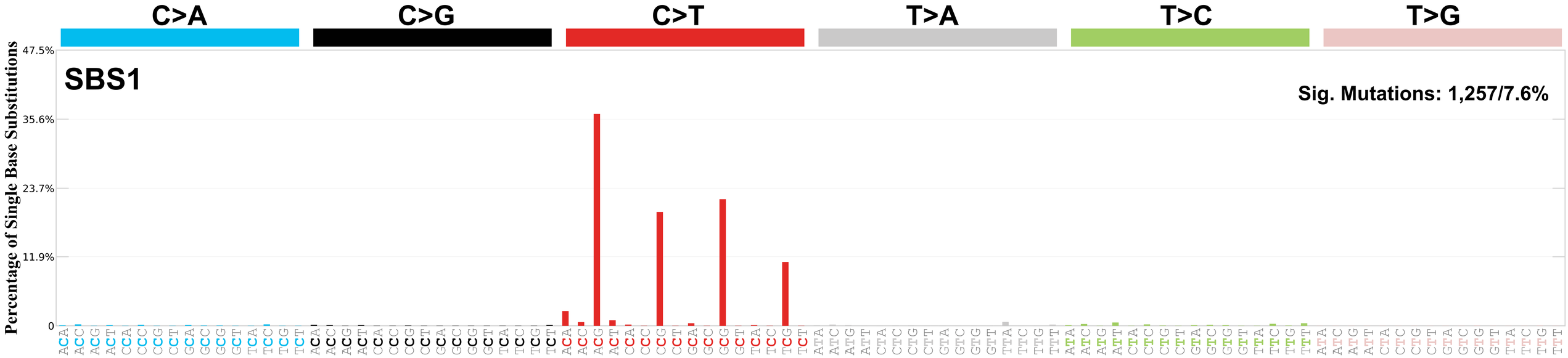
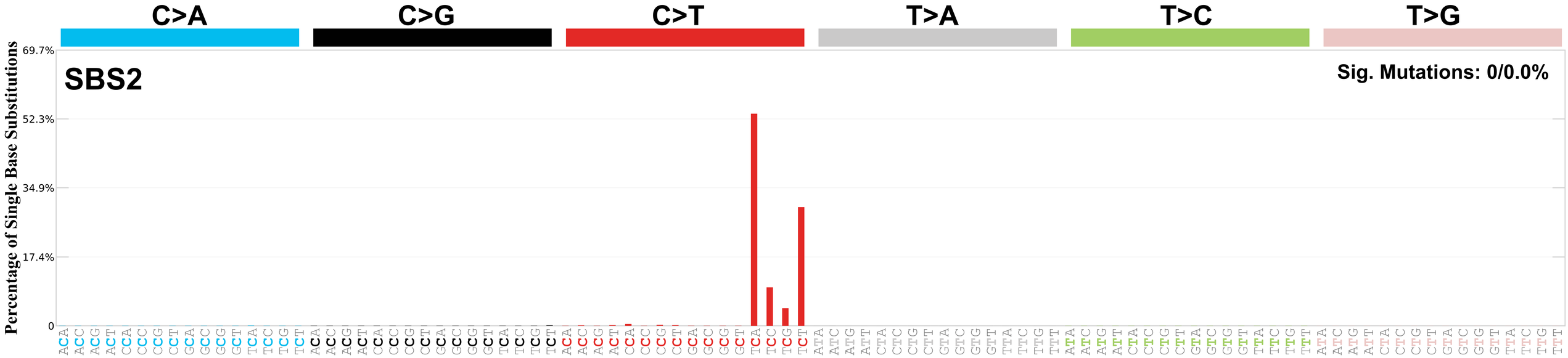
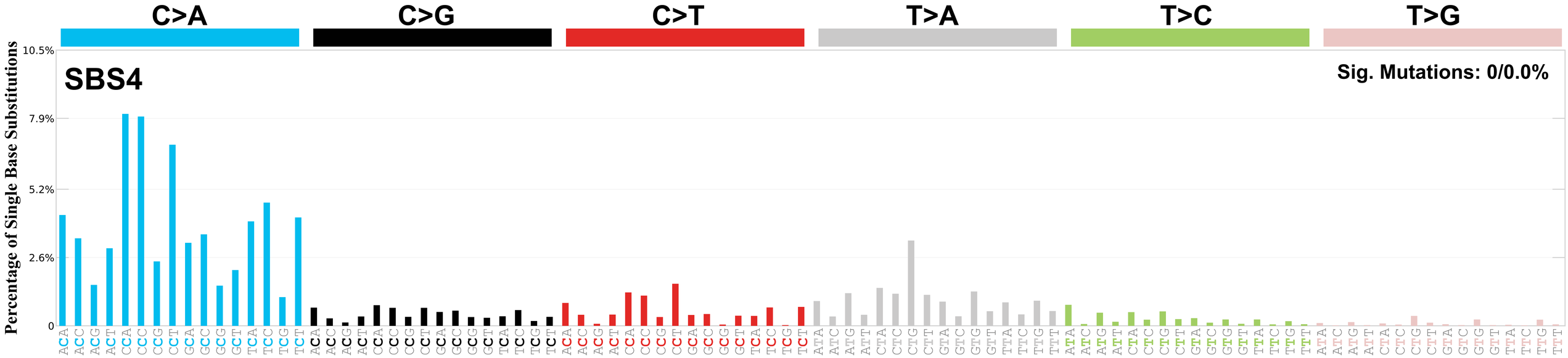

C>A
C>G
C>T
T>A
T>C
T>G
SBS1
Sig. Mutations: 1,257/7.6%
Percentage of Single Base Substitutions
47.5%
35.6%
23.7%
11.9%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS2
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
69.7%
52.3%
34.9%
17.4%
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
SBS4
