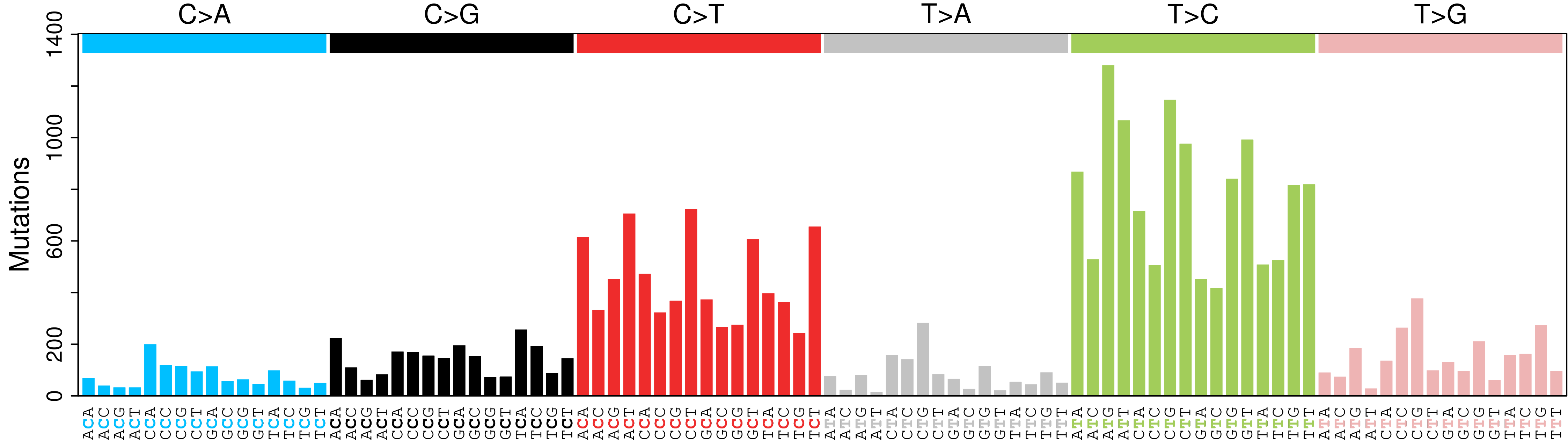


CATD309a (27,085 mutations)



CATD319a (13 mutations)

C>A

C>G

C>T

T>A

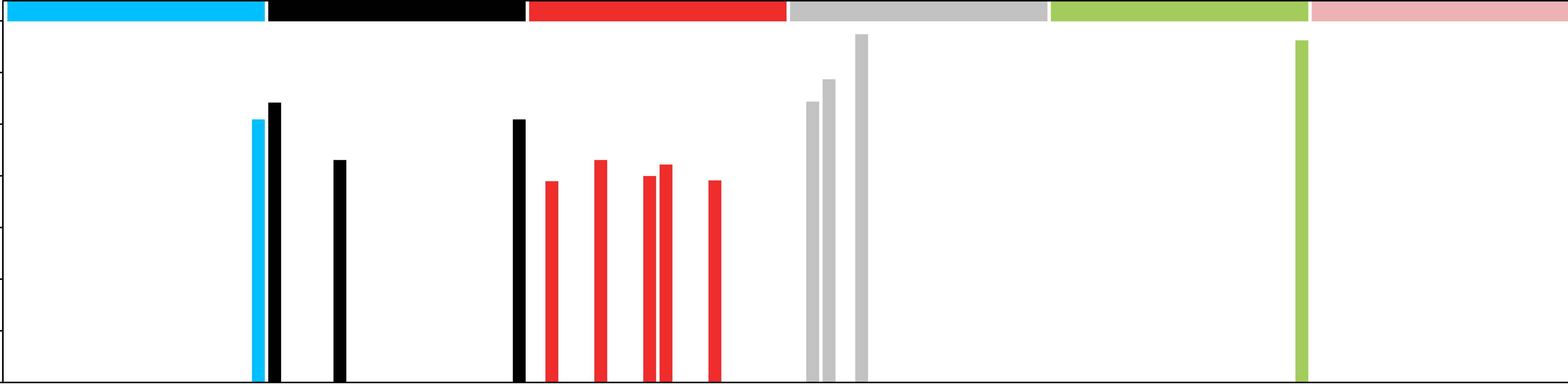
T>C

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



CATD310a (3 mutations)

