

CATD343a (4 mutations)

C>A

C>G

C>T

T>A

T>C

T>G

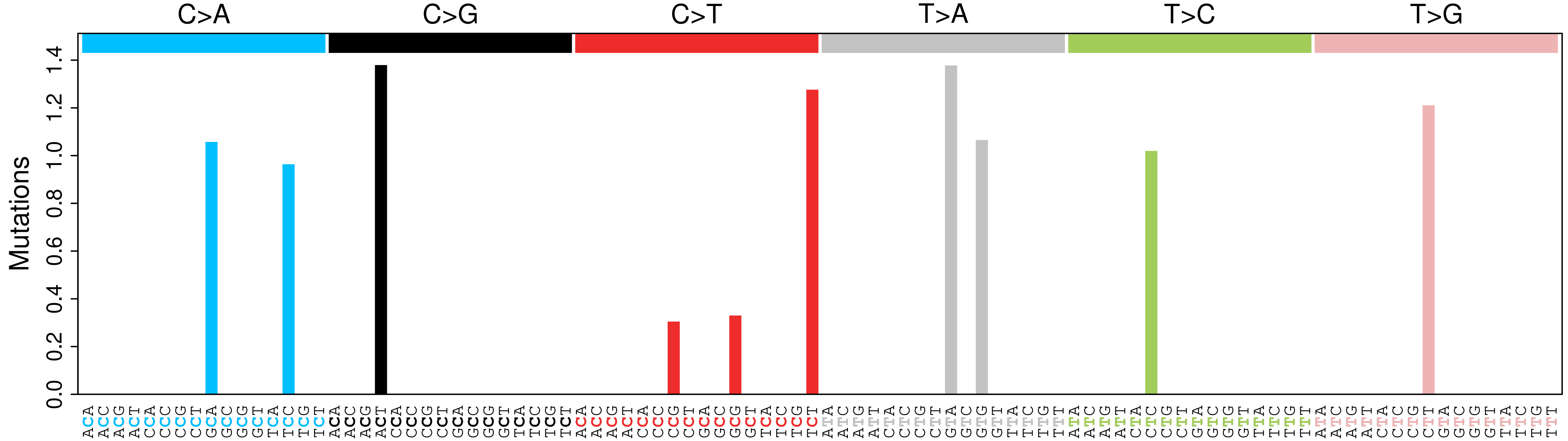
Mutations

1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0

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



CATD336a (10 mutations)



CATD0547a (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]

CATD0558a (2 mutations)