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
10.5%
7.9%
5.2%
2.6%
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
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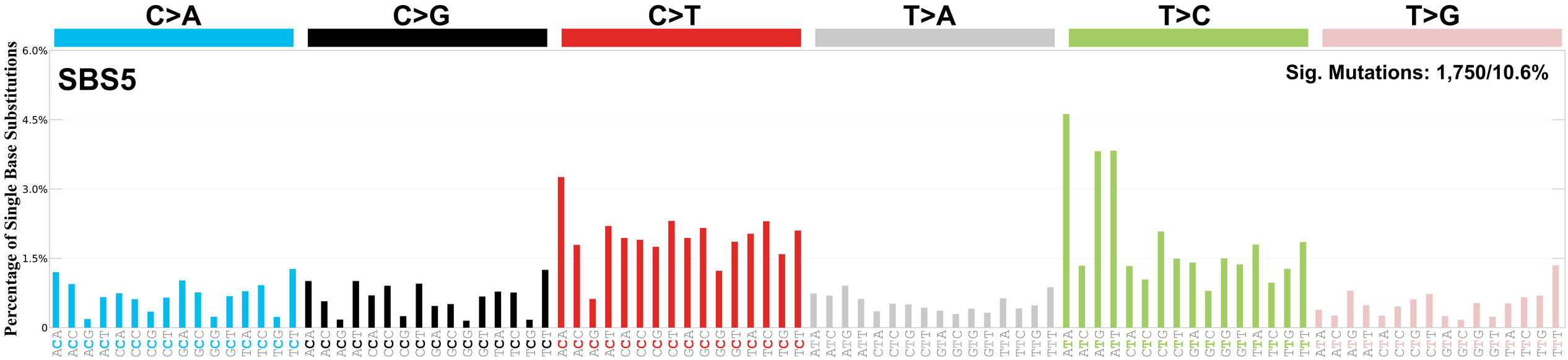
C>A
C>G
C>T
T>A
T>C
T>G
SBS5
Sig. Mutations: 1,750/10.6%
Percentage of Single Base Substitutions
6.0%
4.5%
3.0%
1.5%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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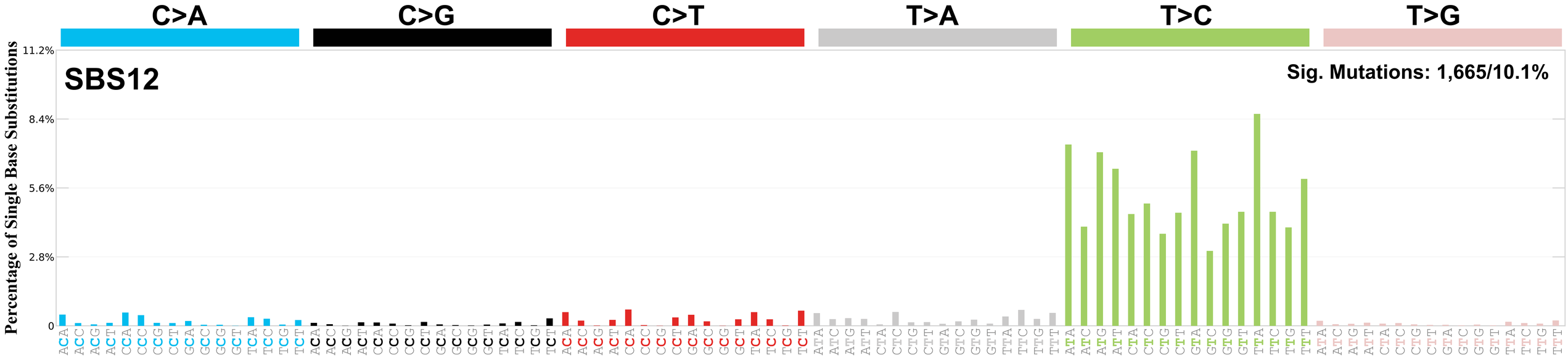
