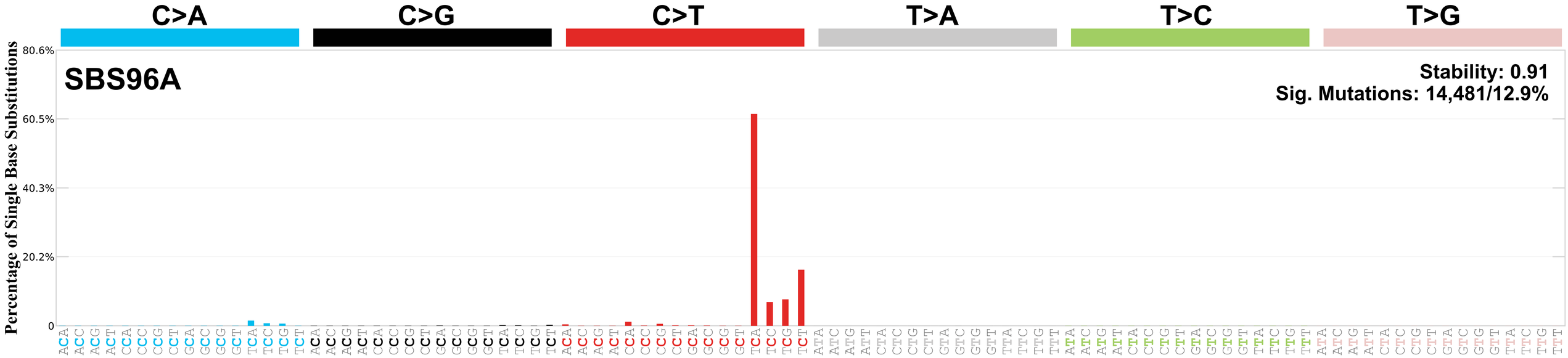
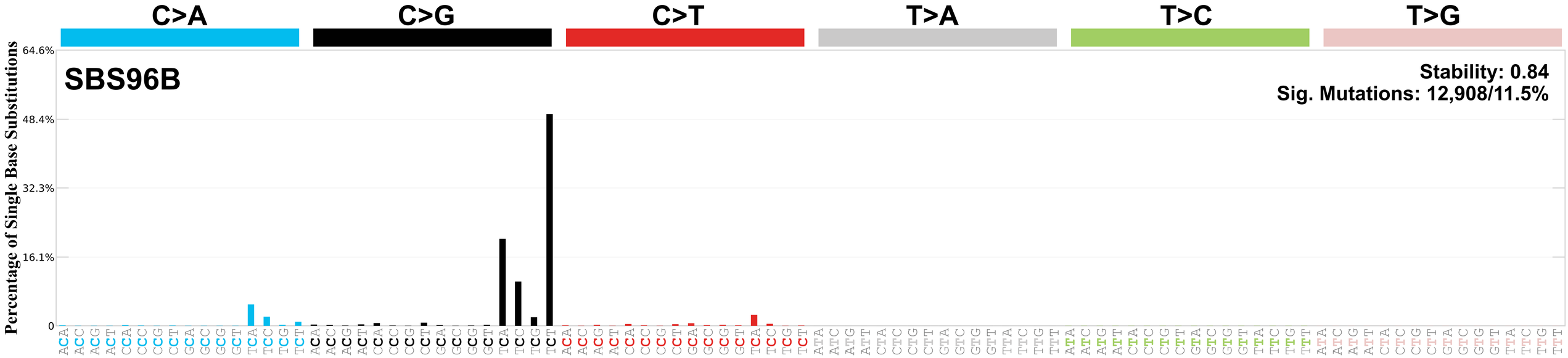
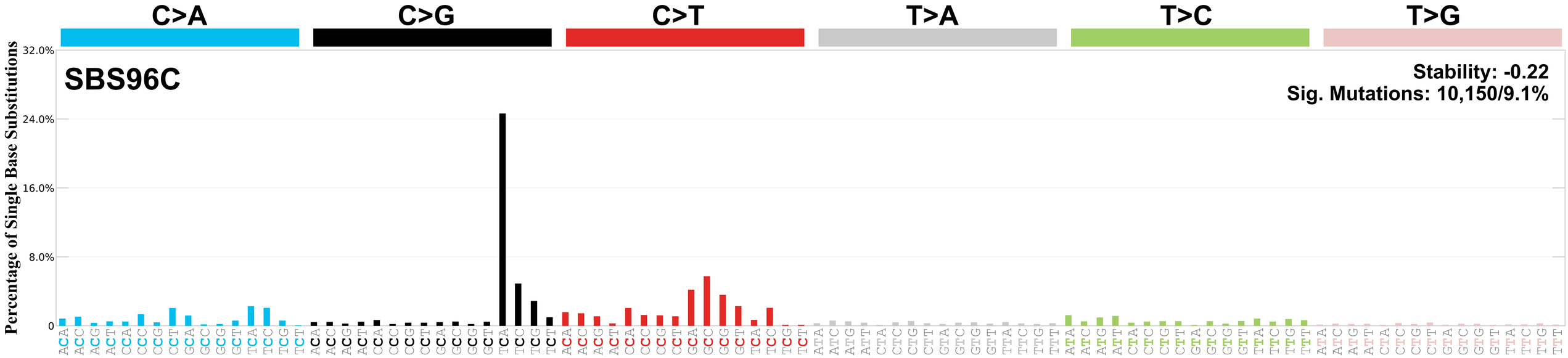
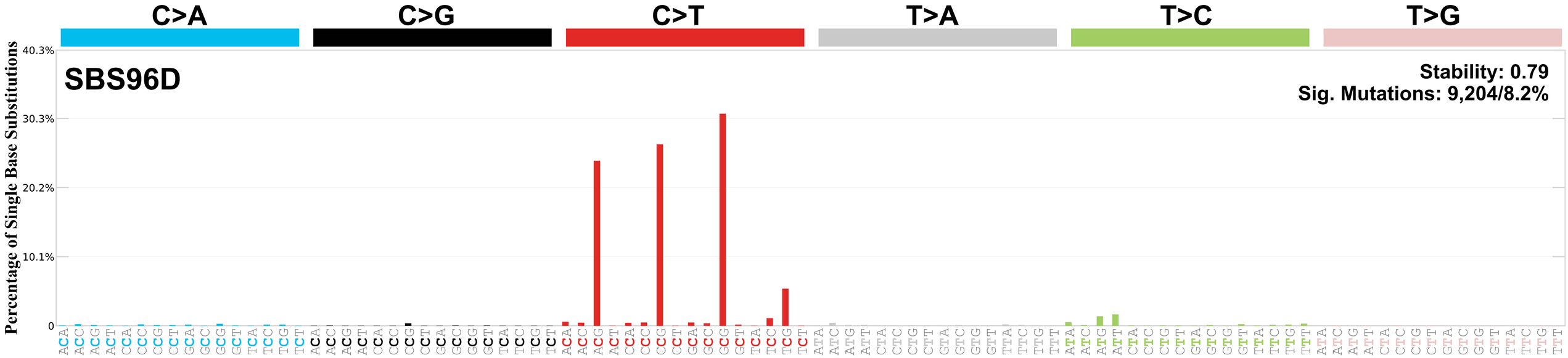
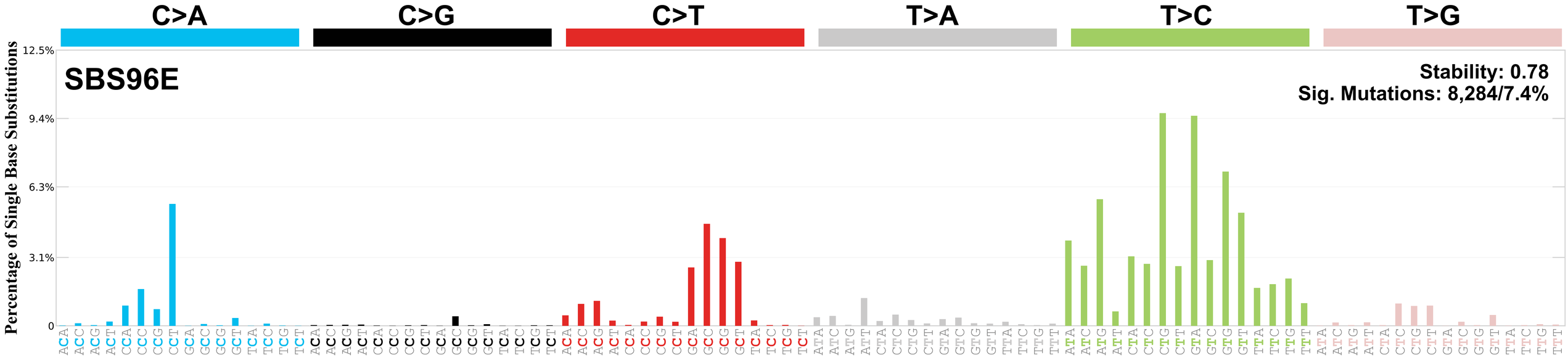
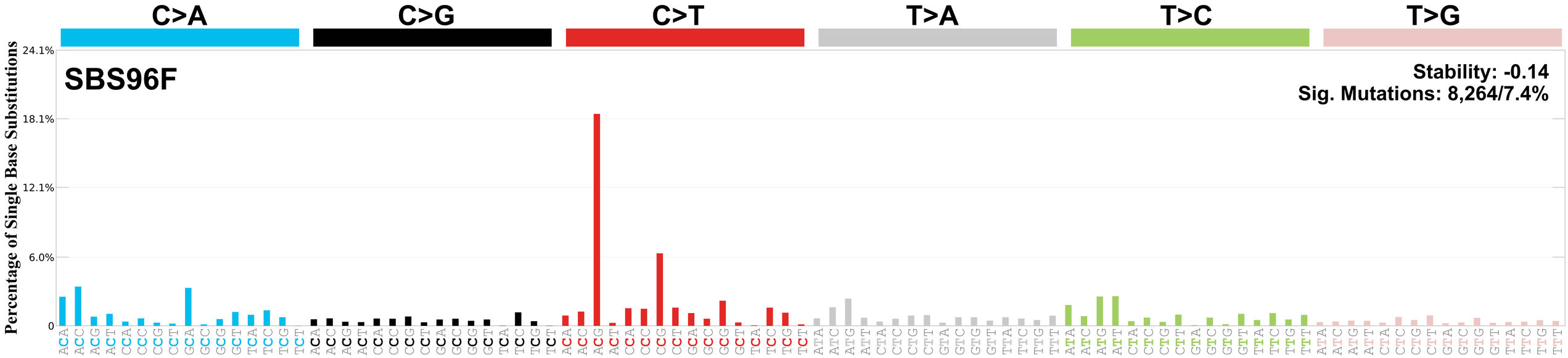

C>A
C>G
C>T
T>A
T>C
T>G
SBS96A
Stability: 0.91
Sig. Mutations: 14,481/12.9%
Percentage of Single Base Substitutions
80.6%
60.5%
40.3%
20.2%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS96B
Stability: 0.84
Sig. Mutations: 12,908/11.5%
