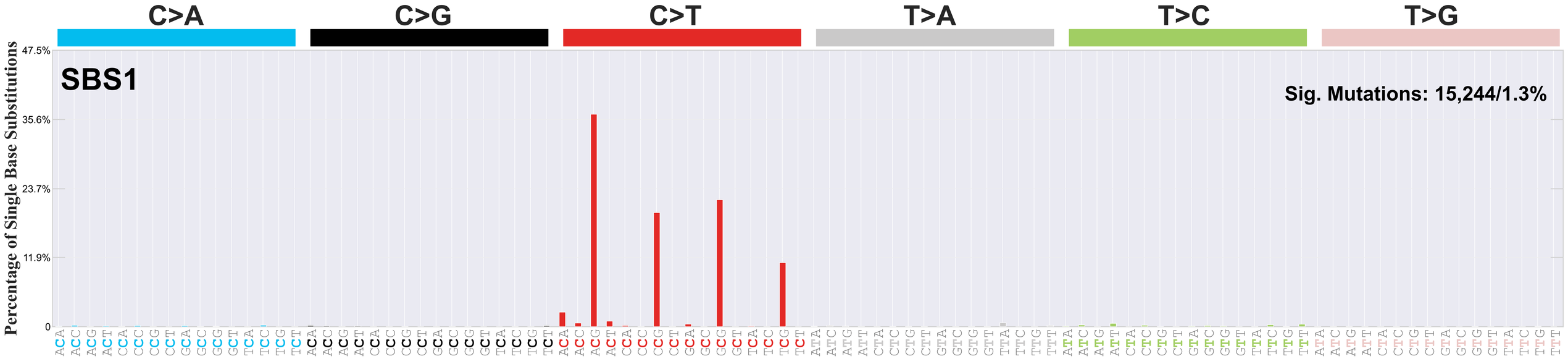
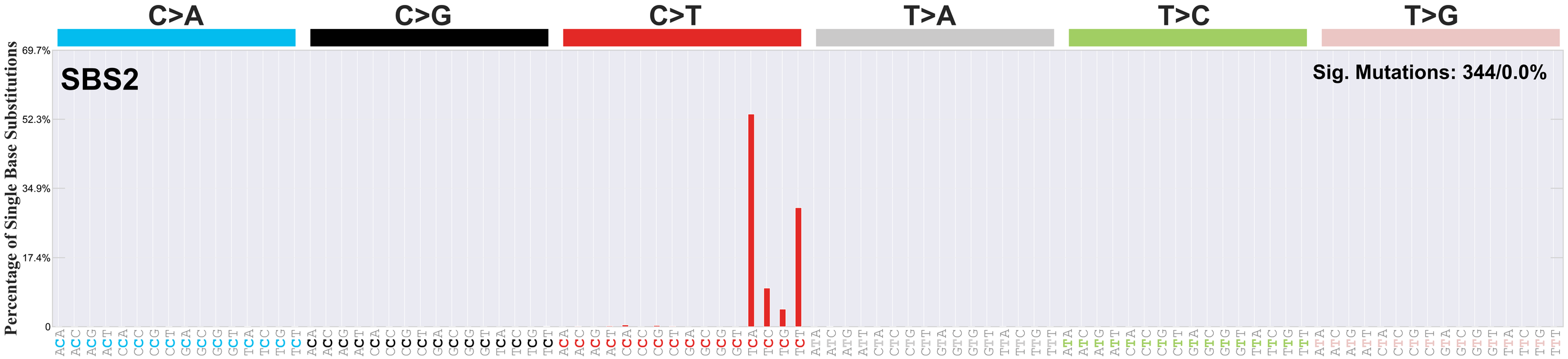
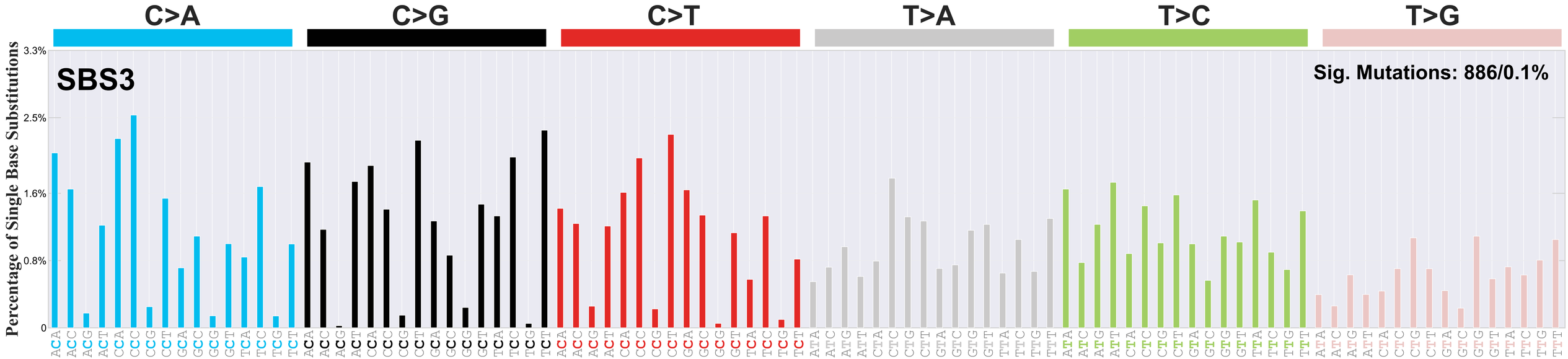

C>A
C>G
C>T
T>A
T>C
T>G
SBS1
Sig. Mutations: 15,244/1.3%
Percentage of Single Base Substitutions
47.5%
35.6%
23.7%
11.9%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS2
Sig. Mutations: 344/0.0%
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: 886/0.1%
Percentage of Single Base Substitutions
3.3%
2.5%
1.6%
0.8%
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
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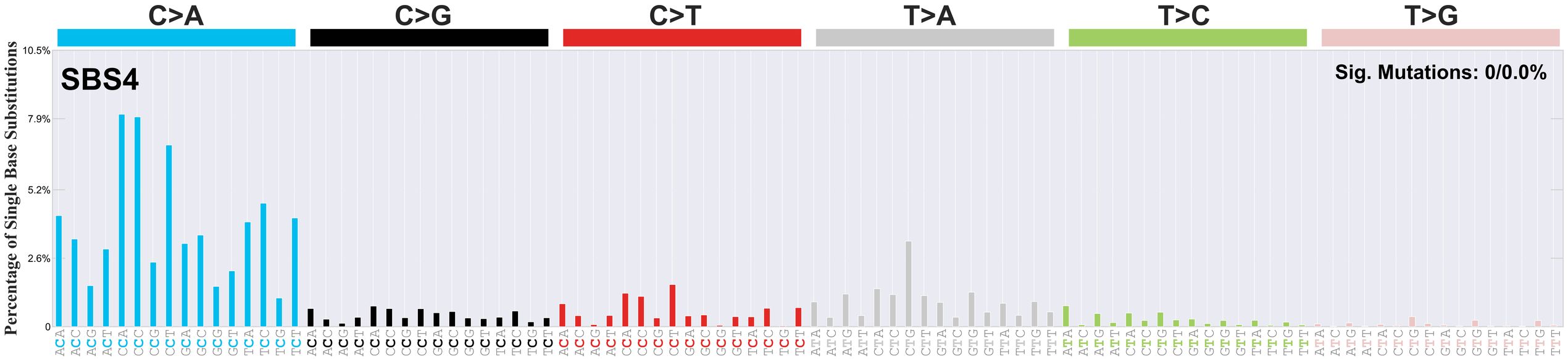
C>A
C>G
C>T
T>A
T>C
T>G
SBS4
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
10.5%
7.9%
5.2%
2.6%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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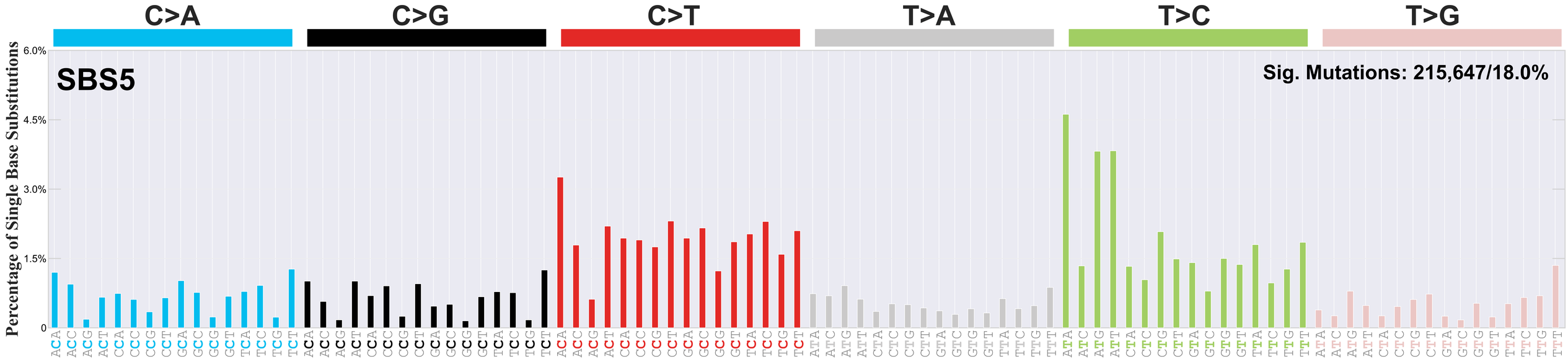
C>A
C>G
C>T
T>A
T>C
T>G
SBS5
Sig. Mutations: 215,647/18.0%
Percentage of Single Base Substitutions
6.0%
4.5%
3.0%
1.5%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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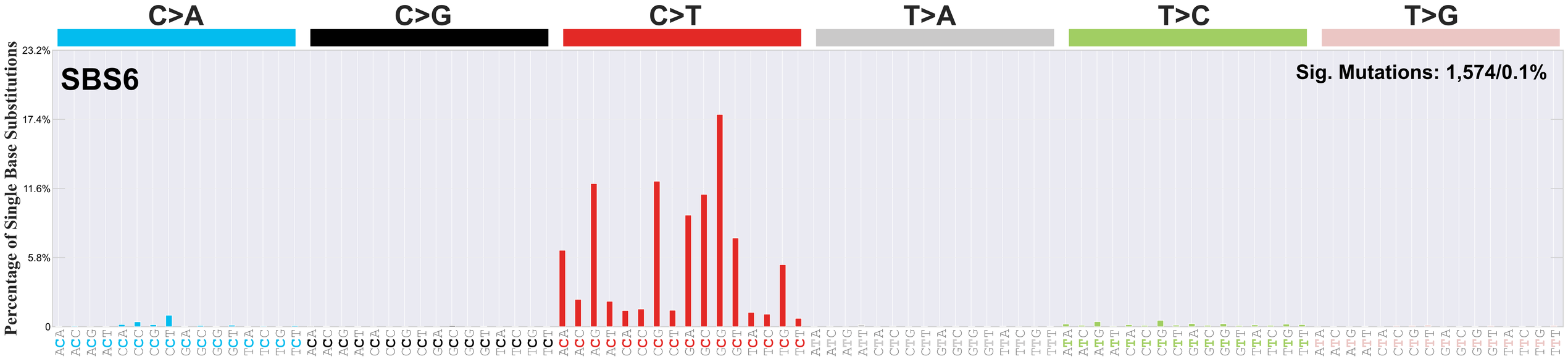
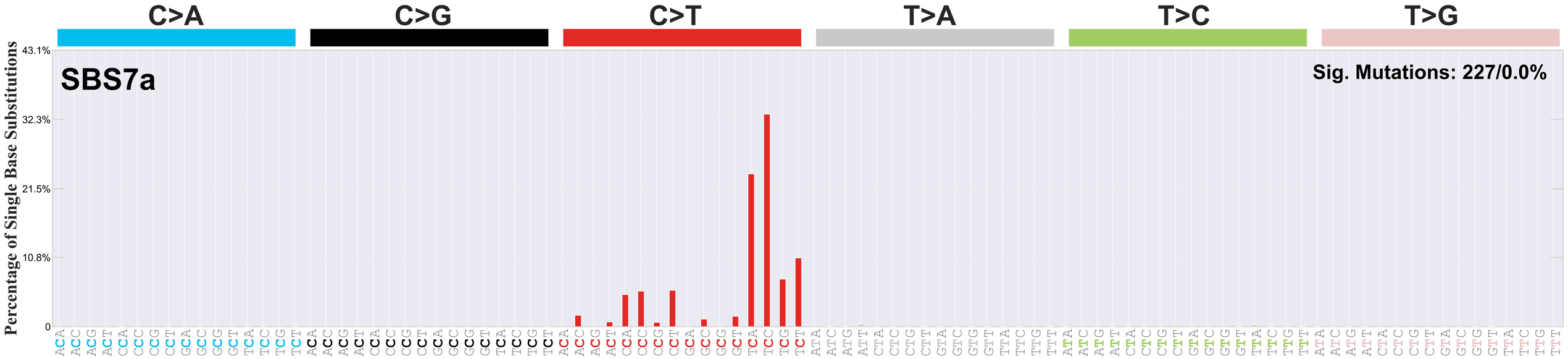
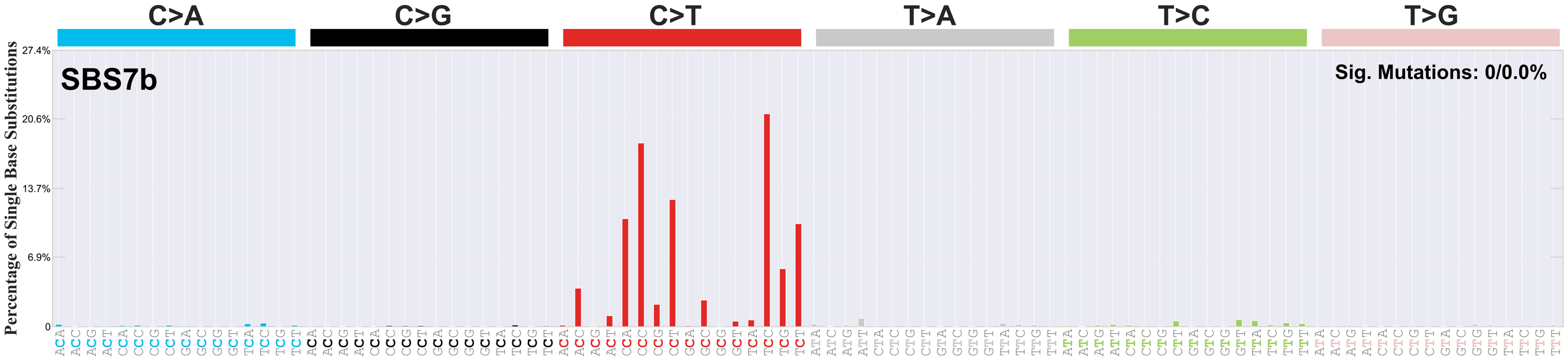
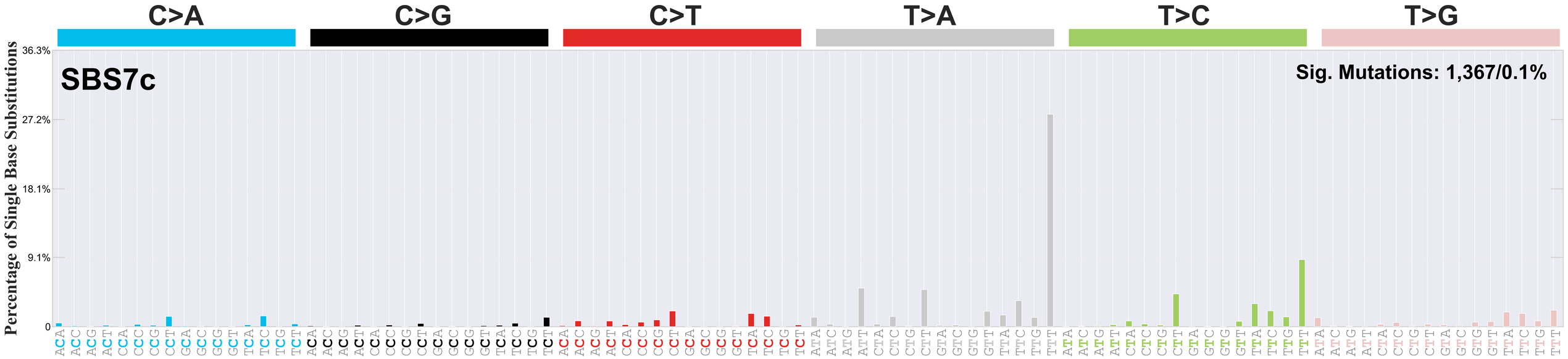
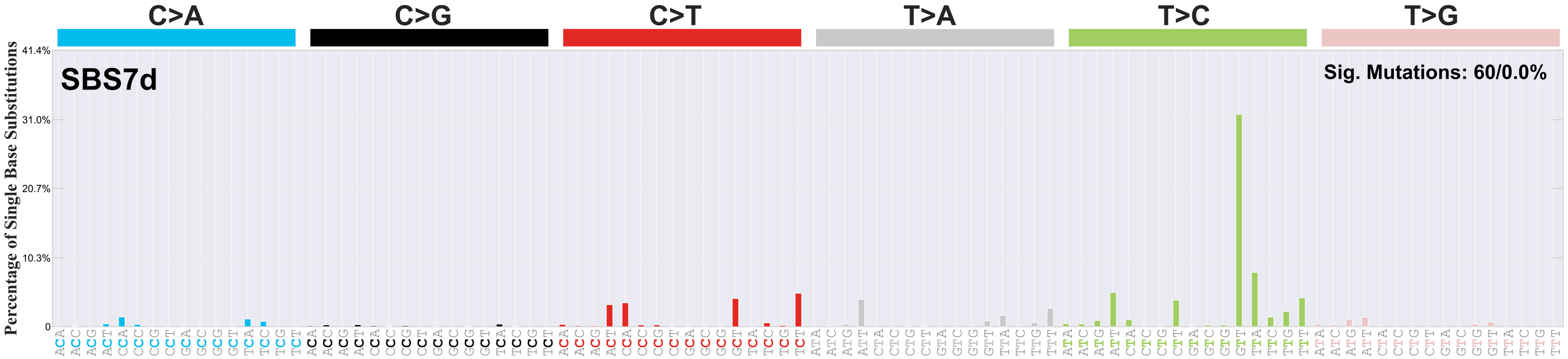
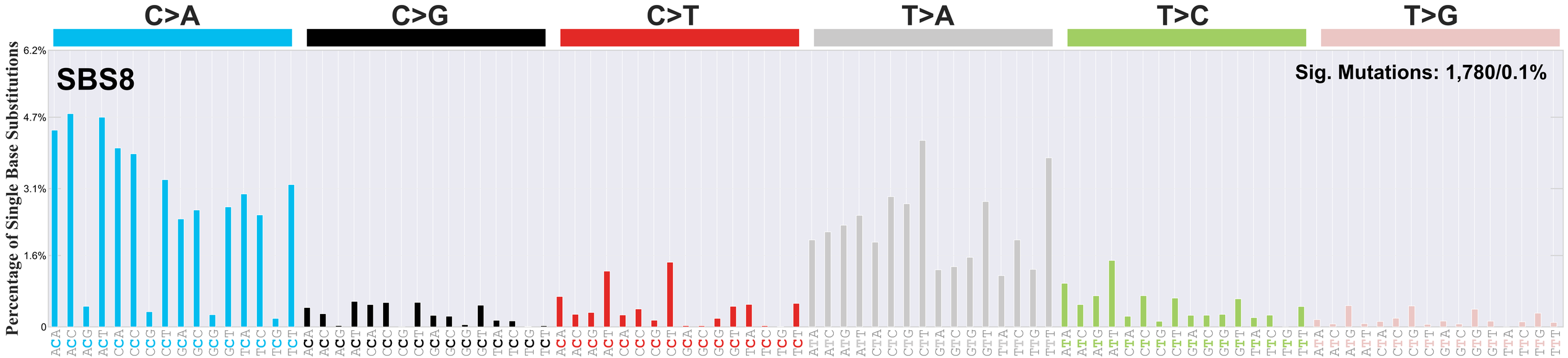

