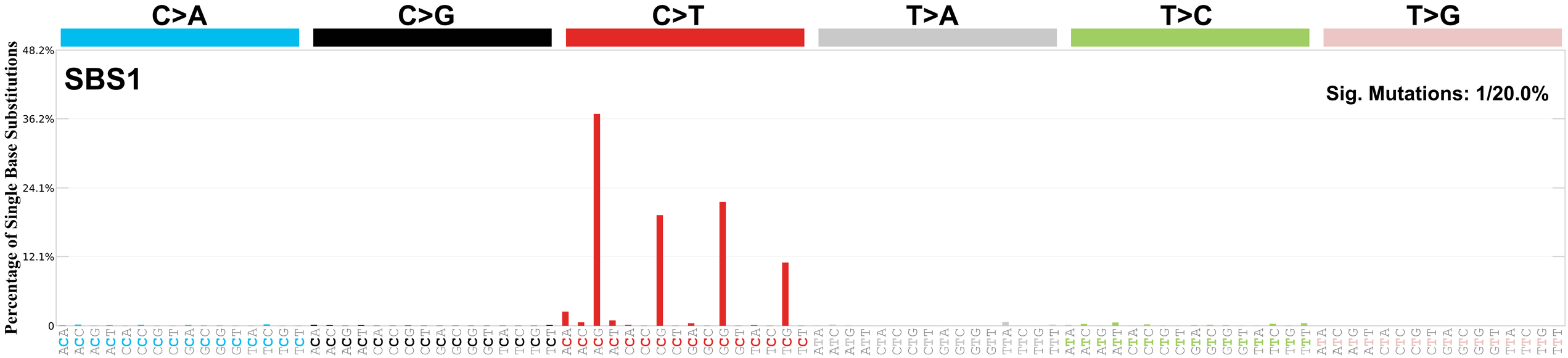
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C>G
C>T
T>A
T>C
T>G
SBS1
Sig. Mutations: 1/20.0%
Percentage of Single Base Substitutions
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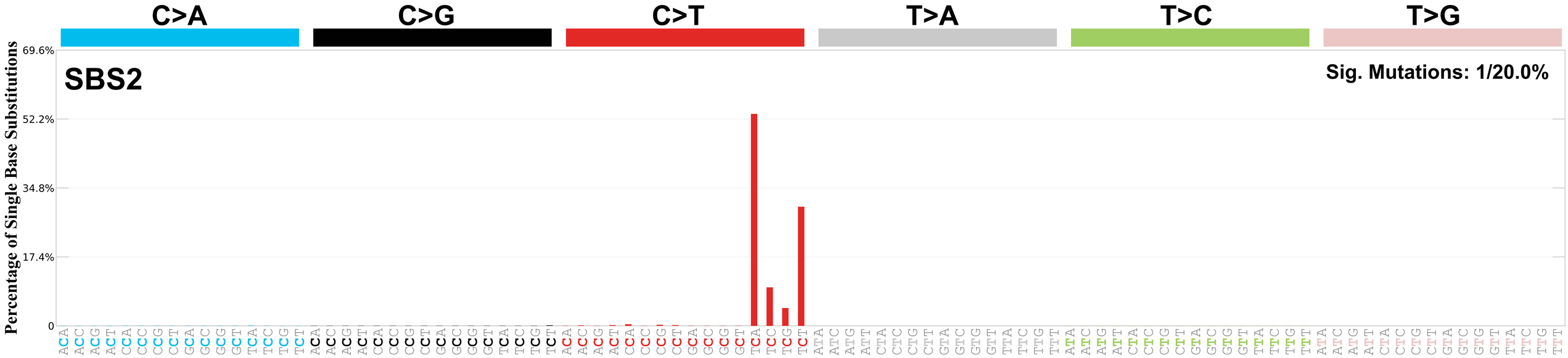
36.2%
24.1%
12.1%
0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C>G
C>T
T>A
T>C
T>G
SBS2
Sig. Mutations: 1/20.0%
Percentage of Single Base Substitutions
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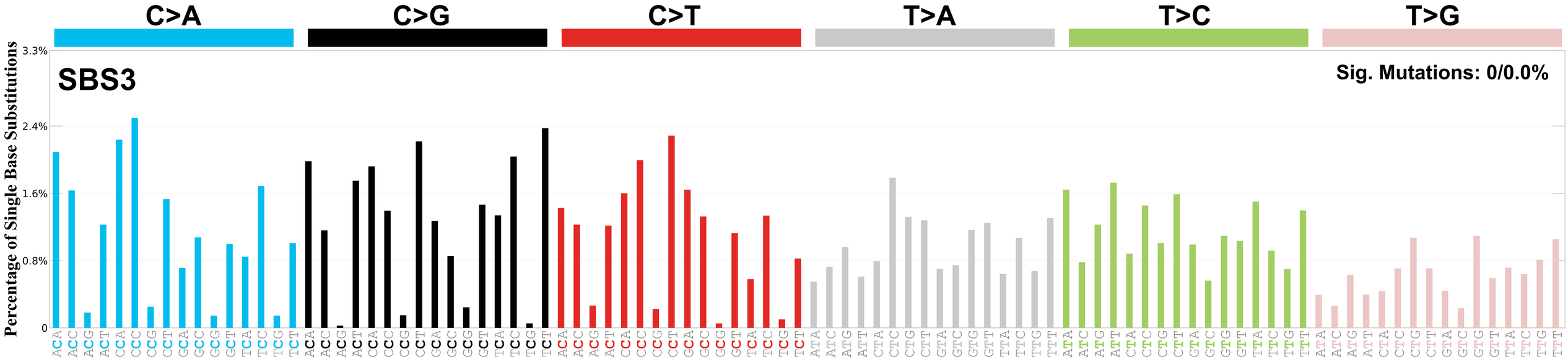
52.2%
34.8%
17.4%
0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C>G
C>T
T>A
T>C
T>G
SBS3
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
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2.4%
1.6%
0.8%
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ATA ATC ATG ATT CTA 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
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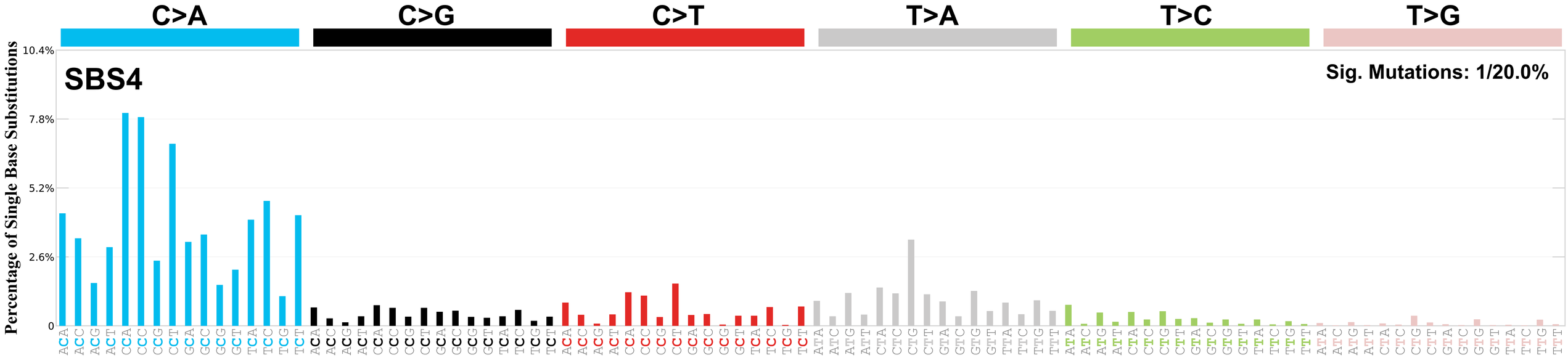
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C>G
C>T
T>A
T>C
T>G
SBS4
Sig. Mutations: 1/20.0%
Percentage of Single Base Substitutions
10.4%
7.8%
5.2%
2.6%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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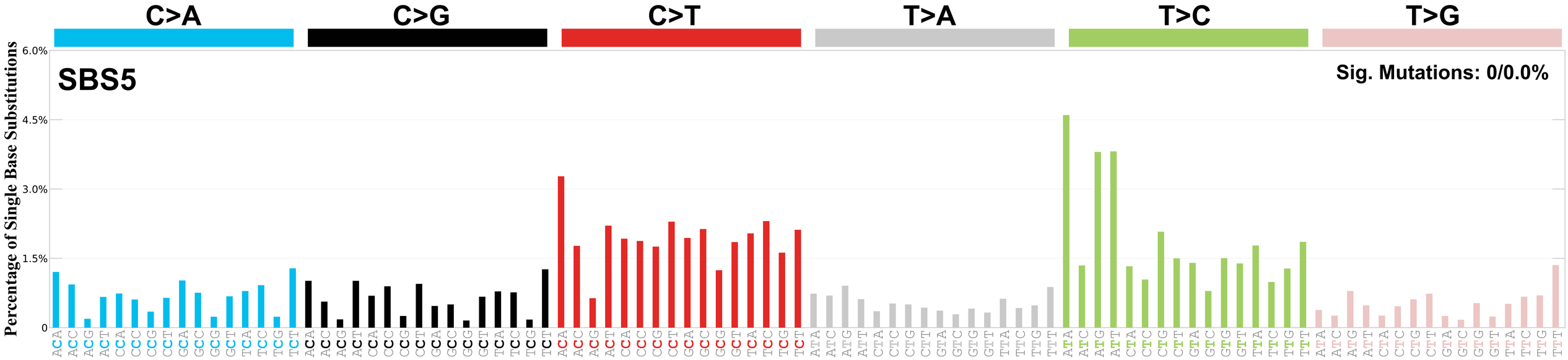
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C>G
C>T
T>A
T>C
T>G
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Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
6.0%
4.5%
3.0%
1.5%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC 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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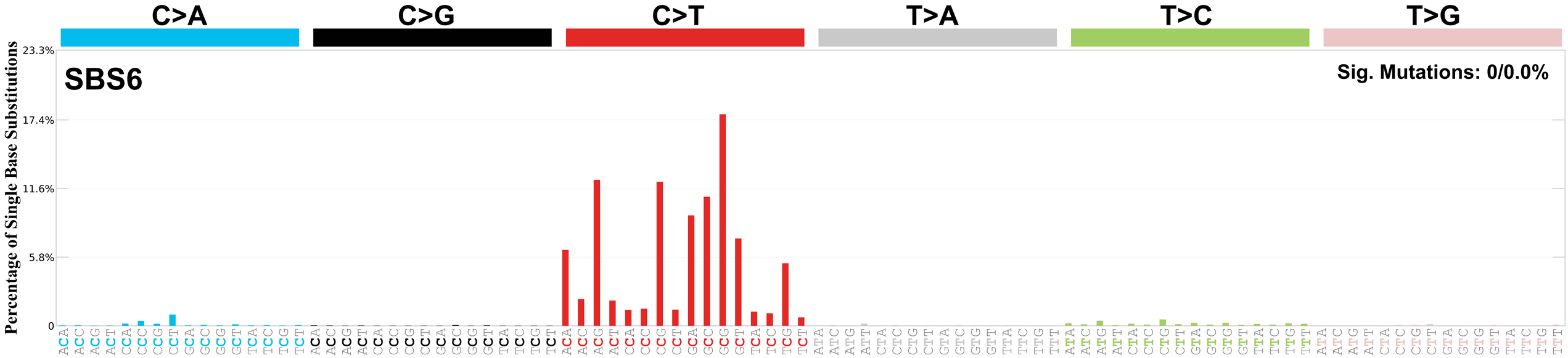
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C>G
C>T
T>A
T>C
T>G
SBS6
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
23.3%
17.4%
11.6%
5.8%
0
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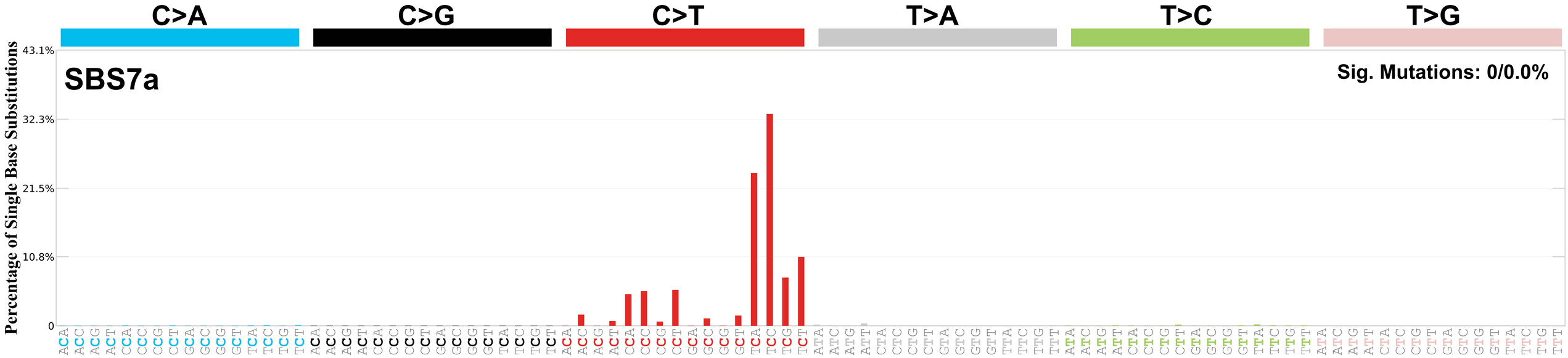
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C>G
C>T
T>A
T>C
T>G
SBS7a
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
43.1%
32.3%
21.5%
10.8%
0
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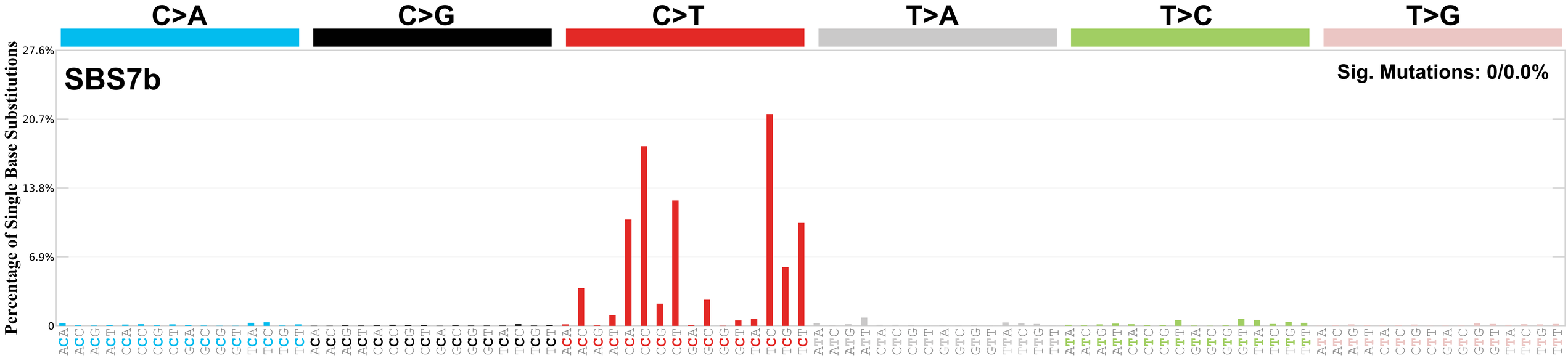
C>A
C>G
C>T
T>A
T>C
T>G
SBS7b
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
27.6%
20.7%
13.8%
6.9%
0
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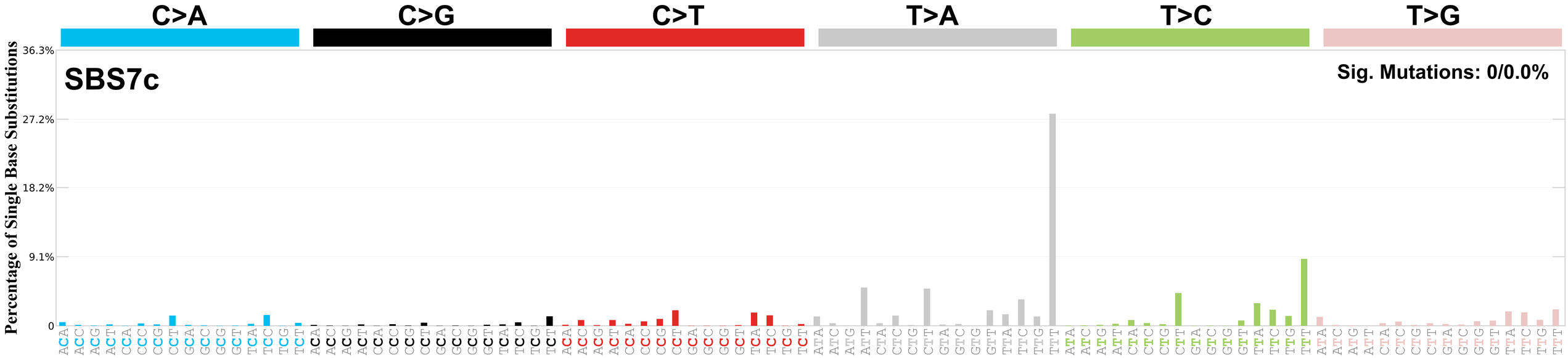
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C>G
C>T
T>A
T>C
T>G
SBS7c
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
36.3%
27.2%
18.2%
9.1%
0
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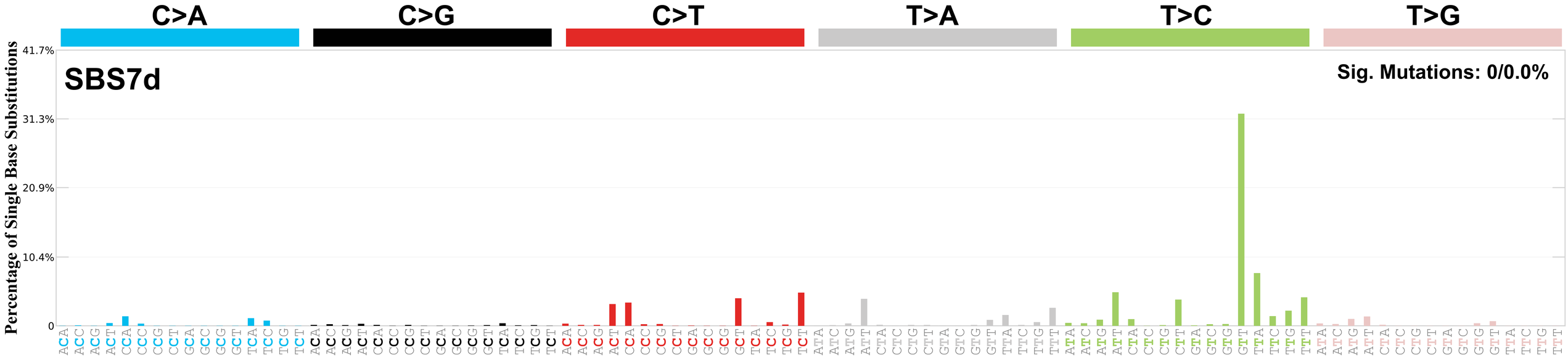
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C>G
C>T
T>A
T>C
T>G
SBS7d
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
41.7%
31.3%
20.9%
10.4%
0
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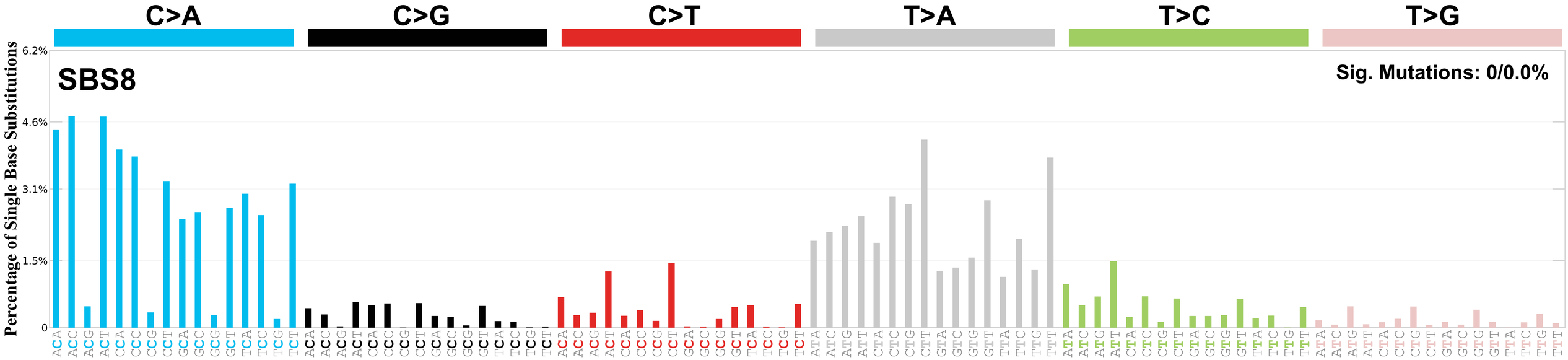
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T>C
T>G
