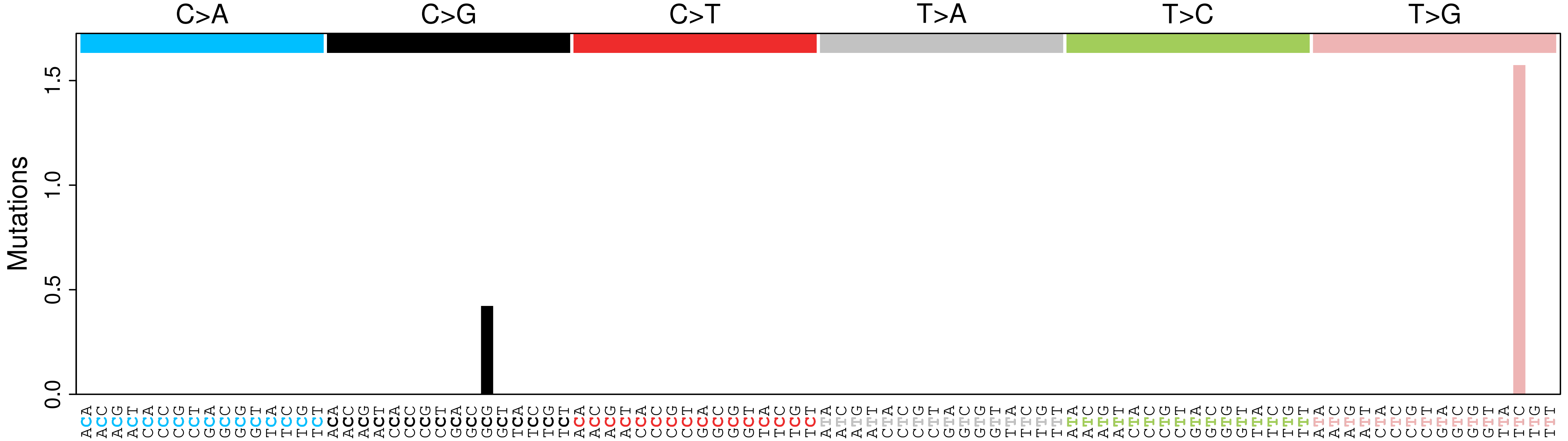


CATD0161a (2 mutations)



CATD0371a (3 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
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
TGA
TGC
TTG
TTT
ATA
ATC
ATG
ATT
CTA
CTC
CTG
CTT
GTA
GTC
GTG
GTT
TGA
TGC
TTG
TTT
TTT

CATD0354a (2 mutations)

$C > A$

$C > G$

$C > T$

T > A

$T > C$

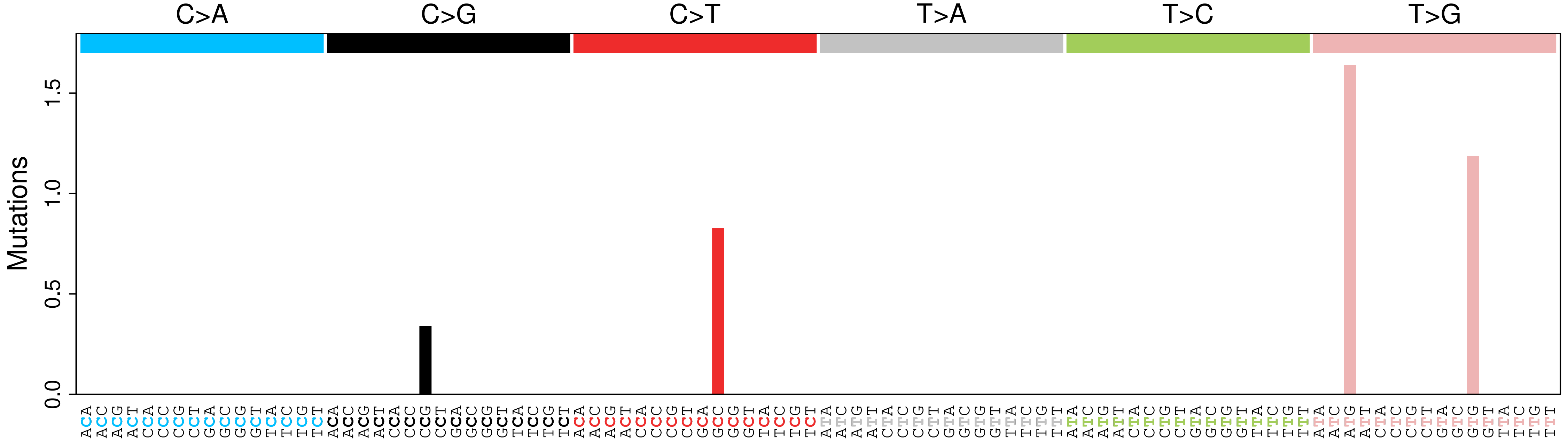
T > G

Mutations

0.0 0.2 0.4 0.6 0.8 1.0 1.2

[illegible]

