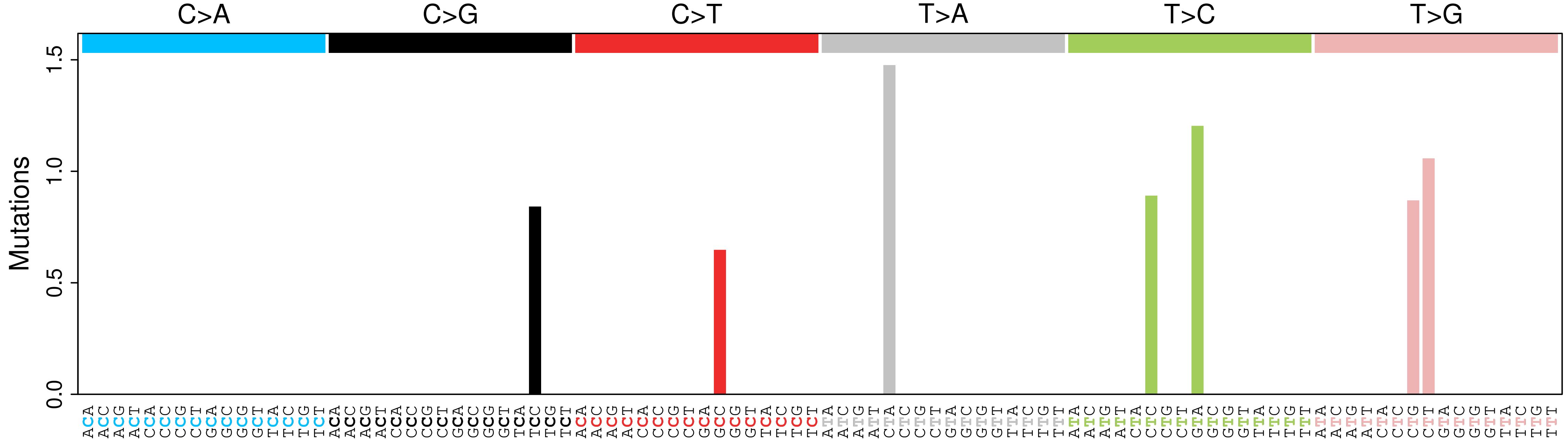


CATD0507a (7 mutations)



CATD0500a (32 mutations)

C > A

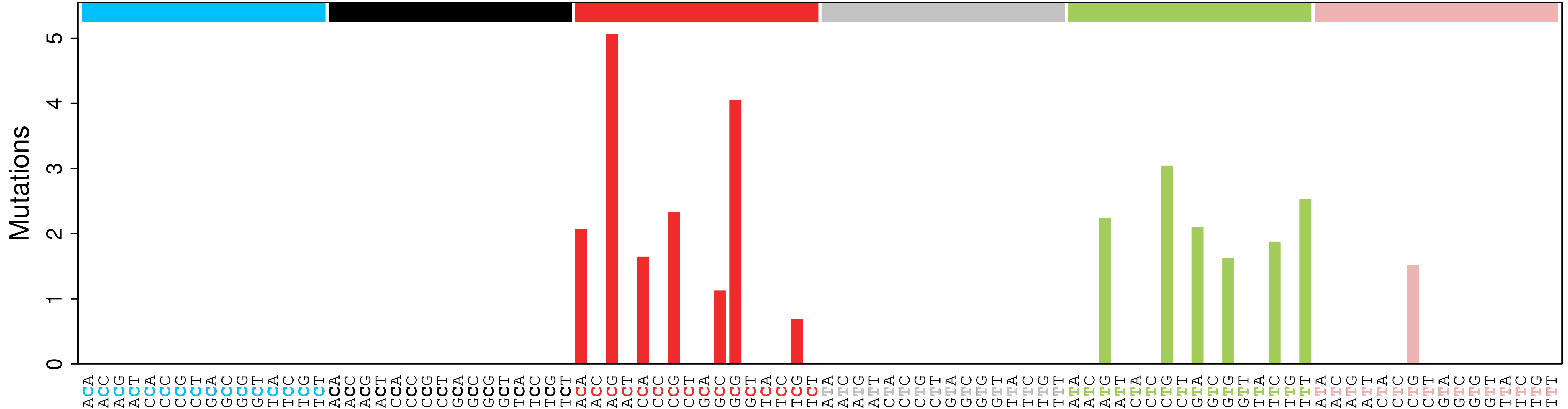
C > G

$C > T$

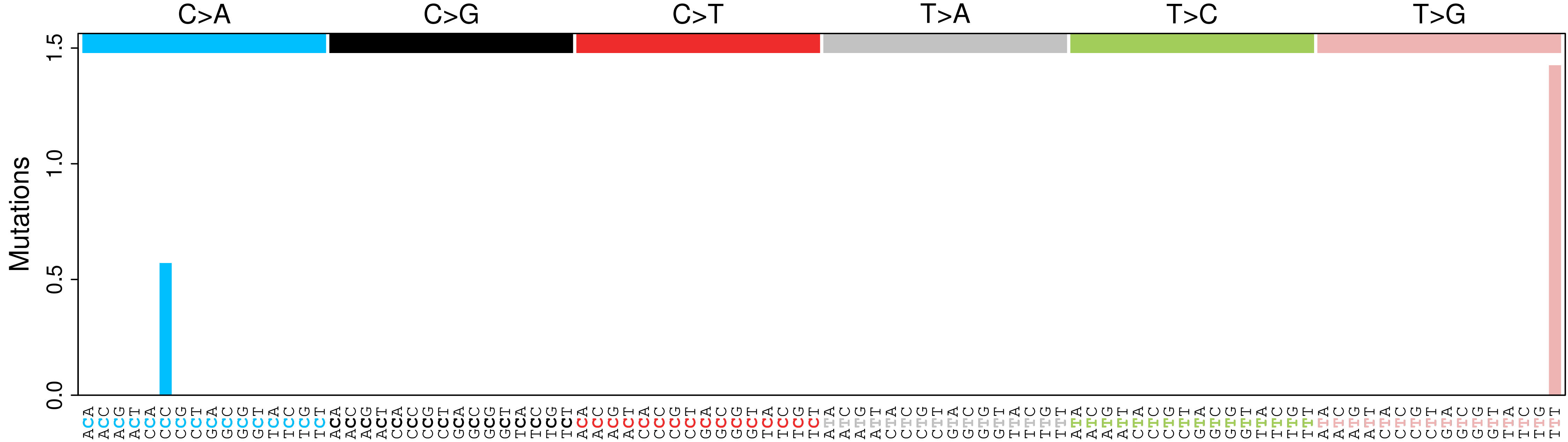
T > A

$$T > C$$

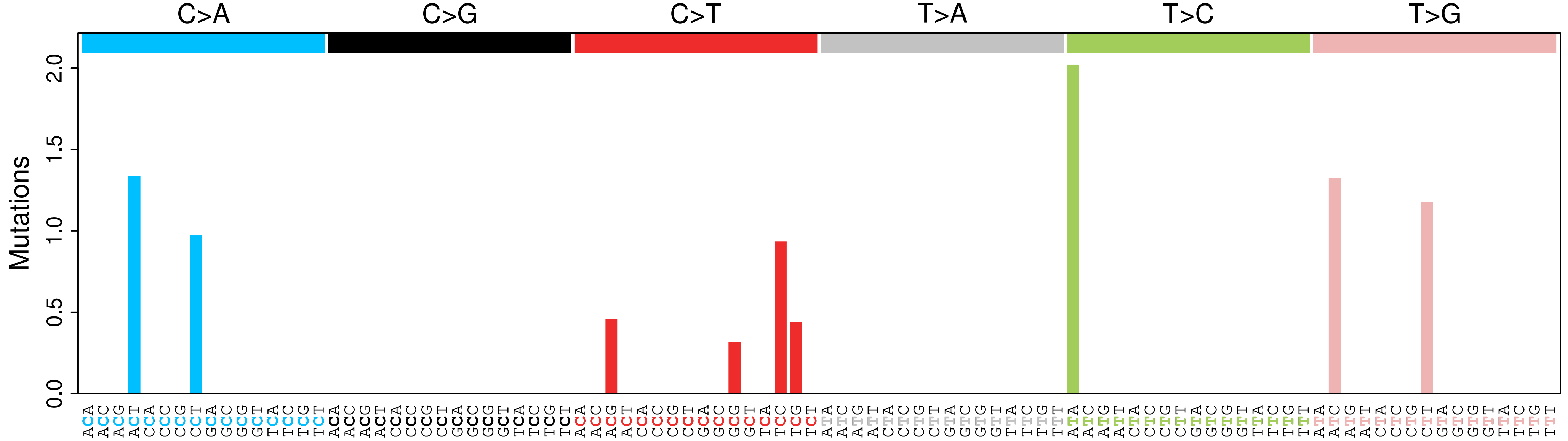
T > G



CATD0467a (2 mutations)



