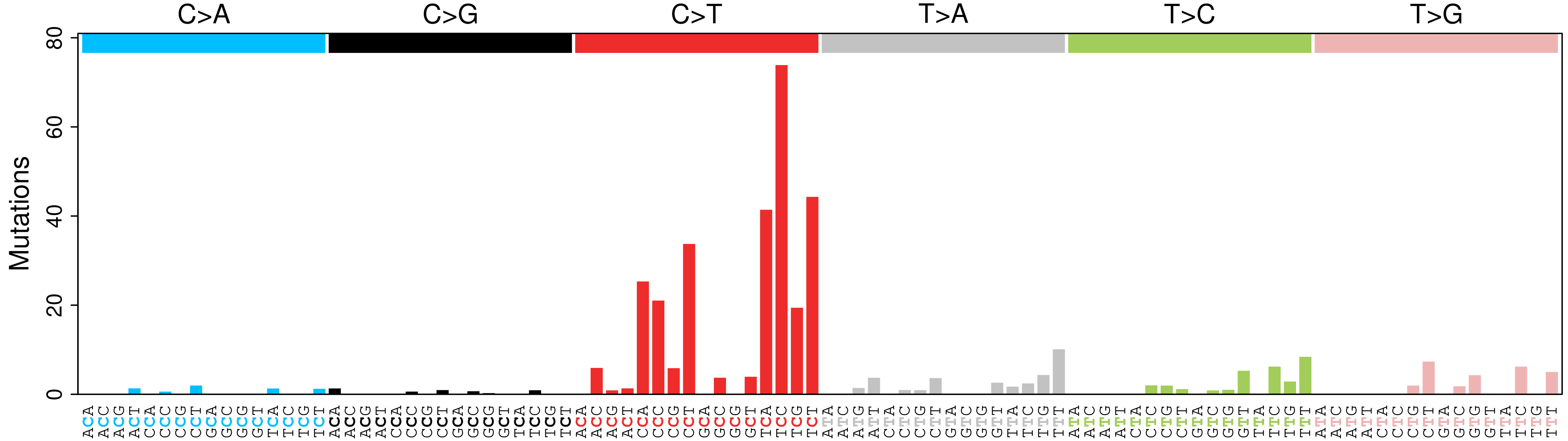
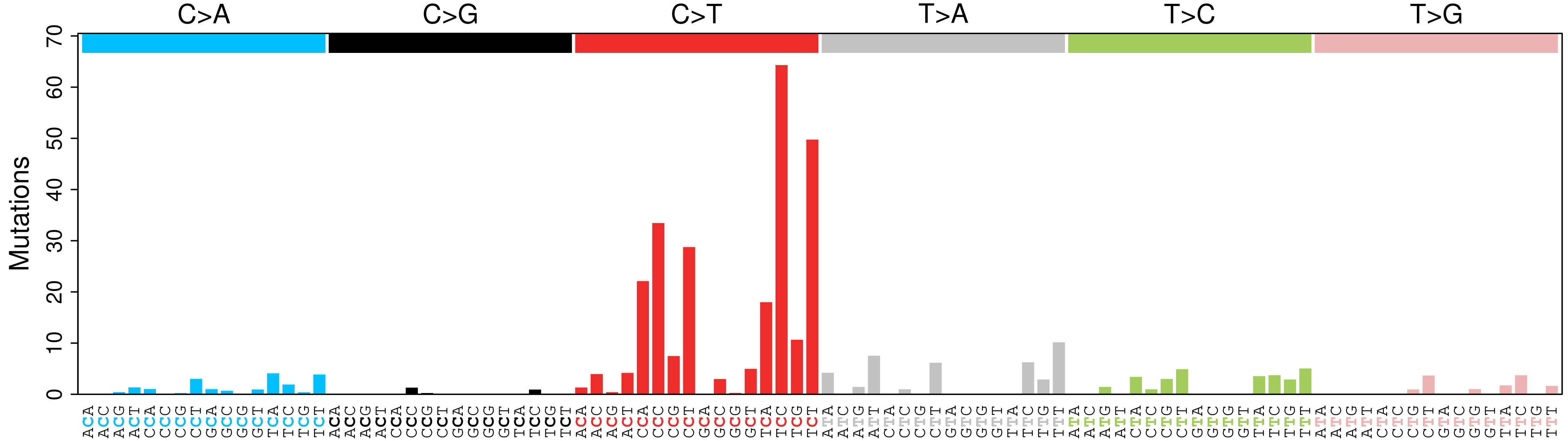


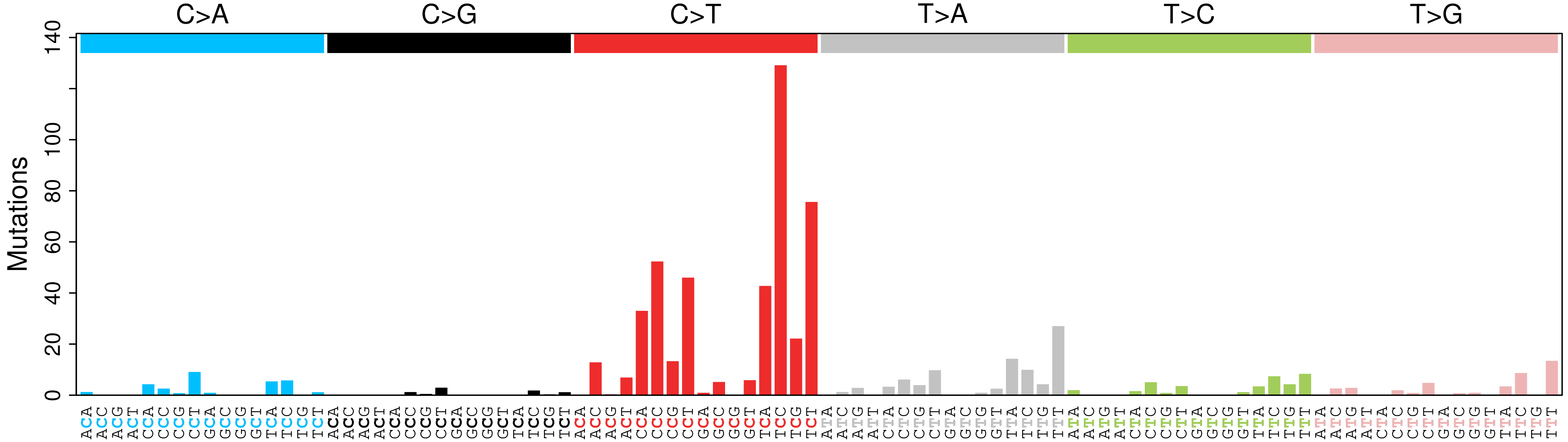
CATD0132a (384 mutations)