C>A
C>G
C>T
T>A
T>C
T>G
SBS6
Sig. Mutations: 1,574/0.1%
Percentage of Single Base Substitutions
23.2%
17.4%
11.6%
5.8%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA 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
SBS7a
Sig. Mutations: 227/0.0%
Percentage of Single Base Substitutions
43.1%
32.3%
21.5%
10.8%
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
SBS7b
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
27.4%
20.6%
13.7%
6.9%
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
SBS7c
Sig. Mutations: 1,367/0.1%
Percentage of Single Base Substitutions
36.3%
27.2%
18.1%
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 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
SBS7d
Sig. Mutations: 60/0.0%
Percentage of Single Base Substitutions
41.4%
31.0%
20.7%
10.3%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS8
Sig. Mutations: 1,780/0.1%
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
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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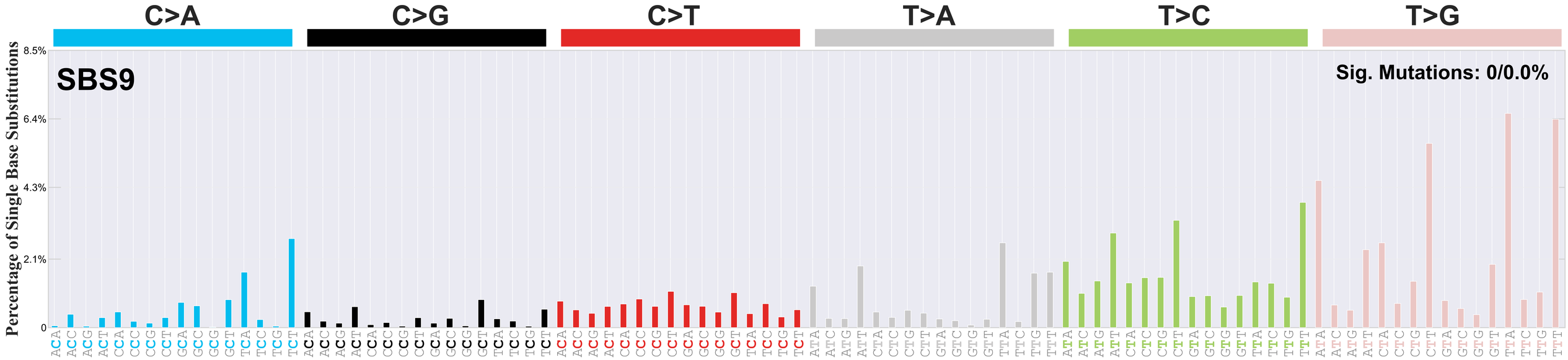
C>A
C>G
C>T
T>A
T>C
T>G
SBS9
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
8.5%
6.4%
4.3%
2.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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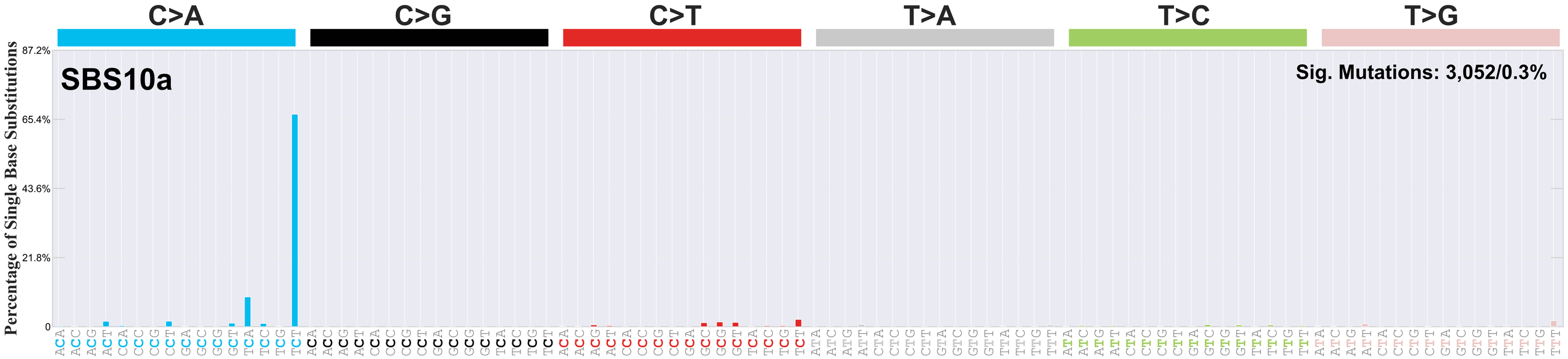
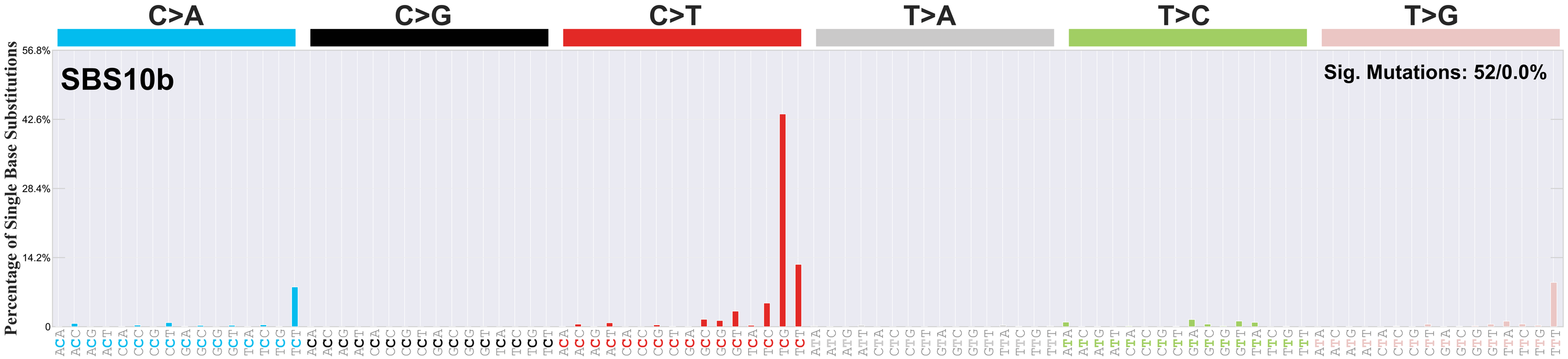
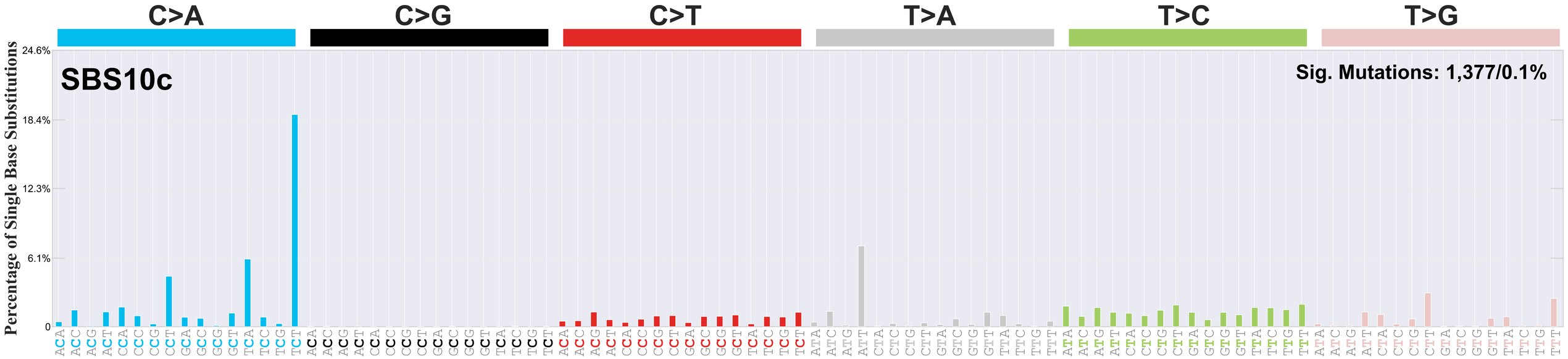

C>A
C>G
C>T
T>A
T>C
T>G
SBS10a
Sig. Mutations: 3,052/0.3%
Percentage of Single Base Substitutions
87.2%
65.4%
43.6%
21.8%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS10b
Sig. Mutations: 52/0.0%
Percentage of Single Base Substitutions
56.8%
42.6%
28.4%
14.2%
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
SBS10c
Sig. Mutations: 1,377/0.1%
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
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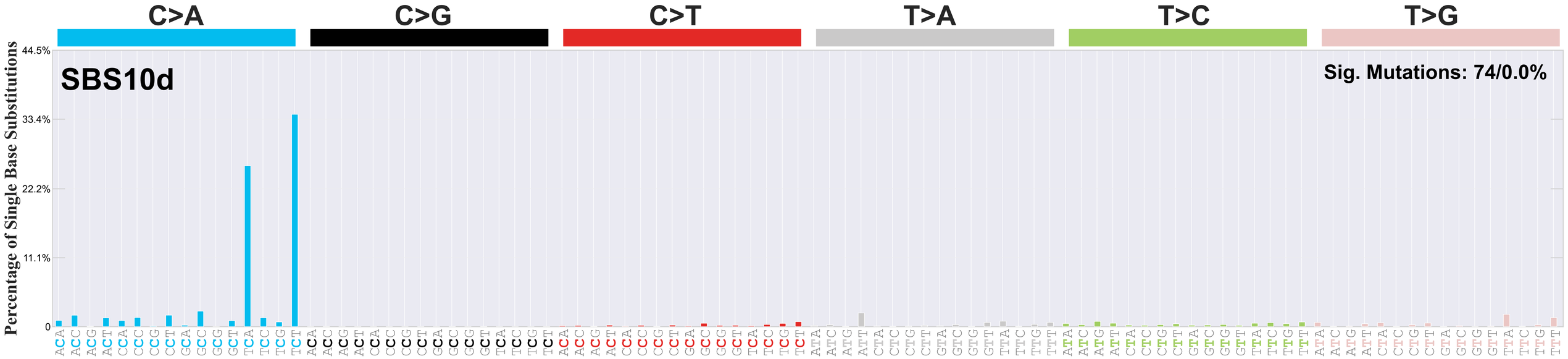
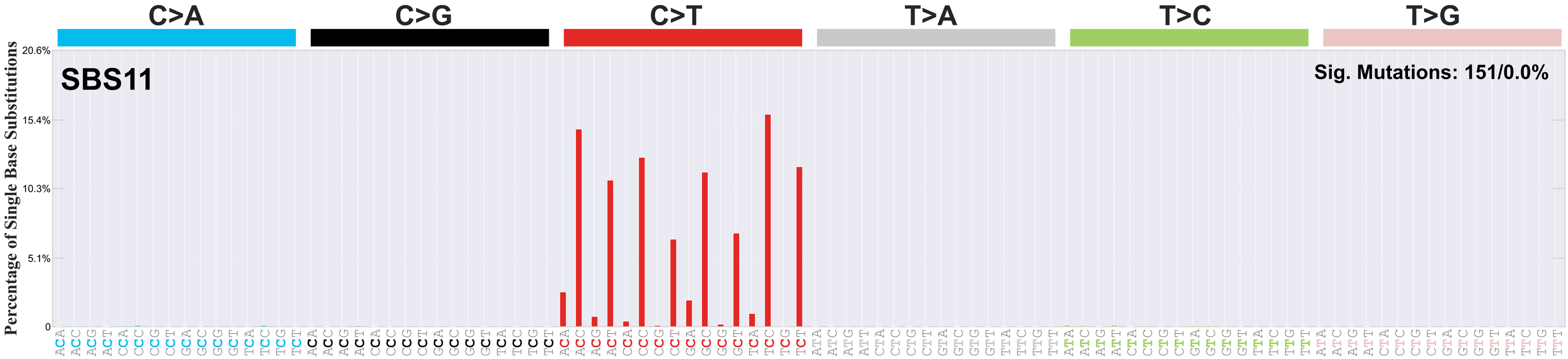
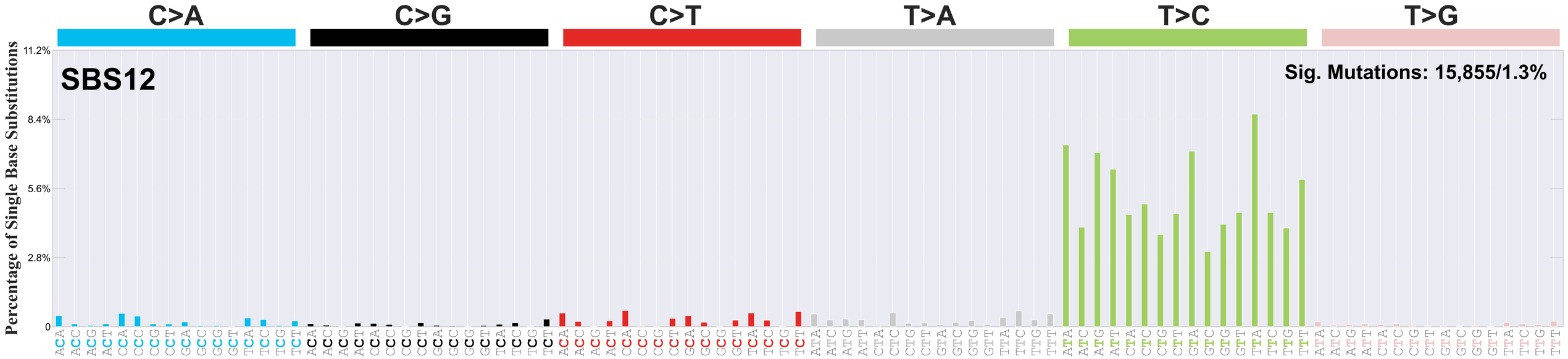
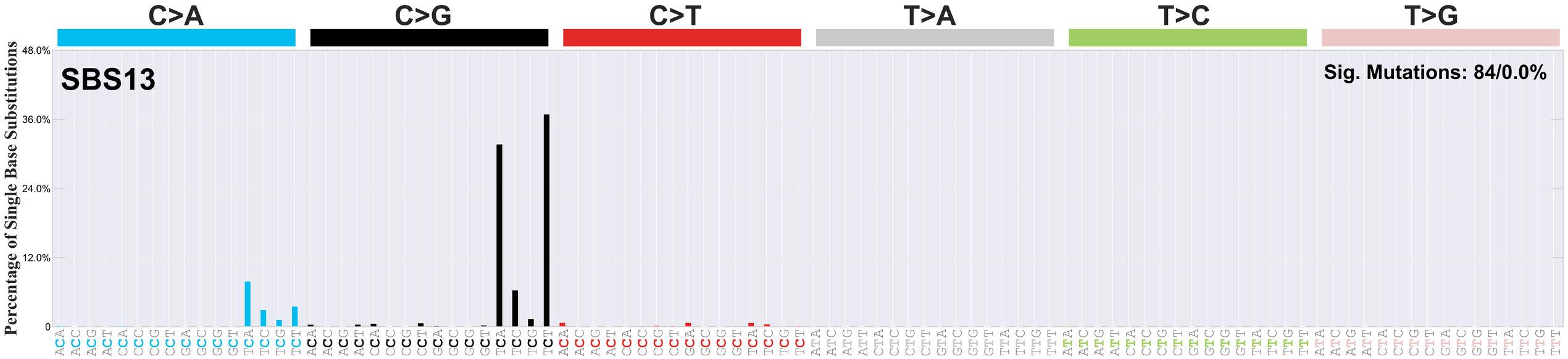
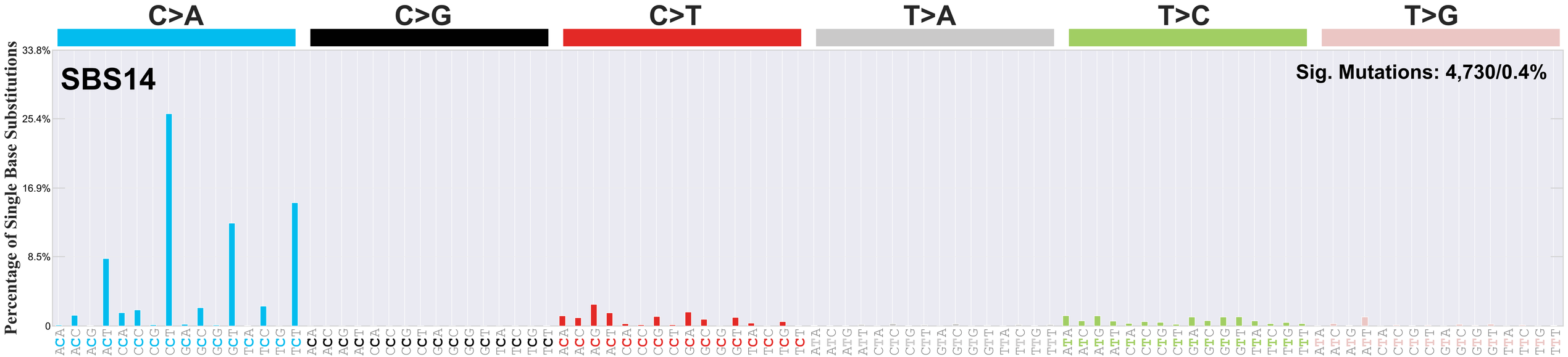