CATD0698a (9 mutations)



CATD0480a (4 mutations)

C>A

C>G

C>T

T>A

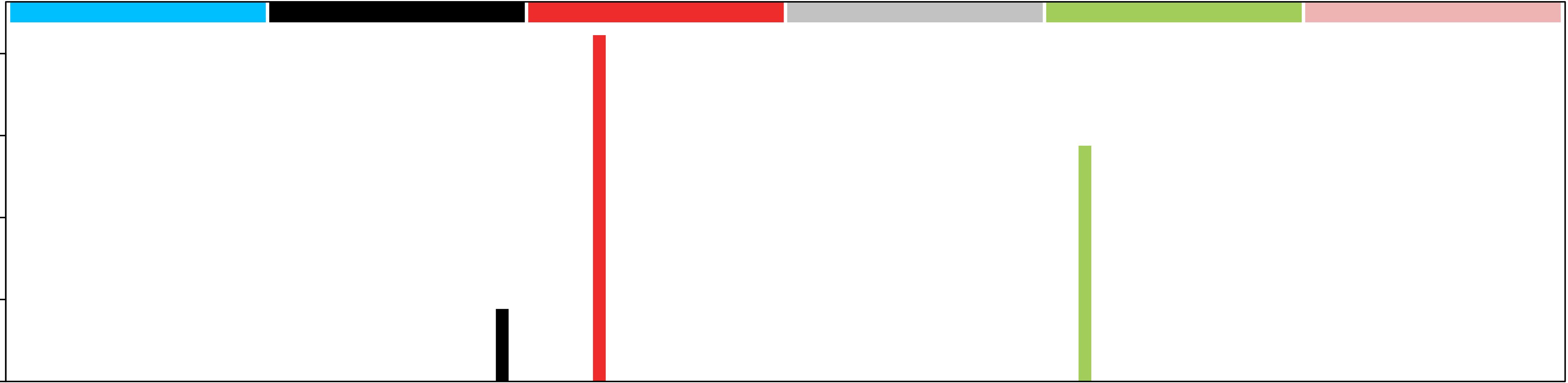
T>C

T>G

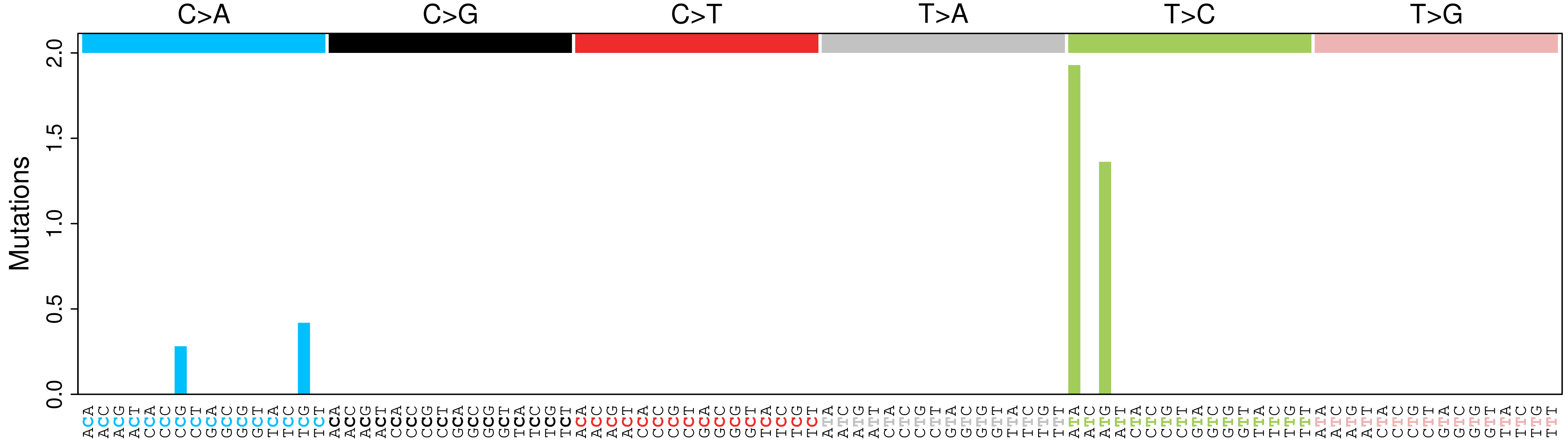
Mutations

2.0
1.5
1.0
0.5
0.0

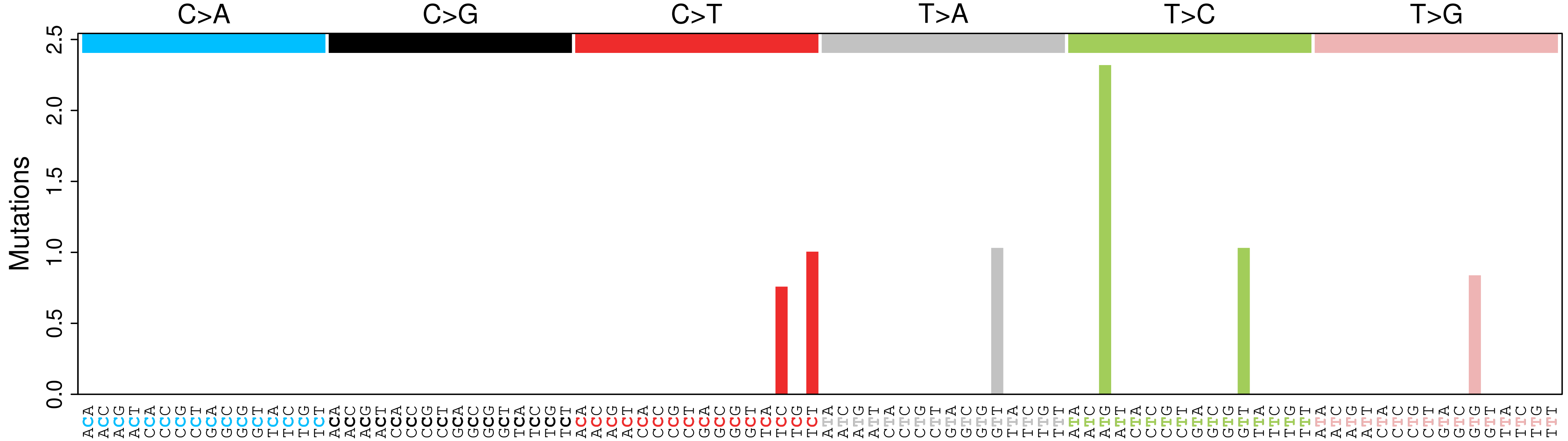
ACA
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TAG
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CTA
CTC
CTG
CTT



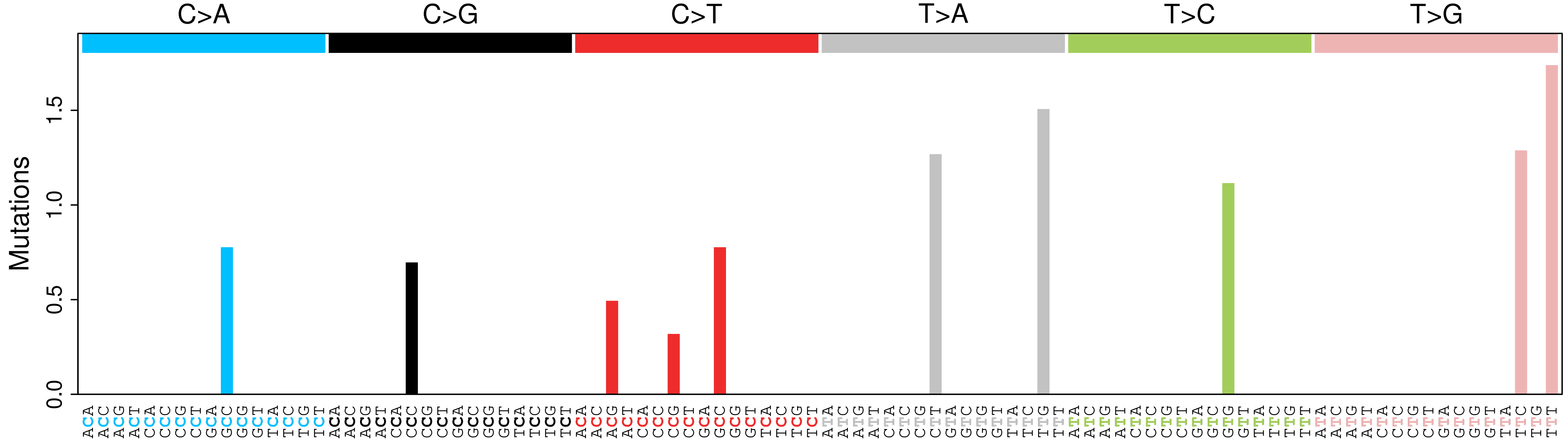
CATD0491a (4 mutations)