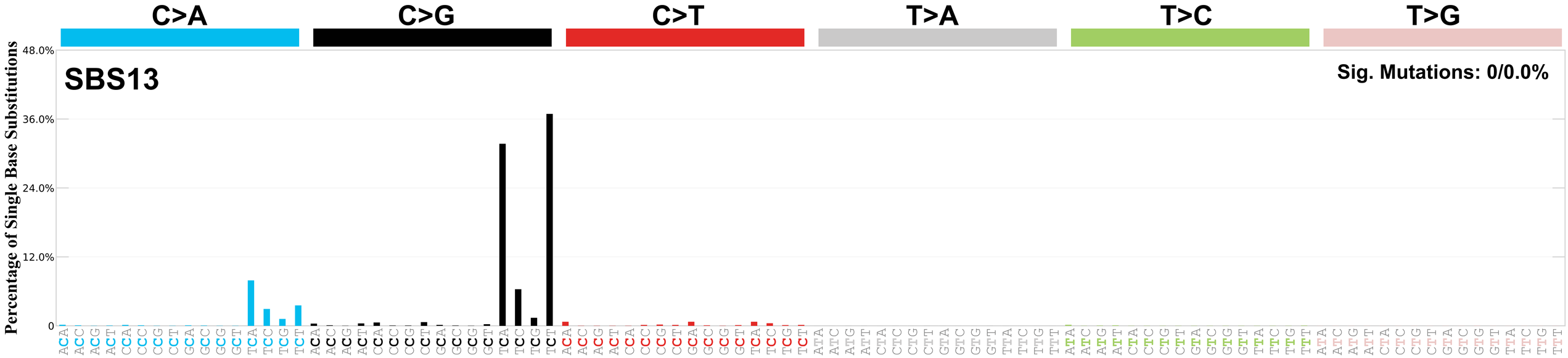
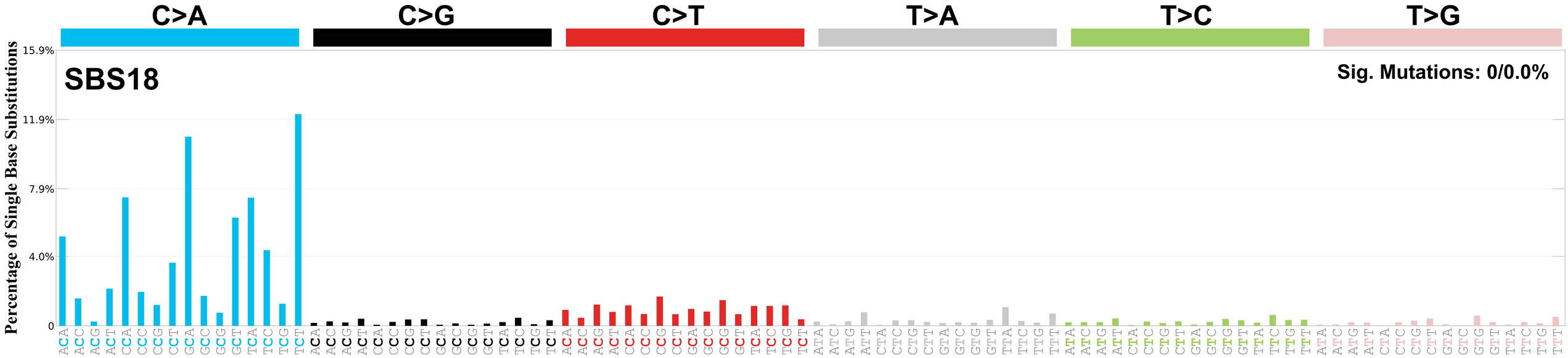

C>A
C>G
C>T
T>A
T>C
T>G
SBS12
Sig. Mutations: 1,665/10.1%
Percentage of Single Base Substitutions
11.2%
8.4%
5.6%
2.8%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA 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 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
SBS13
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
48.0%
36.0%
24.0%