C>A
C>G
C>T
T>A
T>C
T>G
SBS10d
Sig. Mutations: 74/0.0%
Percentage of Single Base Substitutions
44.5%
33.4%
22.2%
11.1%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS11
Sig. Mutations: 151/0.0%
Percentage of Single Base Substitutions
20.6%
15.4%
10.3%
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
SBS12
Sig. Mutations: 15,855/1.3%
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: 84/0.0%
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
SBS14
Sig. Mutations: 4,730/0.4%
Percentage of Single Base Substitutions
33.8%
25.4%
16.9%
8.5%
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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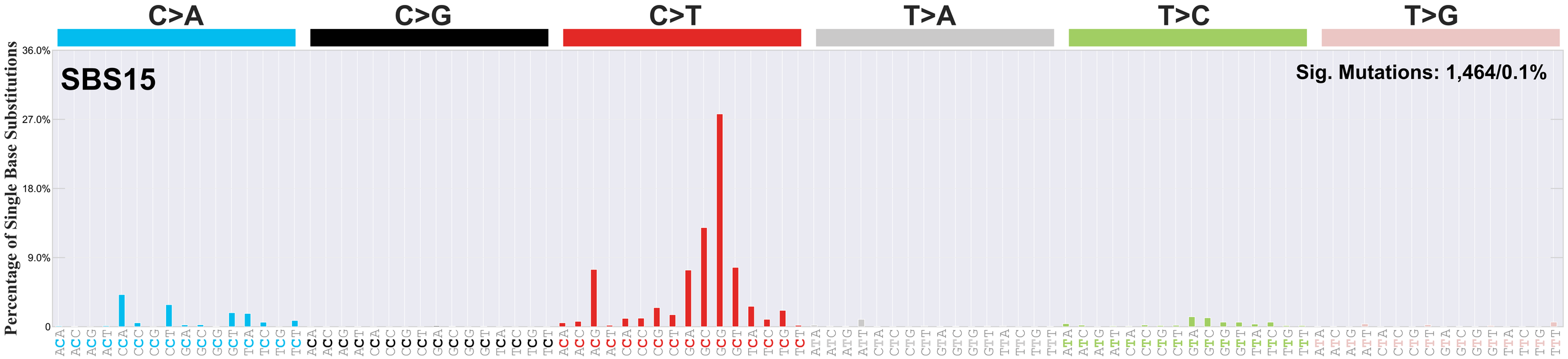
C>A
C>G
C>T
T>A
T>C
T>G
SBS15
Sig. Mutations: 1,464/0.1%
Percentage of Single Base Substitutions
36.0%
27.0%
18.0%
9.0%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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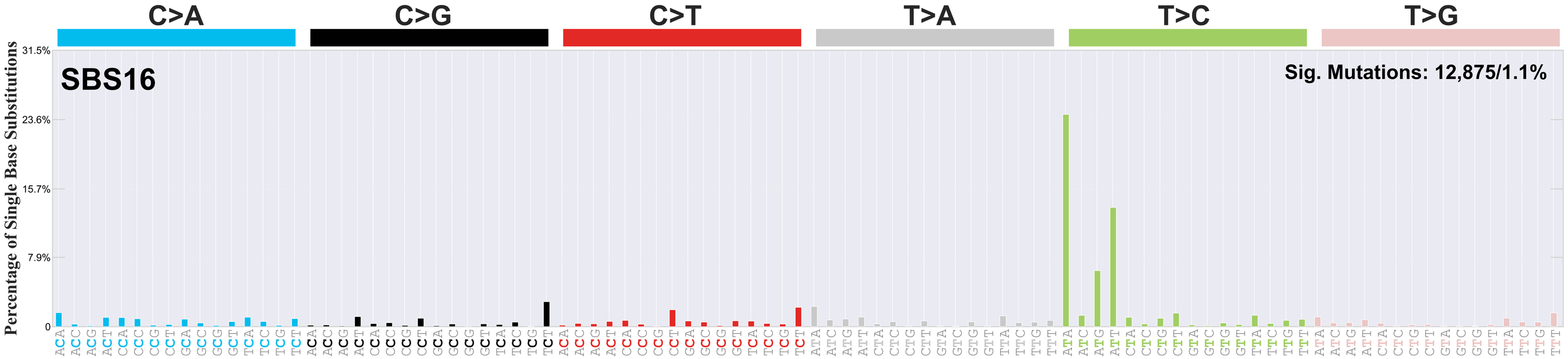
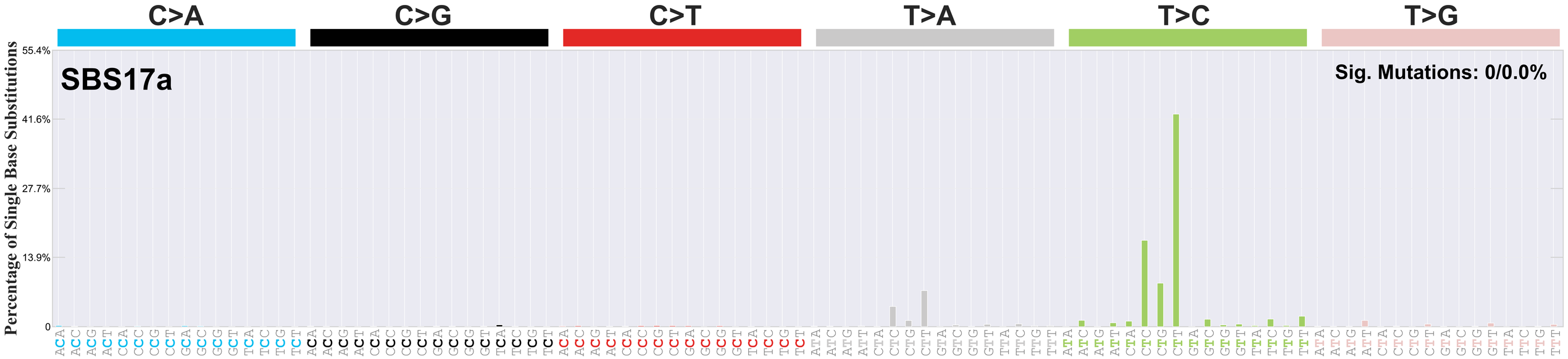
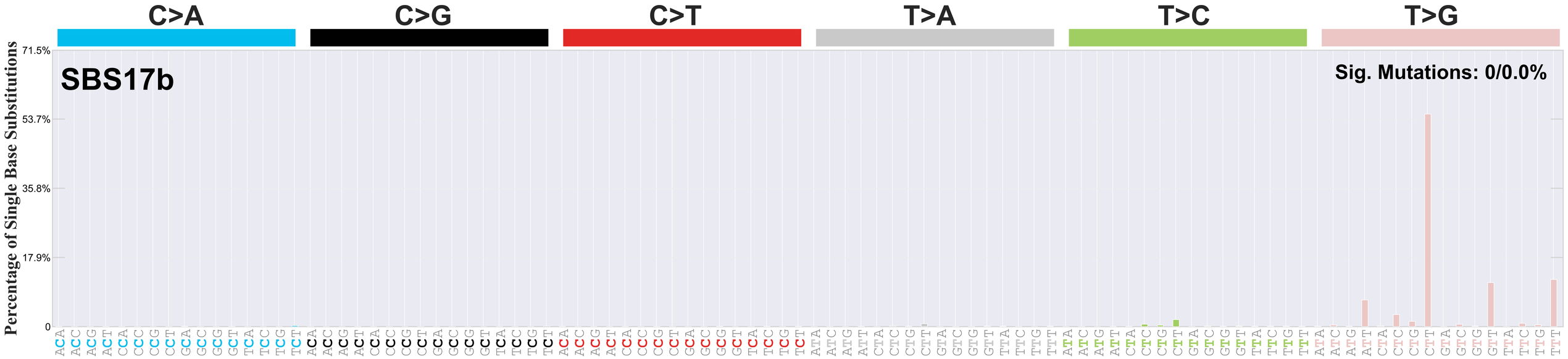
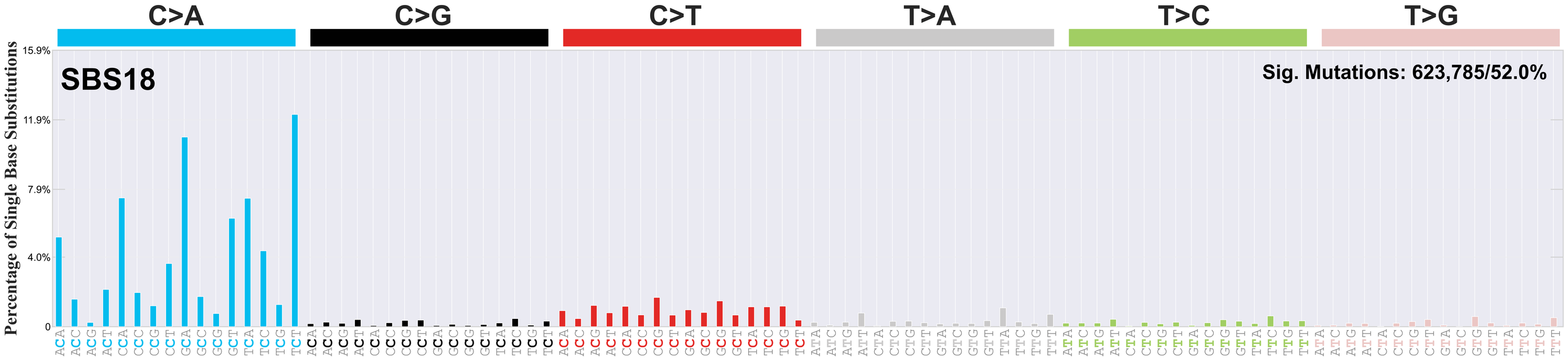

C>A
C>G
C>T
T>A
T>C
T>G
SBS16
Sig. Mutations: 12,875/1.1%
Percentage of Single Base Substitutions
31.5%
23.6%
15.7%
7.9%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA 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
SBS17a
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
55.4%
41.6%
27.7%
13.9%
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: 623,785/52.0%
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
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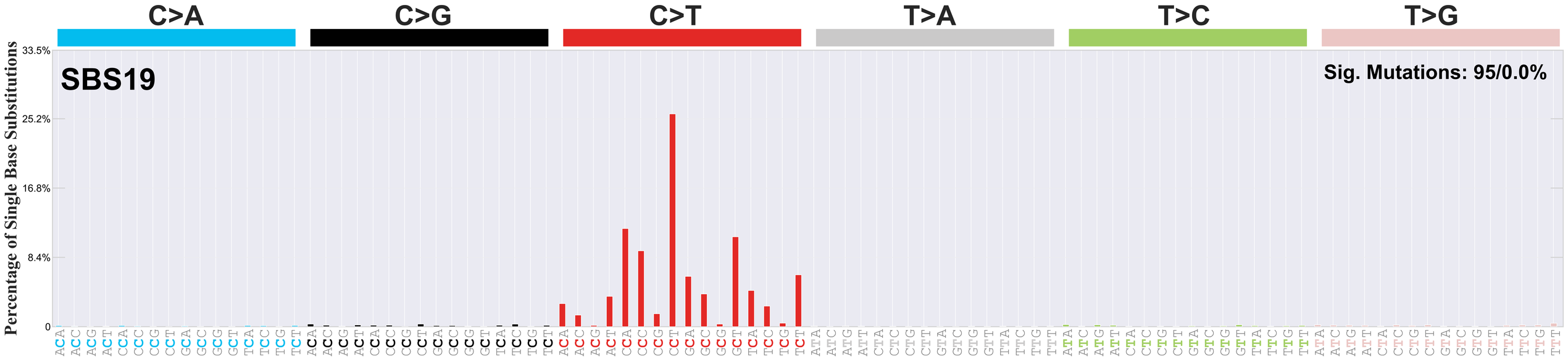
C>A
C>G
C>T
T>A
T>C
T>G
SBS19
Sig. Mutations: 95/0.0%
Percentage of Single Base Substitutions
33.5%
25.2%
16.8%
8.4%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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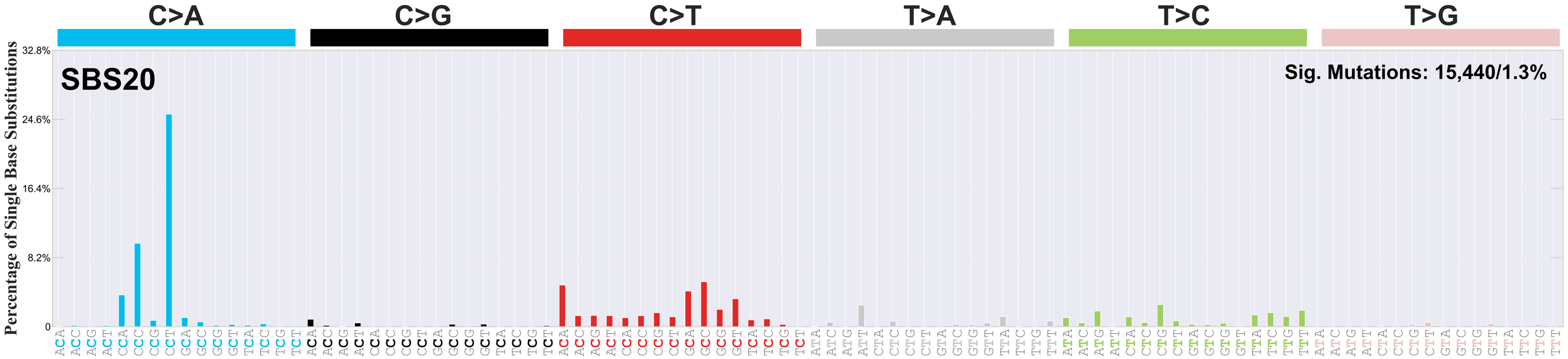
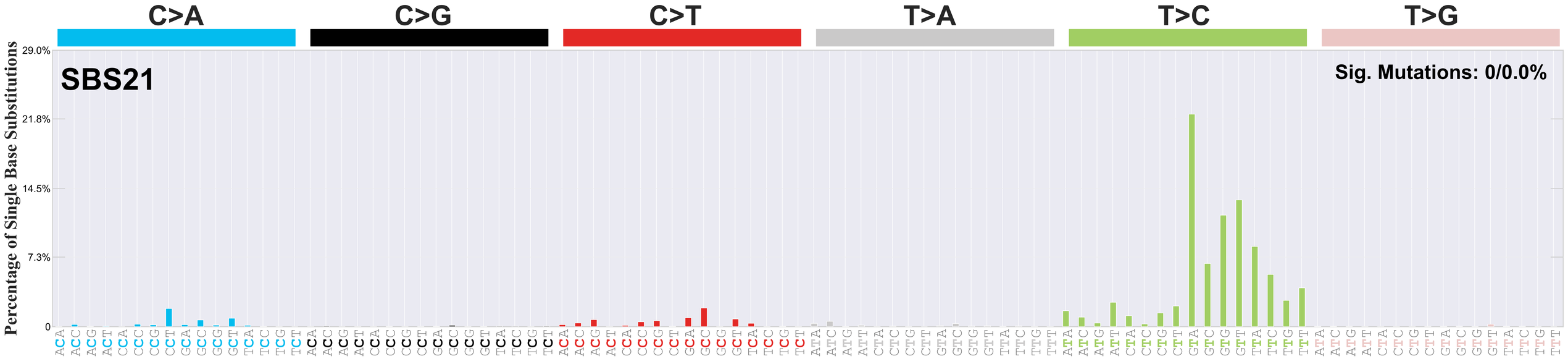

C>A
C>G
C>T
T>A
T>C
T>G
SBS20
Sig. Mutations: 15,440/1.3%
Percentage of Single Base Substitutions
32.8%
24.6%
16.4%
8.2%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA 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
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
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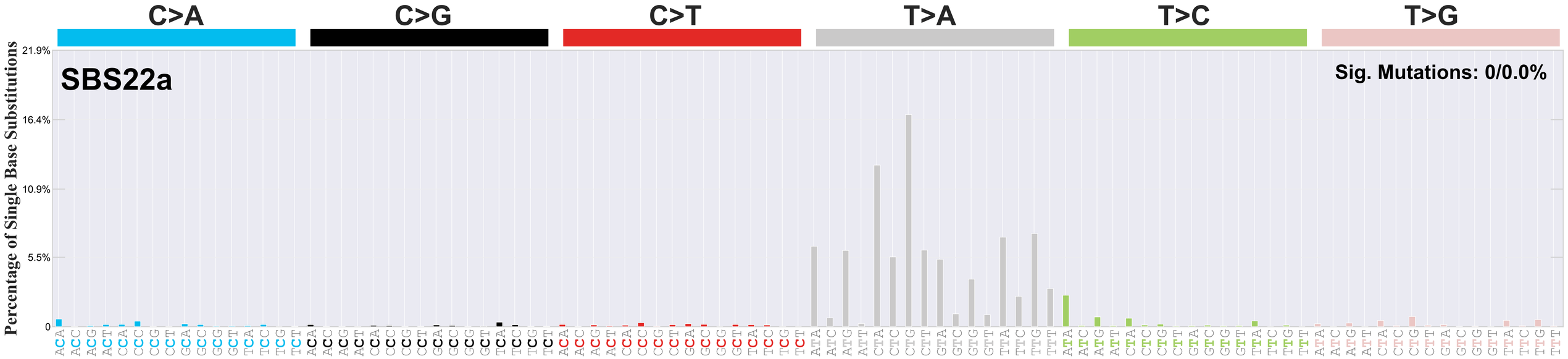
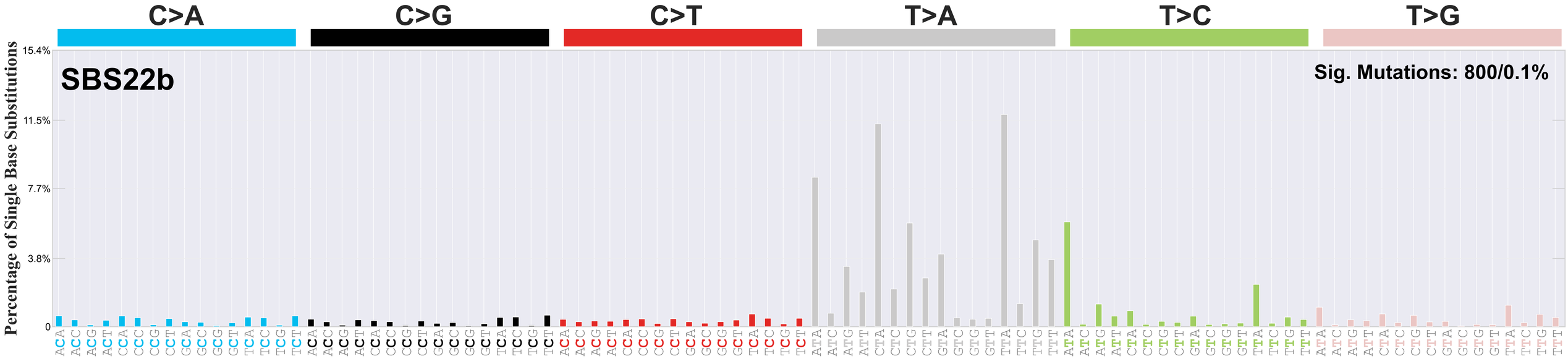

C>A
C>G
C>T
T>A
T>C
T>G
SBS22a
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
21.9%
16.4%
10.9%
5.5%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC 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: 800/0.1%
Percentage of Single Base Substitutions
15.4%
11.5%
7.7%
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
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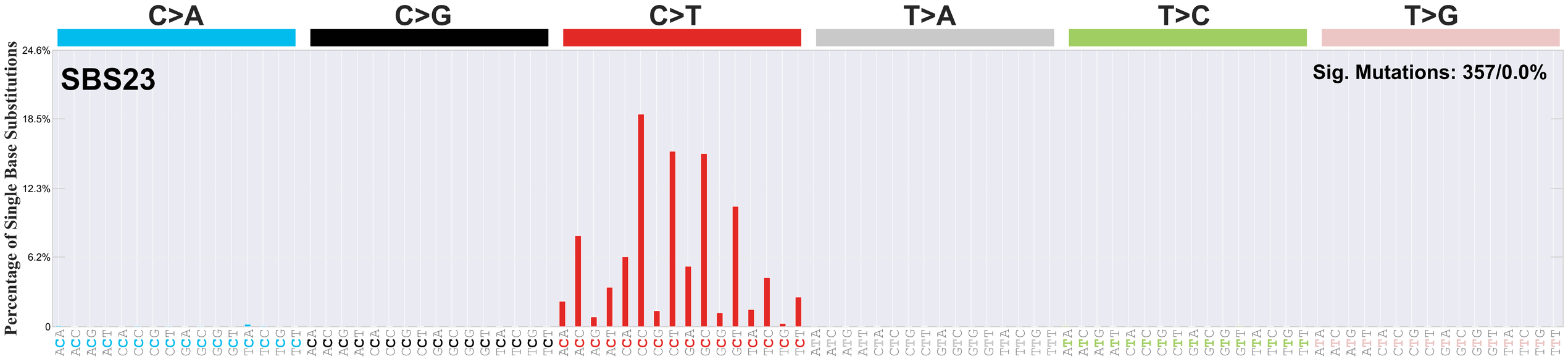
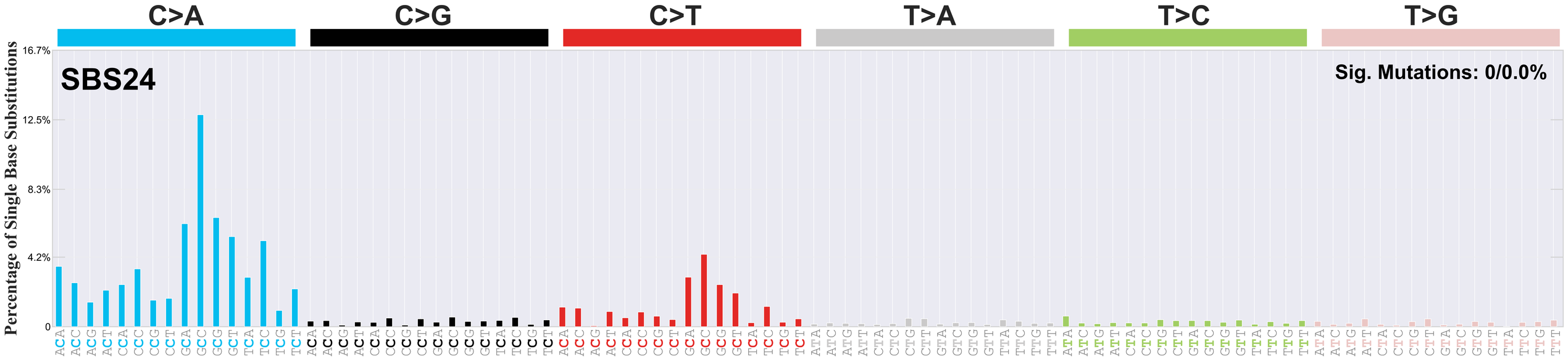