$C > A$

$C > G$

$C > T$

T > A

$T > C$

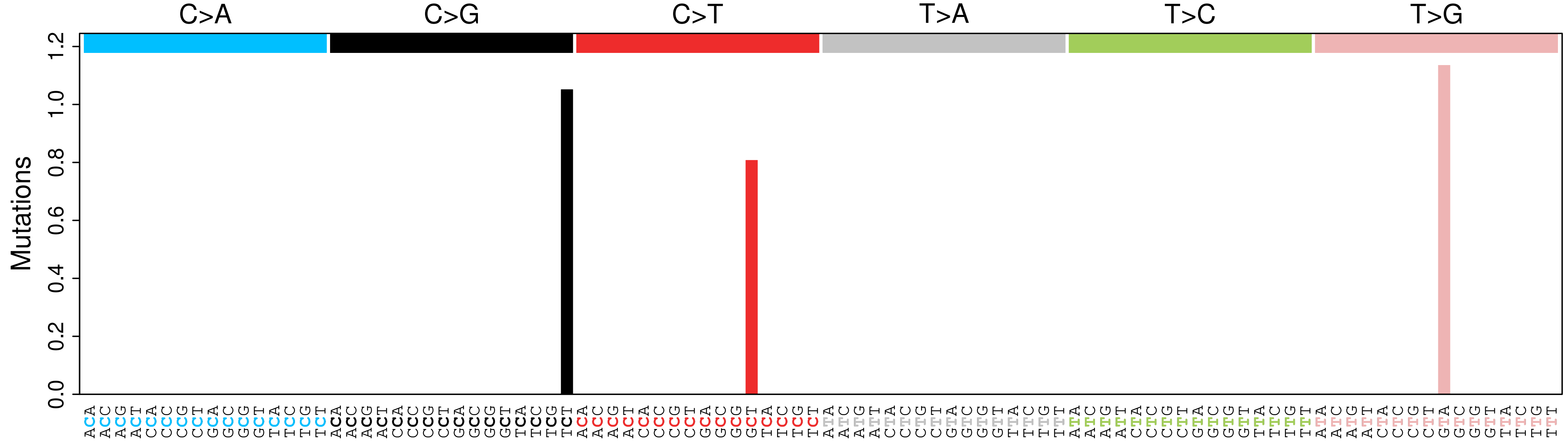
T>G

Mutations

α	N_s^1 (solid)	N_s^2 (dashed)	N_s^3 (dotted)
0.0	0.00	0.00	0.00
0.2	0.15	0.10	0.05
0.4	0.30	0.20	0.10
0.6	0.45	0.30	0.15
0.8	0.60	0.40	0.20
1.0	0.80	0.60	0.40
1.2	0.90	0.70	0.50

[illegible]

CATD337a (3 mutations)



CATD331a (3 mutations)

$C > A$

$C > G$

$C > T$

T>A

 $T > C$

T>G

Mutations

1.5

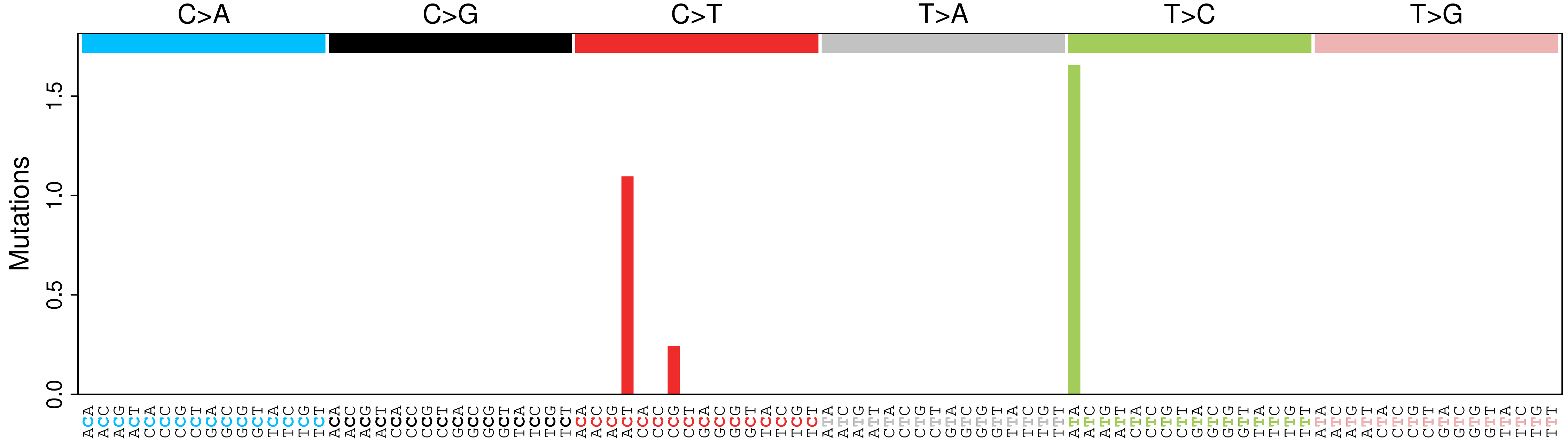
1.0.