12.0%
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
SBS18
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
15.9%
11.9%
7.9%
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
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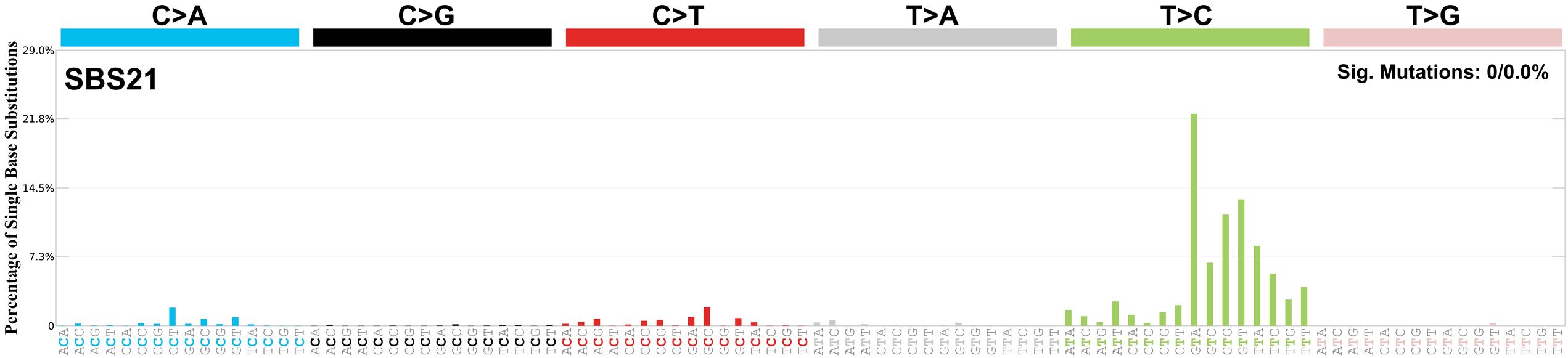
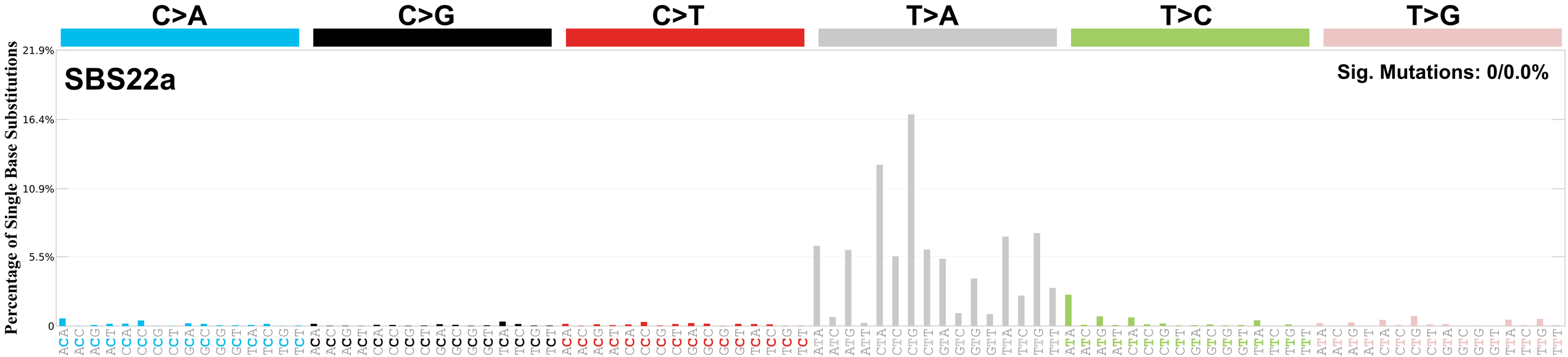
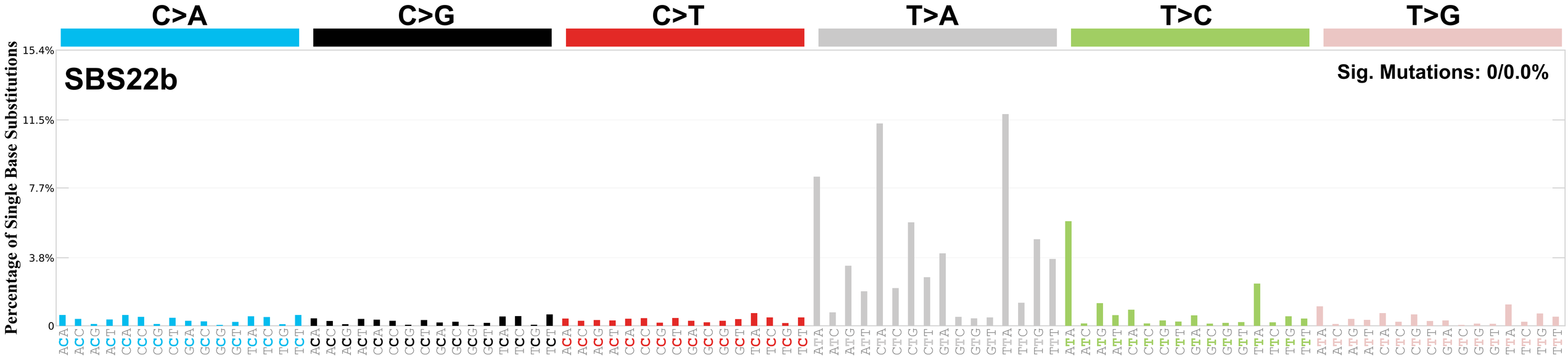

C>A
C>G
C>T
T>A
T>C
T>G
SBS21
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