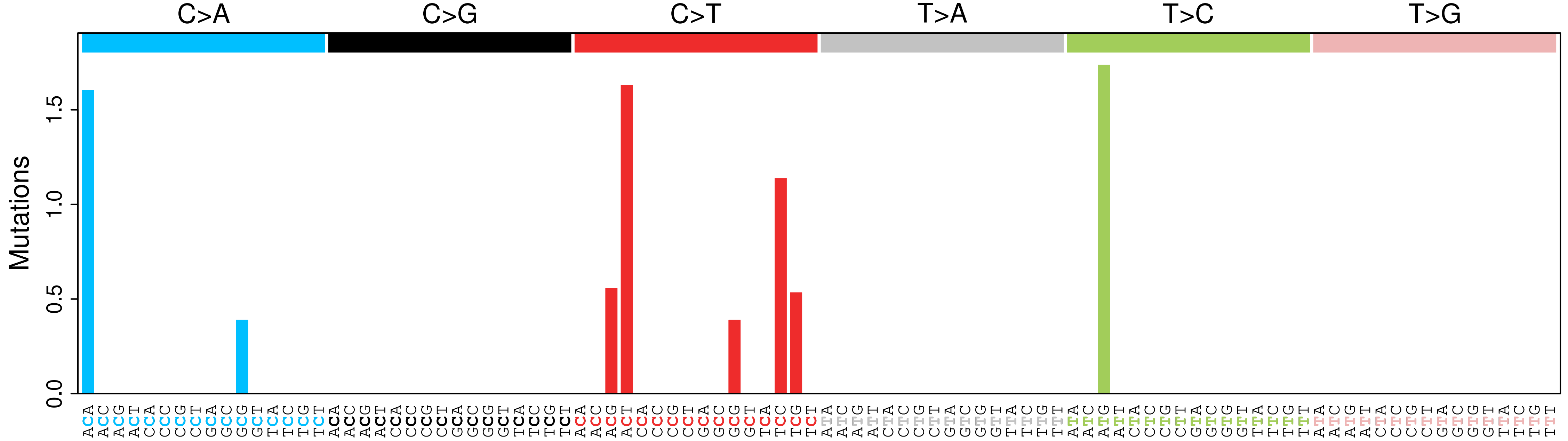
CATD0689a (7 mutations)



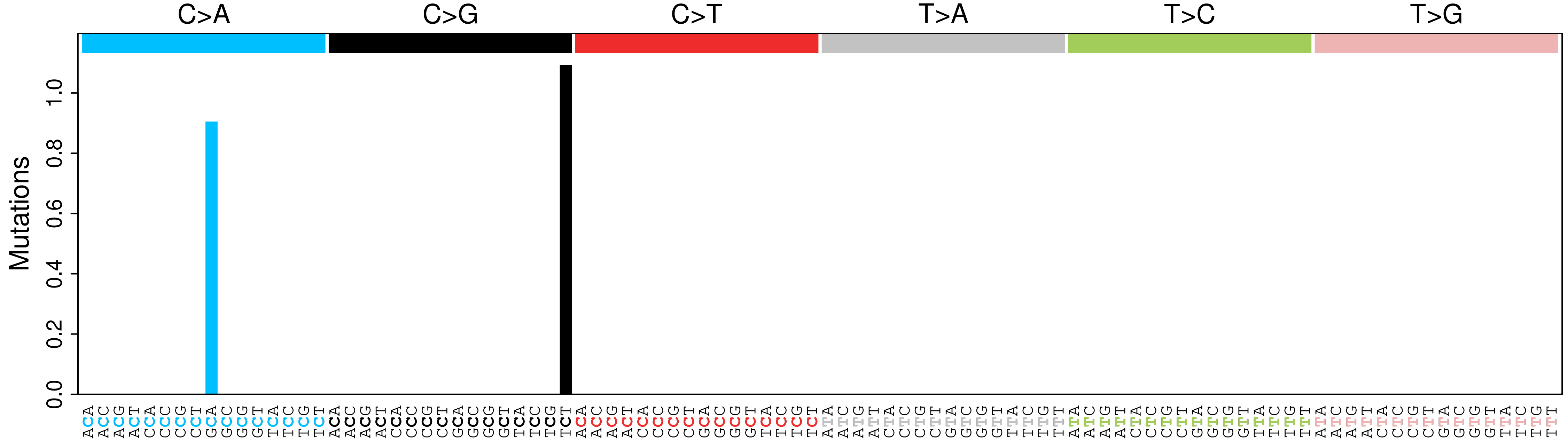
CATD0740a (10 mutations)



CATD0701a (8 mutations)



CATD0495a (2 mutations)



CATD0702a (7 mutations)

