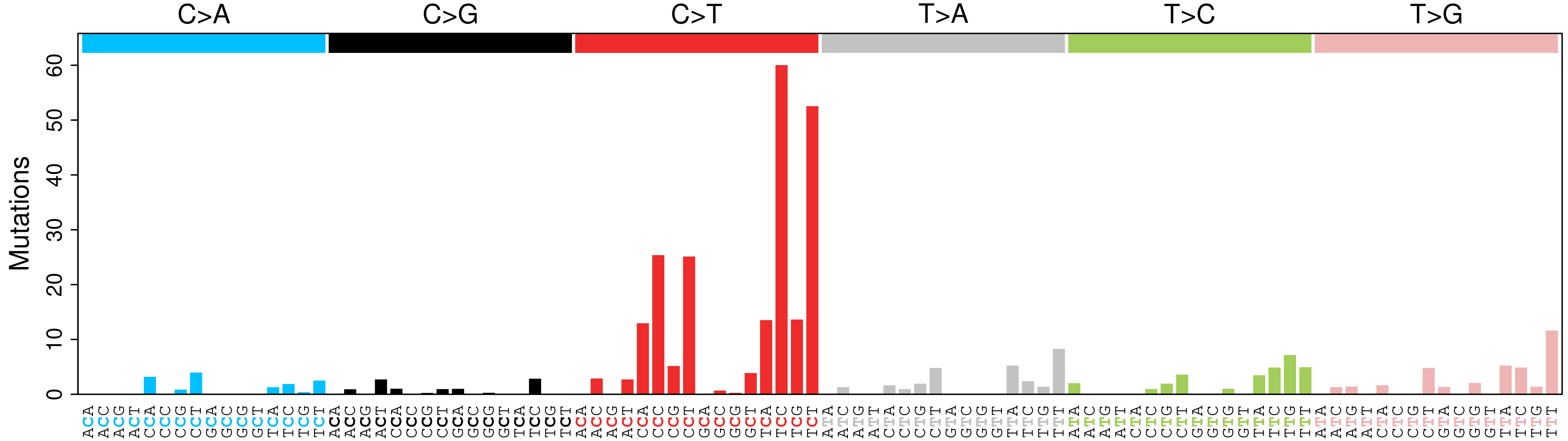
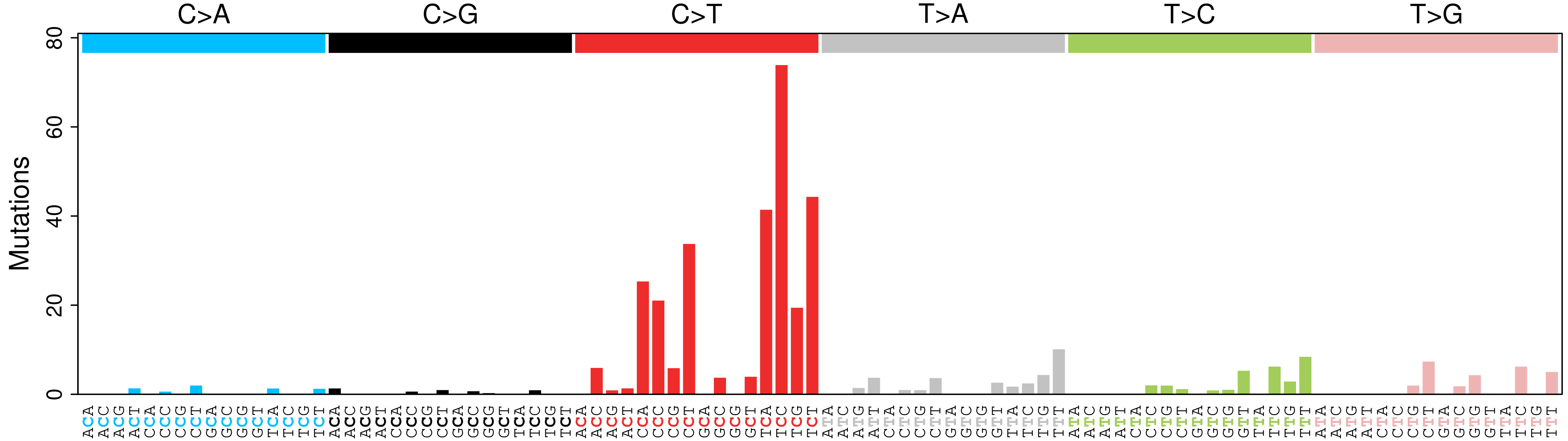


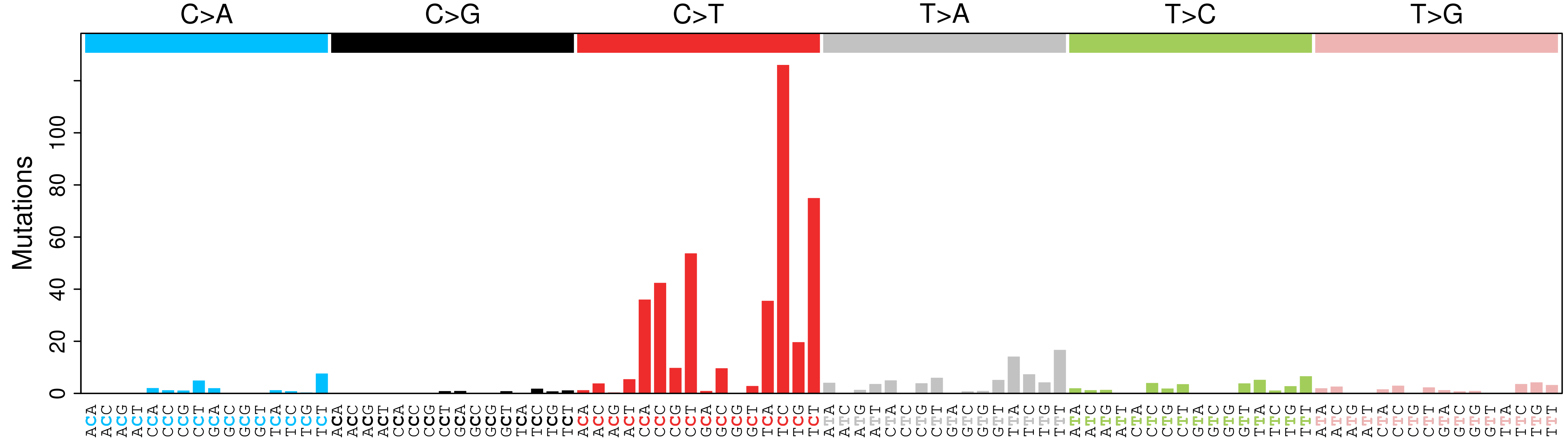
CATD251a (340 mutations)



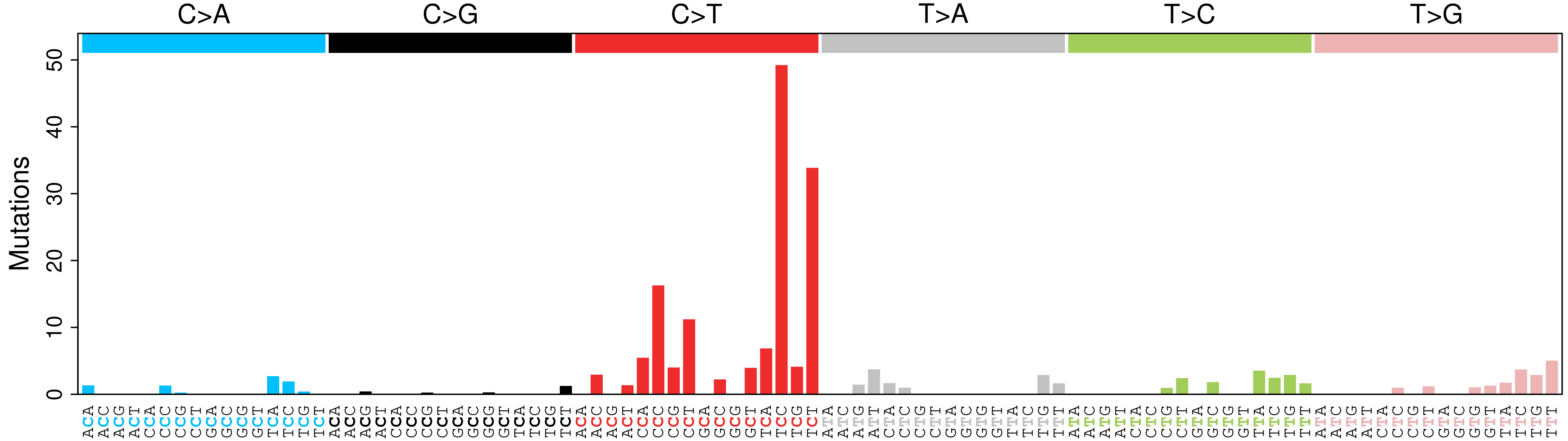
CATD0132a (384 mutations)