$C > A$

$C > G$

 $C > T$

$T > A$

 $T > C$

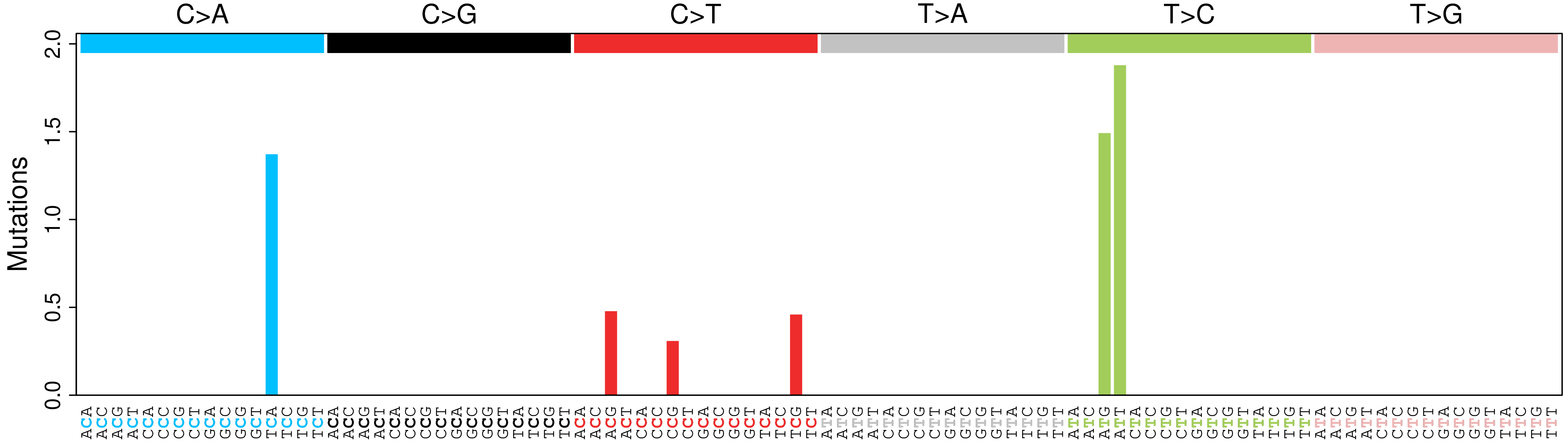
T > G

Mutations

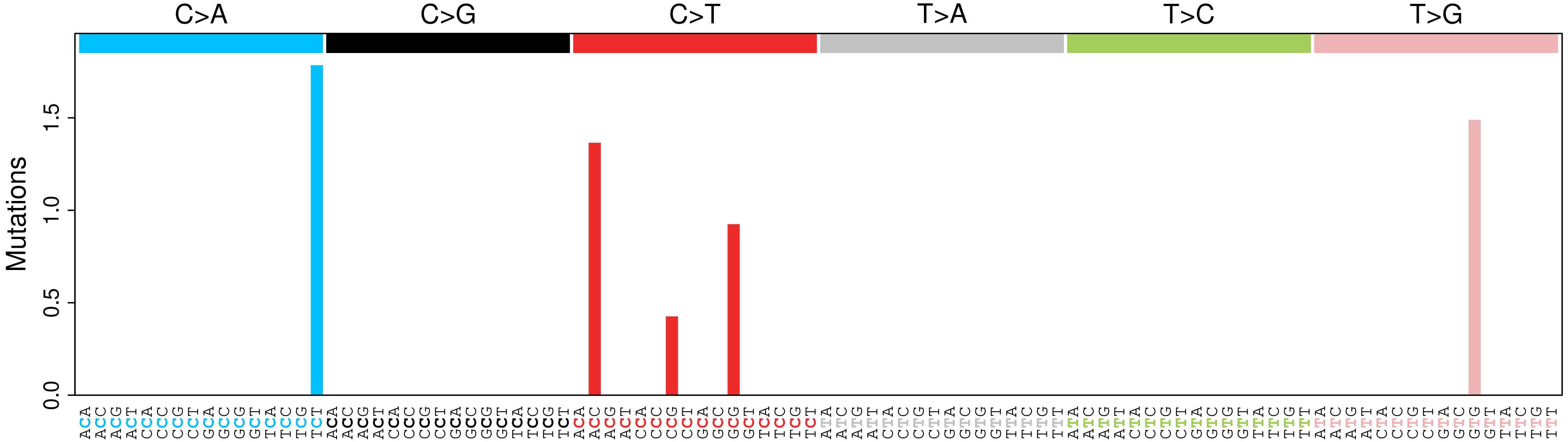
0.0 0.2 0.4 0.6 0.8 1.0 1.2

[illegible]

CATD297a (6 mutations)



CATD323a (6 mutations)



CATD314a (5 mutations)

