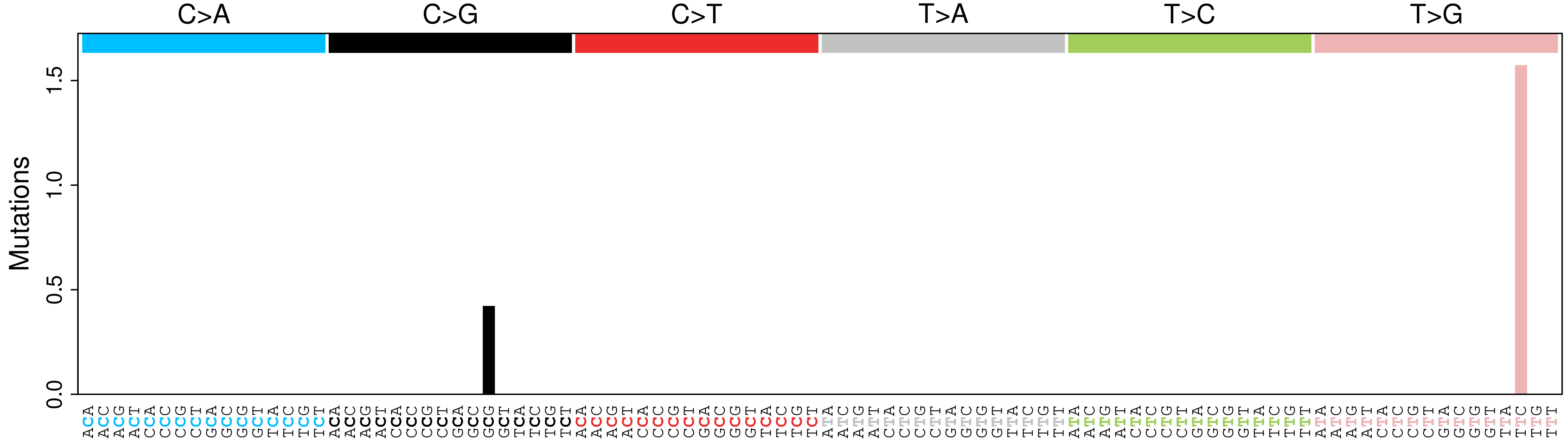
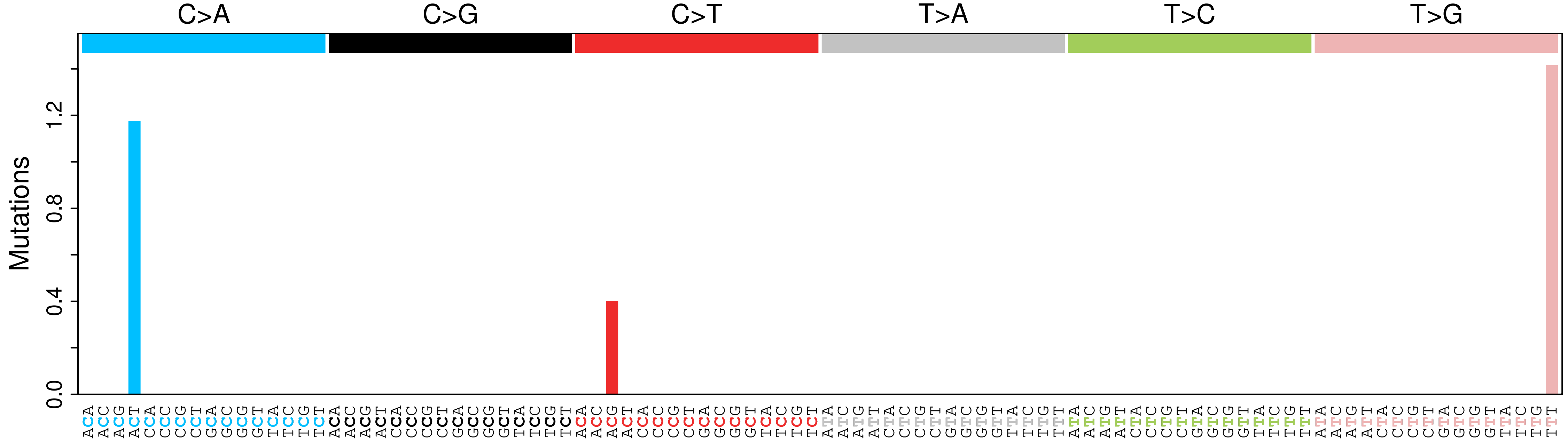


CATD0161a (2 mutations)



CATD0371a (3 mutations)



CATD0354a (2 mutations)

