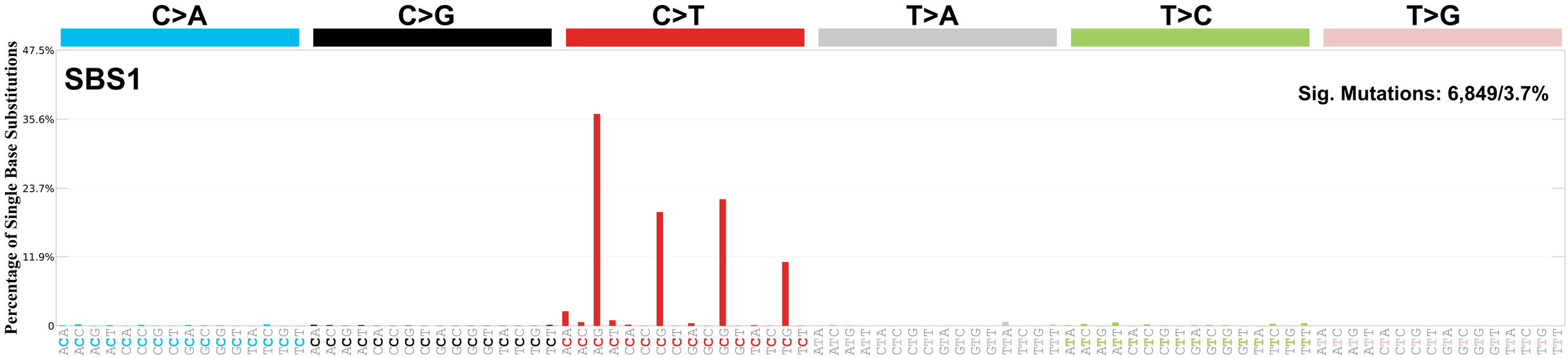
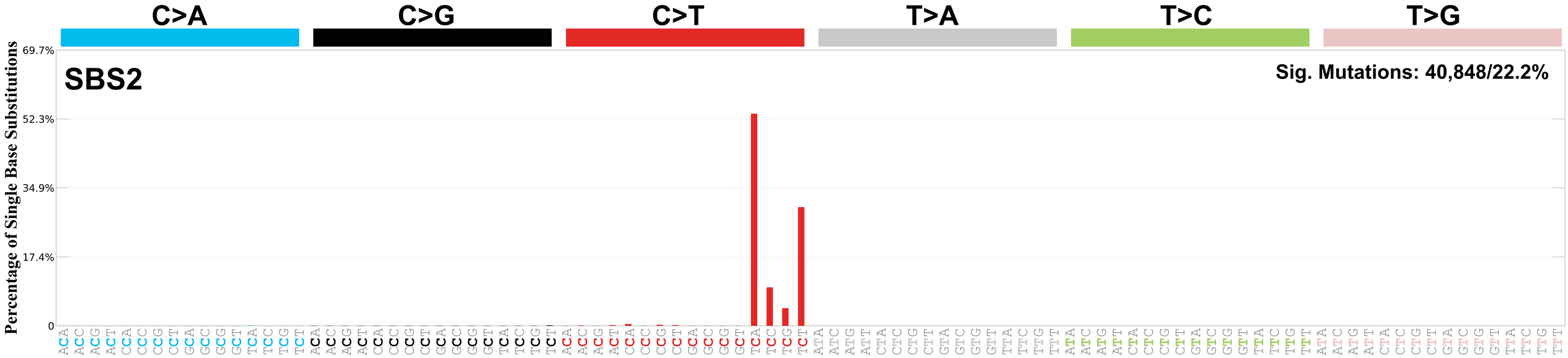
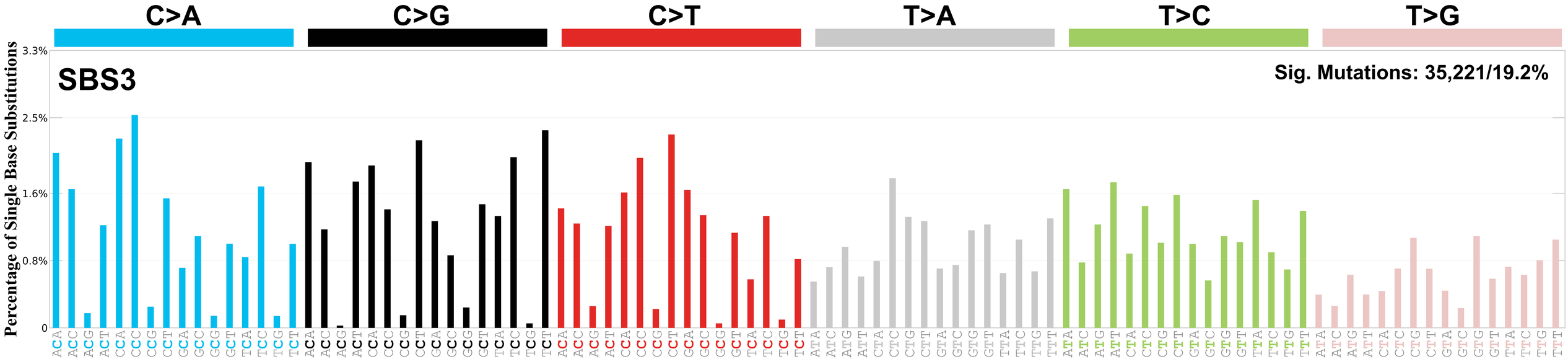
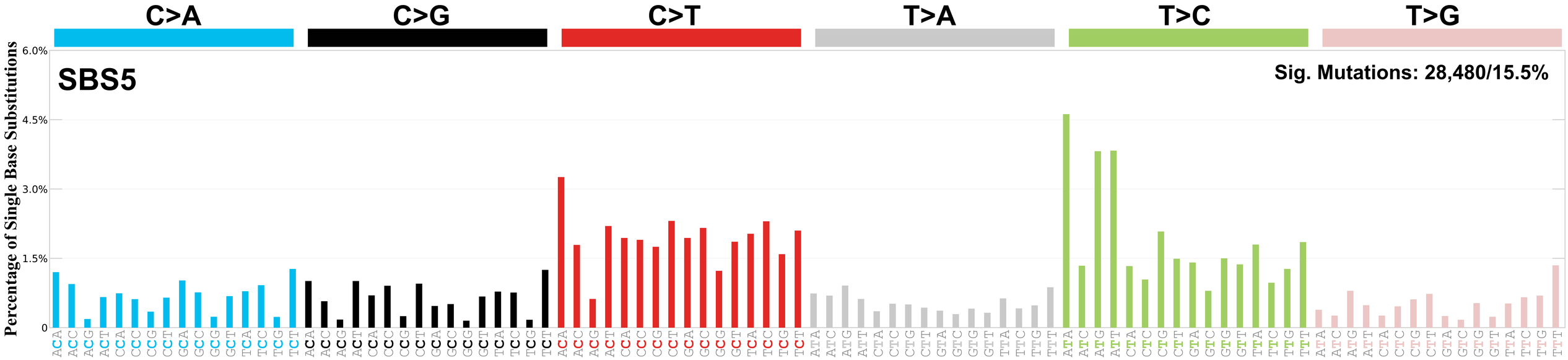

C>A
C>G
C>T
T>A
T>C
T>G
SBS1
Sig. Mutations: 6,849/3.7%
Percentage of Single Base Substitutions
47.5%
35.6%
23.7%
11.9%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS2
Sig. Mutations: 40,848/22.2%
Percentage of Single Base Substitutions
69.7%
52.3%
34.9%