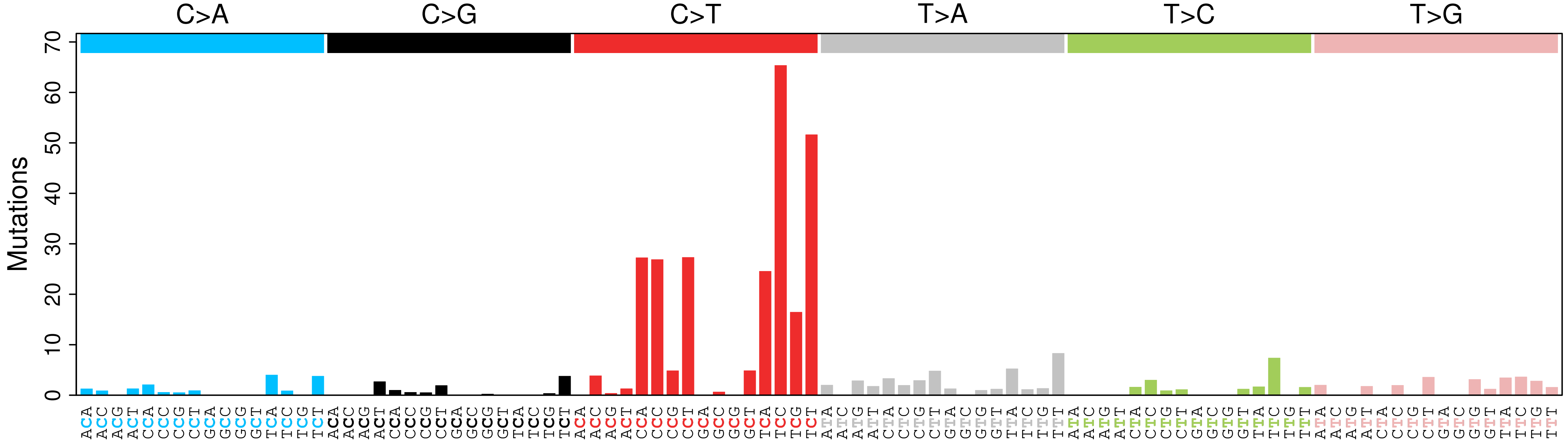
CATD255a (359 mutations)



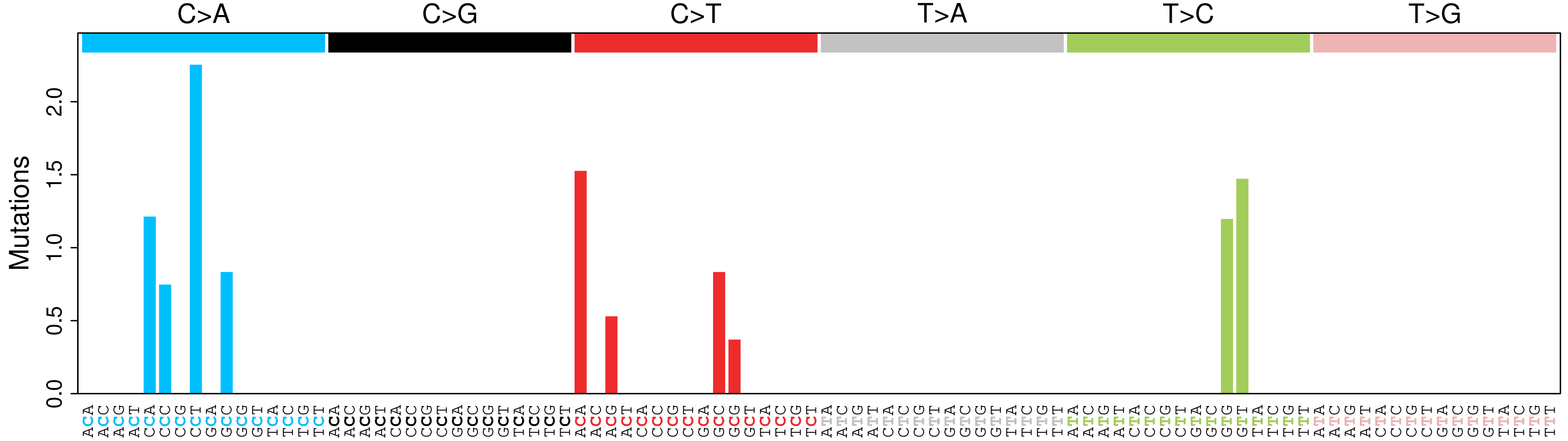
CATD0120a (659 mutations)



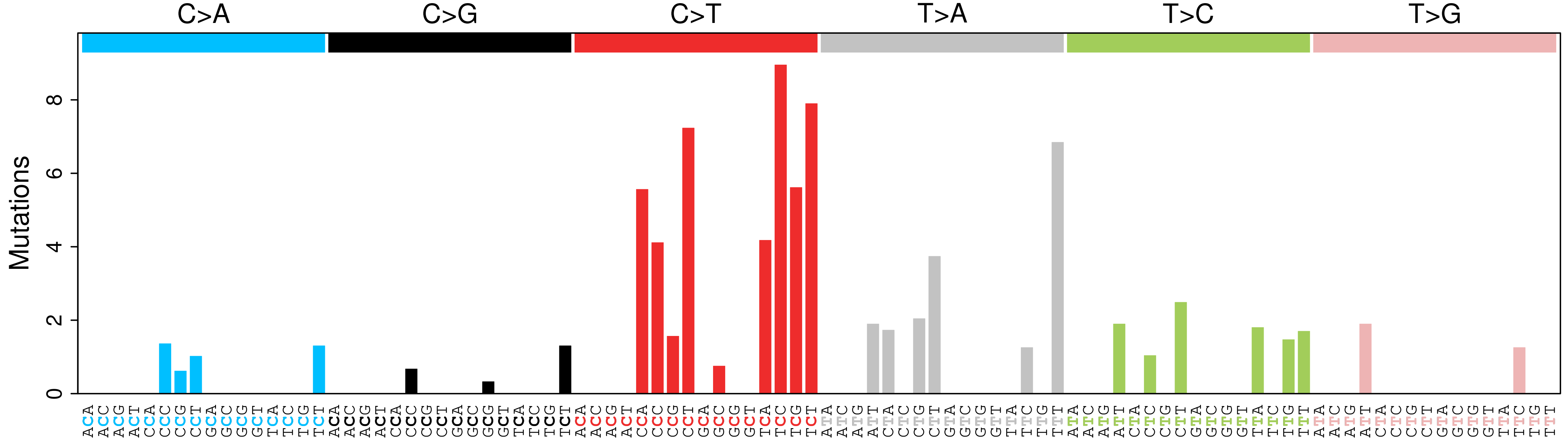
CATD246a (372 mutations)



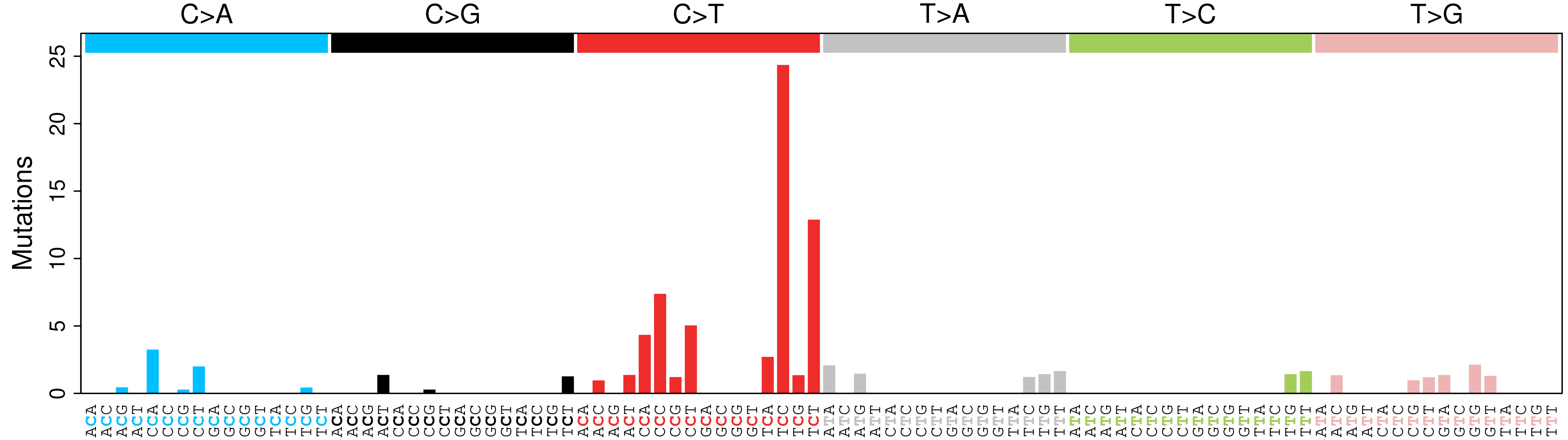
CATD279a (11 mutations)



