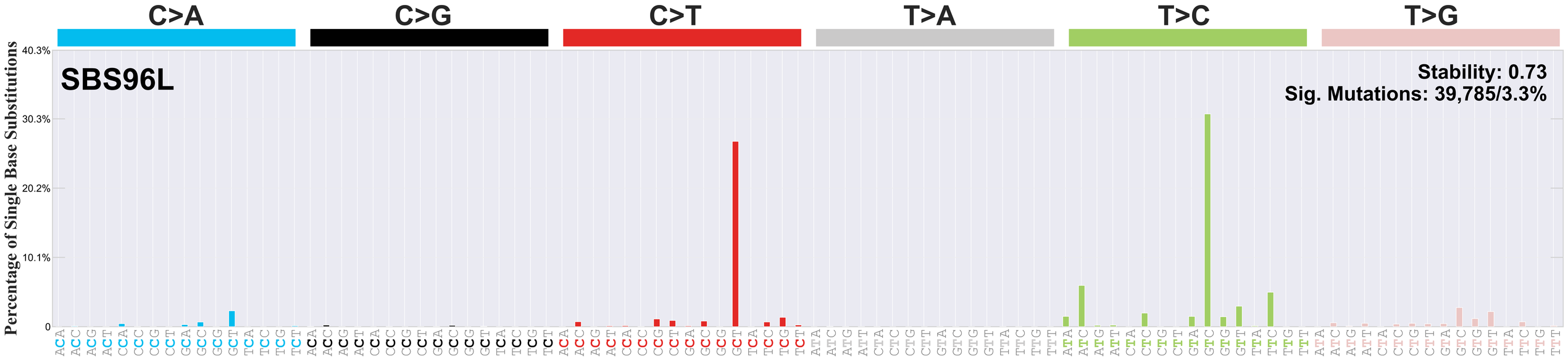

C>A
C>G
C>T
T>A
T>C
T>G
SBS96G
Stability: 0.92
Sig. Mutations: 66,141/5.4%
Percentage of Single Base Substitutions
76.7%
57.5%
38.4%
19.2%
0

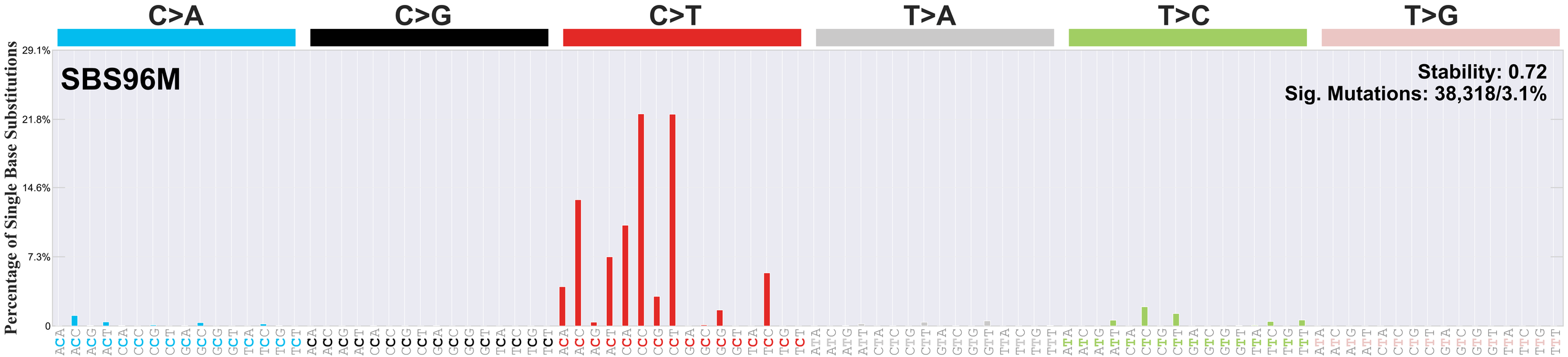

C>A
C>G
C>T
T>A
T>C
T>G
SBS96H
Stability: 0.96
Sig. Mutations: 63,545/5.2%
Percentage of Single Base Substitutions
58.0%
43.5%
29.0%
14.5%
0