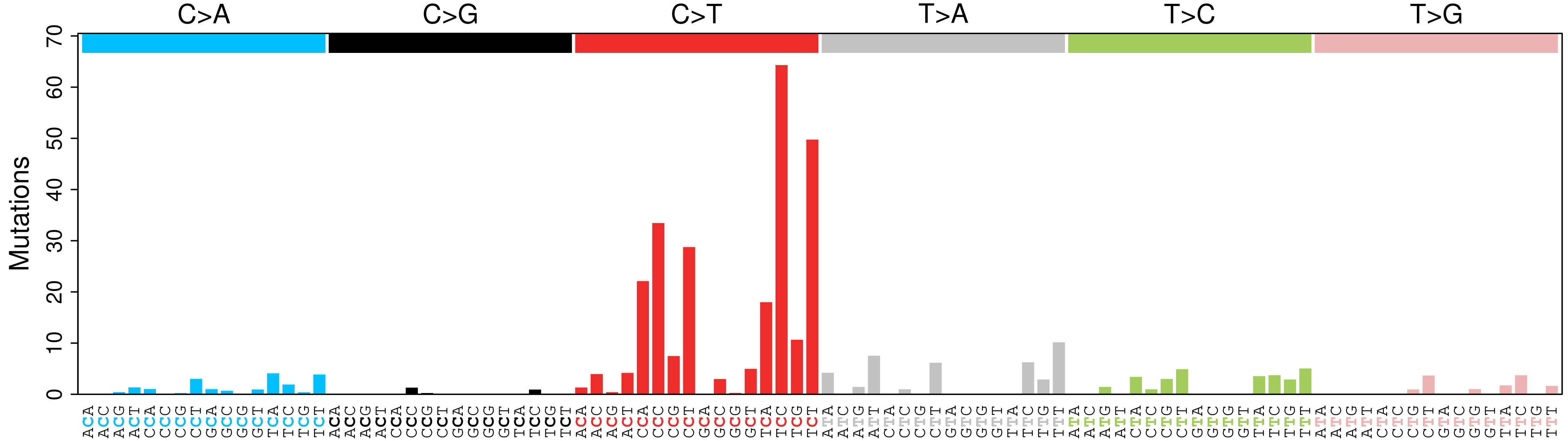
CATD0119a (592 mutations)



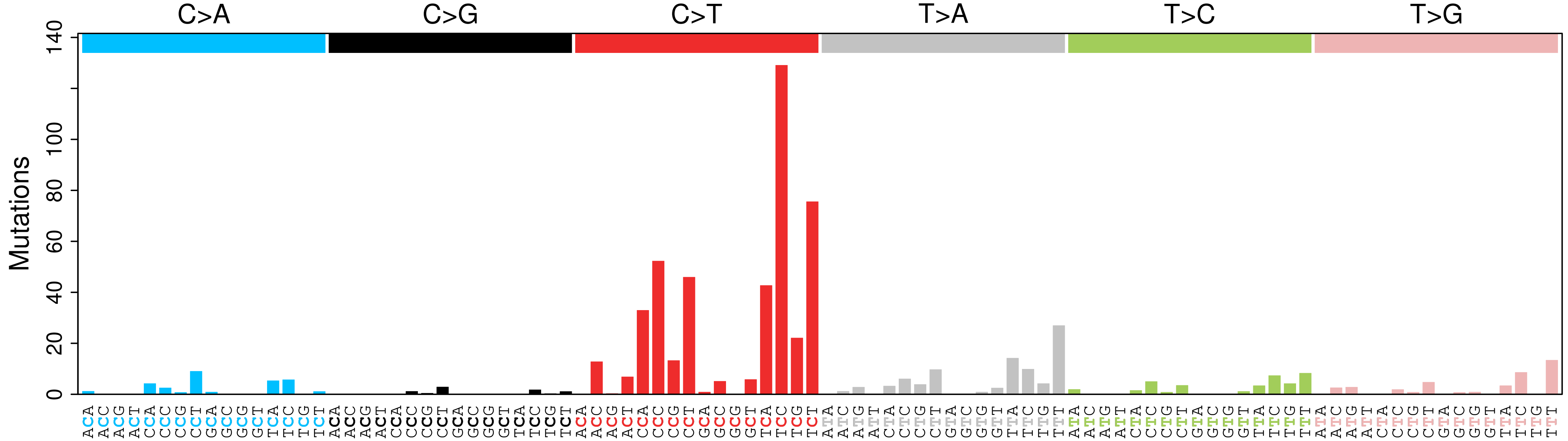
CATD245a (200 mutations)



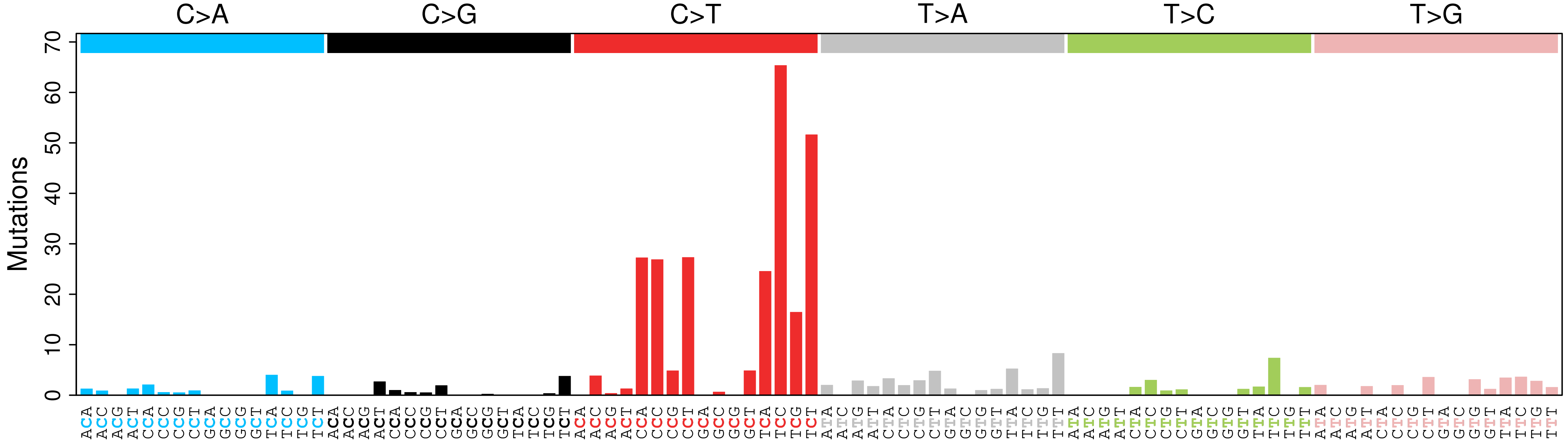
CATD255a (359 mutations)



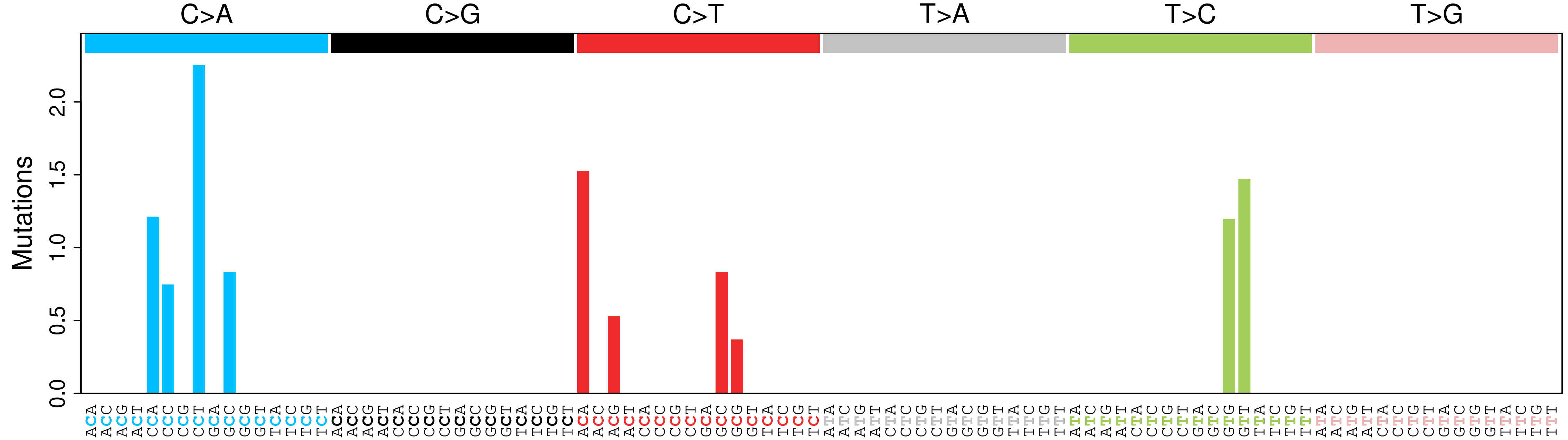
CATD0120a (659 mutations)



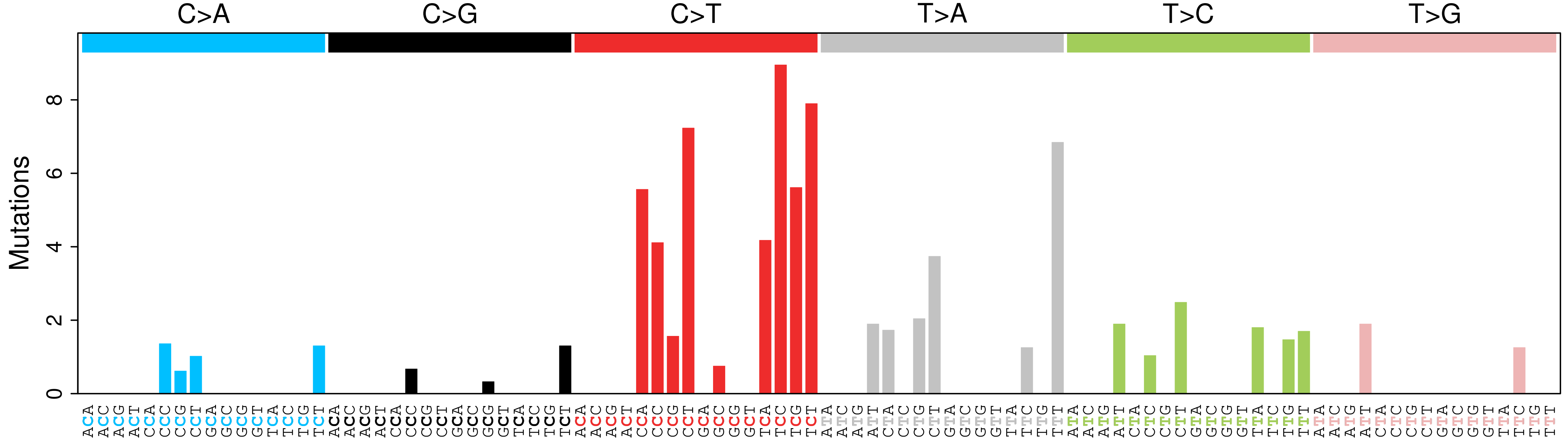
CATD246a (372 mutations)