29.0%
21.8%
14.5%
7.3%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC 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
SBS22a
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
21.9%
16.4%
10.9%
5.5%
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
SBS22b
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
15.4%
11.5%
7.7%
3.8%
0
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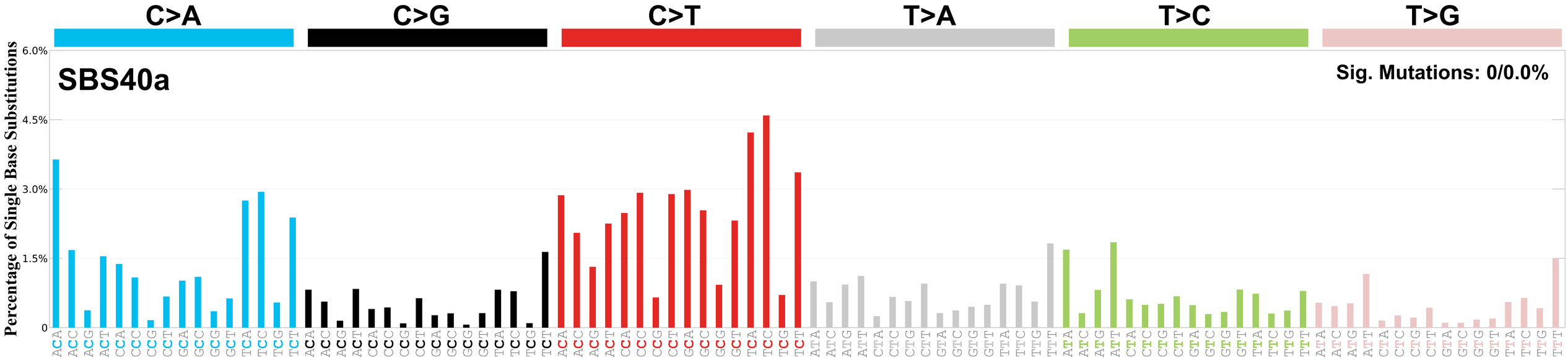
C>A