CATD0372a (4 mutations)



CATD0352a (2 mutations)

$C > A$

C > G

$C > T$

T>A

 $T > C$

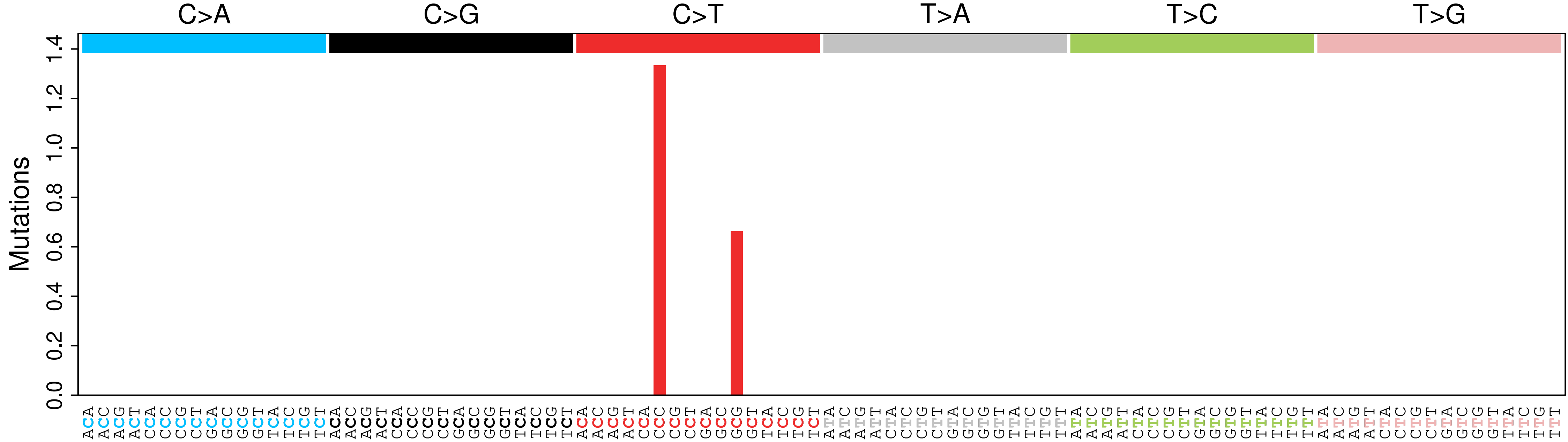
T > G

Mutations

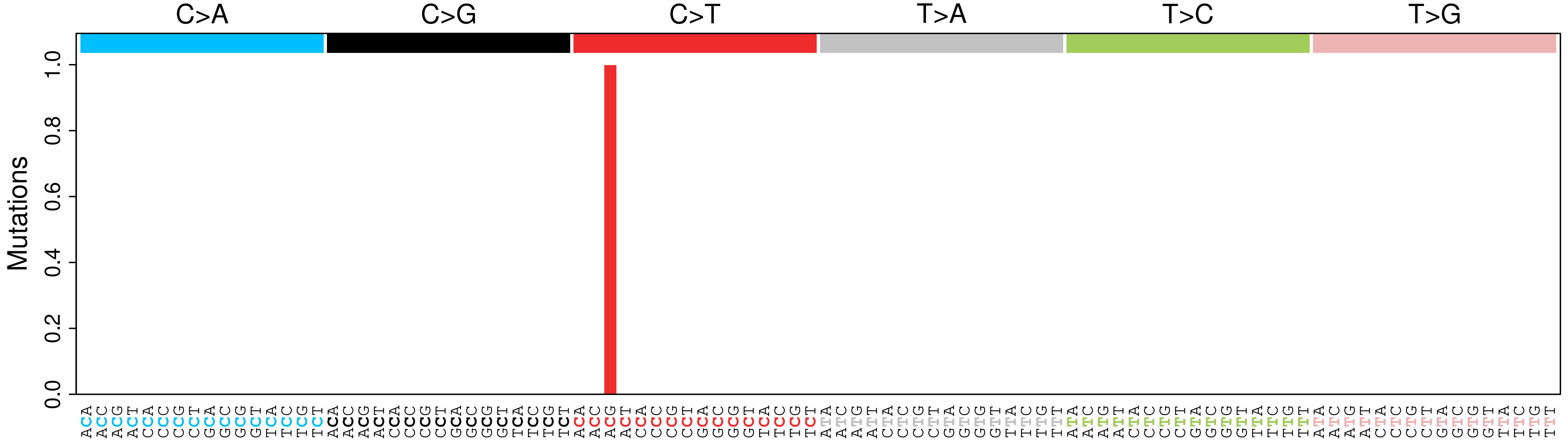
0.0 0.2 0.4 0.6 0.8 1.0 1.2

[illegible]

