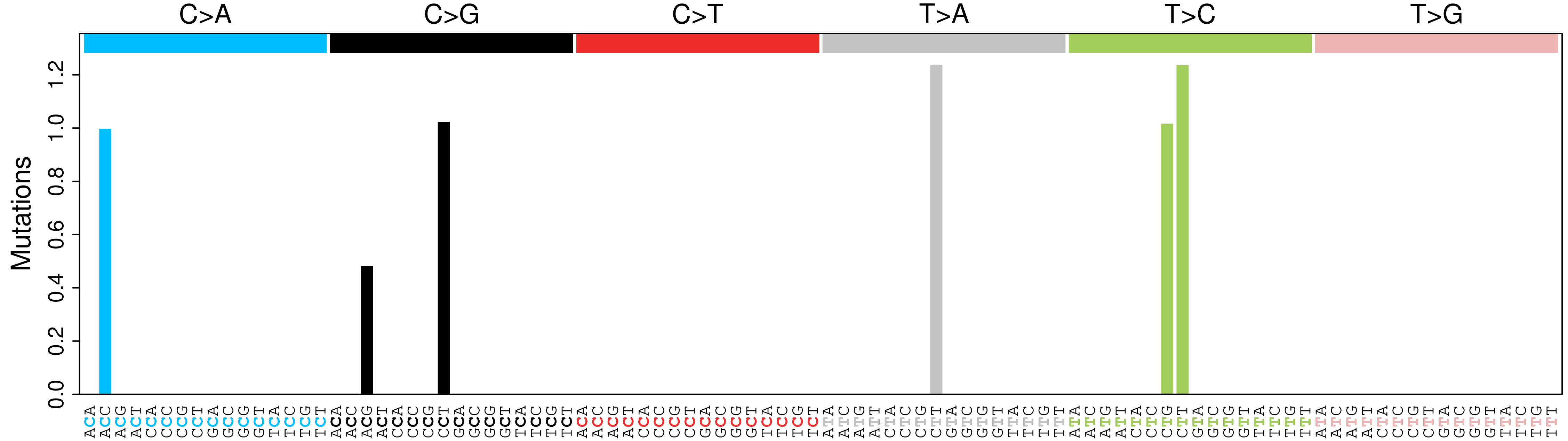


CATD0414a (8 mutations)



CATD0105a (6 mutations)



CATD189a (3 mutations)

C>A

C>G

C>T

T>A

T>C

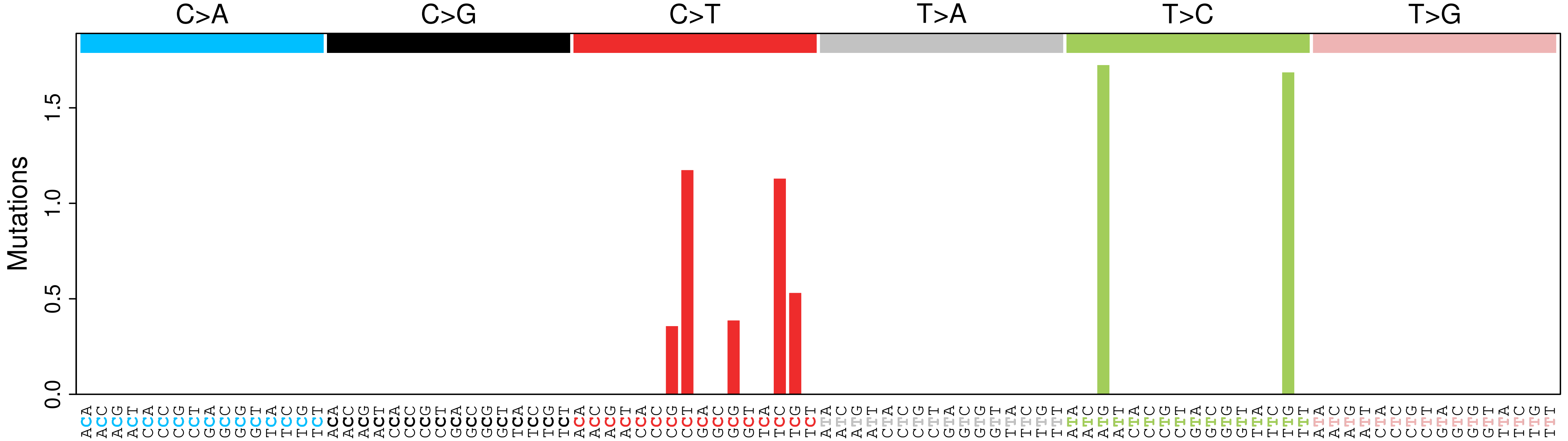
T>G

Mutations

1.4
1.2
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
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

CATD0090a (7 mutations)



CATD0088a (5 mutations)

C>A

C>G

C>T

T>A

T>C

T>G

Mutations

1.2

0.8

0.4

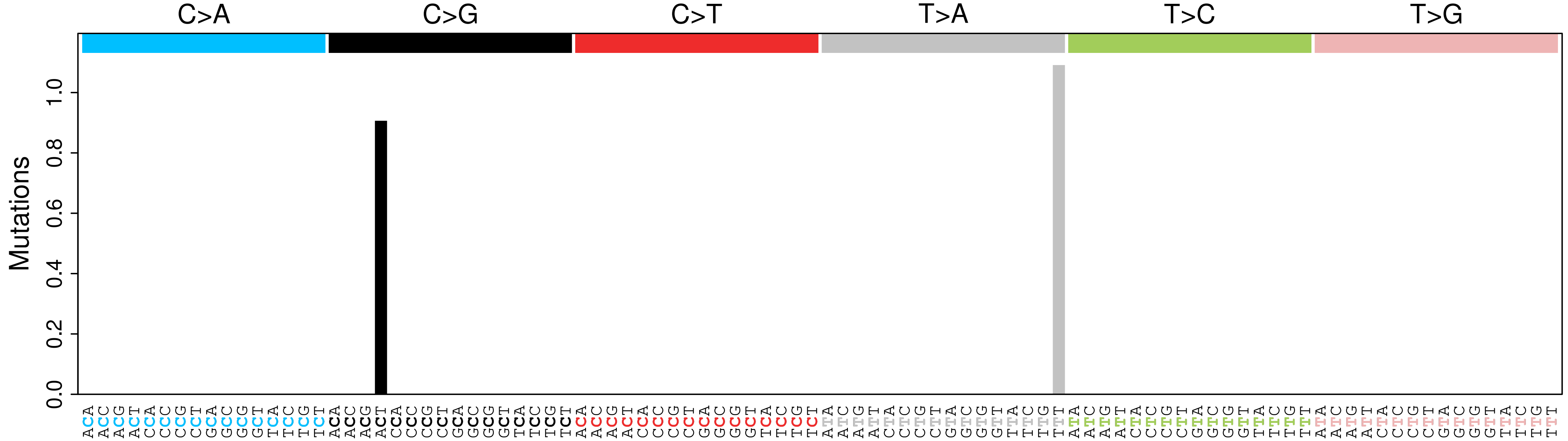
0.0

ACA
ACC
ACG
ACT
CCA
CCC
CCG
CCT
GCA
GCC
GGG
GCT
TCA
TCC
TCG
TCT
ACA
ACC
ACG
ACT
CCA
CCC
CCG
CCT
GCA
GCC
GGG
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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CTA
CTC
CTG
CTT
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GTG
GTT
TTA
TTC
TTG
TTT

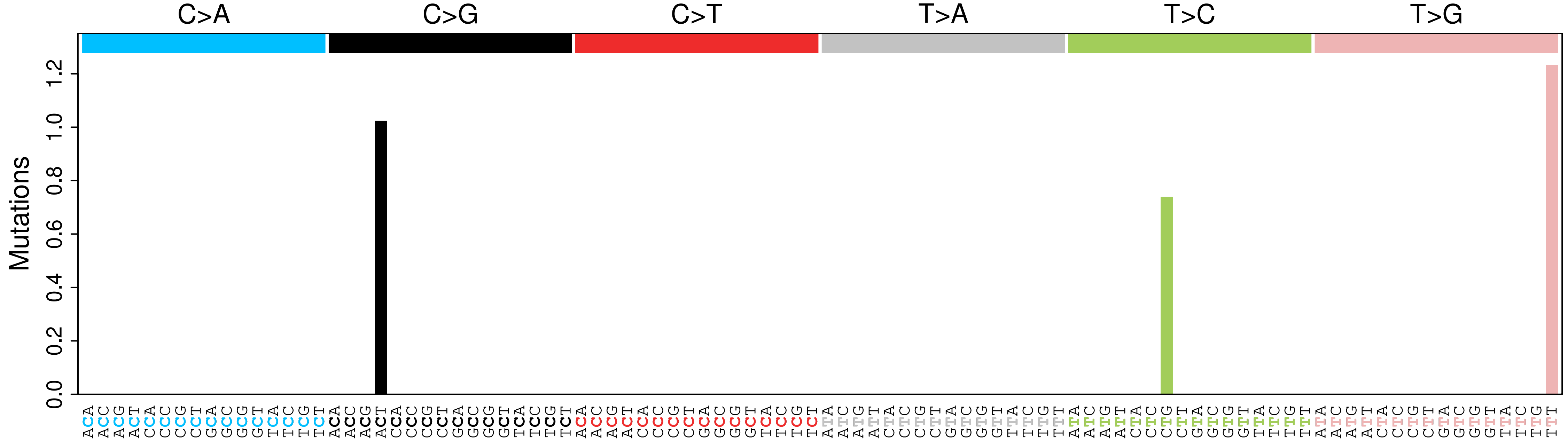
CATD0102a (7 mutations)



CATD0400a (2 mutations)



CATD0095a (3 mutations)



CATD0087a (8 mutations)

C>A

C>G

C>T

T>A

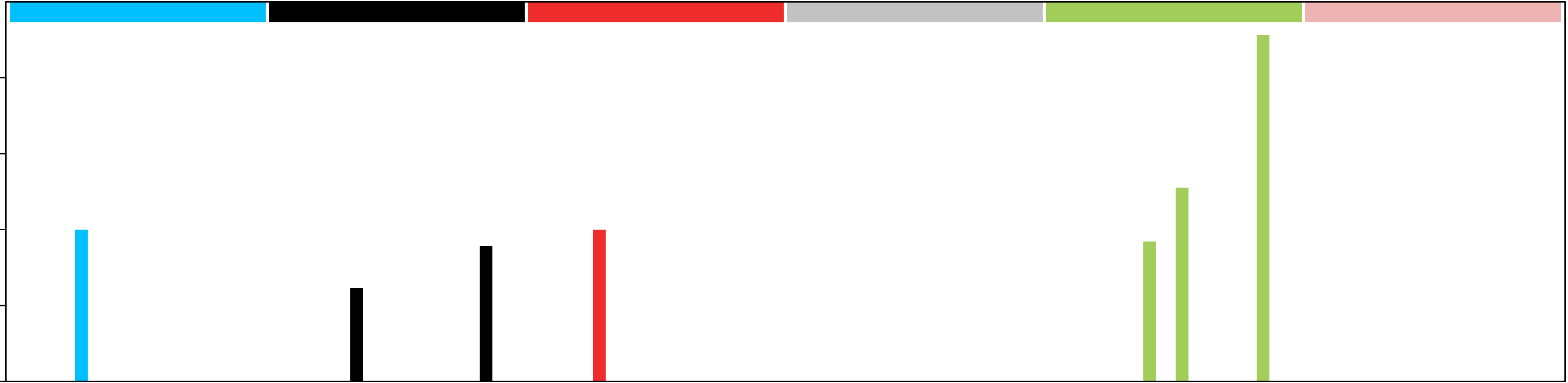
T>C

T>G

Mutations

2.0
1.5
1.0
0.5
0.0

ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GGT GTC TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GGT GTC 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