$C > A$

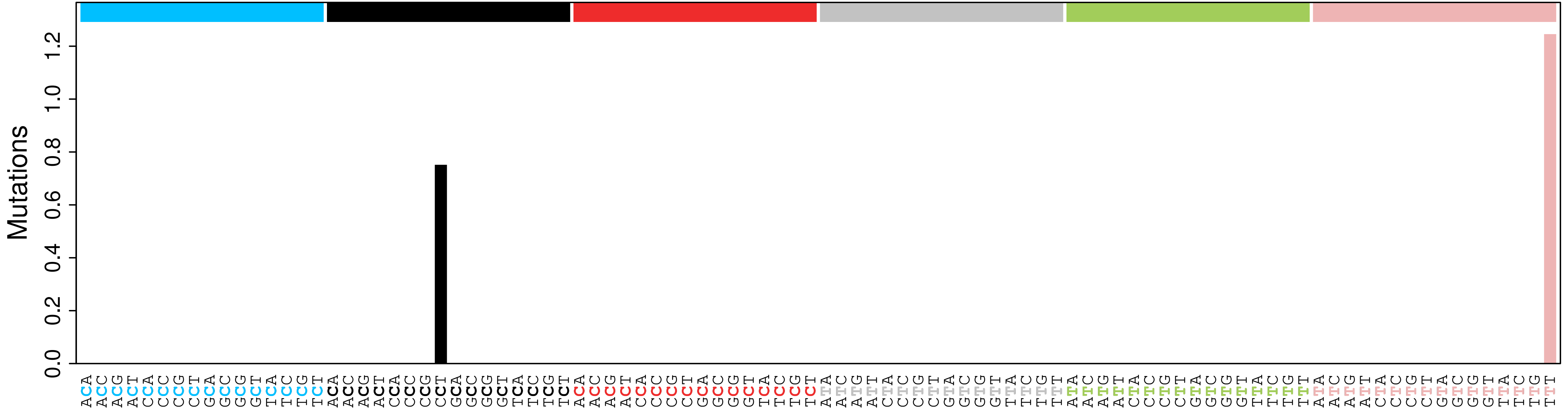
C > G

$C > T$

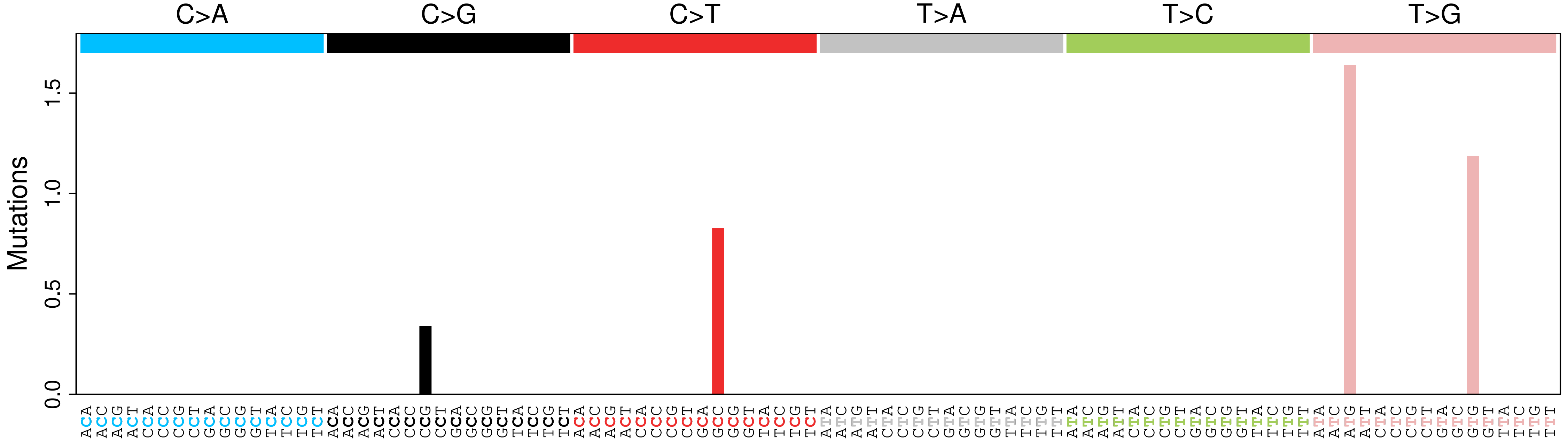
T > A

$$T > C$$

T>G



CATD0372a (4 mutations)



CATD0352a (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]

CATD0366a (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 1.4

[illegible]

CATD0180a (1 mutations)