17.4%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS3
Sig. Mutations: 35,221/19.2%
Percentage of Single Base Substitutions
3.3%
2.5%
1.6%
0.8%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS5
Sig. Mutations: 28,480/15.5%
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
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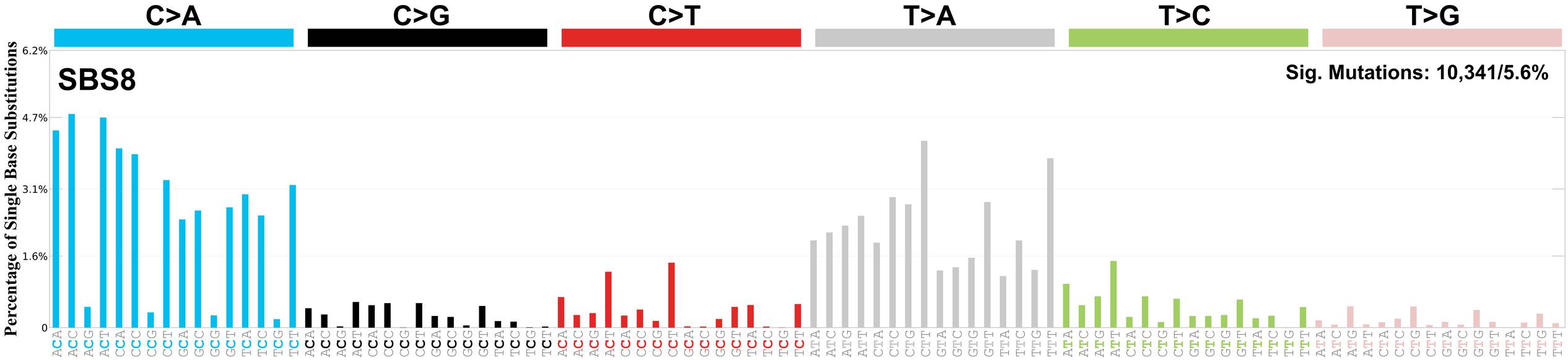
C>A
C>G
C>T
T>A
T>C
T>G
SBS8
Sig. Mutations: 10,341/5.6%
Percentage of Single Base Substitutions
6.2%