0.5

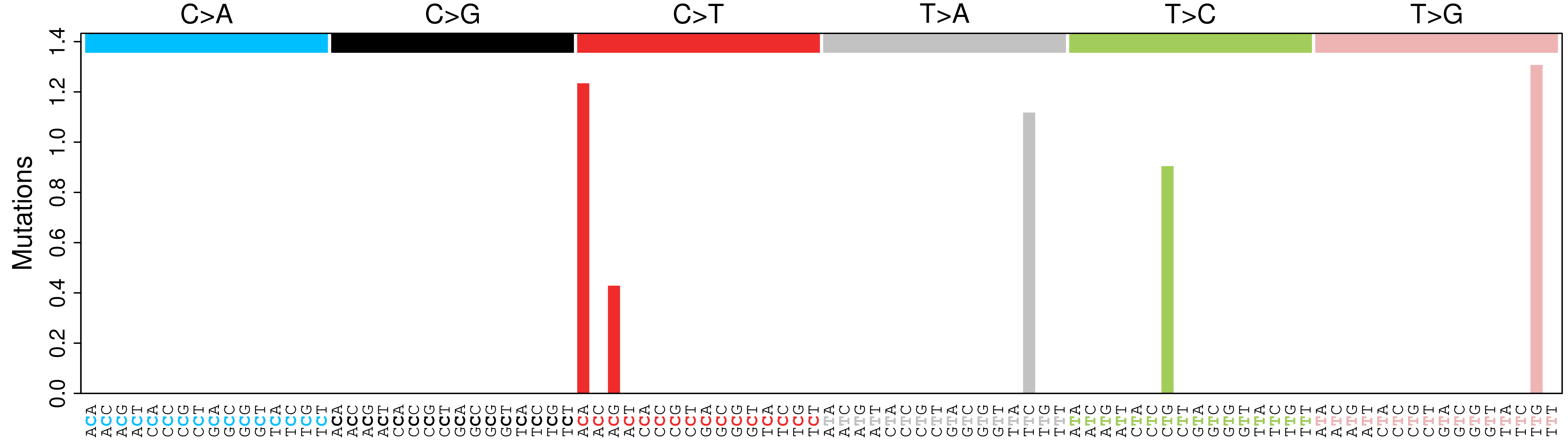
0.0

[illegible]

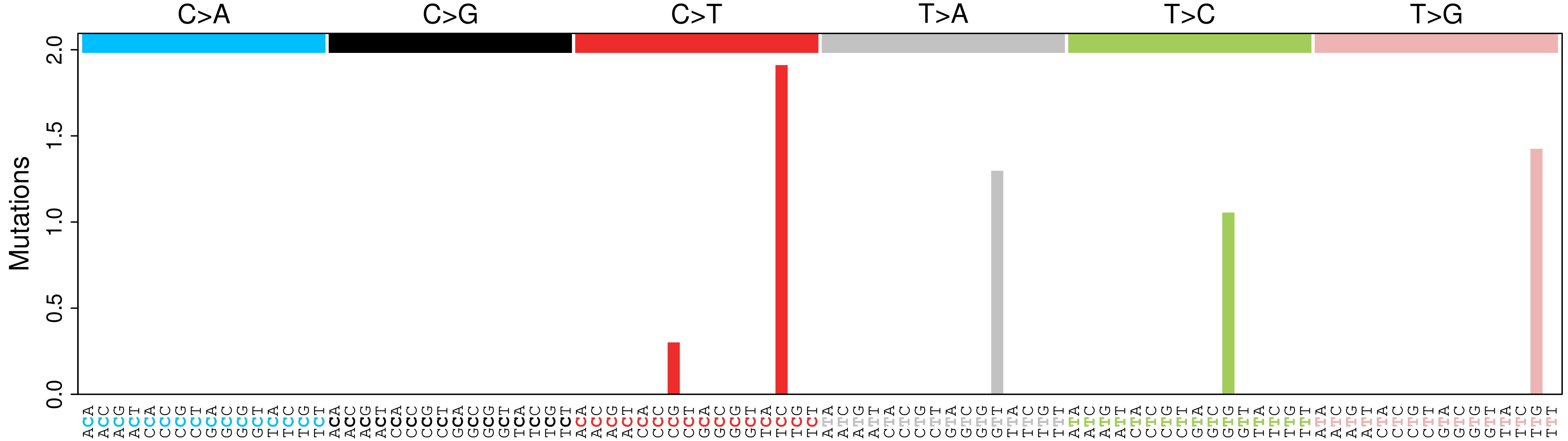
CATD0550a (3 mutations)