$C > A$

C > G

$$C > T$$

T > A

$$T > C$$

T > G

Mutations

1.0

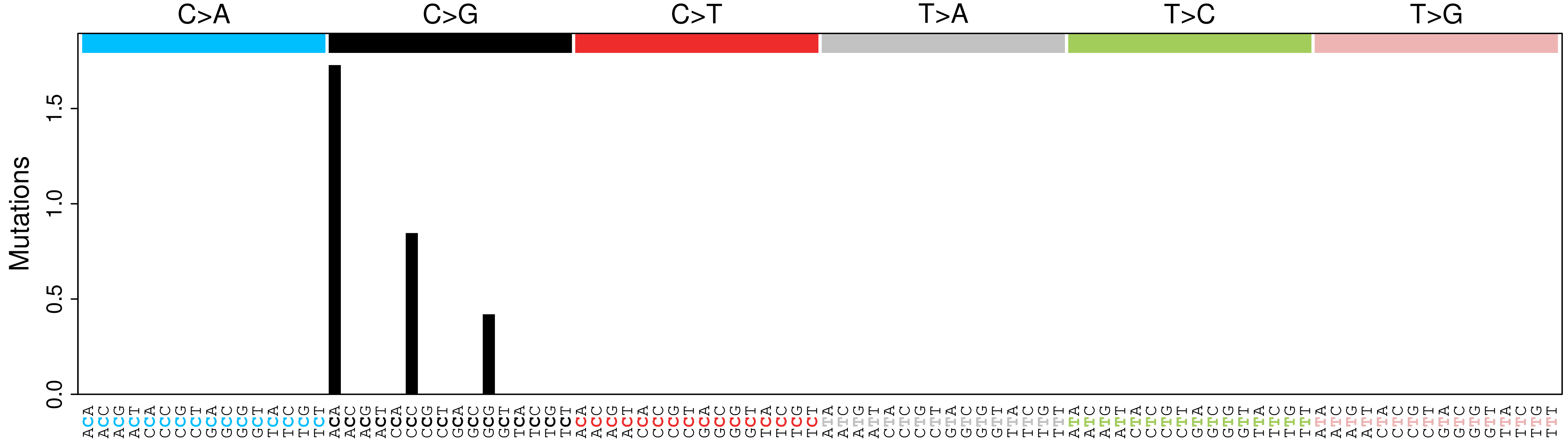
3.0

0

U

[illegible]

CATD0375a (3 mutations)



CATD0351a (2 mutations)