$C > A$

C > G

$$C > T$$

T>A

$T > C$

$T > G$

Mutations

1.5

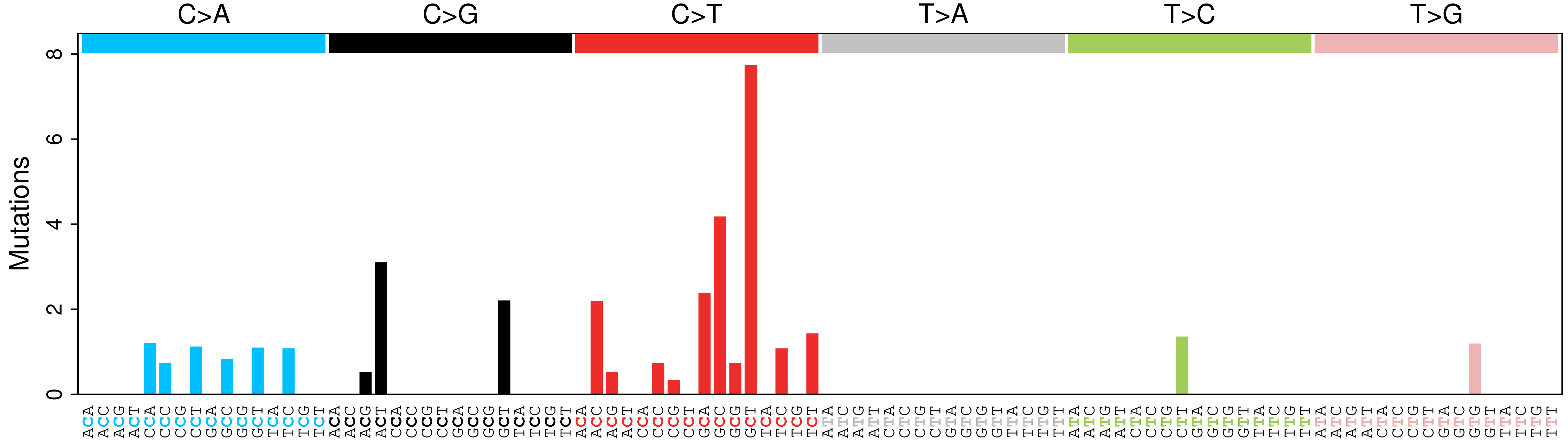
1.0

0.

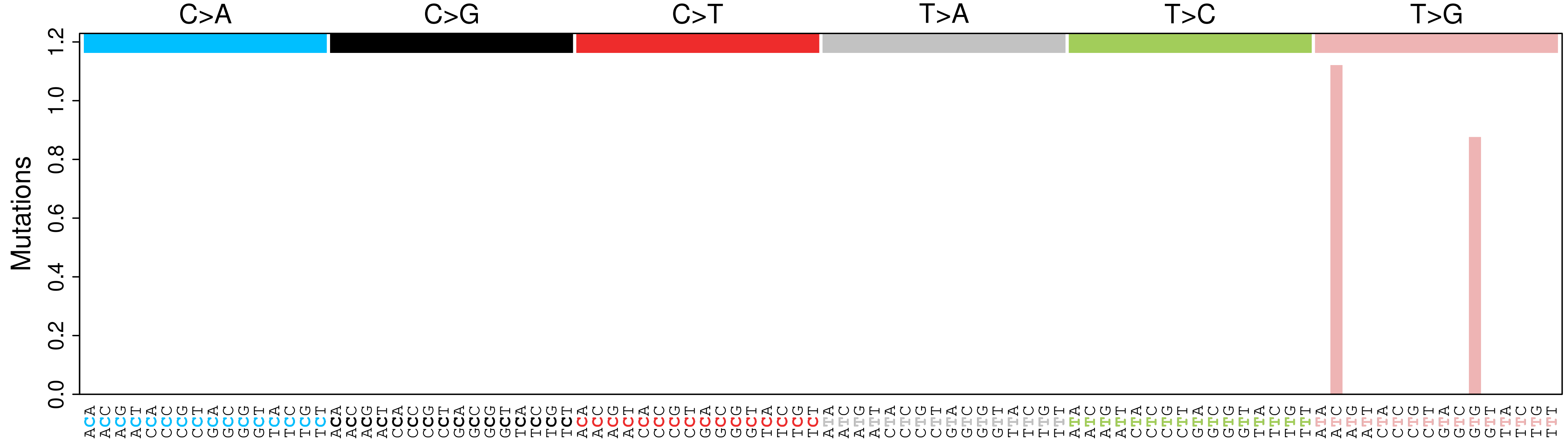
0

[illegible]