CATD0410a (3 mutations)

C>A

C>G

C>T

T>A

T>C

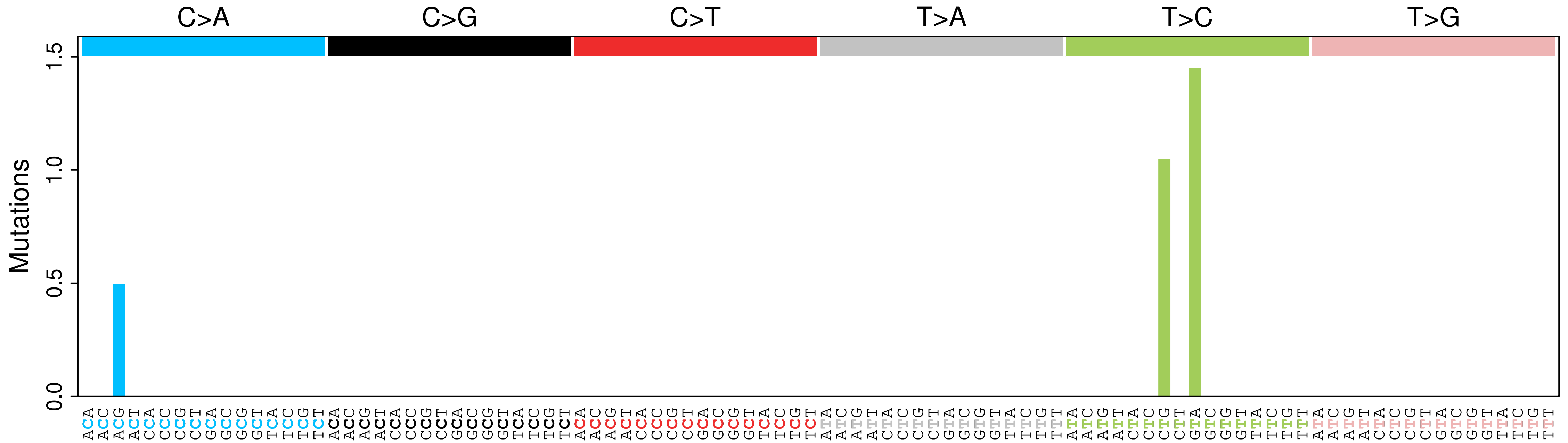
T>G

Mutations

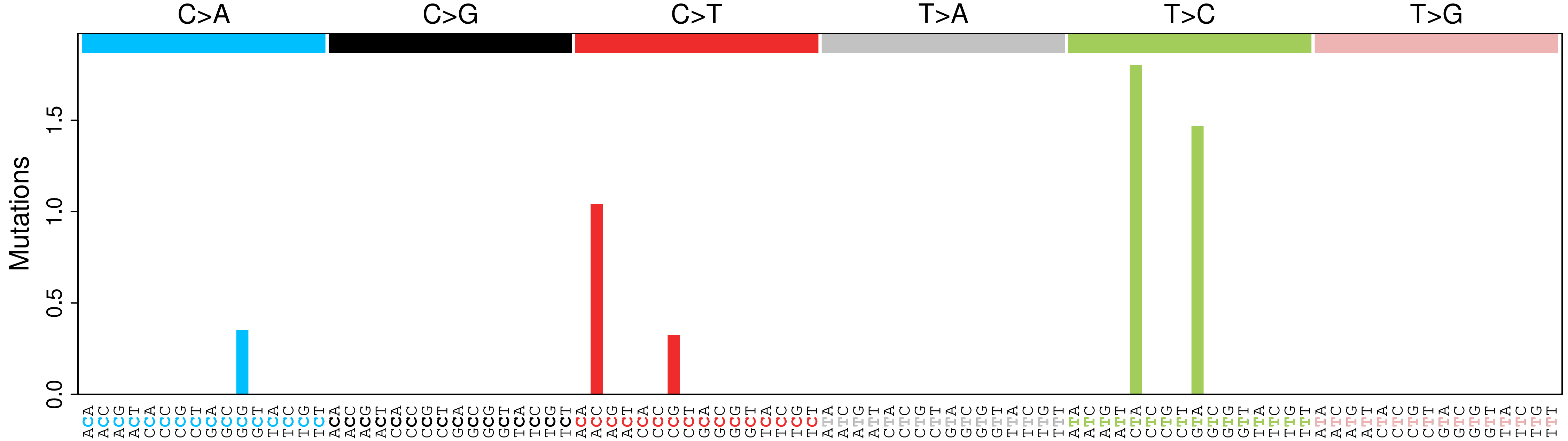
1.2
1.0
0.8
0.6
0.4
0.2
0.0

A C A C A C C C C G C A G C G G T T C A T C C T T A C C A C G A C T C C C C G C C T G C A G C C G G T C A C C G T T C T A T C A T G A T T C T C T G T A T T C T T A T C A T G A T C T A C C T G T A C G T T A C T T G T T A T A T C A T G A T A C C T C T A C G T A C G T T A C G T T T A T C G T T

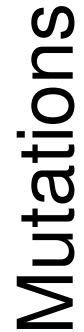
CATD0101a (3 mutations)



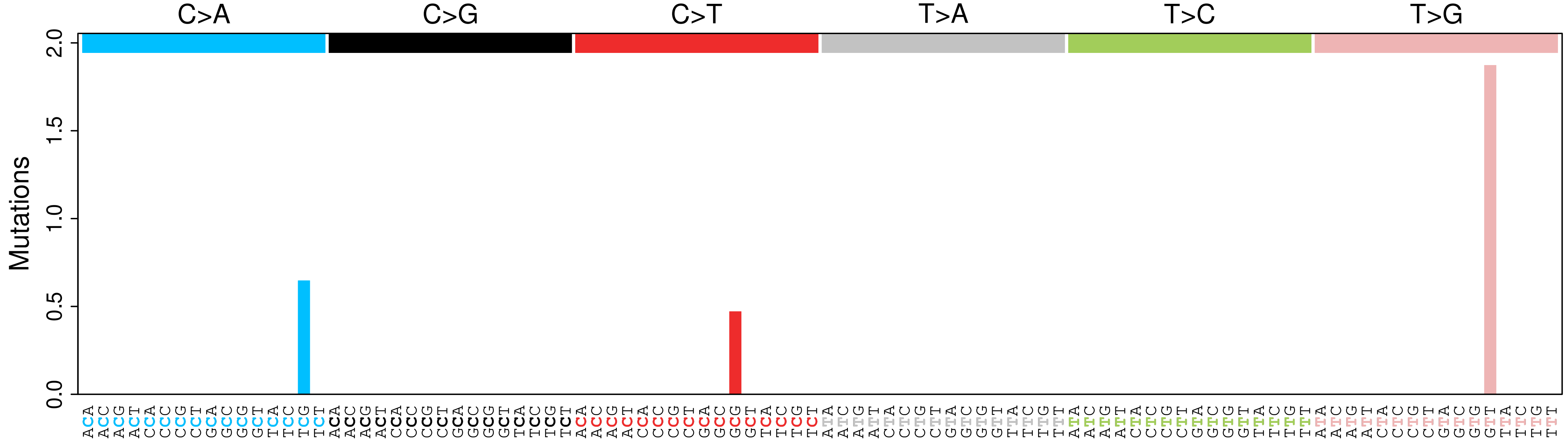
CATD0100a (5 mutations)



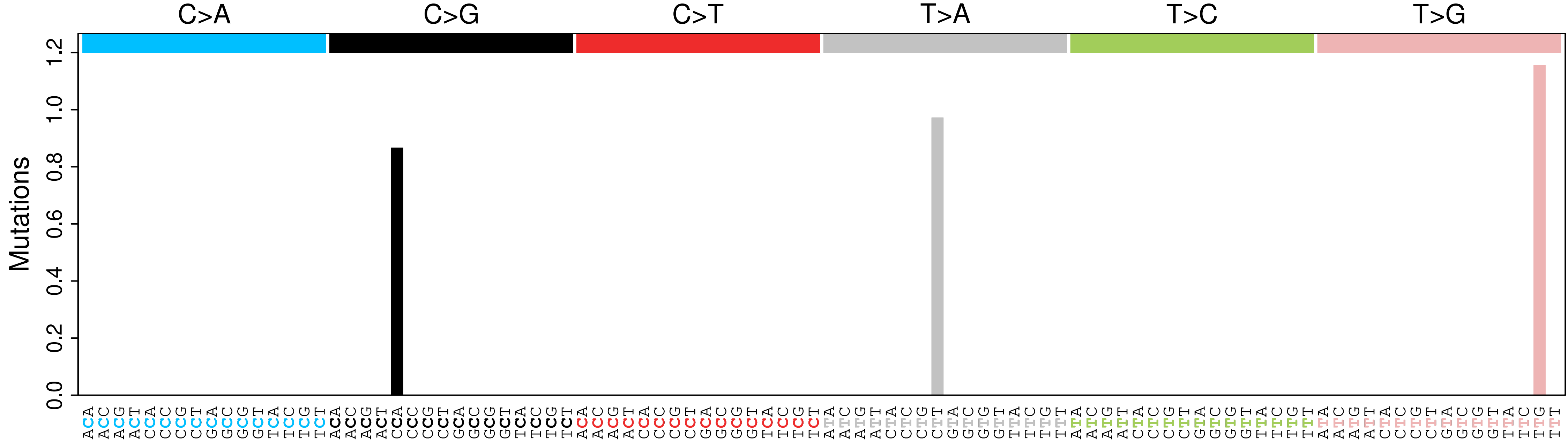
CATD0118a (15 mutations)