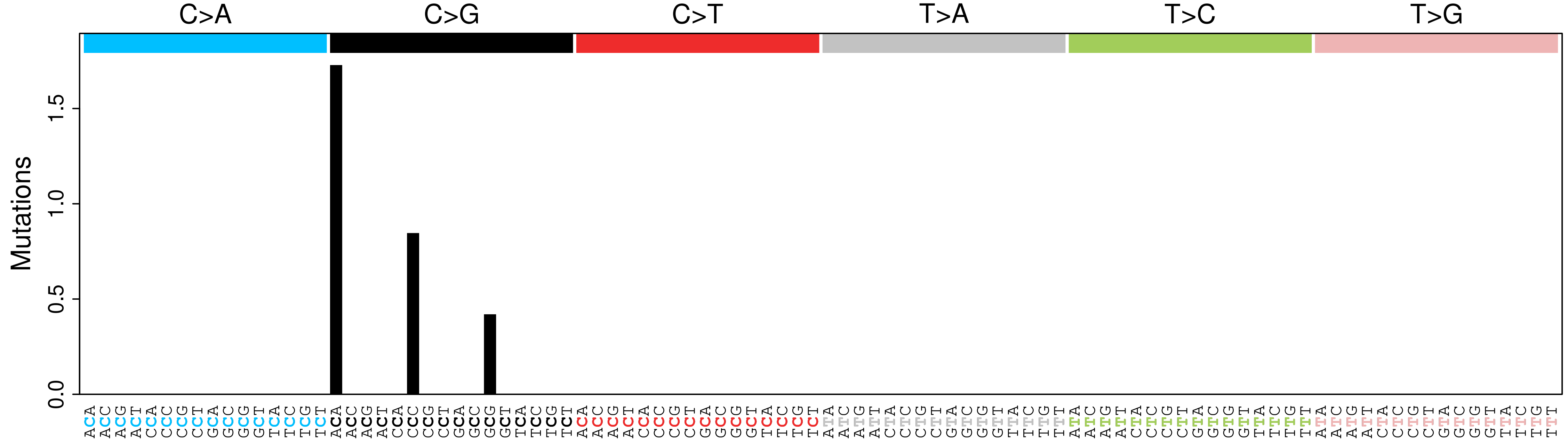
CATD0366a (2 mutations)



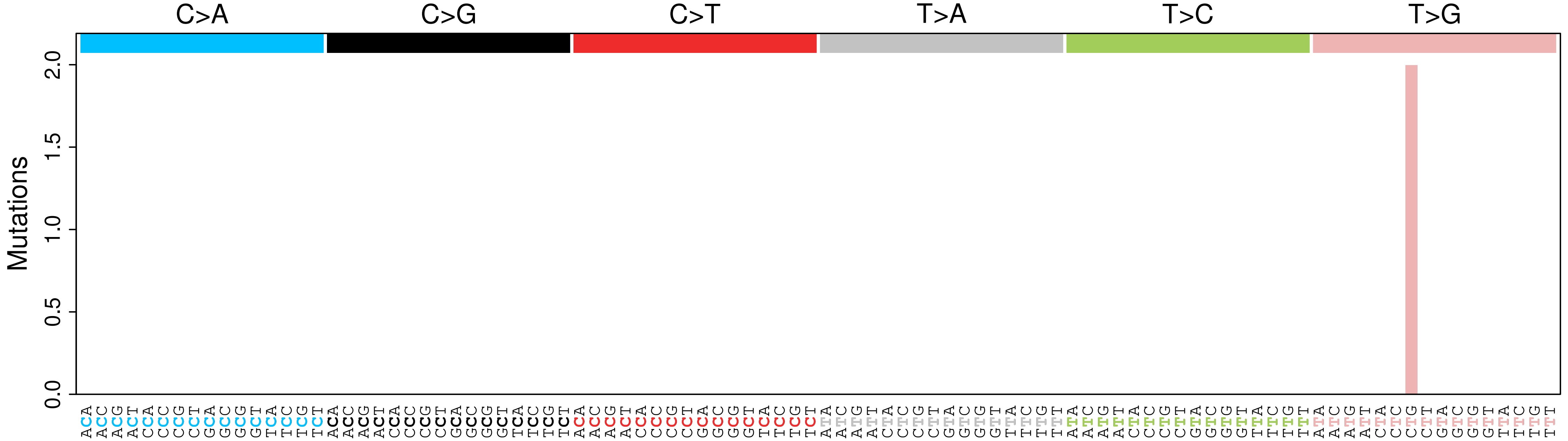
CATD0180a (1 mutations)