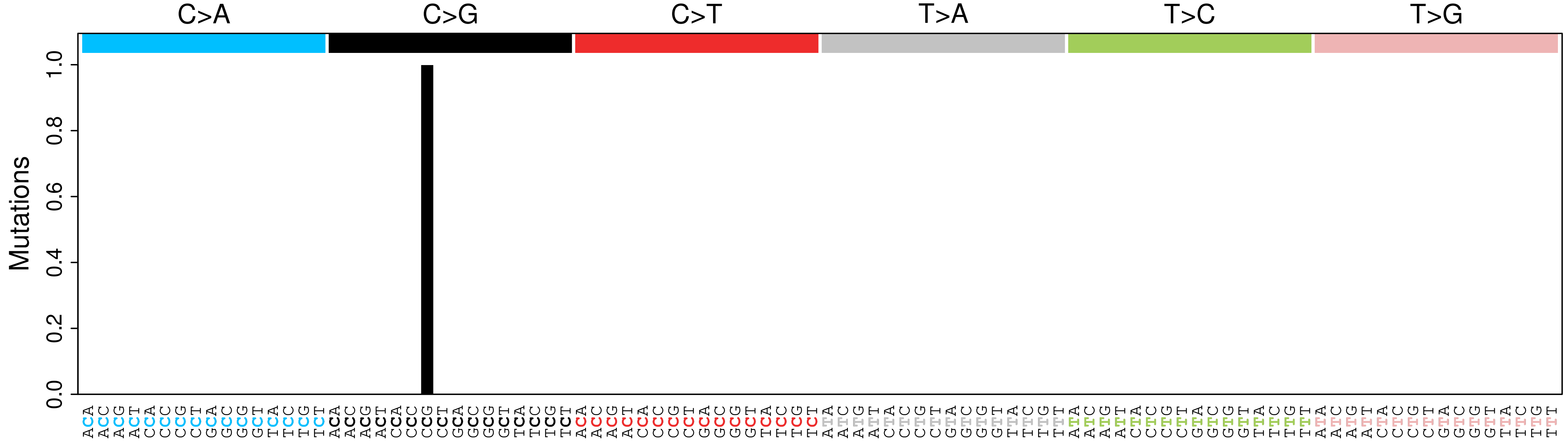
CATD334a (5 mutations)



CATD0557a (6 mutations)



CATD0540a (1 mutations)



CATD344a (1 mutations)

$C > A$

$C > G$

$C > T$

T>A

 $T > C$

T>G

Mutations

1.0

 \circ

1

2

0.

[illegible]

CATD0545a (5 mutations)