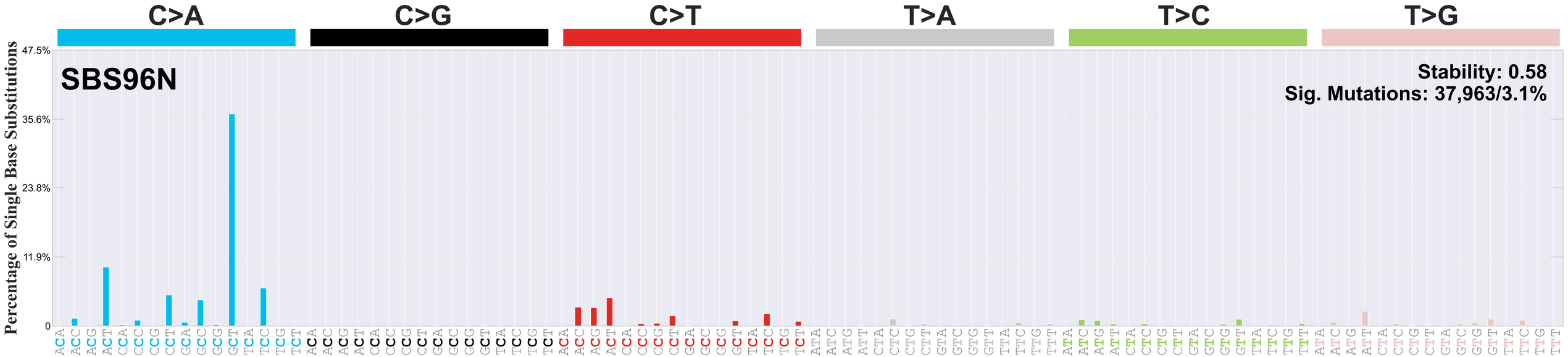

C>A
C>G
C>T
T>A
T>C
T>G
SBS96I
Stability: 0.86
Sig. Mutations: 58,526/4.8%
Percentage of Single Base Substitutions
48.4%
36.3%
24.2%
12.1%
0

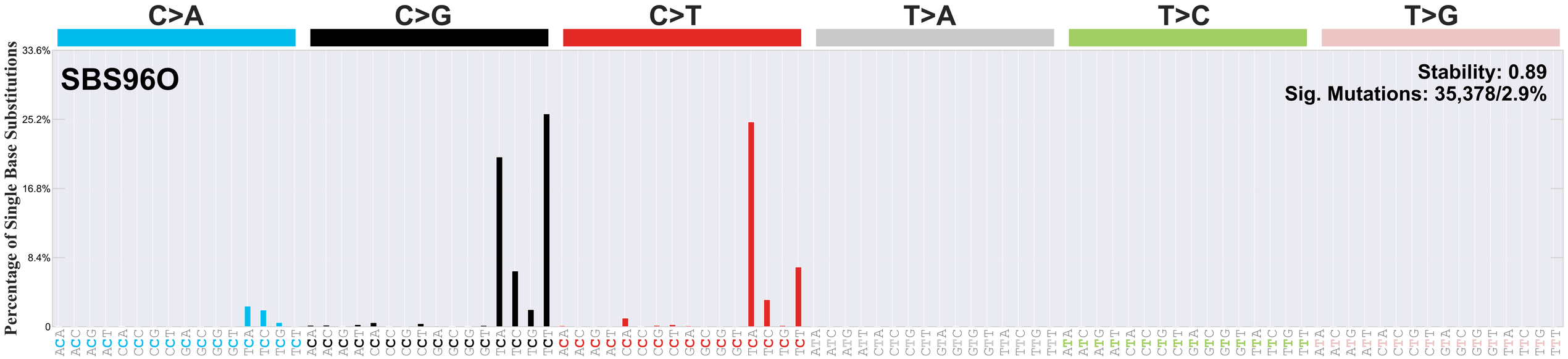

C>A
C>G
C>T
T>A
T>C
T>G
SBS96J
Stability: 0.92
Sig. Mutations: 49,829/4.1%
Percentage of Single Base Substitutions
37.1%
27.9%
18.6%
9.3%
0