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Percentage of Single Base Substitutions
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4.6%
3.1%
1.5%
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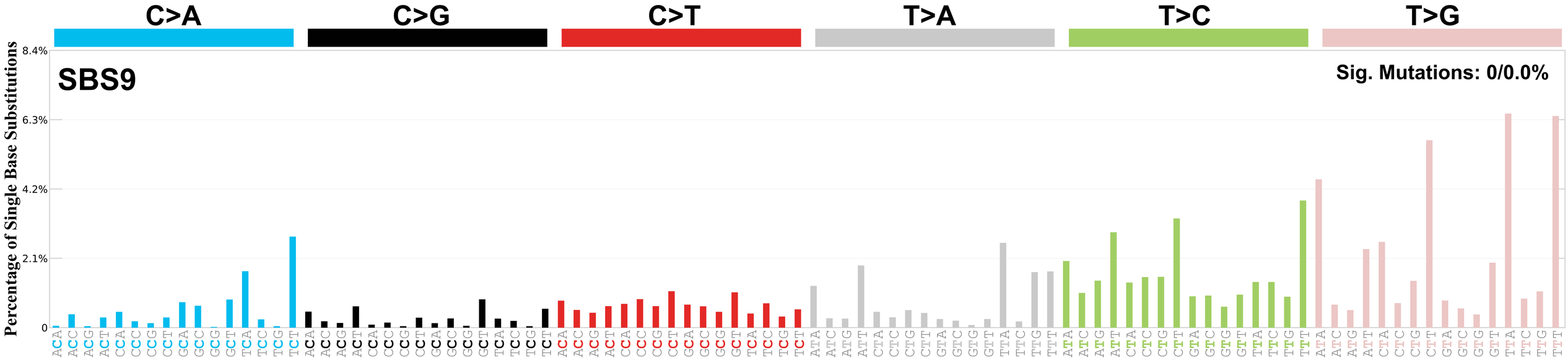
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T>C
T>G
SBS9
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Percentage of Single Base Substitutions
8.4%
6.3%
4.2%
2.1%
0
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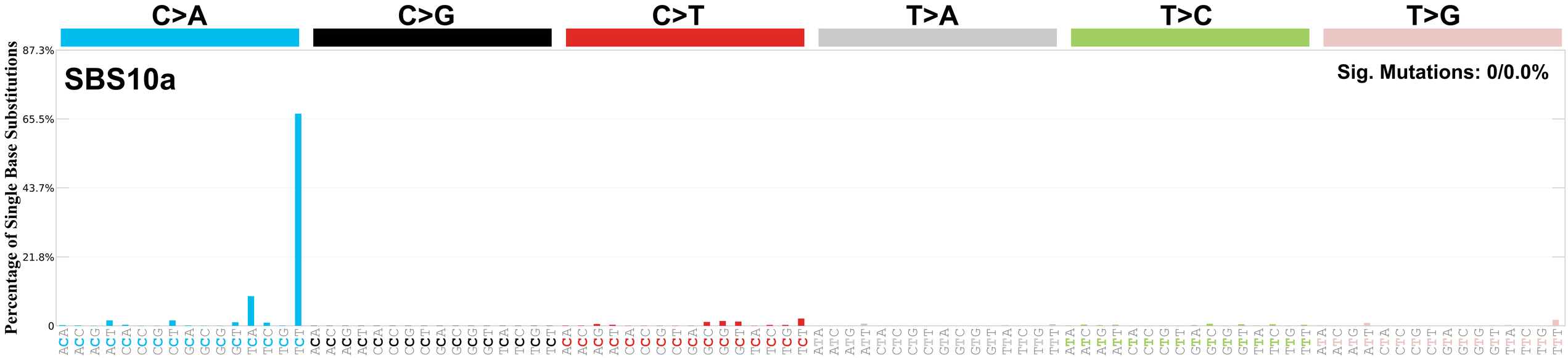
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C>G
C>T
T>A
T>C
T>G
SBS10a
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
87.3%
65.5%
43.7%
21.8%
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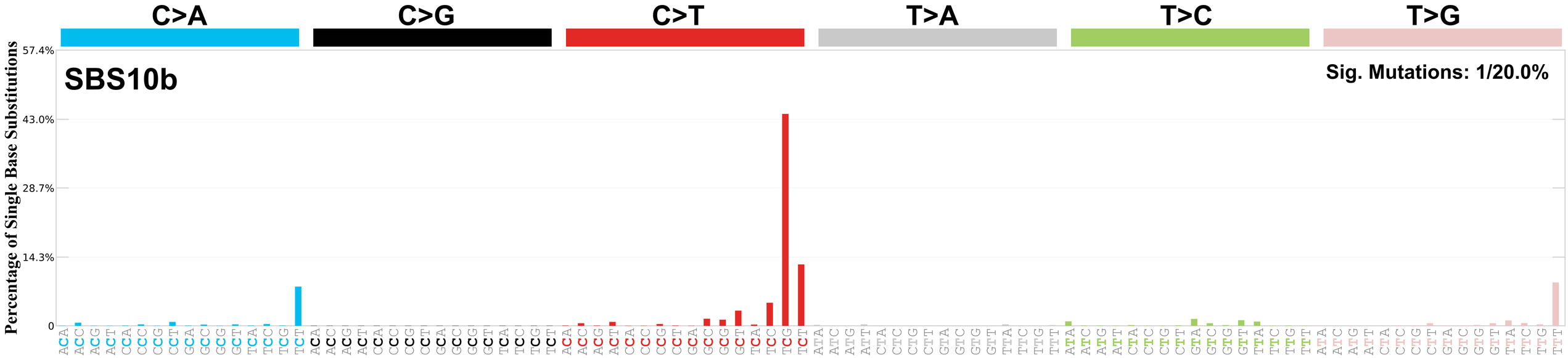
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T>C
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Percentage of Single Base Substitutions
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28.7%
14.3%
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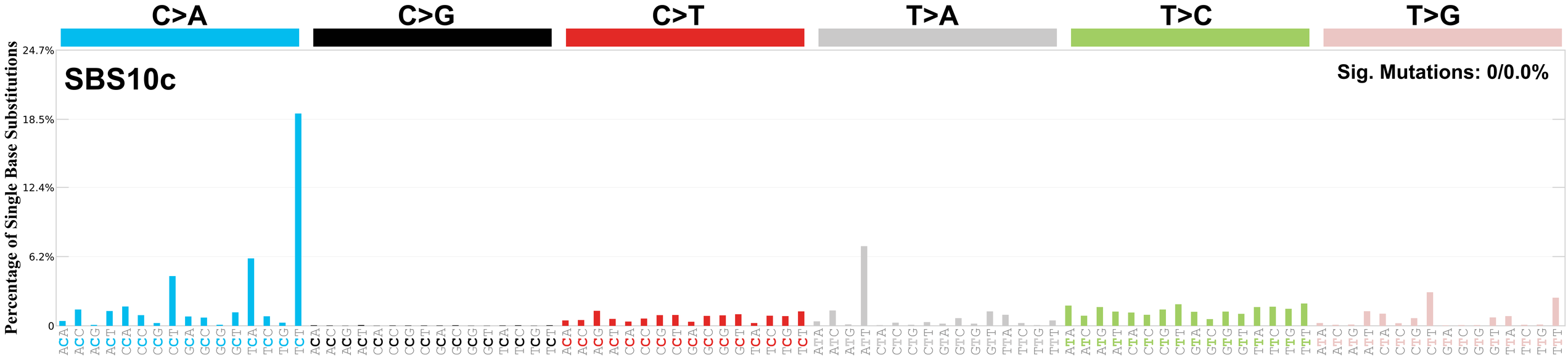
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C>G
C>T
T>A
T>C
T>G
SBS10c
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Percentage of Single Base Substitutions
24.7%
18.5%
12.4%
6.2%
0
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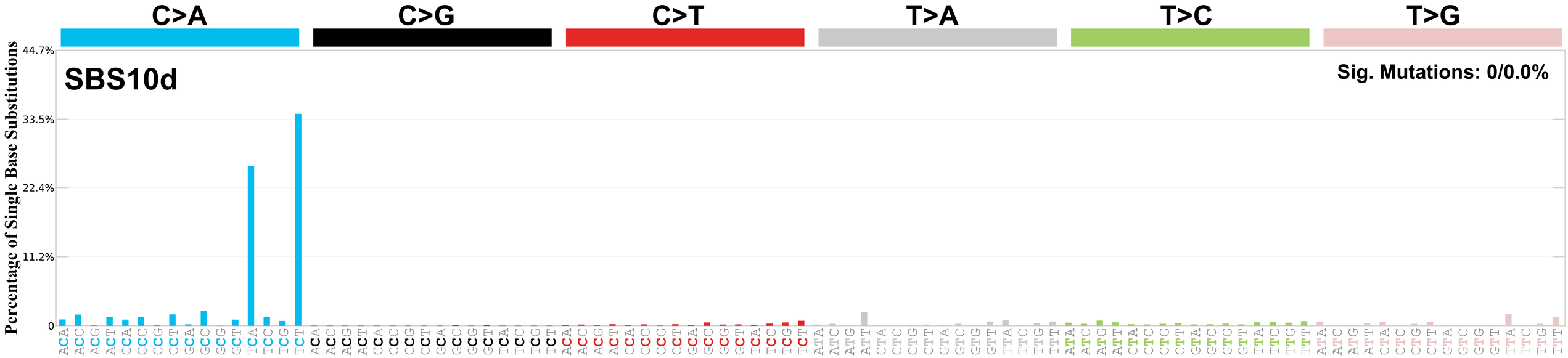
C>A
C>G
C>T
T>A
T>C
T>G
SBS10d
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
44.7%
33.5%
22.4%
11.2%
0
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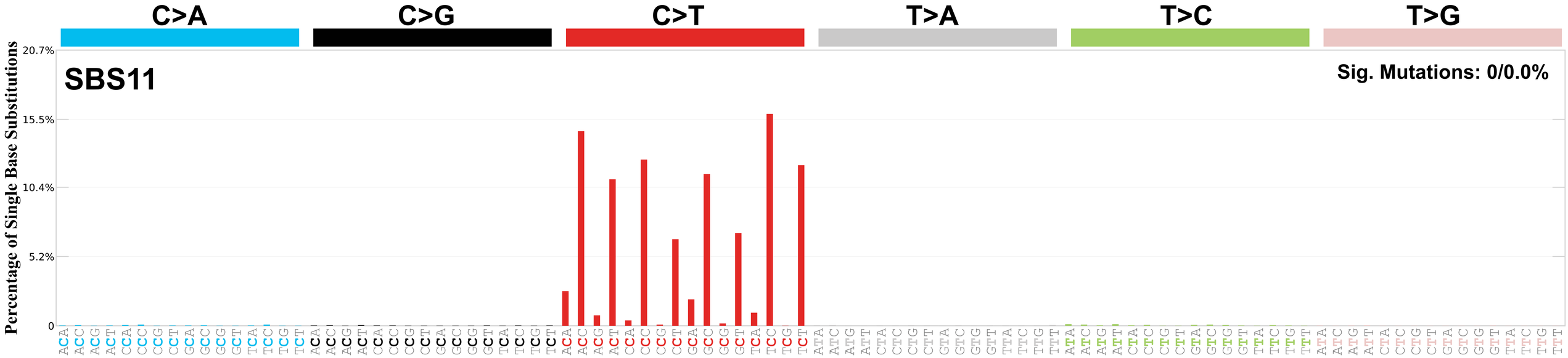
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C>G
C>T
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T>C
T>G
SBS11
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
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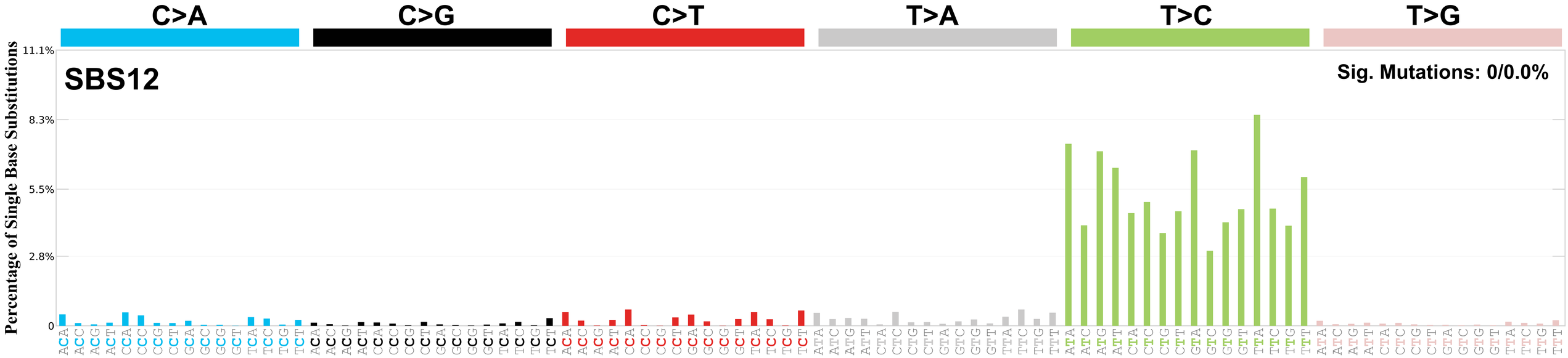
10.4%
5.2%
0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C>G
C>T
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T>C
T>G
SBS12
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
11.1%
8.3%
5.5%
2.8%
0
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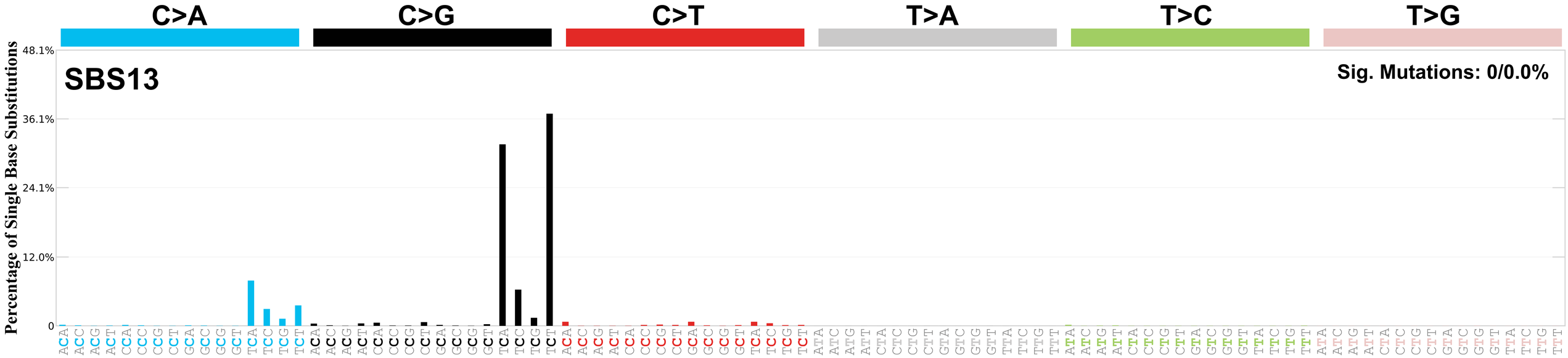
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C>G
C>T
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T>C
T>G
SBS13
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
48.1%
36.1%
24.1%
12.0%
0
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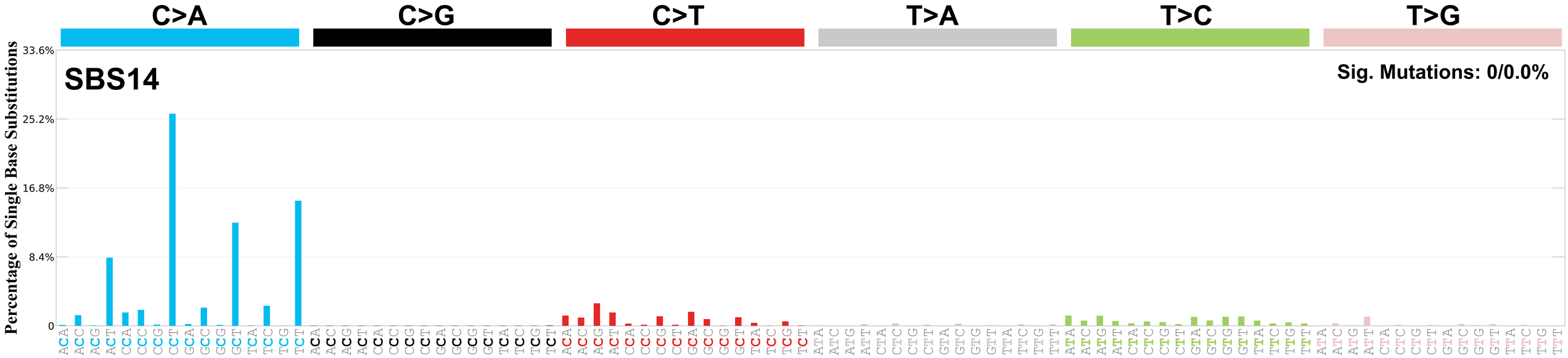
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C>G
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T>C
T>G
SBS14
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Percentage of Single Base Substitutions
33.6%
25.2%
16.8%
8.4%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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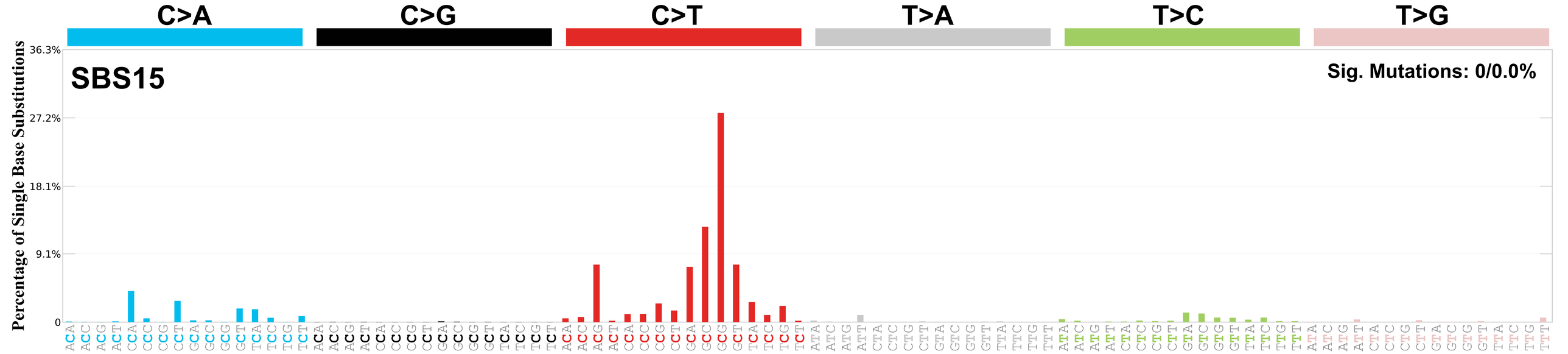
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C>G
C>T
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T>C
T>G
SBS15