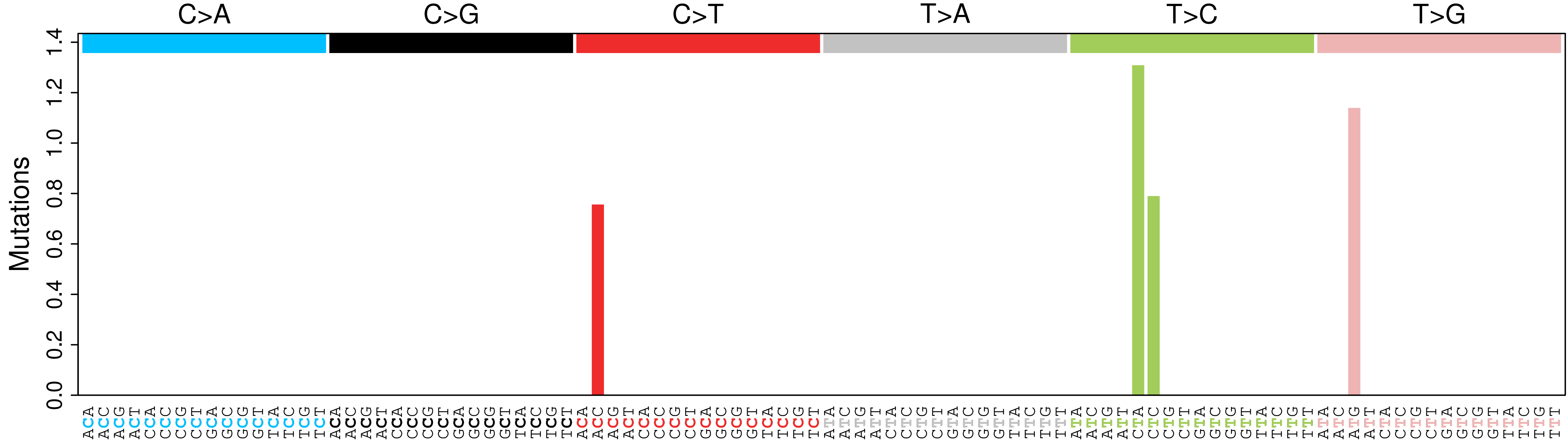
CATD0108a (3 mutations)



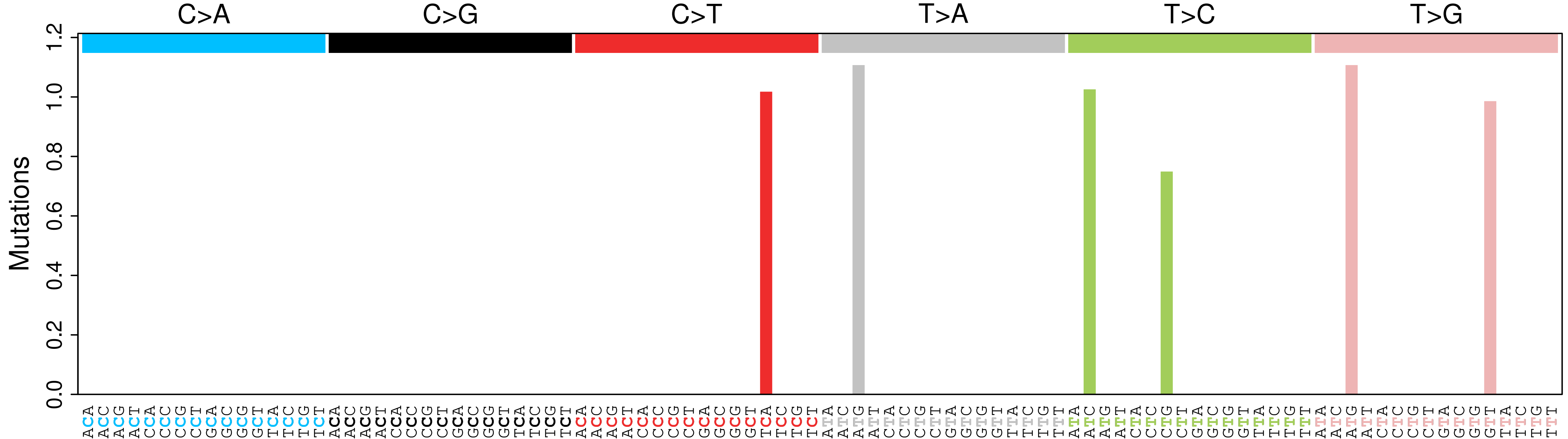
CATD0082a (3 mutations)



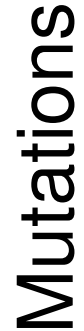
CATD0106a (4 mutations)



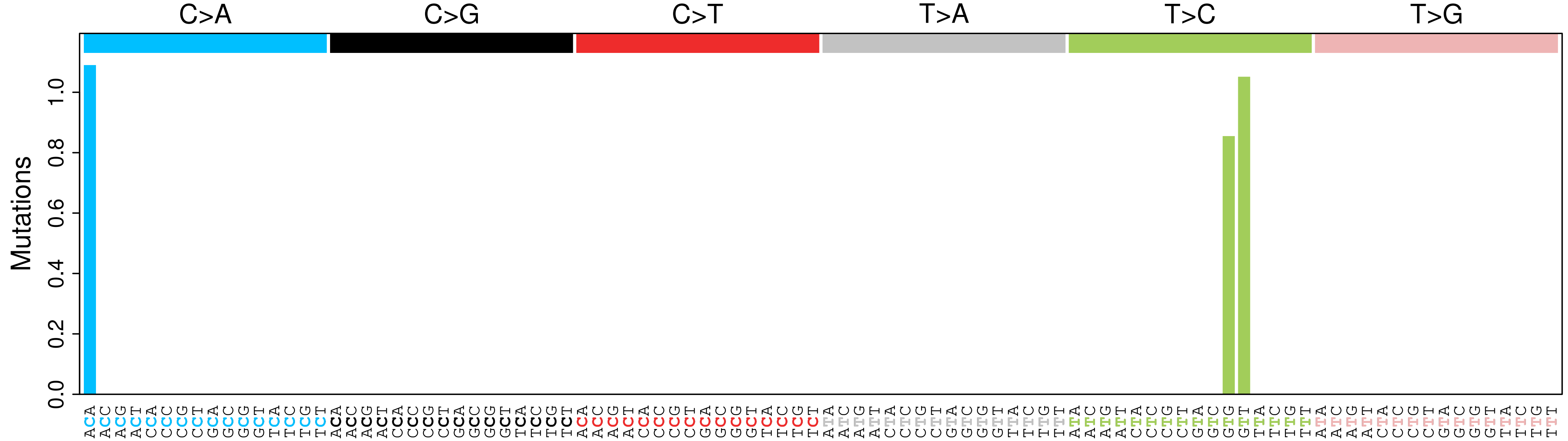
CATD0107a (6 mutations)



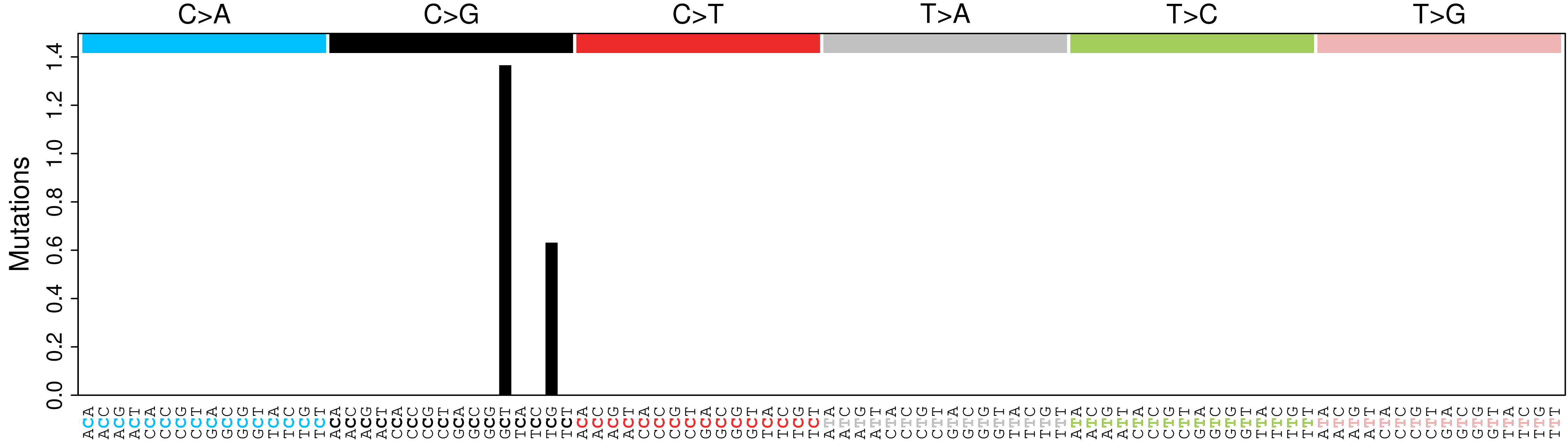
CATD0097a (7 mutations)



CATD0112a (3 mutations)



CATD0412a (2 mutations)



CATD0110a (5 mutations)