C>A

C>G

C>T

T>A

T>C

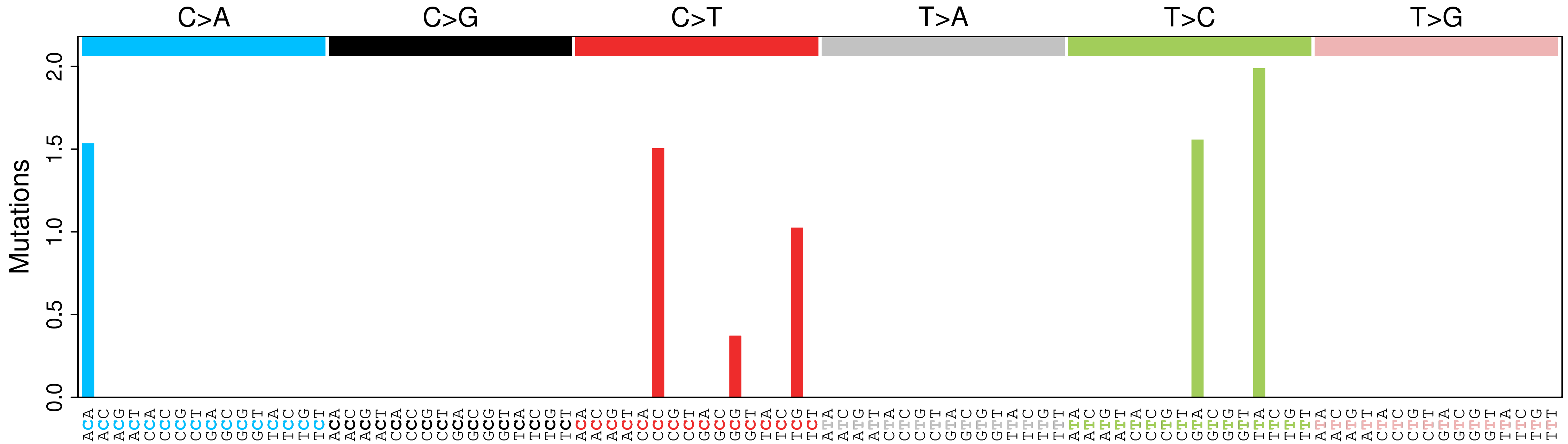
T>G

Mutations

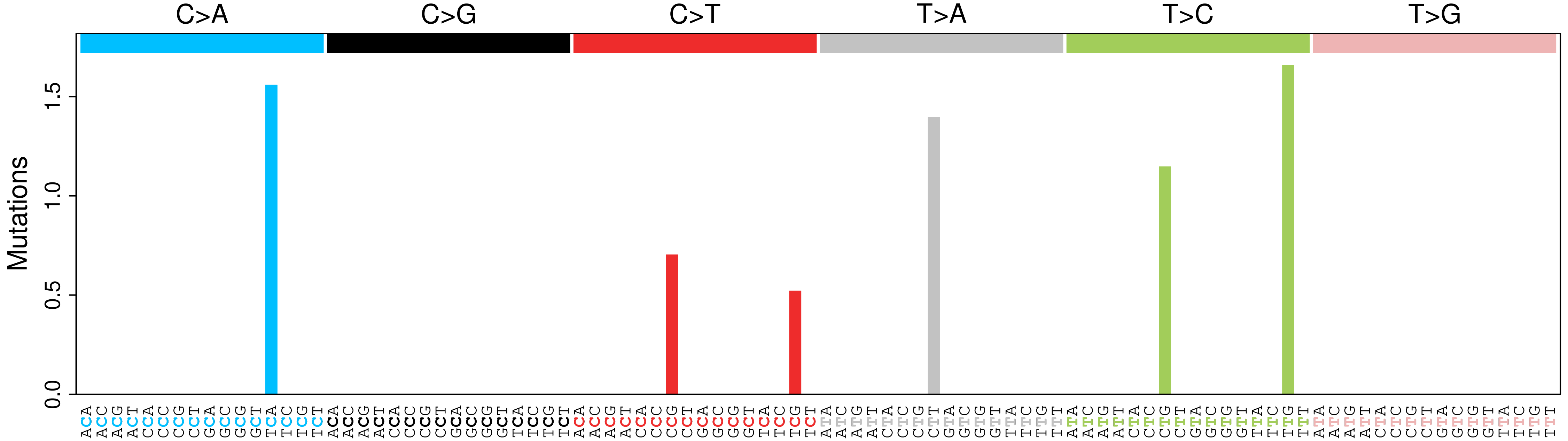
1.5
1.0
0.5
0.0

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

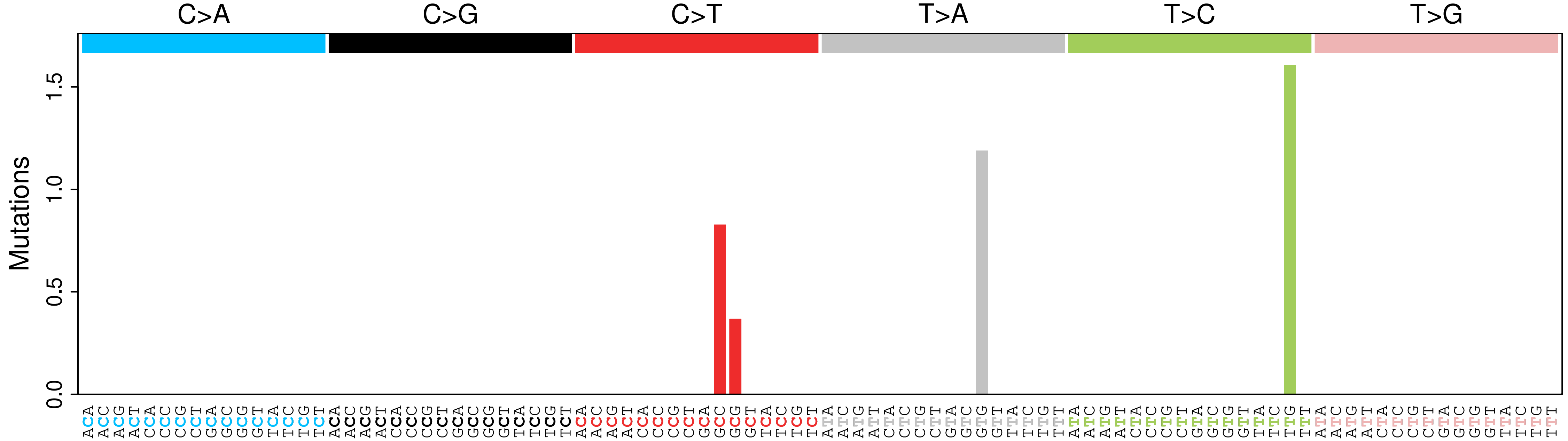
CATD0505a (8 mutations)



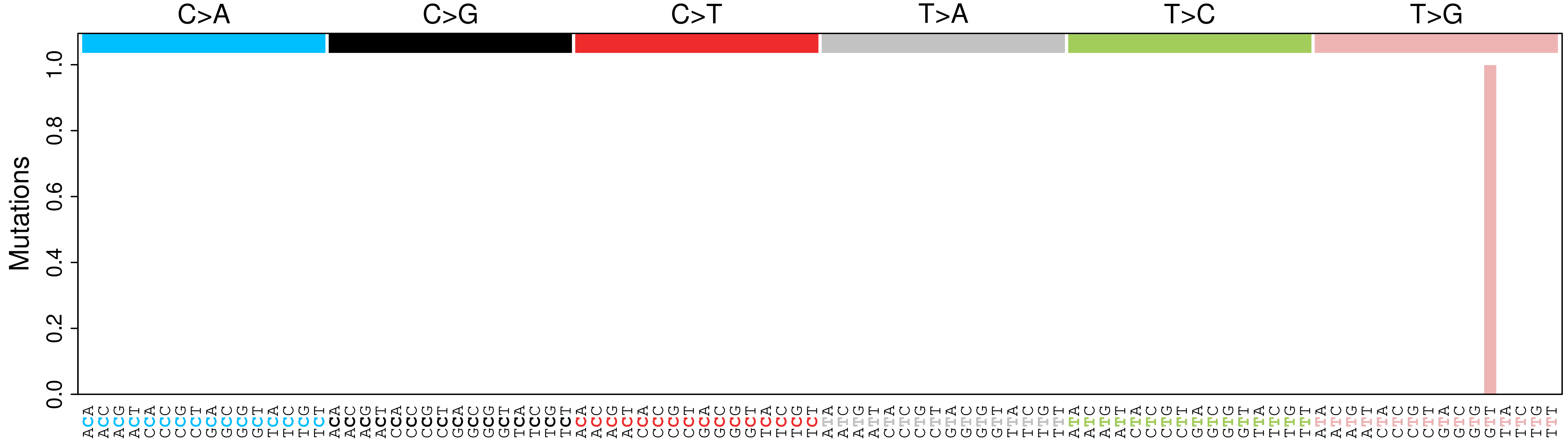
CATD0482a (7 mutations)



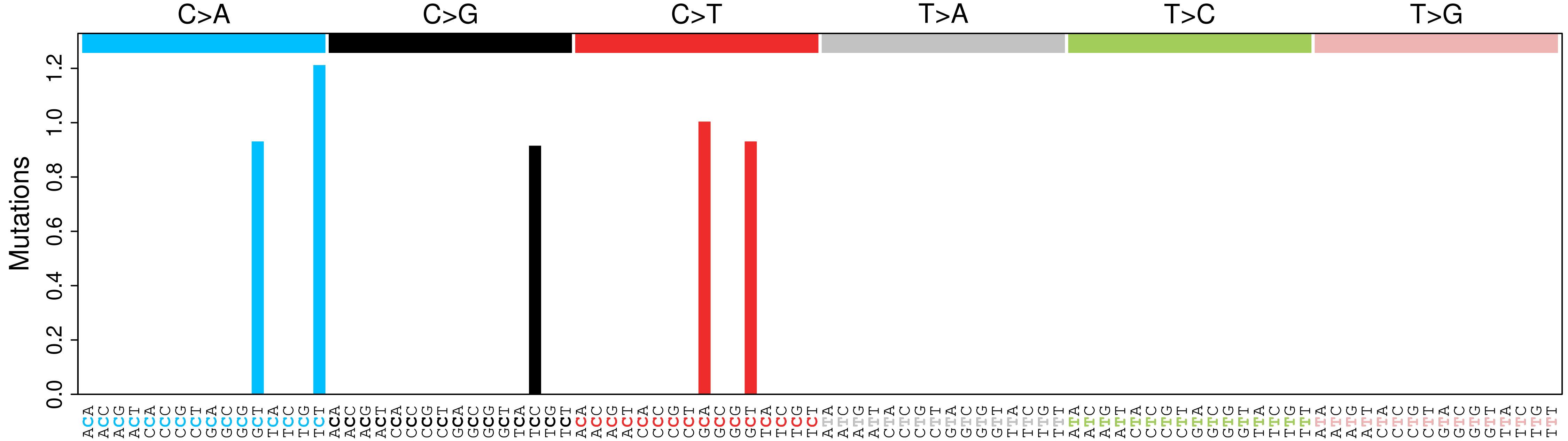
CATD0694a (4 mutations)