C>A
C>G
C>T
T>A
T>C
T>G
SBS23
Sig. Mutations: 357/0.0%
Percentage of Single Base Substitutions
24.6%
18.5%
12.3%
6.2%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS24
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
16.7%
12.5%
8.3%
4.2%
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
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ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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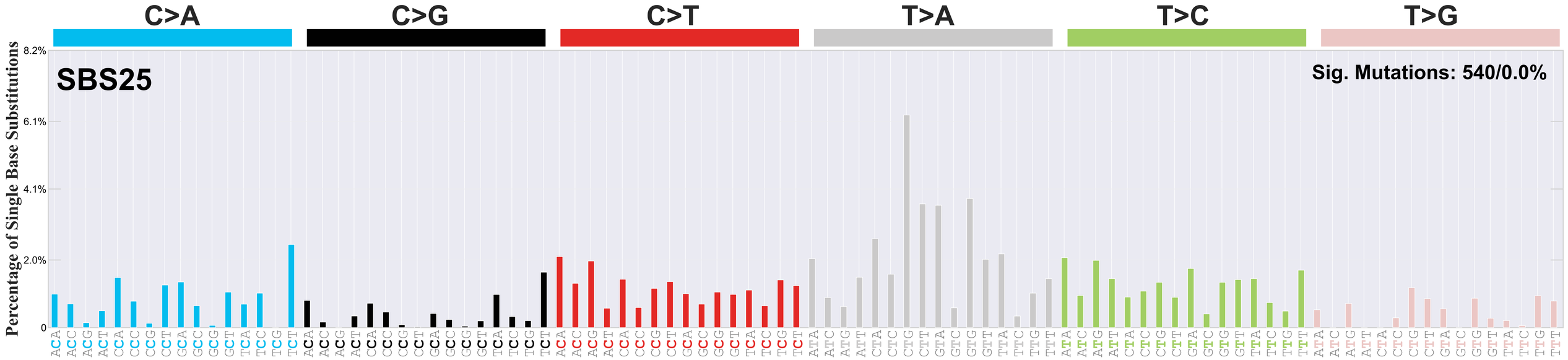
C>A
C>G
C>T
T>A
T>C
T>G
SBS25
Sig. Mutations: 540/0.0%
Percentage of Single Base Substitutions
8.2%
6.1%
4.1%
2.0%
0
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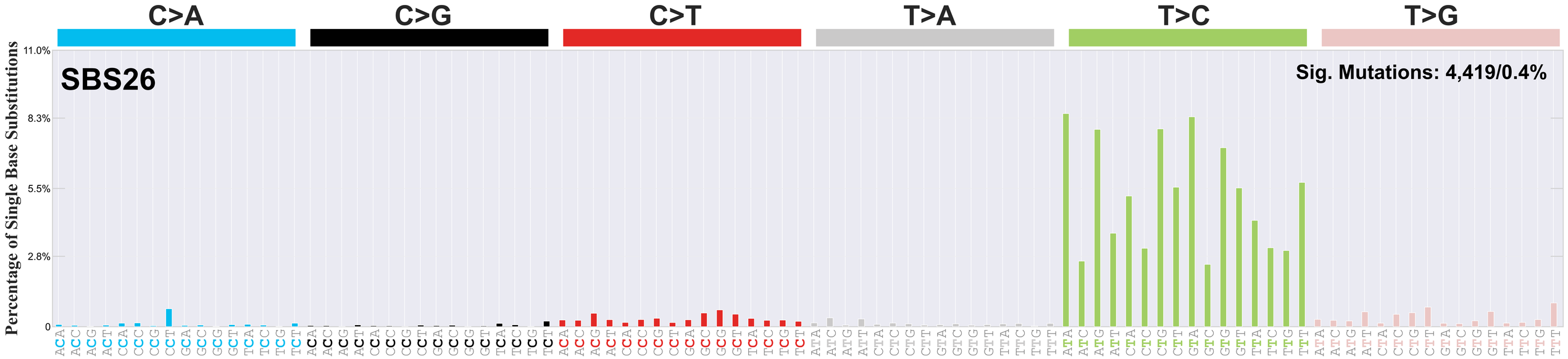
C>A
C>G
C>T
T>A
T>C
T>G
SBS26
Sig. Mutations: 4,419/0.4%
Percentage of Single Base Substitutions
11.0%
8.3%
5.5%
2.8%
0
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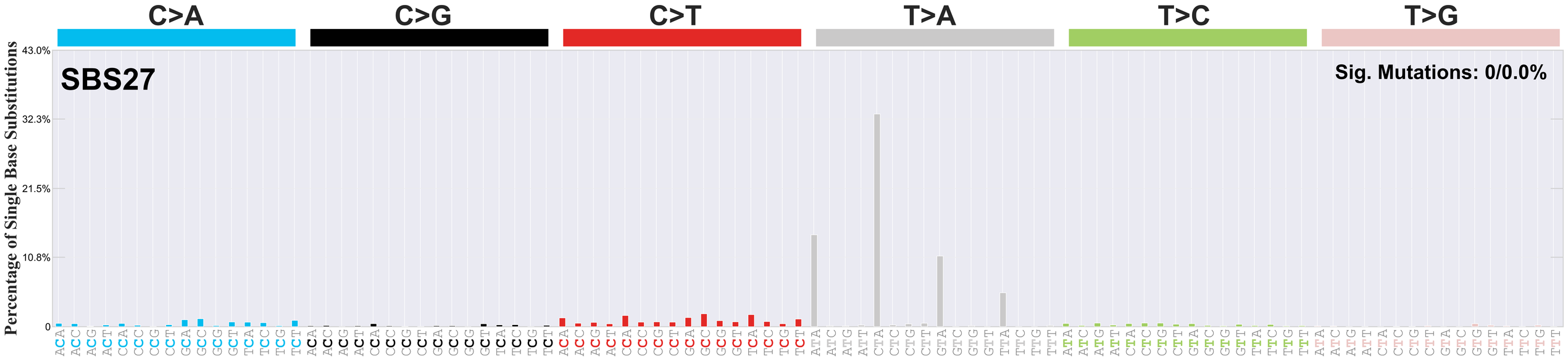
C>A
C>G
C>T
T>A
T>C
T>G
SBS27
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
43.0%
32.3%
21.5%
10.8%
0
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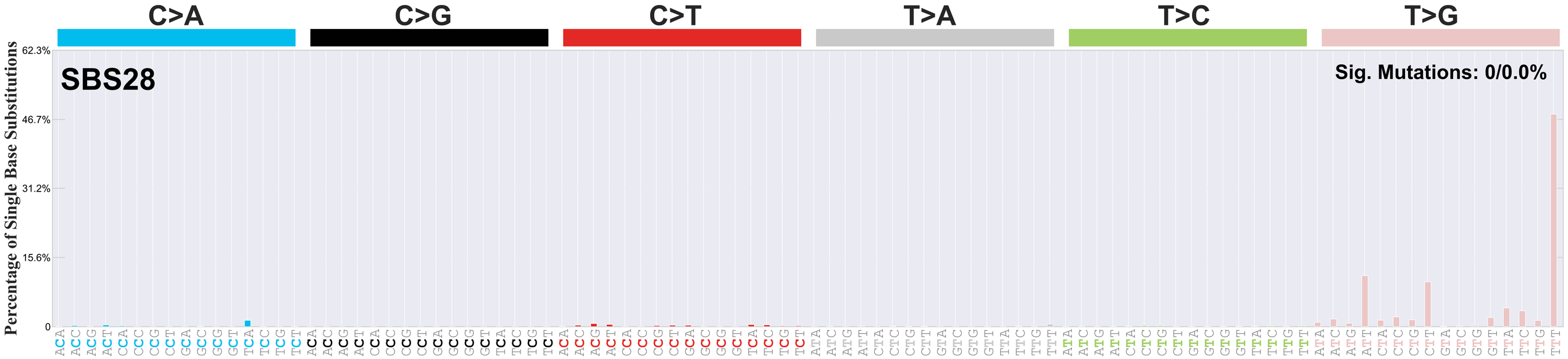
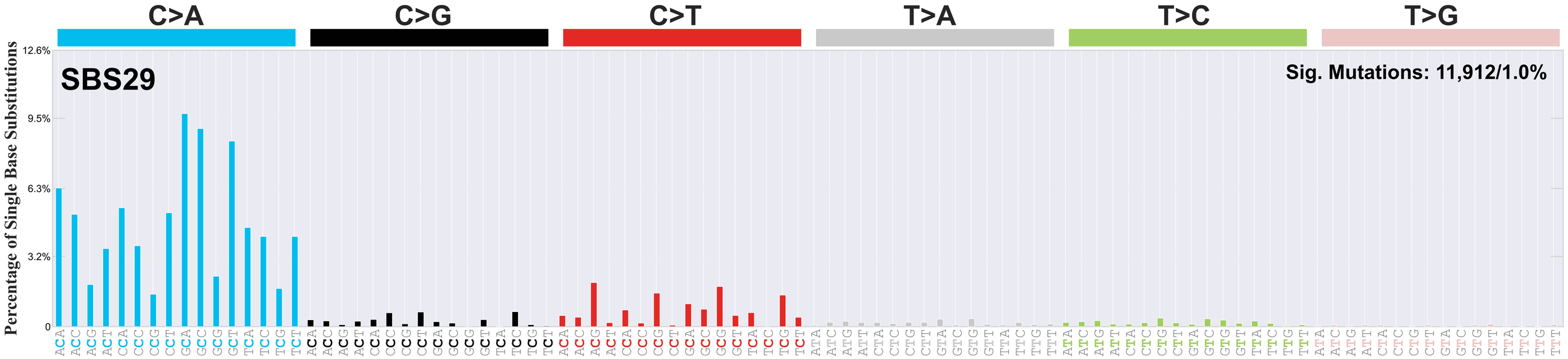

C>A
C>G
C>T
T>A
T>C
T>G
SBS28
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
62.3%
46.7%
31.2%
15.6%
0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C>G
C>T
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T>C
T>G
SBS29
Sig. Mutations: 11,912/1.0%
Percentage of Single Base Substitutions
12.6%
9.5%
6.3%
3.2%
0
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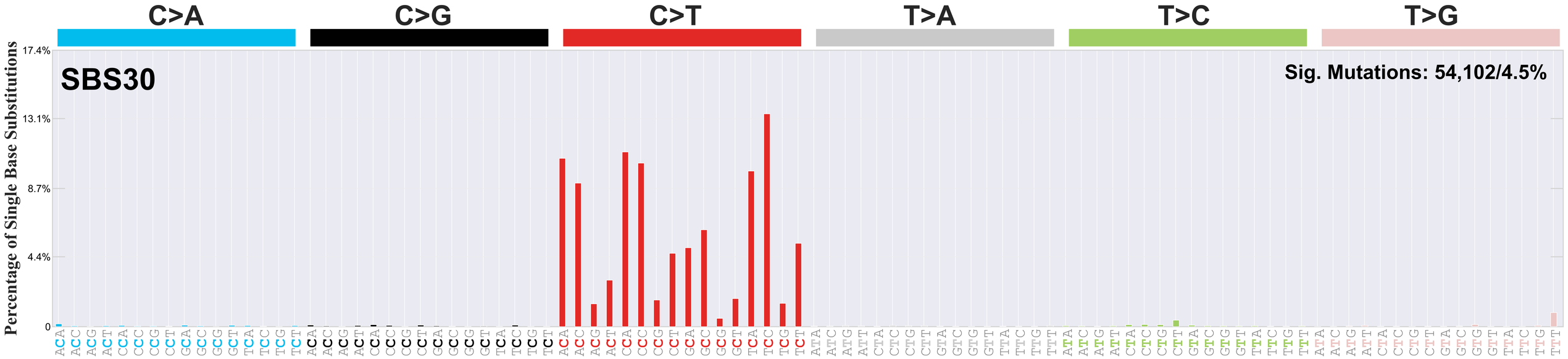
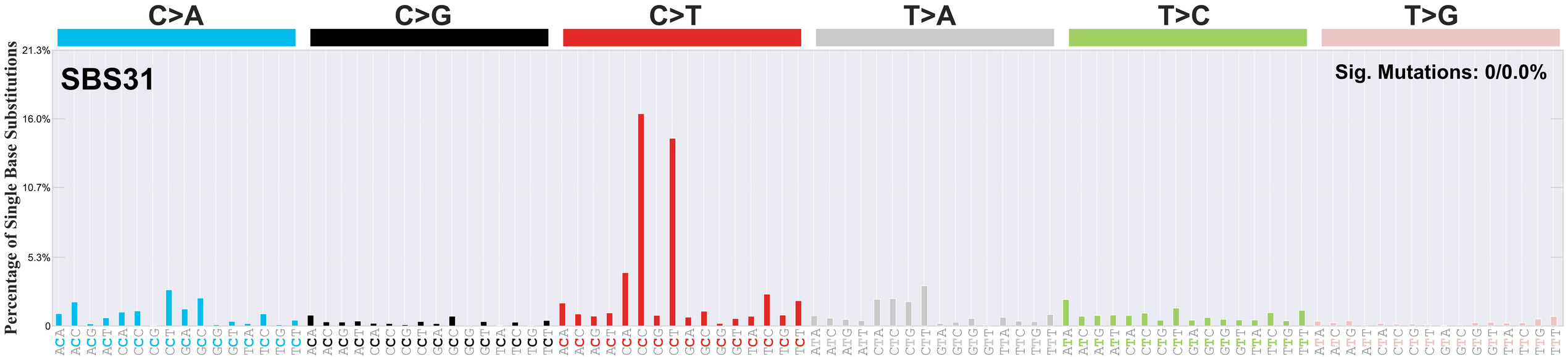

C>A
C>G
C>T
T>A
T>C
T>G
SBS30
Sig. Mutations: 54,102/4.5%
Percentage of Single Base Substitutions
17.4%
13.1%
8.7%
4.4%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA 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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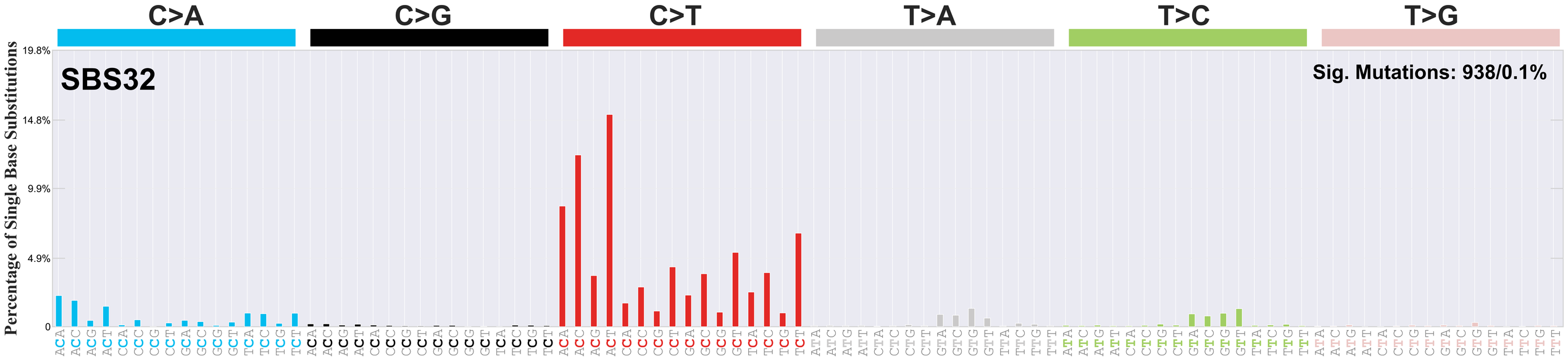
C>G
C>T
T>A
T>C
T>G
SBS31
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
21.3%
16.0%
10.7%
5.3%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG 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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C>G
C>T
T>A
T>C
T>G
SBS32
Sig. Mutations: 938/0.1%
Percentage of Single Base Substitutions
19.8%
14.8%
9.9%
4.9%
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
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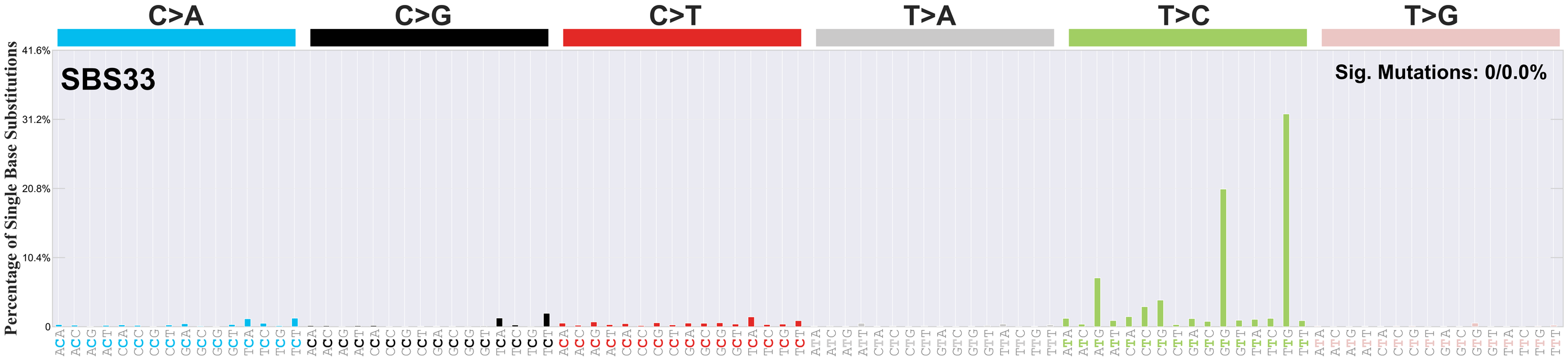
C>A
C>G
C>T
T>A
T>C
T>G
SBS33
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
41.6%
31.2%
20.8%
10.4%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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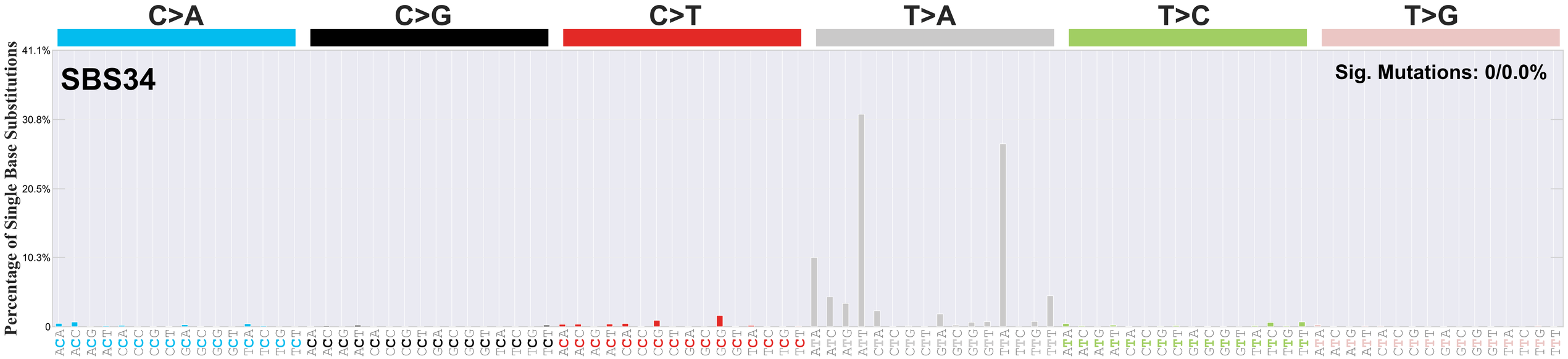
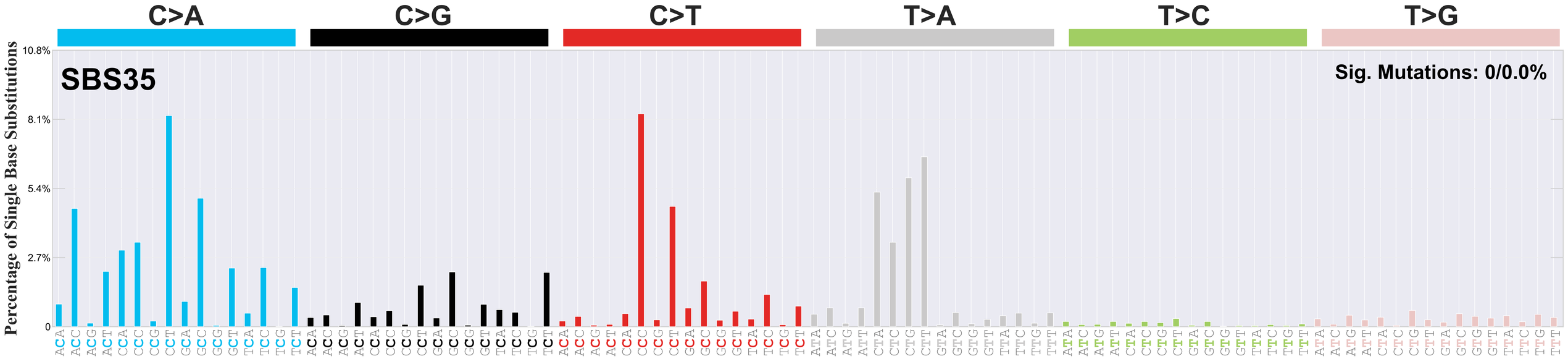