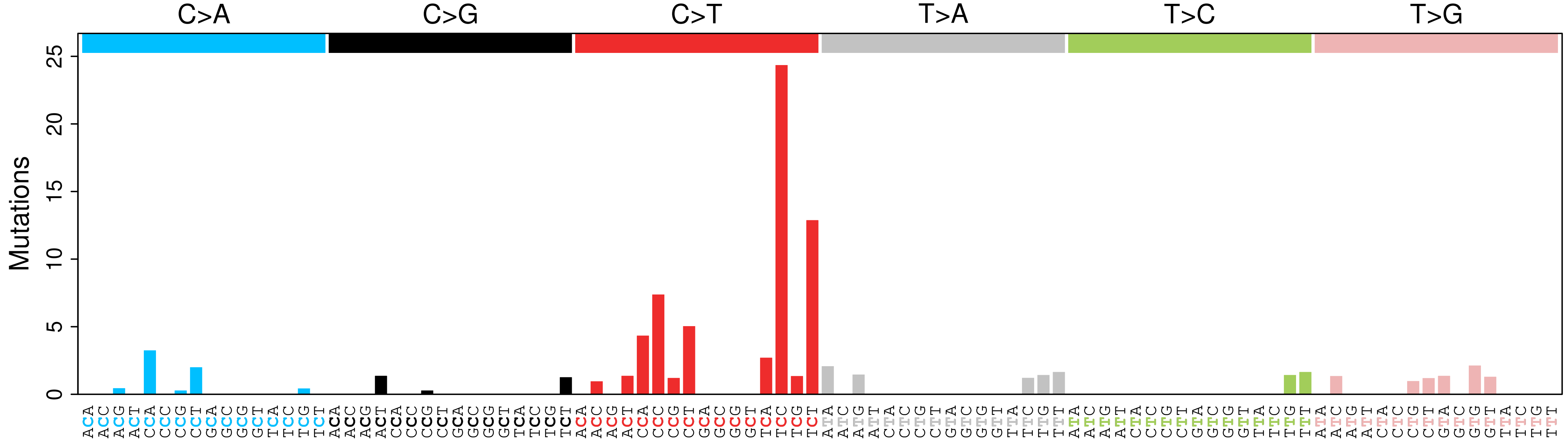
CATD279a (11 mutations)



CATD261a (84 mutations)



CATD280a (91 mutations)



CATD275a (1 mutations)

$C > A$

$C > G$

$C > T$

$T > A$

 $T > C$

T>G

Mutations

1.0

3.0

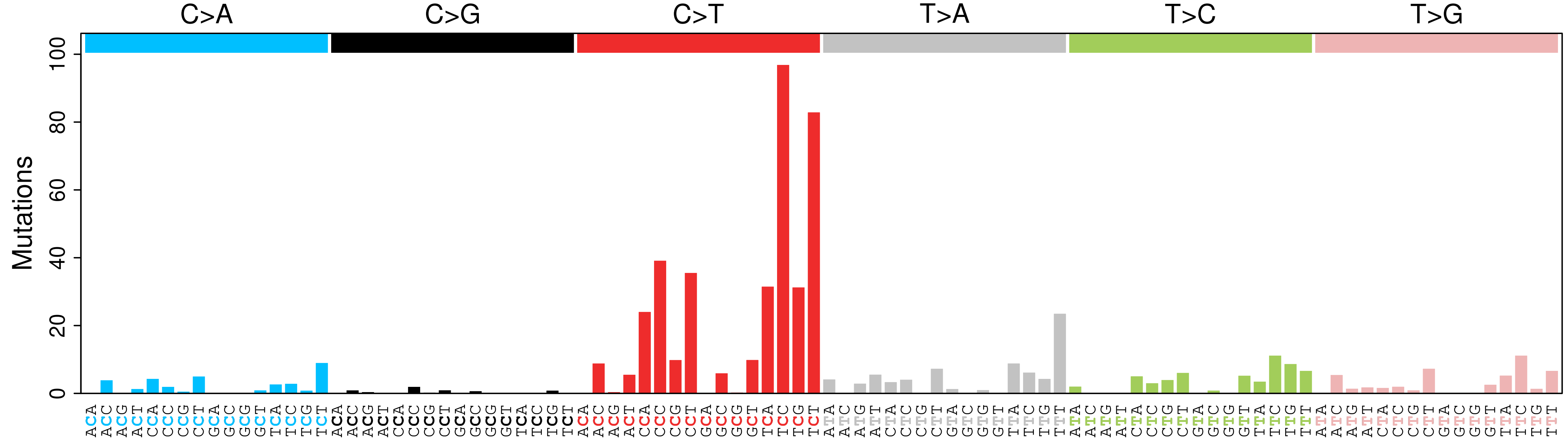
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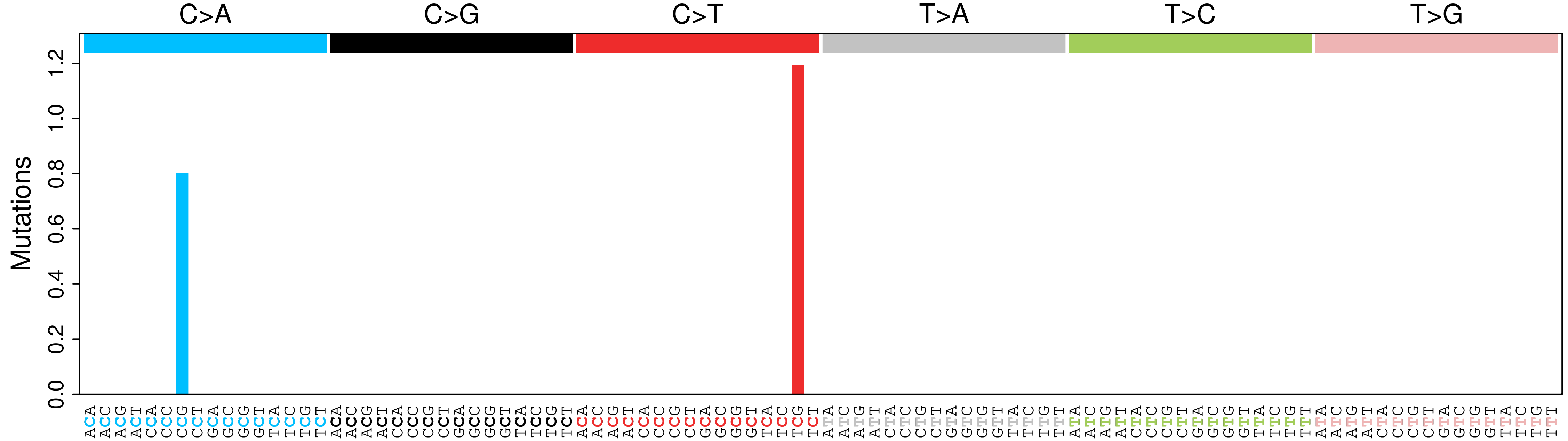
U

[illegible]

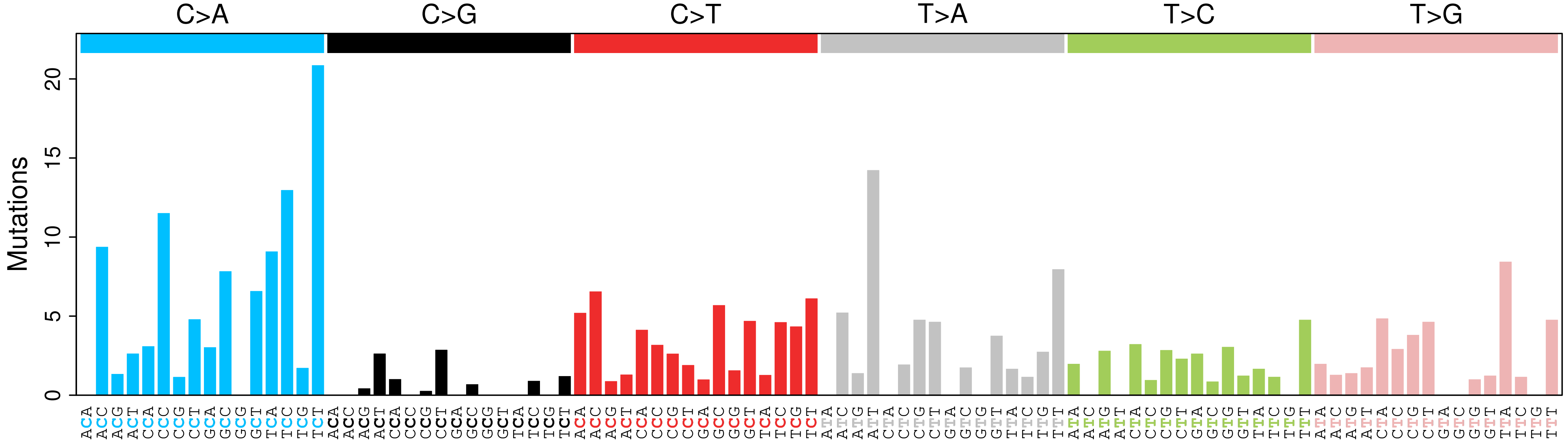
CATD253a (603 mutations)