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

 \circ

0

U

[illegible]

CATD267a (2 mutations)

$C > A$

C > G

$$C > T$$

T > A

$$T > C$$

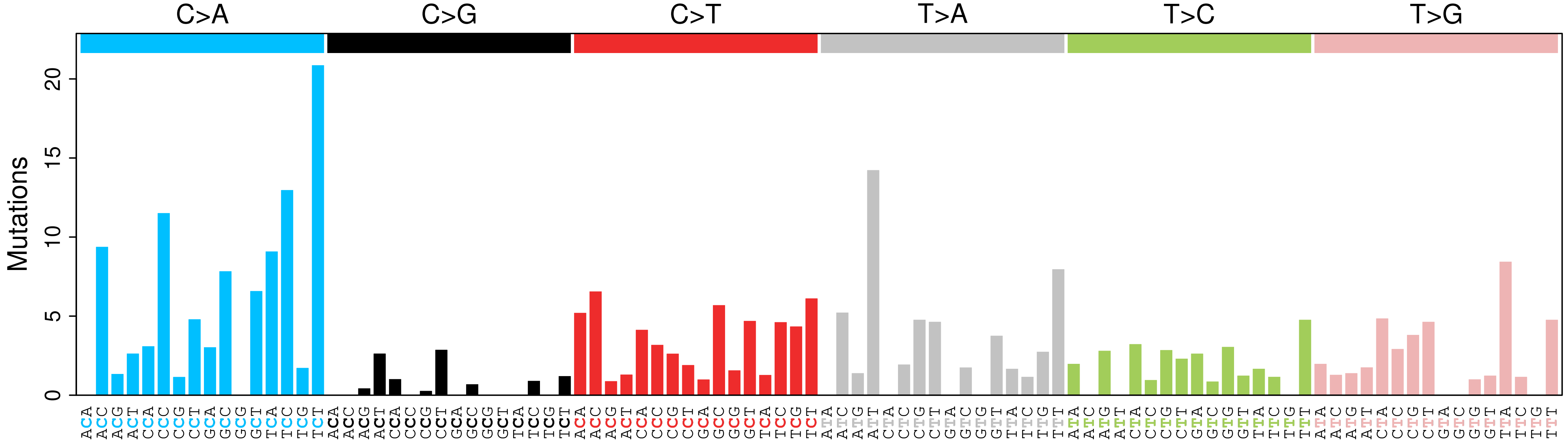
T>G

Mutations

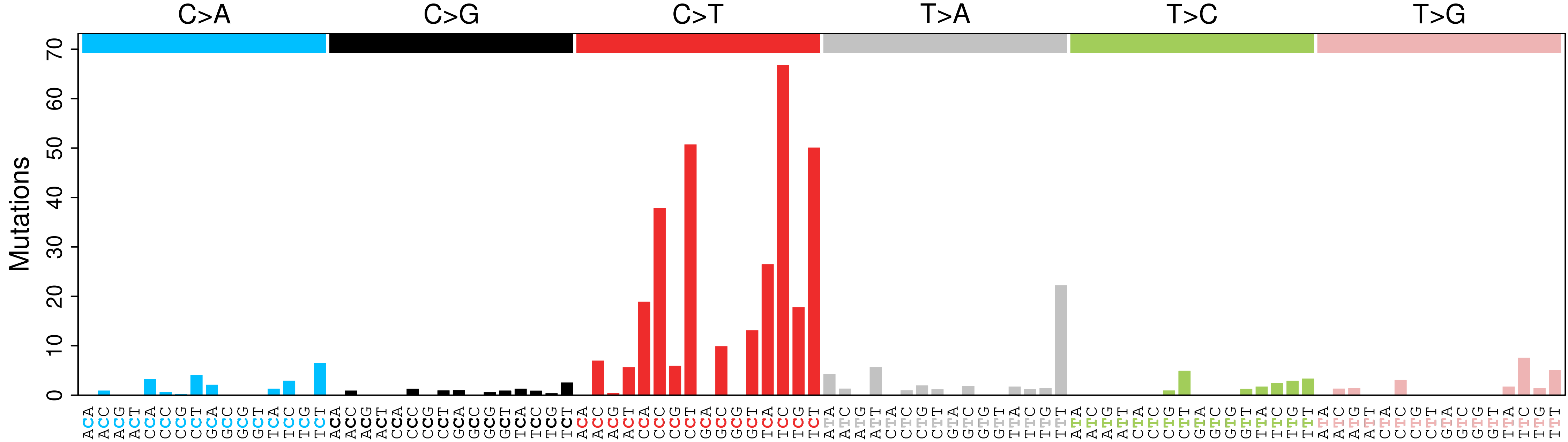
0.0 0.2 0.4 0.6 0.8 1.0 1.2

[illegible]

CATD186a (283 mutations)



CATD0632c (431 mutations)



CATD0126a (105 mutations)