$C > A$

$C > G$

$C > T$

T > A

$T > C$

T > G

Mutations

2.0

1.5

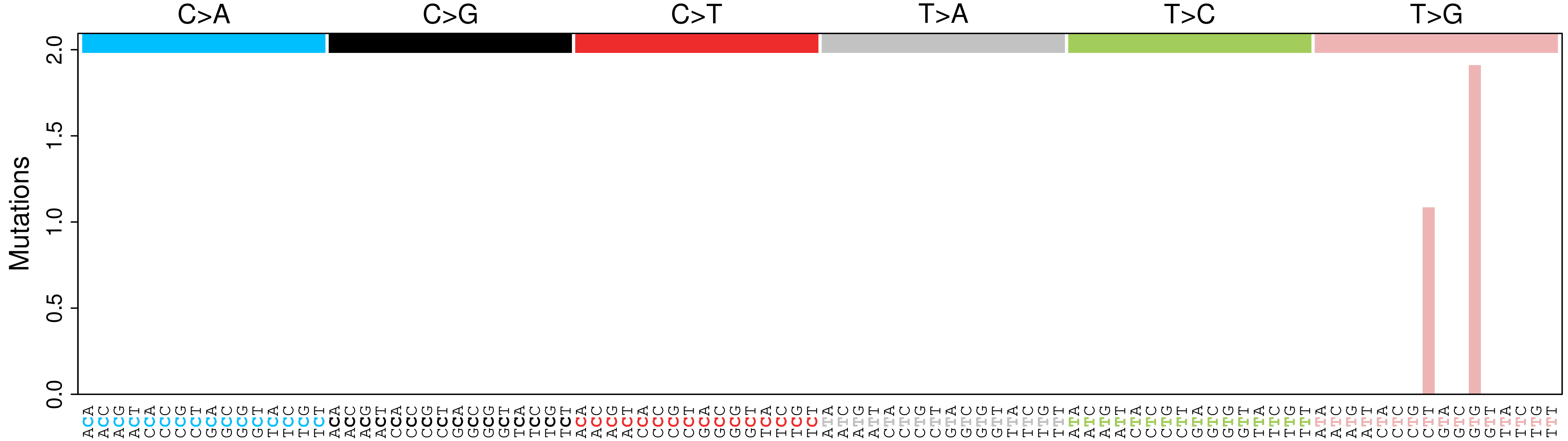
1.0

0.5

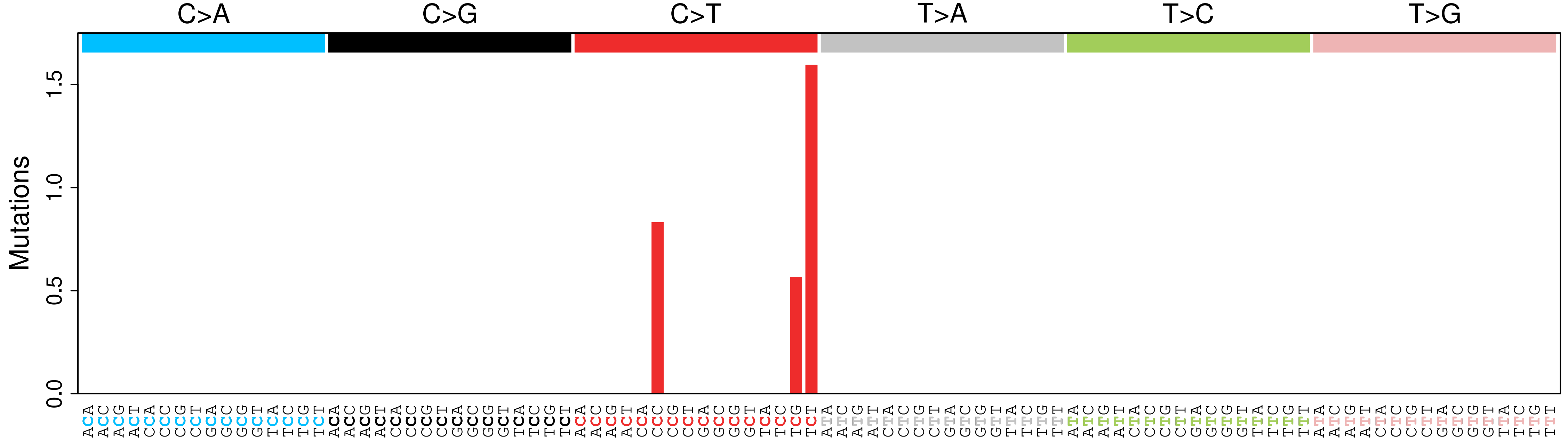
0.

[illegible]

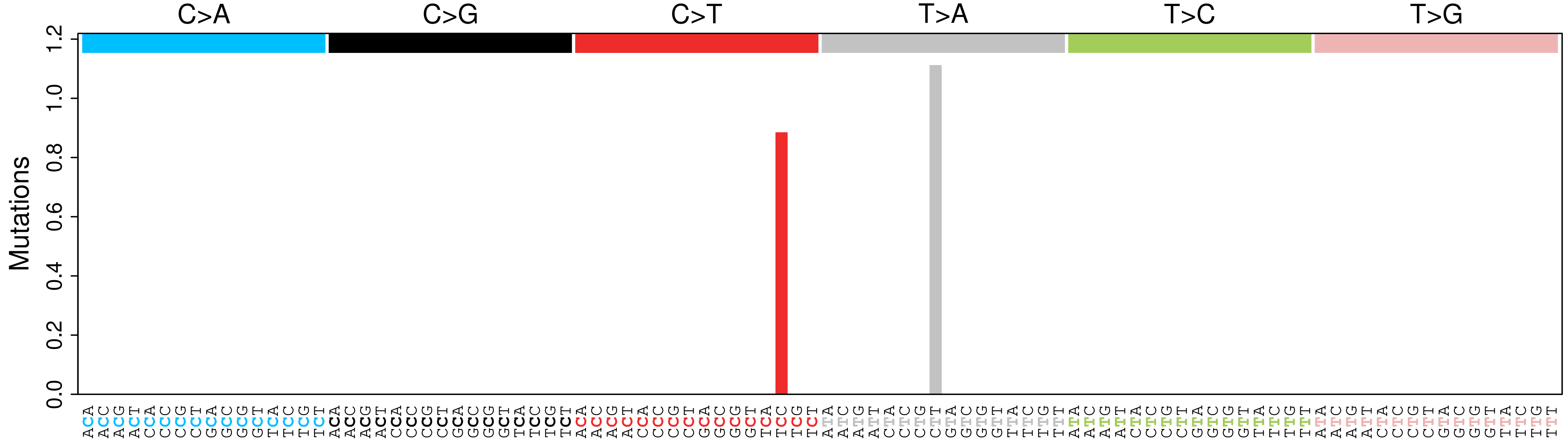
CATD0182a (3 mutations)



CATD0184a (3 mutations)



CATD0179a (2 mutations)



CATD0370a (2 mutations)