C>A

C>G

C>T

T>A

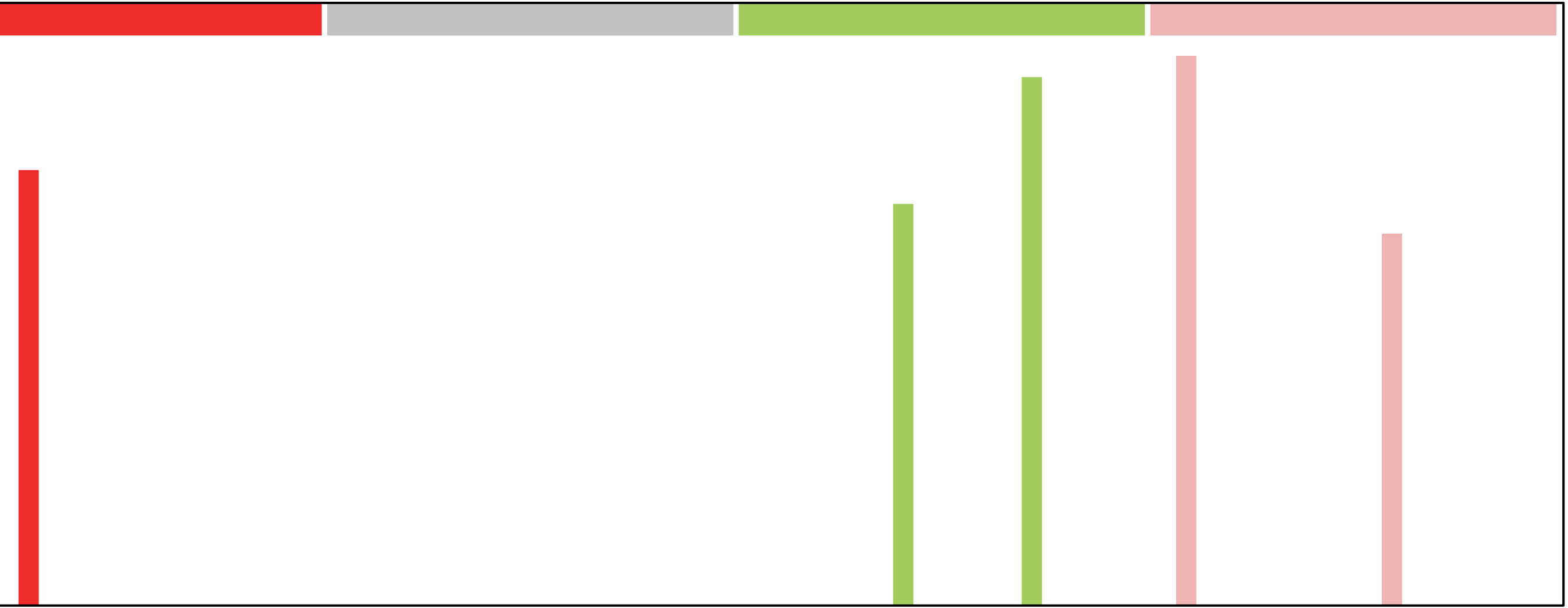
T>C

T>G

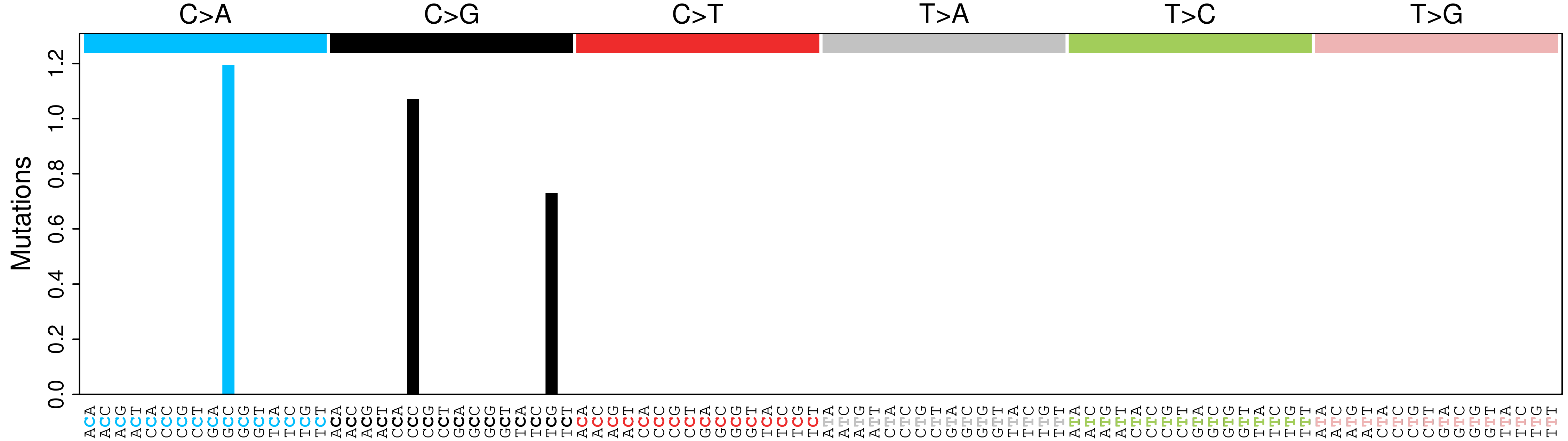
Mutations

1.2
1.0
0.8
0.6
0.4
0.2
0.0

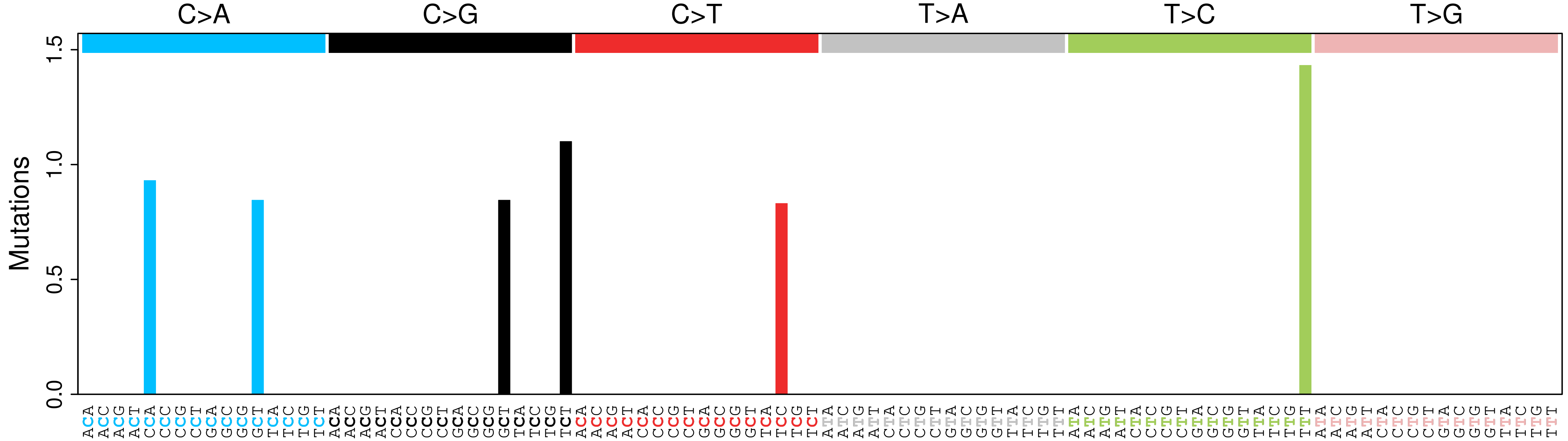
ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ACA ACC ACG ACT CCA CCC CCG CCT GCA GCC GCG GCT TCA TCC TCG TCT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT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



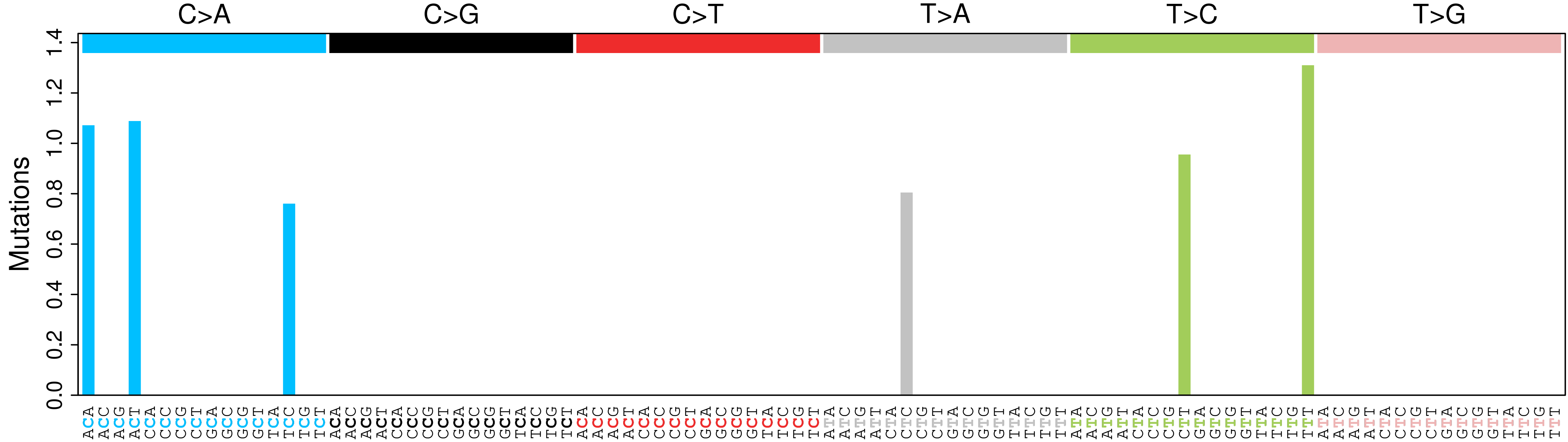
CATD0117a (3 mutations)



CATD0084a (6 mutations)



CATD0081a (6 mutations)



CATD0092a (3 mutations)

$C > A$

$C > G$

$C > T$

T > A

$T > C$

T > G

Mutations

1.2

80.

0.4

0.0

[illegible]

CATD0111a (5 mutations)

C>A

C>G

C>T

T>A

T>C

T>G

Mutations

1.5

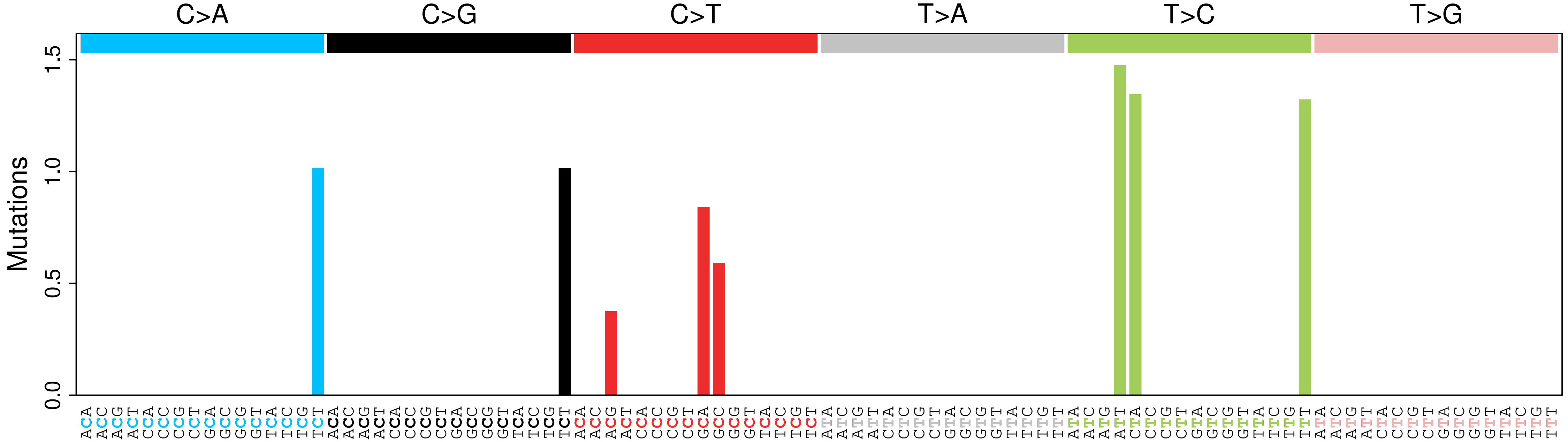
1.0

0.5

0.0

ACA
ACC
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
TCG
TCT
ATA
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CTA
CTC
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GTA
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GTG
GTT
TTA
TTC
TTG
TTT
ATA
ATC
ATG
ATT
CTA
CTC
CTG
CTT
GTA
GTC
GTG
GTT
TTA
TTC
TTG
TTT

CATD0114a (8 mutations)



CATD0103a (13 mutations)