$C > A$

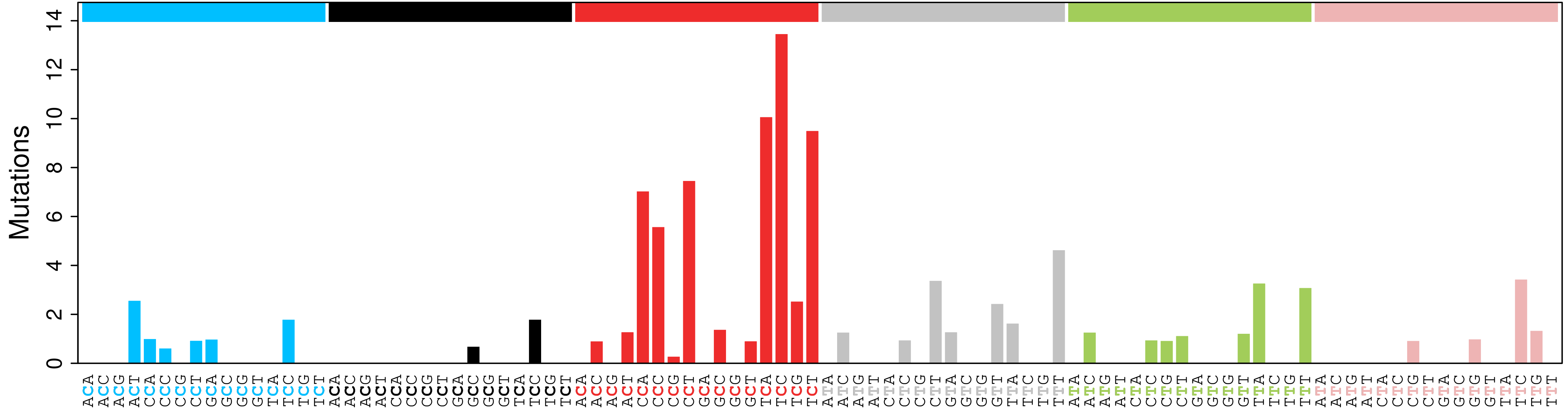
C > G

$$C > T$$

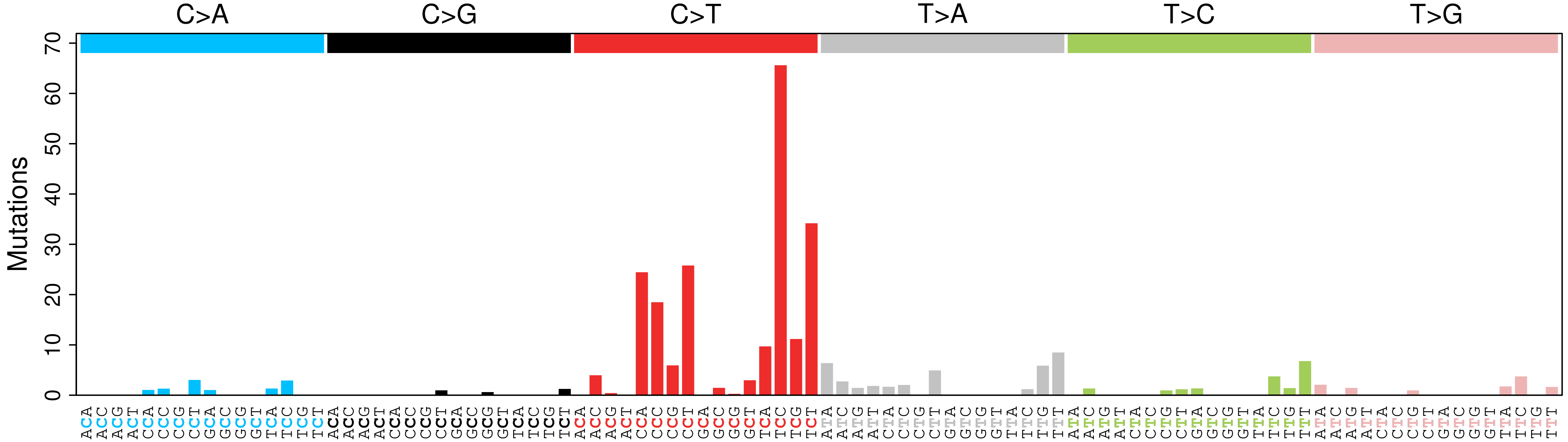
T > A

 $T > C$

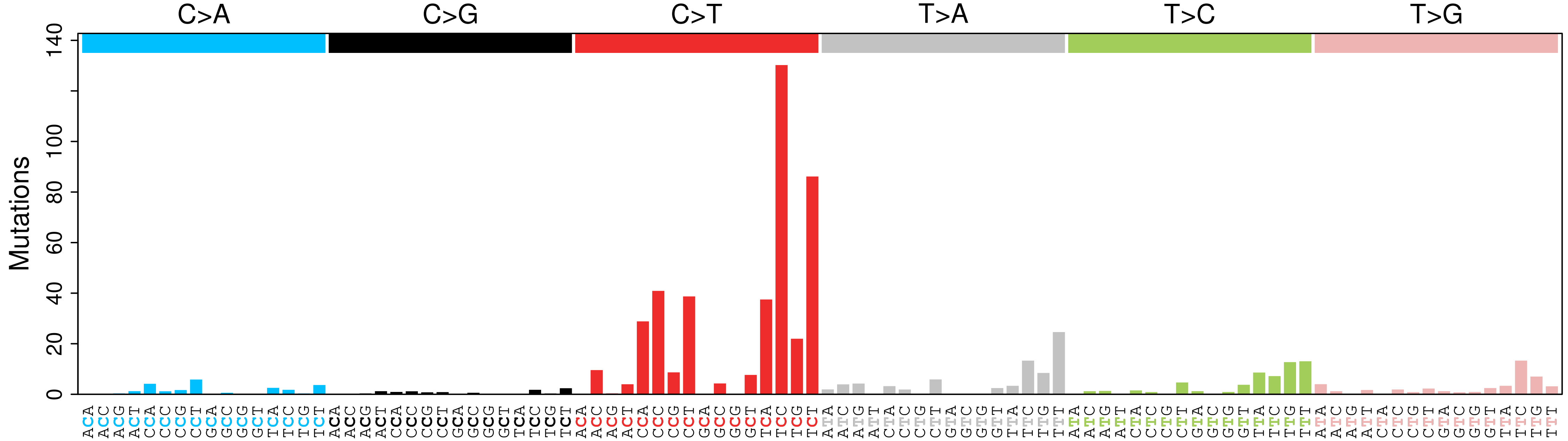
T>G



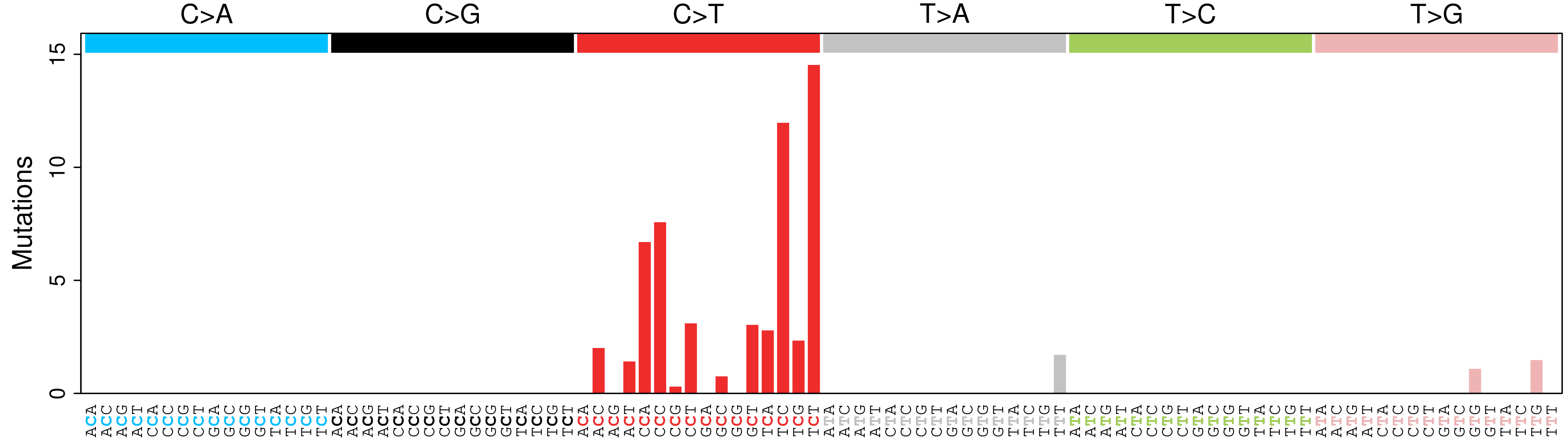
CATD274a (286 mutations)



CATD264a (637 mutations)



CATD0135a (61 mutations)



CATD282a (135 mutations)