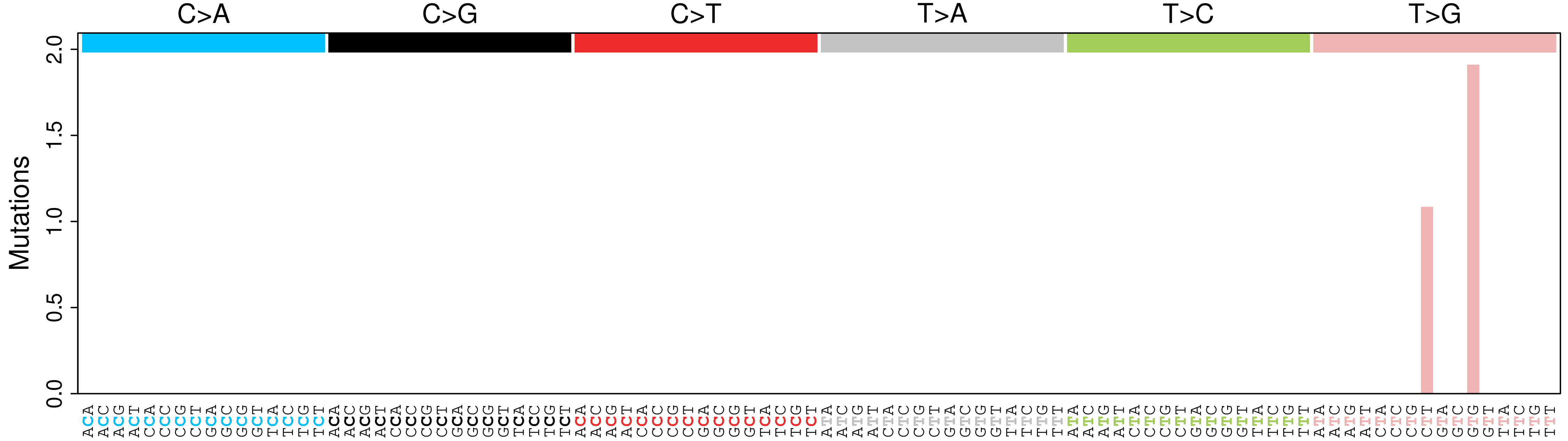
CATD0375a (3 mutations)



CATD0351a (2 mutations)



CATD0182a (3 mutations)



CATD0184a (3 mutations)

$C > A$

$C > G$

$C > T$

T > A

$T > C$

T > G

Mutations

5.