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
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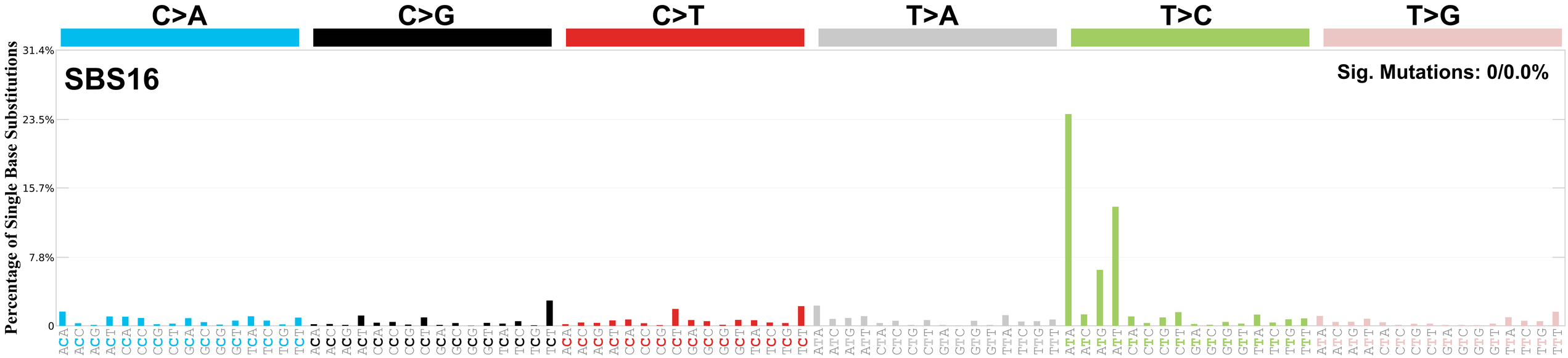
18.1%
9.1%
0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C>T
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T>C
T>G
SBS16
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
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23.5%
15.7%
7.8%
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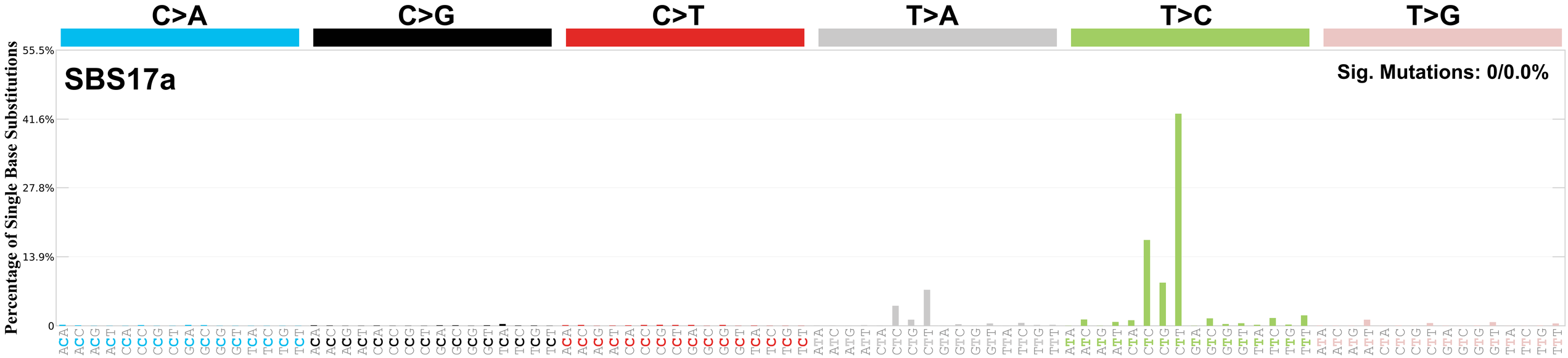
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C>G
C>T
T>A
T>C
T>G
SBS17a
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
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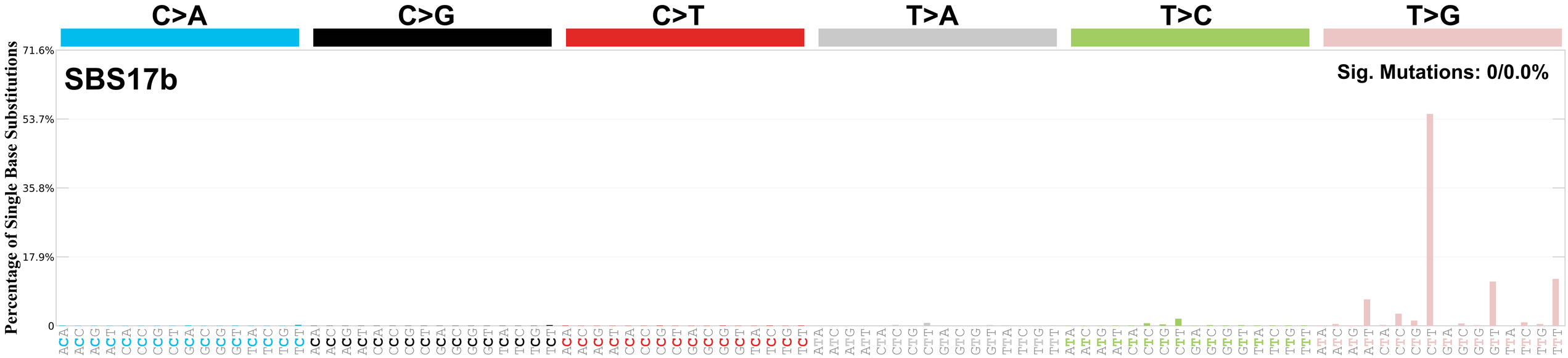
27.8%
13.9%
0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C>G
C>T
T>A
T>C
T>G
SBS17b
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
71.6%
53.7%
35.8%
17.9%
0
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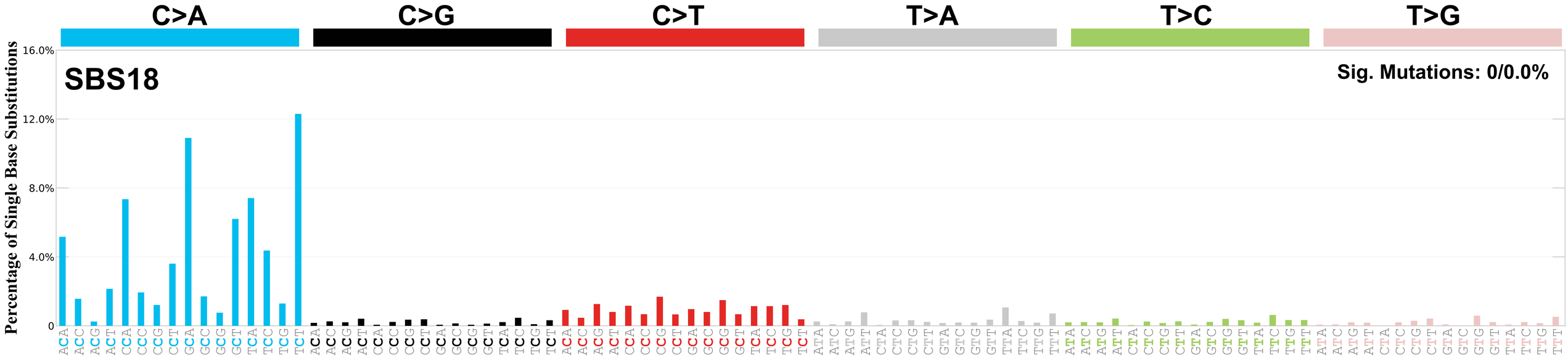
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T>C
T>G
SBS18
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Percentage of Single Base Substitutions
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8.0%
4.0%
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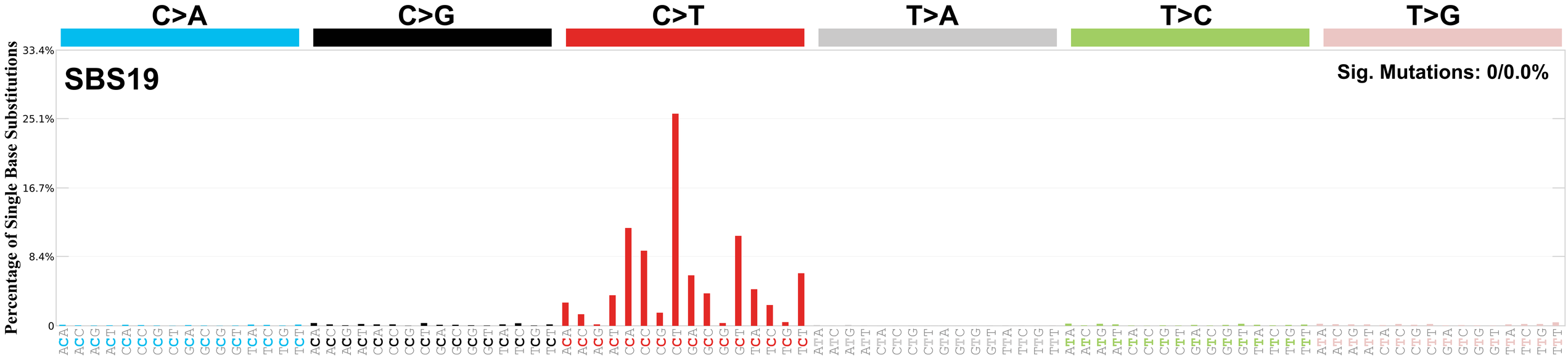
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C>G
C>T
T>A
T>C
T>G
SBS19
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Percentage of Single Base Substitutions
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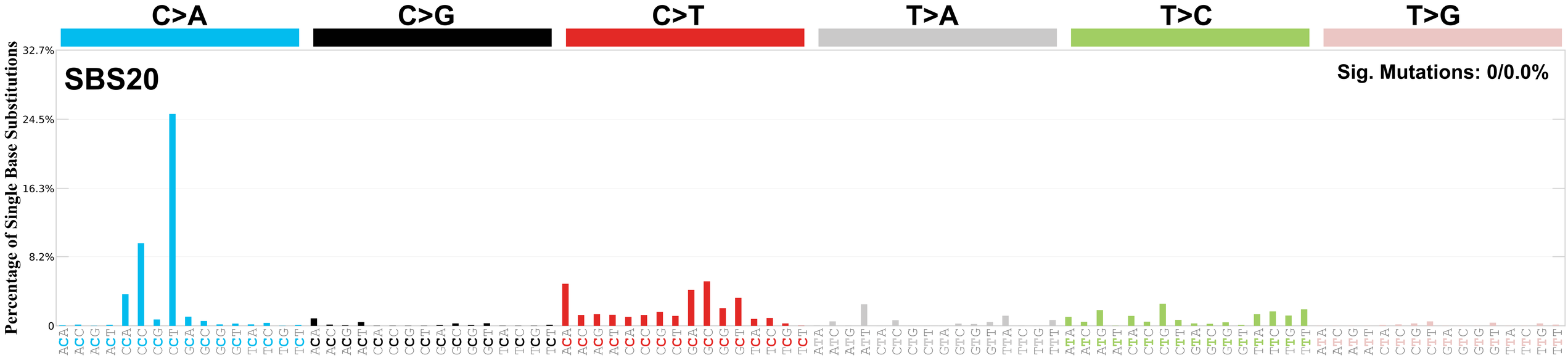
16.7%
8.4%
0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C>T
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T>C
T>G
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Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
32.7%
24.5%
16.3%
8.2%
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ACA 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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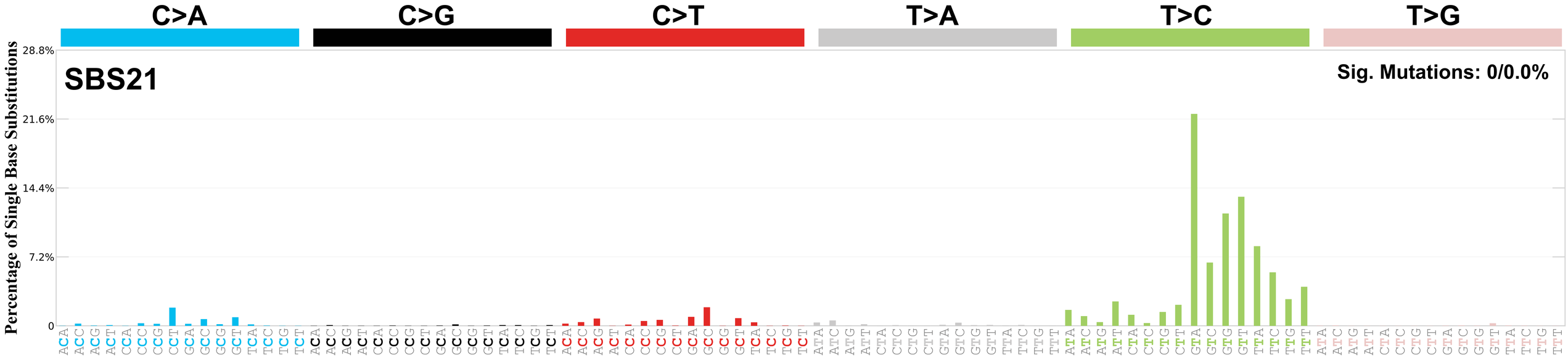
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C>G
C>T
T>A
T>C
T>G
SBS21
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
28.8%
21.6%
14.4%
7.2%
0
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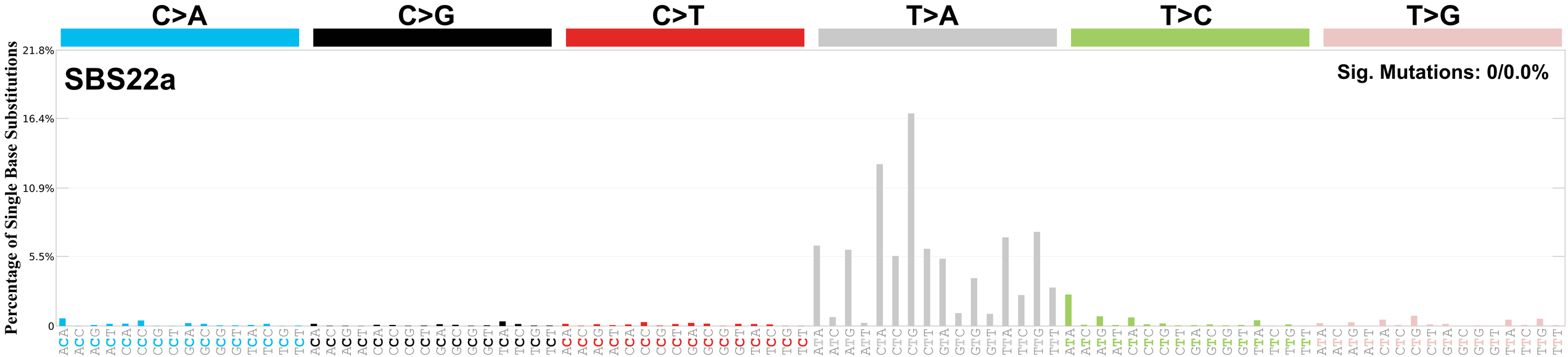
C>A
C>G
C>T
T>A
T>C
T>G
SBS22a
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
21.8%
16.4%
10.9%
5.5%
0
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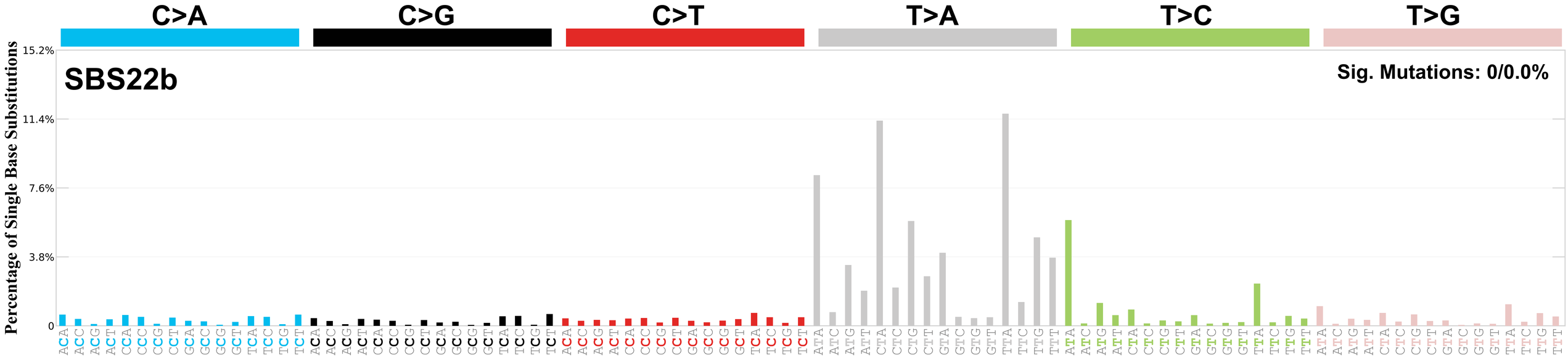
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C>G
C>T
T>A
T>C
T>G
SBS22b
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
15.2%
11.4%
7.6%
3.8%
0
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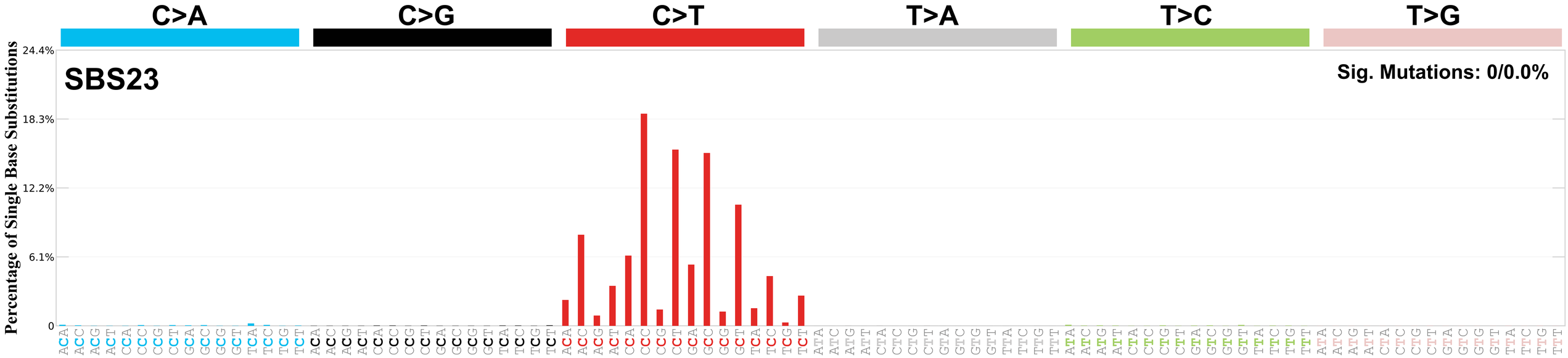
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T>C
T>G
SBS23
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
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18.3%
12.2%
6.1%
0