C > A

C > G

$$C > T$$

$T > A$

$T > C$

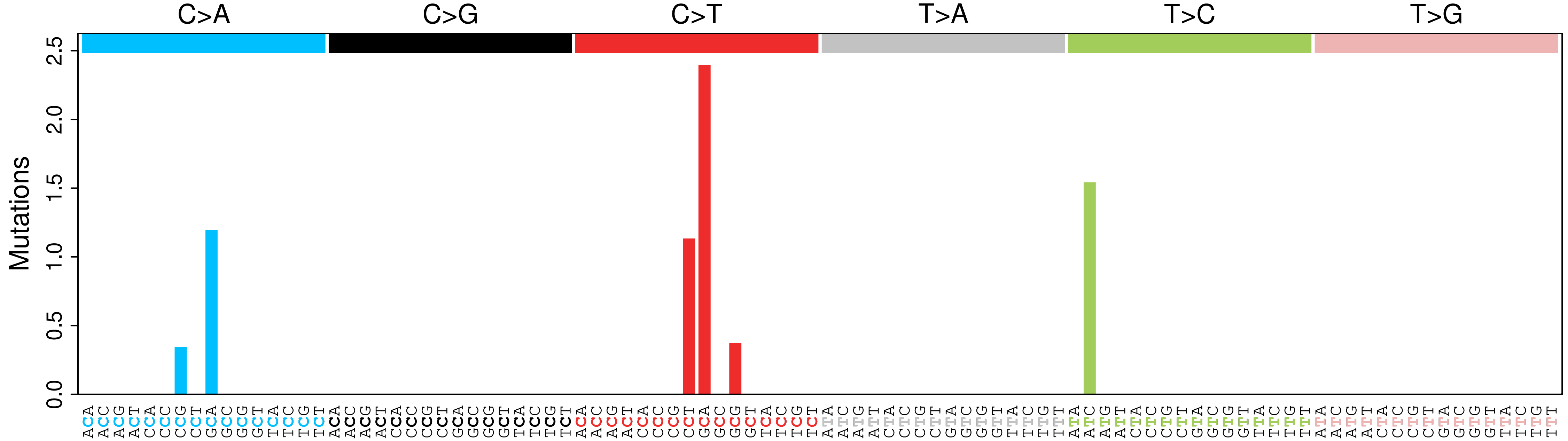
T>G

Mutations

0.0 0.5 1.0 1.5 2.0

AACGTAACCAGTAACTAACCAACAATCCCGTCGGTTACTCCTTACTCGTACCGGTACGCCGAAGATTATAAAGAATACTTGTTATAGTAGTAGTGCCTGTTATCATGTTA

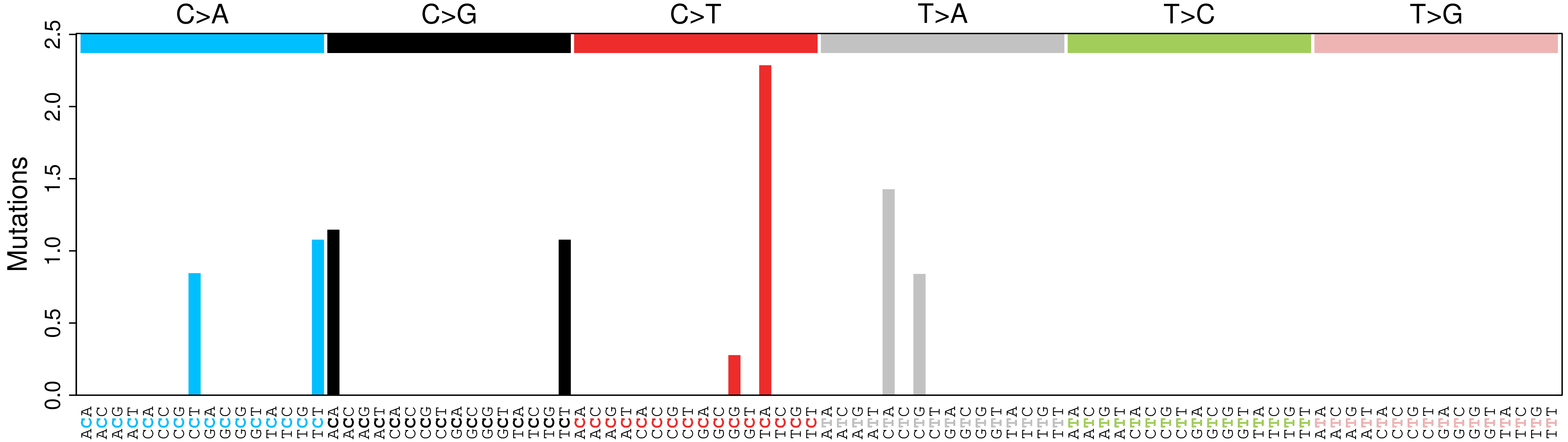
CATD0099a (7 mutations)



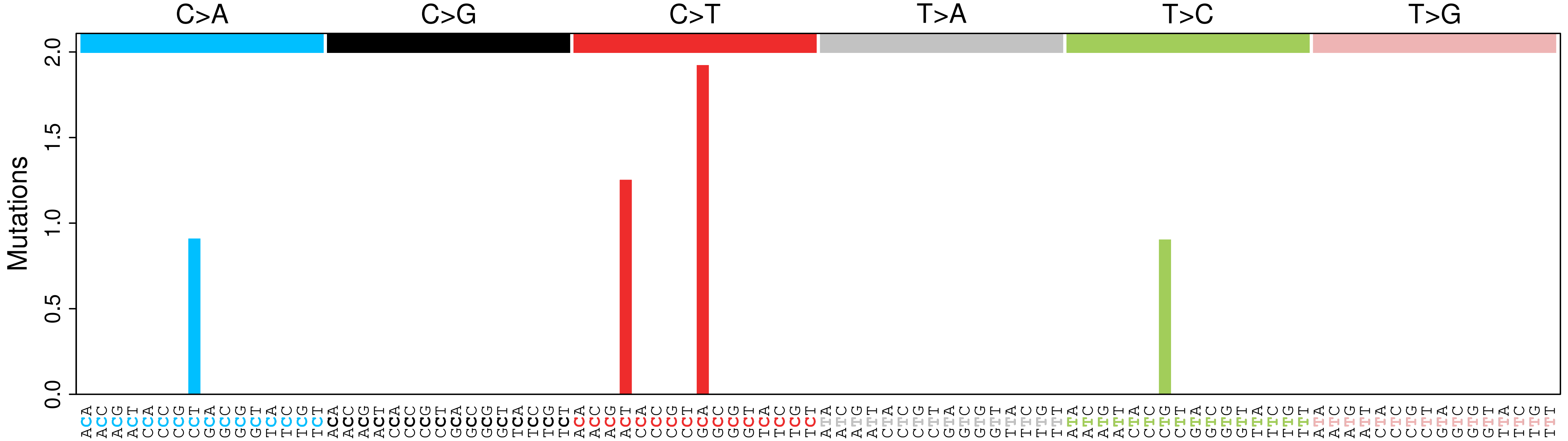
CATD0091a (6 mutations)



CATD0086a (9 mutations)



CATD0405a (5 mutations)



CATD188a (7 mutations)

C>A

C>G

C>T

T>A

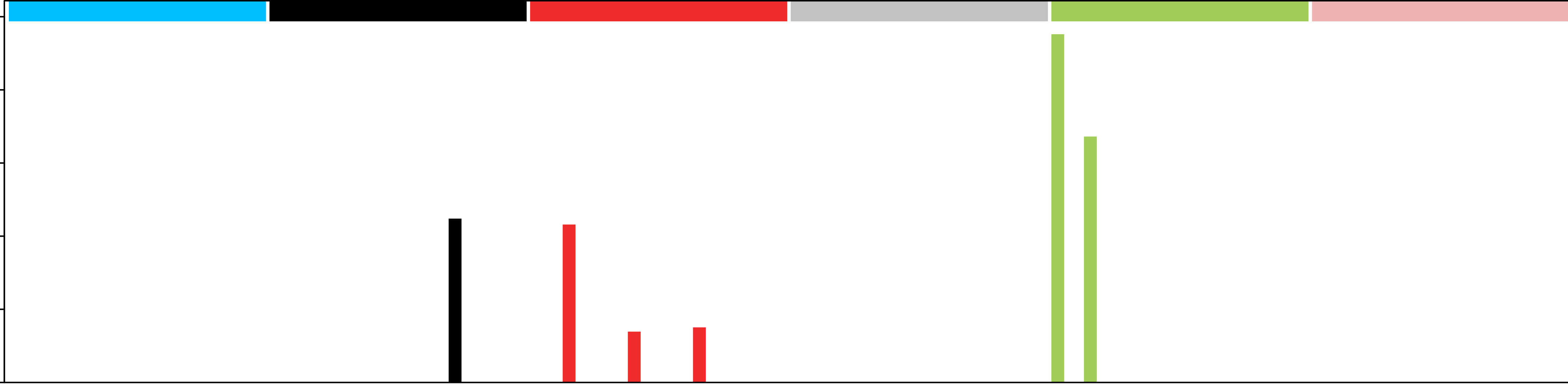
T>C

T>G

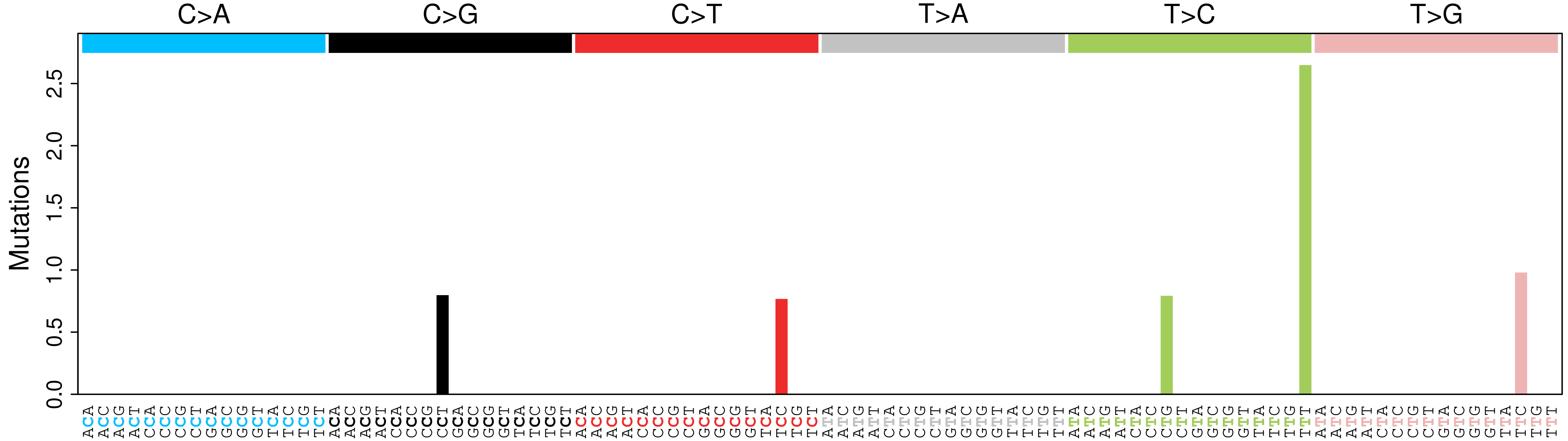
Mutations

2.5
2.0
1.5
1.0
0.5
0.0

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



CATD0401a (6 mutations)



CATD0096a (2 mutations)