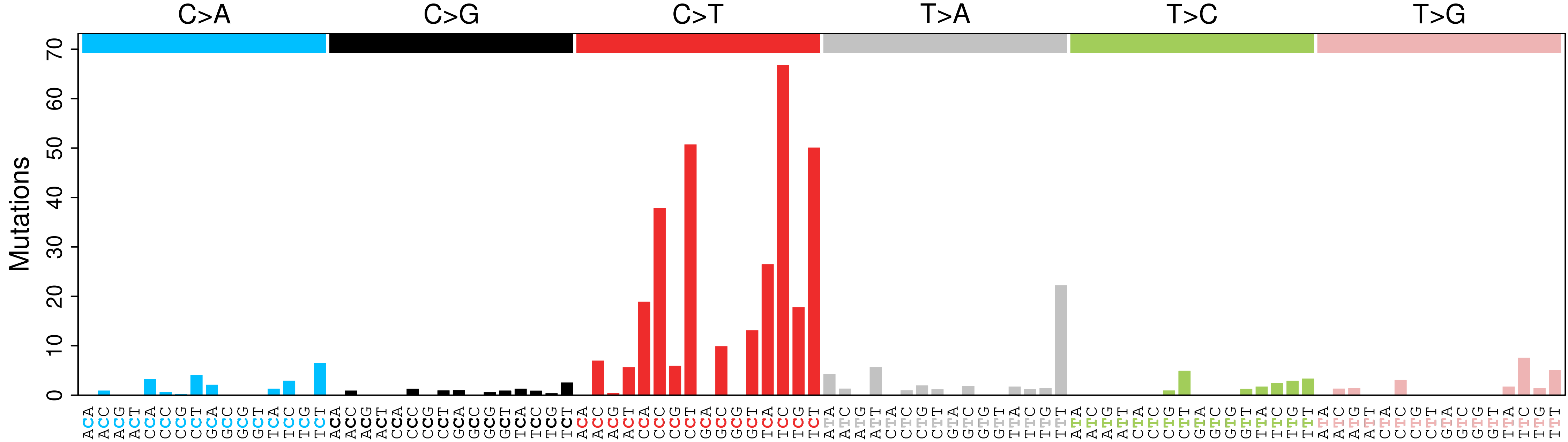
CATD267a (2 mutations)



CATD186a (283 mutations)



CATD0632c (431 mutations)



CATD0126a (105 mutations)

$C > A$

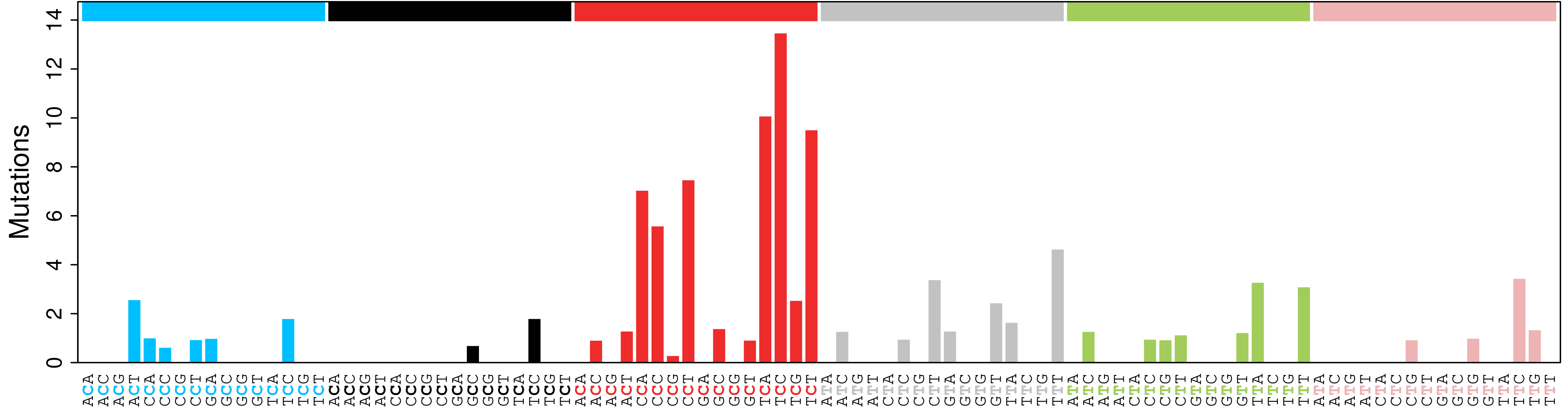
C > G

$$C > T$$

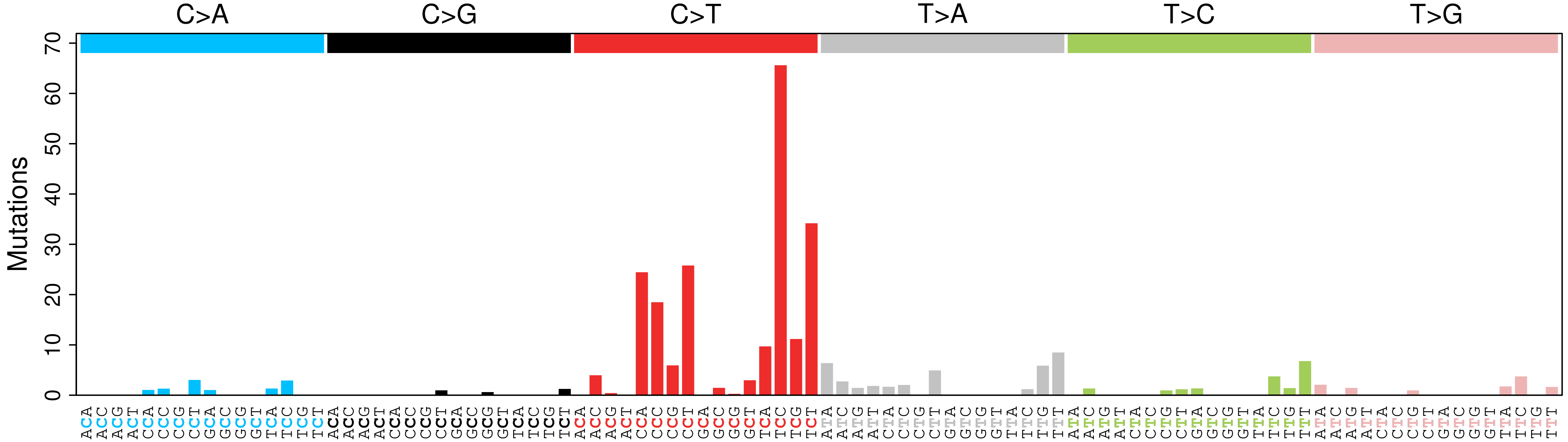
T > A

 $T > C$

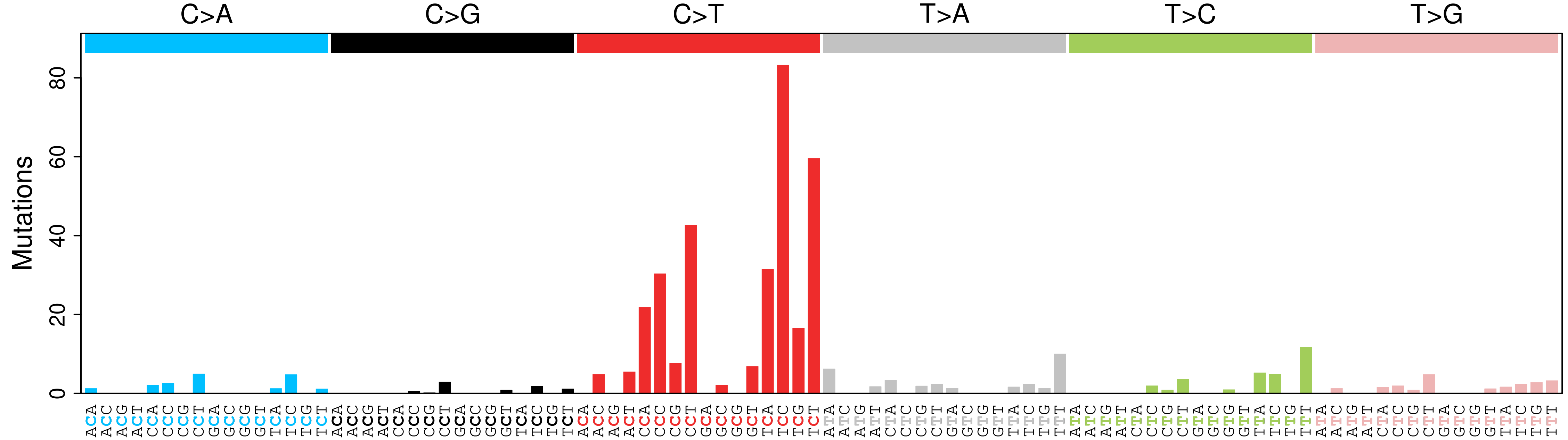
T>G



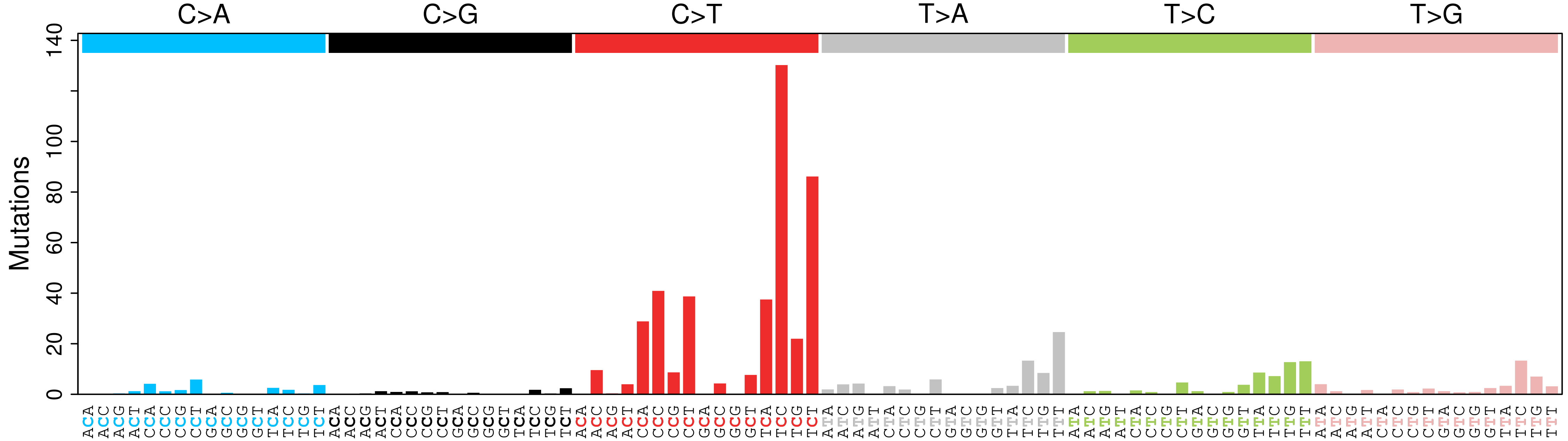
CATD274a (286 mutations)