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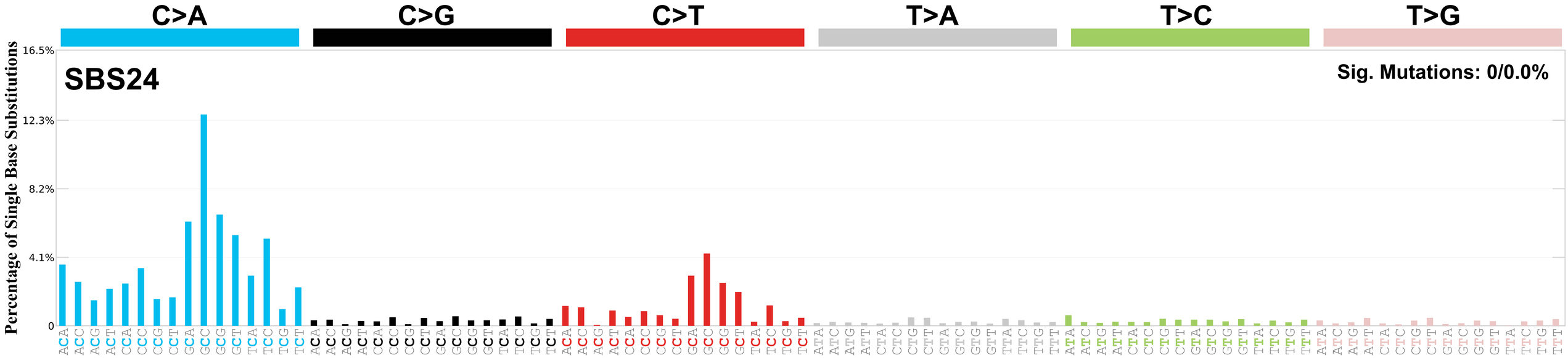
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SBS24
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
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12.3%
8.2%
4.1%
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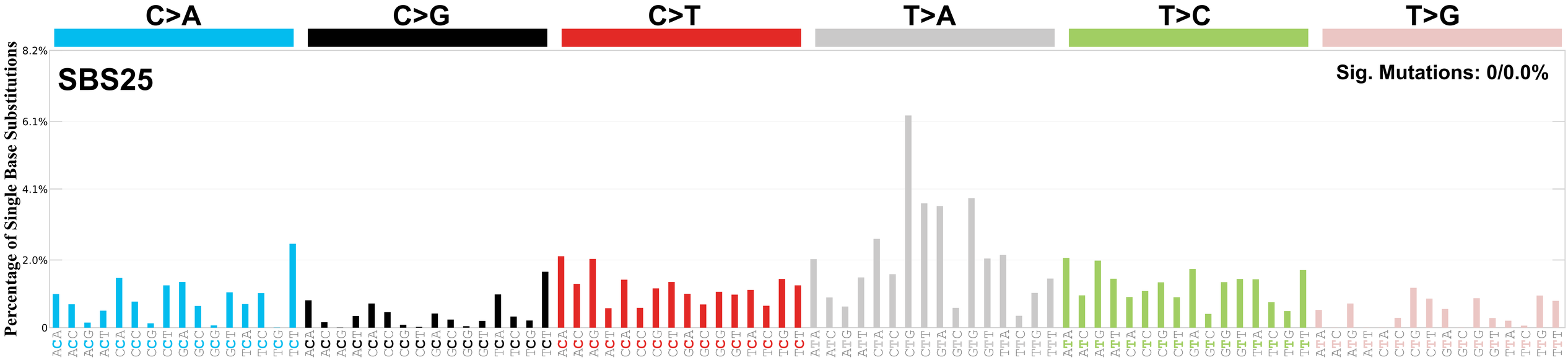
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T>C
T>G
SBS25
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
8.2%
6.1%
4.1%
2.0%
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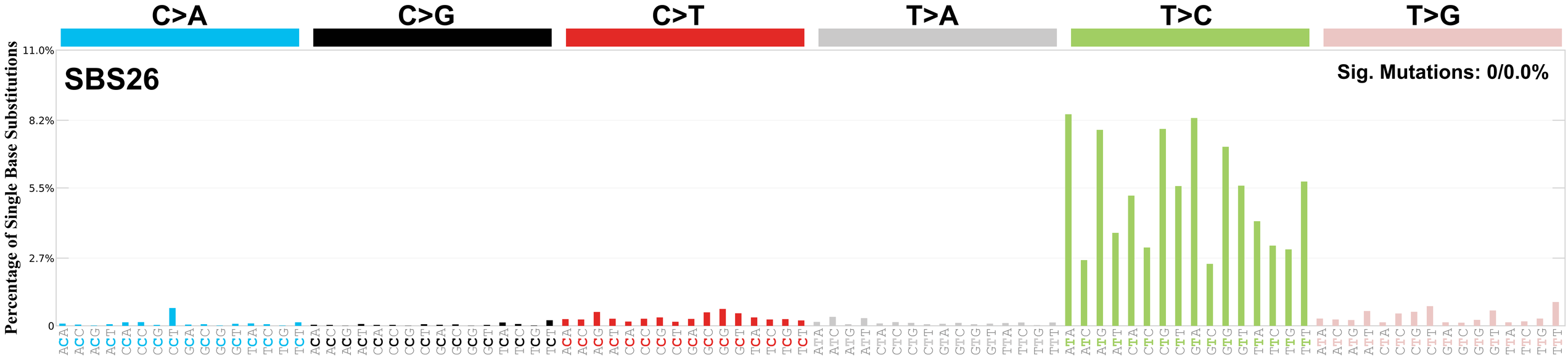
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Percentage of Single Base Substitutions
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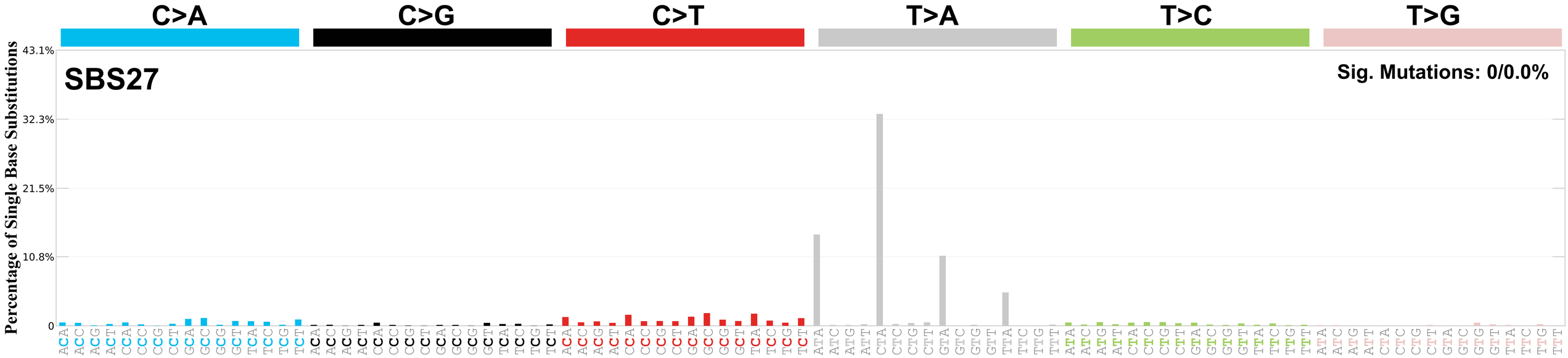
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Percentage of Single Base Substitutions
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21.5%
10.8%
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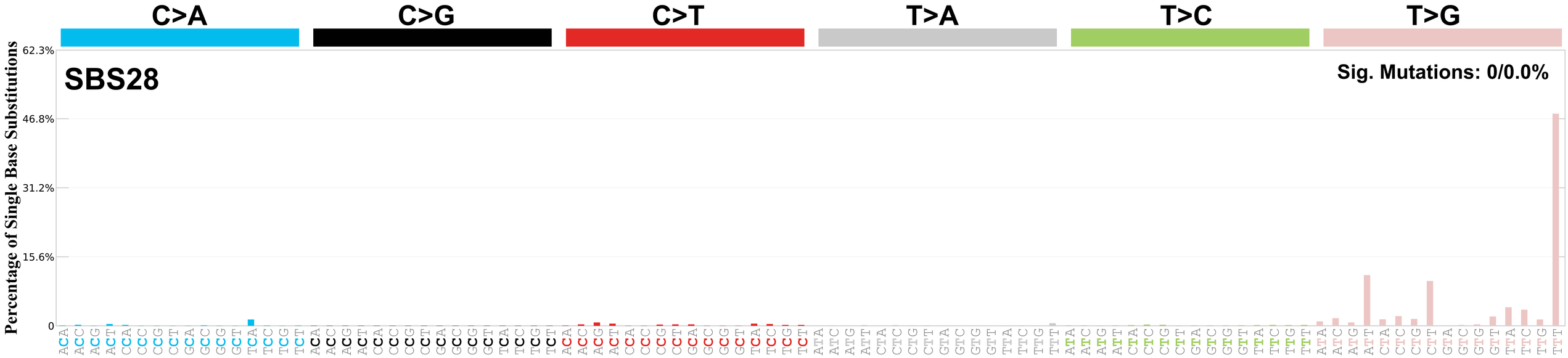
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Percentage of Single Base Substitutions
62.3%
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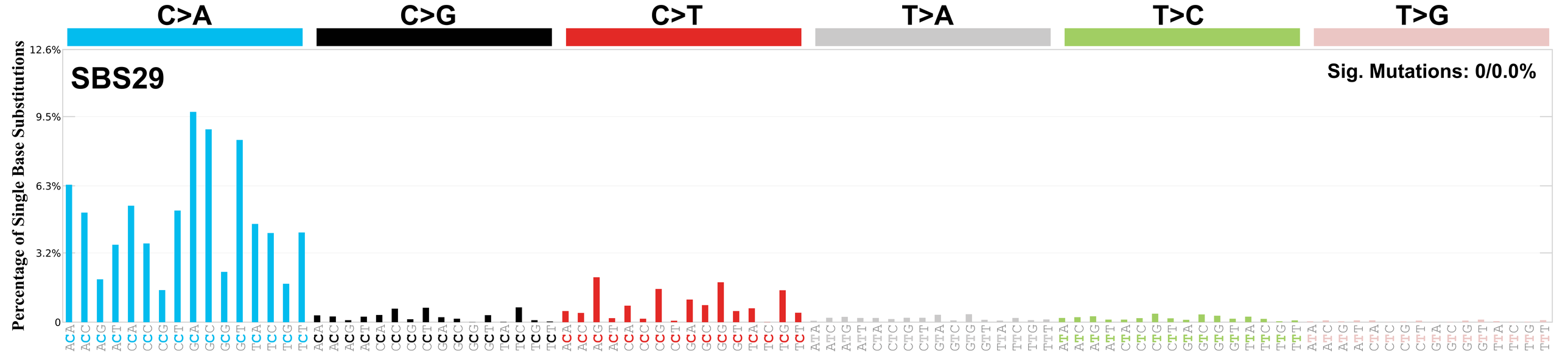
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SBS29
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Percentage of Single Base Substitutions
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6.3%
3.2%
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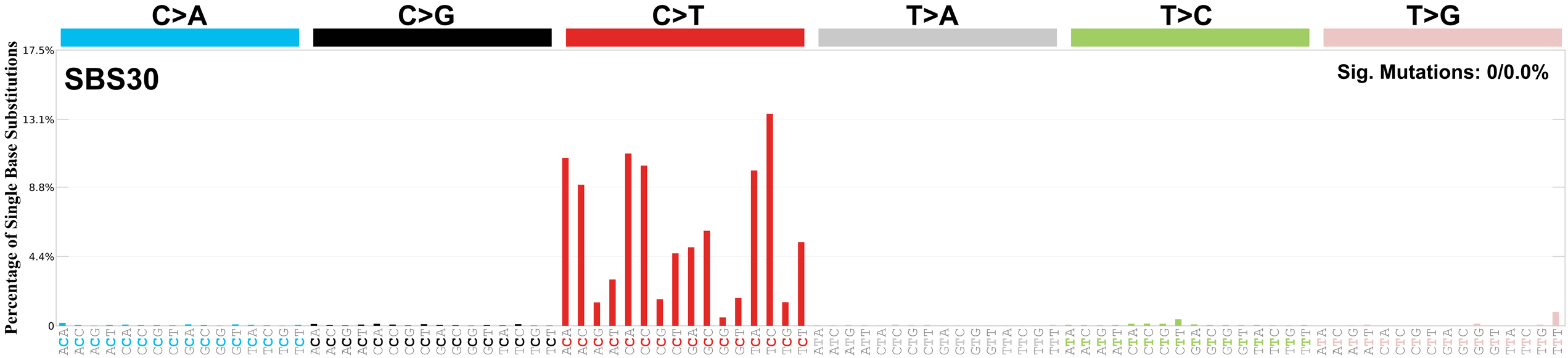
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T>G
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Percentage of Single Base Substitutions
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8.8%
4.4%
0
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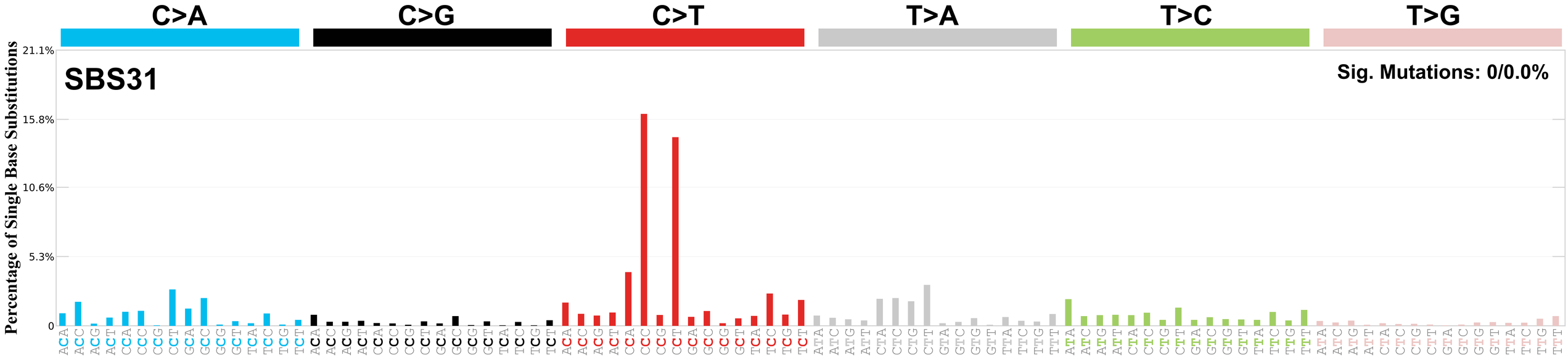
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T>G
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Percentage of Single Base Substitutions
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10.6%
5.3%
0
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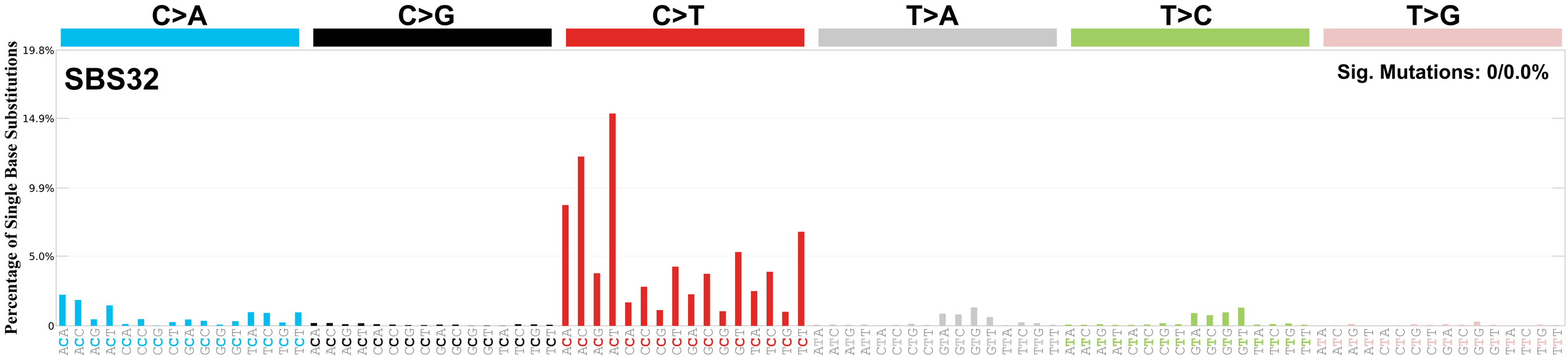
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C>T
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T>C
T>G
SBS32
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
19.8%
14.9%
9.9%
5.0%
0
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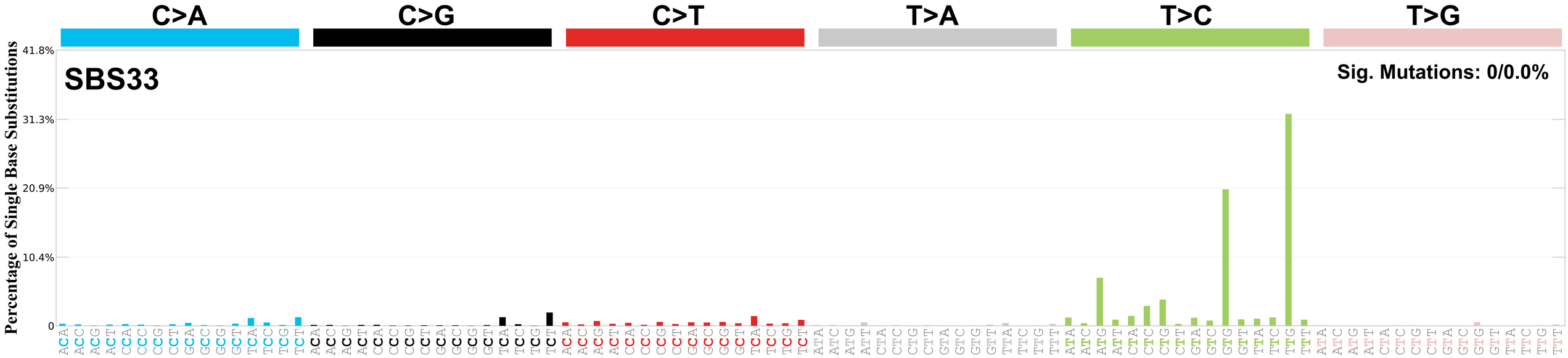
C>A
C>G
C>T
T>A
T>C
T>G
SBS33
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
41.8%
31.3%
20.9%
10.4%
0
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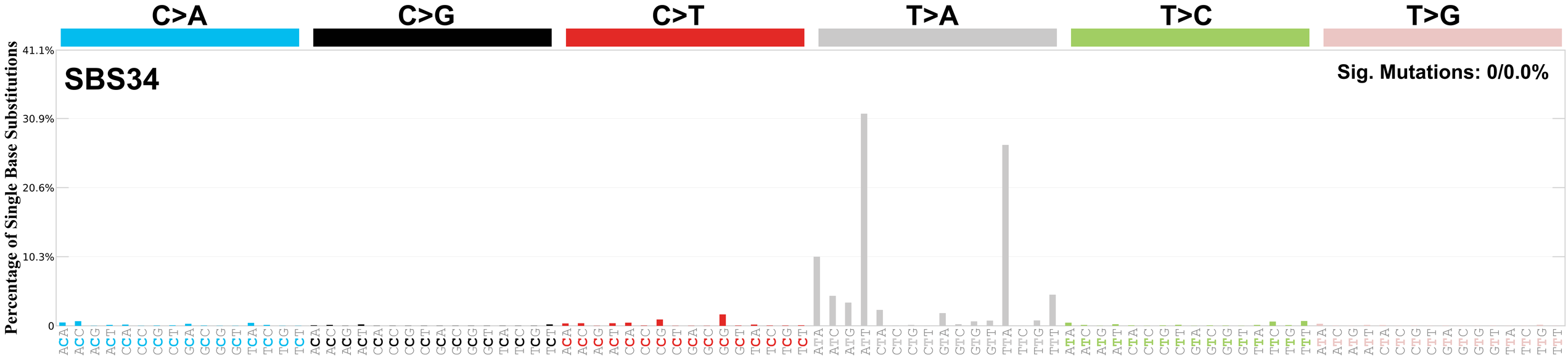
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C>G
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T>G
SBS34
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Percentage of Single Base Substitutions
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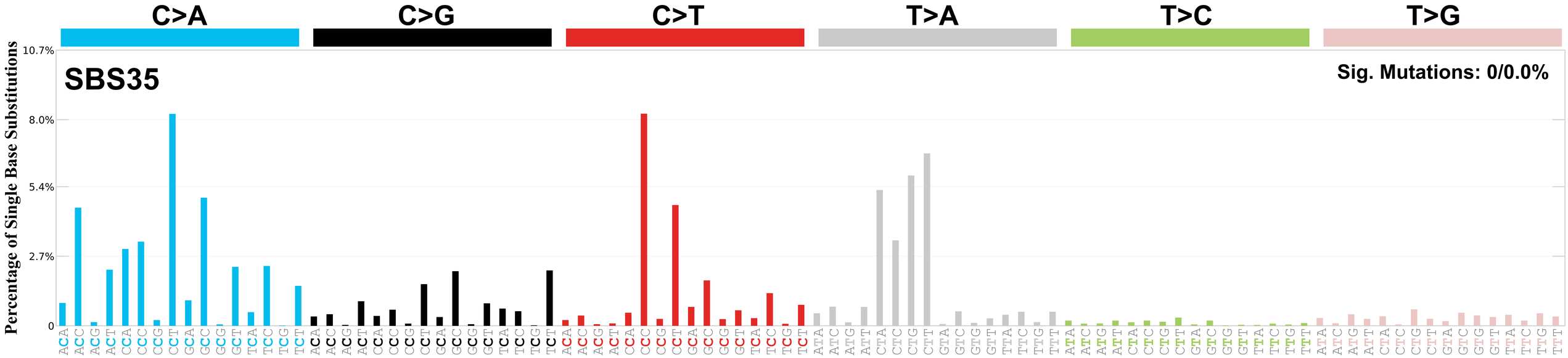
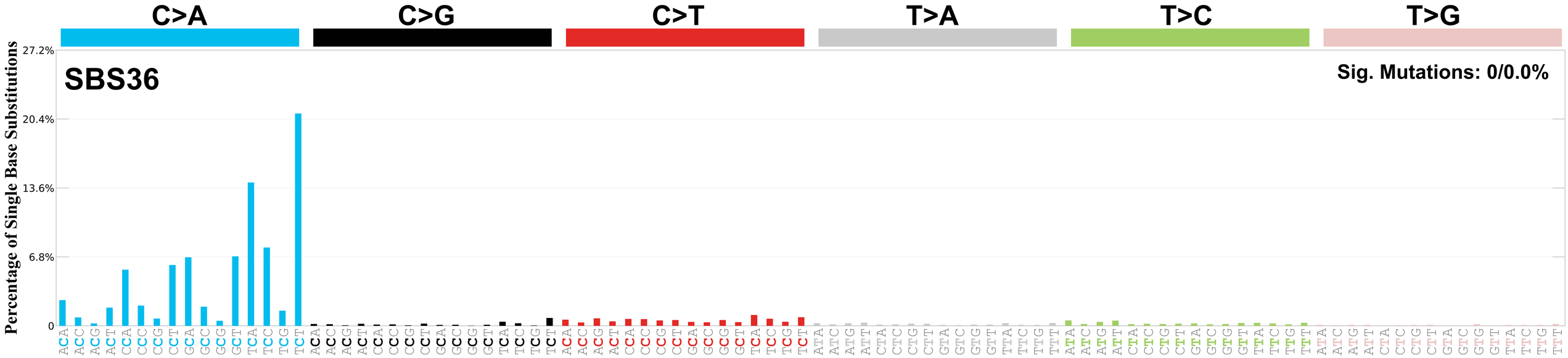
20.6%