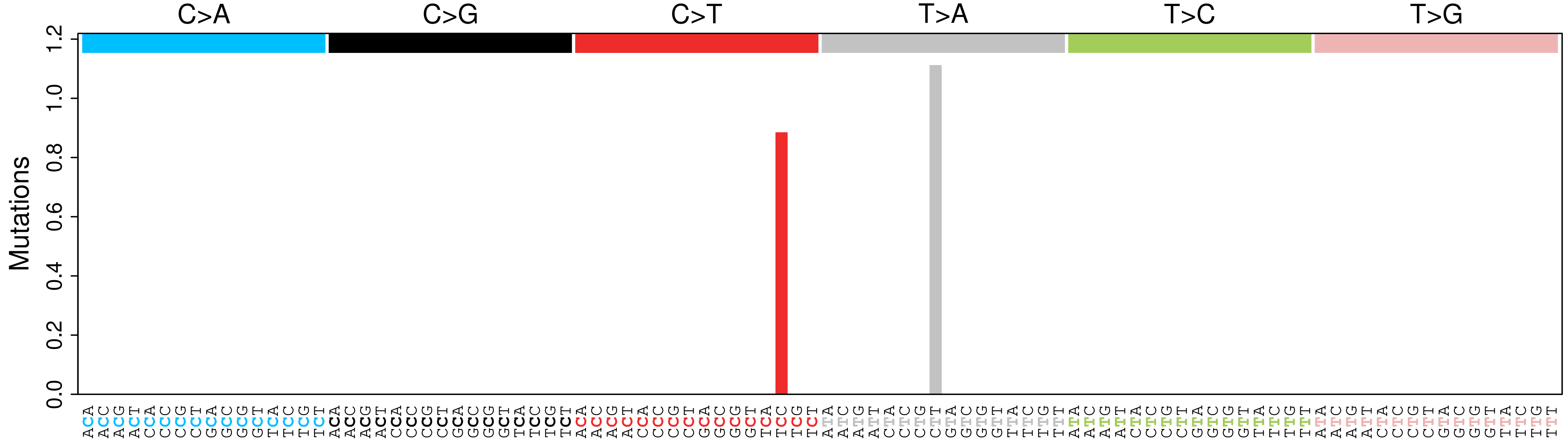
1.0

0.5

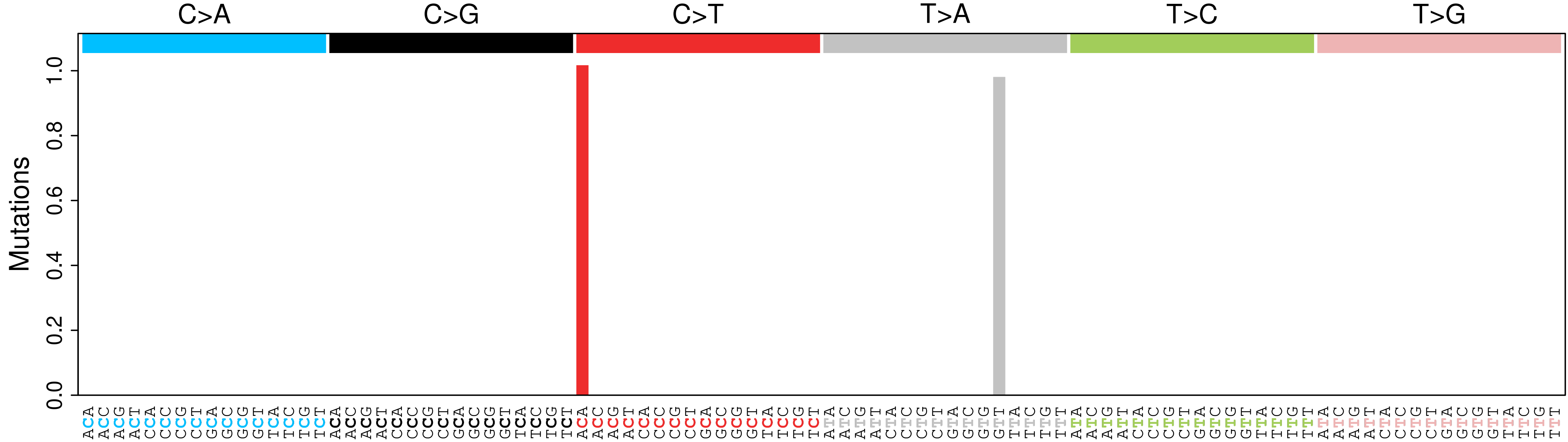
0.

[illegible]

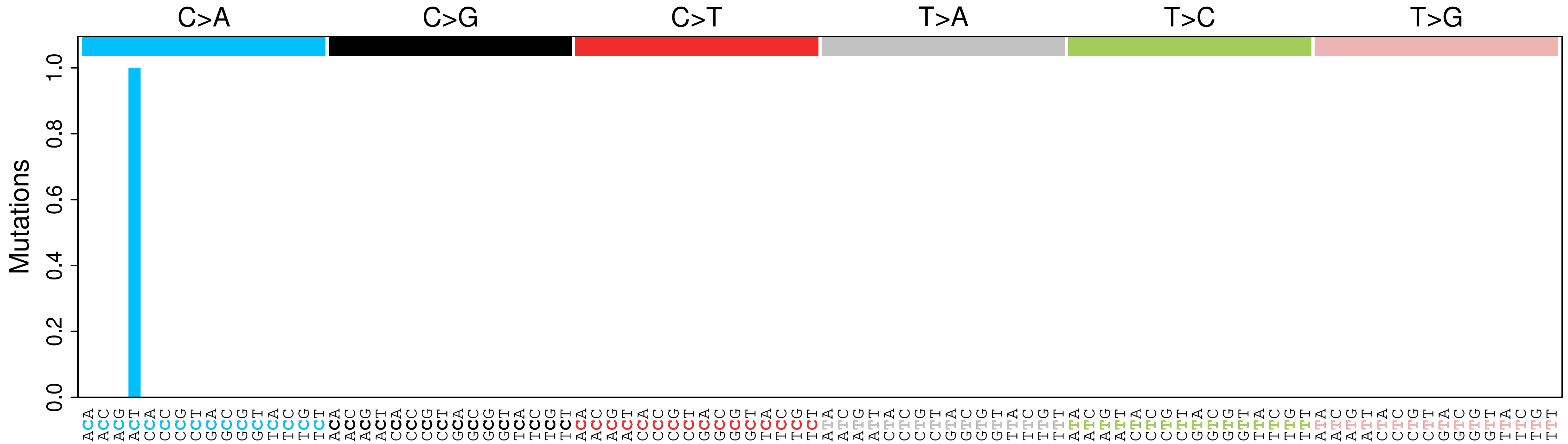
CATD0179a (2 mutations)