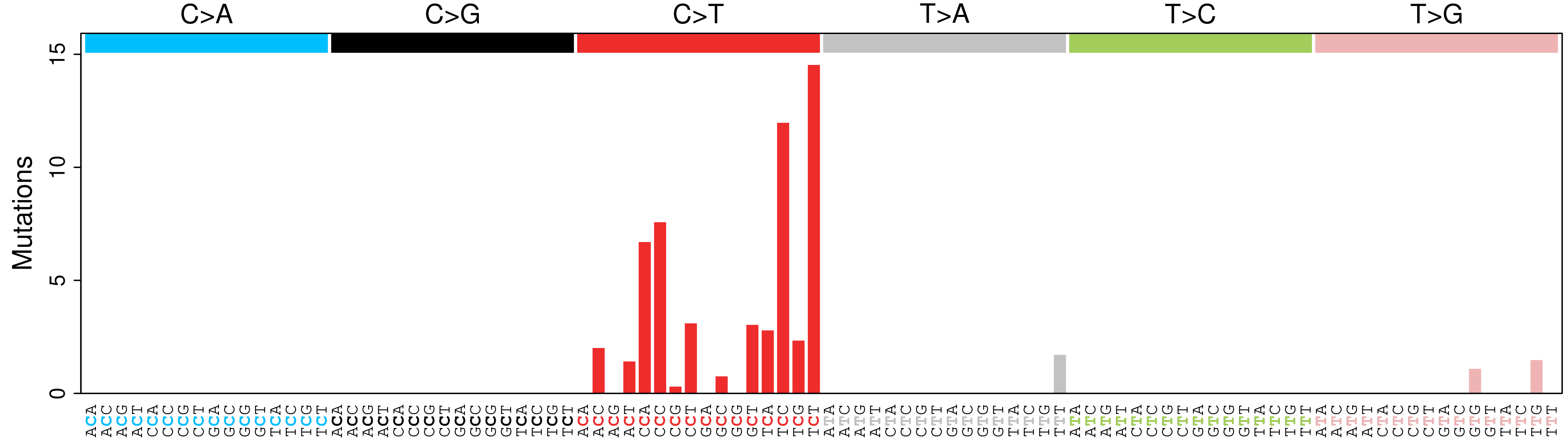
CATD278a (428 mutations)



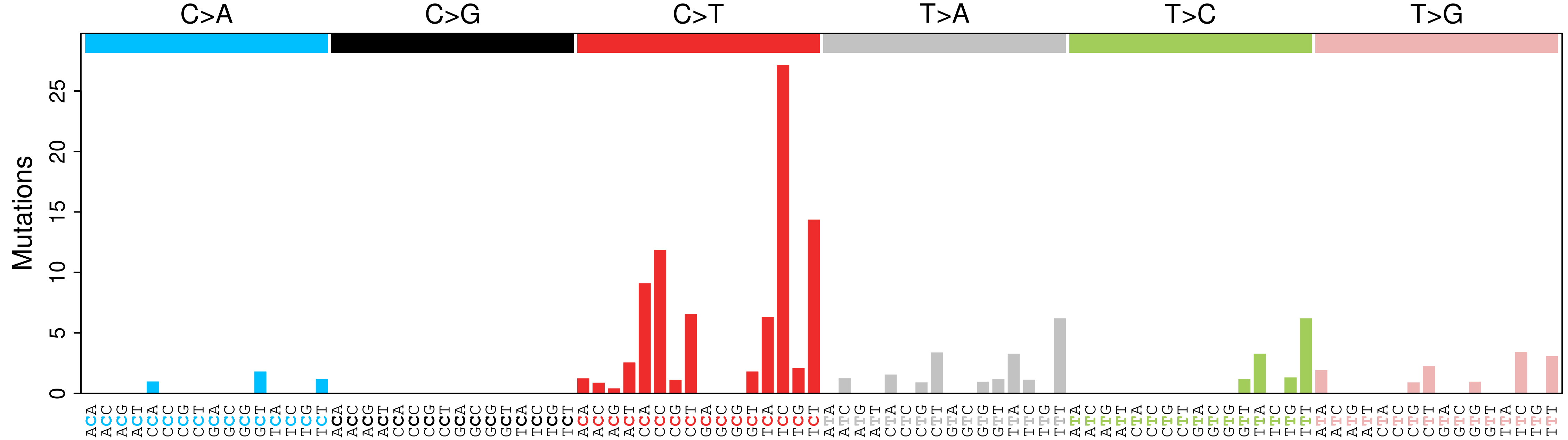
CATD264a (637 mutations)



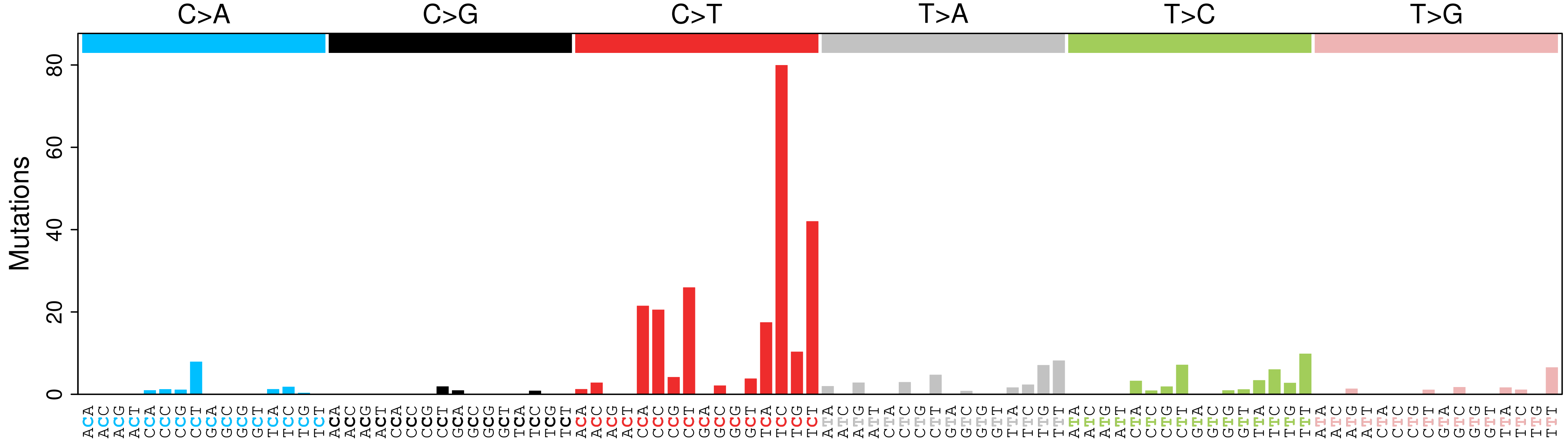
CATD0135a (61 mutations)



CATD282a (135 mutations)



CATD250a (339 mutations)



CATD254a (60 mutations)