C>G
C>T
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T>C
T>G
SBS40a
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
6.0%
4.5%
3.0%
1.5%
0
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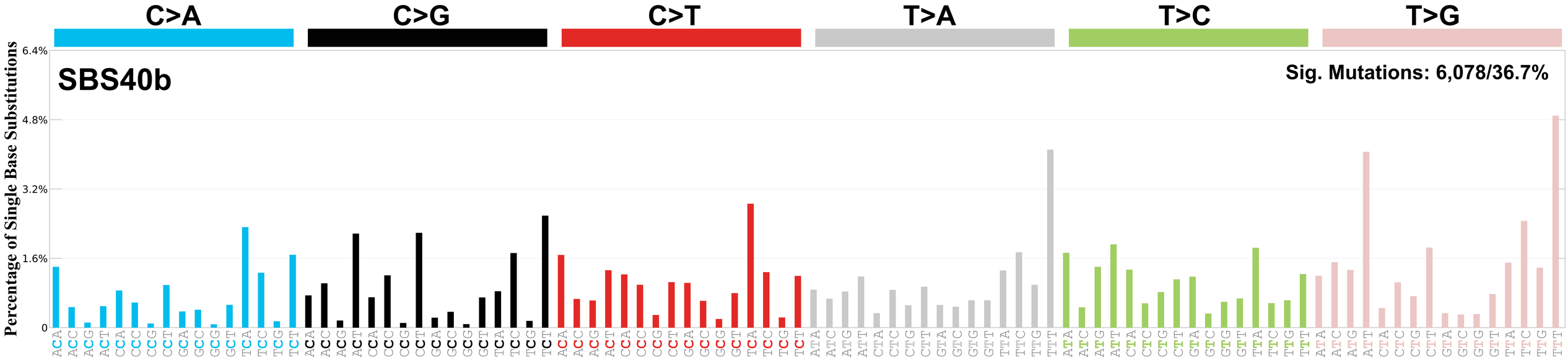
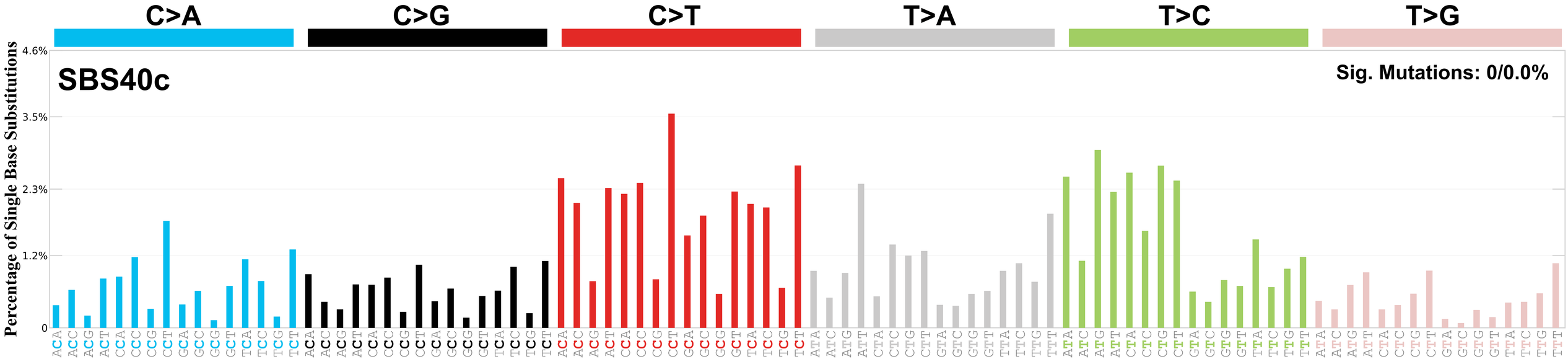

C>A
C>G
C>T
T>A
T>C
T>G
SBS40b
Sig. Mutations: 6,078/36.7%
Percentage of Single Base Substitutions
6.4%
4.8%
3.2%