4.7%
3.1%
1.6%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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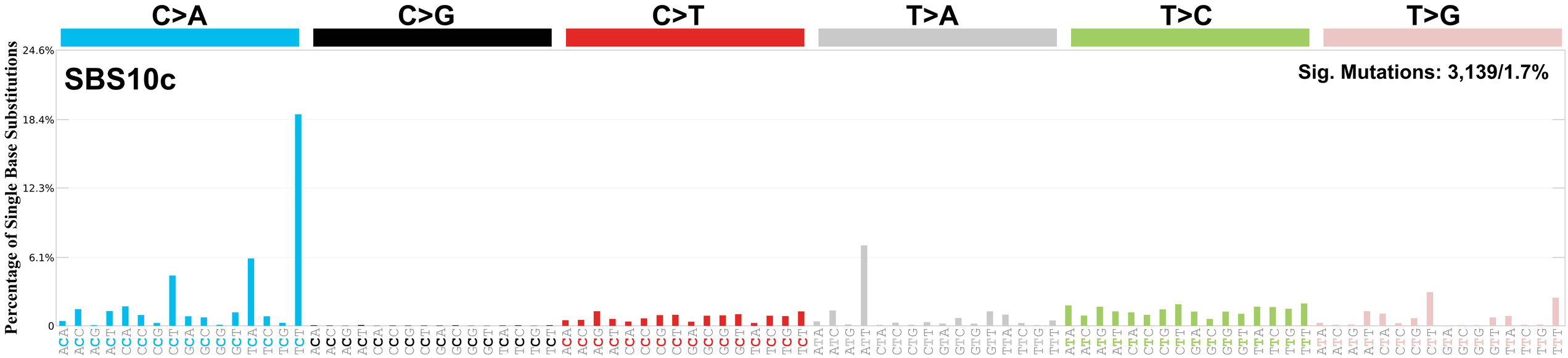
C>A
C>G
C>T
T>A
T>C
T>G
SBS10c
Sig. Mutations: 3,139/1.7%
Percentage of Single Base Substitutions
24.6%
18.4%
12.3%
6.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA 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
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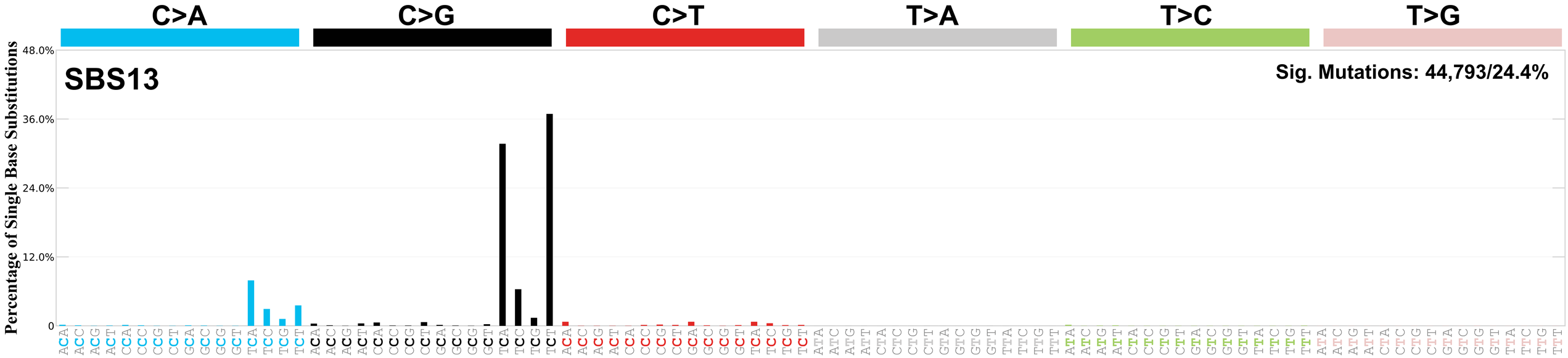