Percentage of Single Base Substitutions
64.6%
48.4%
32.3%
16.1%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS96C
Stability: -0.22
Sig. Mutations: 10,150/9.1%
Percentage of Single Base Substitutions
32.0%
24.0%
16.0%
8.0%
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
SBS96D
Stability: 0.79
Sig. Mutations: 9,204/8.2%
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
SBS96E
Stability: 0.78
Sig. Mutations: 8,284/7.4%
Percentage of Single Base Substitutions
12.5%
9.4%
6.3%
3.1%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS96F
Stability: -0.14
Sig. Mutations: 8,264/7.4%
Percentage of Single Base Substitutions
24.1%
18.1%
12.1%
6.0%
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
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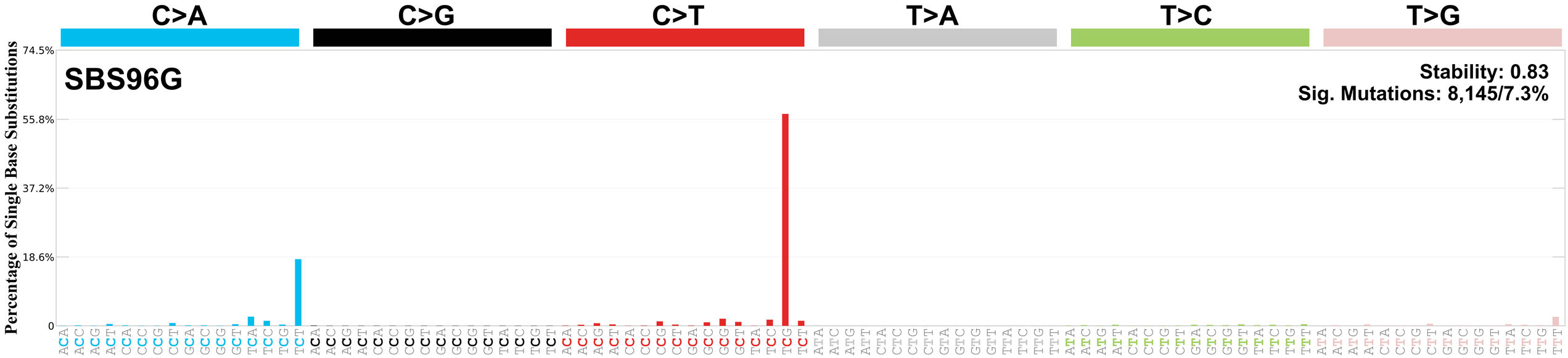
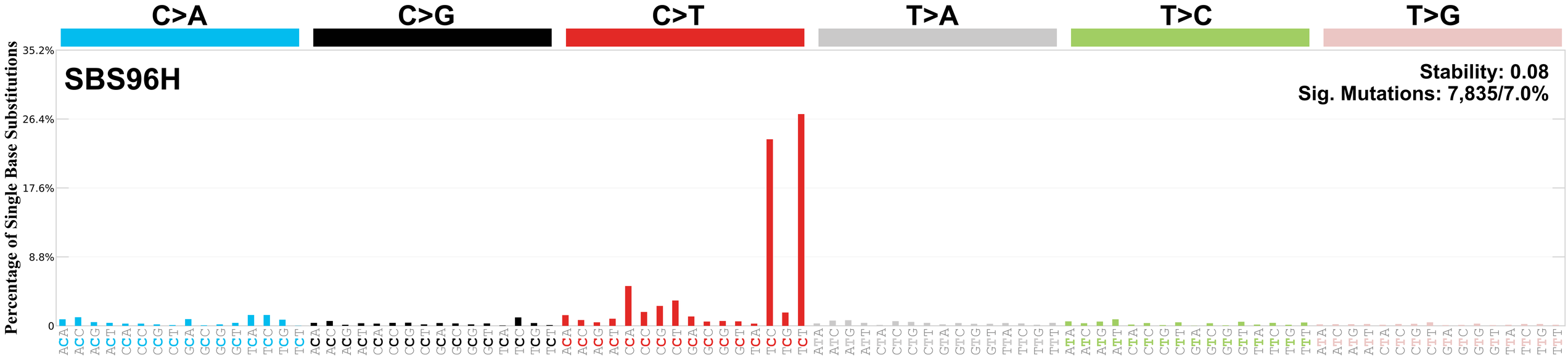
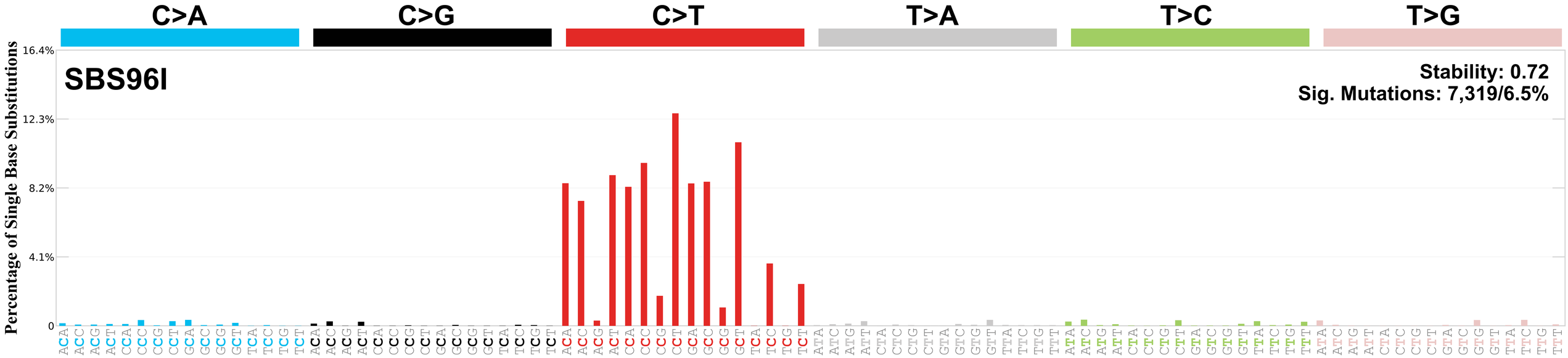
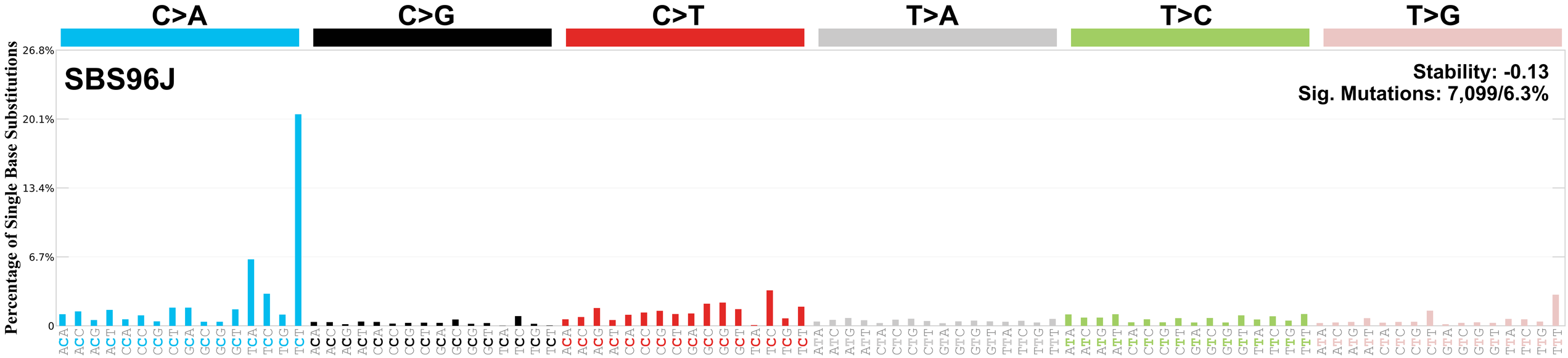

C>A
C>G
C>T
T>A
T>C
T>G
SBS96G
Stability: 0.83