C > A

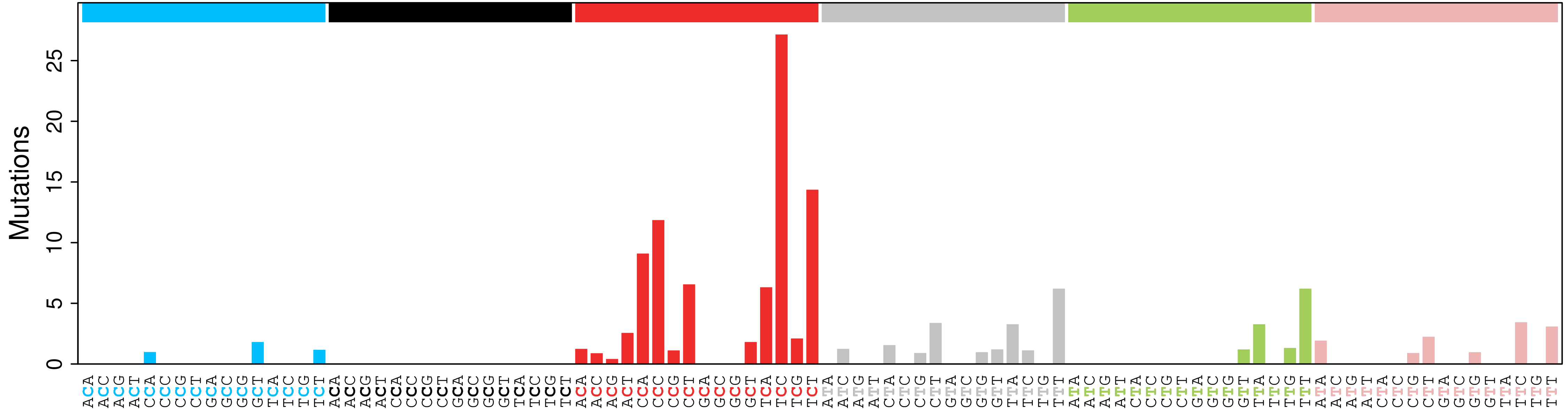
C > G

$C > T$

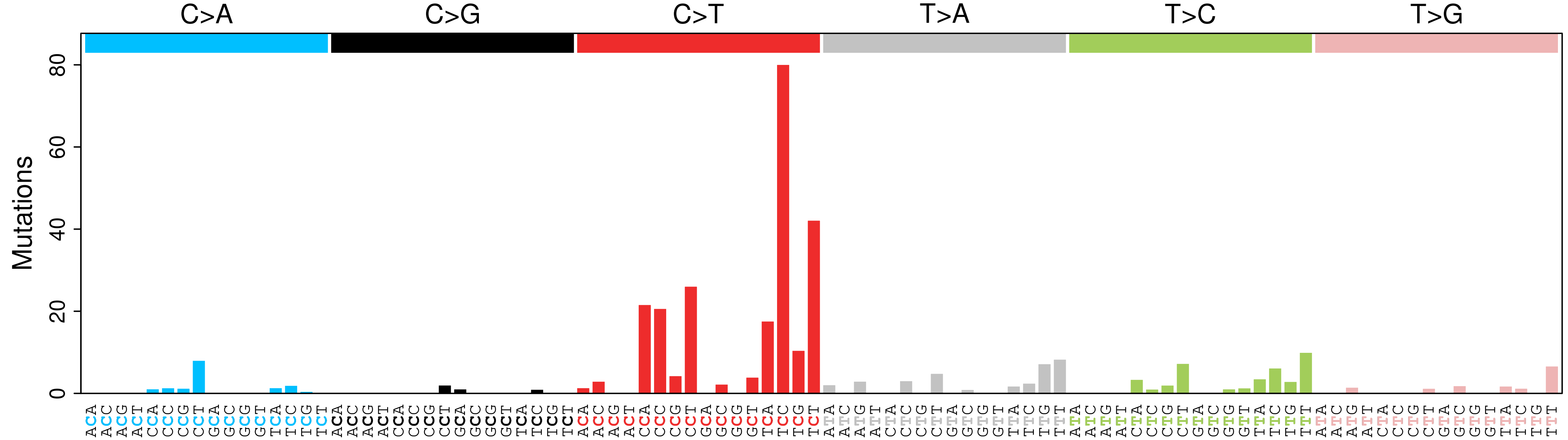
T > A

$T > C$

T>G



CATD250a (339 mutations)



CATD254a (60 mutations)