$C > A$

$C > G$

$C > T$

T > A

$T > C$

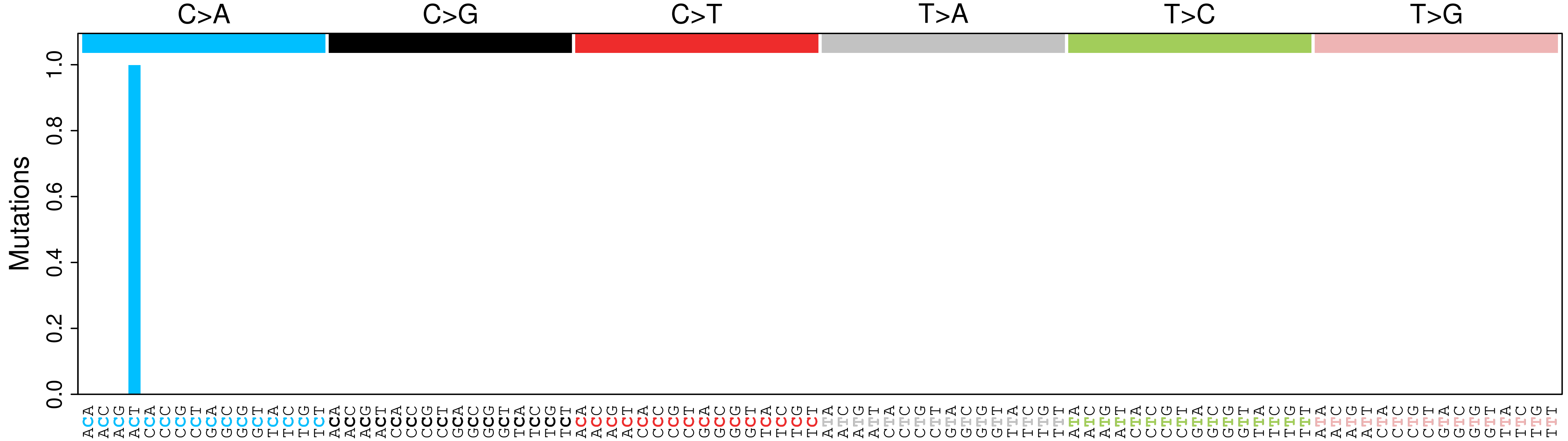
T > G

Mutations

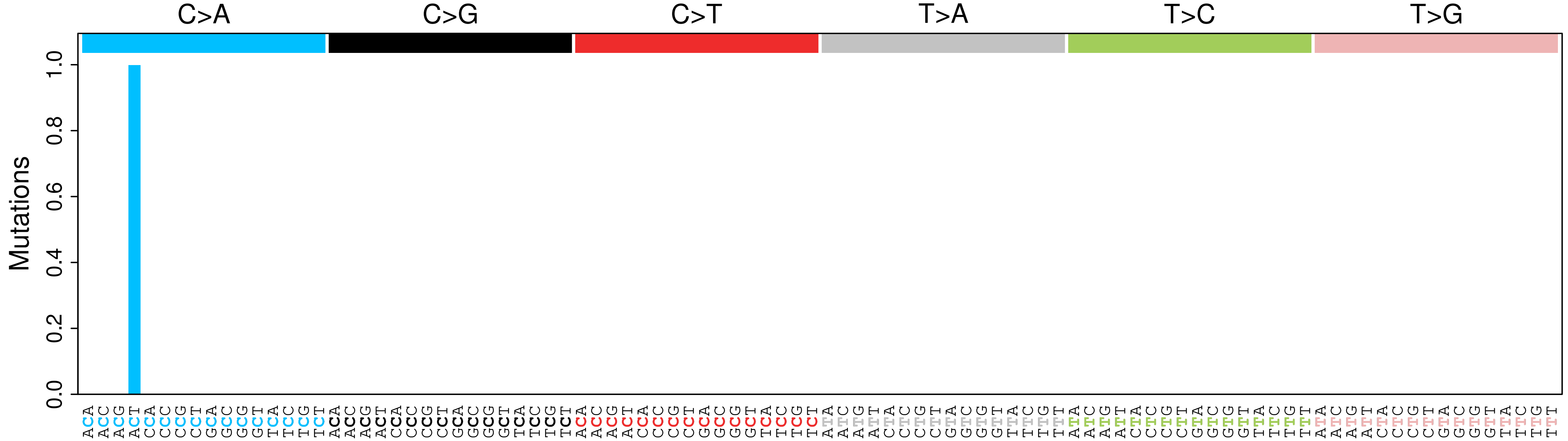
0.0 0.2 0.4 0.6 0.8 1.0

[illegible]

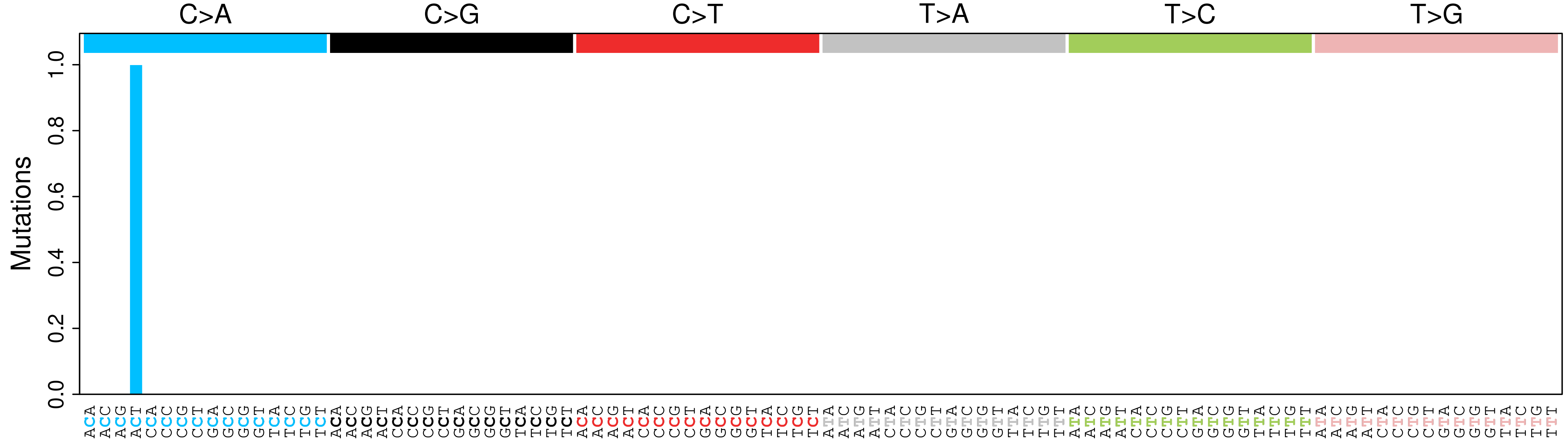
CATD0167a (1 mutations)