$C > A$

C > G

$$C > T$$

T > A

$$T > C$$

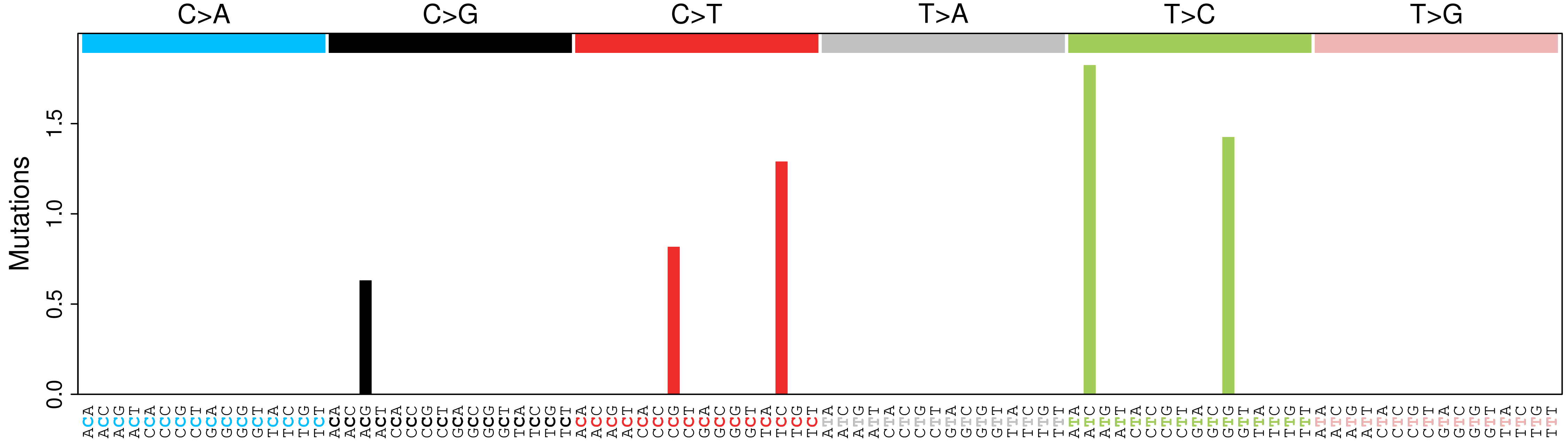
T > G

Mutations

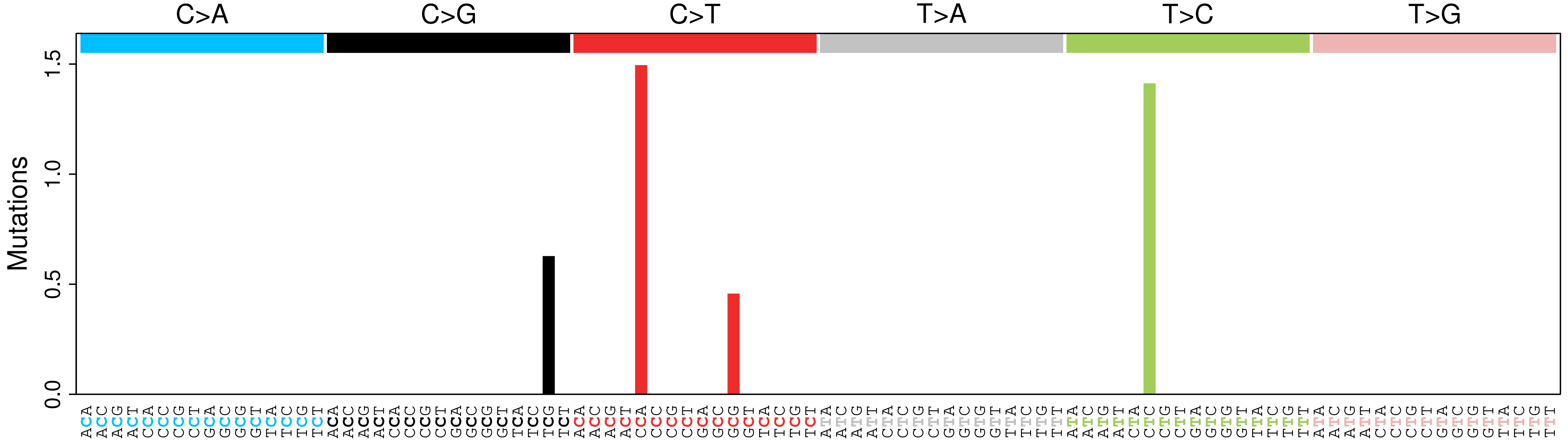
0.0 0.2 0.4 0.6 0.8 1.0

[illegible]

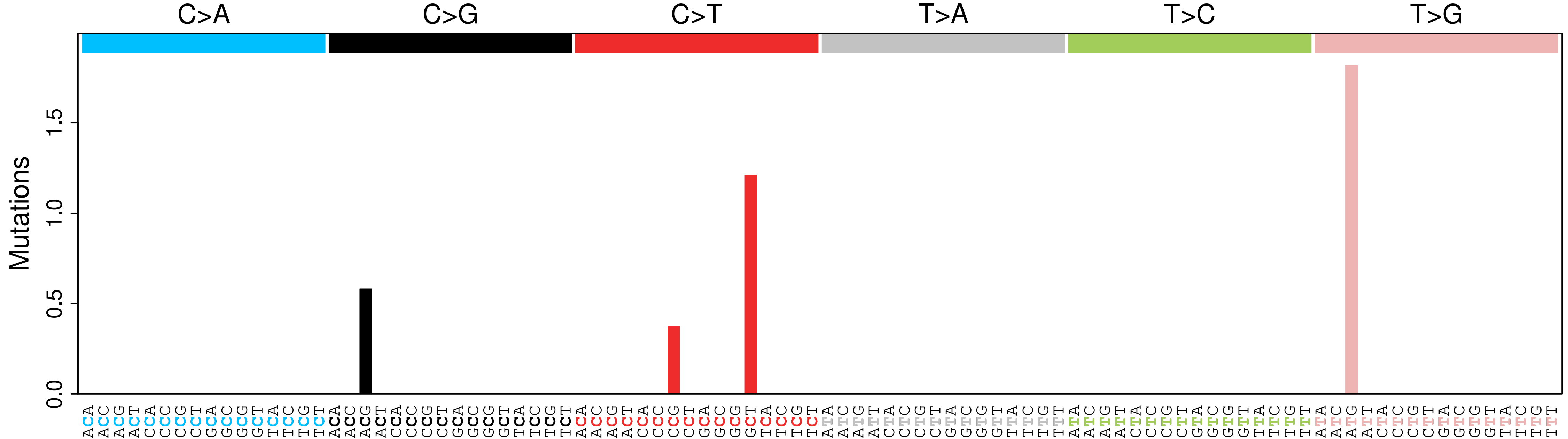
CATD0411a (6 mutations)



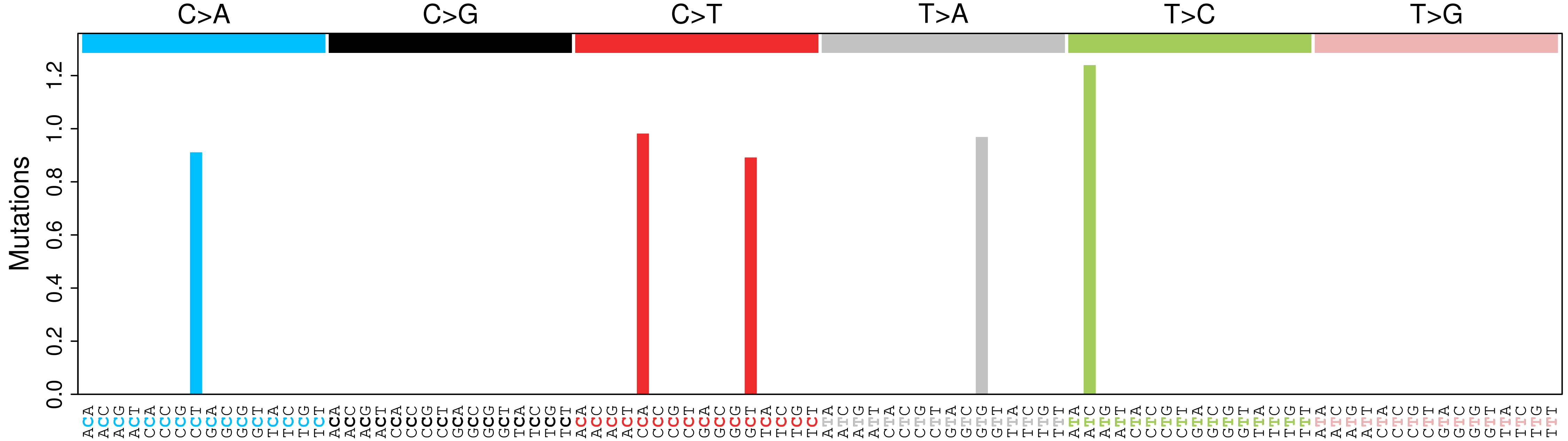
CATD0113a (4 mutations)



CATD0403a (4 mutations)



CATD0085a (5 mutations)



CATD190a (5 mutations)

$C > A$

C>G

$C > T$

T > A

$$T > C$$

T>G

Mutations

2.0

1.5

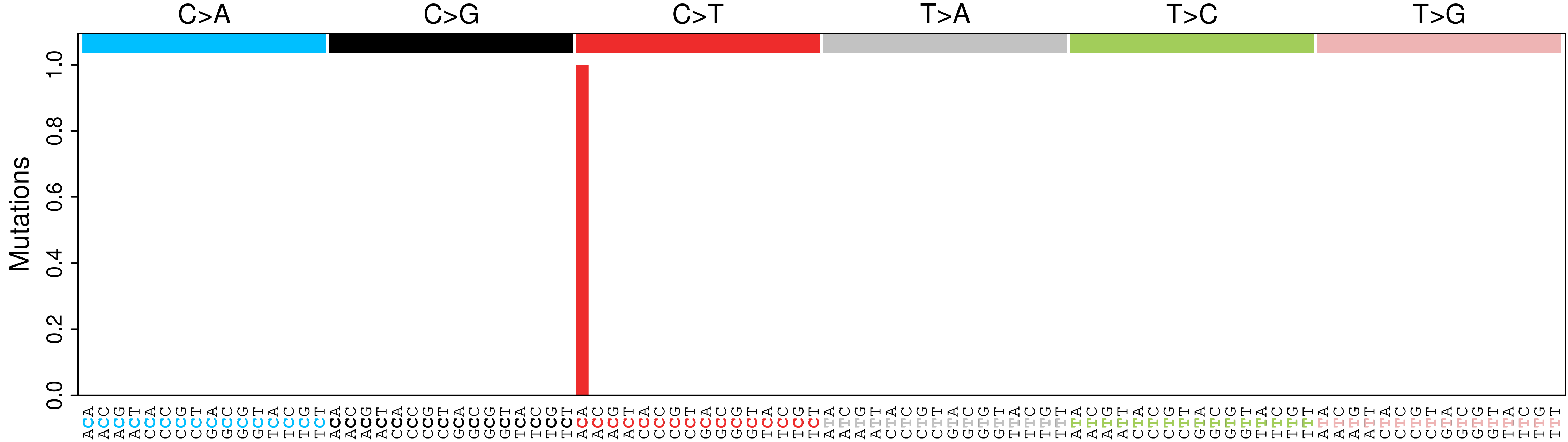
1.