C>A

C>G

C>T

T>A

T>C

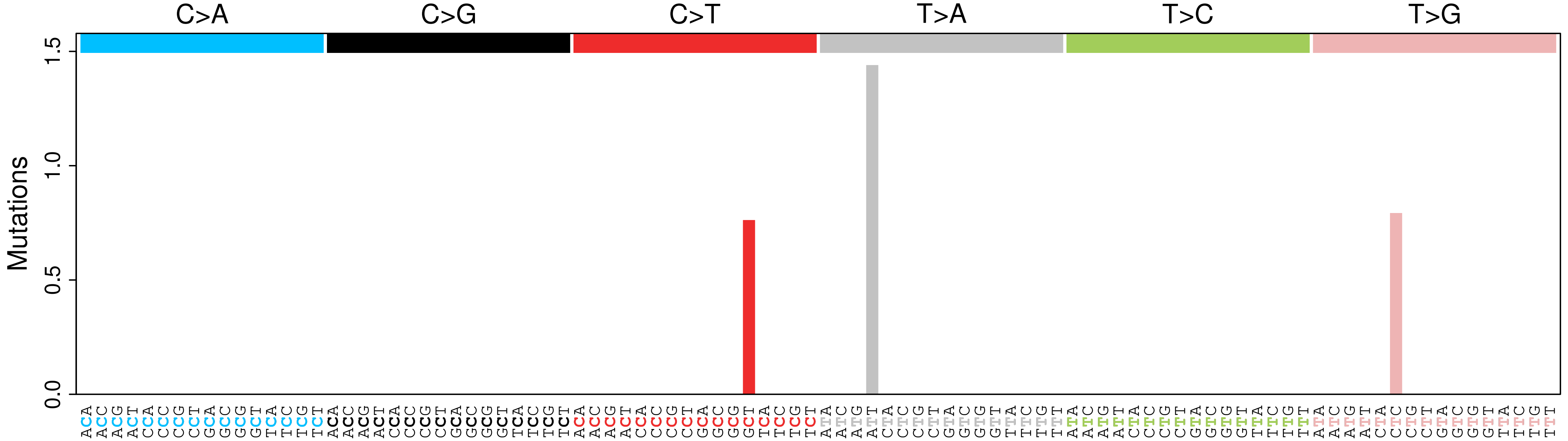
T>G

Mutations

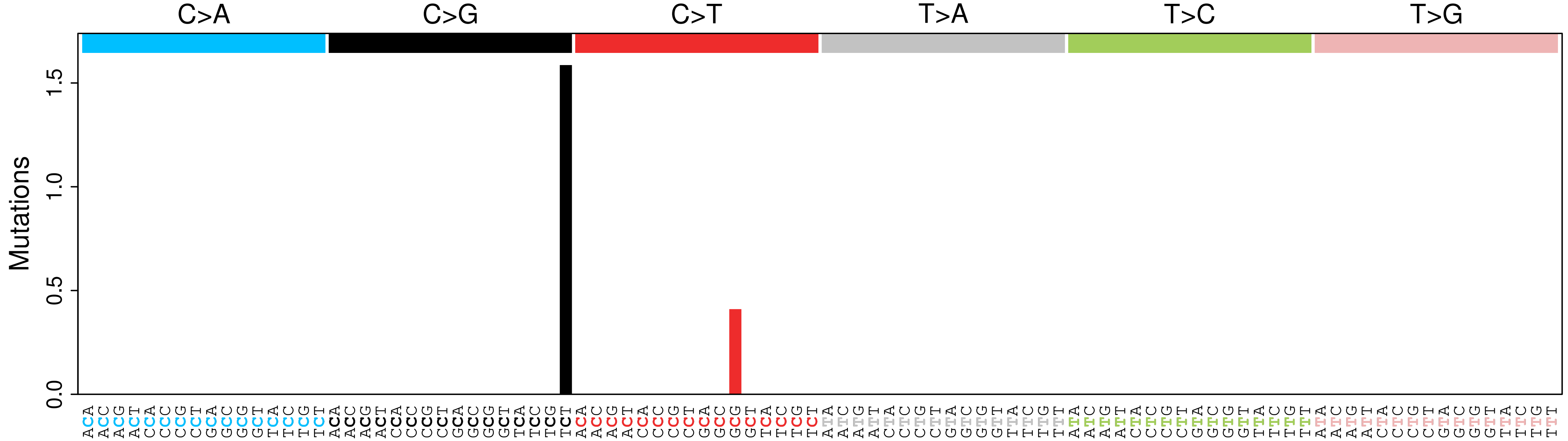
0.0 0.2 0.4 0.6 0.8 1.0 1.2 1.4

ACA
ACC
ACG
ACT
CCA
CCC
CCG
CCT
GCA
GCC
GGG
GGT
TCA
TCC
TCG
TCT
ACA
ACC
ACG
ACT
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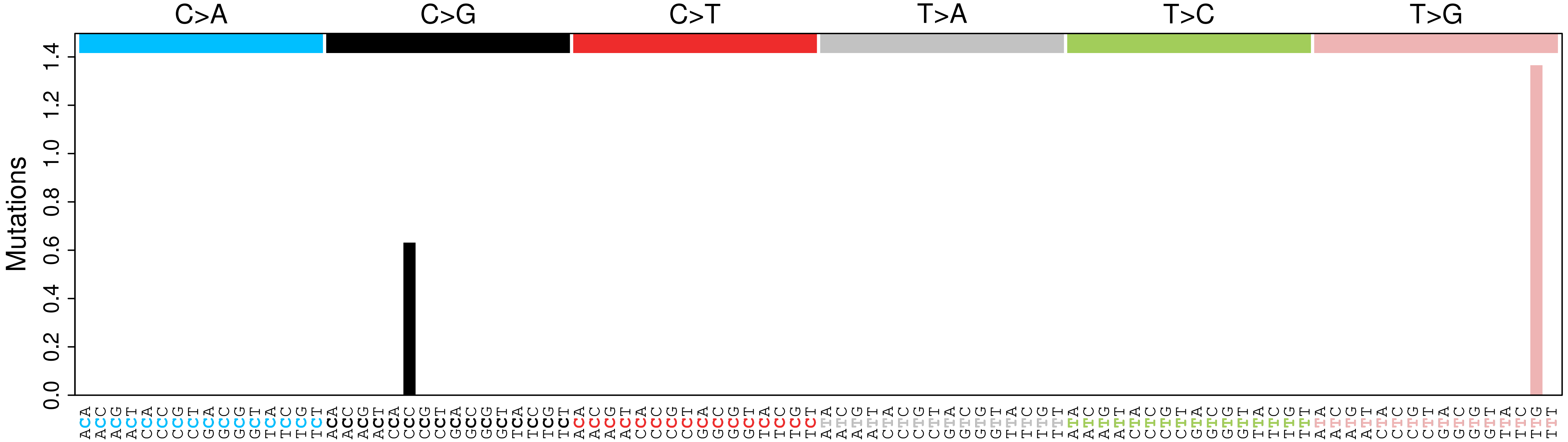
CATD0554a (3 mutations)