C>A
C>G
C>T
T>A
T>C
T>G
SBS34
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
41.1%
30.8%
20.5%
10.3%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC 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
SBS35
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
10.8%
8.1%
5.4%
2.7%
0
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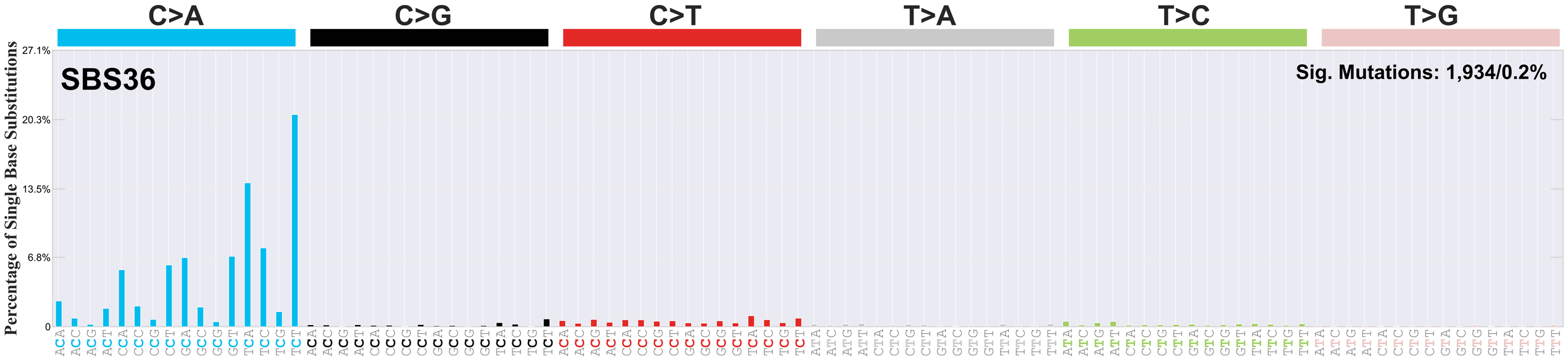
C>A
C>G
C>T
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T>C
T>G
SBS36
Sig. Mutations: 1,934/0.2%
Percentage of Single Base Substitutions
27.1%
20.3%
13.5%
6.8%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA 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
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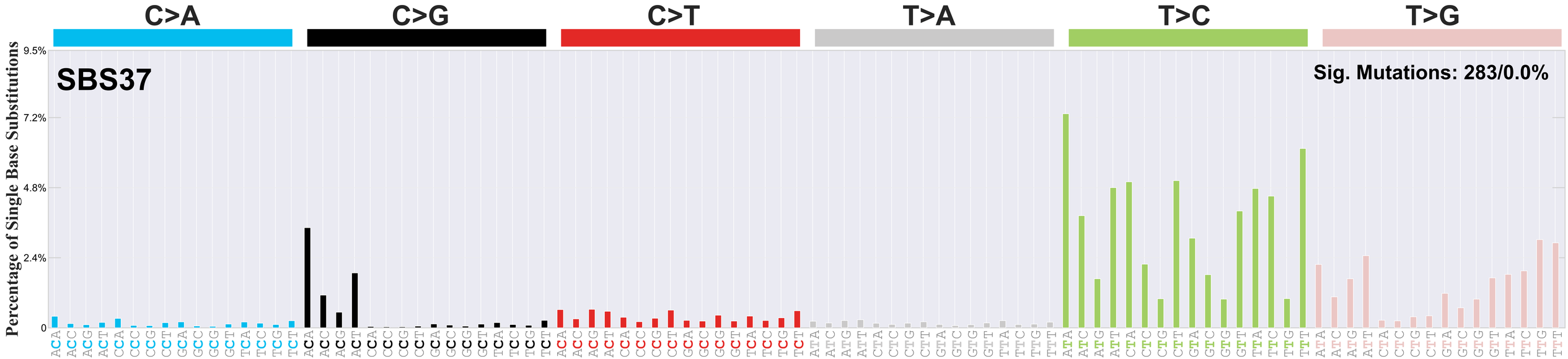
C>A
C>G
C>T
T>A
T>C
T>G
SBS37
Sig. Mutations: 283/0.0%
Percentage of Single Base Substitutions
9.5%
7.2%
4.8%
2.4%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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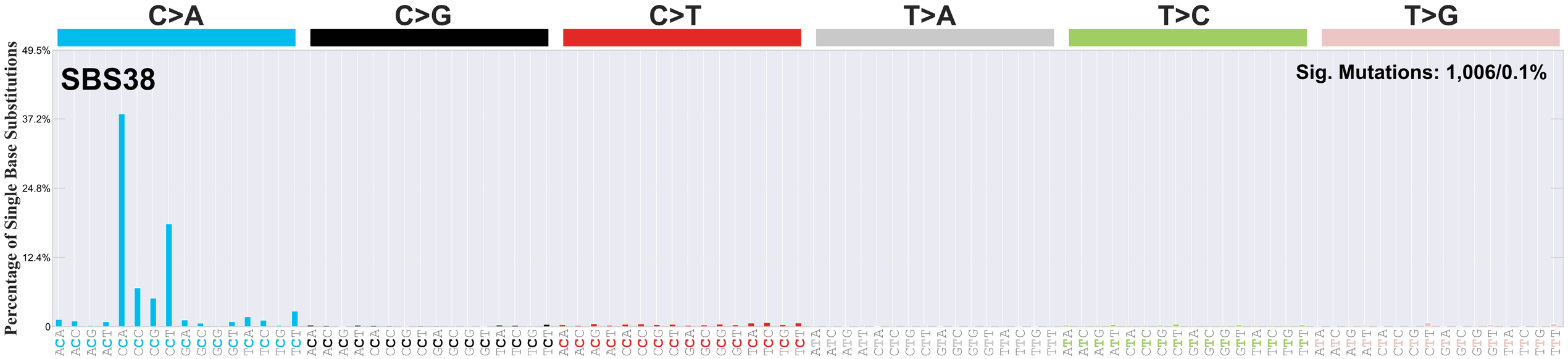
C>A
C>G
C>T
T>A
T>C
T>G
SBS38
Sig. Mutations: 1,006/0.1%
Percentage of Single Base Substitutions
49.5%
37.2%
24.8%
12.4%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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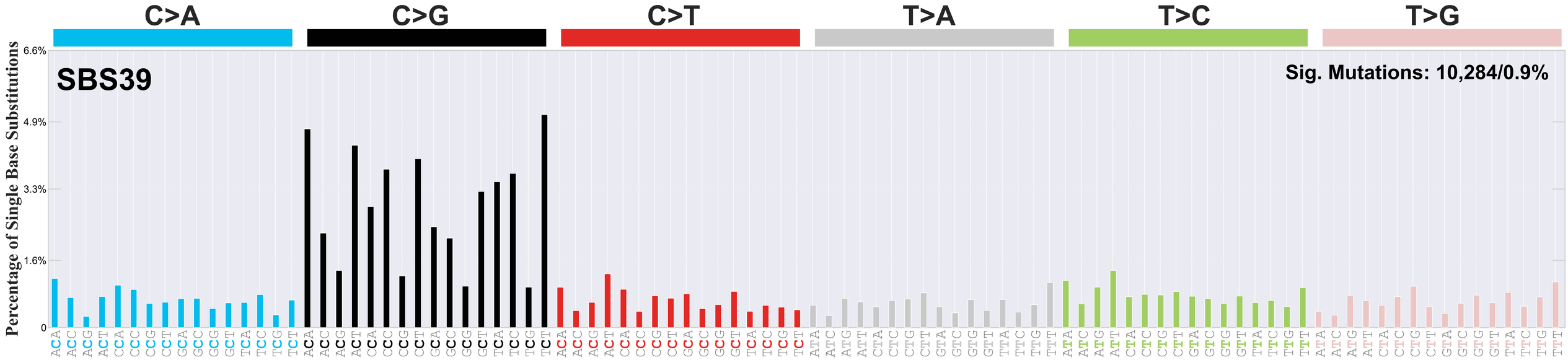
C>A
C>G
C>T
T>A
T>C
T>G
SBS39
Sig. Mutations: 10,284/0.9%
Percentage of Single Base Substitutions
6.6%
4.9%
3.3%
1.6%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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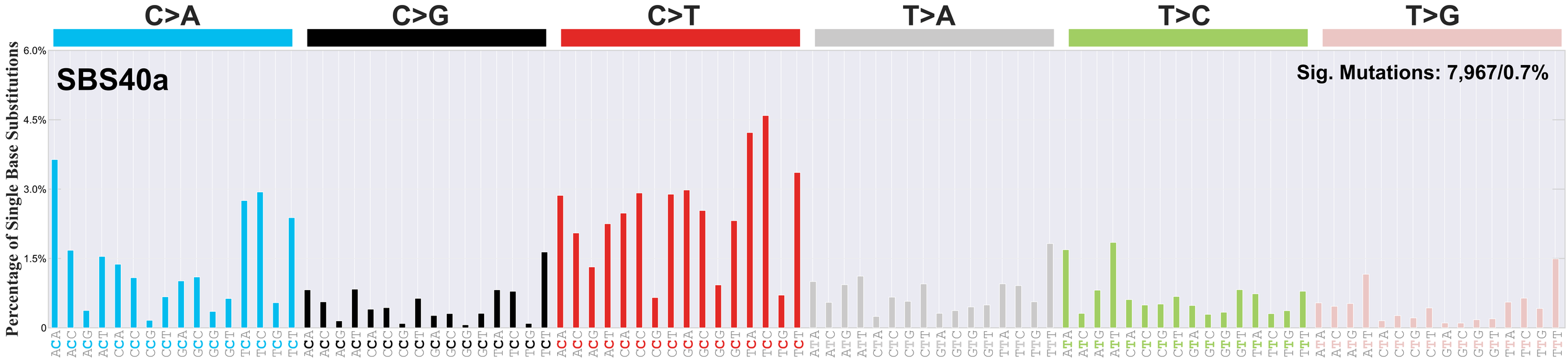
C>A
C>G
C>T
T>A
T>C
T>G
SBS40a
Sig. Mutations: 7,967/0.7%
Percentage of Single Base Substitutions
6.0%
4.5%
3.0%
1.5%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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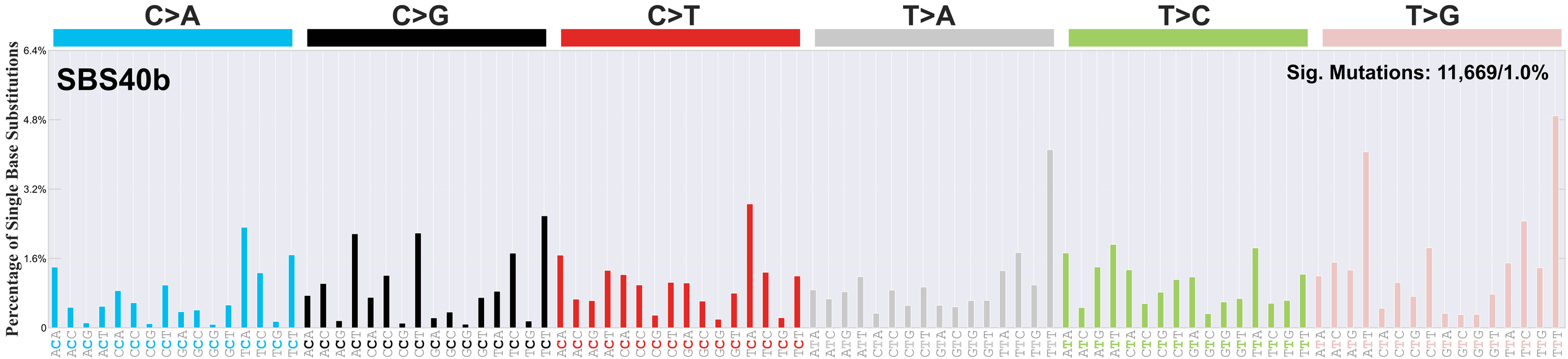
C>A
C>G
C>T
T>A
T>C
T>G
SBS40b
Sig. Mutations: 11,669/1.0%
Percentage of Single Base Substitutions
6.4%
4.8%
3.2%
1.6%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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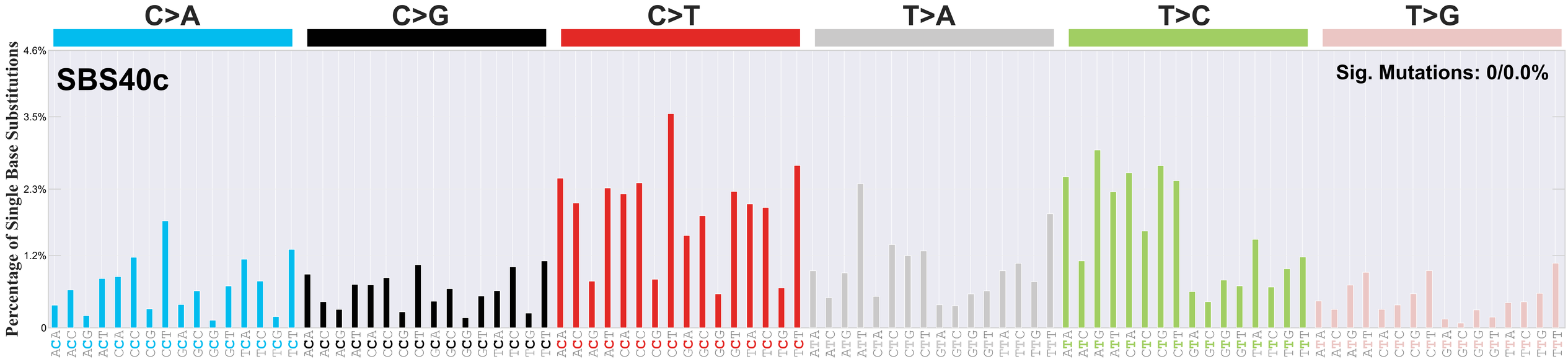
C>A
C>G
C>T
T>A
T>C
T>G
SBS40c
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
4.6%
3.5%
2.3%
1.2%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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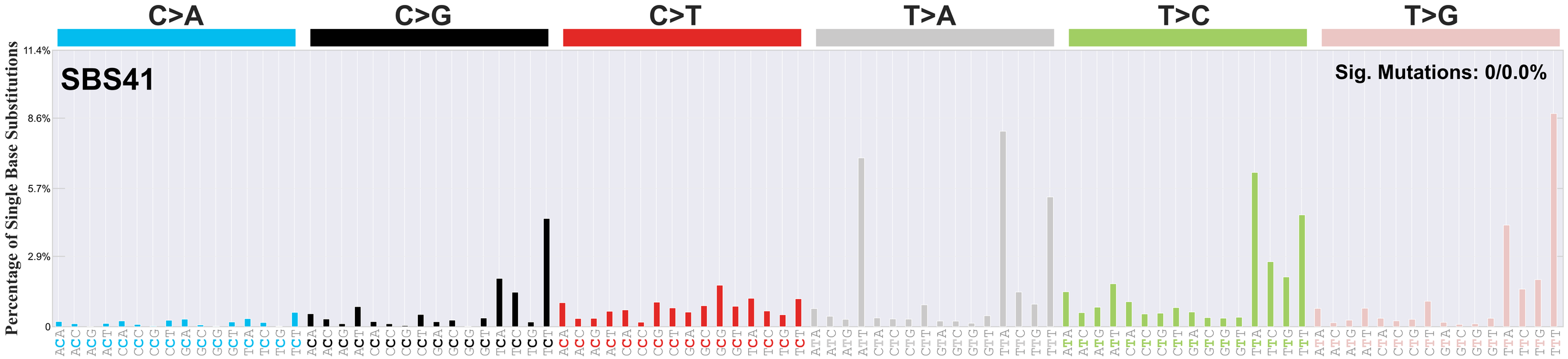
C>A
C>G
C>T
T>A
T>C
T>G
SBS41
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
11.4%
8.6%
5.7%
2.9%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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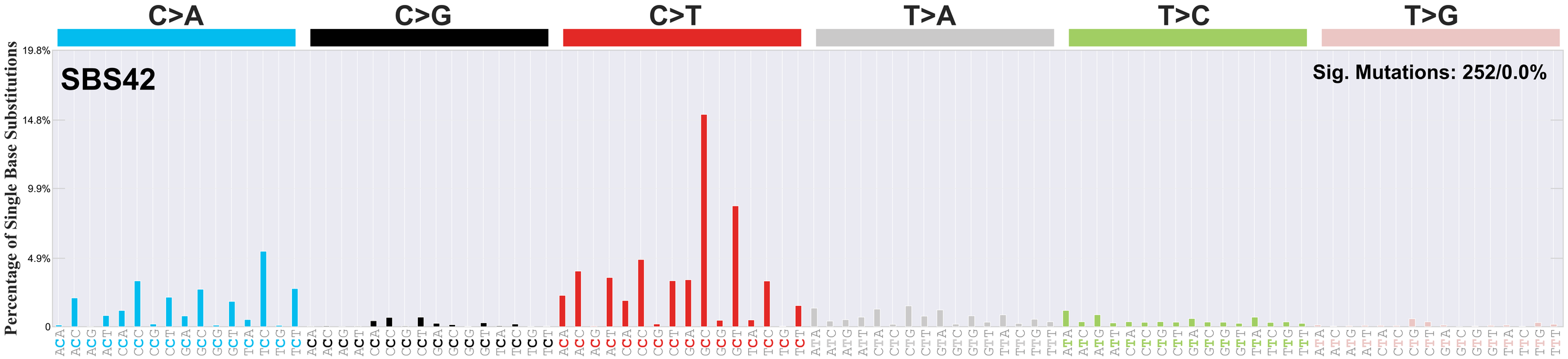
C>A
C>G
C>T
T>A
T>C
T>G
SBS42
Sig. Mutations: 252/0.0%
Percentage of Single Base Substitutions
19.8%
14.8%
9.9%
4.9%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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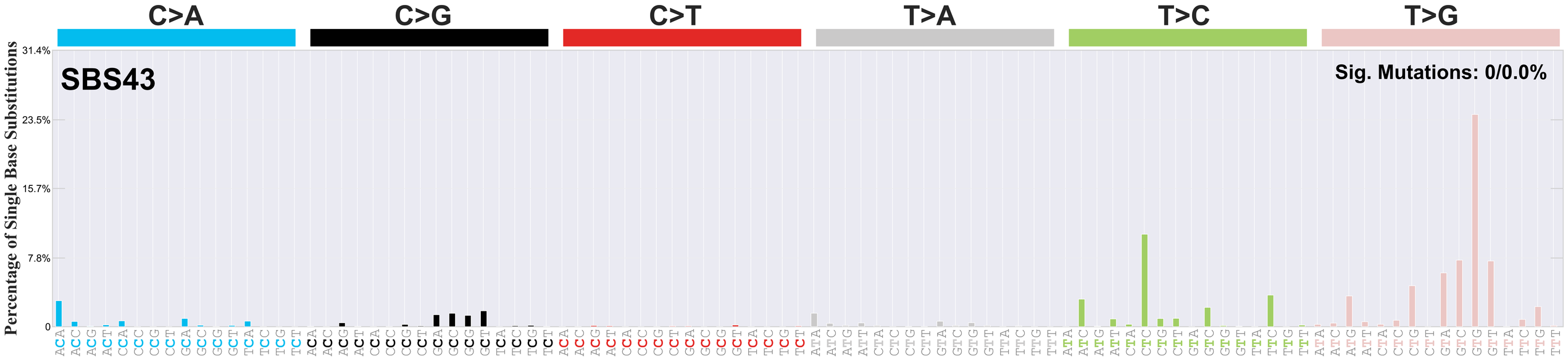
C>A
C>G
C>T
T>A
T>C
T>G
SBS43
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
31.4%
23.5%
15.7%
7.8%
0
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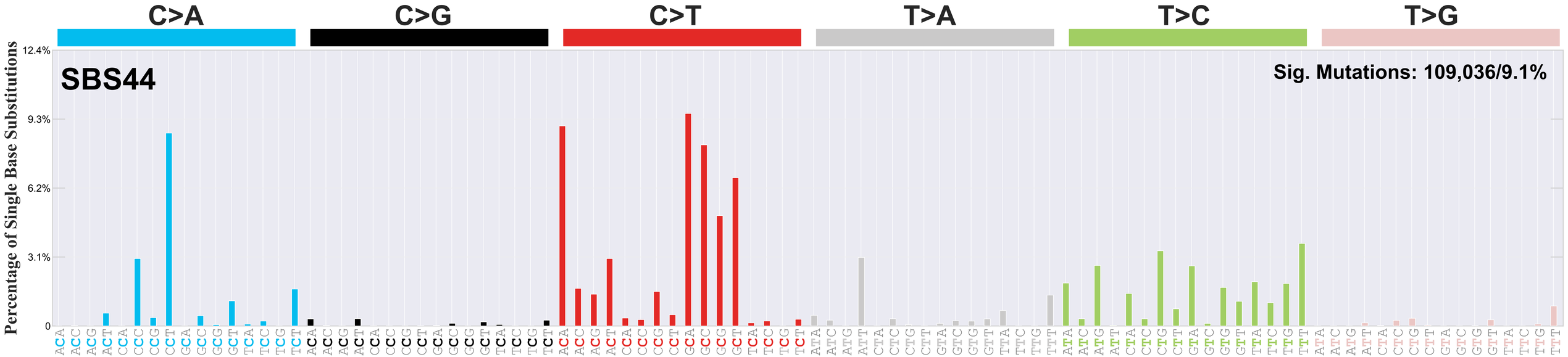
C>A
C>G
C>T
T>A
T>C
T>G
SBS44
Sig. Mutations: 109,036/9.1%
Percentage of Single Base Substitutions
12.4%
9.3%
6.2%
3.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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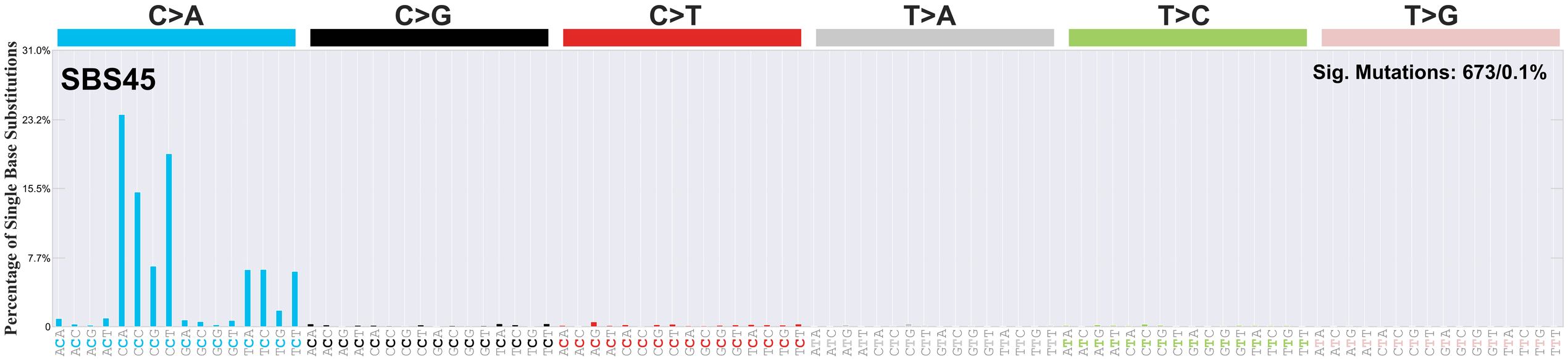
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C>G
C>T
T>A
T>C
T>G
SBS45
Sig. Mutations: 673/0.1%
Percentage of Single Base Substitutions
31.0%
23.2%
15.5%
7.7%
0
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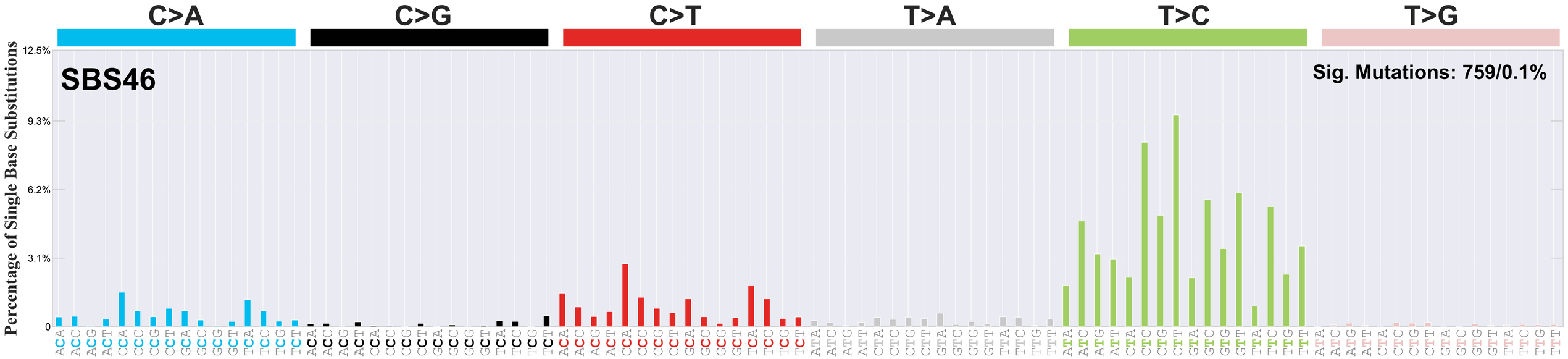
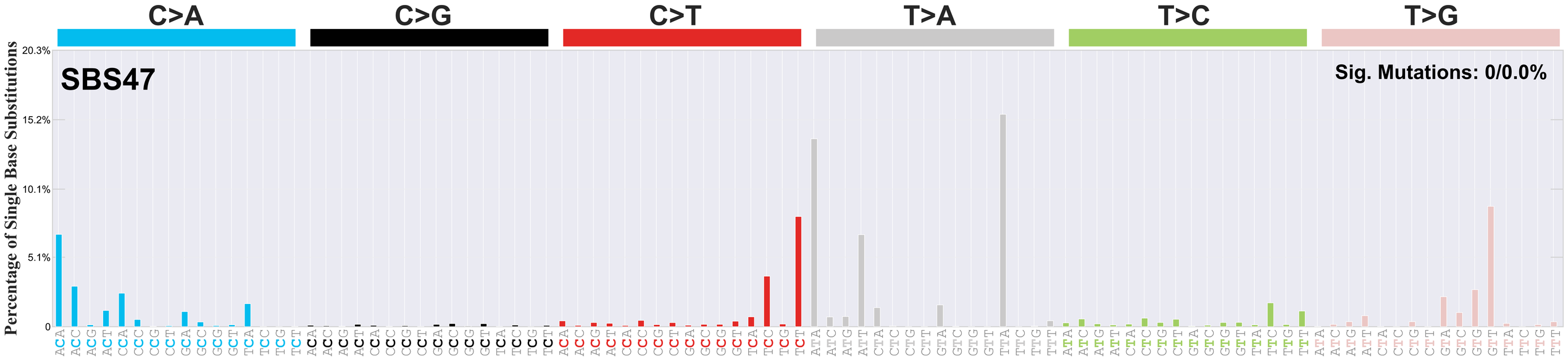