10.3%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT


C>A
C>G
C>T
T>A
T>C
T>G
SBS35
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
10.7%
8.0%
5.4%
2.7%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS36
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
27.2%
20.4%
13.6%
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
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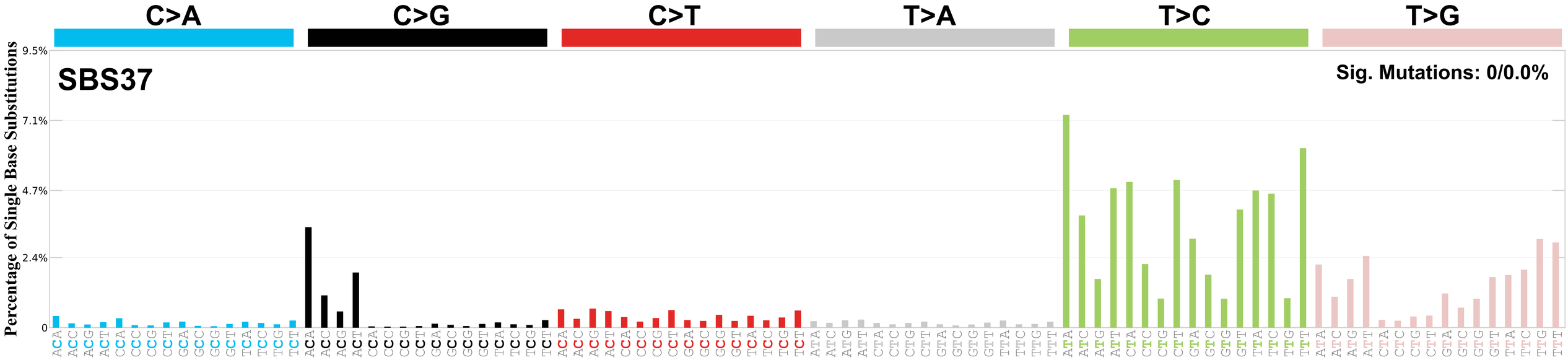
C>A
C>G
C>T
T>A
T>C
T>G
SBS37
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
9.5%
7.1%
4.7%
2.4%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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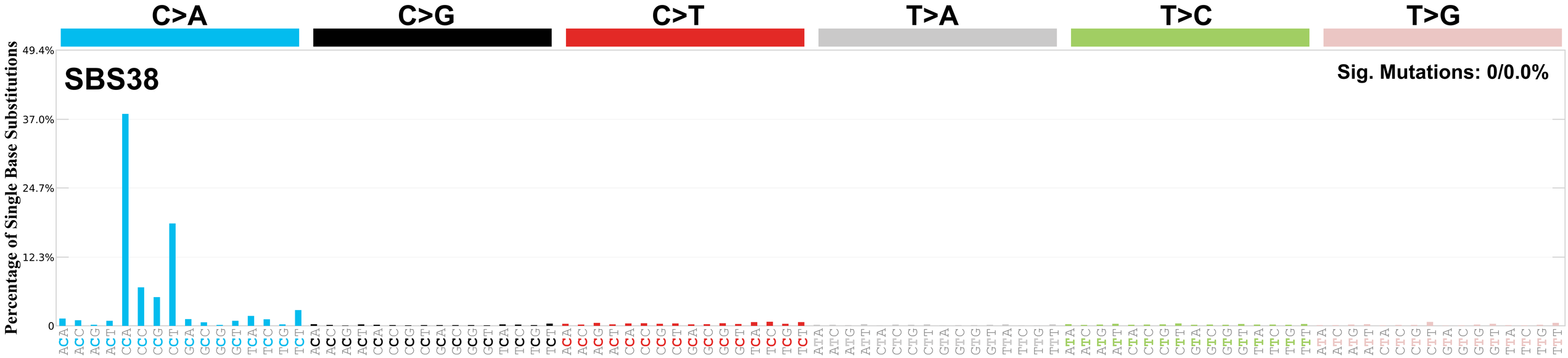
C>A
C>G
C>T
T>A
T>C
T>G
SBS38
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
49.4%
37.0%
24.7%
12.3%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC 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
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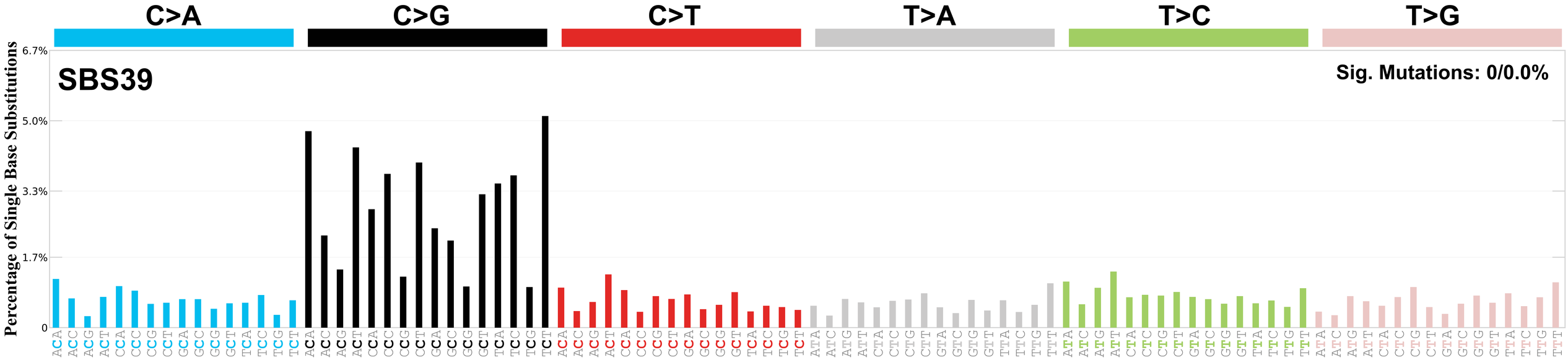
C>A
C>G
C>T
T>A
T>C
T>G
SBS39
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
6.7%
5.0%
3.3%
1.7%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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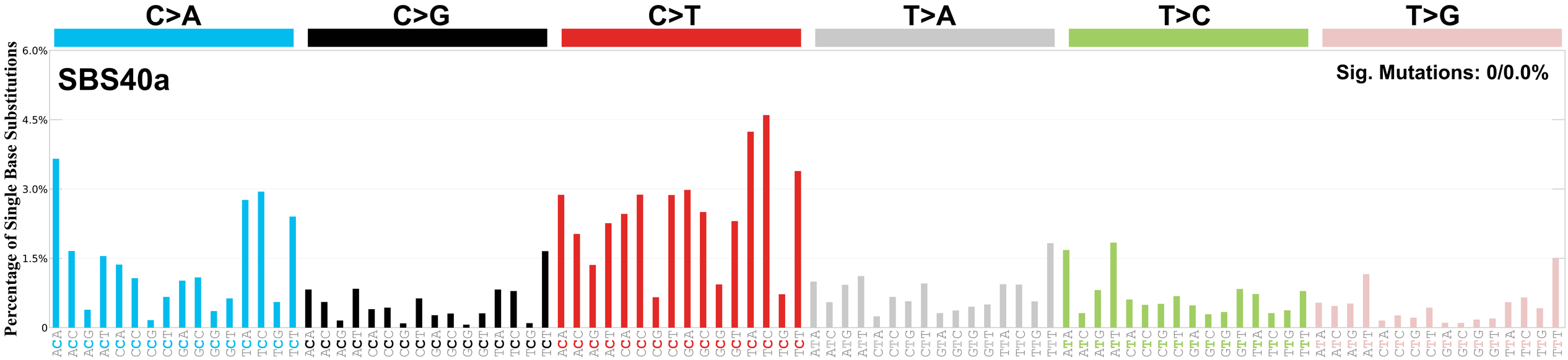
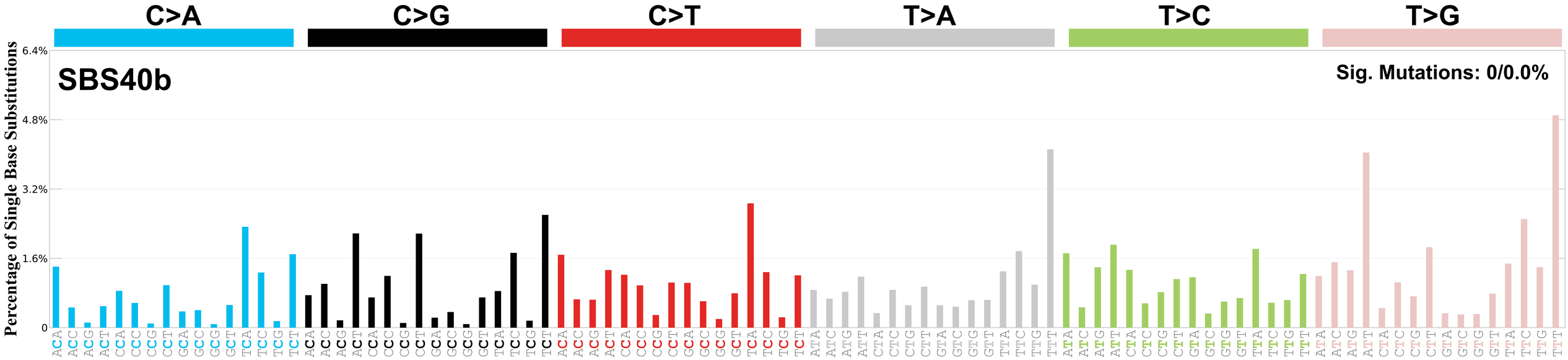

C>A
C>G
C>T
T>A
T>C
T>G
SBS40a
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
6.0%
4.5%
3.0%
1.5%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT 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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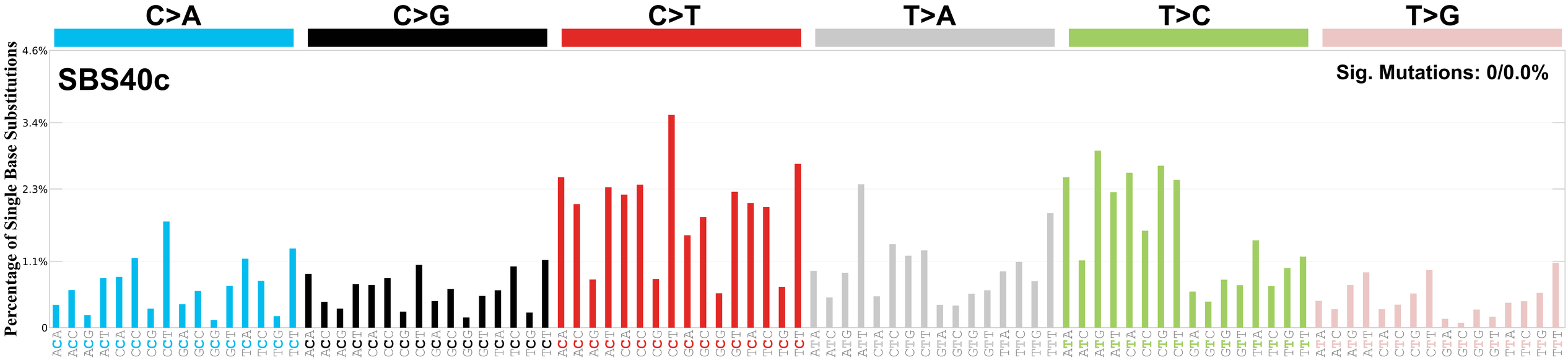
C>G
C>T
T>A
T>C
T>G
SBS40b
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
6.4%
4.8%
3.2%
1.6%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT 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
SBS40c
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
4.6%
3.4%
2.3%
1.1%
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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ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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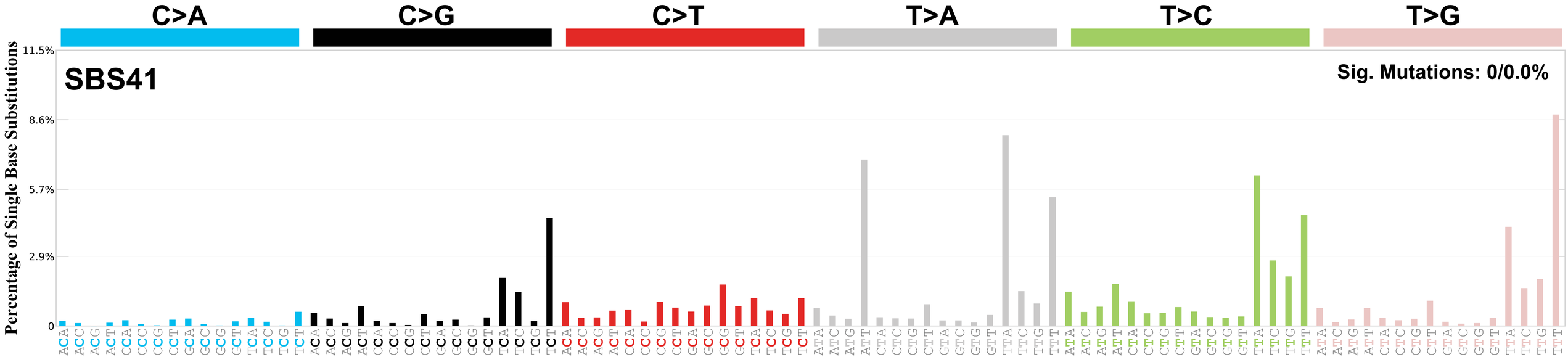
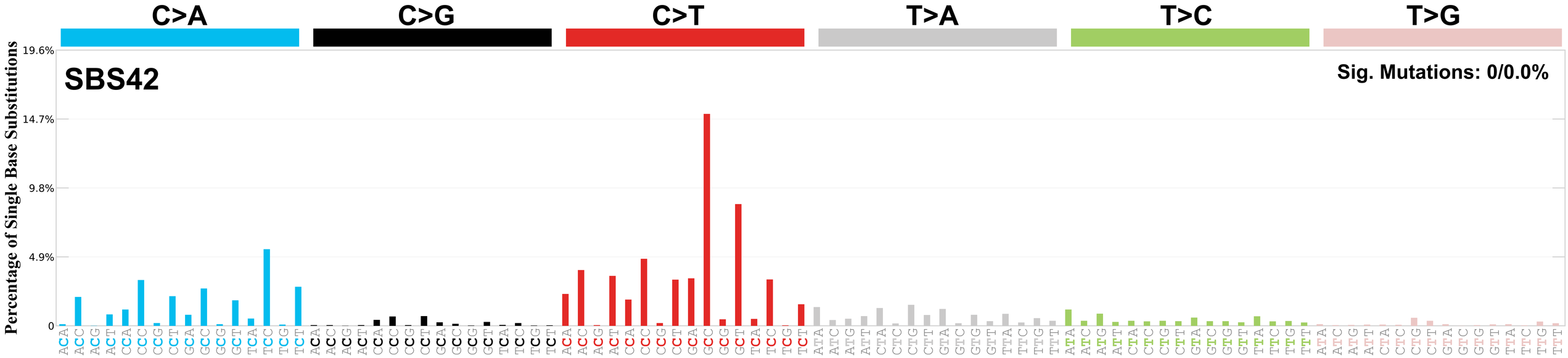

C>A
C>G
C>T
T>A
T>C
T>G
SBS41
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
11.5%
8.6%
5.7%
2.9%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG 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 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
SBS42
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
19.6%
14.7%
9.8%
4.9%
0
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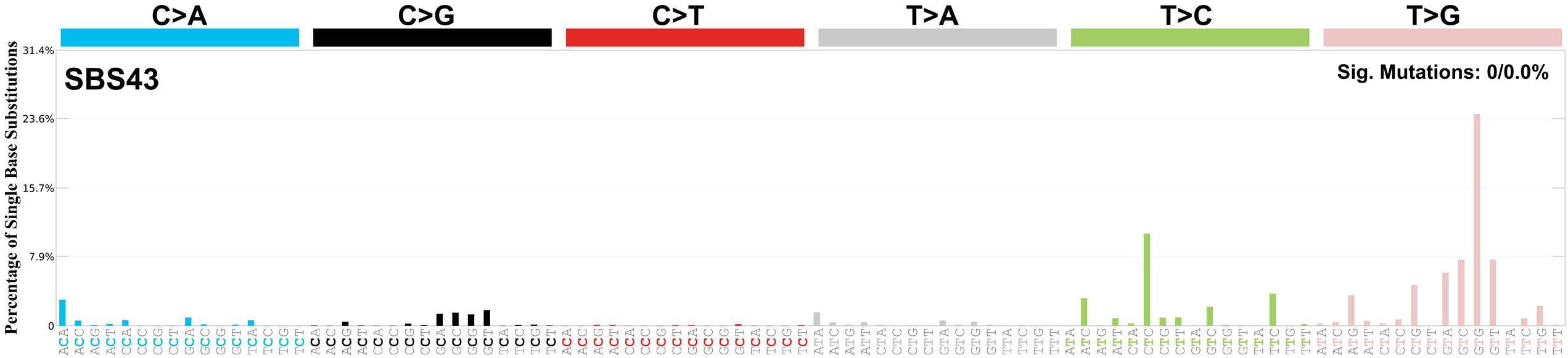
C>A
C>G
C>T
T>A
T>C
T>G
SBS43
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
31.4%
23.6%
15.7%
7.9%
0
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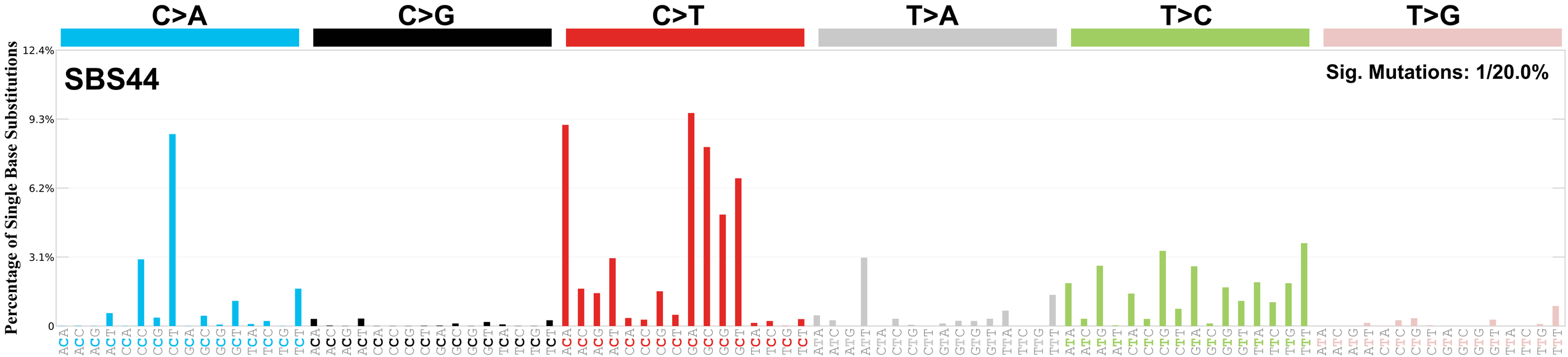
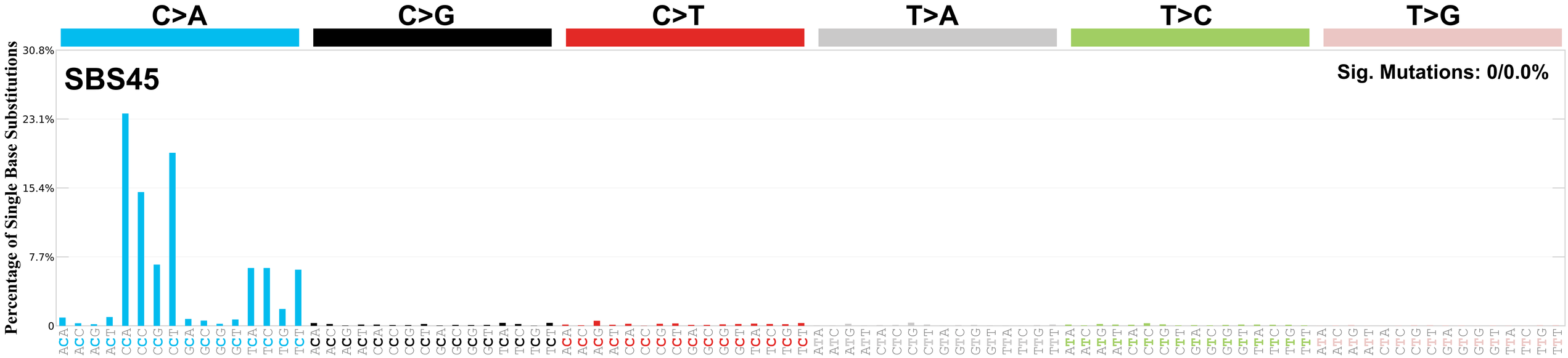

C>A
C>G
C>T
T>A
T>C
T>G
SBS44
Sig. Mutations: 1/20.0%
Percentage of Single Base Substitutions
12.4%