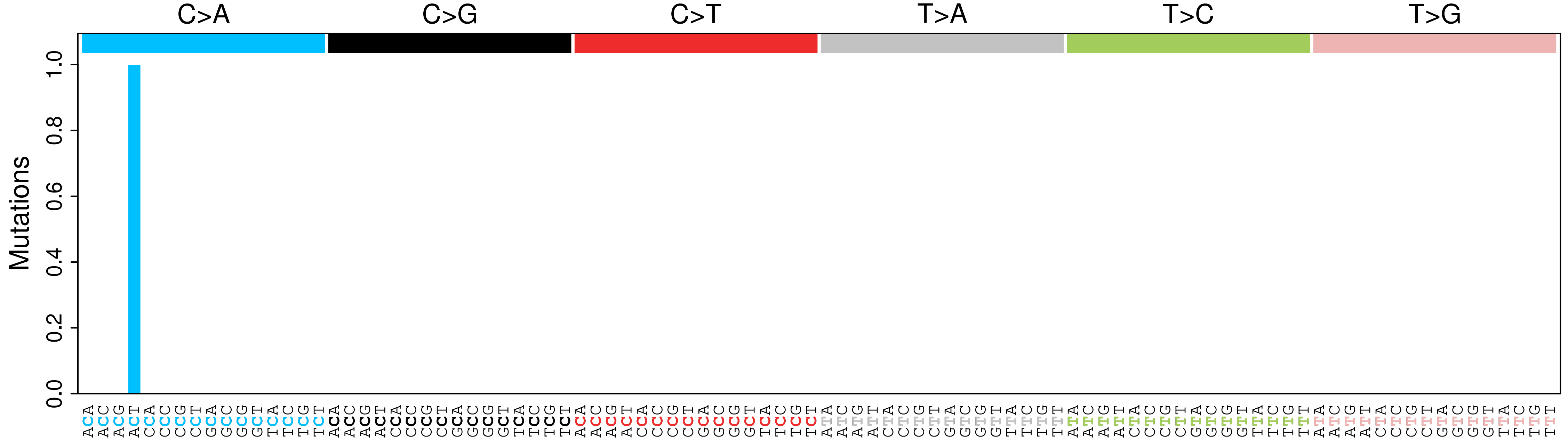
CATD0370a (2 mutations)



CATD0174a (1 mutations)



CATD0175a (1 mutations)



CATD0181a (2 mutations)