CATD0541a (2 mutations)



CATD0556a (2 mutations)



CATD335a (1 mutations)

$C > A$

$C > G$

$C > T$

T>A

 $T > C$

T>G

Mutations

1.0

 \circ

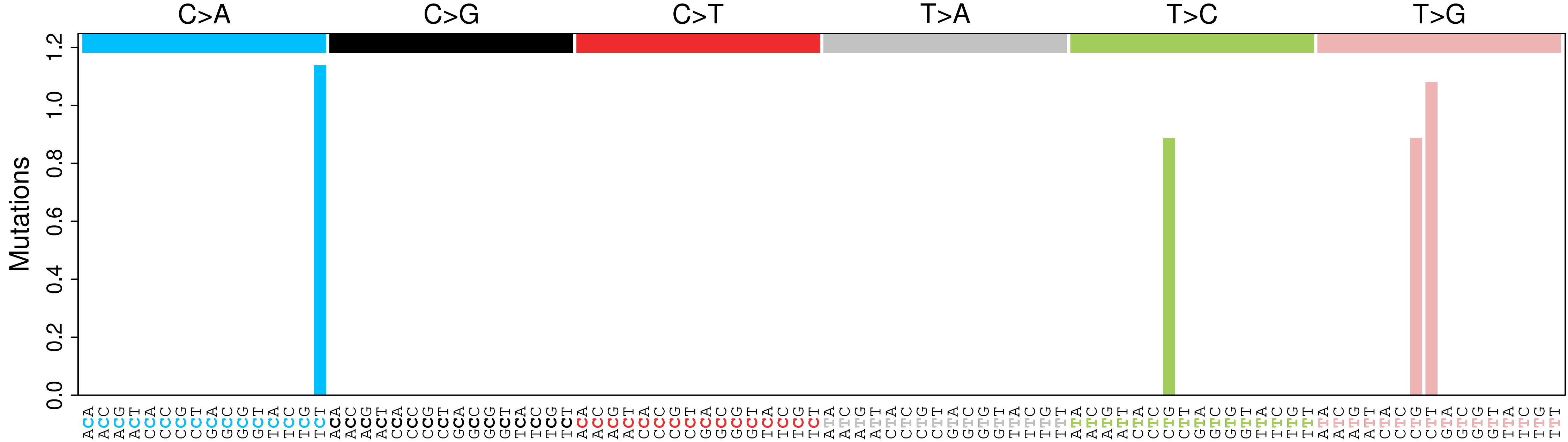
0

0

0.0

[illegible]

CATD0546a (4 mutations)



CATD338a (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]

CATD332a (1 mutations)

$C > A$

C > G

$C > T$

T > A

$$T > C$$

T>G

Mutations

1.0

 \circ

0

0

0.0

[illegible]

CATD339a (1 mutations)