CATD0174a (1 mutations)



CATD0175a (1 mutations)



CATD0181a (2 mutations)

C>A

C>G

C>T

T>A

T>C

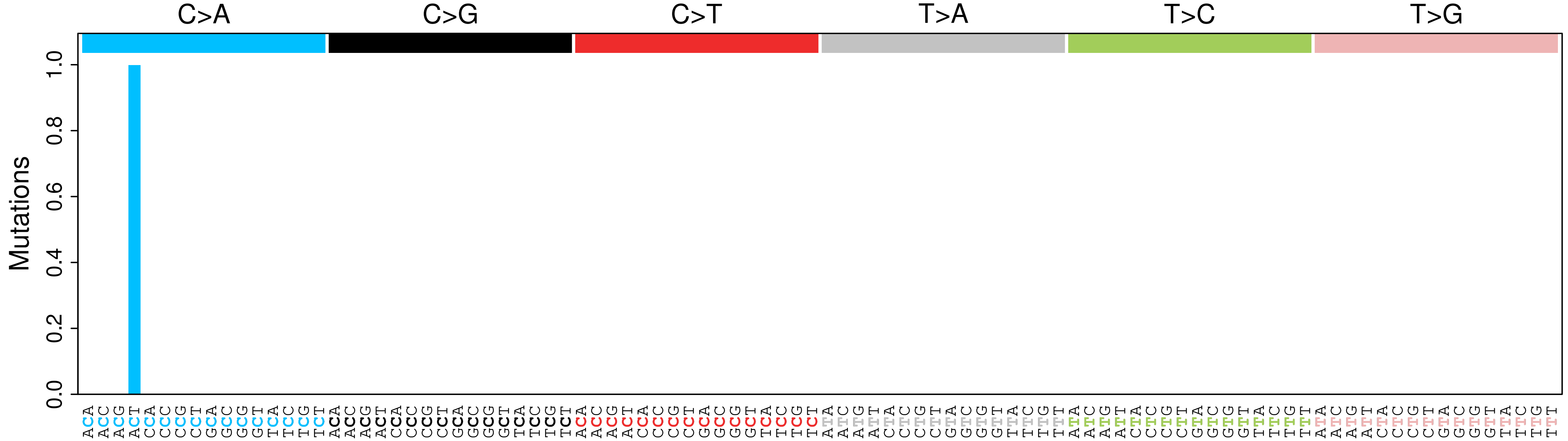
T>G

Mutations

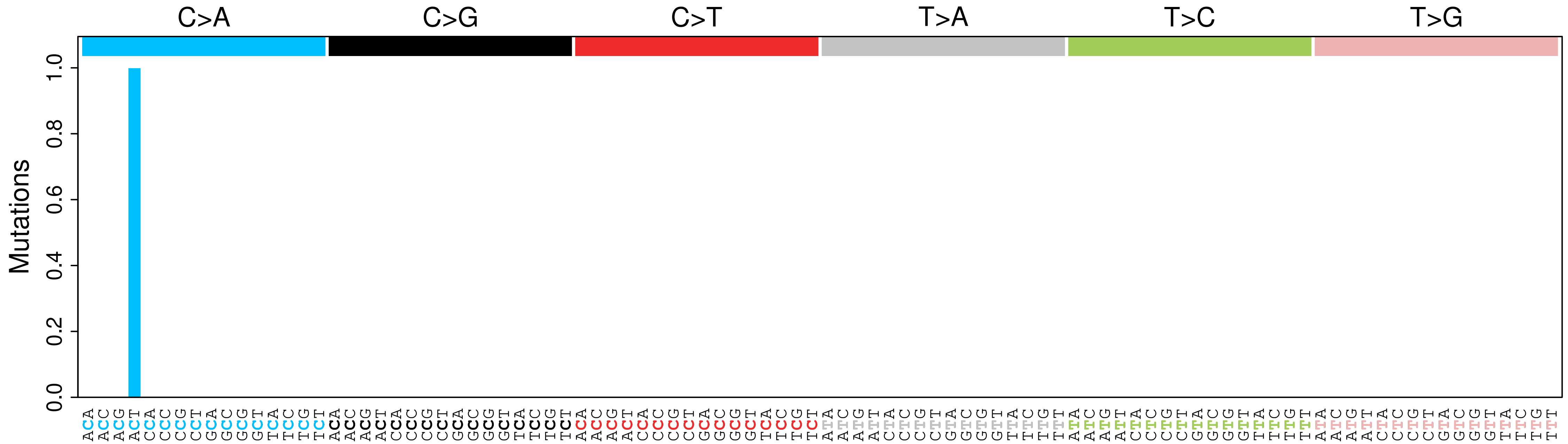
1.2
1.0
0.8
0.6
0.4
0.2
0.0

ACA
ACC
ACG
ACT
CCA
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CCG
CCT
GCA
GCC
GGG
GGT
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TCC
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ACA