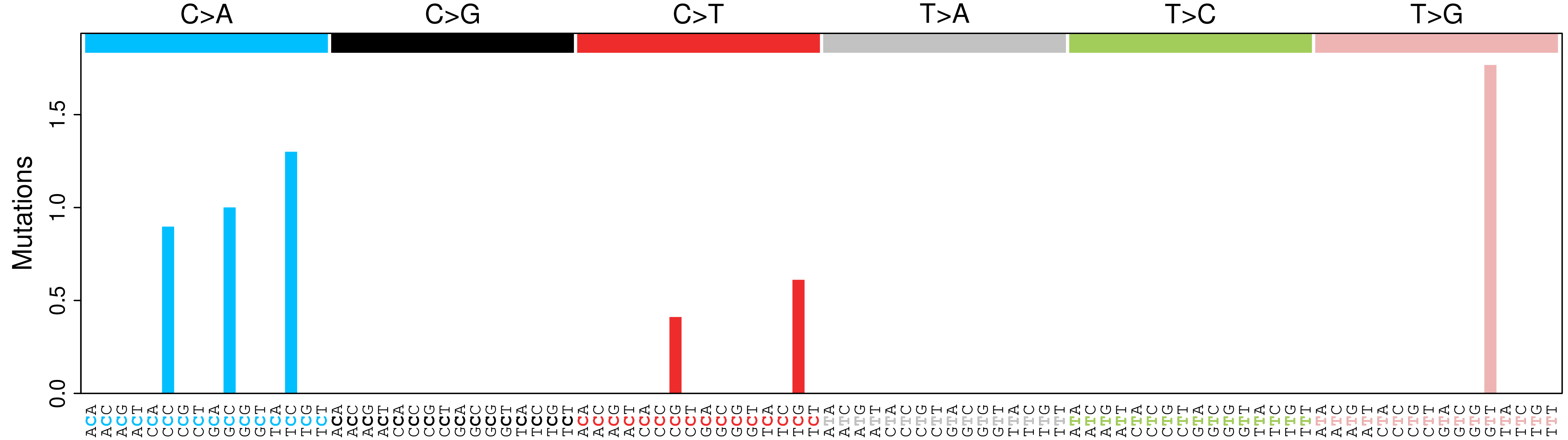
CATD0499a (1 mutations)



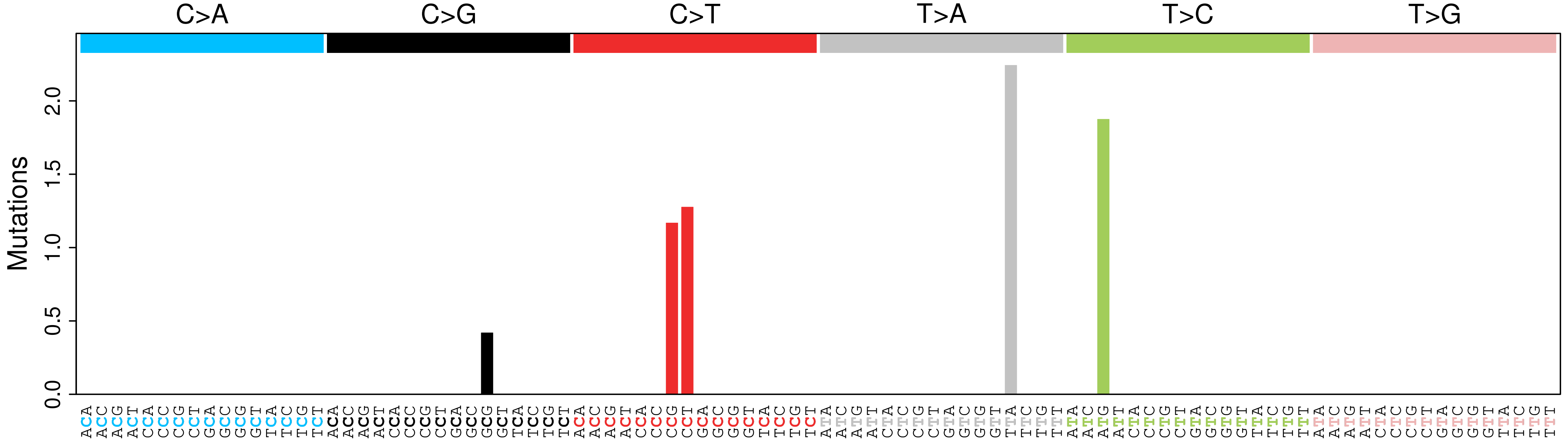
CATD0504a (5 mutations)



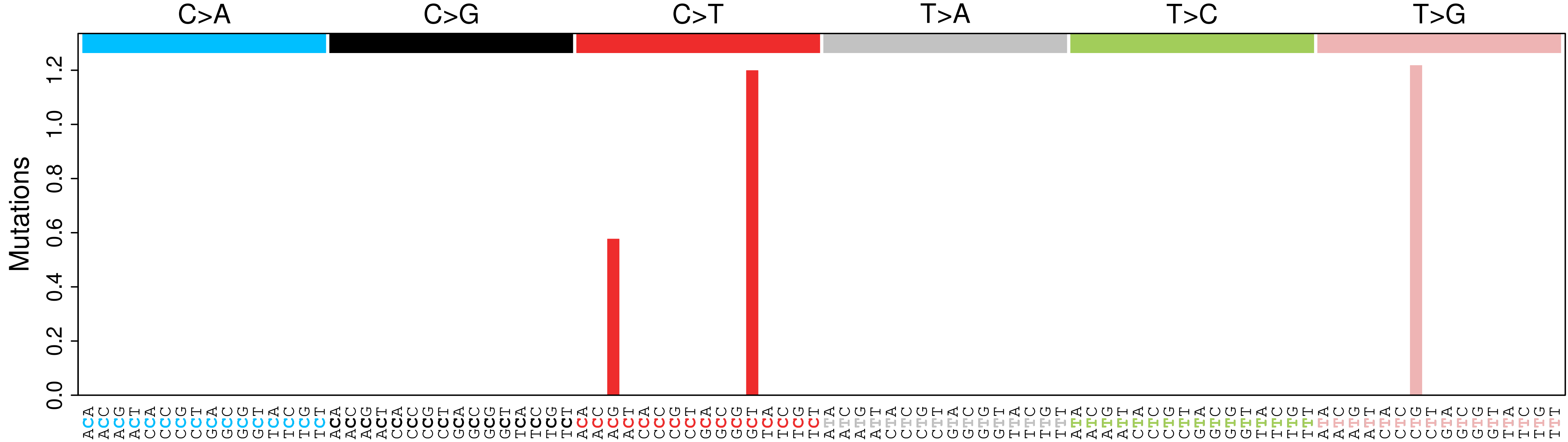
CATD0700a (6 mutations)



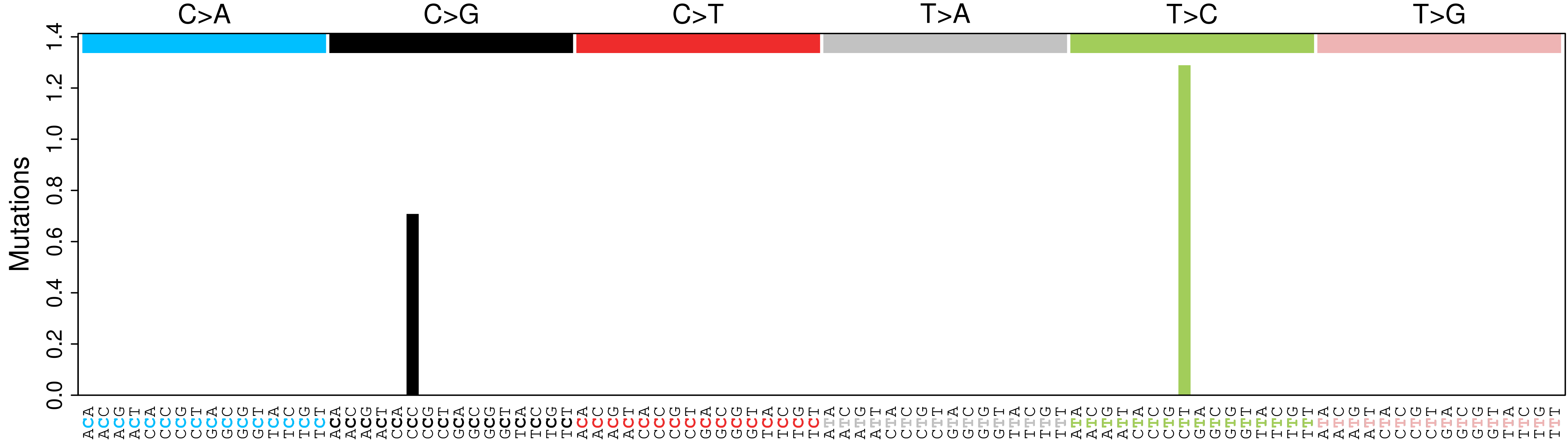
CATD0469a (7 mutations)