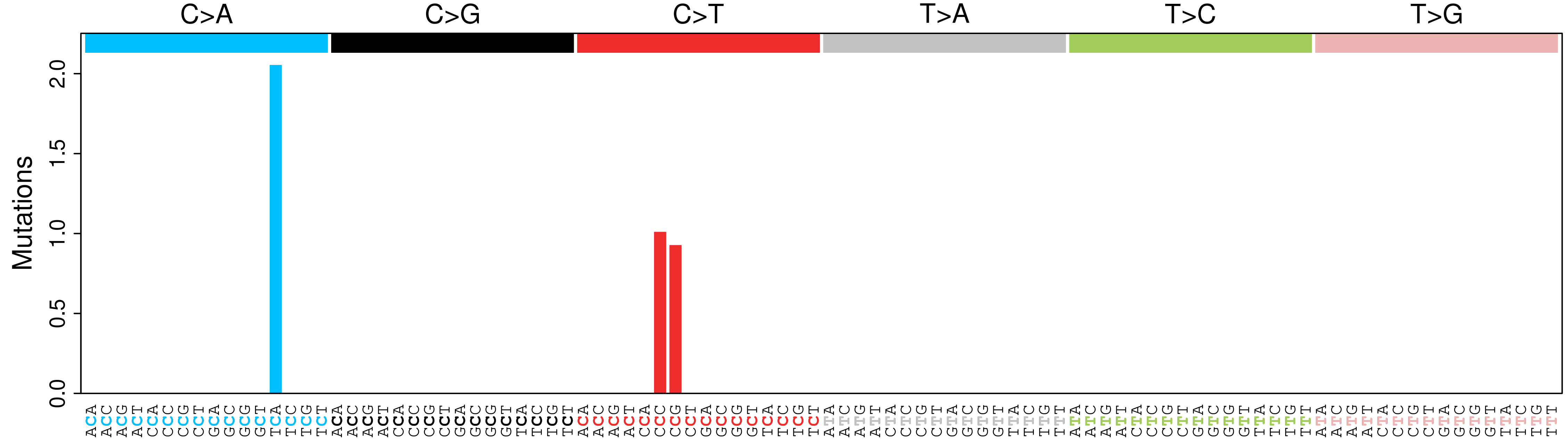
CATD329a (36 mutations)



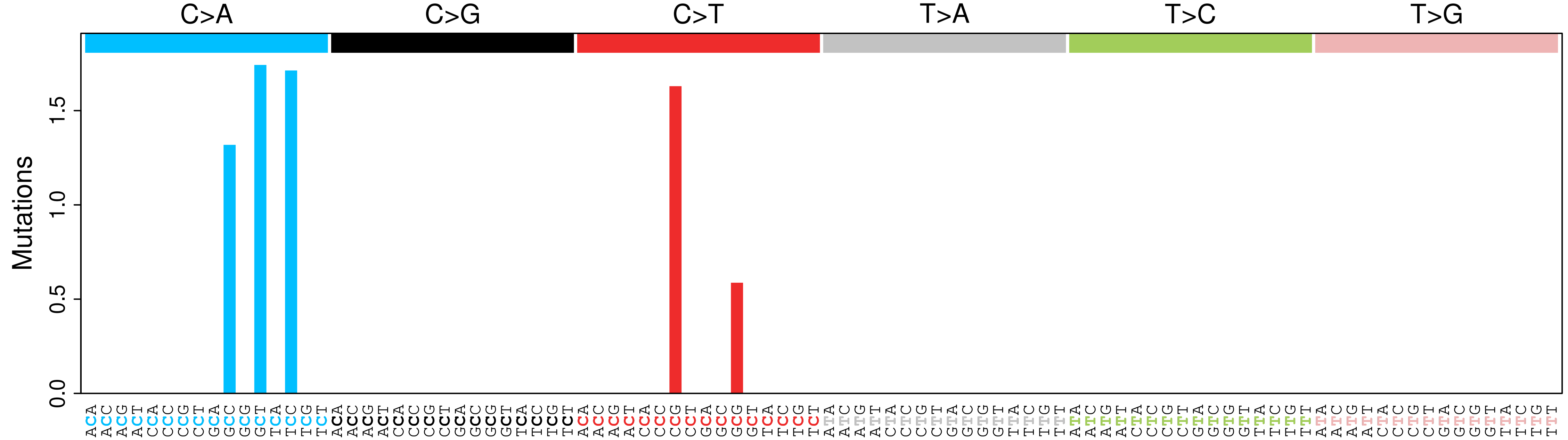
CATD311a (2 mutations)



CATD306a (4 mutations)



CATD300a (7 mutations)



CATD328a (8 mutations)