$C > A$

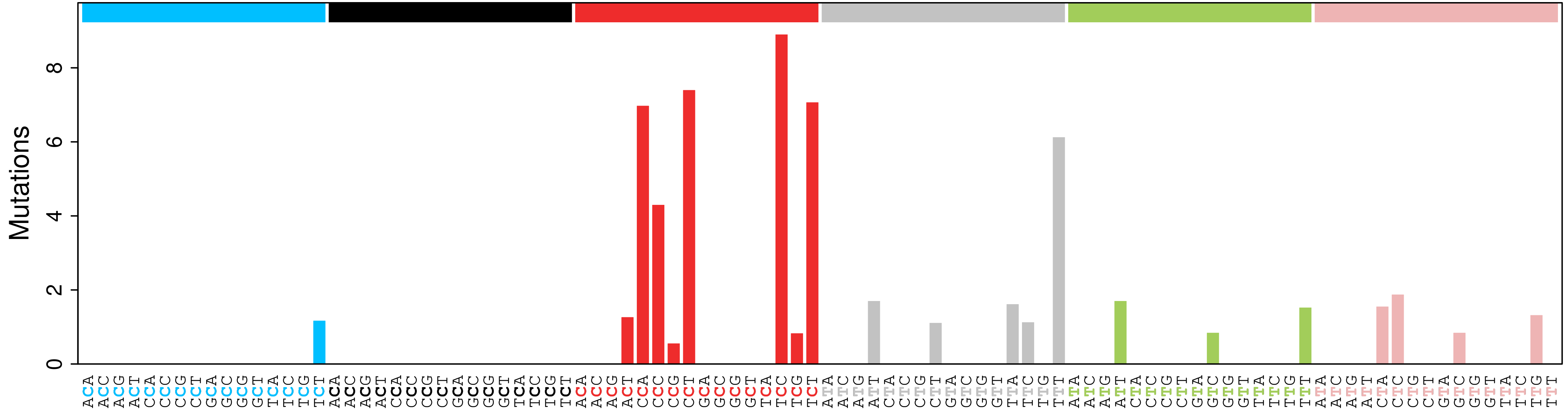
$C > G$

$C > T$

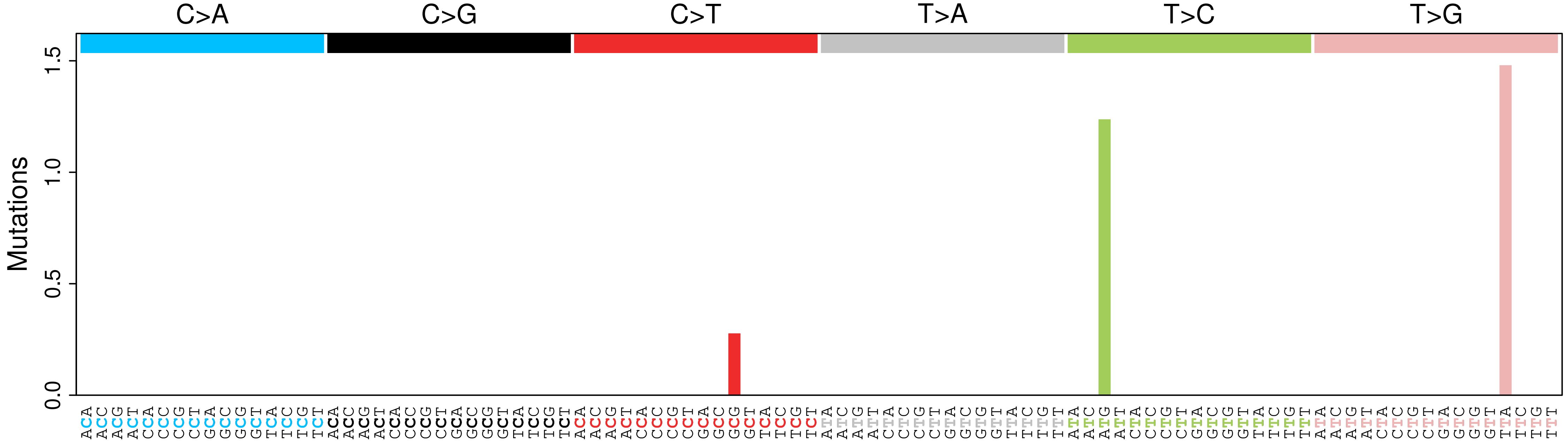
T > A

$T > C$

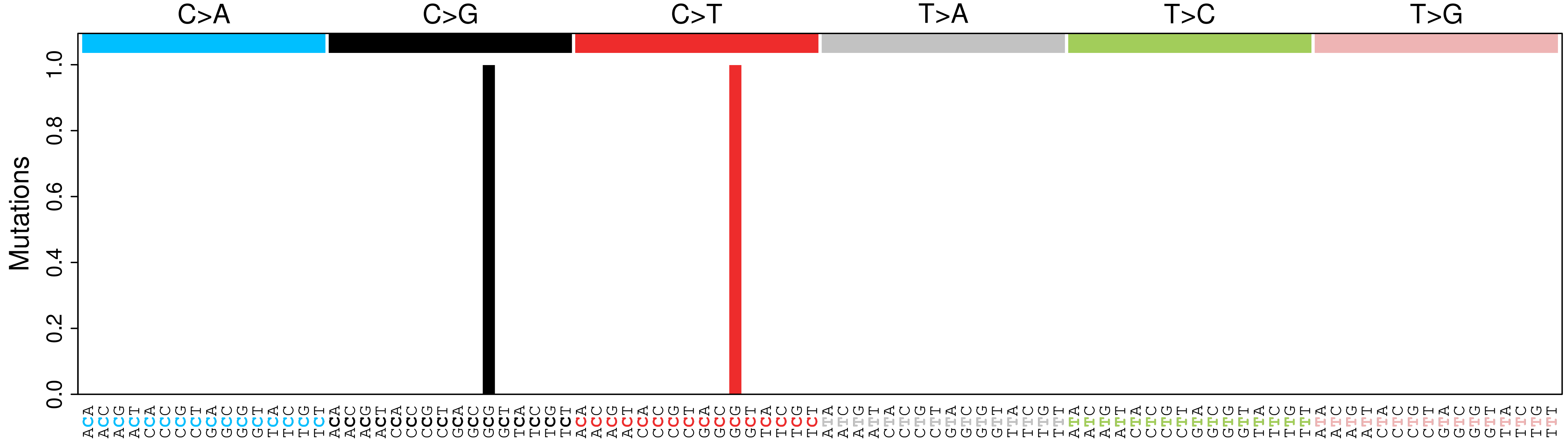
T > G



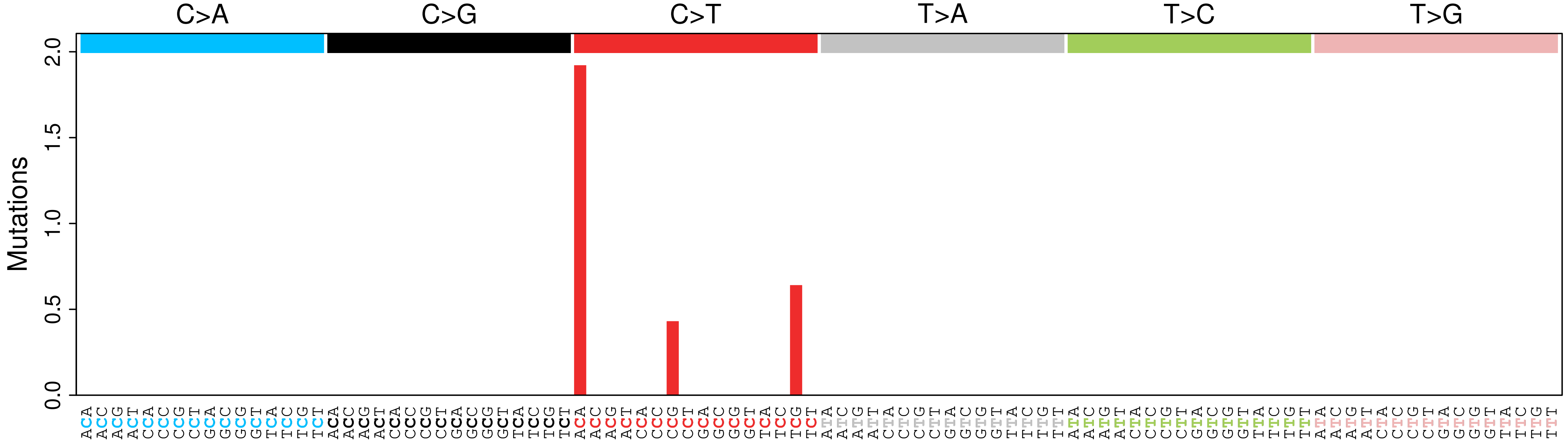
CATD0124a (3 mutations)



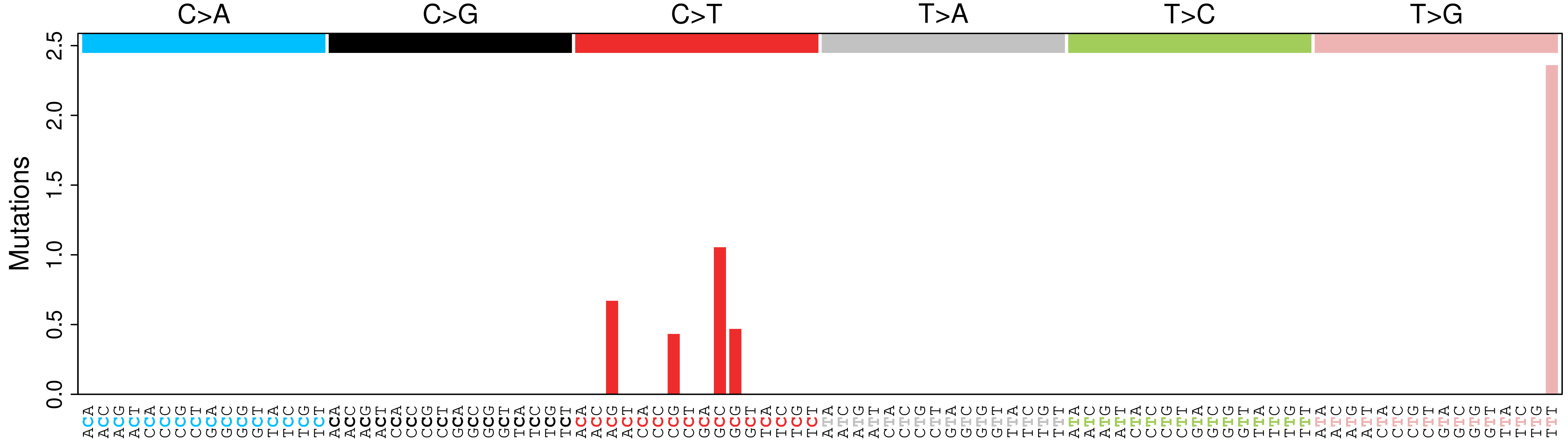
CATD0129a (2 mutations)



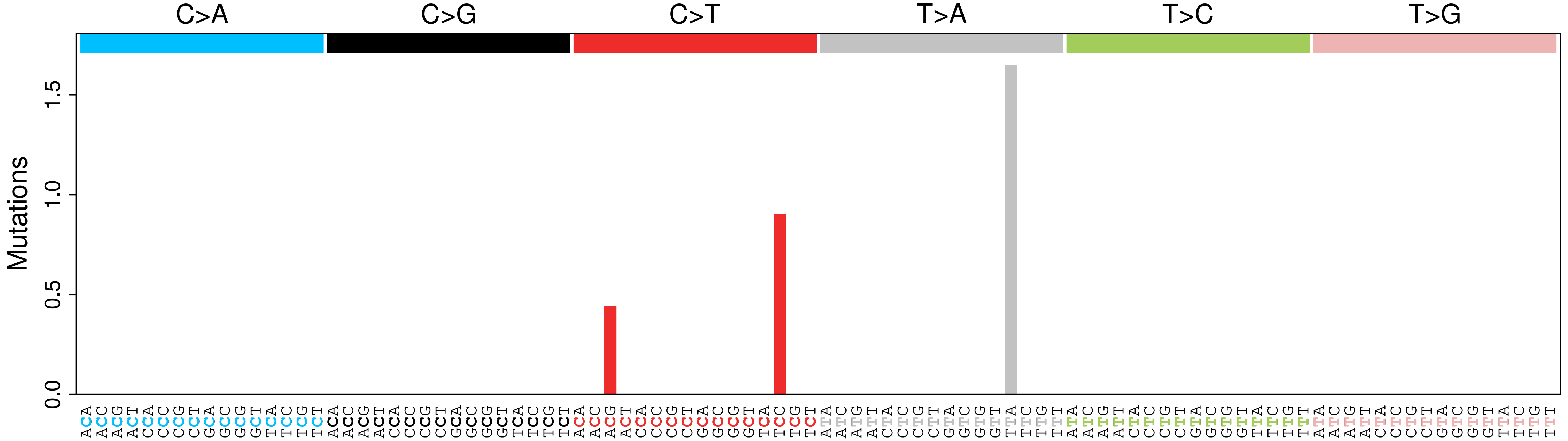
CATD0130a (3 mutations)