9.3%
6.2%
3.1%
0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C>T
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T>C
T>G
SBS45
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Percentage of Single Base Substitutions
30.8%
23.1%
15.4%
7.7%
0
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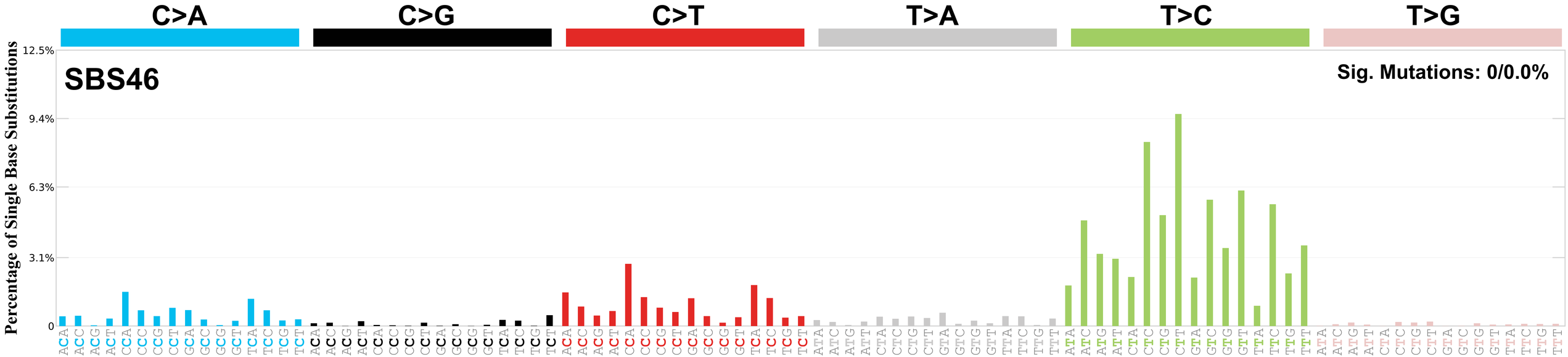
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T>G
SBS46
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Percentage of Single Base Substitutions
12.5%
9.4%
6.3%
3.1%
0
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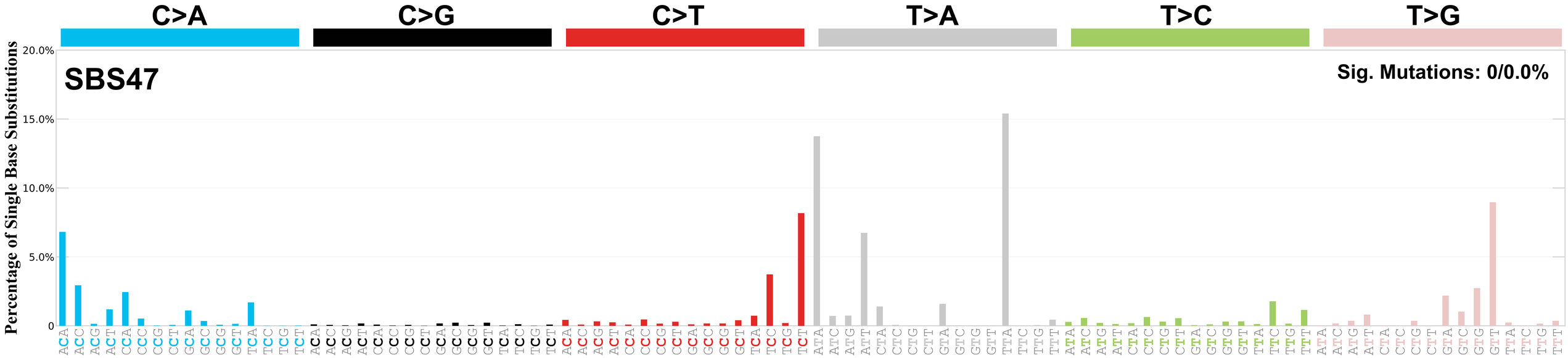
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C>T
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T>C
T>G
SBS47
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
20.0%
15.0%
10.0%
5.0%
0
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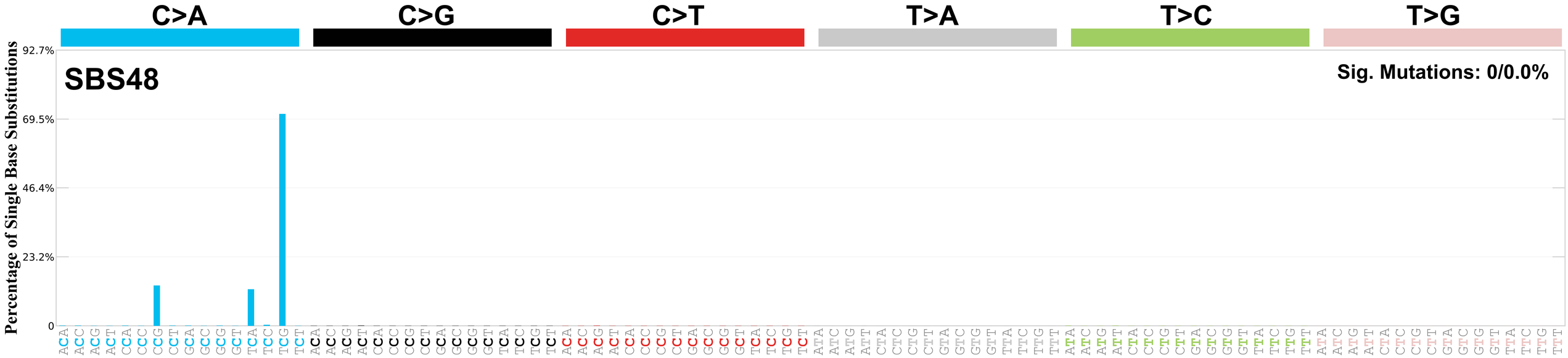
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T>C
T>G
SBS48
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
92.7%
69.5%
46.4%
23.2%
0
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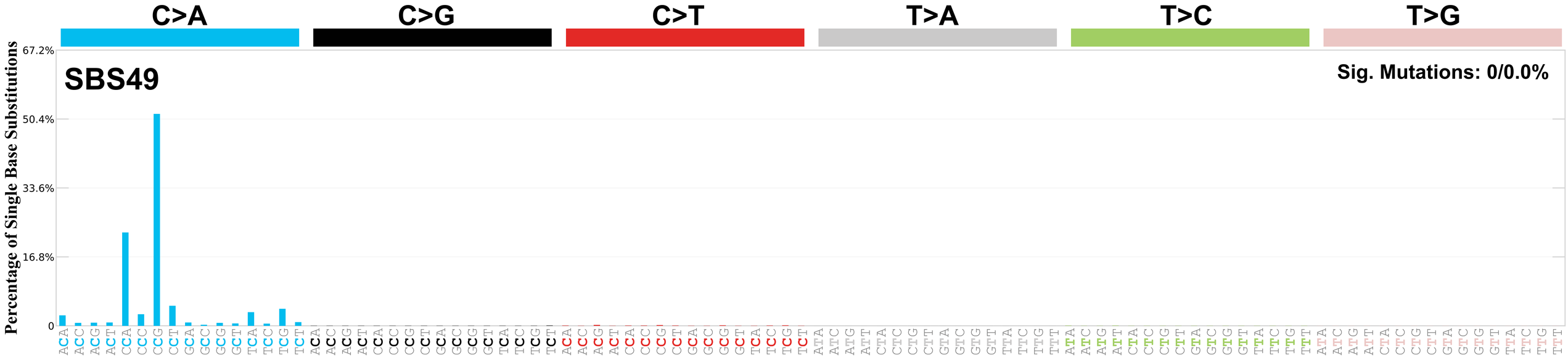
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C>G
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T>C
T>G
SBS49
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
67.2%
50.4%
33.6%
16.8%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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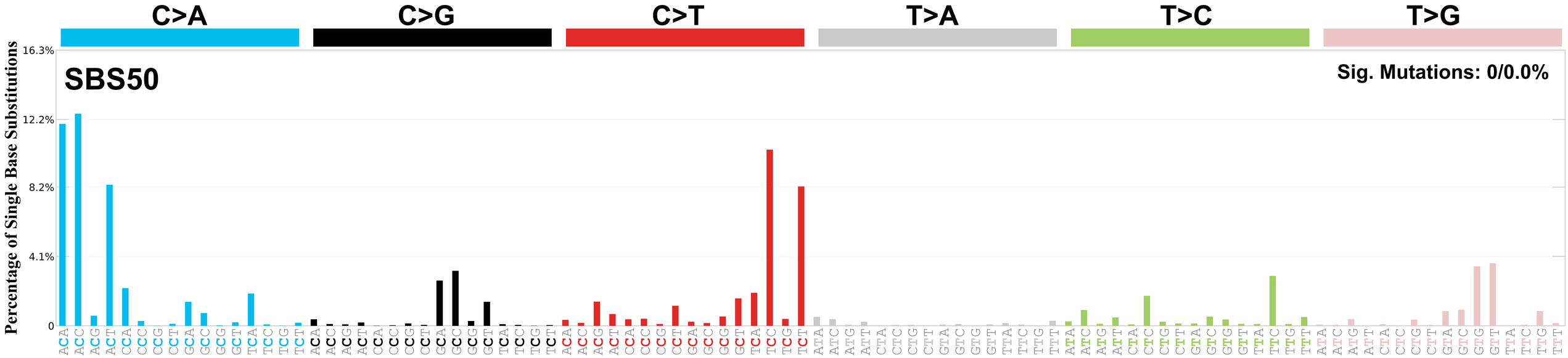
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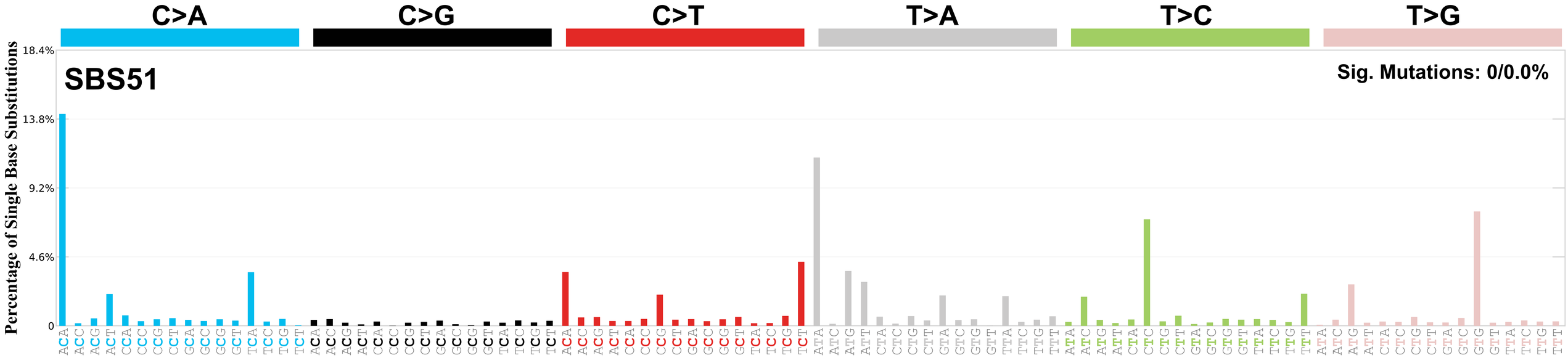
T>C
T>G
SBS50
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
16.3%
12.2%
8.2%
4.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ATA ATC 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
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T>C
T>G
SBS51
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
18.4%
13.8%
9.2%
4.6%
0
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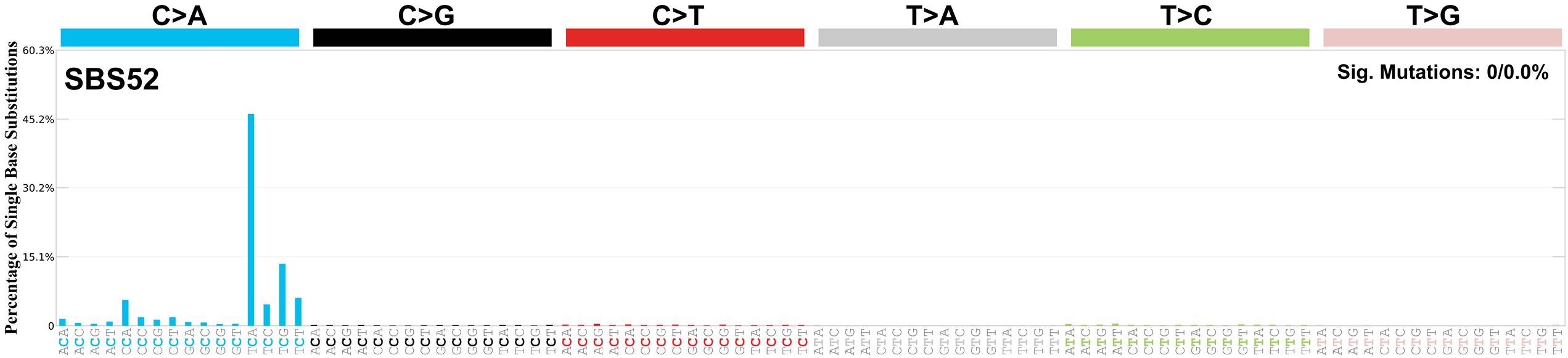
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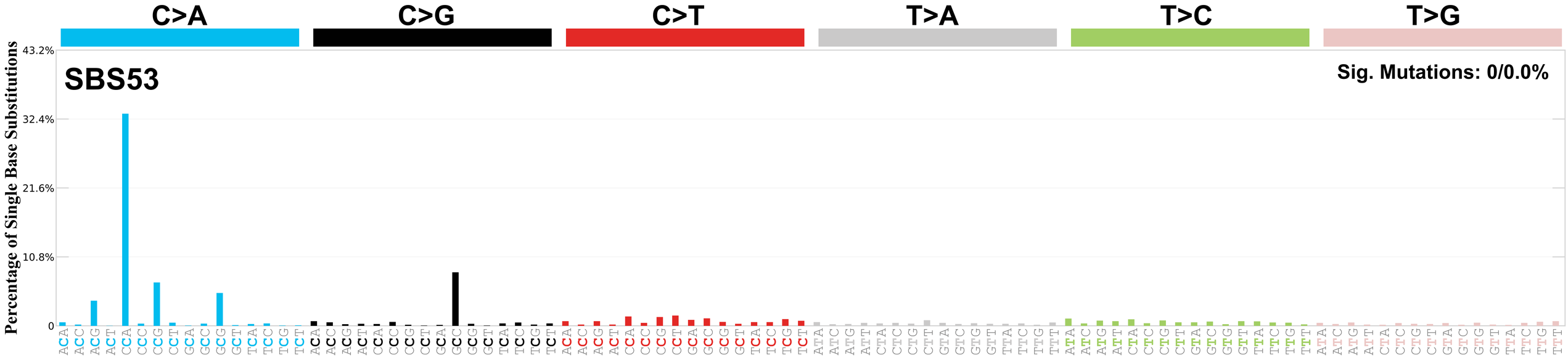
C>G
C>T
T>A
T>C
T>G
SBS52
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
60.3%
45.2%
30.2%
15.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG 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
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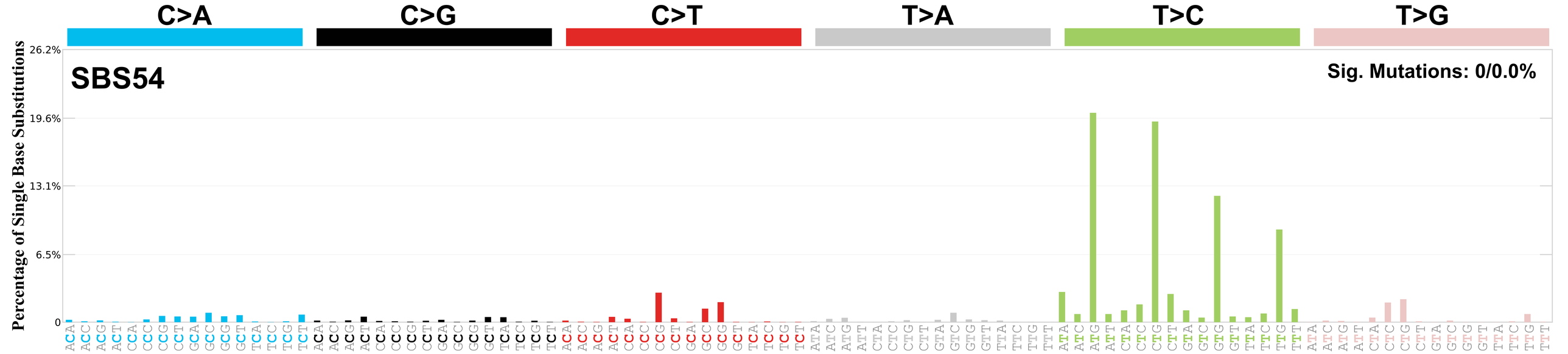
T>G
SBS53
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
43.2%
32.4%
21.6%
10.8%
0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C>G
C>T
T>A
T>C
T>G
SBS54
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
26.2%
19.6%
13.1%
6.5%
0
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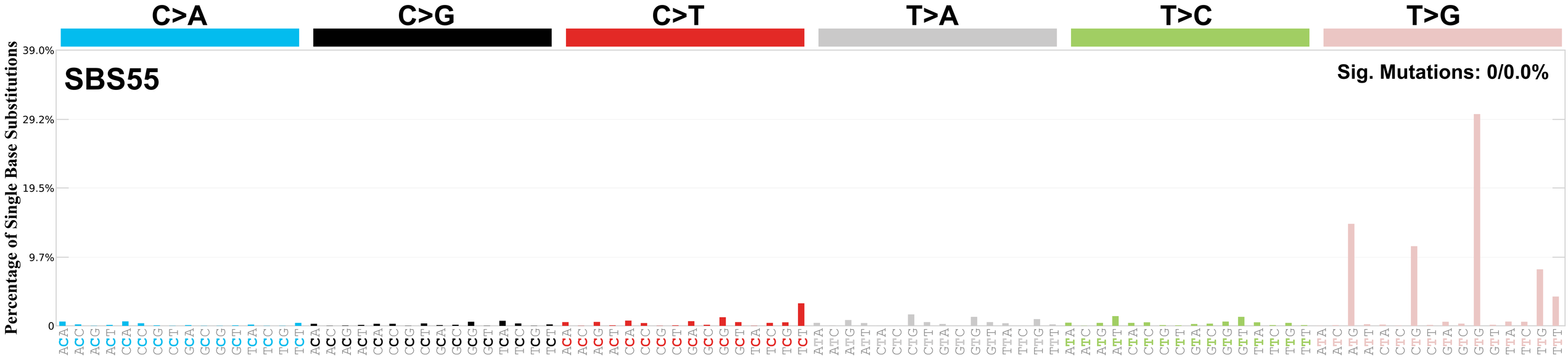
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C>G
C>T
T>A
T>C
T>G
SBS55
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
39.0%
29.2%
19.5%