C>A

C>G

C>T

T>A

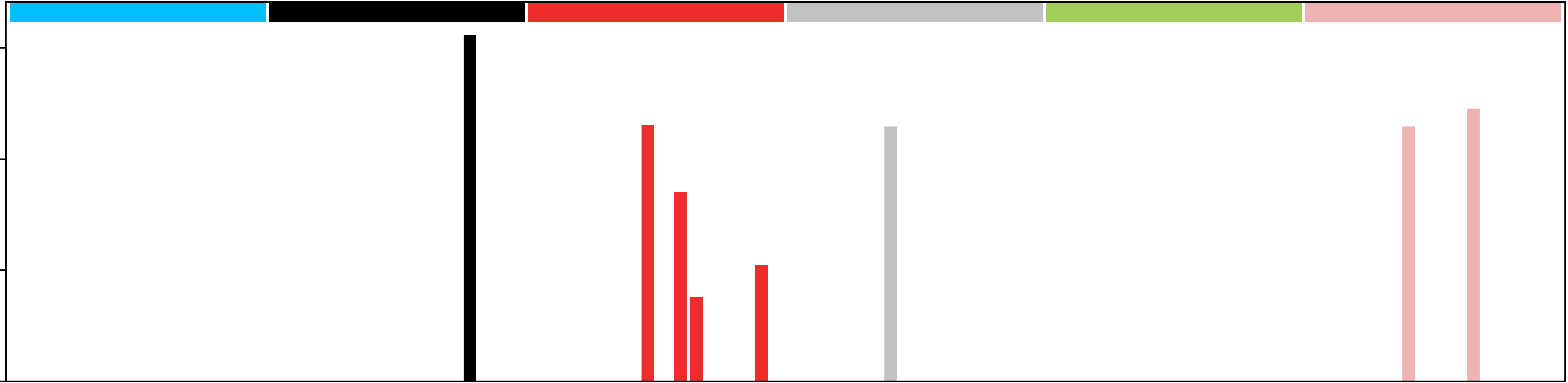
T>C

T>G

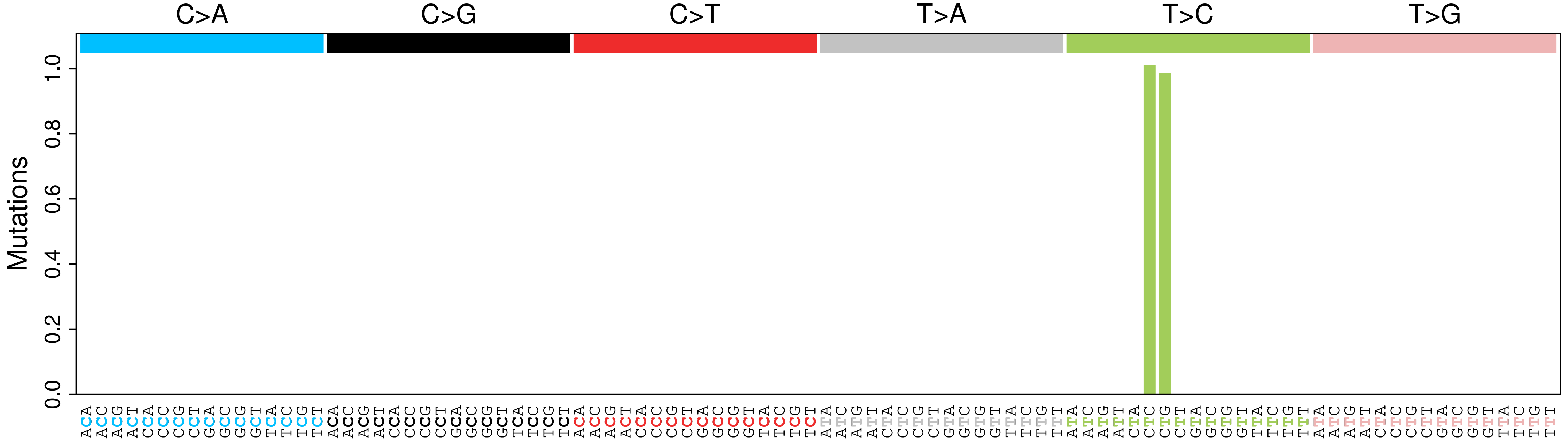
Mutations

1.5
1.0
0.5
0.0

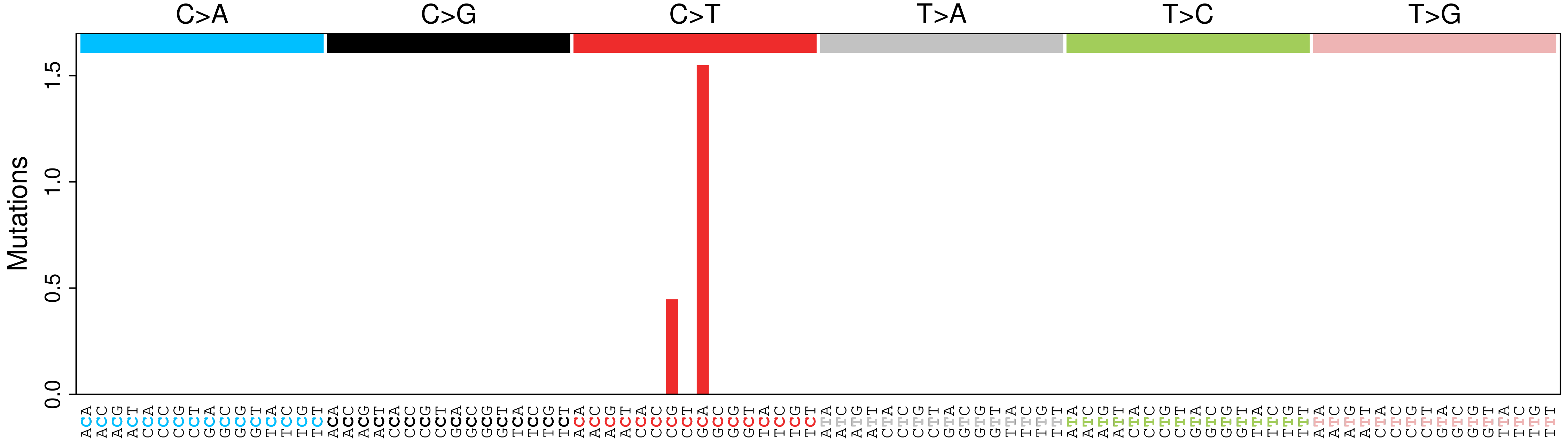
ACA ACC AGT ACT CCA CCC CCT CCA GCC GGT GGT TCA TCC TCG TCT ACA ACC AGT ACT CCA CCC CCT CCA GCC GGT GGT TCA TCC TCG TCT ATA ATC ATG ATT CTA CTC CTG CTT GTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CCT CTT CTA GTC GTG GTT TTA TTC TTG TTT ATA ATC ATG ATT CTA CTC CTG CTT CTA GTC GTG GTT TTA TTC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