C>A

C>G

C>T

T>A

T>C

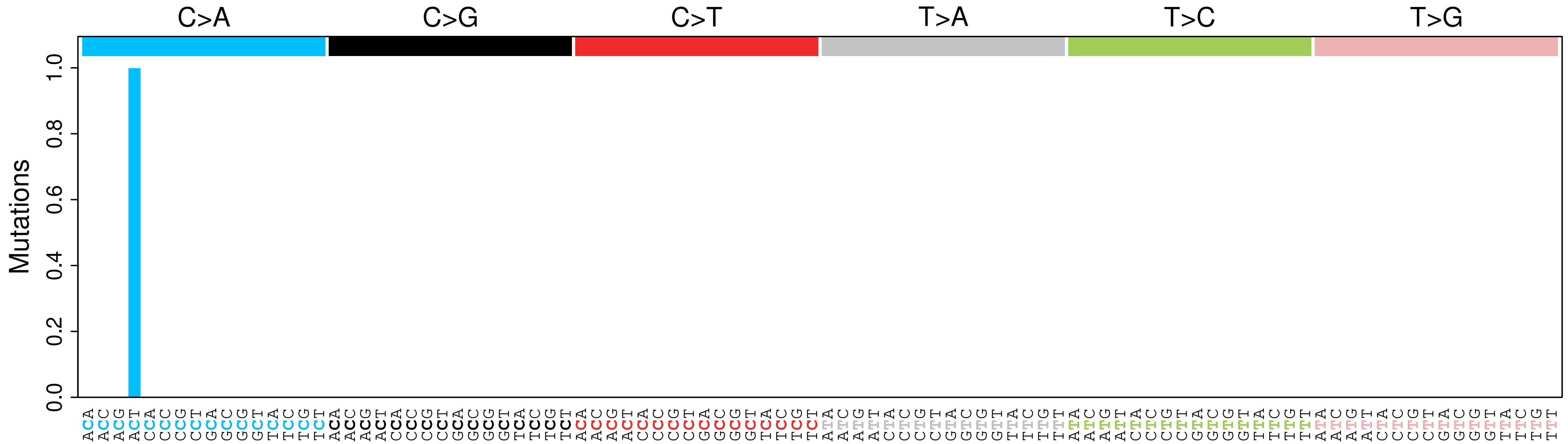
T>G

Mutations

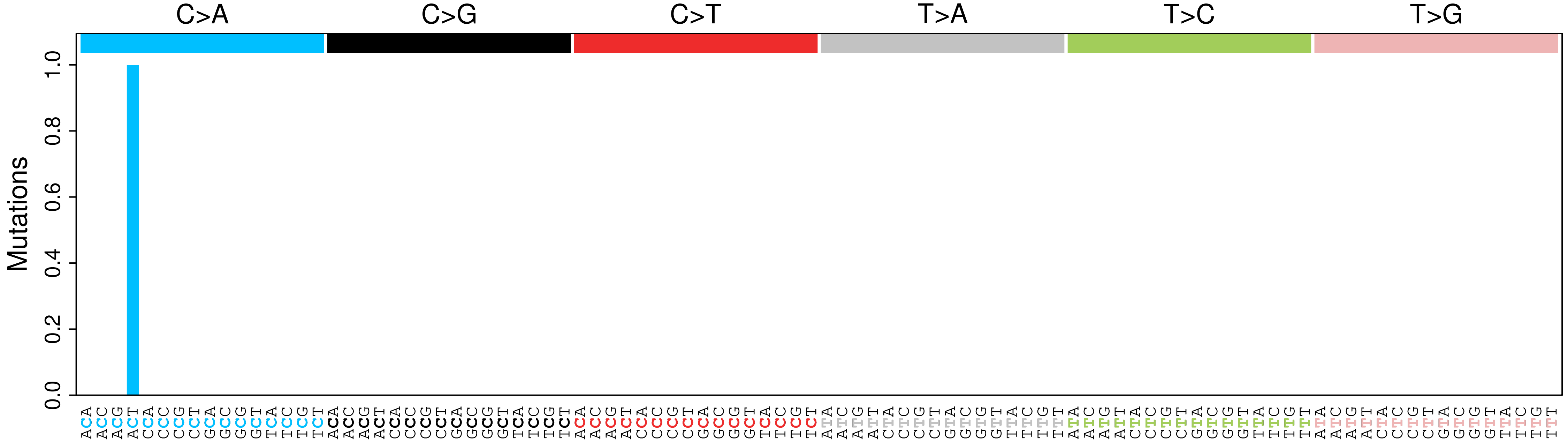
1.2
1.0
0.8
0.6
0.4
0.2
0.0

ACA
ACC
ACG
ACT
CCA
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
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CTA
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CTA
CTC
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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

CATD0355a (1 mutations)



CATD0362a (1 mutations)



CATD0363a (1 mutations)

C>A

C>G

C>T

T>A

T>C

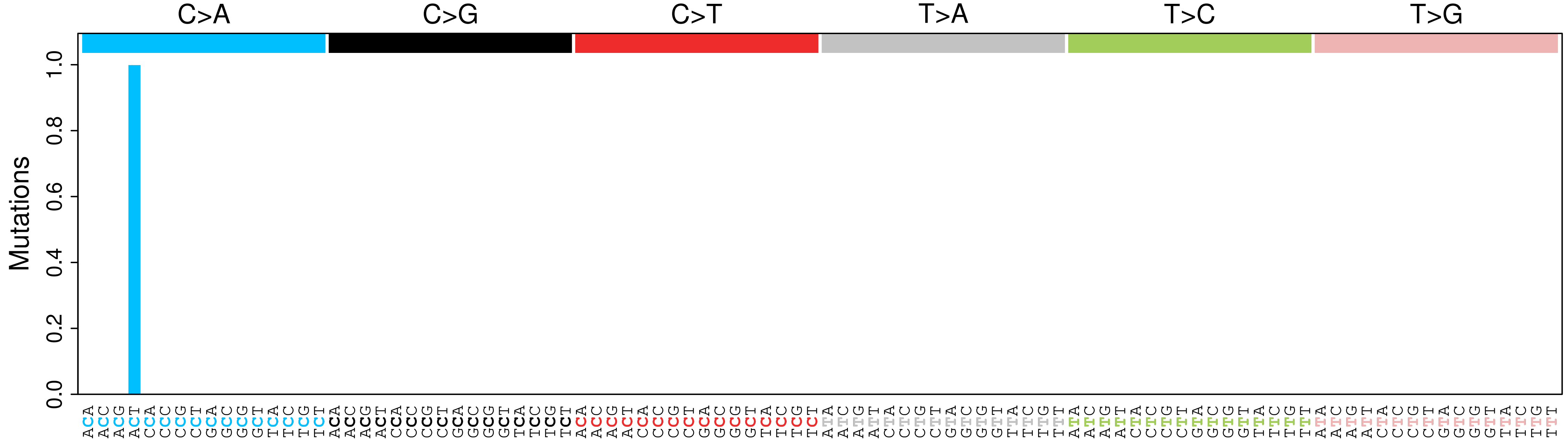
T>G

Mutations

1.0
0.8
0.6
0.4
0.2
0.0

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

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
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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TCT
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ATC
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CTA
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TTT
ATA
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CTA
CTC
CTG
CTT
GTA
GTC
GTG
GTT
TTA
TTC
TTG
TTT

CATD0376a (2 mutations)