C>A
C>G
C>T
T>A
T>C
T>G
SBS46
Sig. Mutations: 759/0.1%
Percentage of Single Base Substitutions
12.5%
9.3%
6.2%
3.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC 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
SBS47
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
20.3%
15.2%
10.1%
5.1%
0
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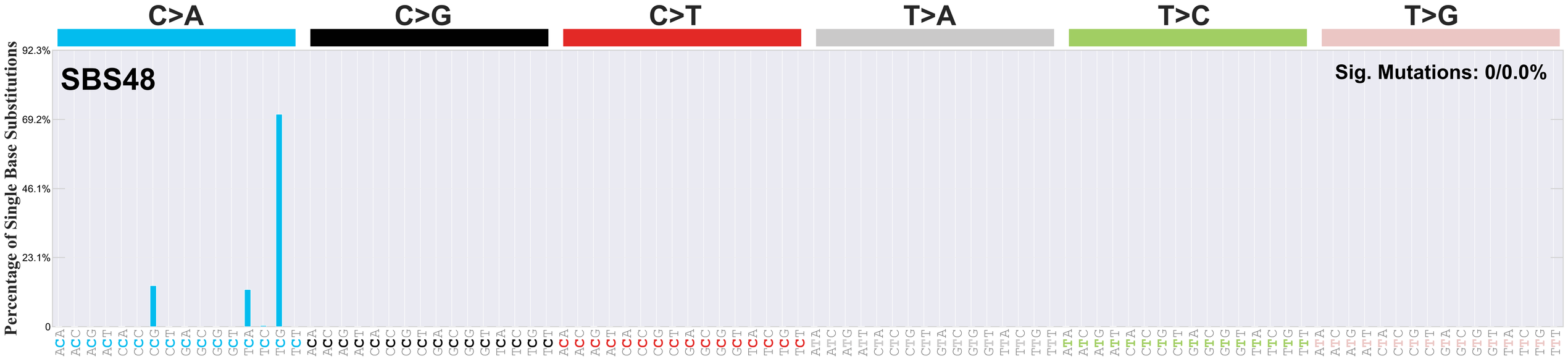
C>A
C>G
C>T
T>A
T>C
T>G
SBS48
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
92.3%
69.2%
46.1%
23.1%
0
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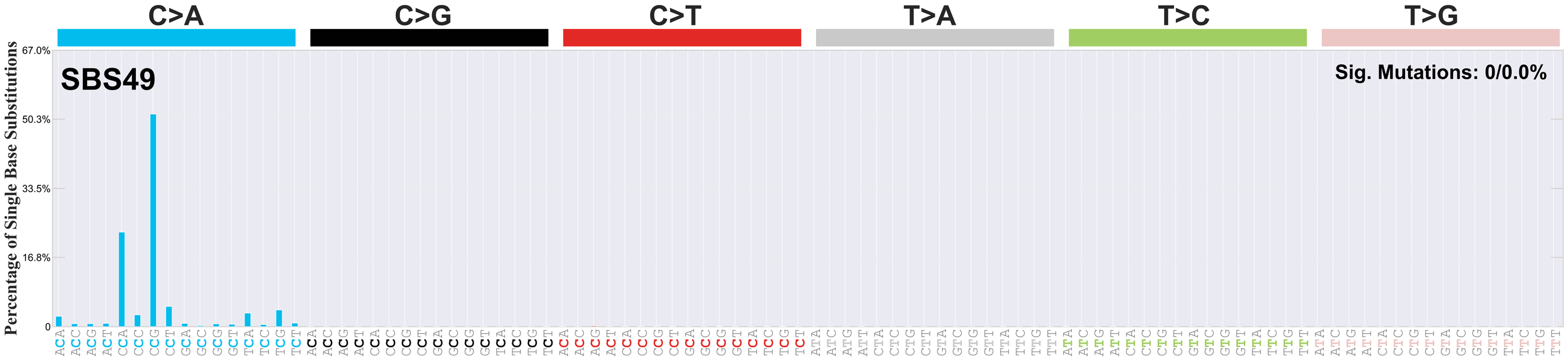
C>A
C>G
C>T
T>A
T>C
T>G
SBS49
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
67.0%
50.3%
33.5%
16.8%
0
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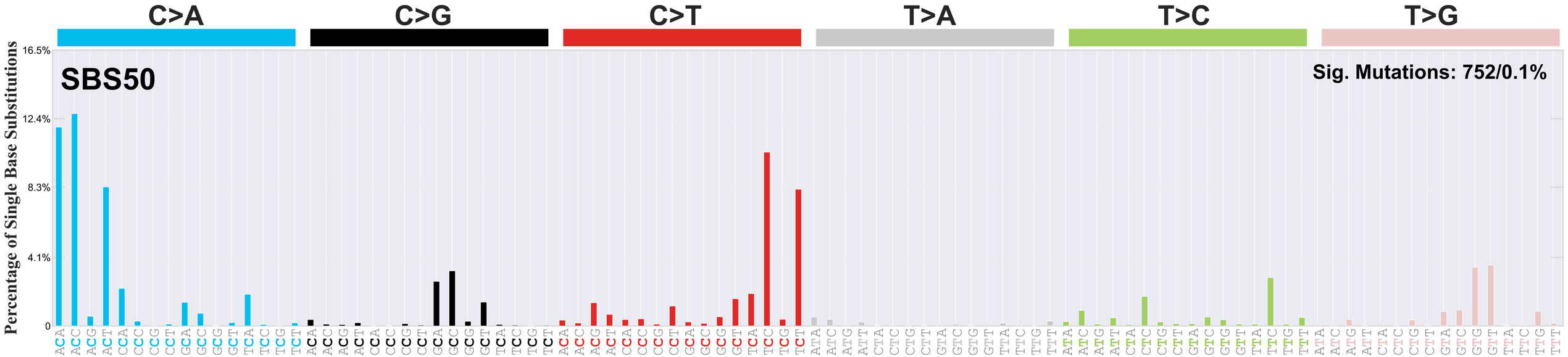
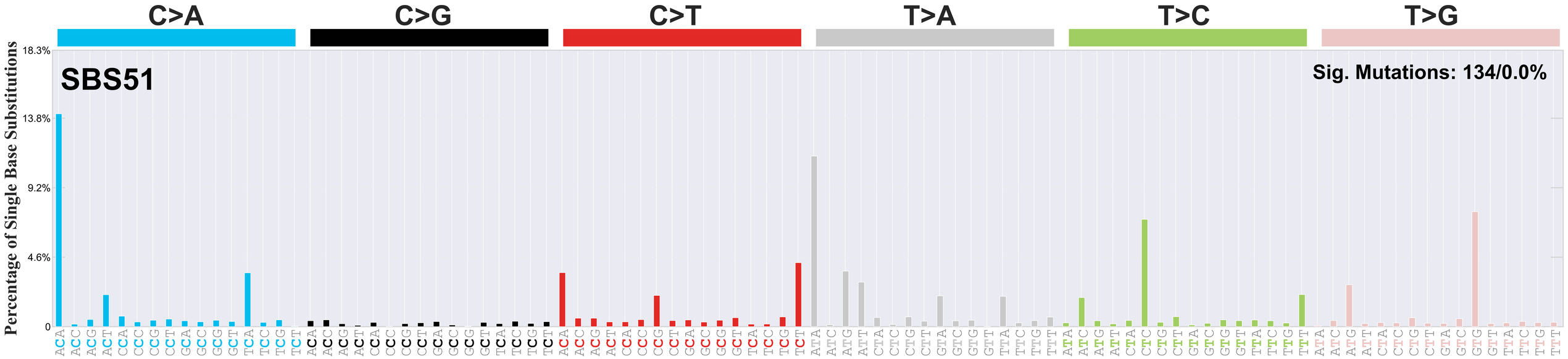

C>A
C>G
C>T
T>A
T>C
T>G
SBS50
Sig. Mutations: 752/0.1%
Percentage of Single Base Substitutions
16.5%
12.4%
8.3%
4.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC 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
SBS51
Sig. Mutations: 134/0.0%
Percentage of Single Base Substitutions
18.3%
13.8%
9.2%
4.6%
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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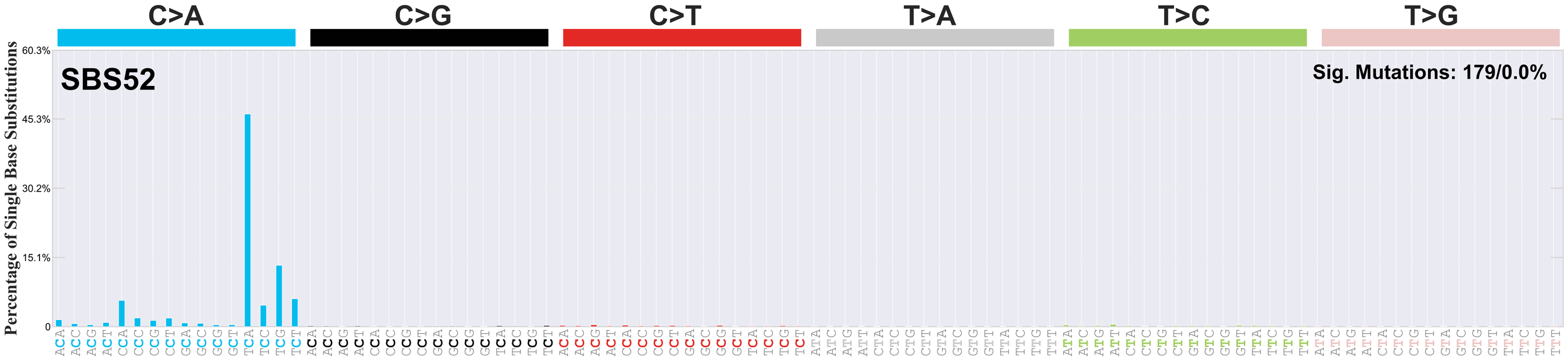
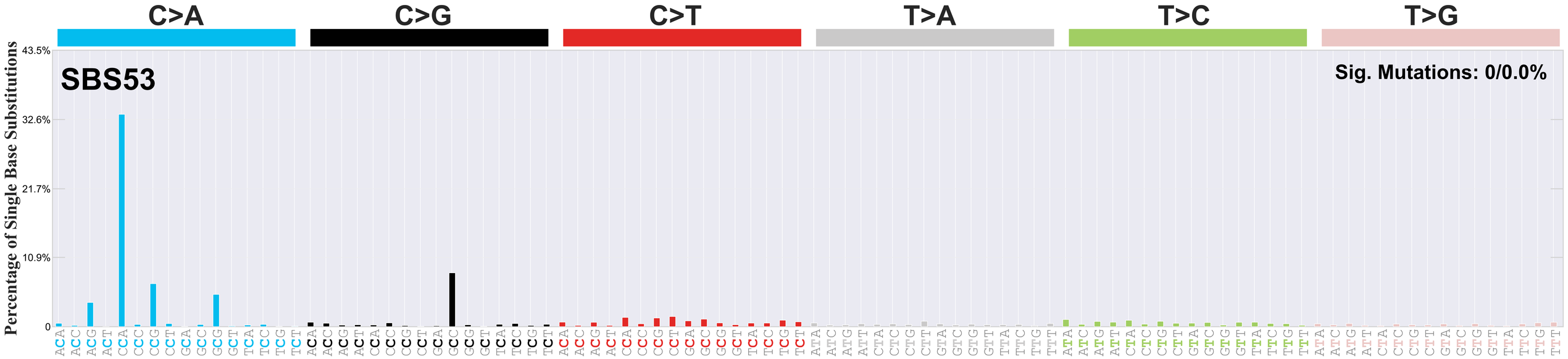

C>A
C>G
C>T
T>A
T>C
T>G
SBS52
Sig. Mutations: 179/0.0%
Percentage of Single Base Substitutions
60.3%
45.3%
30.2%
15.1%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS53
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
43.5%
32.6%
21.7%
10.9%
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
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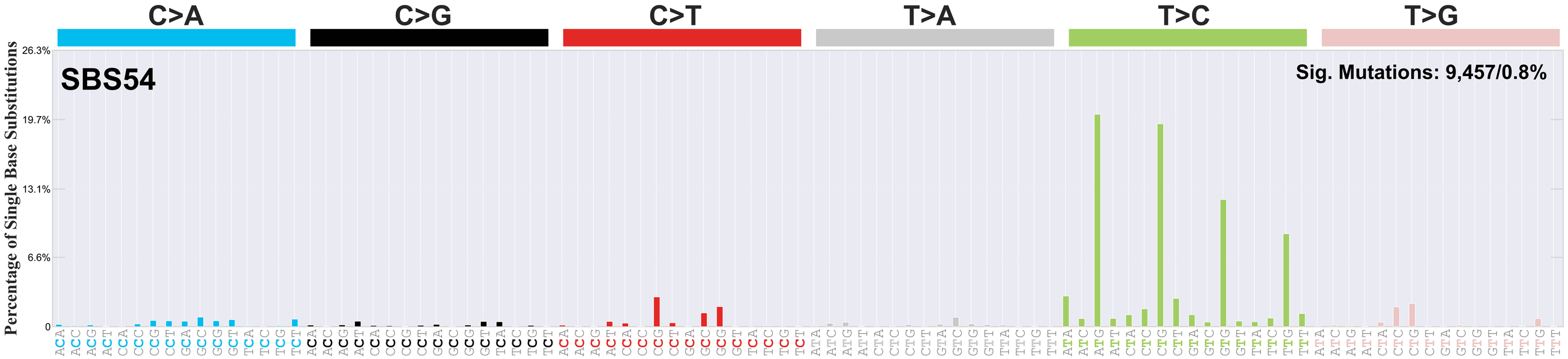
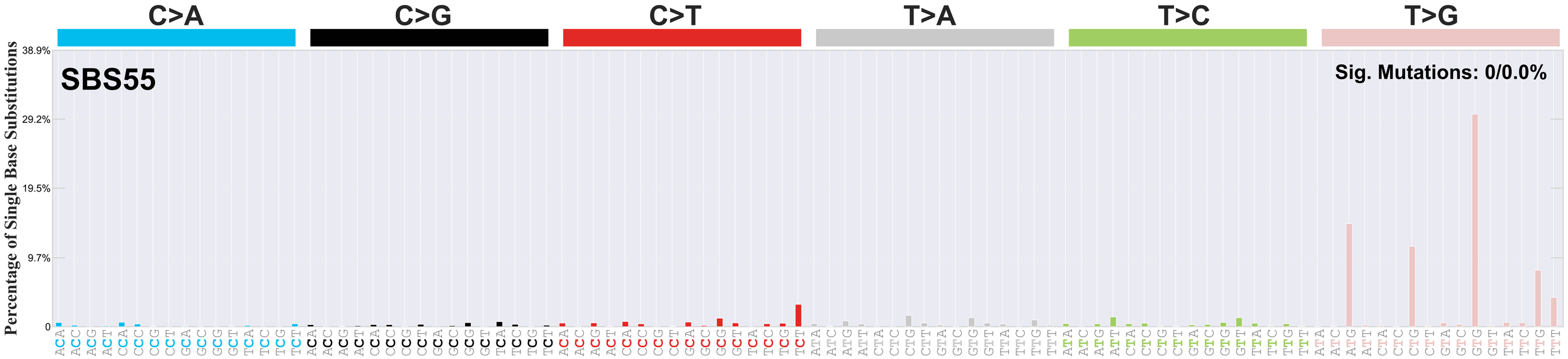