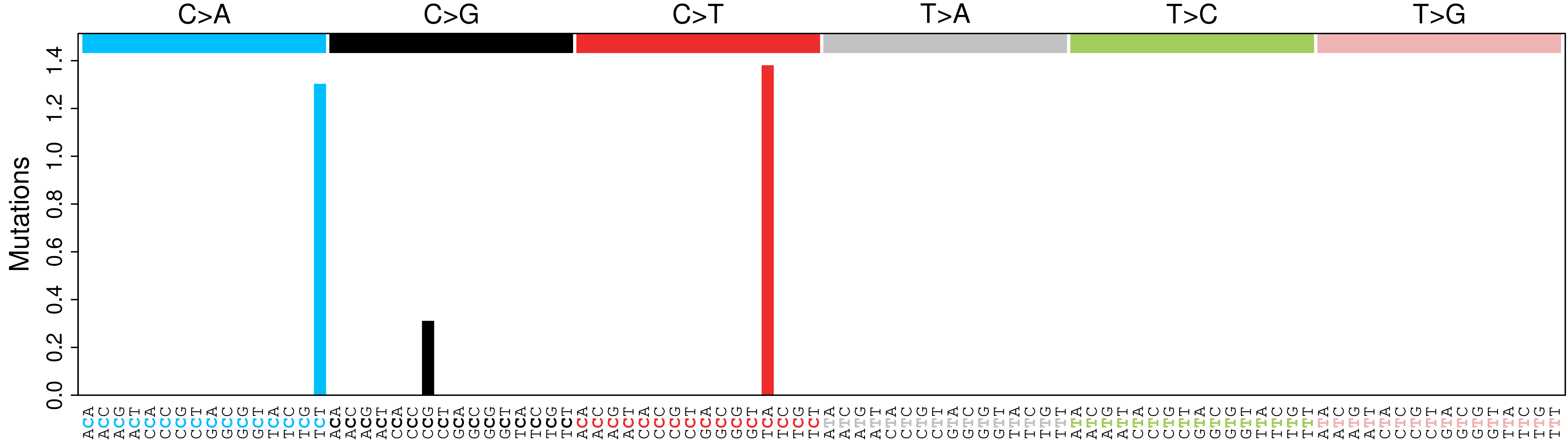
CATD0140a (5 mutations)



CATD0125a (3 mutations)



CATD0134a (3 mutations)



CATD258a (8 mutations)

C>A

C>G

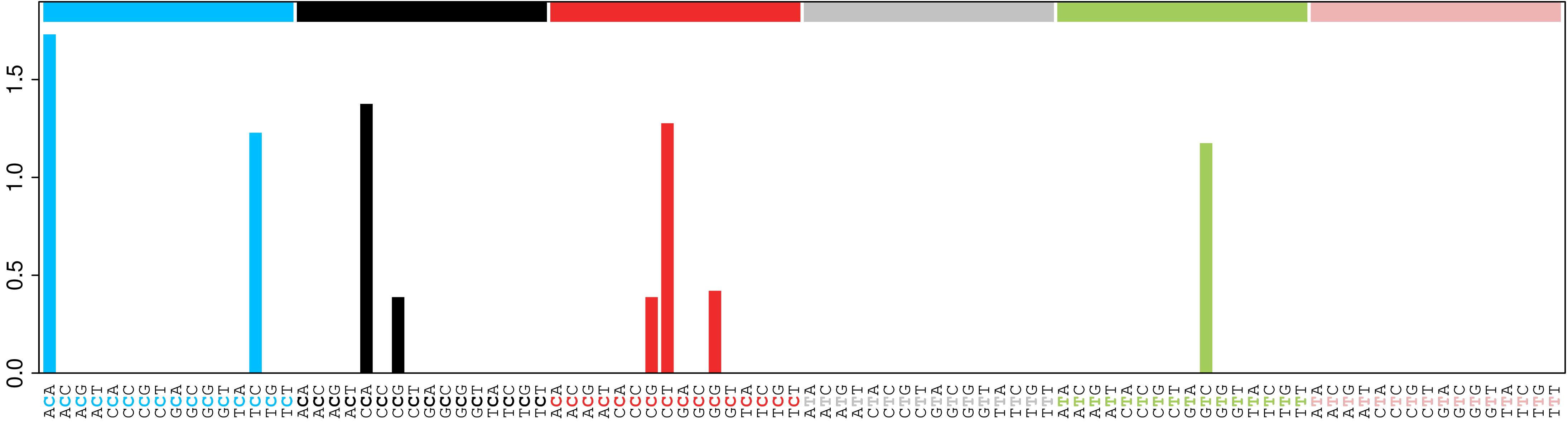
C>T

T>A

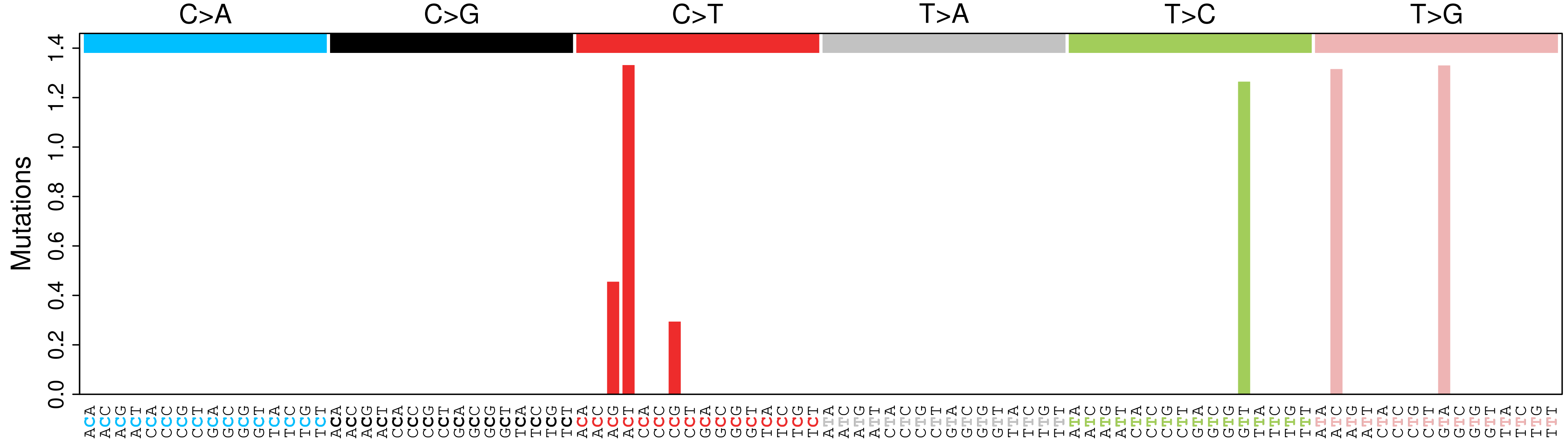
T>C

T>G

Mutations



CATD257a (6 mutations)



CATD0139a (7 mutations)