Sig. Mutations: 8,145/7.3%
Percentage of Single Base Substitutions
74.5%
55.8%
37.2%
18.6%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS96H
Stability: 0.08
Sig. Mutations: 7,835/7.0%
Percentage of Single Base Substitutions
35.2%
26.4%
17.6%
8.8%
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


C>A
C>G
C>T
T>A
T>C
T>G
SBS96I
Stability: 0.72
Sig. Mutations: 7,319/6.5%
Percentage of Single Base Substitutions
16.4%
12.3%
8.2%
4.1%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS96J
Stability: -0.13
Sig. Mutations: 7,099/6.3%
Percentage of Single Base Substitutions
26.8%
20.1%
13.4%
6.7%
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
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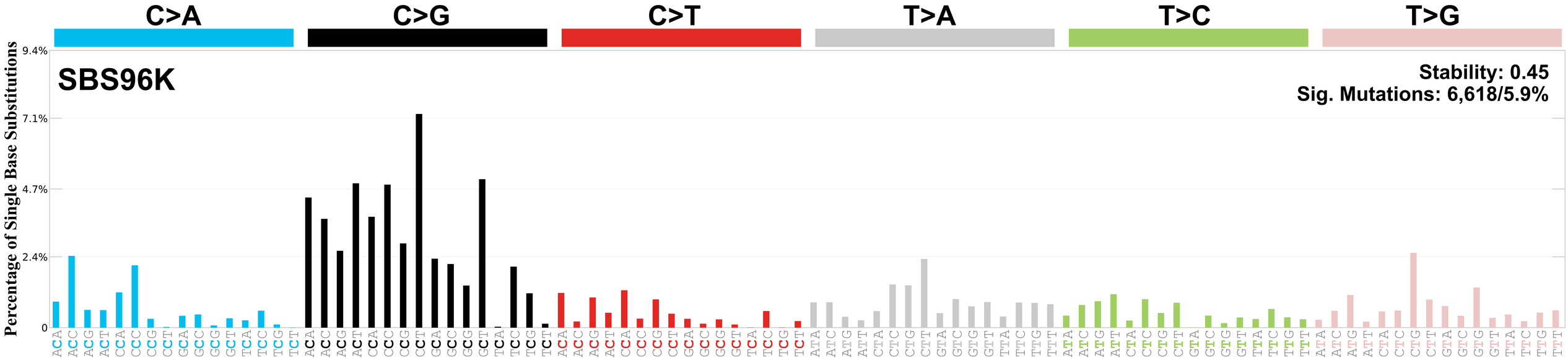
C>A
C>G
C>T
T>A
T>C
T>G
SBS96K
Stability: 0.45
Sig. Mutations: 6,618/5.9%
Percentage of Single Base Substitutions
9.4%
7.1%
4.7%
2.4%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC 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