C>A
C>G
C>T
T>A
T>C
T>G
SBS54
Sig. Mutations: 9,457/0.8%
Percentage of Single Base Substitutions
26.3%
19.7%
13.1%
6.6%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA 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


C>A
C>G
C>T
T>A
T>C
T>G
SBS55
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
38.9%
29.2%
19.5%
9.7%
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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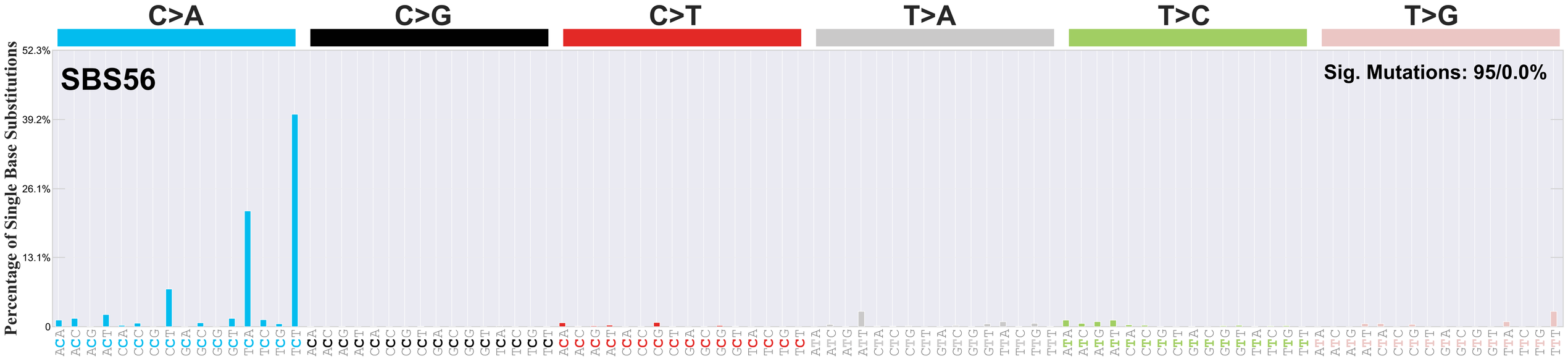
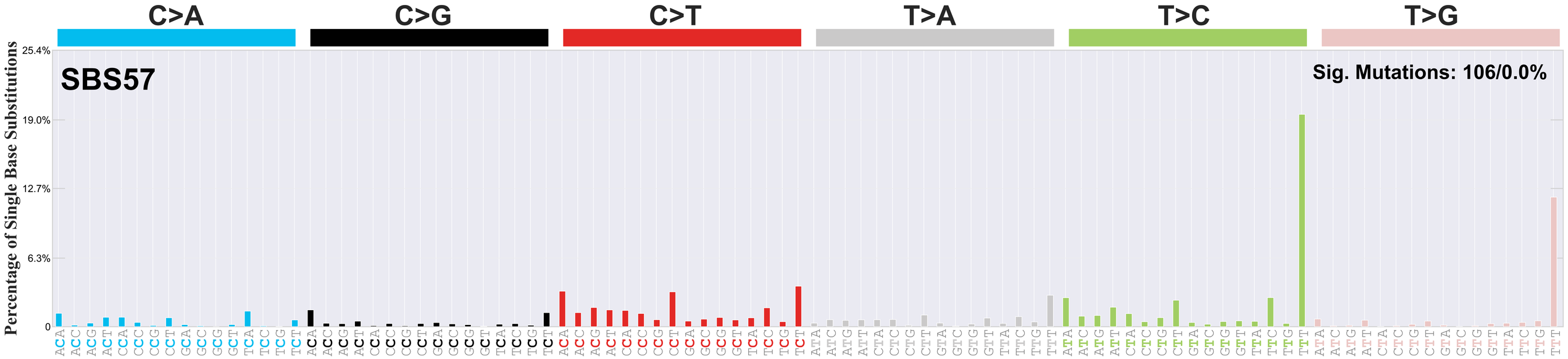

C>A
C>G
C>T
T>A
T>C
T>G
SBS56
Sig. Mutations: 95/0.0%
Percentage of Single Base Substitutions
52.3%
39.2%
26.1%
13.1%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS57
Sig. Mutations: 106/0.0%
Percentage of Single Base Substitutions
25.4%
19.0%
12.7%
6.3%
0
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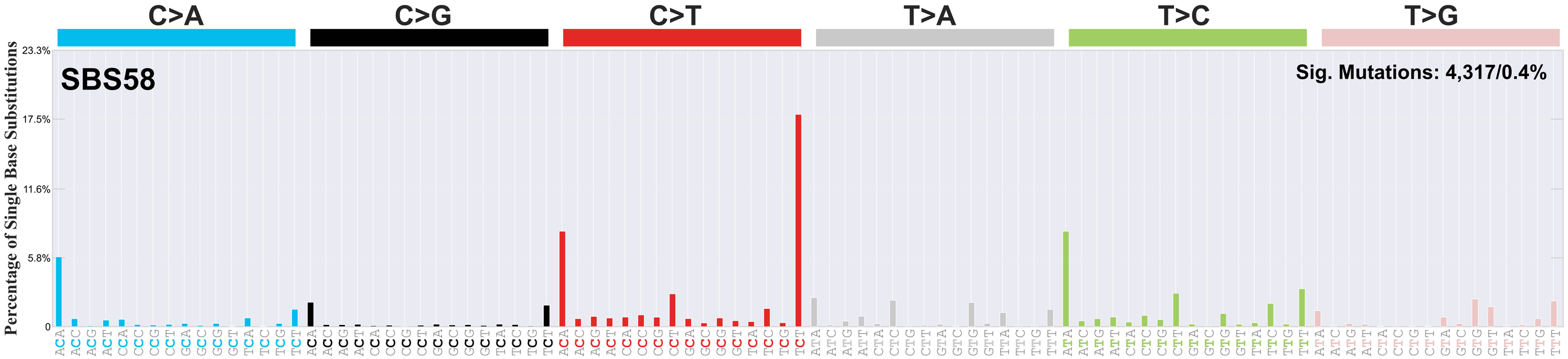
C>A
C>G
C>T
T>A
T>C
T>G
SBS58
Sig. Mutations: 4,317/0.4%
Percentage of Single Base Substitutions
23.3%
17.5%
11.6%
5.8%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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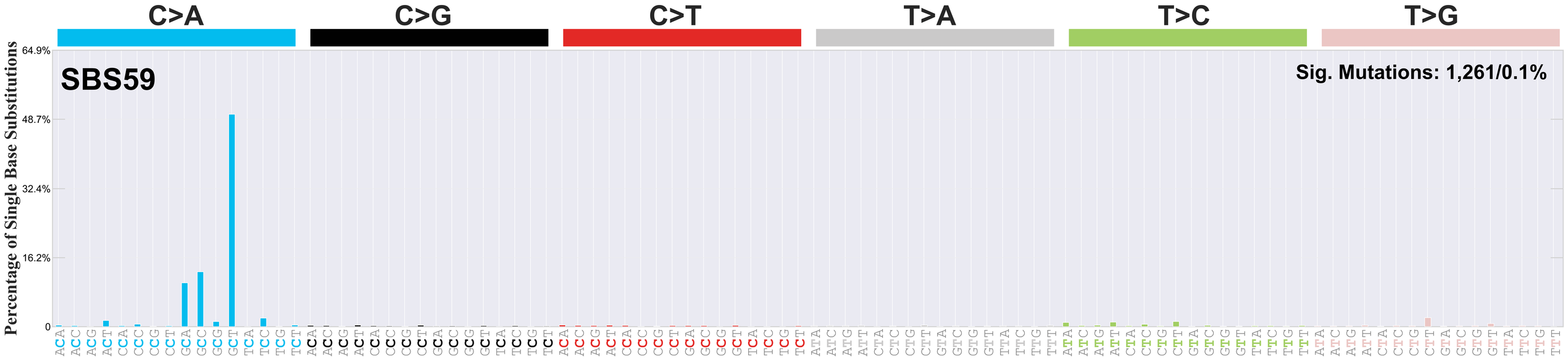
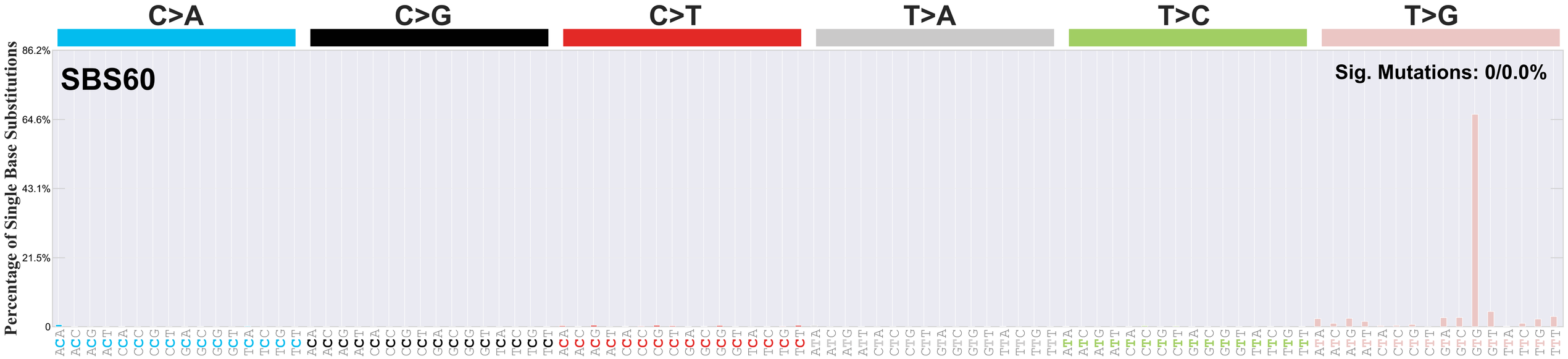
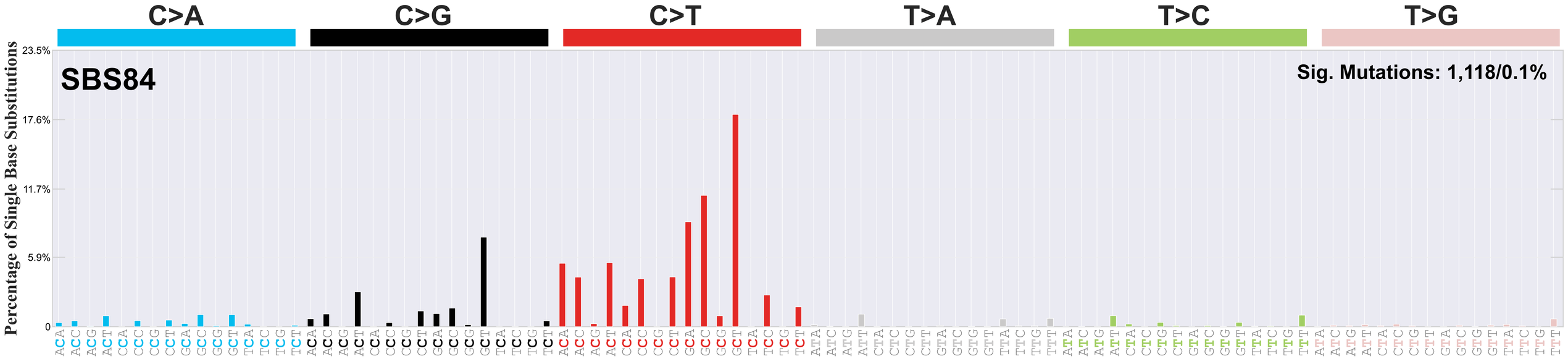

C>A
C>G
C>T
T>A
T>C
T>G
SBS59
Sig. Mutations: 1,261/0.1%
Percentage of Single Base Substitutions
64.9%
48.7%
32.4%
16.2%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA 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
SBS60
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
86.2%
64.6%
43.1%
21.5%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS84
Sig. Mutations: 1,118/0.1%
Percentage of Single Base Substitutions
23.5%
17.6%
11.7%
5.9%
0
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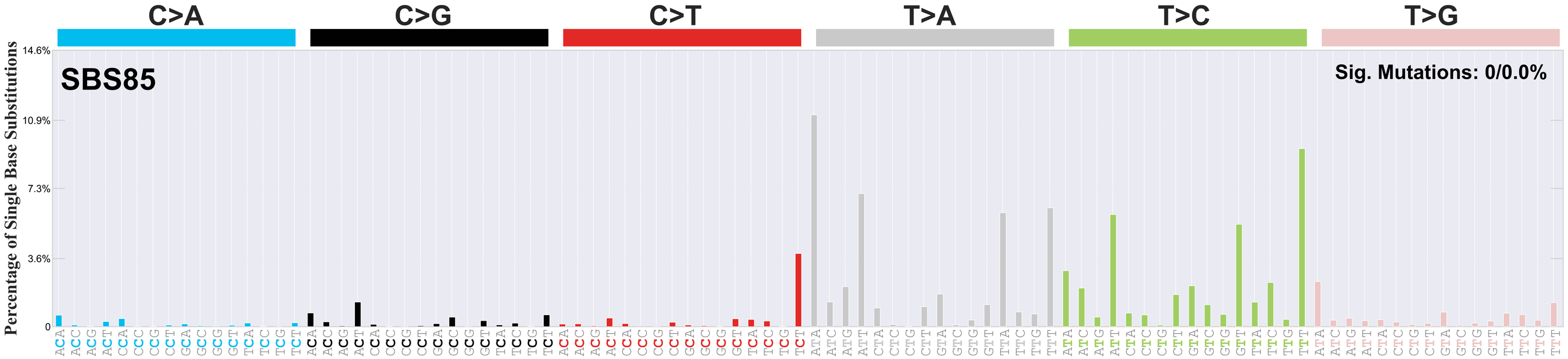
C>A
C>G
C>T
T>A
T>C
T>G
SBS85
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
14.6%
10.9%
7.3%
3.6%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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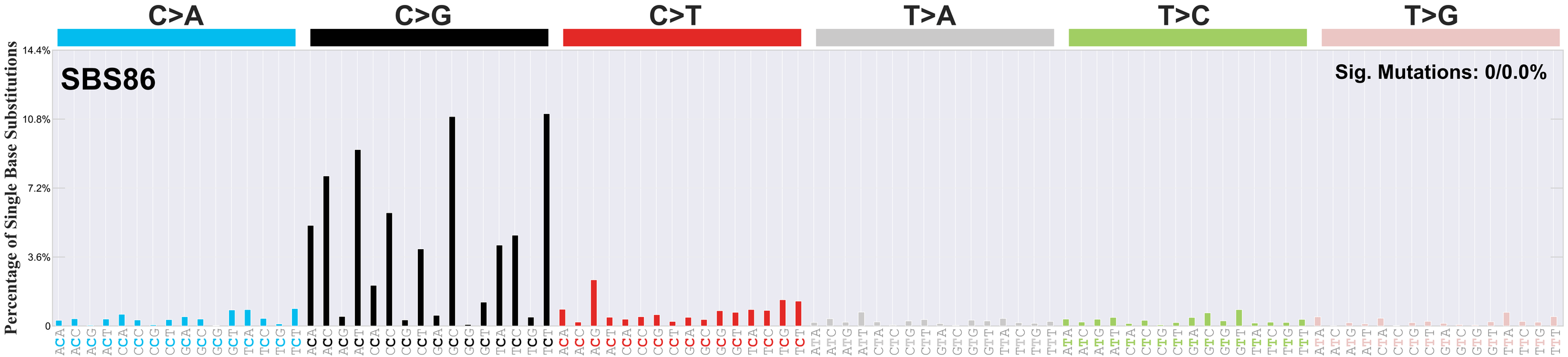
C>A
C>G
C>T
T>A
T>C
T>G
SBS86
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
14.4%
10.8%
7.2%
3.6%
0
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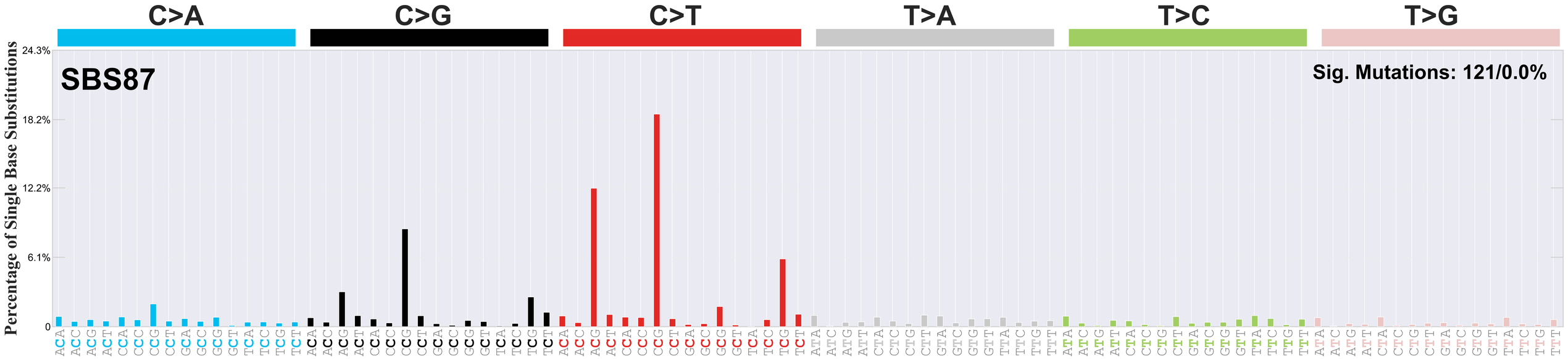
C>A
C>G
C>T
T>A
T>C
T>G
SBS87
Sig. Mutations: 121/0.0%
Percentage of Single Base Substitutions
24.3%
18.2%
12.2%
6.1%
0
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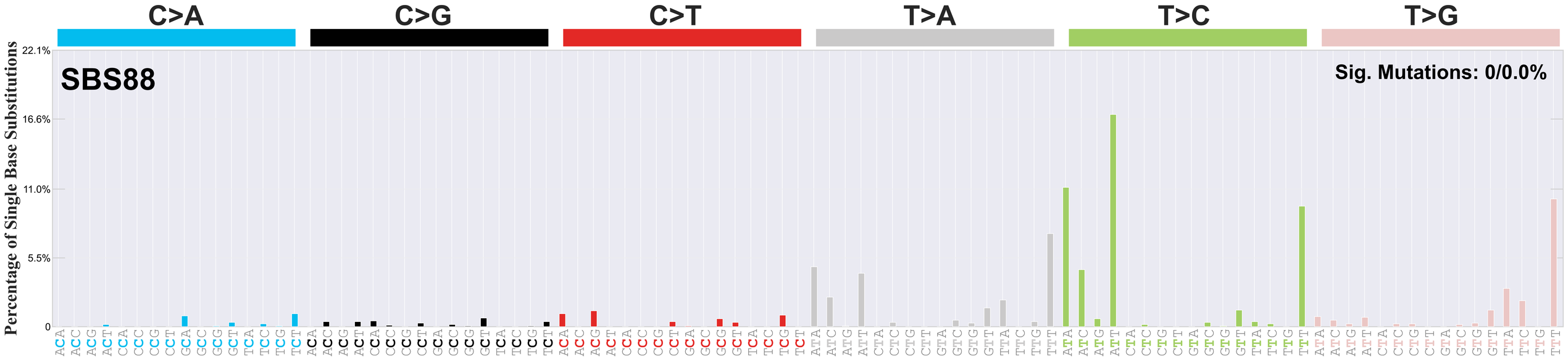
C>A
C>G
C>T
T>A
T>C
T>G
SBS88
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
22.1%
16.6%
11.0%
5.5%
0
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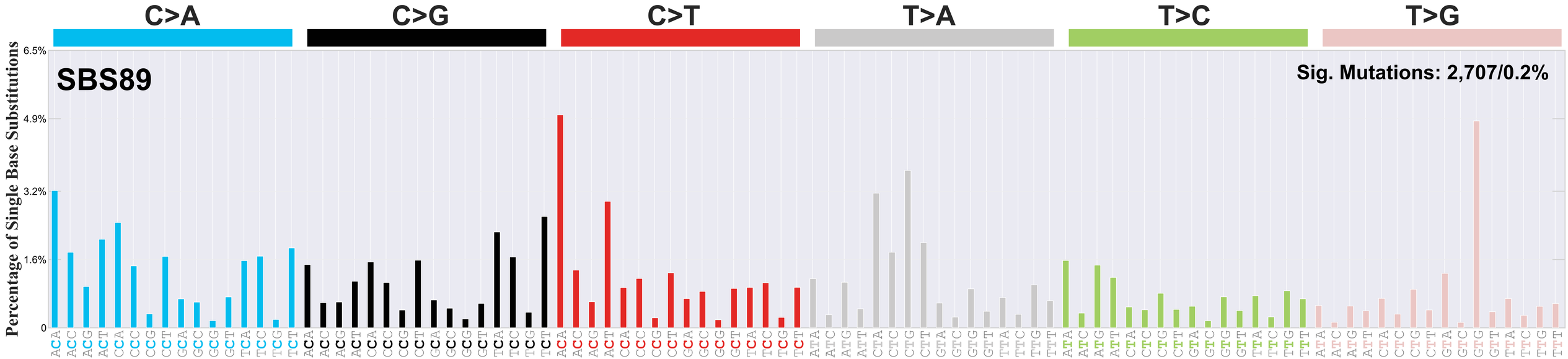
C>A
C>G
C>T
T>A
T>C
T>G
SBS89
Sig. Mutations: 2,707/0.2%
Percentage of Single Base Substitutions
6.5%
4.9%
3.2%
1.6%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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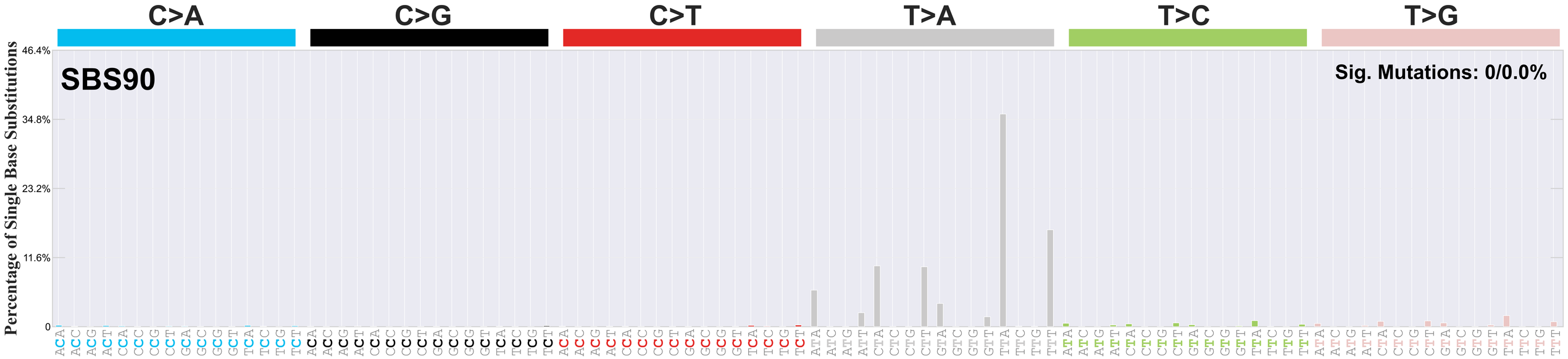
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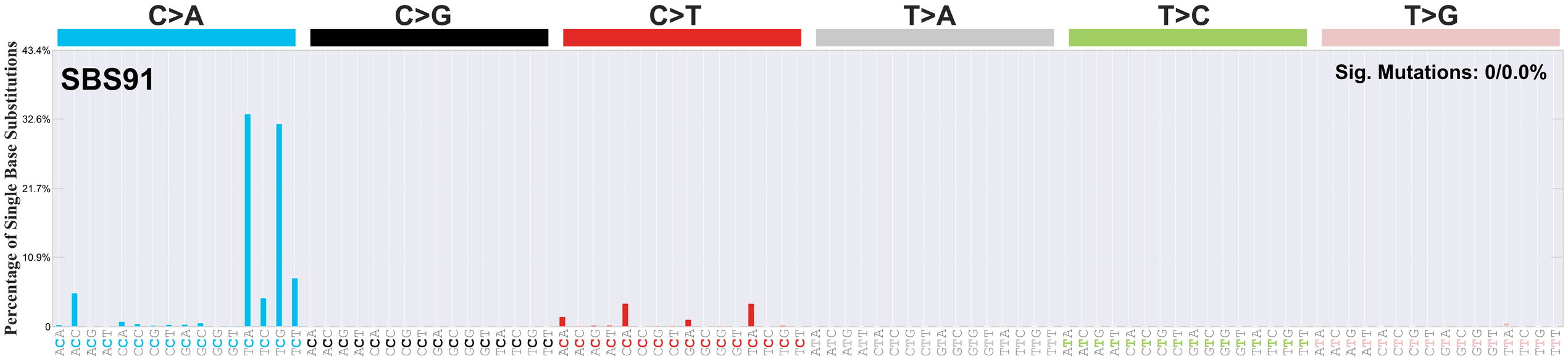
C>G
C>T
T>A
T>C
T>G
SBS90
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
46.4%
34.8%
23.2%
11.6%
0


