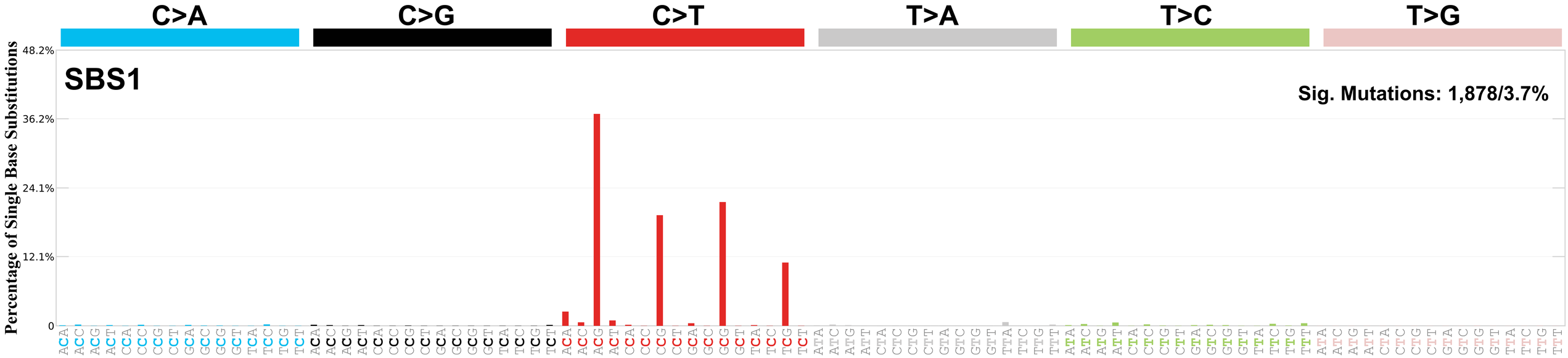
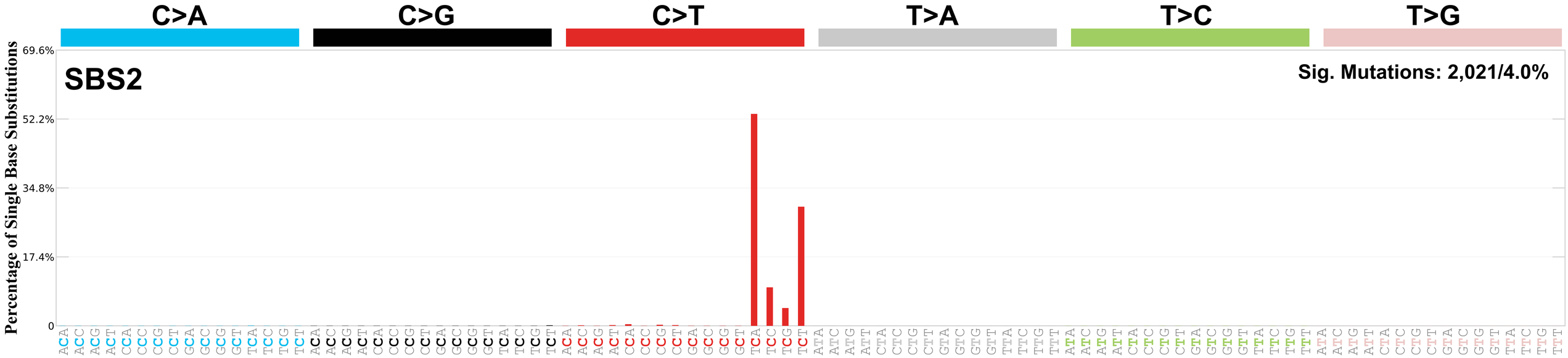
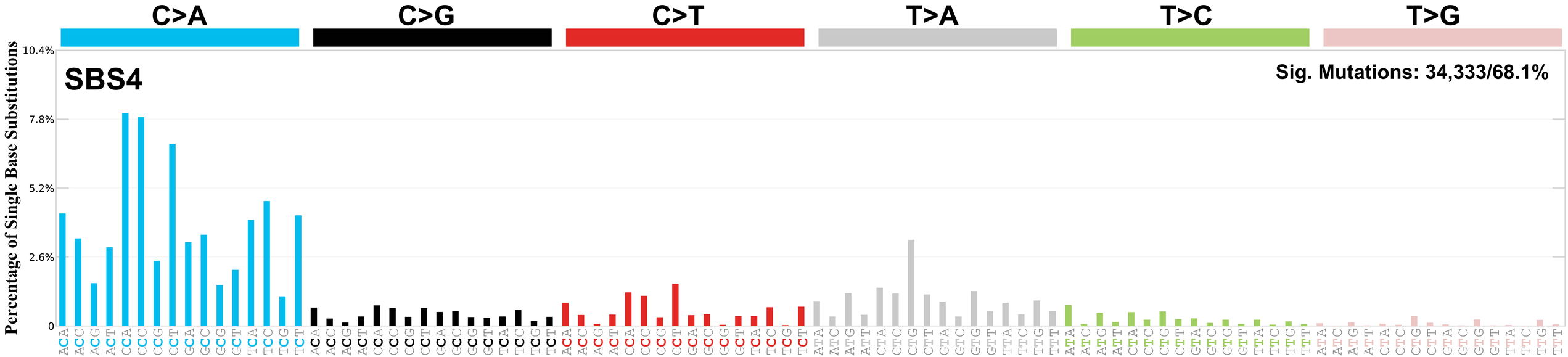
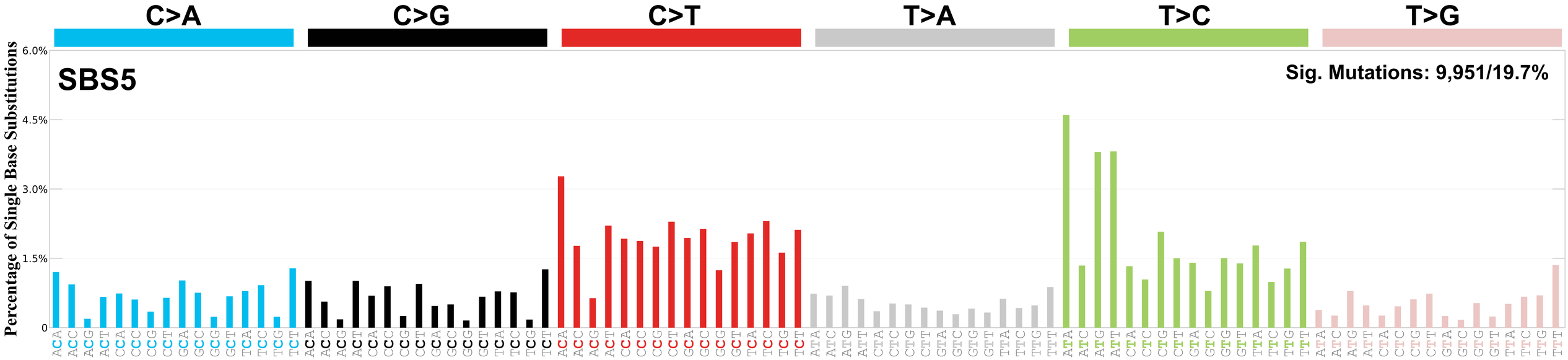
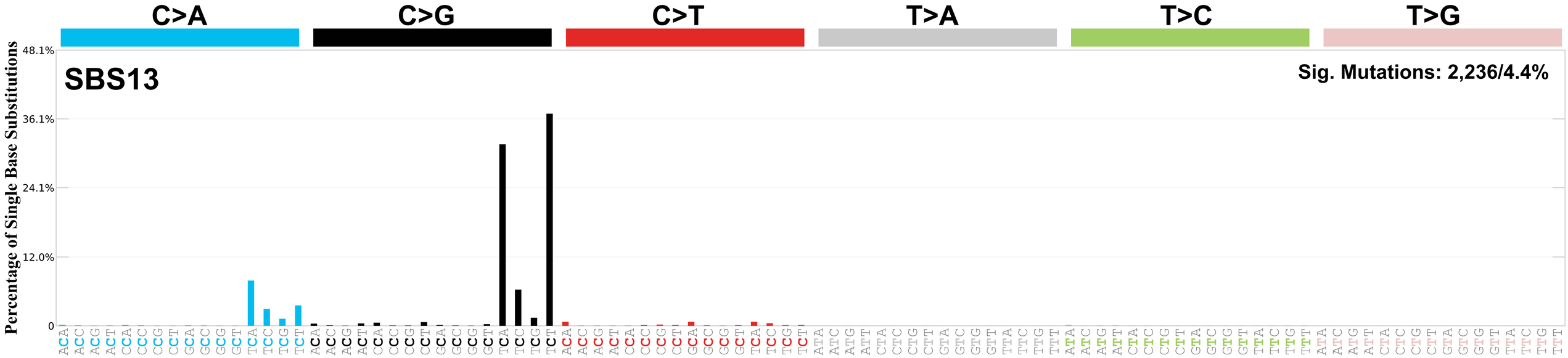

C>A
C>G
C>T
T>A
T>C
T>G
SBS1
Sig. Mutations: 1,878/3.7%
Percentage of Single Base Substitutions
48.2%
36.2%
24.1%
12.1%
0
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA 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
SBS2
Sig. Mutations: 2,021/4.0%
Percentage of Single Base Substitutions
69.6%
52.2%
34.8%
17.4%
0


C>A
C>G
C>T
T>A
T>C
T>G
SBS4
Sig. Mutations: 34,333/68.1%
Percentage of Single Base Substitutions
10.4%
7.8%
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
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
SBS5
Sig. Mutations: 9,951/19.7%
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
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
SBS13
Sig. Mutations: 2,236/4.4%
Percentage of Single Base Substitutions
48.1%
36.1%
24.1%
12.0%
0