CATD0674a (2 mutations)



CATD318a (2 mutations)



CATD301a (6 mutations)

C>A

C>G

C>T

T>A

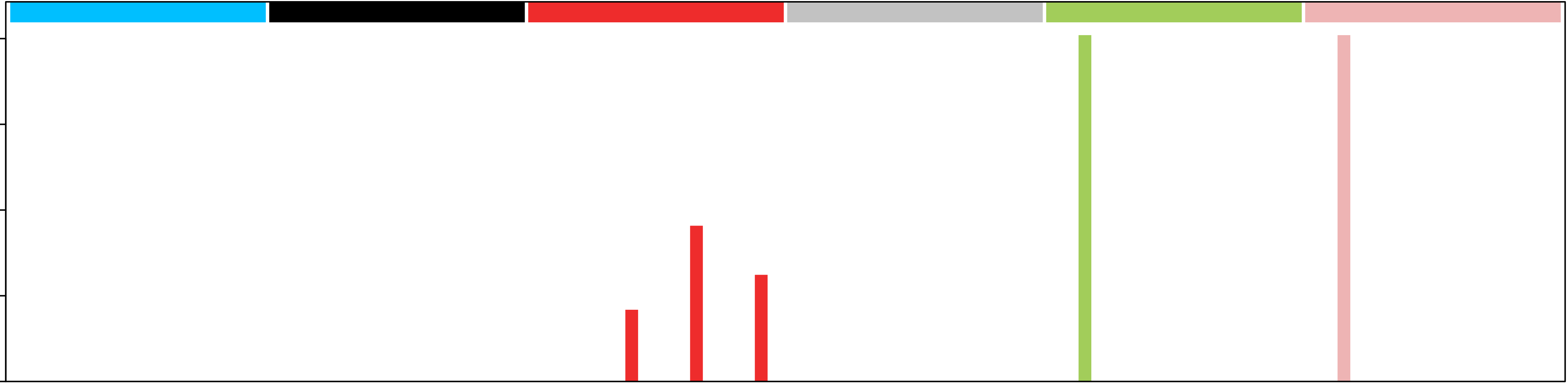
T>C

T>G

Mutations

2.0
1.5
1.0
0.5
0.0

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



CATD308a (1 mutations)