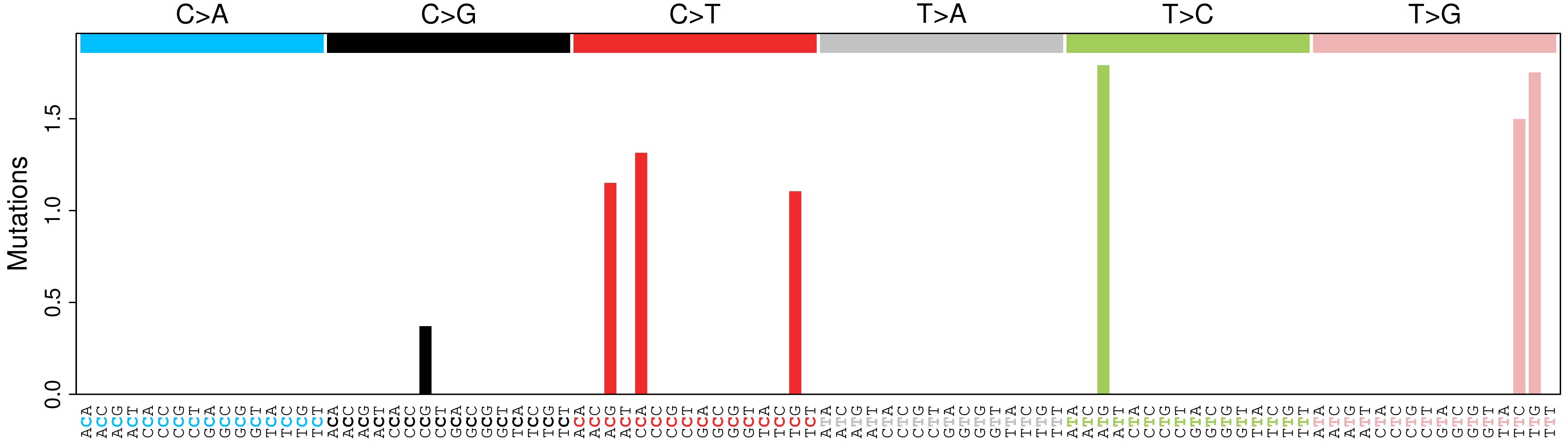
CATD0468a (3 mutations)



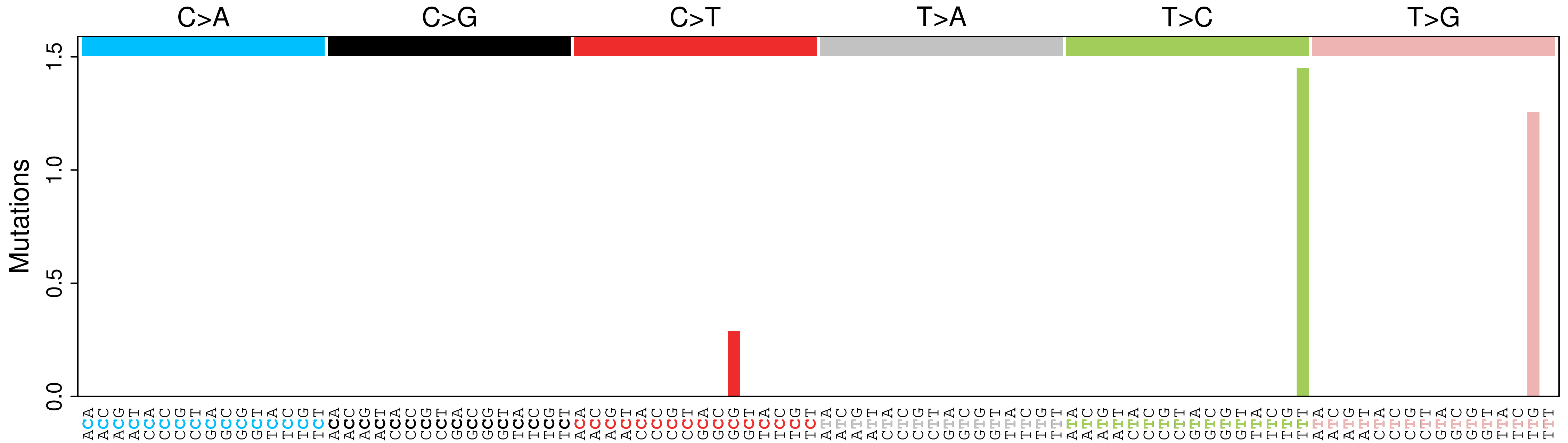
CATD0691a (2 mutations)



CATD0479a (9 mutations)



CATD0688a (3 mutations)



CATD0494a (6 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]

CATD0742a (2 mutations)

$C > A$

$C > G$

$C > T$

T > A

$T > C$

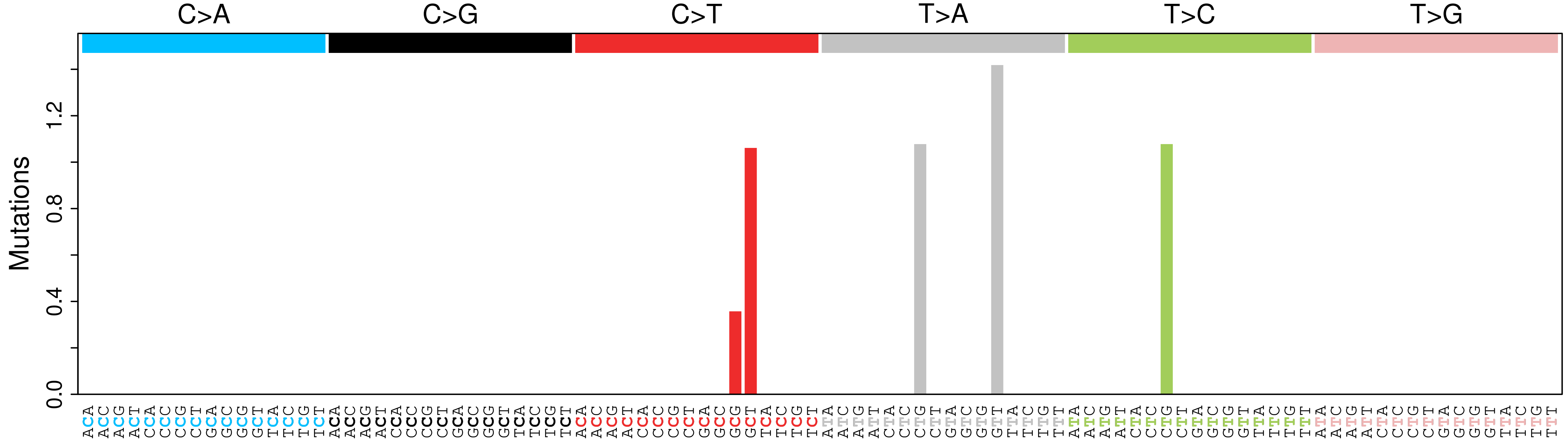
T > G

Mutations

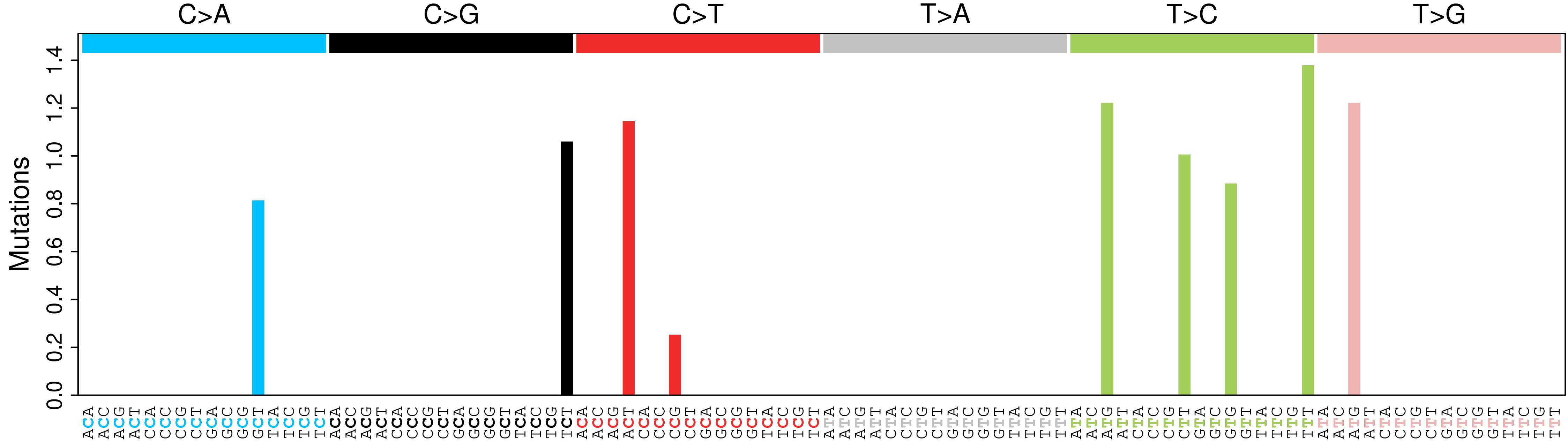
0.0 0.2 0.4 0.6 0.8 1.0 1.2

[illegible]