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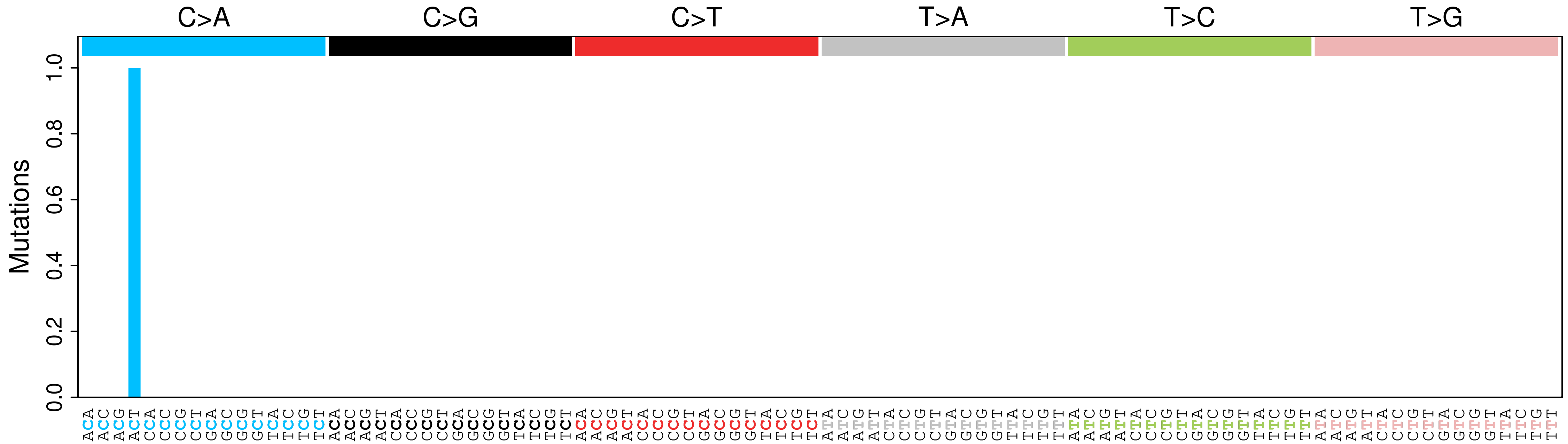
CATD0355a (1 mutations)



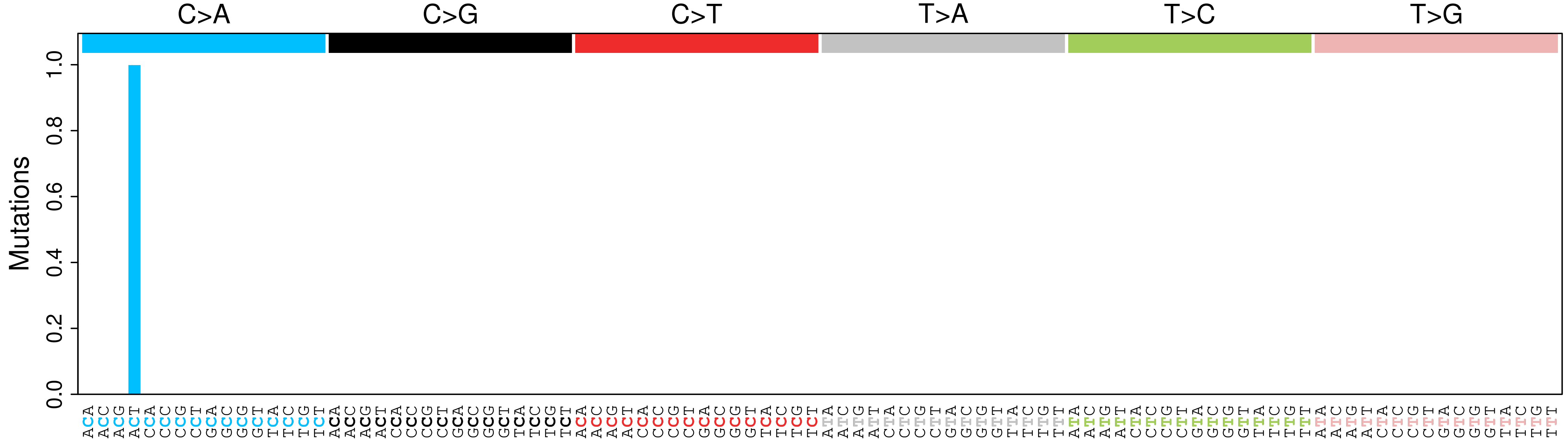
CATD0362a (1 mutations)



CATD0363a (1 mutations)



CATD0365a (1 mutations)



CATD0177a (2 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
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CCG
CCT
GCA
GCC
GGG
GCT
TCA
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GTC
GTG
GTT
TTA
TTC
TTG
TTT