9.7%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC 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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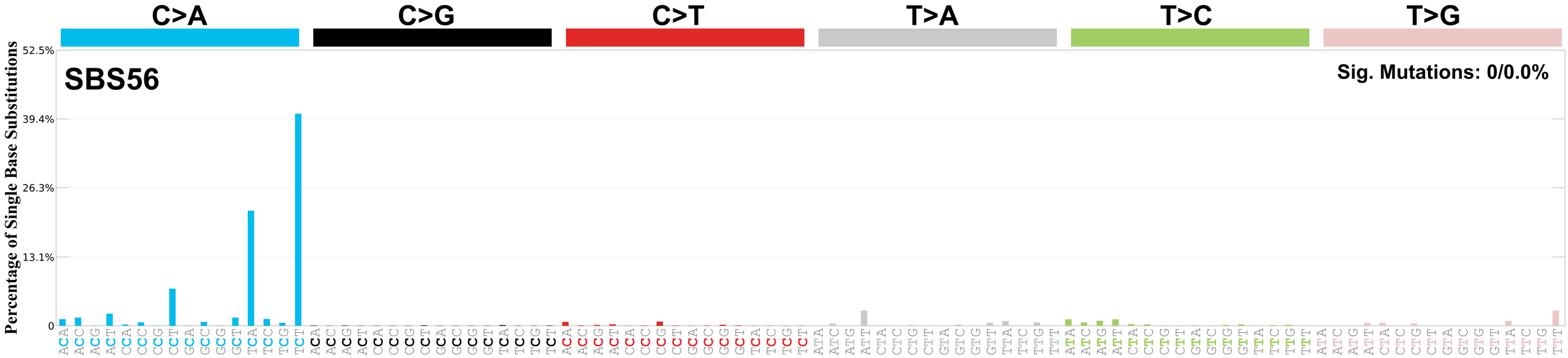
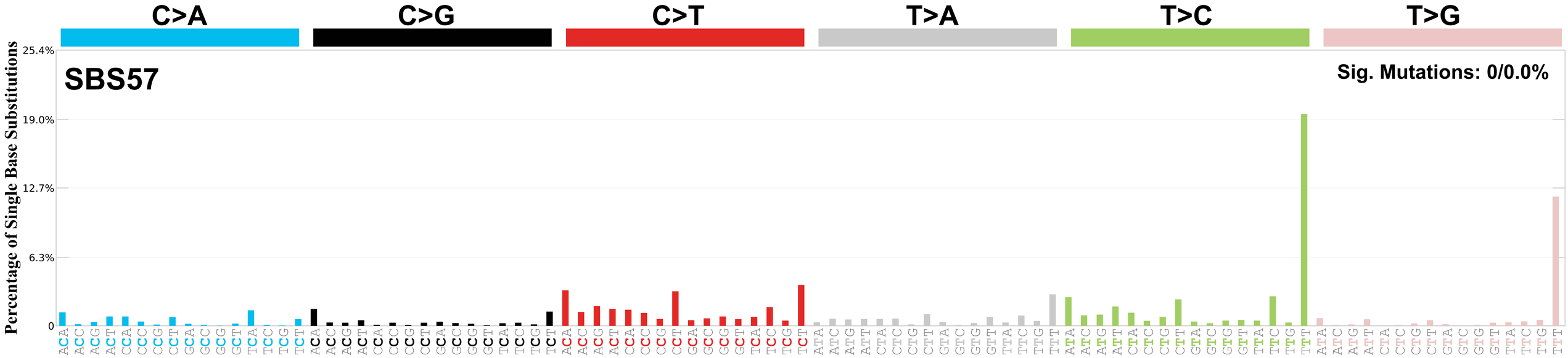

C>A
C>G
C>T
T>A
T>C
T>G
SBS56
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
52.5%
39.4%
26.3%
13.1%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS57
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
25.4%
19.0%
12.7%
6.3%
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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ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT
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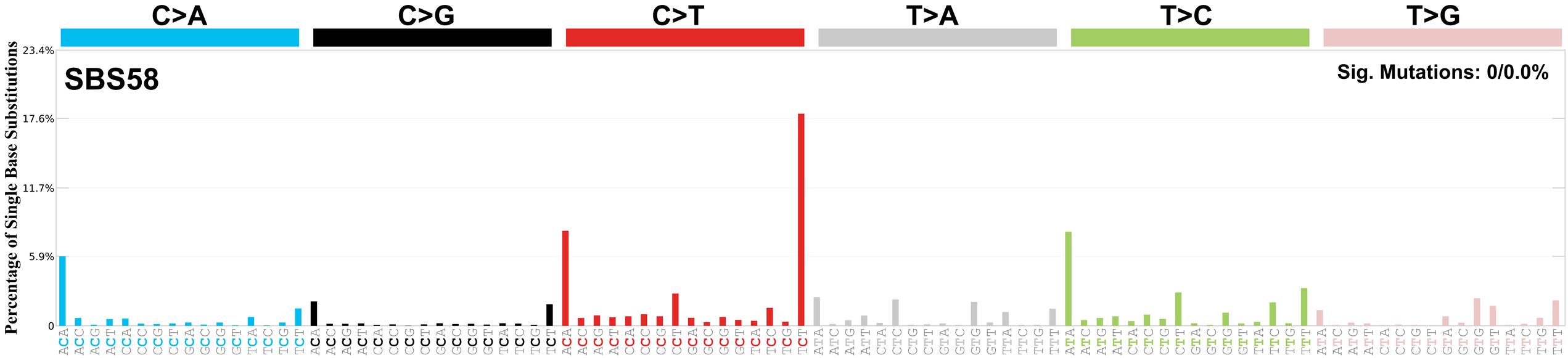
C>A
C>G
C>T
T>A
T>C
T>G
SBS58
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
23.4%
17.6%
11.7%
5.9%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC 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
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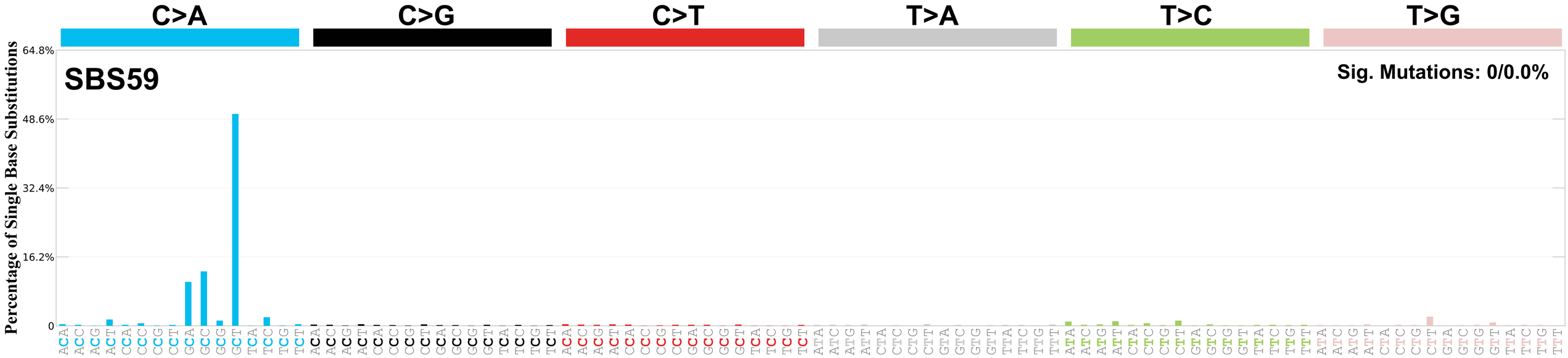
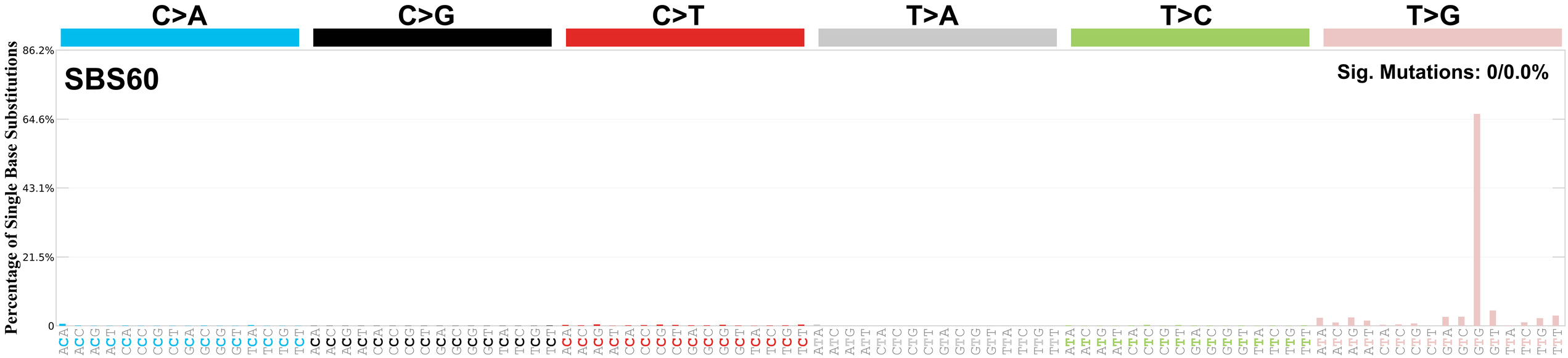

C>A
C>G
C>T
T>A
T>C
T>G
SBS59
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
64.8%
48.6%
32.4%
16.2%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC 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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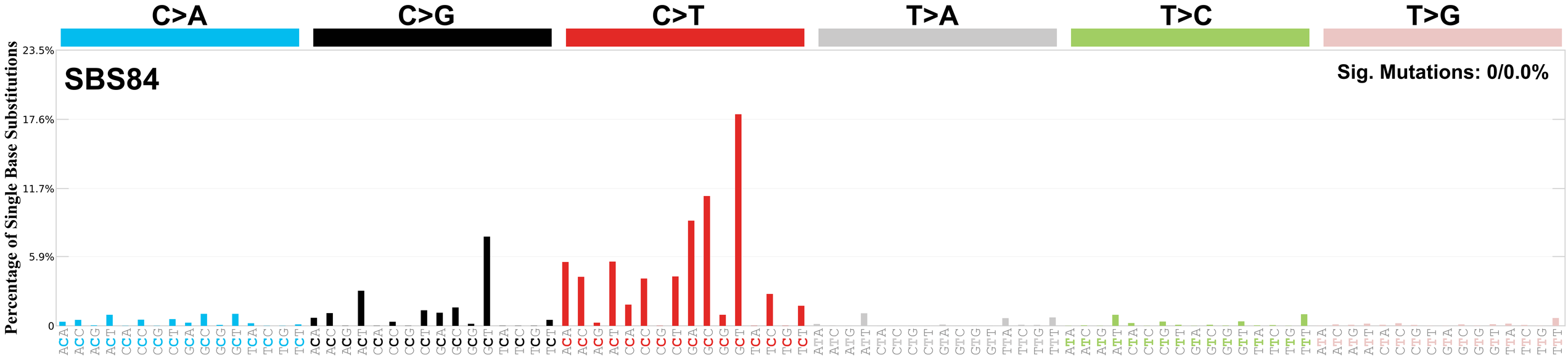
T>C
T>G
SBS60
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
86.2%
64.6%
43.1%
21.5%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ATA ATC 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 ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT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C>G
C>T
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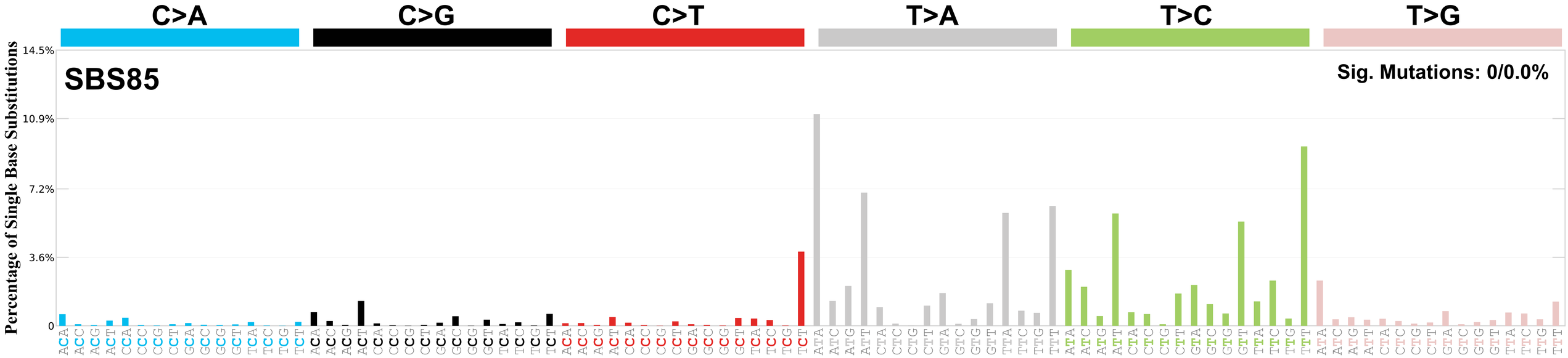
T>C
T>G
SBS84
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
23.5%
17.6%
11.7%
5.9%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ATA ATC 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 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
SBS85
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
14.5%
10.9%
7.2%
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
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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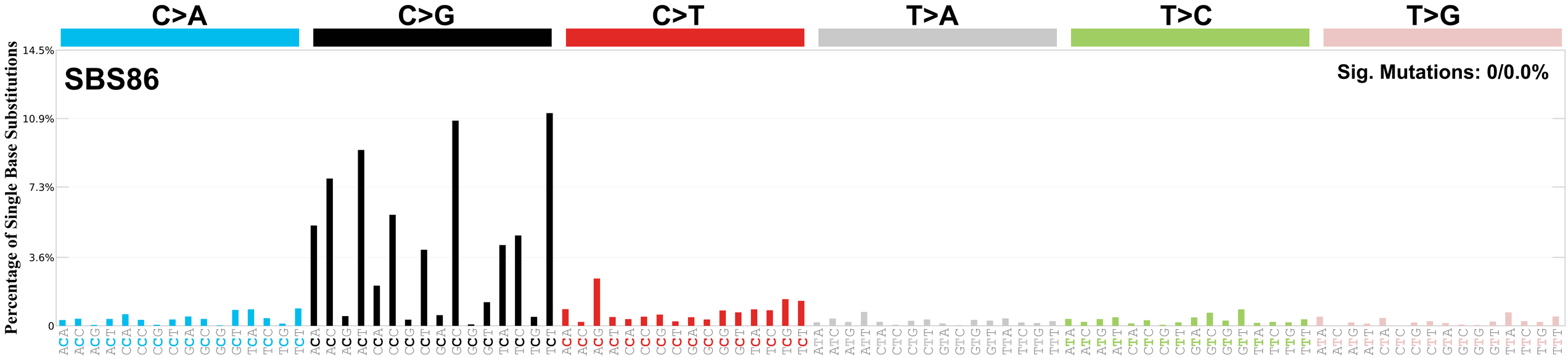
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C>G
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T>C
T>G
SBS86
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
14.5%
10.9%
7.3%
3.6%
0
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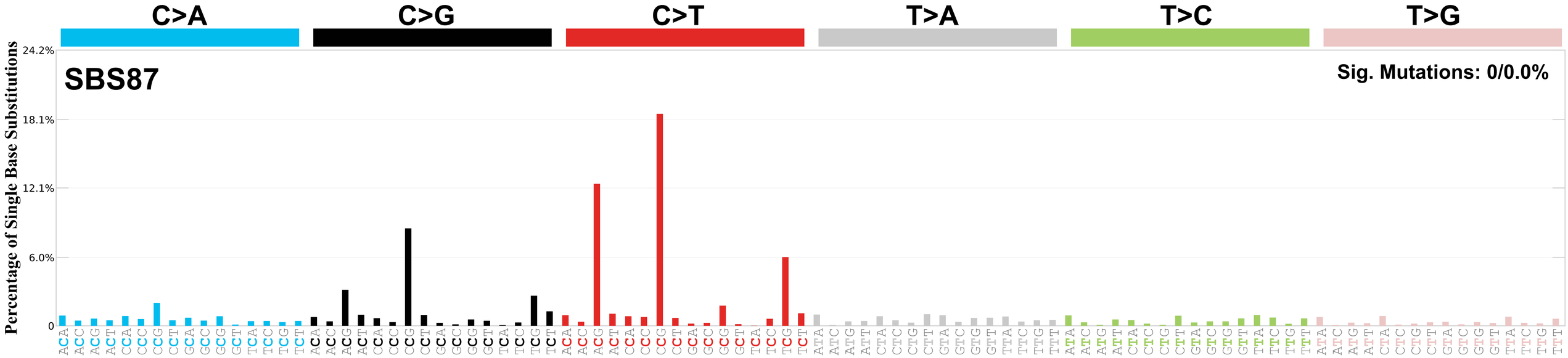
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C>G
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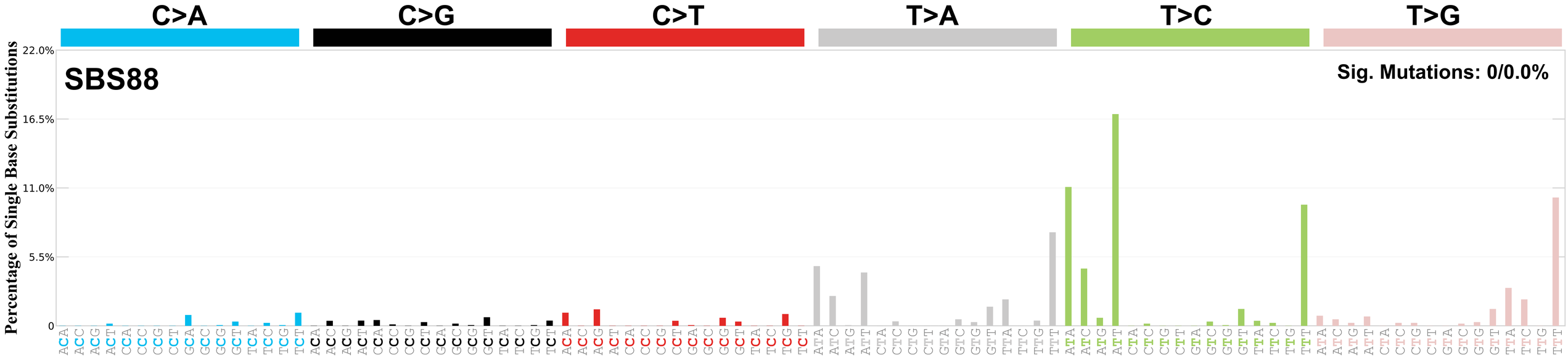
T>A
T>C
T>G
SBS87
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
24.2%
18.1%
12.1%
6.0%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ATA 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


C>A
C>G