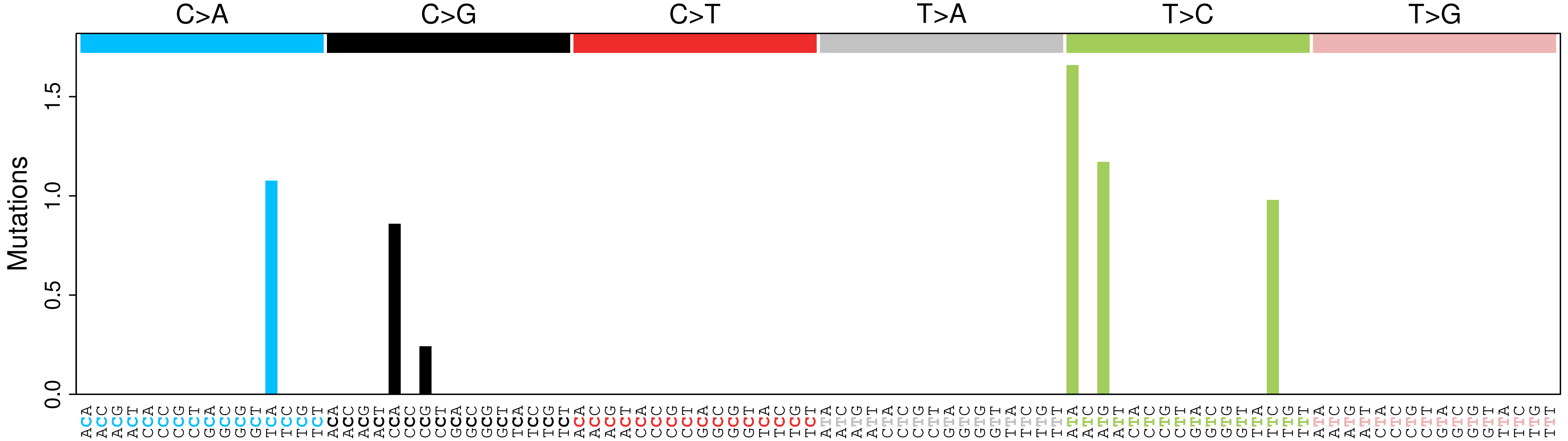
CATD0746a (5 mutations)



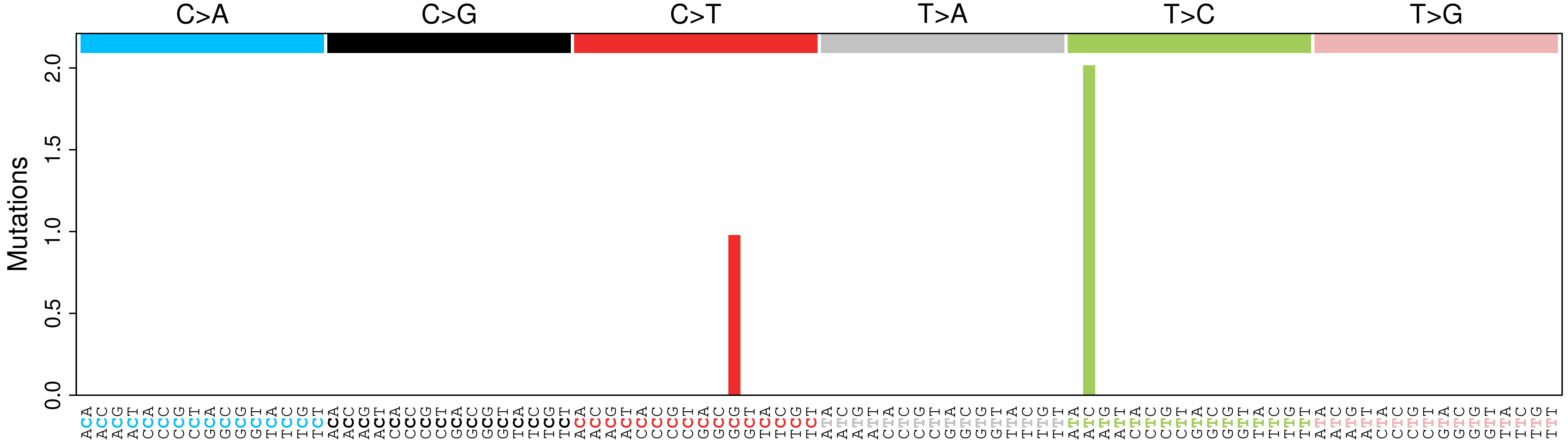
CATD0745a (9 mutations)



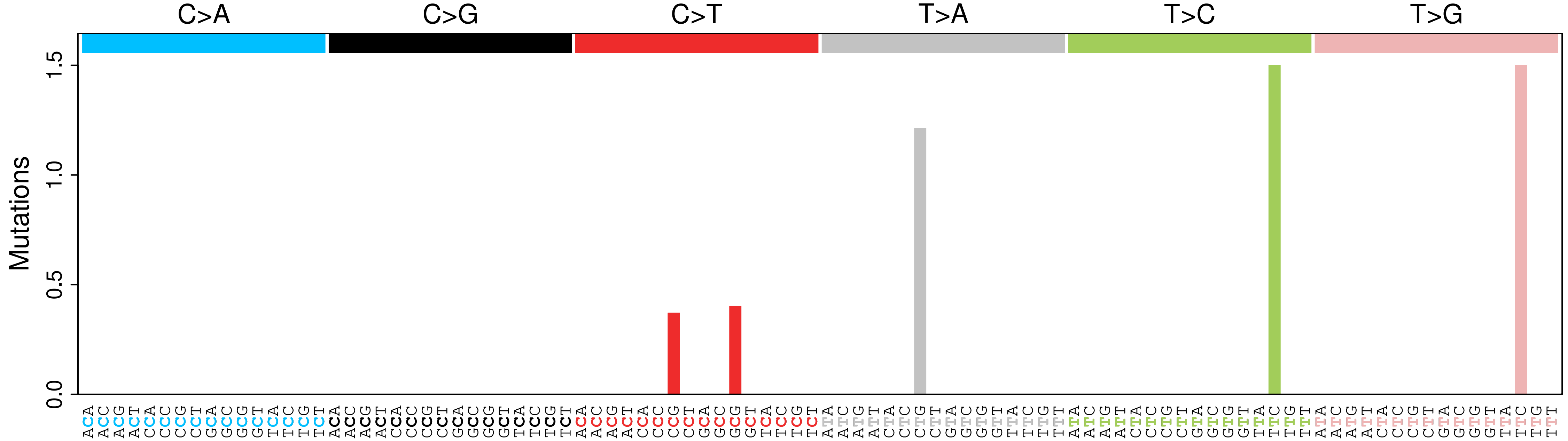
CATD0475a (6 mutations)