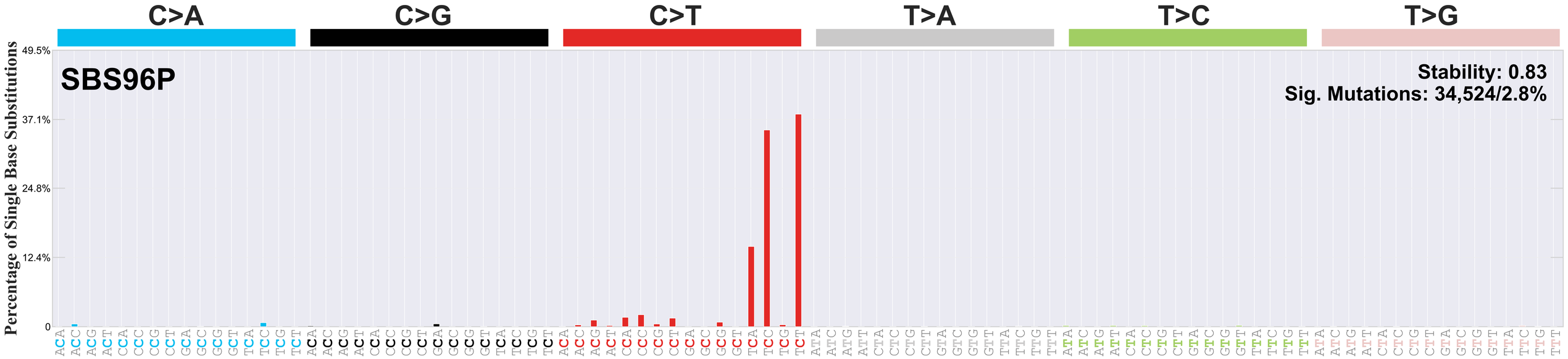

C>A
C>G
C>T
T>A
T>C
T>G
SBS96K
Stability: 0.93
Sig. Mutations: 46,248/3.8%
Percentage of Single Base Substitutions
39.2%
29.4%
19.6%
9.8%
0

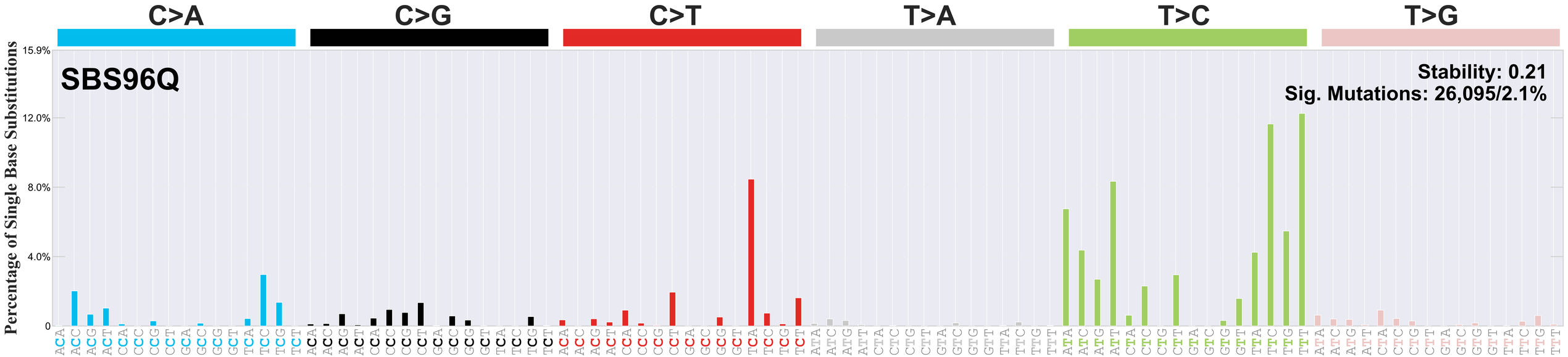

C>A
C>G
C>T
T>A
T>C
T>G
SBS96L
Stability: 0.73
Sig. Mutations: 39,785/3.3%
Percentage of Single Base Substitutions
40.3%
30.3%
20.2%
10.1%
0