$C > A$

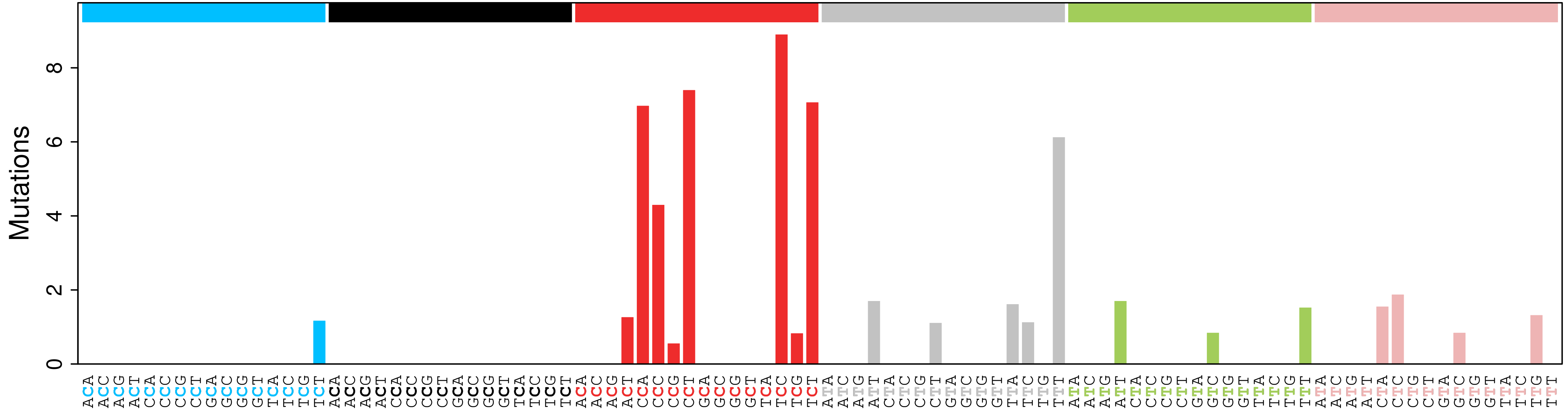
$C > G$

$C > T$

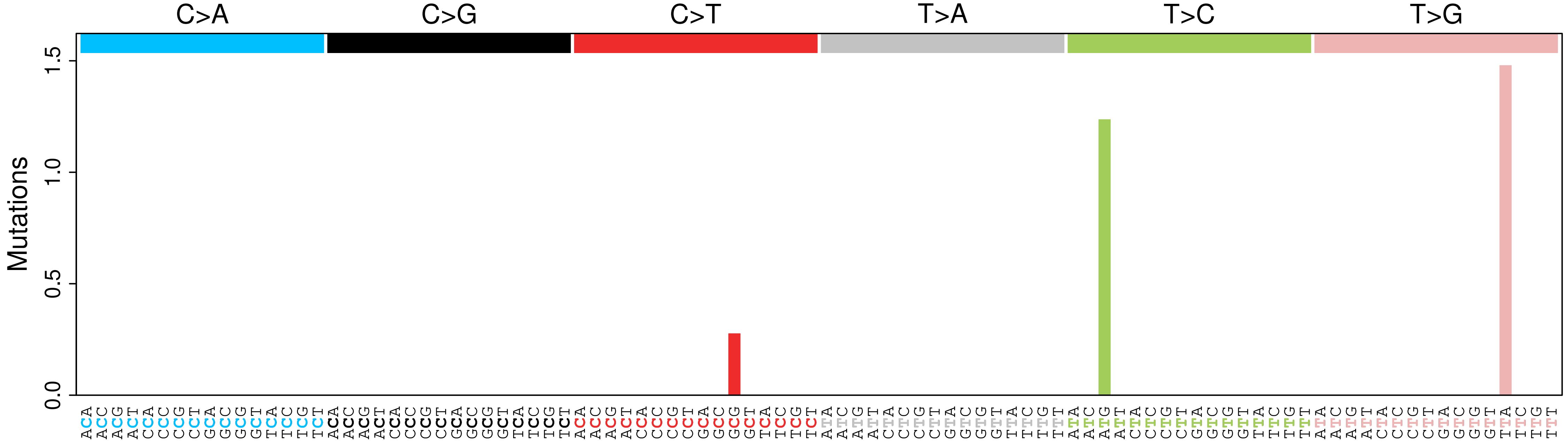
T > A

$T > C$

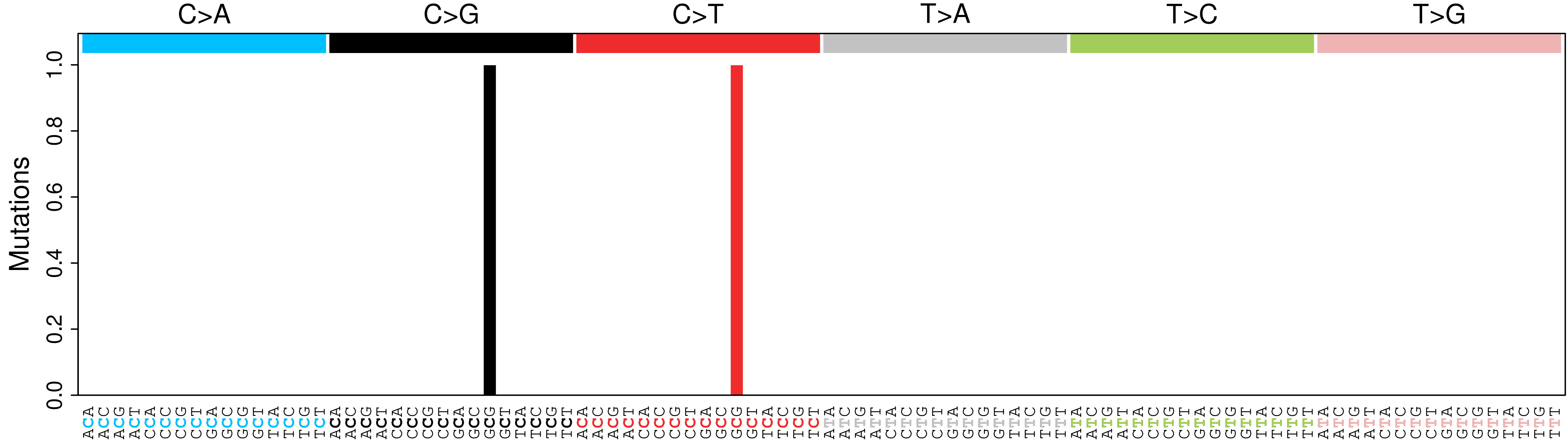
T > G



CATD0124a (3 mutations)



CATD0129a (2 mutations)



CATD0130a (3 mutations)

C > A

C > G

$C > T$

T > A

$$T > C$$

T > G

2.0

1.5

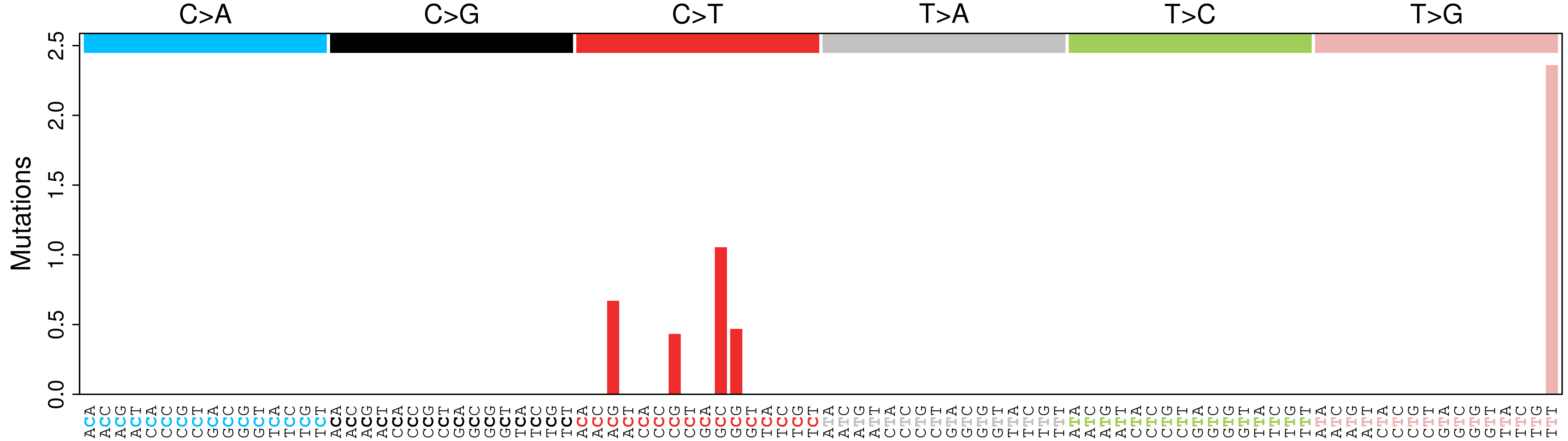
1.0

5.

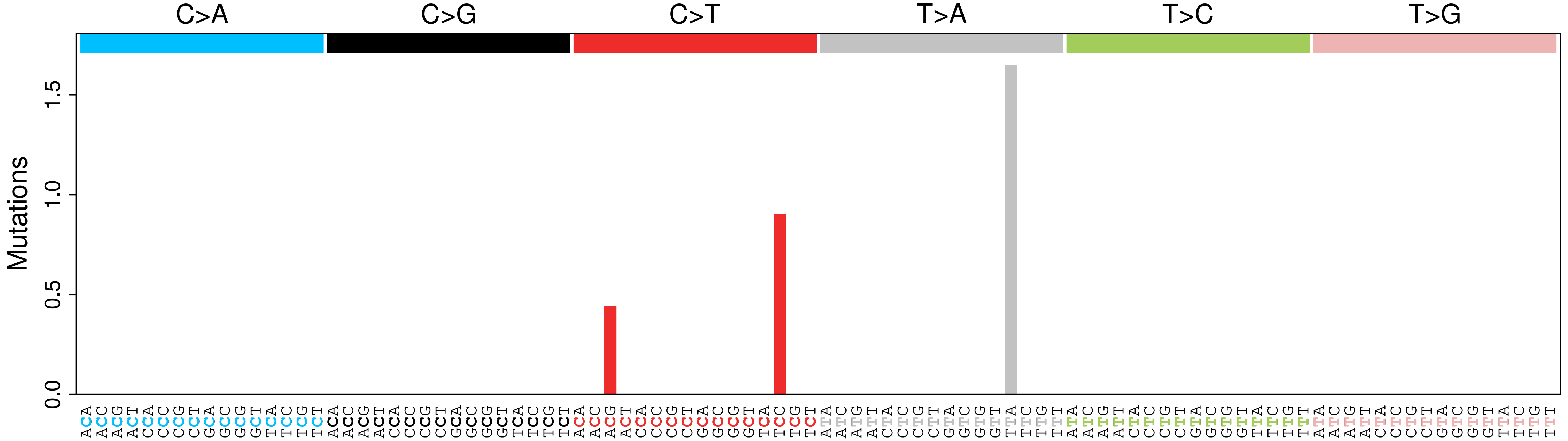
0.

[illegible]

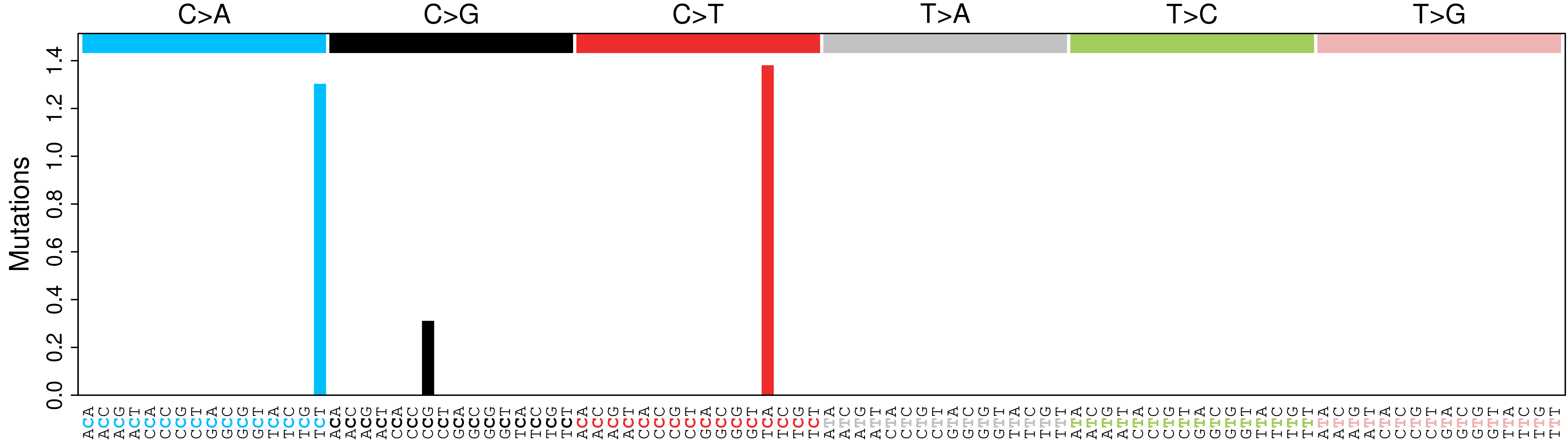
CATD0140a (5 mutations)