CATD0376a (2 mutations)

$C > A$

$C > G$

$C > T$

T > A

$T > C$

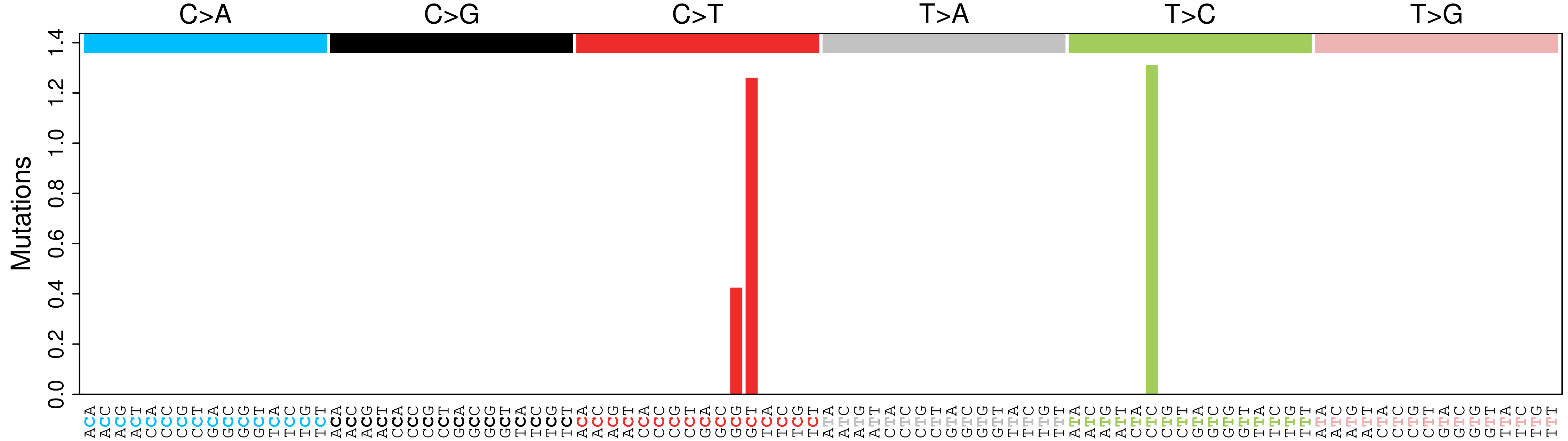
T > G

Mutations

0.0 0.2 0.4 0.6 0.8 1.0 1.2

[illegible]

CATD0367a (3 mutations)



CATD0364a (1 mutations)

C > A

C > G

$C > T$

T > A

$$T > C$$

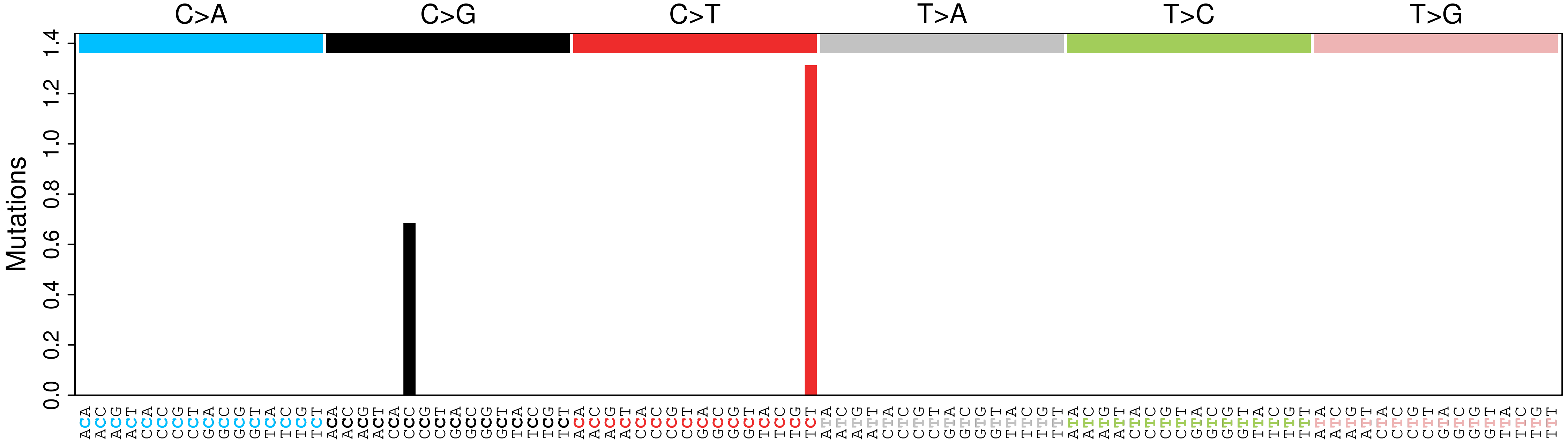
T > G

Mutations

0.0 0.2 0.4 0.6 0.8 1.0

[illegible]

CATD0671a (2 mutations)



CATD0163a (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]

CATD0368a (3 mutations)