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T>A
T>C
T>G
SBS88
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
22.0%
16.5%
11.0%
5.5%
0
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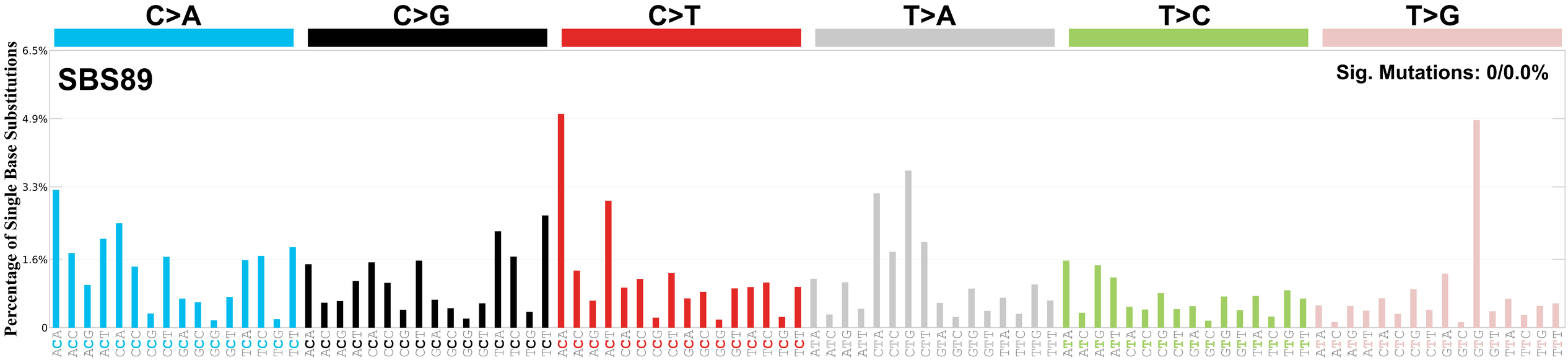
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C>T
T>A
T>C
T>G
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Percentage of Single Base Substitutions
6.5%
4.9%
3.3%
1.6%
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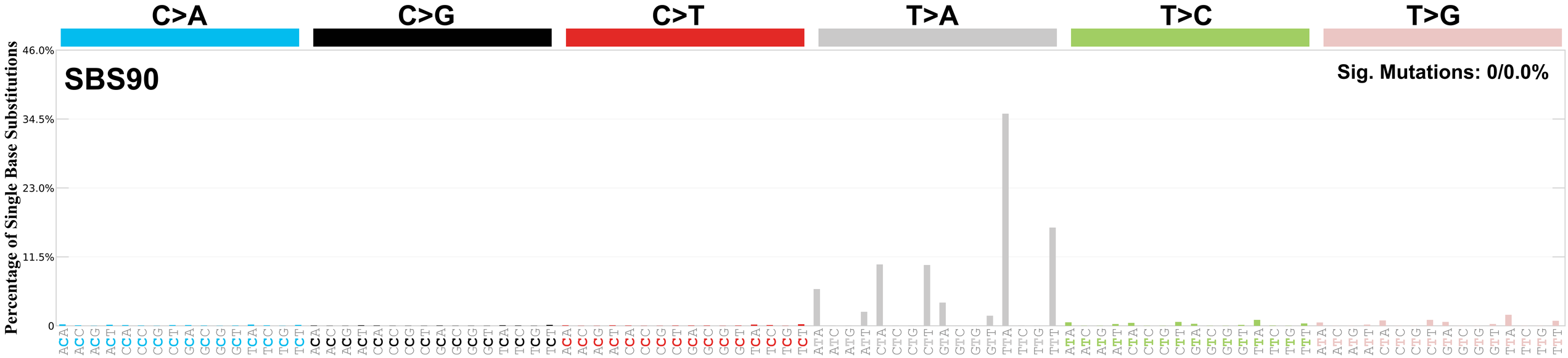
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T>C
T>G
SBS90
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Percentage of Single Base Substitutions
46.0%
34.5%
23.0%
11.5%
0
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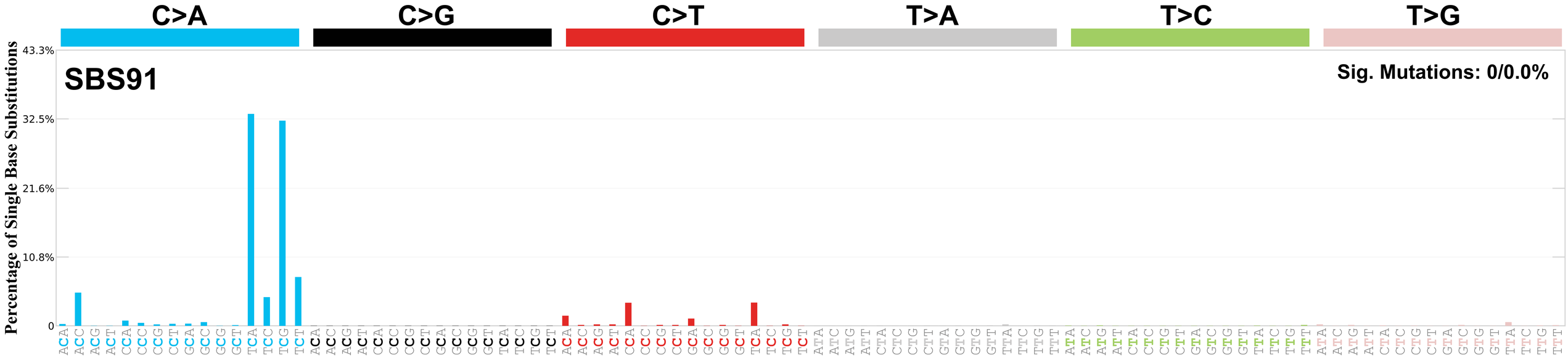
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C>G
C>T
T>A
T>C
T>G
SBS91
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
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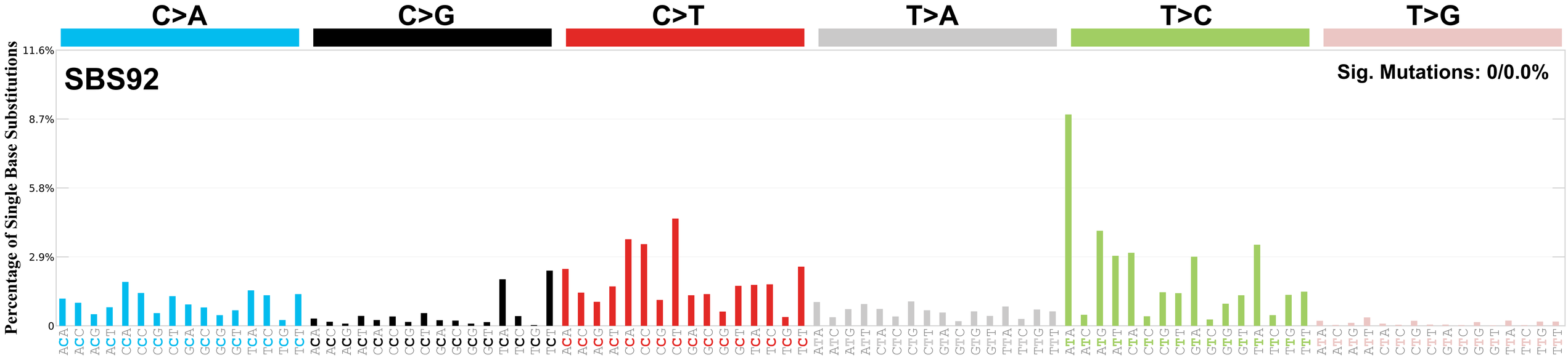
21.6%
10.8%
0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T>G
SBS92
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
11.6%
8.7%
5.8%
2.9%
0
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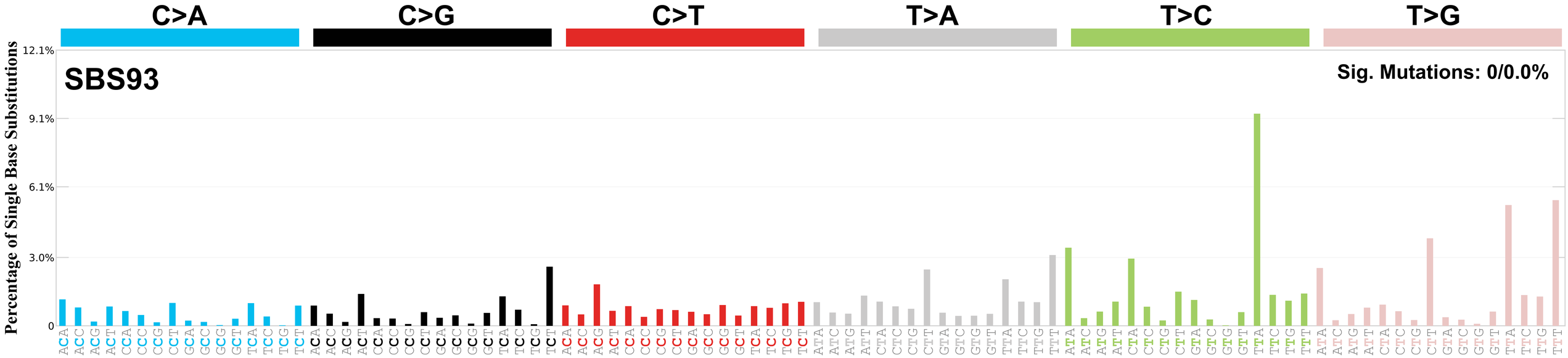
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T>C
T>G
SBS93
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
12.1%
9.1%
6.1%
3.0%
0
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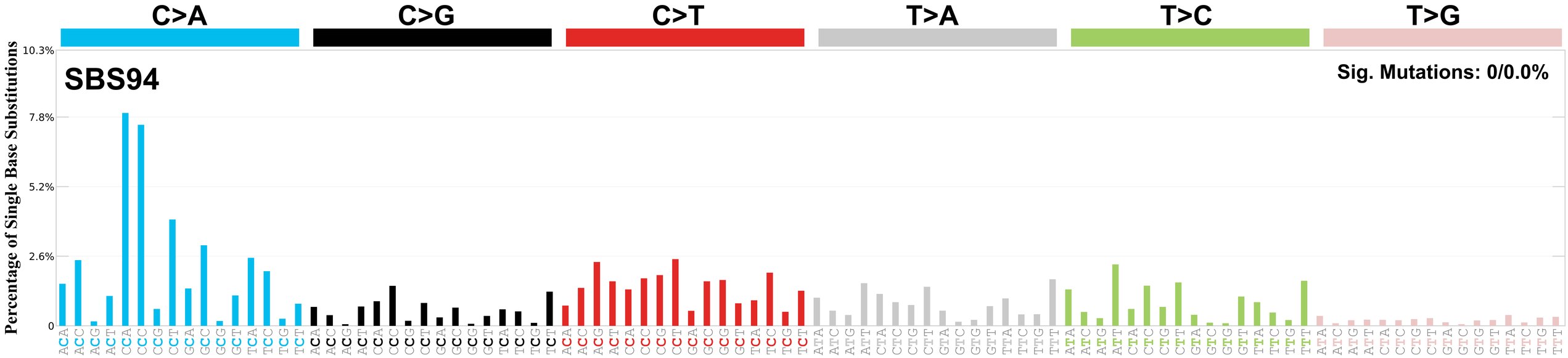
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C>T
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T>C
T>G
SBS94
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
10.3%
7.8%
5.2%
2.6%
0
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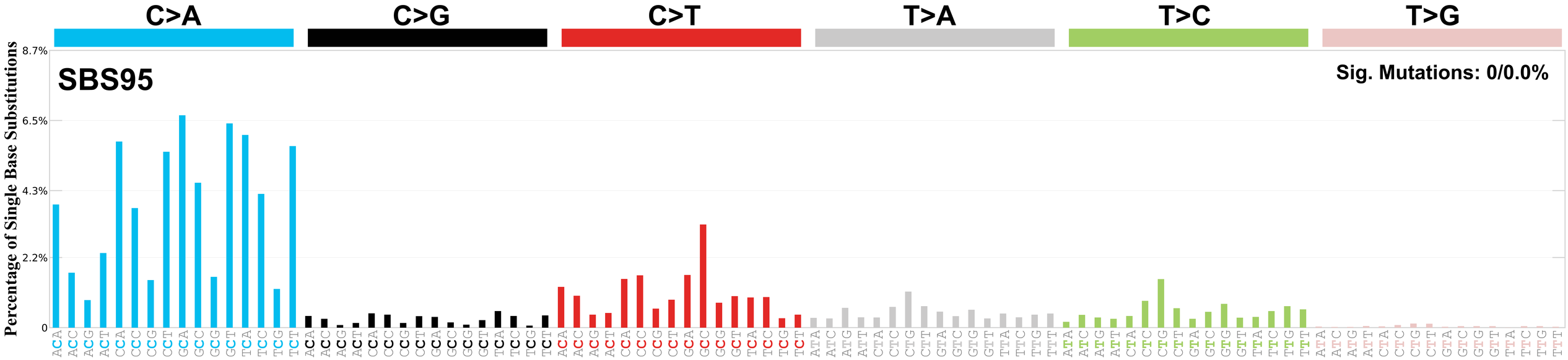
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C>G
C>T
T>A
T>C
T>G
SBS95
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
8.7%
6.5%
4.3%
2.2%
0
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ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
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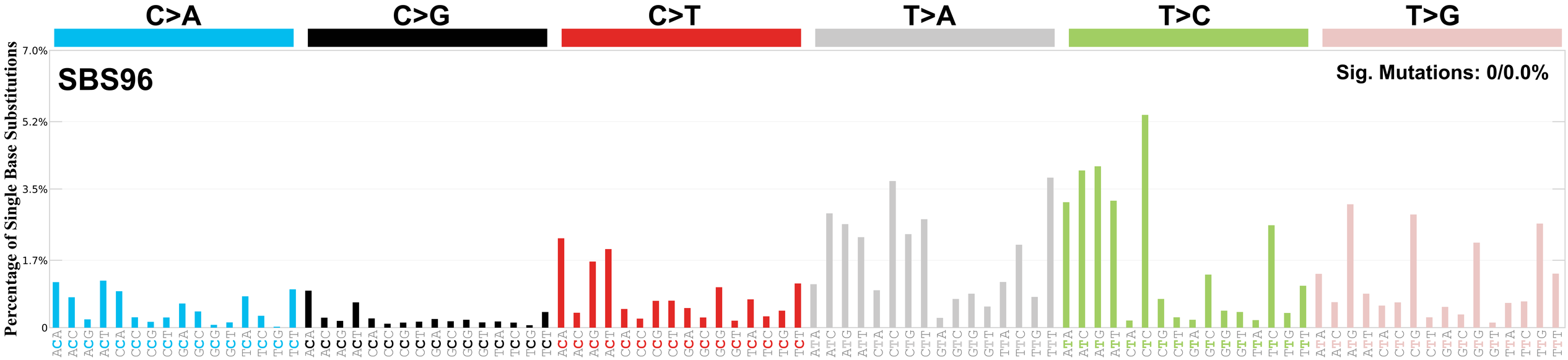
C>A
C>G
C>T
T>A
T>C
T>G
SBS96
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
7.0%
5.2%
3.5%
1.7%
0
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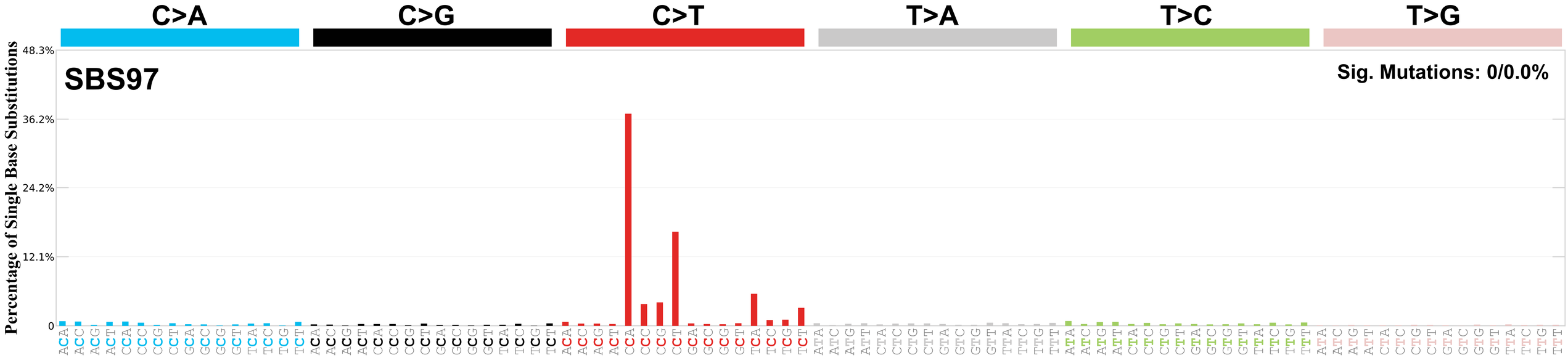
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C>G
C>T
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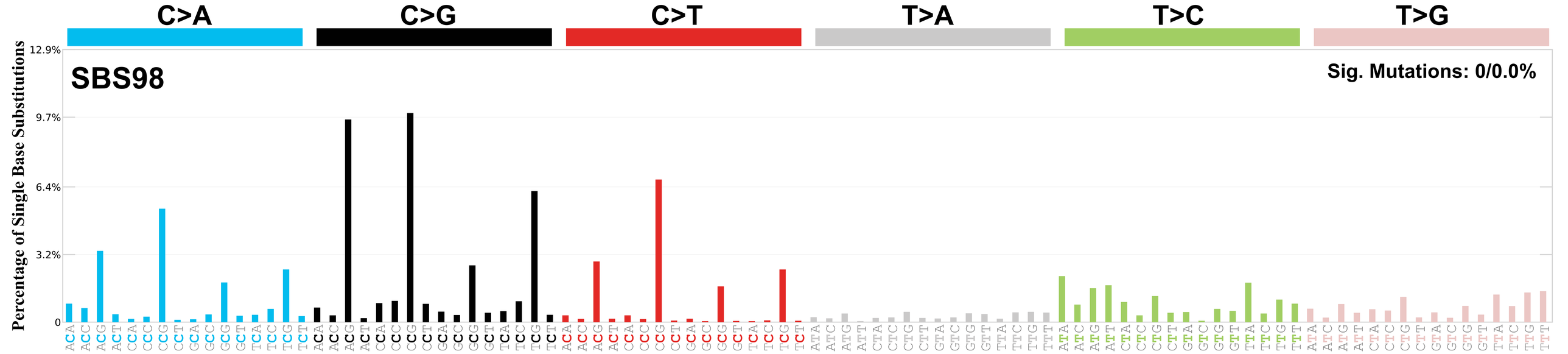
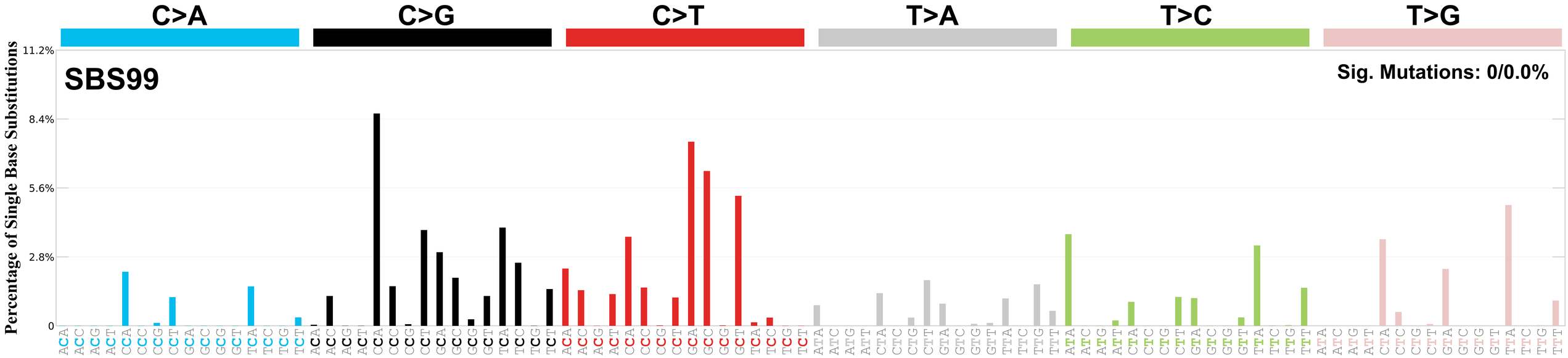
T>G
SBS97
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
48.3%
36.2%
24.2%
12.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT
ATA ATC ATG 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
SBS98
Sig. Mutations: 0/0.0%
Percentage of Single Base Substitutions
12.9%
9.7%
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
SBS99
Sig. Mutations: 0/0.0%
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