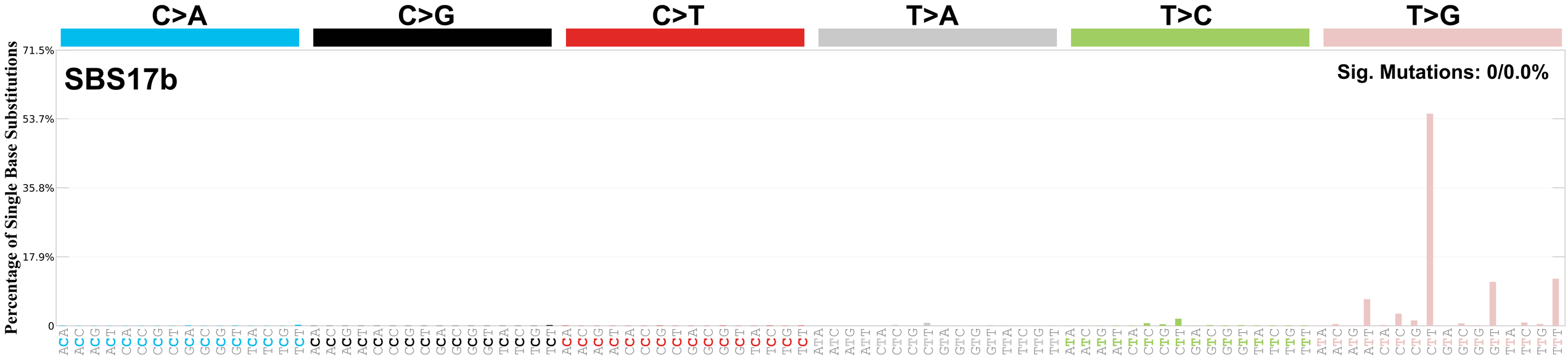
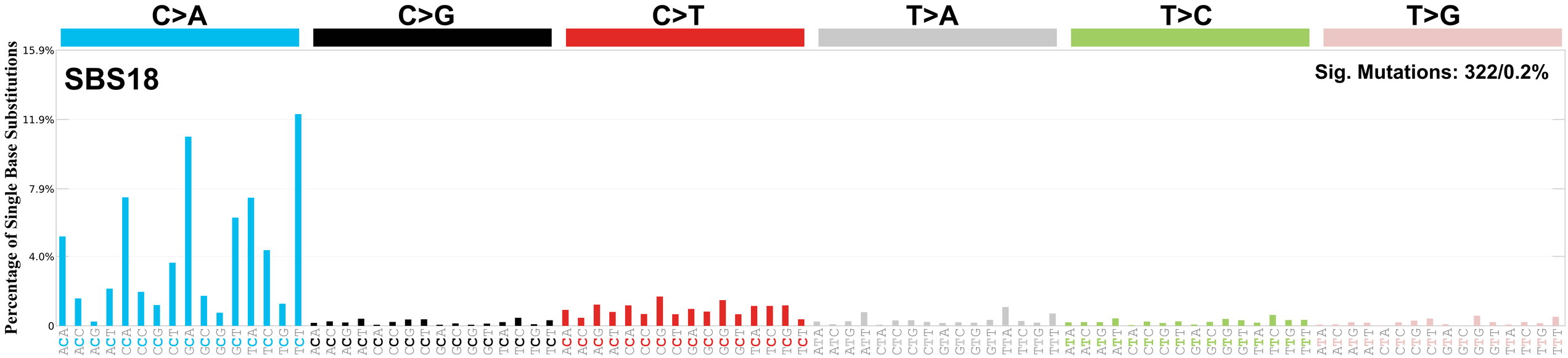

C>A
C>G
C>T
T>A
T>C
T>G
SBS13
Sig. Mutations: 44,793/24.4%
Percentage of Single Base Substitutions
48.0%
36.0%
24.0%
12.0%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS17b
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
71.5%
53.7%
35.8%
17.9%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS18
Sig. Mutations: 322/0.2%