0

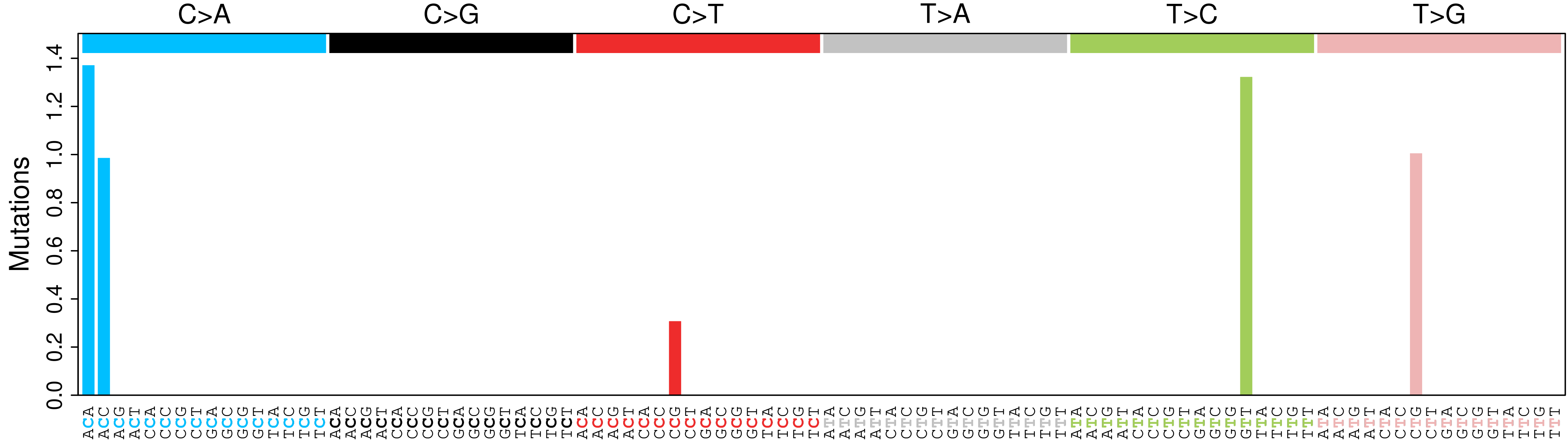
0

[illegible]

CATD0109a (1 mutations)



CATD0415a (5 mutations)



CATD191a (2 mutations)

$C > A$

$C > G$

$C > T$

$T > A$

 $T > C$

T>G

Mutations

1.0

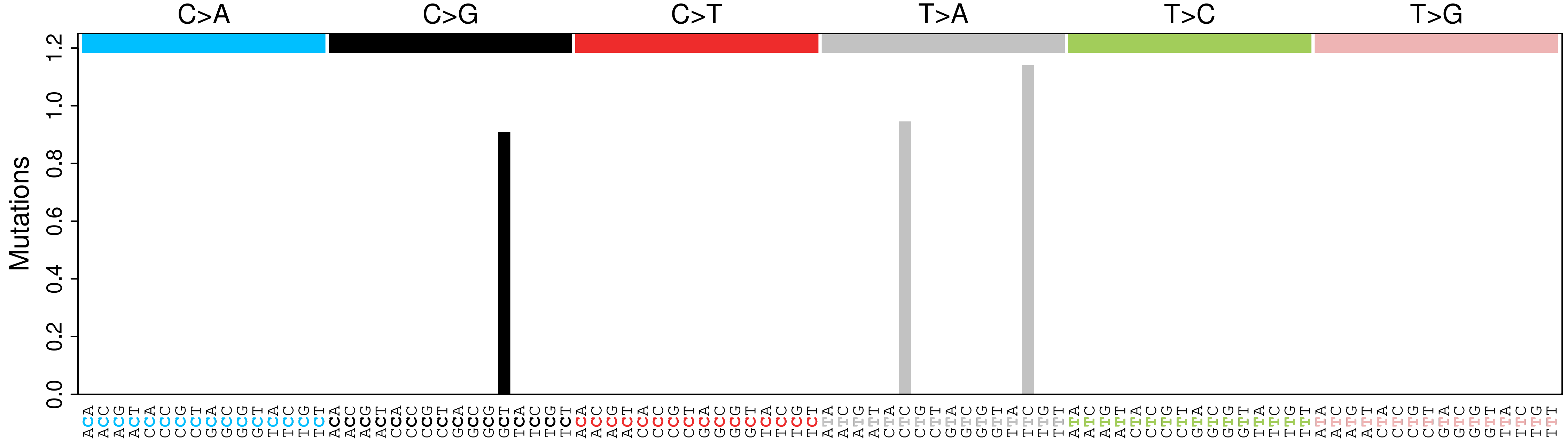
30.

0

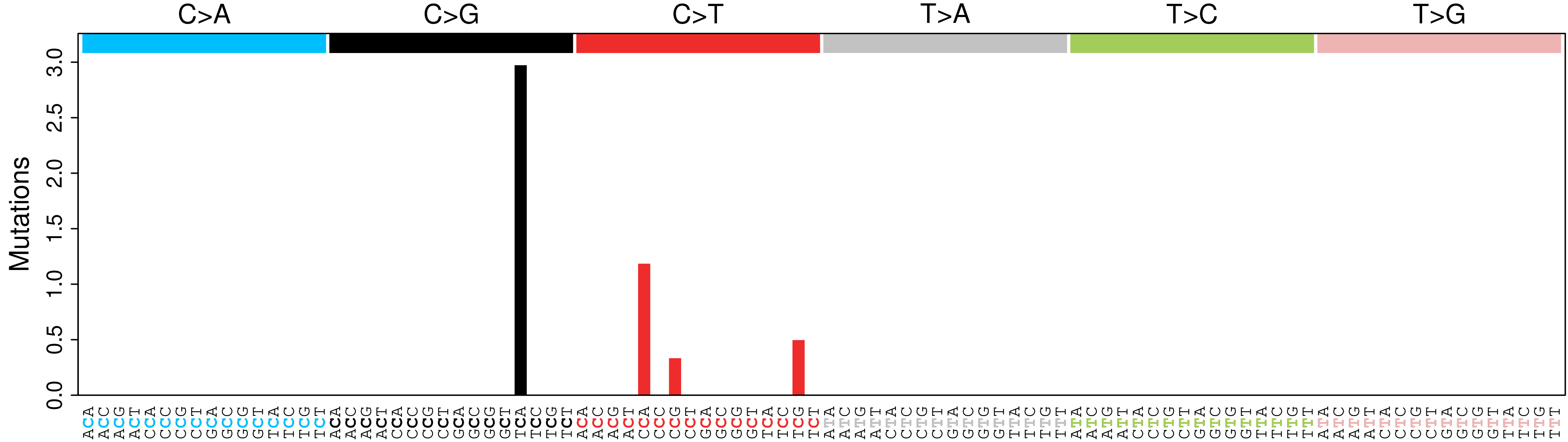
0

[illegible]

CATD0093a (3 mutations)



CATD0407a (5 mutations)



CATD0413a (2 mutations)

C > A

C > G

$C > T$

T > A

$$T > C$$

T>G

Mutations

1.0

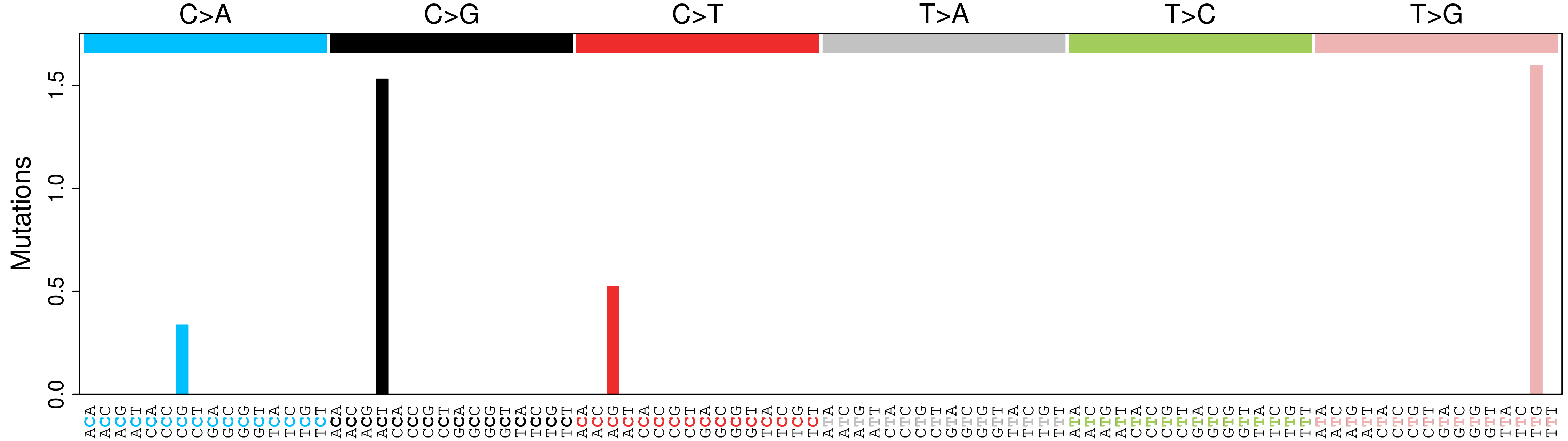
3.0

0

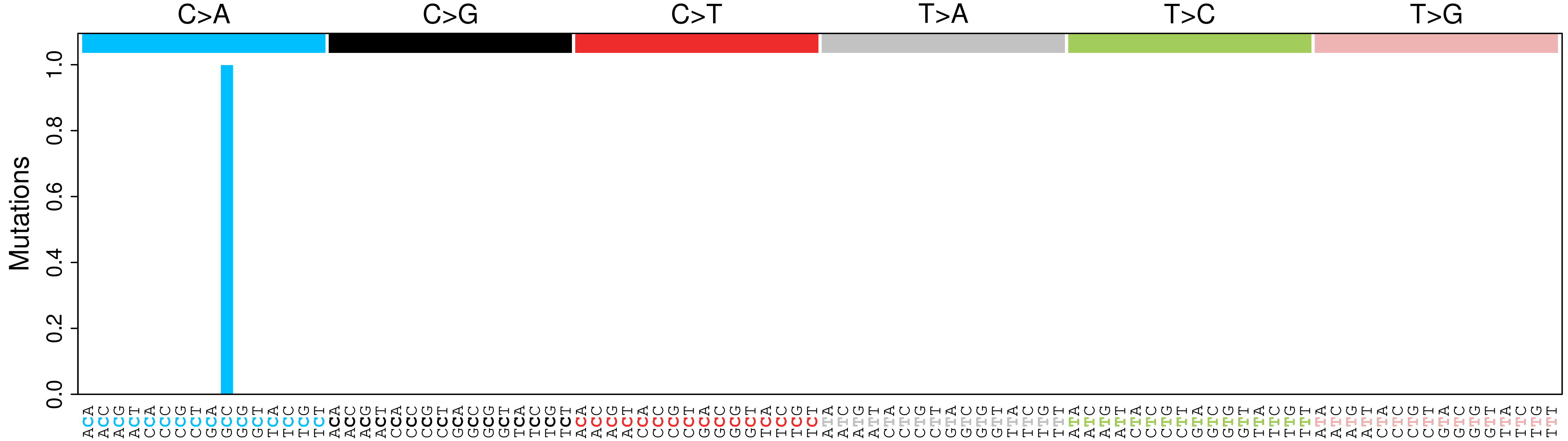
C

[illegible]