$C > A$

$C > G$

$C > T$

$T > A$

 $T > C$

T>G

Mutations

1.0

3.0

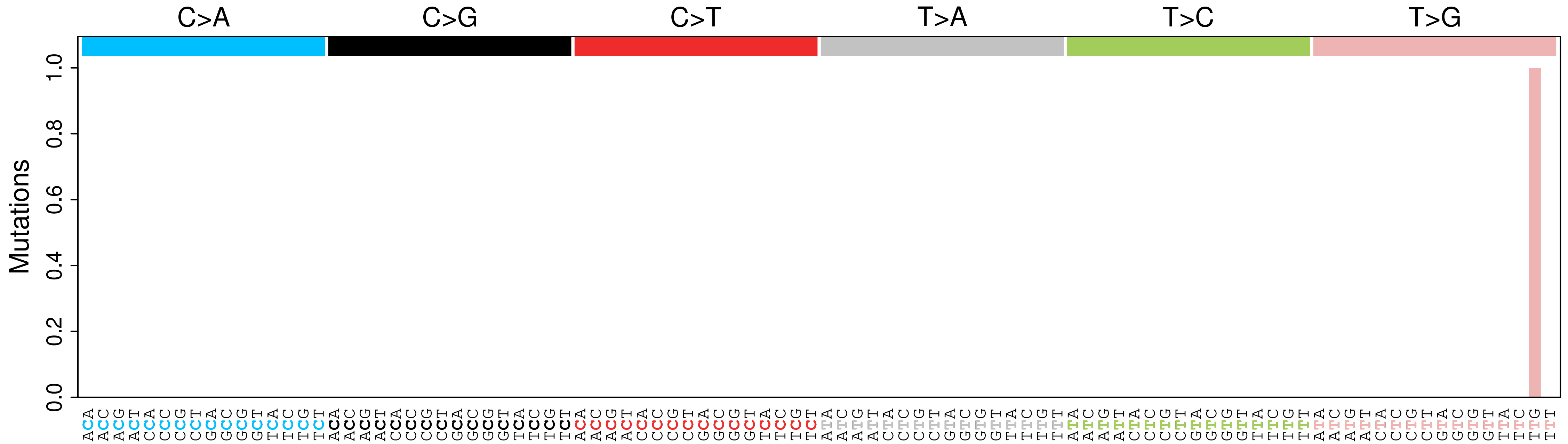
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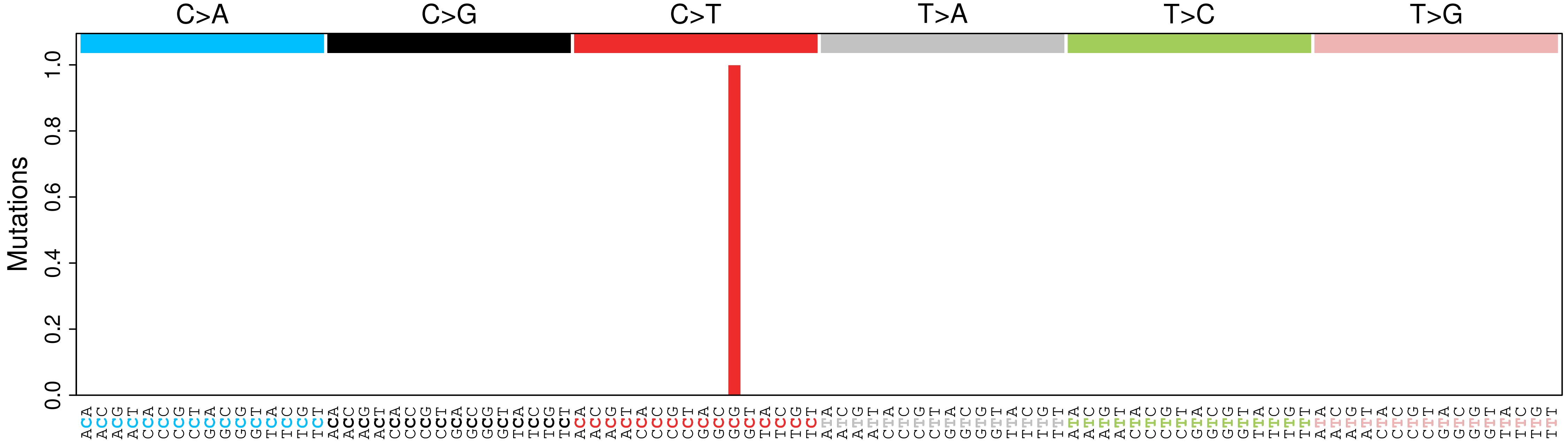
U

[illegible]

CATD0555a (1 mutations)



CATD0551a (1 mutations)



CATD345a (7 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 1.4