$C > A$

$C > G$

 $C > T$

$T > A$

 $T > C$

T > G

Mutations

1.0

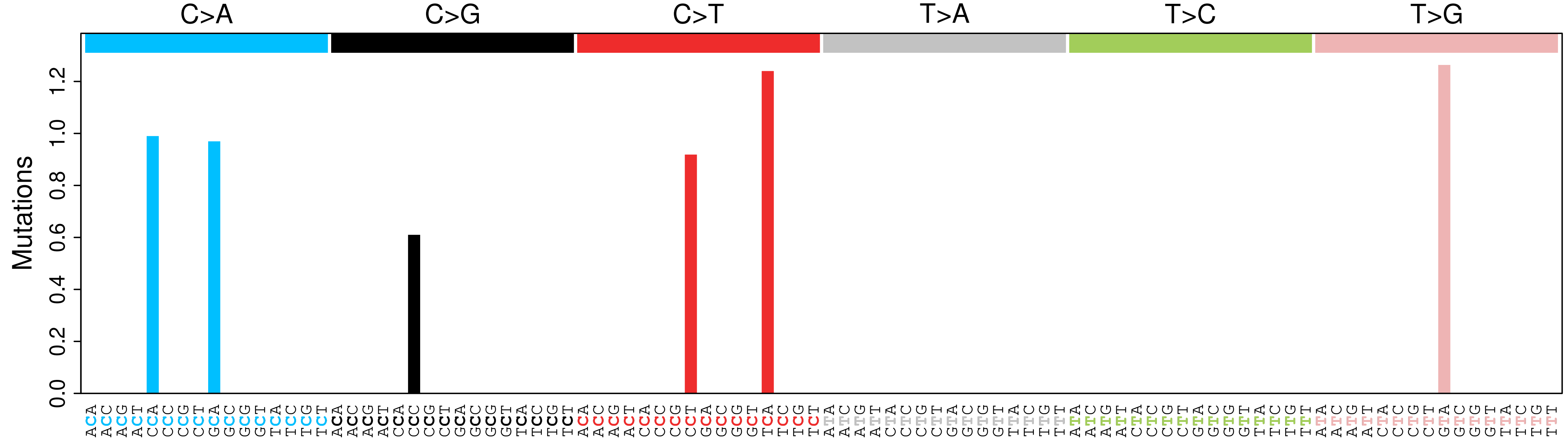
0

2

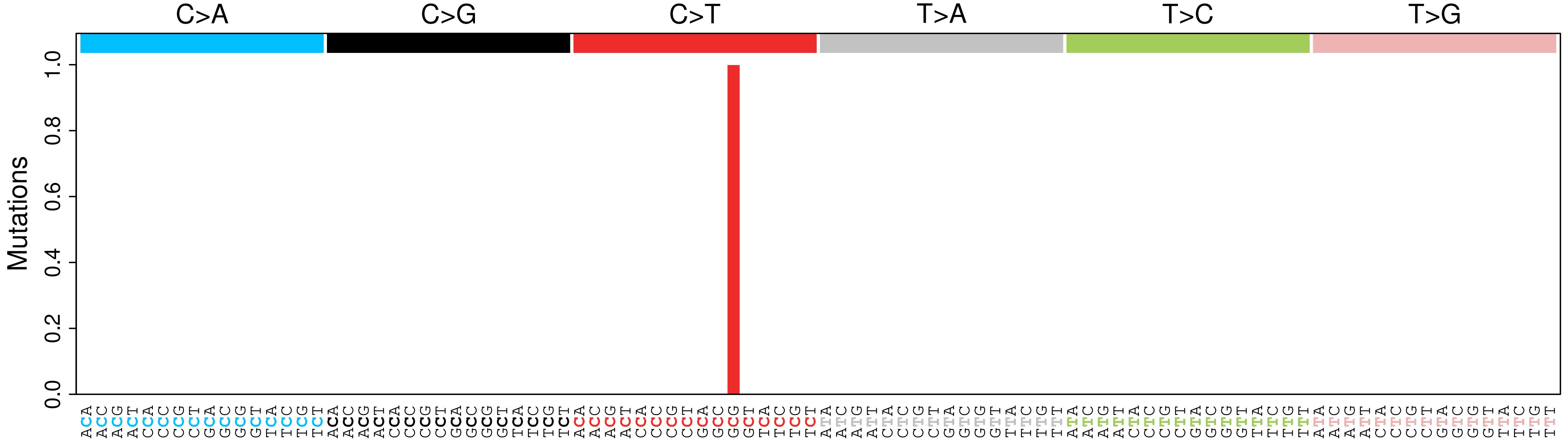
0.

[illegible]

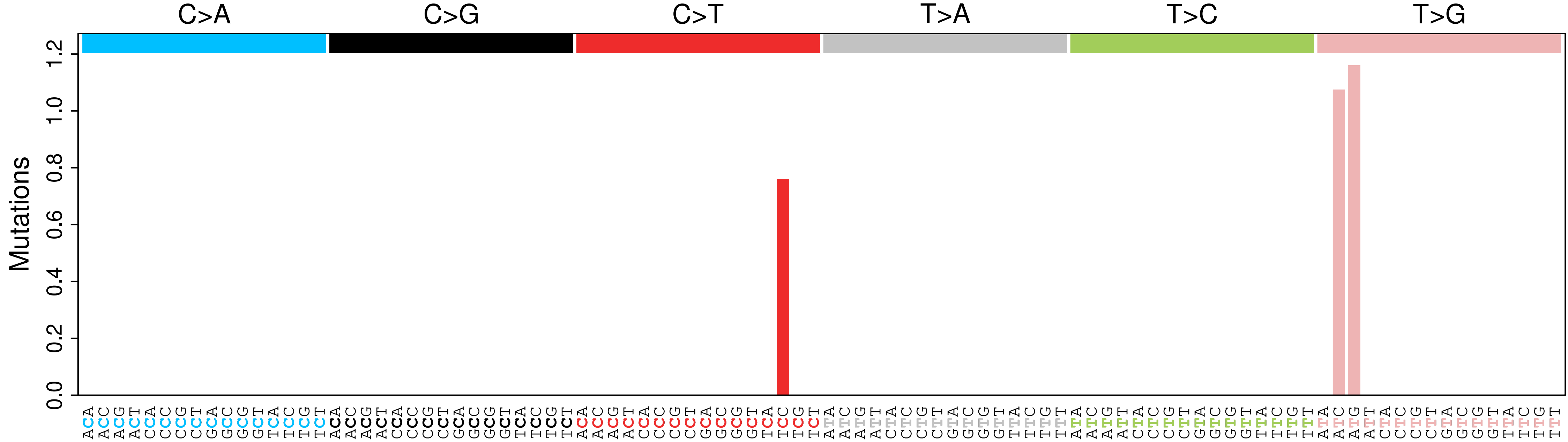
CATD296a (6 mutations)