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
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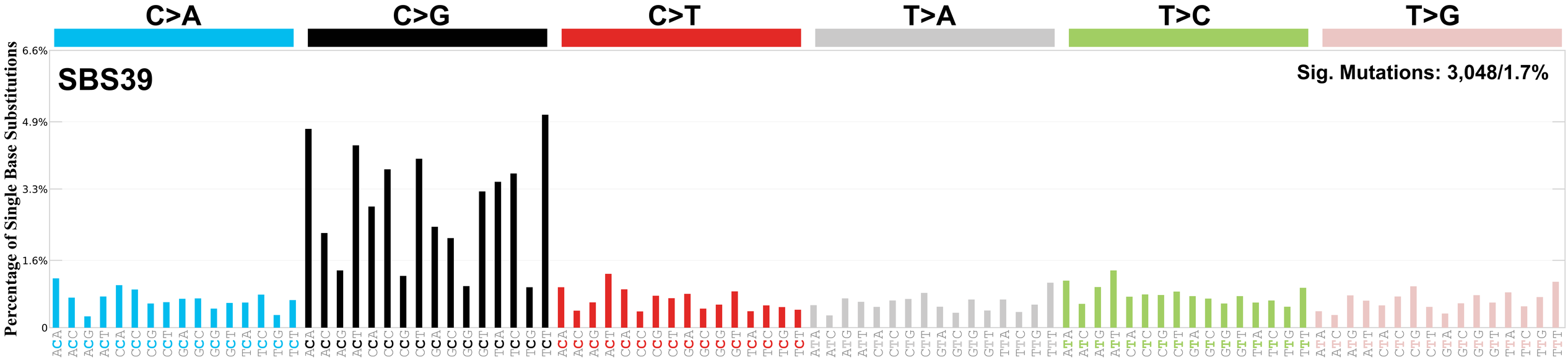
C>A
C>G
C>T
T>A
T>C
T>G
SBS39
Sig. Mutations: 3,048/1.7%
Percentage of Single Base Substitutions
6.6%
4.9%
3.3%
1.6%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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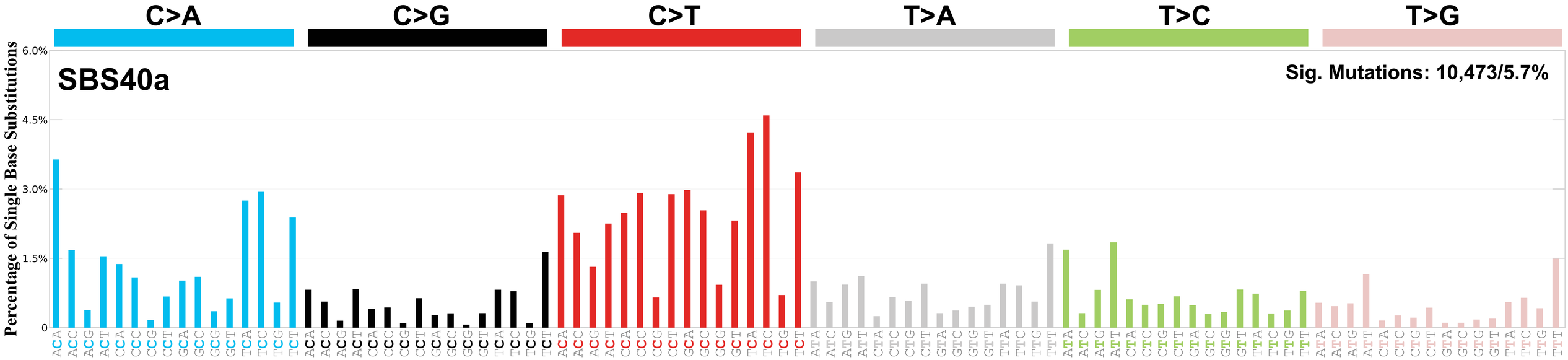
C>A
C>G
C>T
T>A
T>C
T>G
SBS40a
Sig. Mutations: 10,473/5.7%