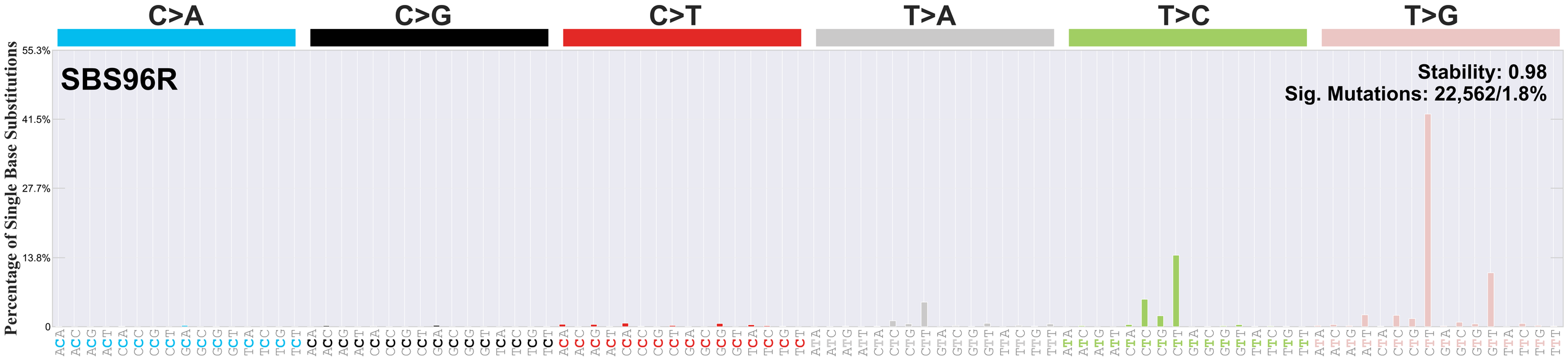

C>A
C>G
C>T
T>A
T>C
T>G
SBS96M
Stability: 0.72
Sig. Mutations: 38,318/3.1%
Percentage of Single Base Substitutions
29.1%
21.8%
14.6%
7.3%
0

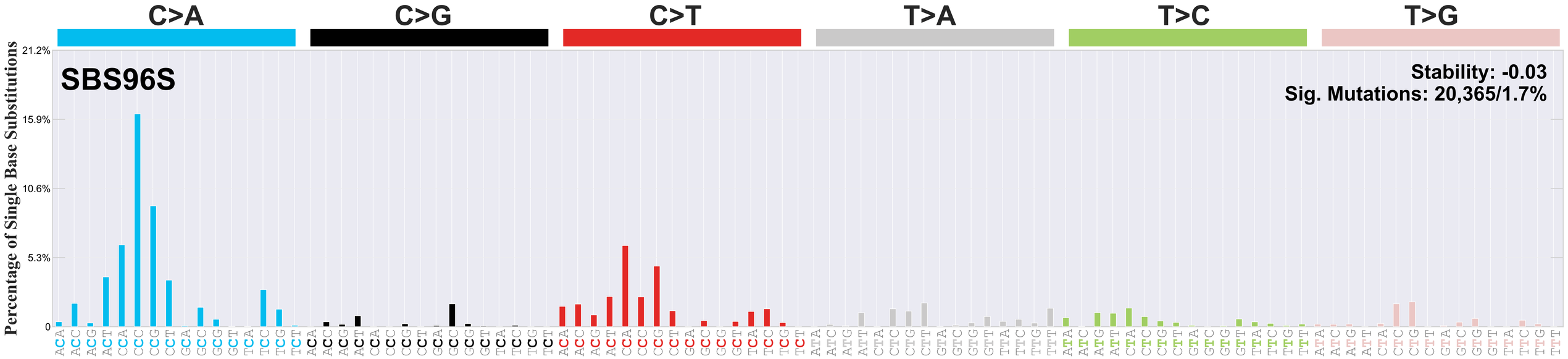

C>A
C>G
C>T
T>A
T>C
T>G
SBS96N
Stability: 0.58
Sig. Mutations: 37,963/3.1%
Percentage of Single Base Substitutions
47.5%
35.6%
23.8%
11.9%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT 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