C>A
C>G
C>T
T>A
T>C
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SBS91
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
43.4%
32.6%
21.7%
10.9%
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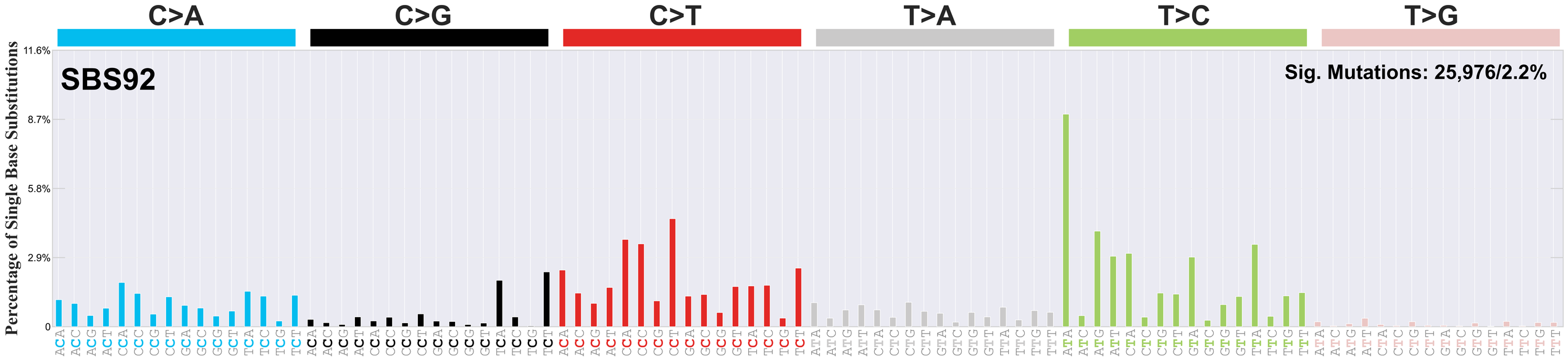
C>A
C>G
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T>C
T>G
SBS92
Sig. Mutations: 25,976/2.2%
Percentage of Single Base Substitutions
11.6%
8.7%
5.8%
2.9%
0
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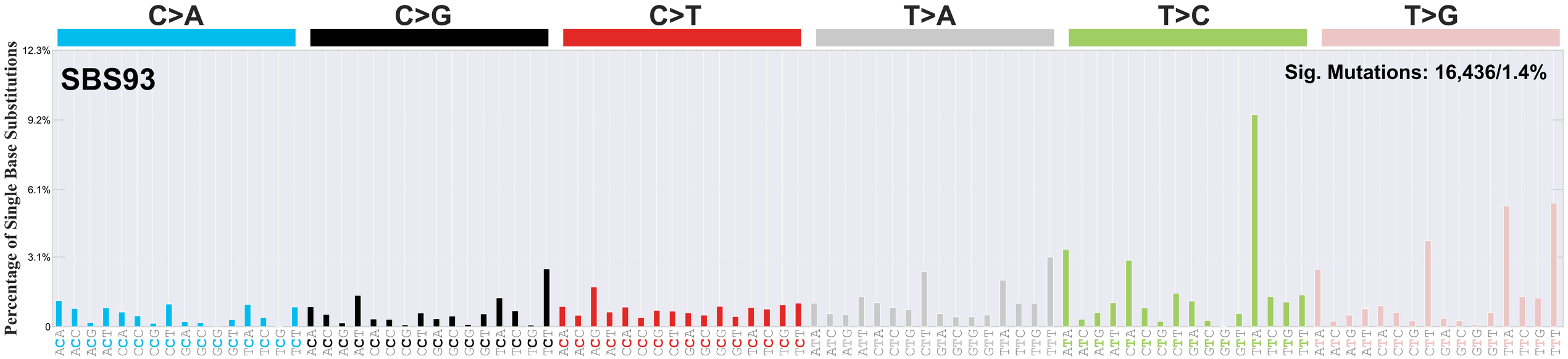
C>A
C>G
C>T
T>A
T>C
T>G
SBS93
Sig. Mutations: 16,436/1.4%
Percentage of Single Base Substitutions
12.3%
9.2%
6.1%
3.1%
0
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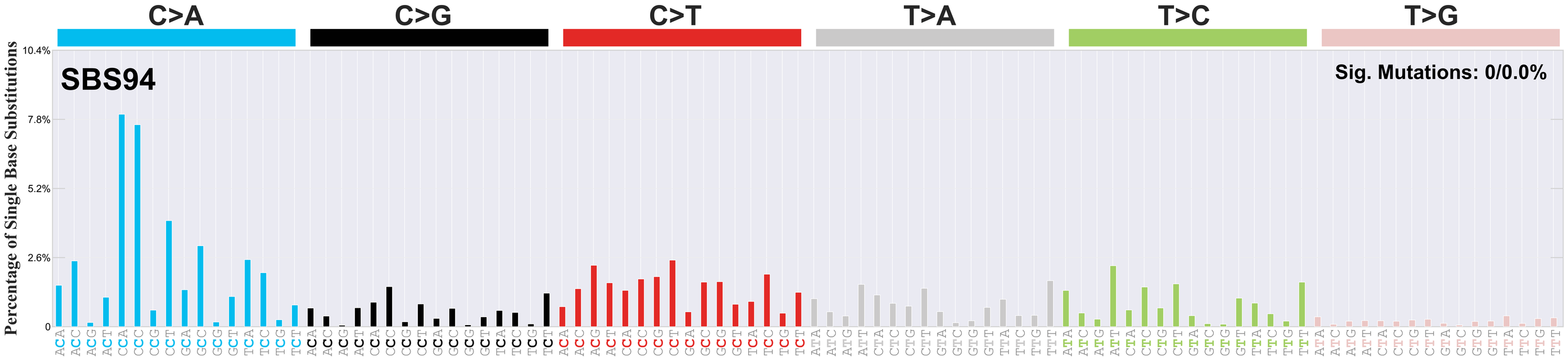
C>A
C>G
C>T
T>A
T>C
T>G
SBS94
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
10.4%
7.8%
5.2%
2.6%
0
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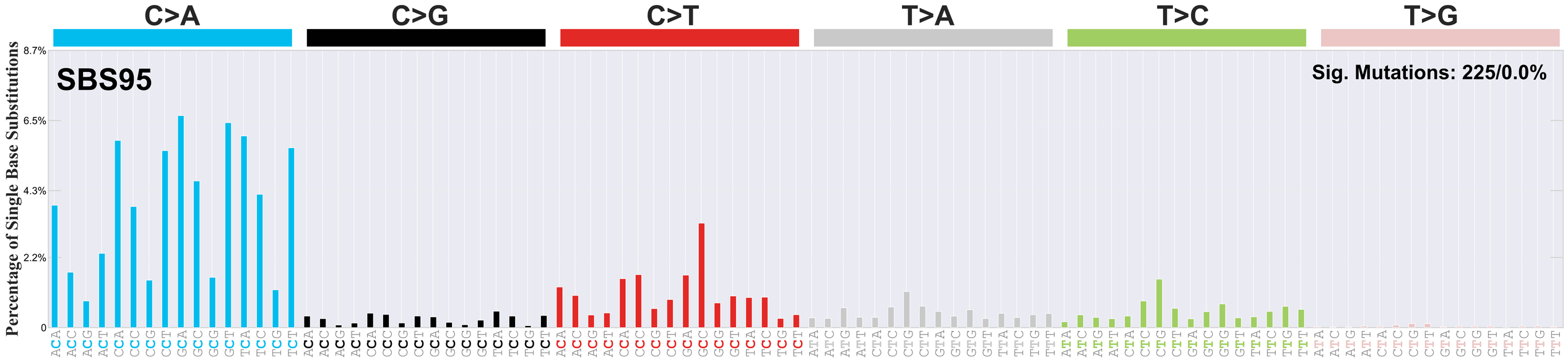
C>A
C>G
C>T
T>A
T>C
T>G
SBS95
Sig. Mutations: 225/0.0%
Percentage of Single Base Substitutions
8.7%
6.5%
4.3%
2.2%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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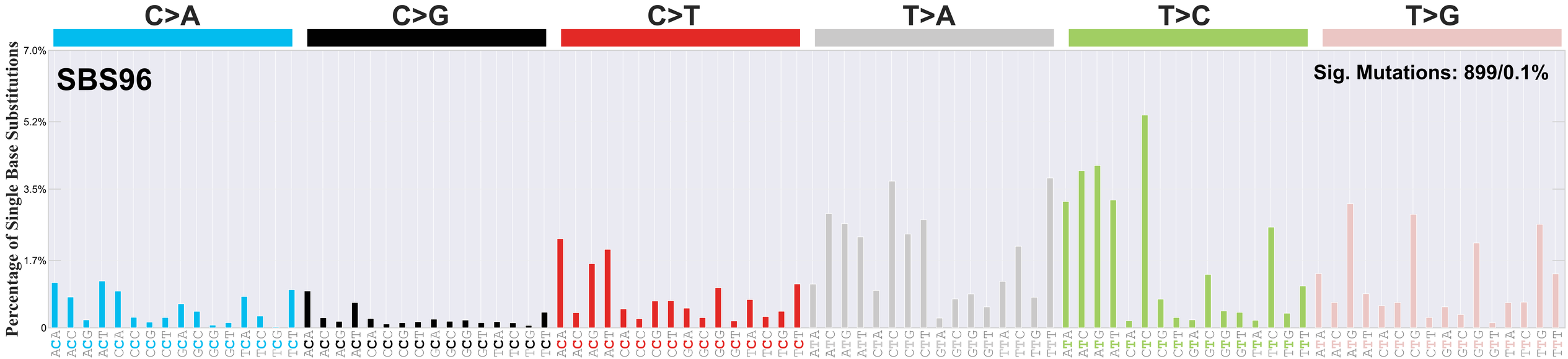
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C>G
C>T
T>A
T>C
T>G
SBS96
Sig. Mutations: 899/0.1%
Percentage of Single Base Substitutions
7.0%
5.2%
3.5%
1.7%
0
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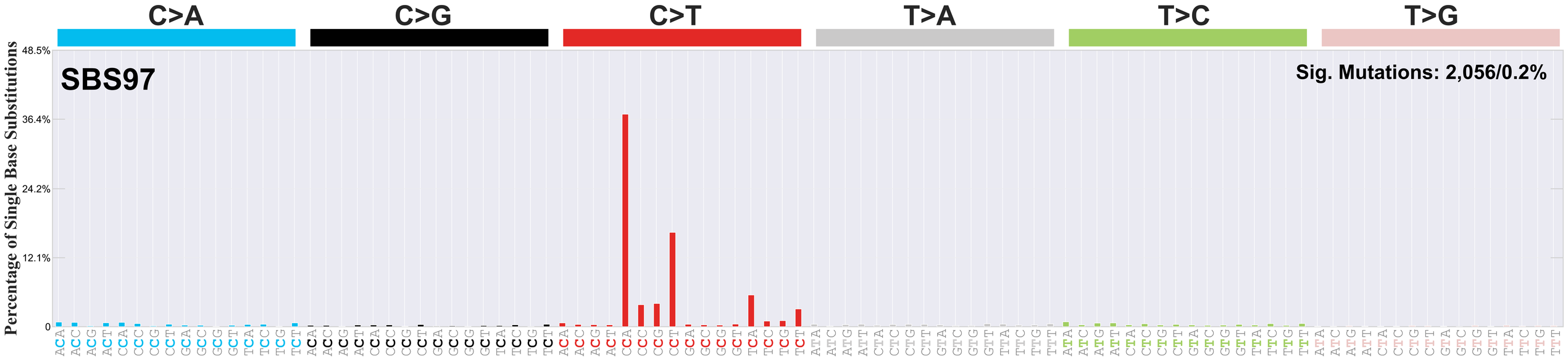
C>A
C>G
C>T
T>A
T>C
T>G
SBS97
Sig. Mutations: 2,056/0.2%
Percentage of Single Base Substitutions
48.5%
36.4%
24.2%
12.1%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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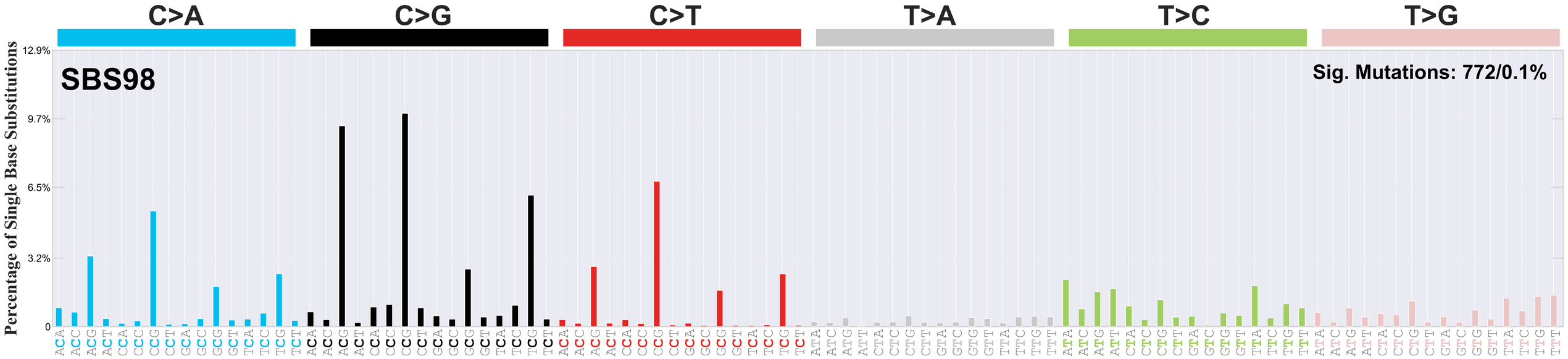
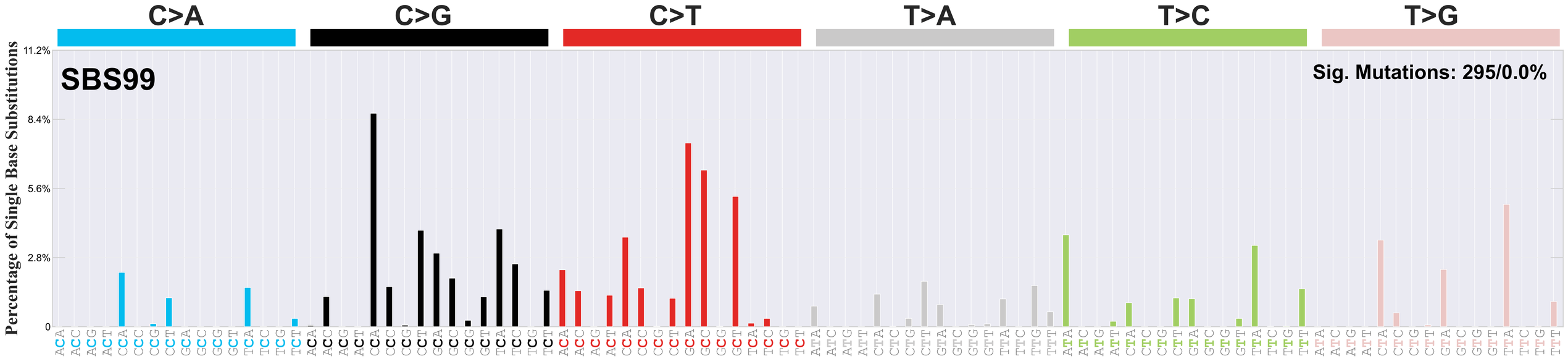
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT


C>A
C>G
C>T
T>A
T>C
T>G
SBS98
Sig. Mutations: 772/0.1%
Percentage of Single Base Substitutions
12.9%
9.7%
6.5%
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
SBS99
Sig. Mutations: 295/0.0%
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