Percentage of Single Base Substitutions
6.0%
4.5%
3.0%
1.5%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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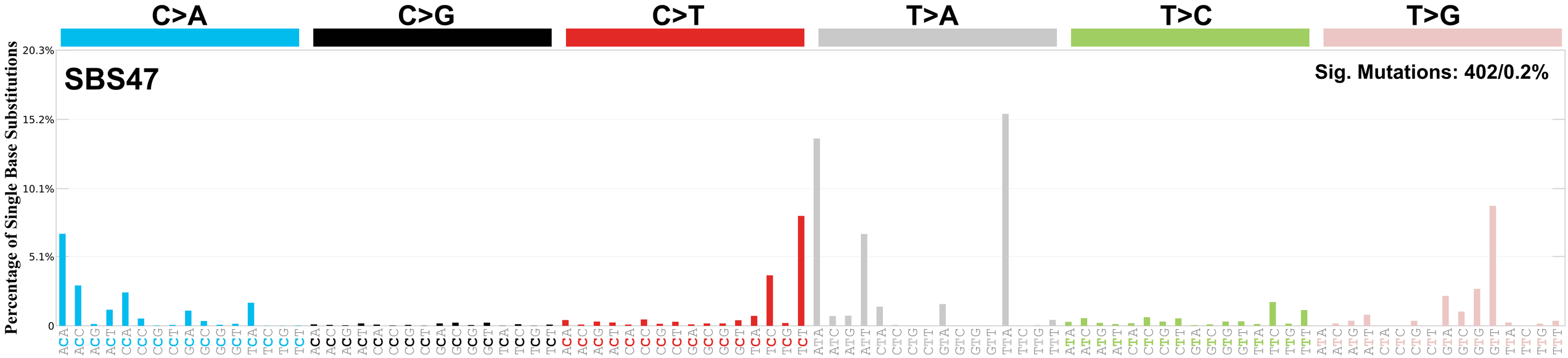
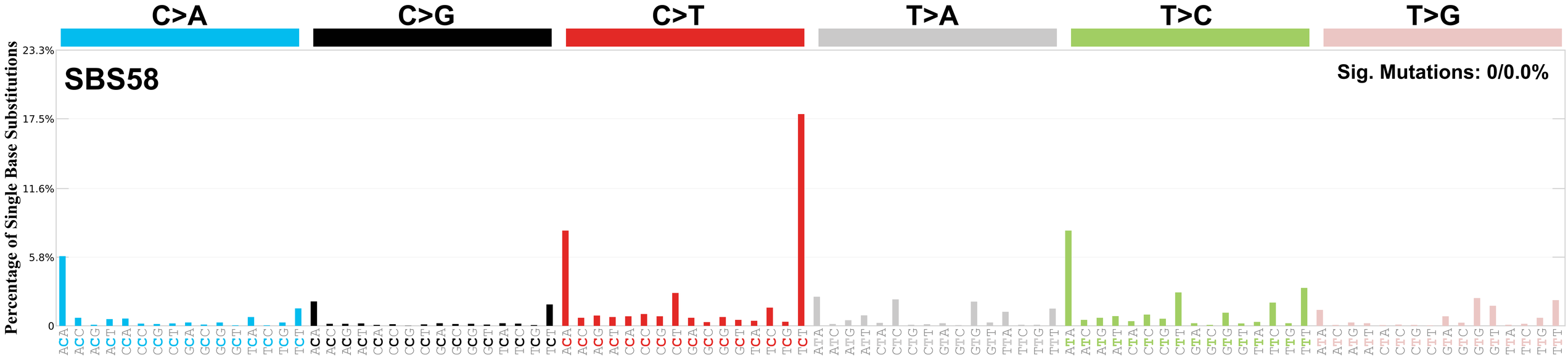

C>A
C>G
C>T
T>A
T>C
T>G
SBS47
Sig. Mutations: 402/0.2%
Percentage of Single Base Substitutions
20.3%
15.2%
10.1%
5.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC 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