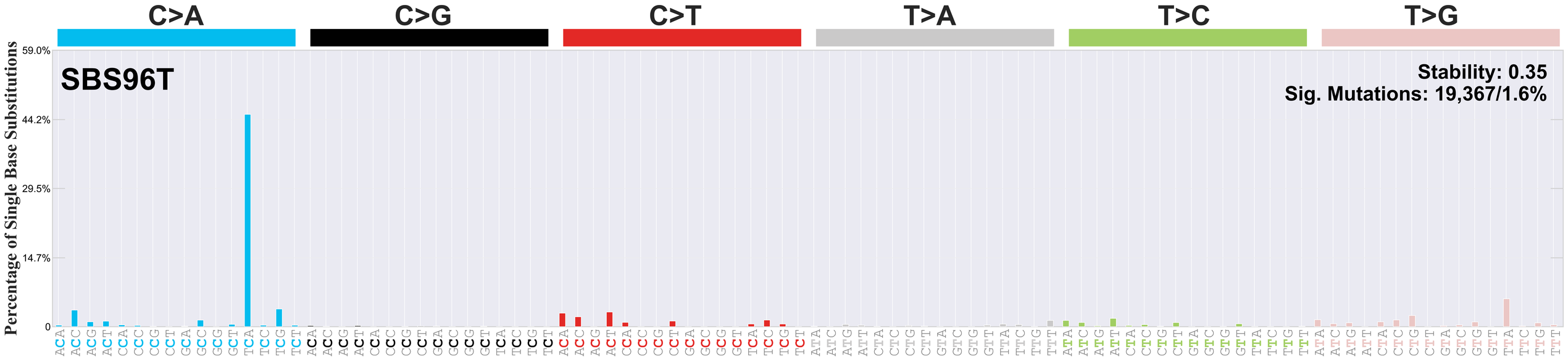

C>A
C>G
C>T
T>A
T>C
T>G
SBS96O
Stability: 0.89
Sig. Mutations: 35,378/2.9%
Percentage of Single Base Substitutions
33.6%
25.2%
16.8%
8.4%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA 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

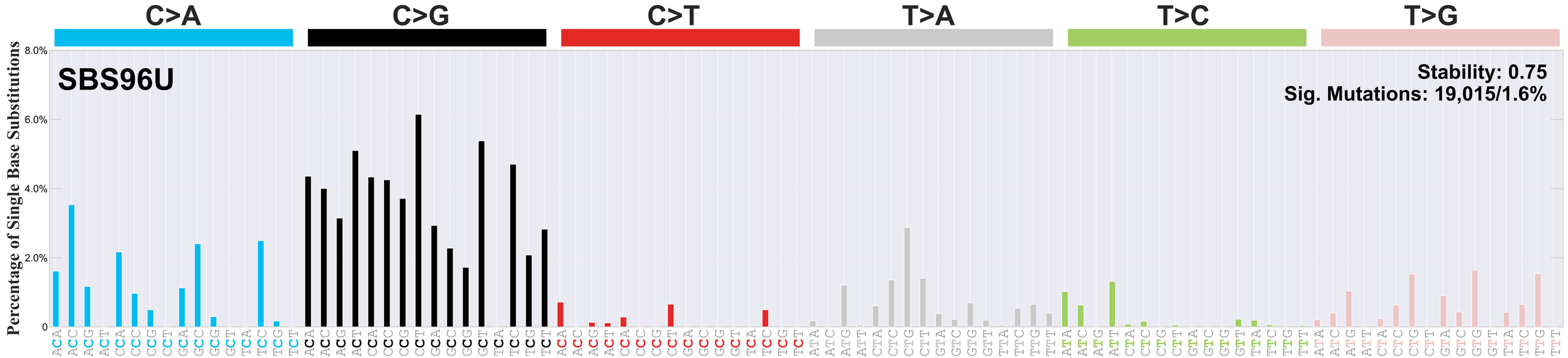

C>A
C>G
C>T
T>A
T>C
T>G
SBS96P
Stability: 0.83
Sig. Mutations: 34,524/2.8%
Percentage of Single Base Substitutions
49.5%
37.1%
24.8%
12.4%
0