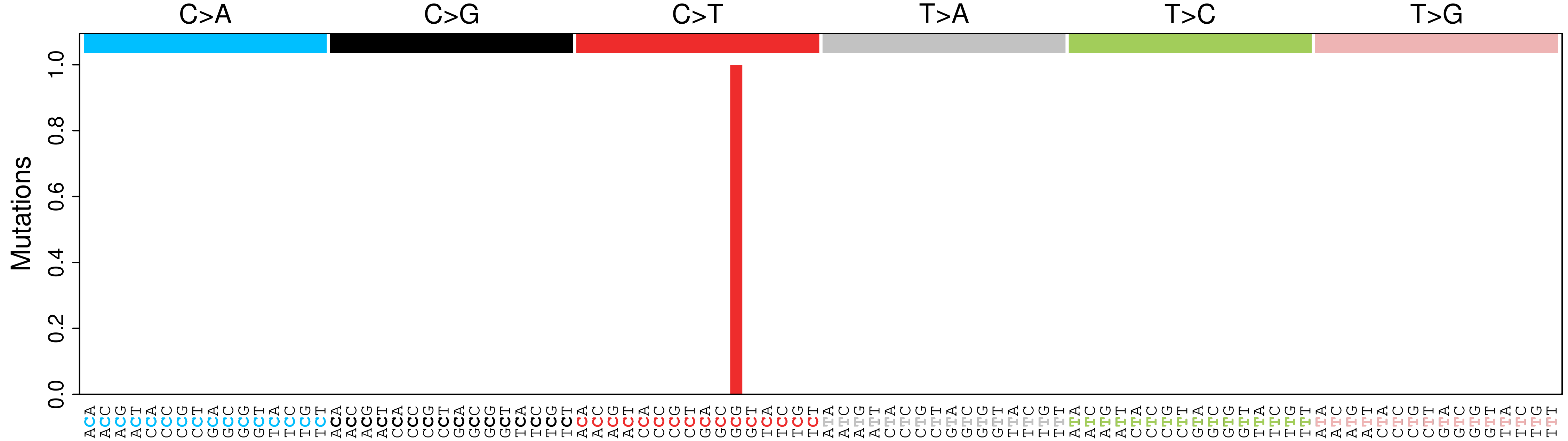
CATD0409a (4 mutations)



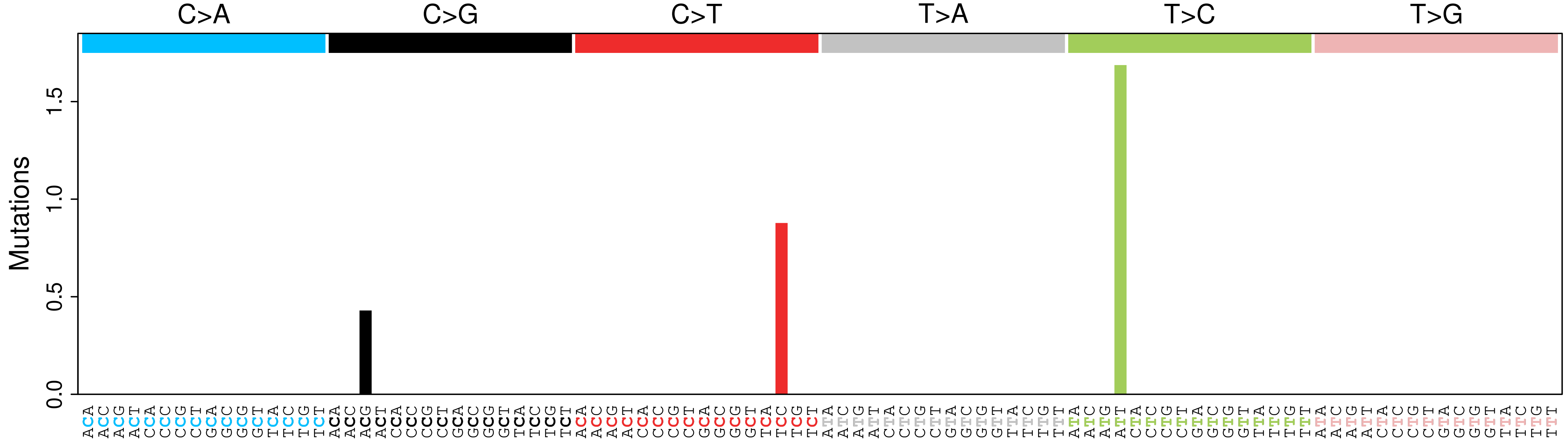
CATD0116a (1 mutations)



CATD0406a (1 mutations)



CATD0089a (3 mutations)



CATD0115a (2 mutations)

$C > A$

$C > G$

$C > T$

T > A

$T > C$

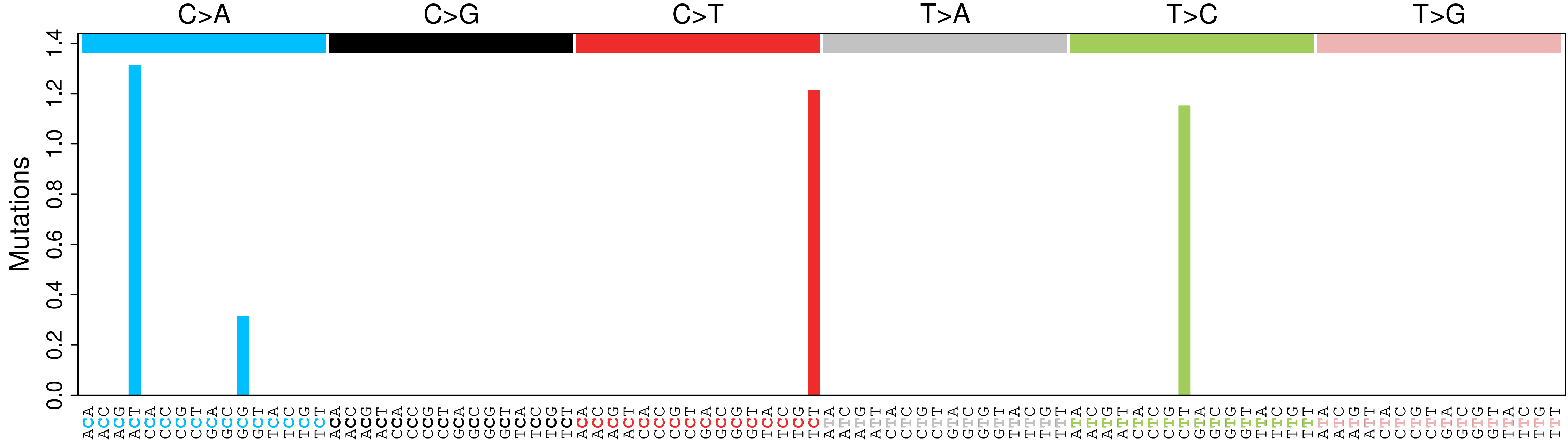
T > G

Mutations

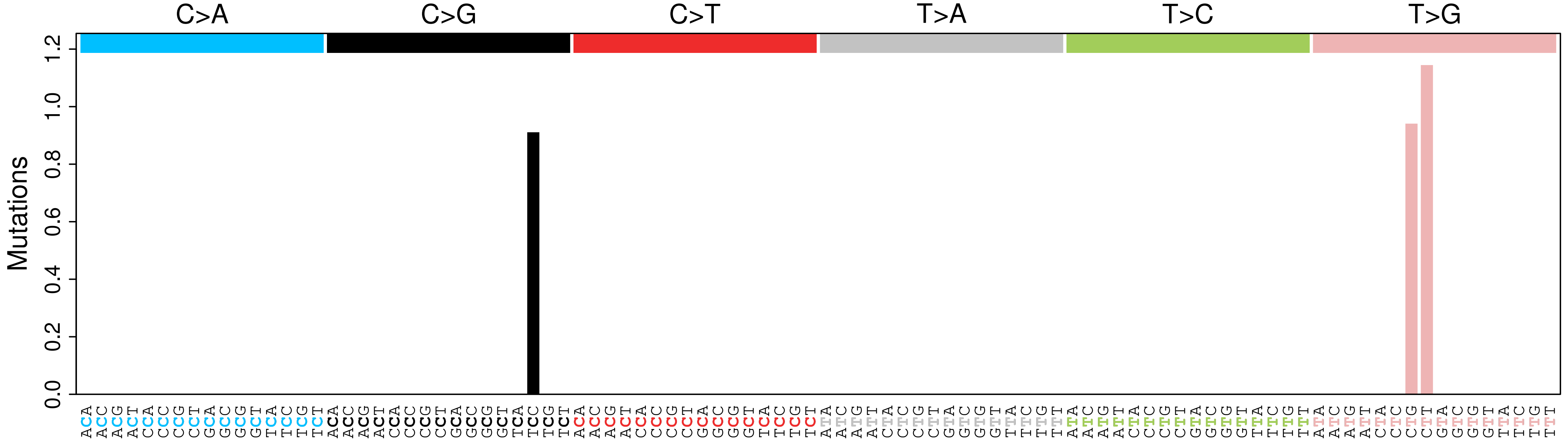
0.0 0.2 0.4 0.6 0.8 1.0 1.2

[illegible]

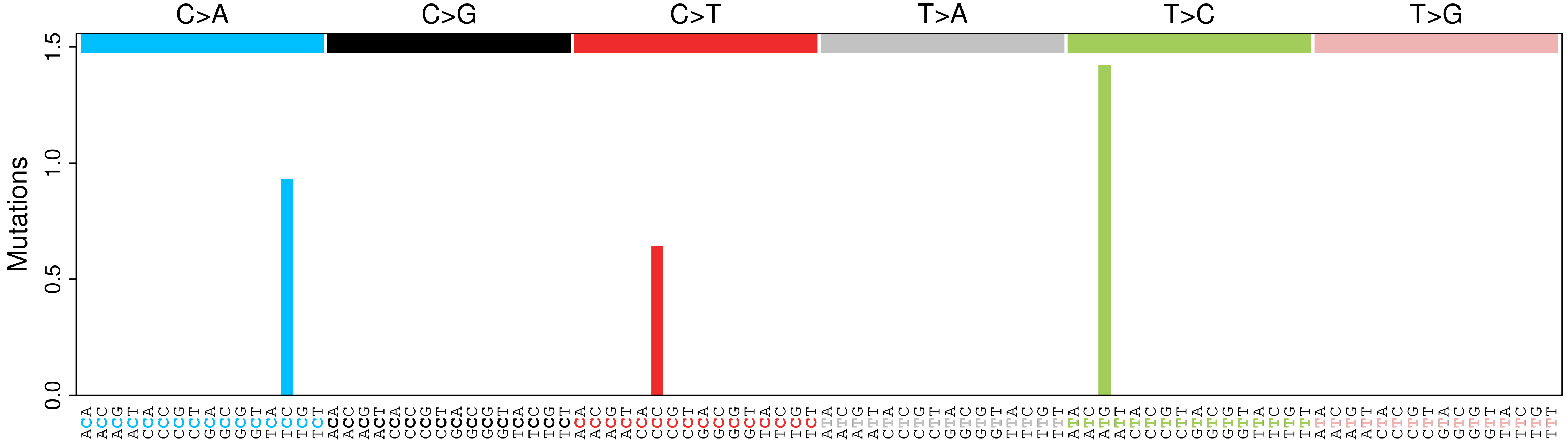
CATD0098a (4 mutations)



CATD0402a (3 mutations)



CATD0404a (3 mutations)



CATD0408a (4 mutations)