C>A

C>G

C>T

T>A

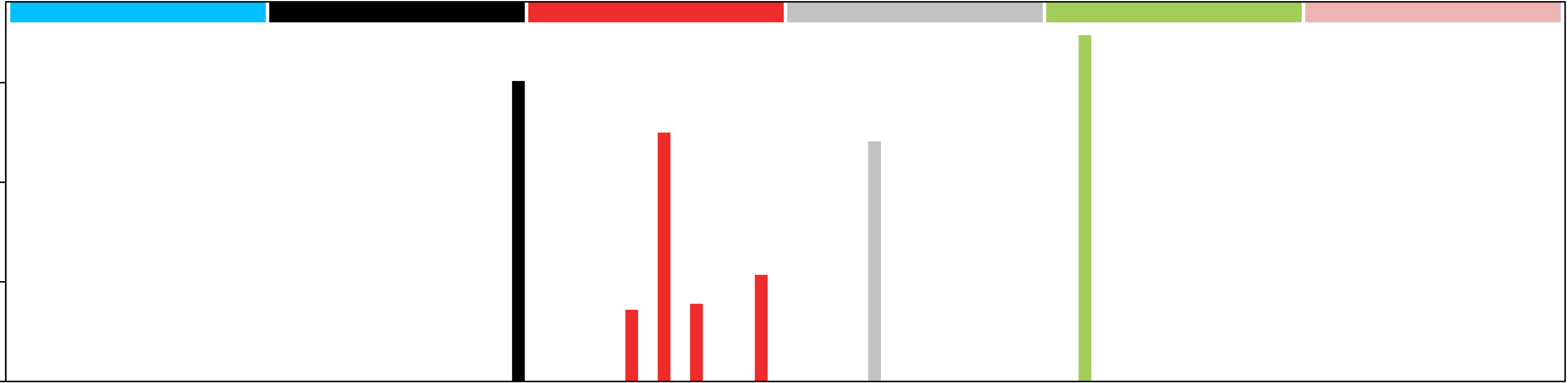
T>C

T>G

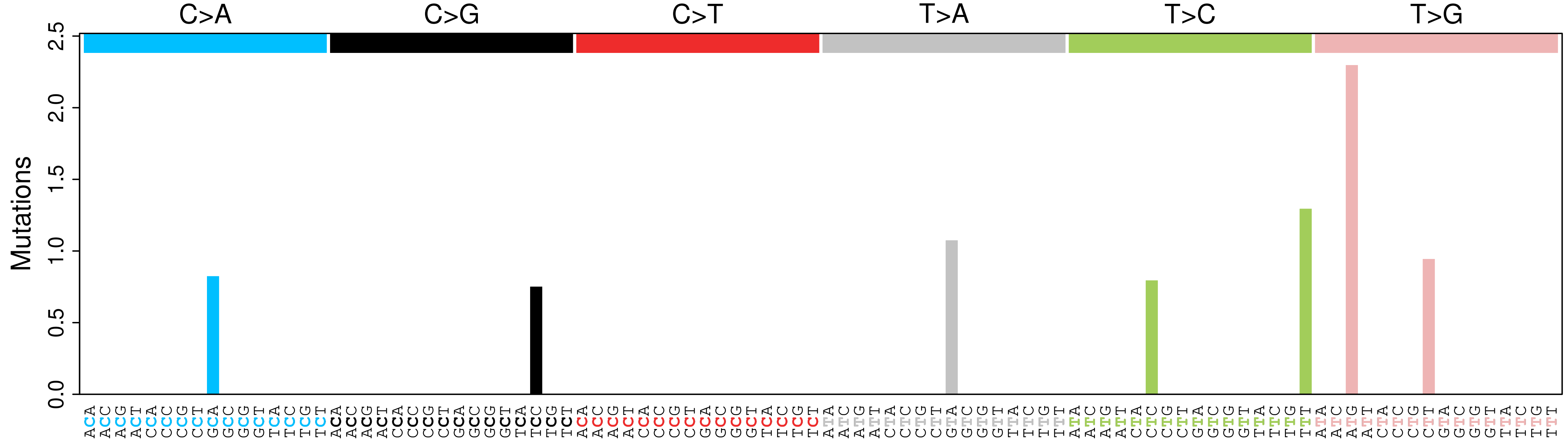
Mutations

1.5
1.0
0.5
0.0

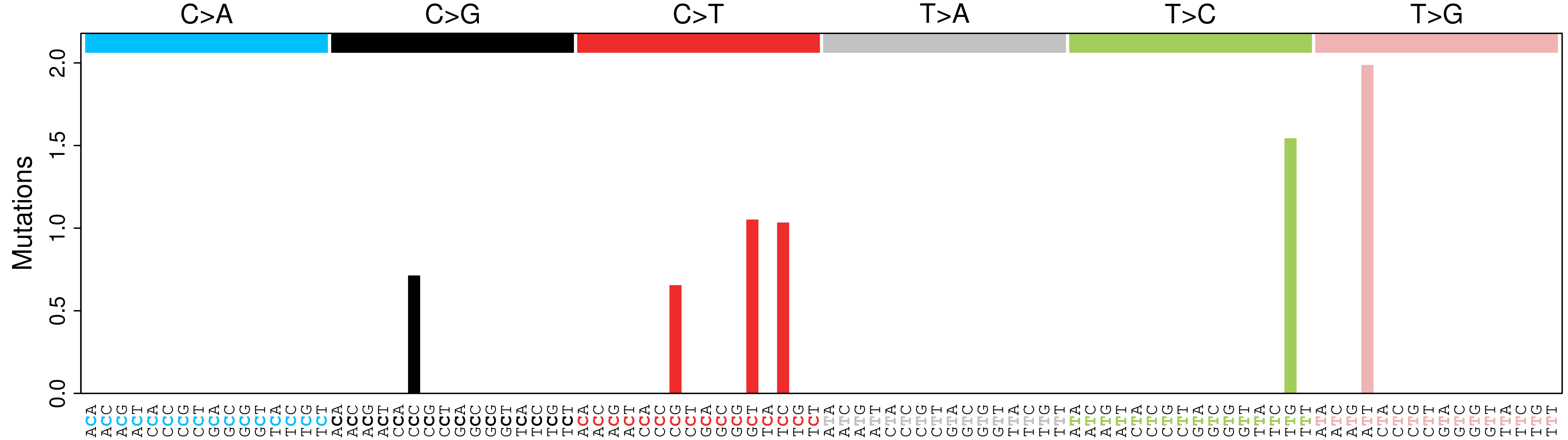
ACA ACC AGT ACT CCA CCC CCT CCA GCC GGT GGT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCG GCA GCC GCG GGT TCA TCC TCG TCT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTT GTC GTG GTT TTA TTC TTG TTT



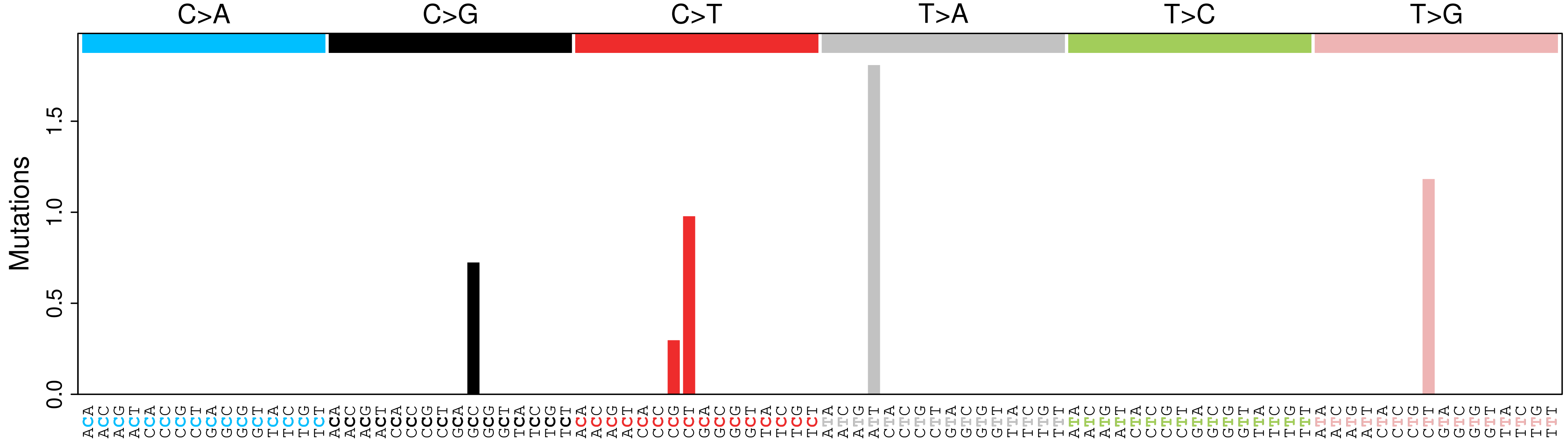
CATD0137a (8 mutations)



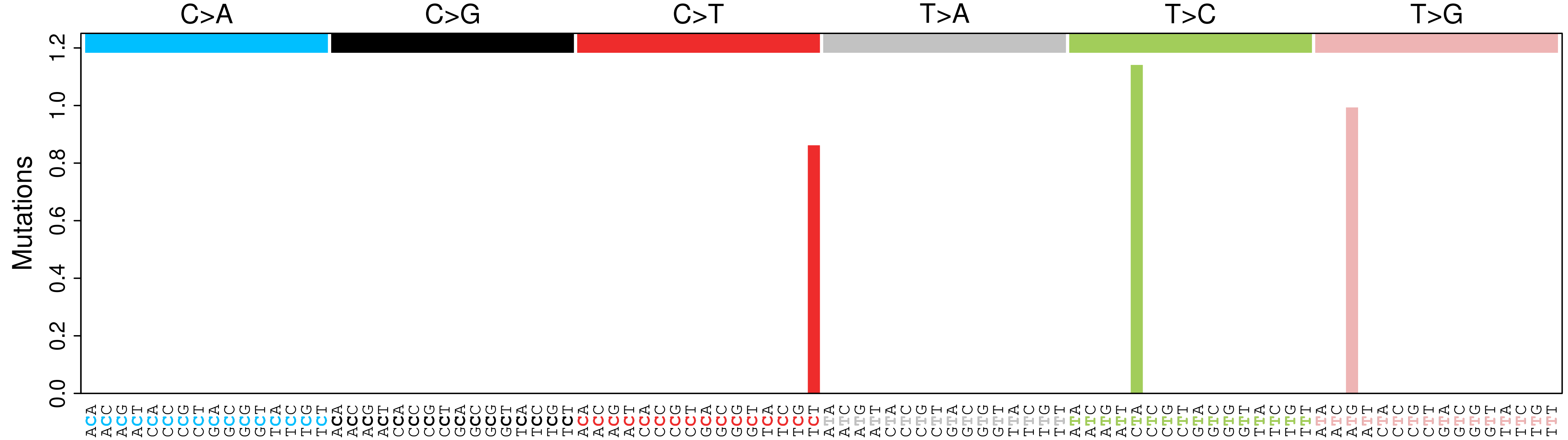
CATD259a (7 mutations)



CATD0127a (5 mutations)



CATD277a (3 mutations)



CATD281a (2 mutations)

C>A

C>G

C>T

T>A

T>C

T>G

Mutations

1.0
0.8
0.6
0.4
0.2
0.0

ACA
ACC
ACG
ACT
CCA
CCC
CCG
CCT
GCA
GCC
GGG
GGT
TCA
TCC
TCG
TCT
ACA
ACC
ACG
ACT
CCA
CCC
CCG
CCT
GCA
GCC
GGG
GGT
TCA
TCC
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GTA
GTC
GTG
GTT
TGA
TGC
TGT
TTA
TTC
TTC
TTC
TTC

CATD0133a (1 mutations)

$C > A$

$C > G$

$C > T$

T > A

$T > C$

T > G

Mutations

0.0 0.2 0.4 0.6 0.8 1.0

[illegible]