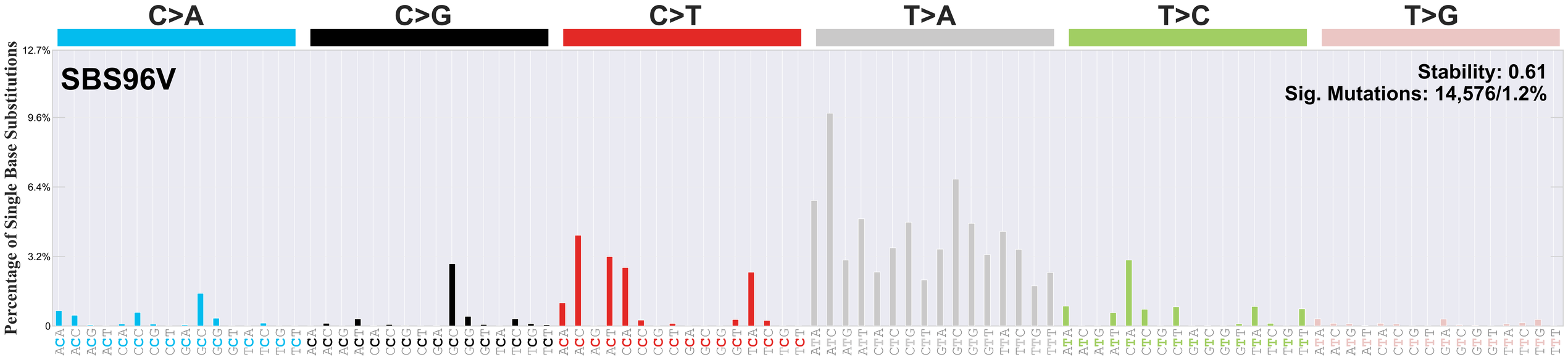

C>A
C>G
C>T
T>A
T>C
T>G
SBS96Q
Stability: 0.21
Sig. Mutations: 26,095/2.1%
Percentage of Single Base Substitutions
15.9%
12.0%
8.0%
4.0%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA 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

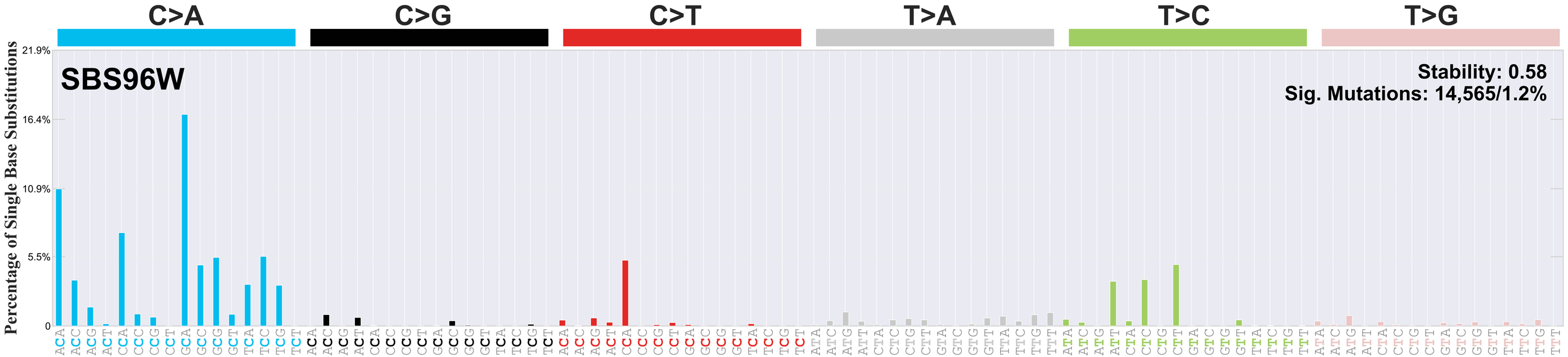

C>A
C>G
C>T
T>A
T>C
T>G
SBS96R
Stability: 0.98
Sig. Mutations: 22,562/1.8%
Percentage of Single Base Substitutions
55.3%
41.5%
27.7%
13.8%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS96S
Stability: -0.03
Sig. Mutations: 20,365/1.7%
Percentage of Single Base Substitutions
21.2%
15.9%
10.6%
5.3%
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 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: 0.35
Sig. Mutations: 19,367/1.6%
Percentage of Single Base Substitutions
59.0%
44.2%
29.5%
14.7%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS96U
Stability: 0.75
Sig. Mutations: 19,015/1.6%
Percentage of Single Base Substitutions
8.0%
6.0%
4.0%
2.0%
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 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
SBS96V
Stability: 0.61
Sig. Mutations: 14,576/1.2%
Percentage of Single Base Substitutions
12.7%
9.6%
6.4%
3.2%
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: 0.58
Sig. Mutations: 14,565/1.2%
Percentage of Single Base Substitutions
21.9%
16.4%
10.9%
5.5%
0