CATD0125a (3 mutations)



CATD0134a (3 mutations)



CATD258a (8 mutations)

C>A

C>G

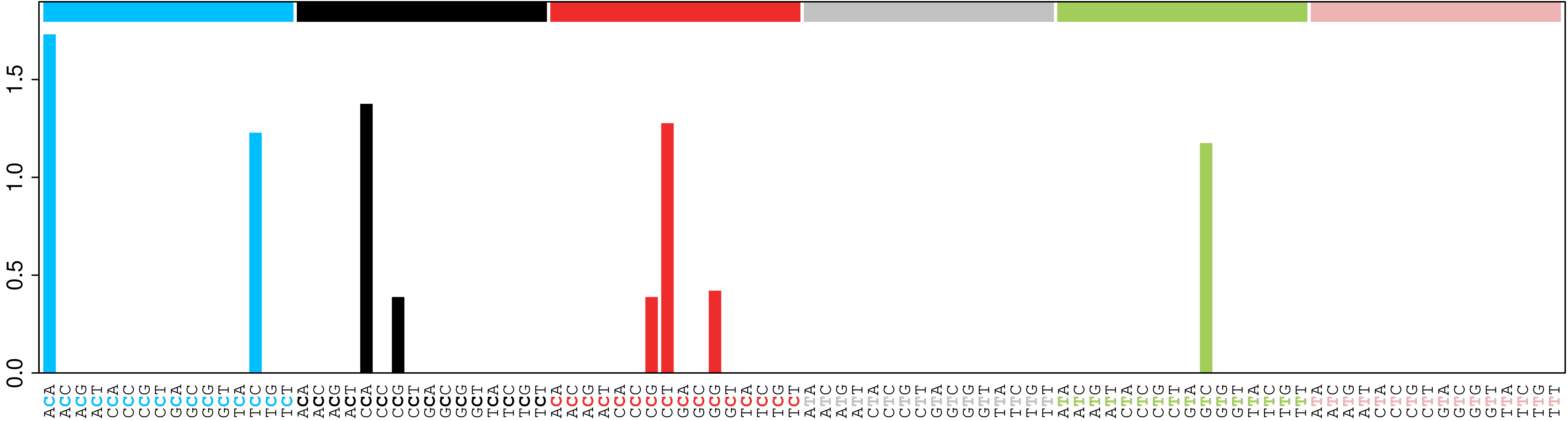
C>T

T>A

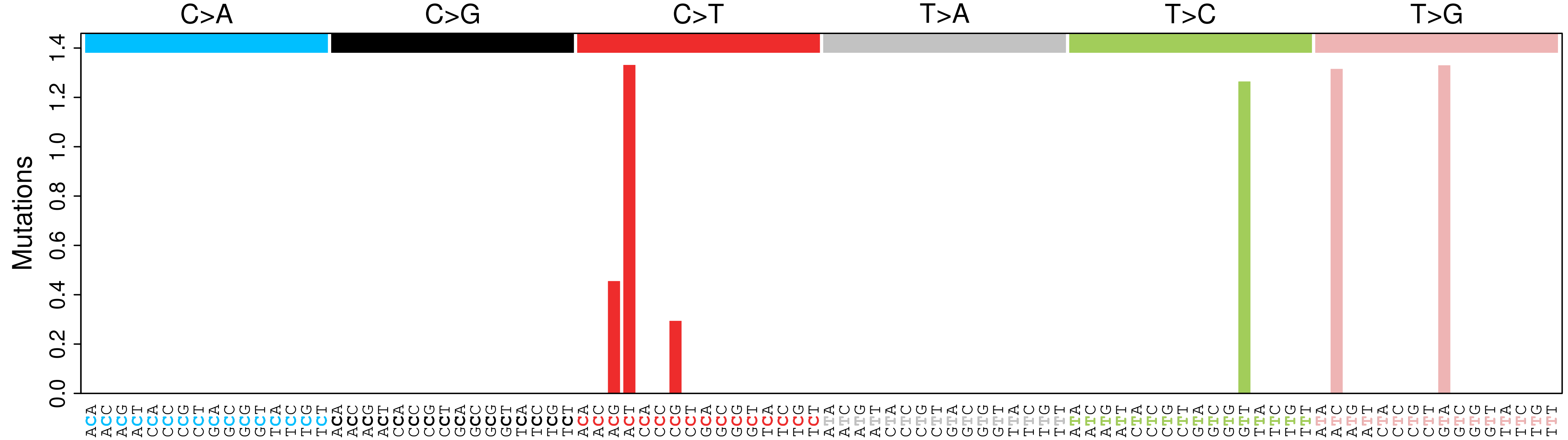
T>C

T>G

Mutations



CATD257a (6 mutations)



CATD0139a (7 mutations)

C>A

C>G

C>T

T>A

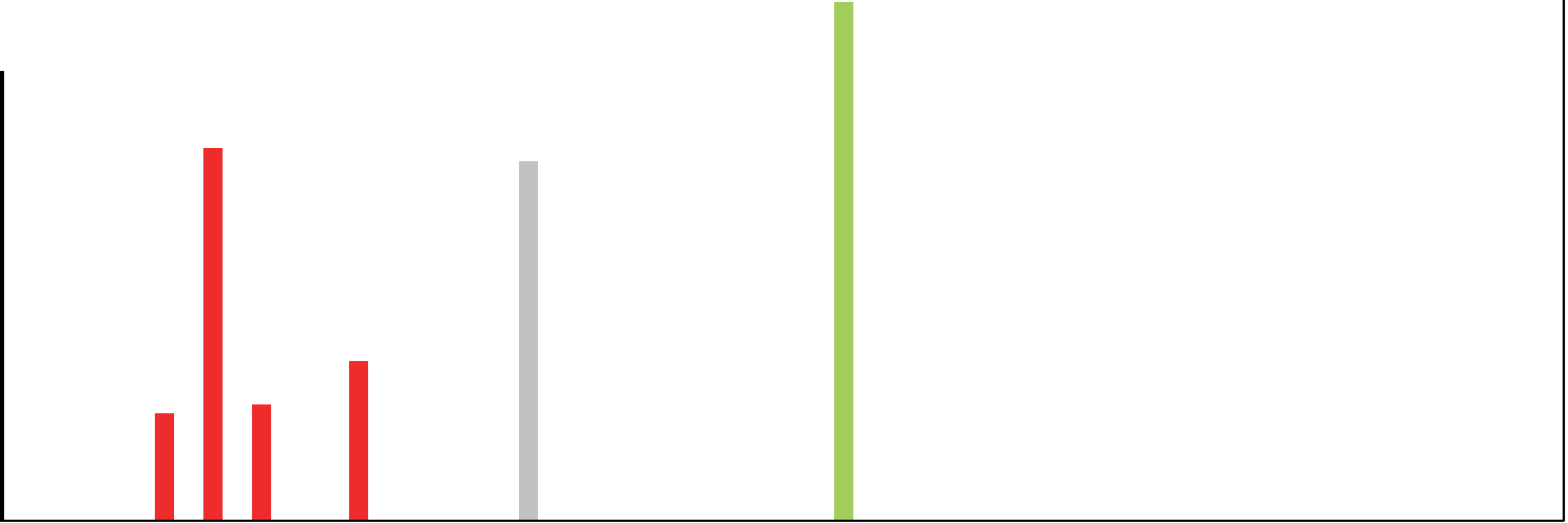
T>C

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)