CATD0675a (1 mutations)



CATD0676a (3 mutations)



CATD326a (6 mutations)

$C > A$

C > G

$C > T$

T > A

$$T > C$$

$T > G$

1.5

1.0

0.5

0.0

[illegible]

CATD0677a (2 mutations)

C > A

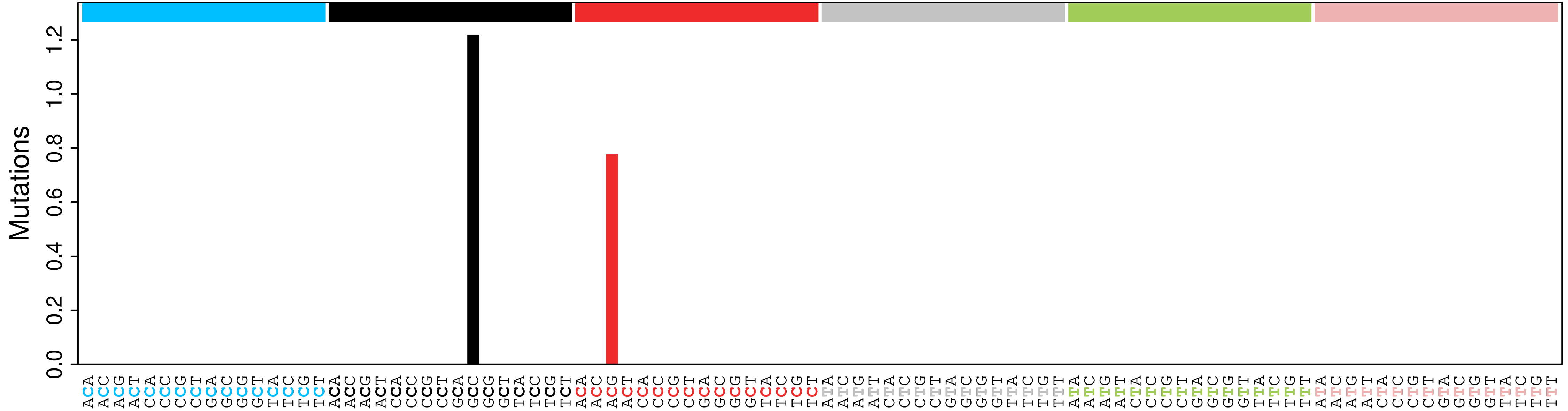
C > G

$$C > T$$

T > A

$$T > C$$

$T > G$



CATD299a (2 mutations)

$C > A$

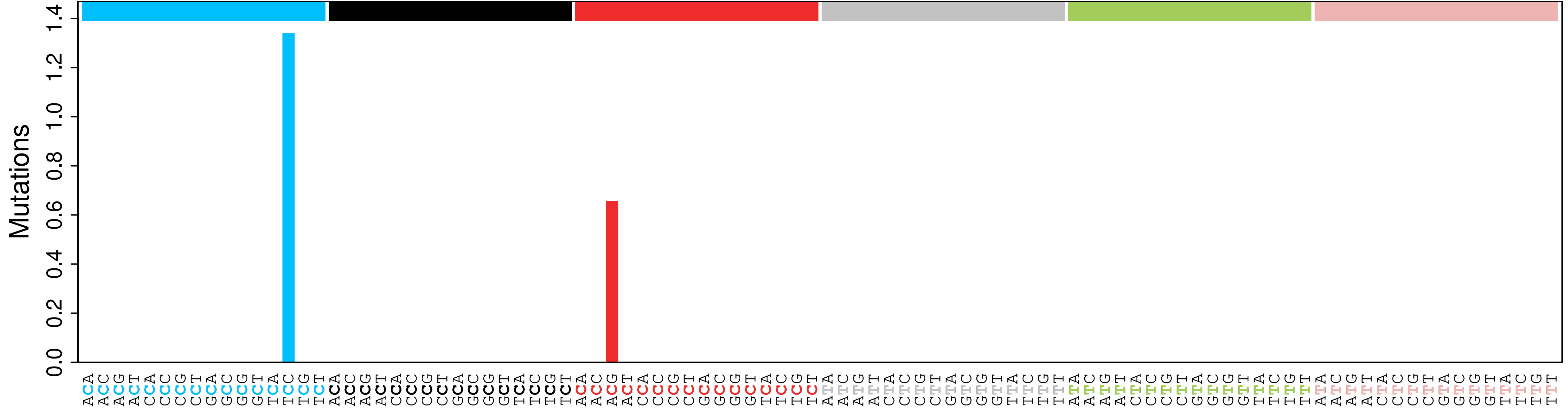
C>G

$$C > T$$

T > A

$$T > C$$

T>G



CATD317a (1 mutations)

$C > A$

$C > G$

 $C > T$

$T > A$

 $T > C$

T > G

Mutations

1.0

0

2

0.

[illegible]

CATD307a (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]