C > A

C > G

$C > T$

T > A

$$T > C$$

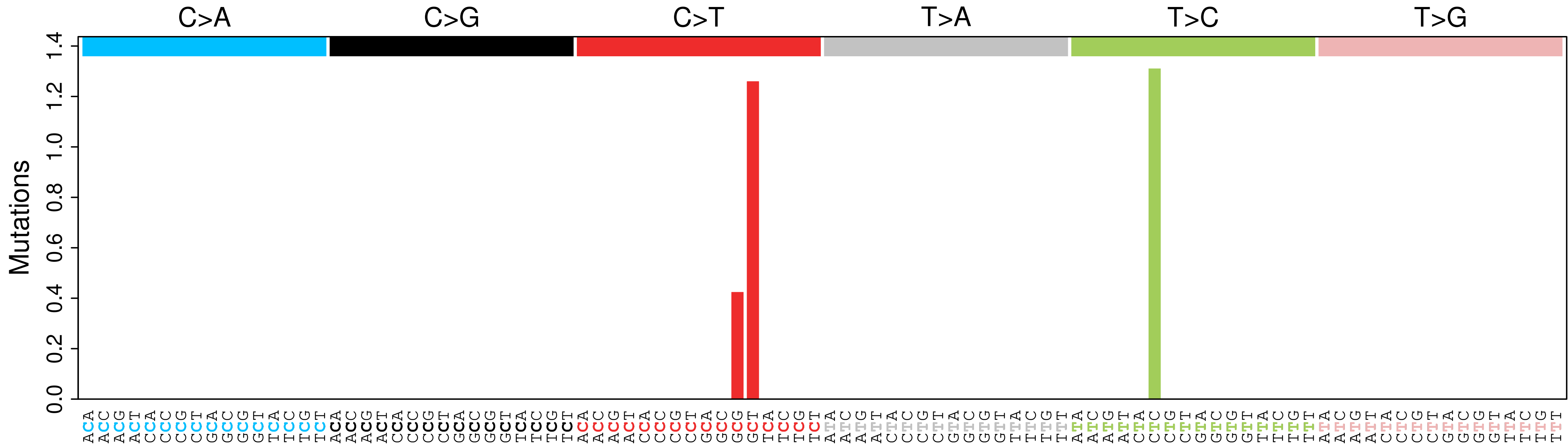
T > G

Mutations

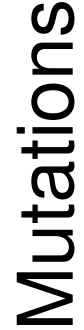
p	N_s^1 (solid)	N_s^2 (dashed)	N_s^3 (dotted)
0.0	1.00	1.00	1.00
0.2	0.80	0.90	0.95
0.4	0.60	0.75	0.85
0.6	0.40	0.55	0.70
0.8	0.20	0.35	0.50
1.0	0.00	0.15	0.30
1.2	0.00	0.00	0.00

[illegible]

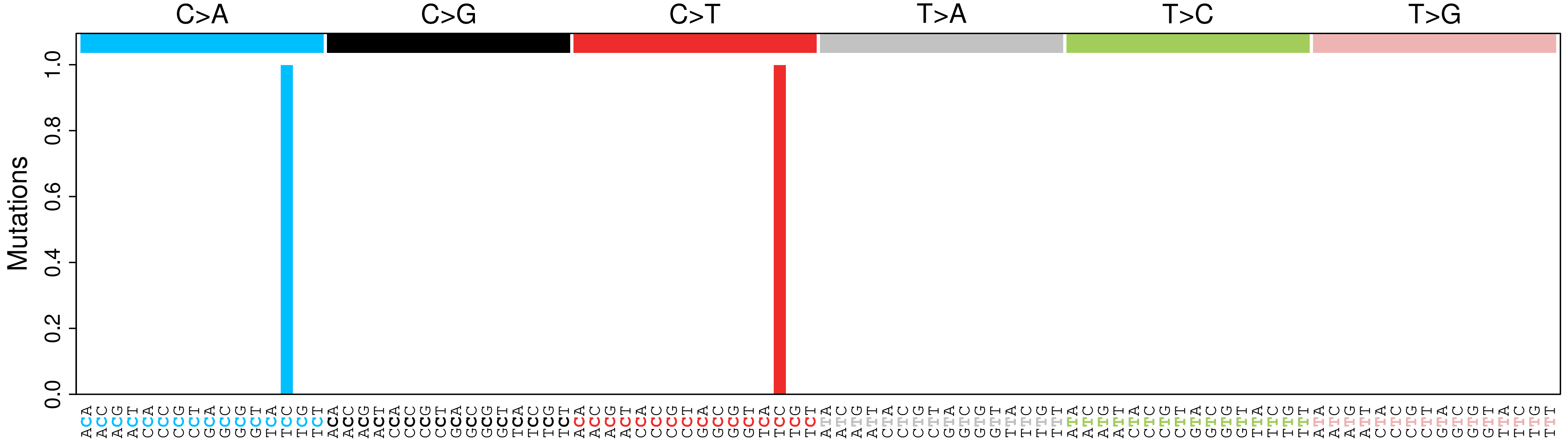
CATD0367a (3 mutations)



CATD0671a (2 mutations)



CATD0163a (2 mutations)



CATD0368a (3 mutations)