SBS58
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
23.3%
17.5%
11.6%
5.8%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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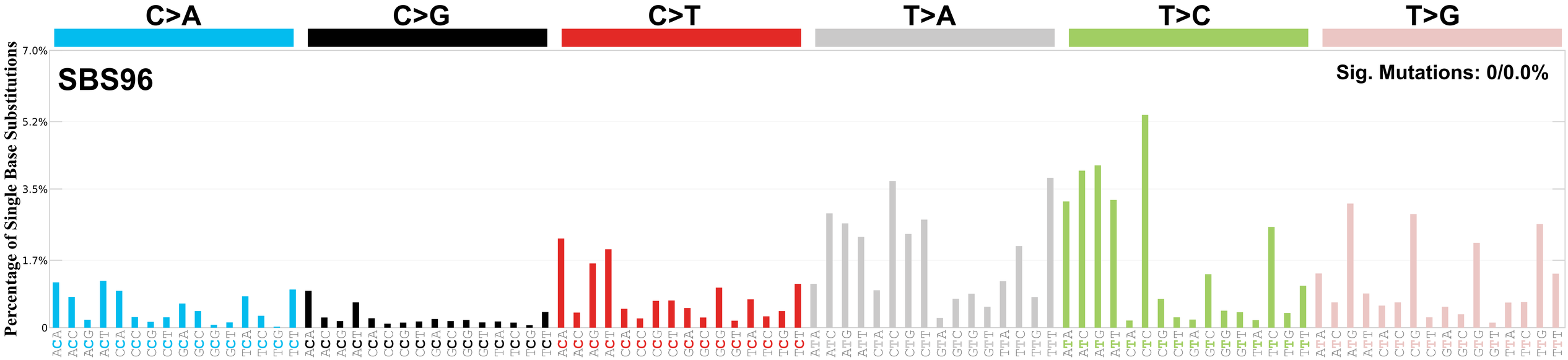
C>A
C>G
C>T
T>A
T>C
T>G
SBS96
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
7.0%
5.2%
3.5%
1.7%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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