1.6%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA 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
SBS40c
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
4.6%
3.5%
2.3%
1.2%
0
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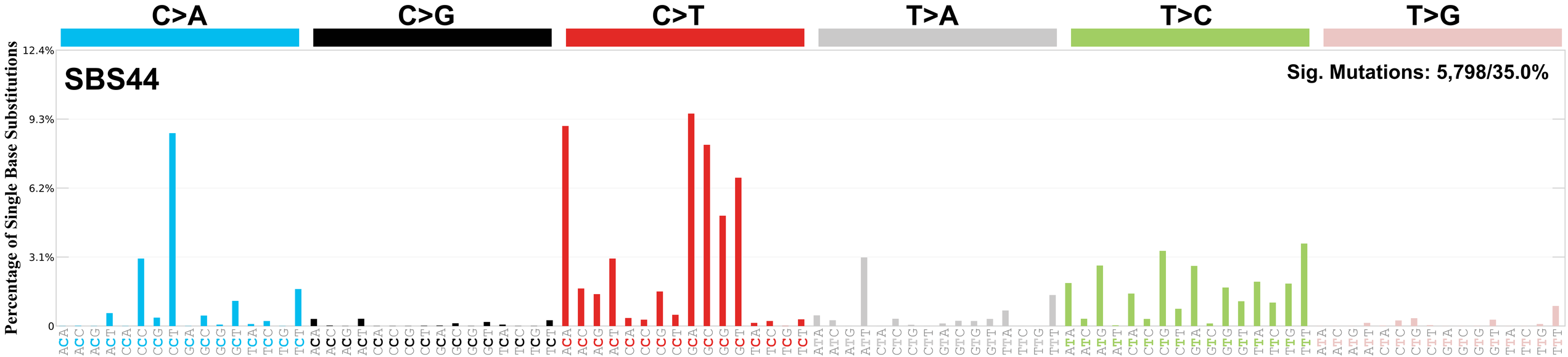
C>A
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C>T
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T>C
T>G
SBS44
Sig. Mutations: 5,798/35.0%
Percentage of Single Base Substitutions
12.4%
9.3%
6.2%
3.1%
0