CATD271a (5 mutations)

C>A

C>G

C>T

T>A

T>C

T>G

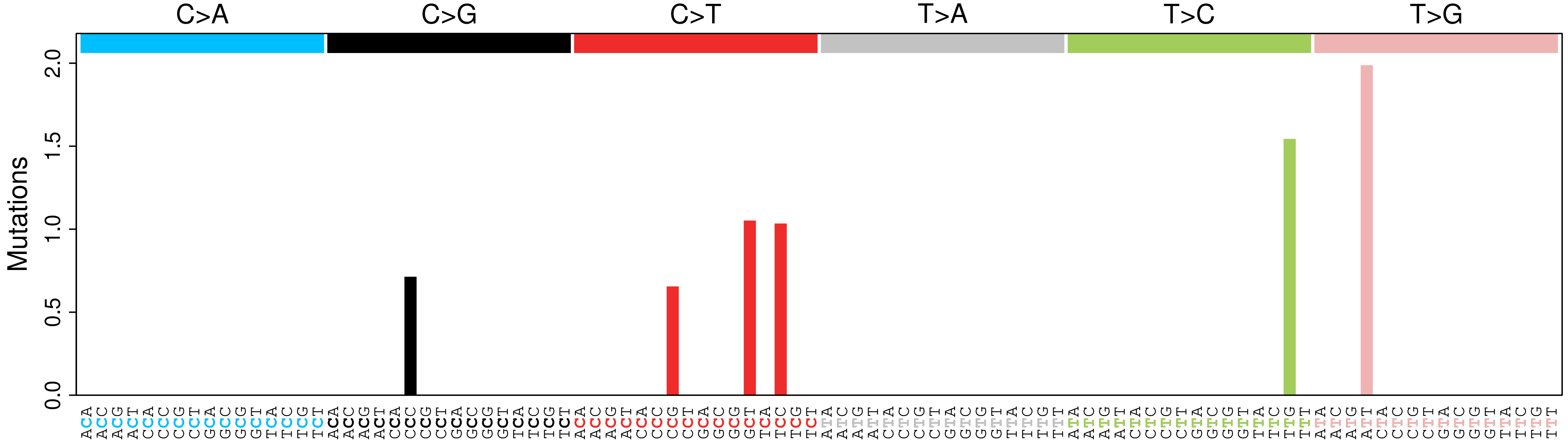
Mutations

1.5
1.0
0.5
0.0

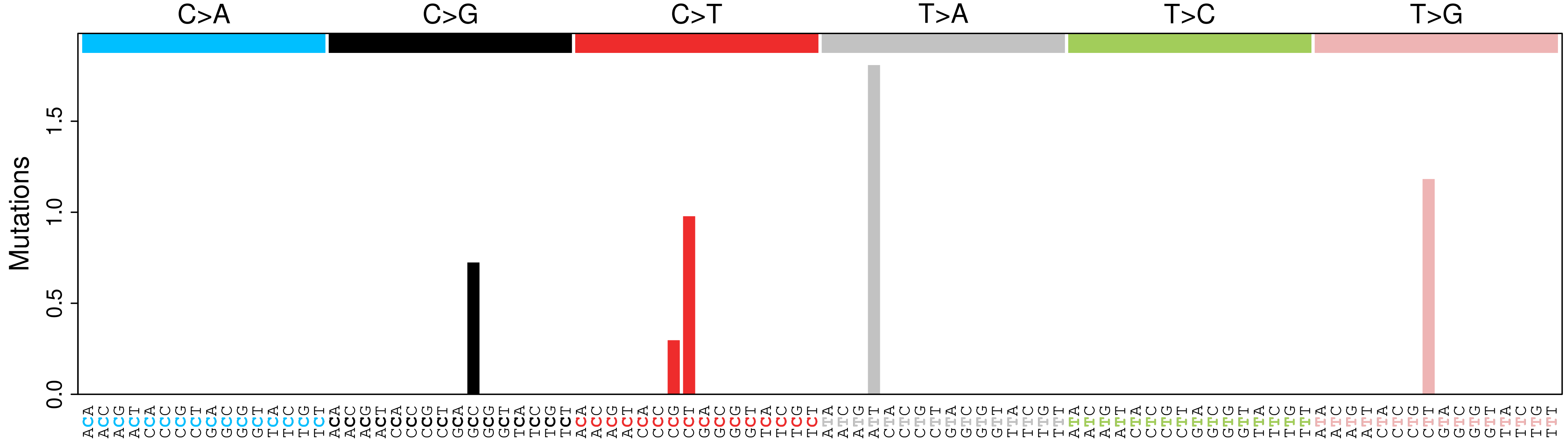
ACA ACC AGT ACT CCA CCC CCG CCT GCA GCC GGT GCA GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GGT GCA GCG GCT TCA TCC TCG TCT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GCA GCG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GCA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



CATD259a (7 mutations)



CATD0127a (5 mutations)



CATD277a (3 mutations)

$C > A$

C > G

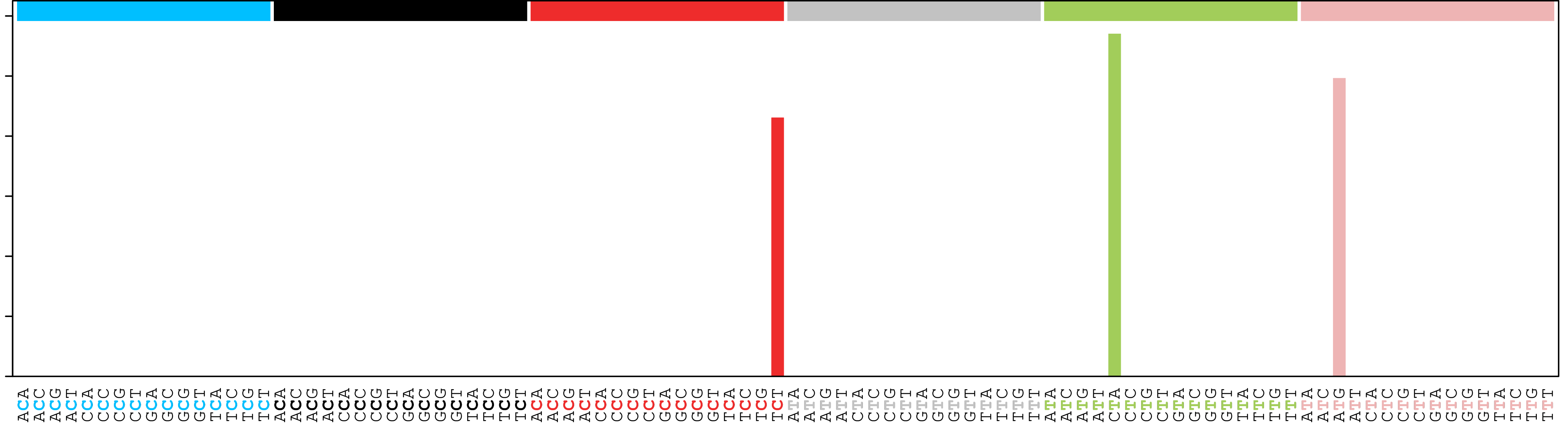
$$C > T$$

T>A

$T > C$

$T > G$

0.0 0.2 0.4 0.6 0.8 1.0 1.2

[illegible]

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
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GTT
TTA
TTC
TTG
TTT
ATA
ATC
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ATT
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CTG
CTT
GTA
GTC
GTG
GTT
TTA
TTC
TTG
TTT

CATD0133a (1 mutations)