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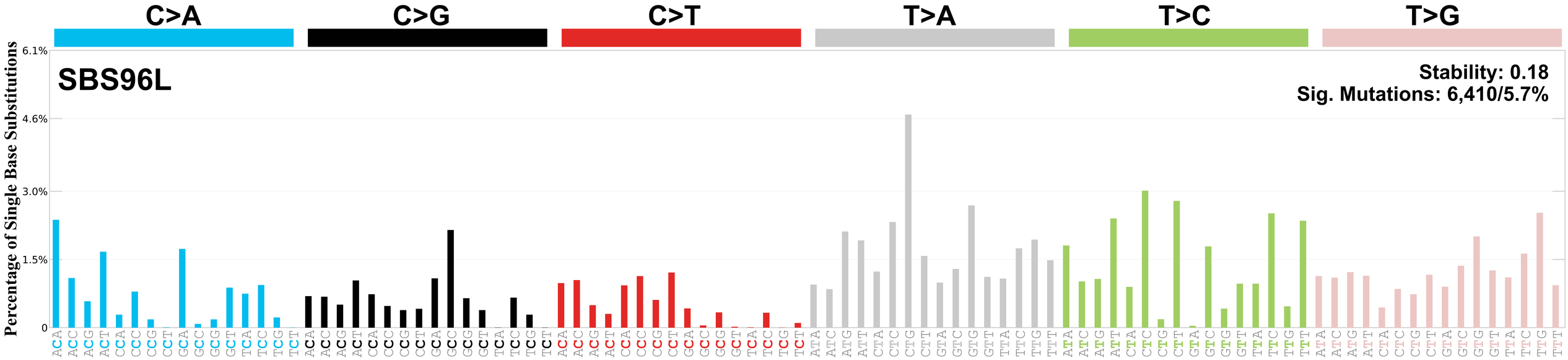
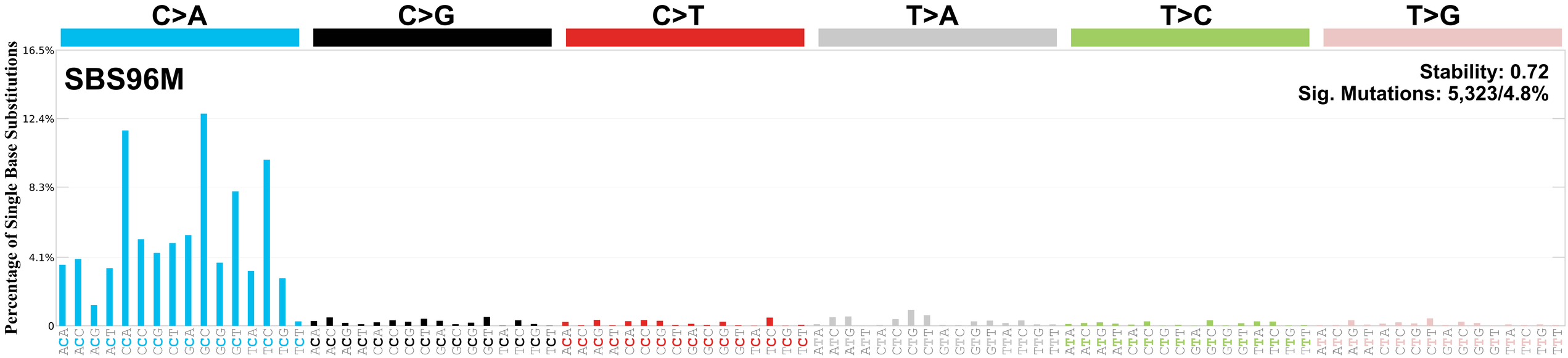

C>A
C>G
C>T
T>A
T>C
T>G
SBS96L
Stability: 0.18
Sig. Mutations: 6,410/5.7%
Percentage of Single Base Substitutions
6.1%
4.6%
3.0%
1.5%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC 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
SBS96M
Stability: 0.72
Sig. Mutations: 5,323/4.8%
Percentage of Single Base Substitutions
16.5%
12.4%
8.3%
4.1%
0