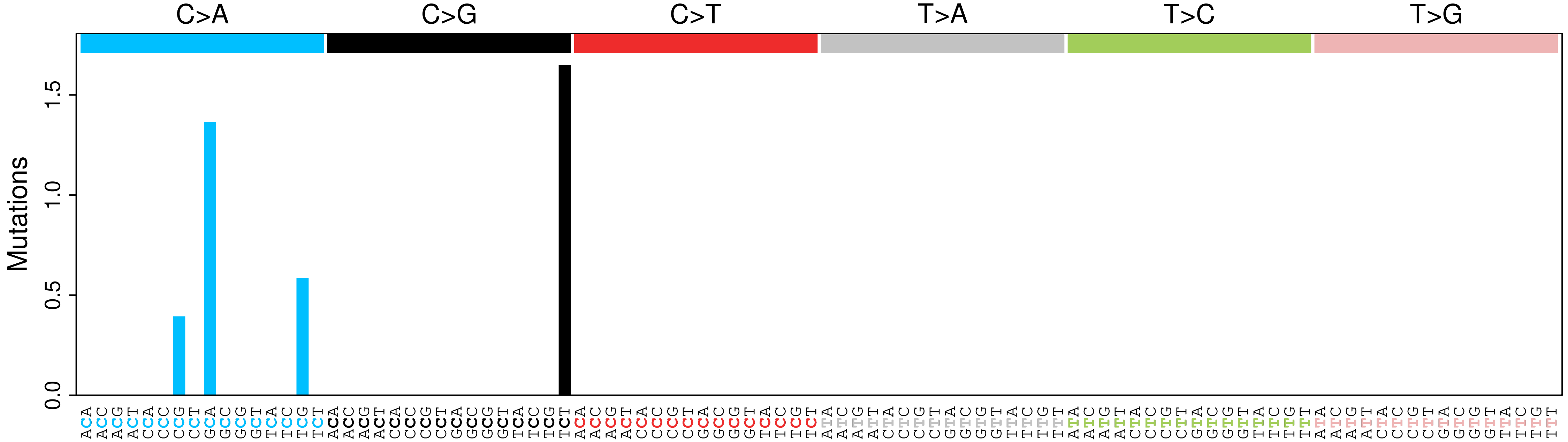
CATD0503a (3 mutations)



CATD0743a (5 mutations)



CATD0737a (4 mutations)



CATD0478a (4 mutations)

$C > A$

$C > G$

$C > T$

T>A

 $T > C$

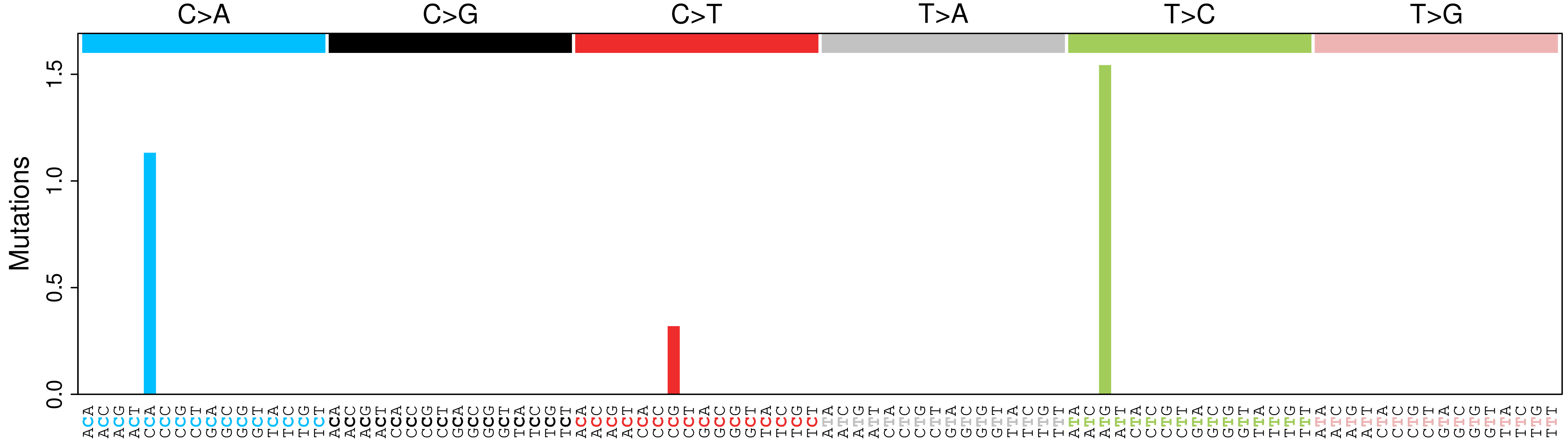
T>G

Mutations

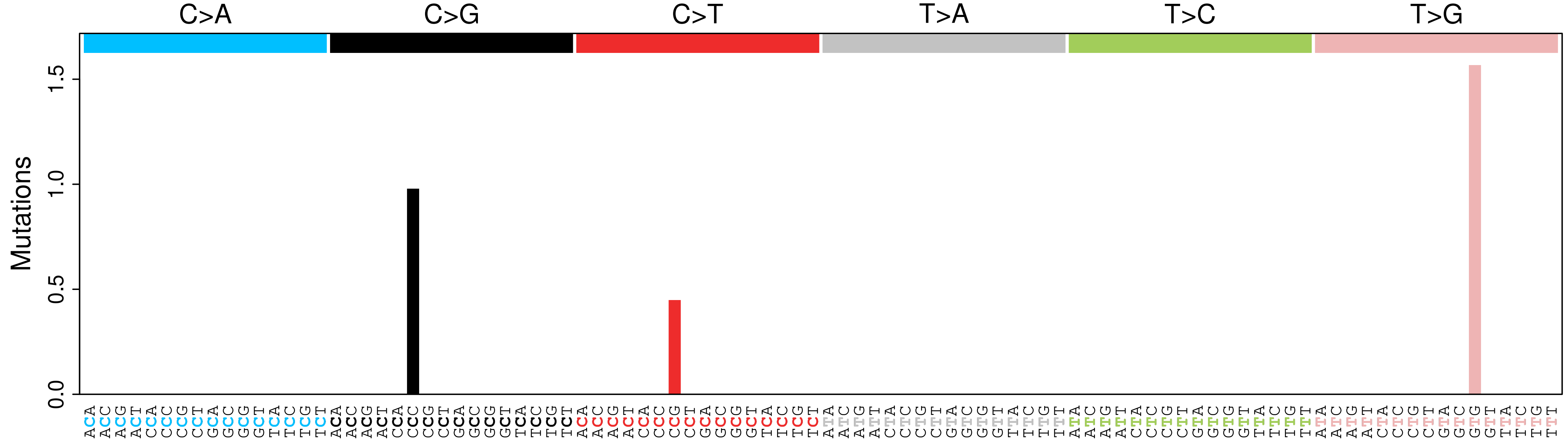
0.0 0.2 0.4 0.6 0.8 1.0 1.2 1.4

[illegible]

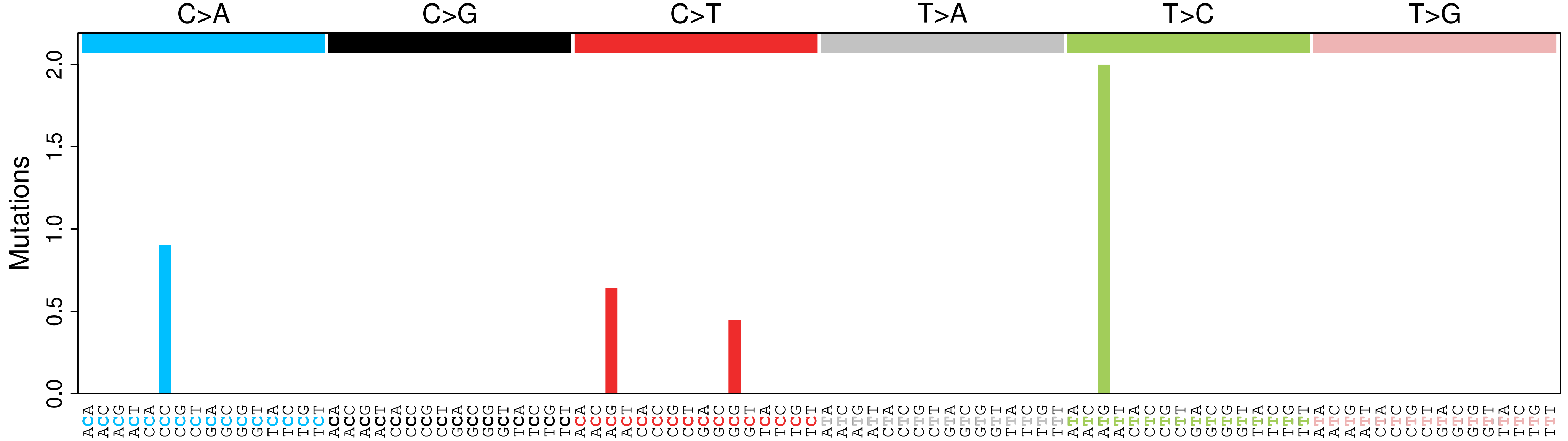
CATD0488a (3 mutations)



CATD0697a (3 mutations)



CATD0485a (4 mutations)



CATD0486a (4 mutations)

C>A

C>G

C>T

T>A

T>C

T>G

Mutations

1.2

0.8

0.4

0.0

ACA
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TTT

CATD0487a (3 mutations)

C>A

C>G

C>T

T>A

T>C

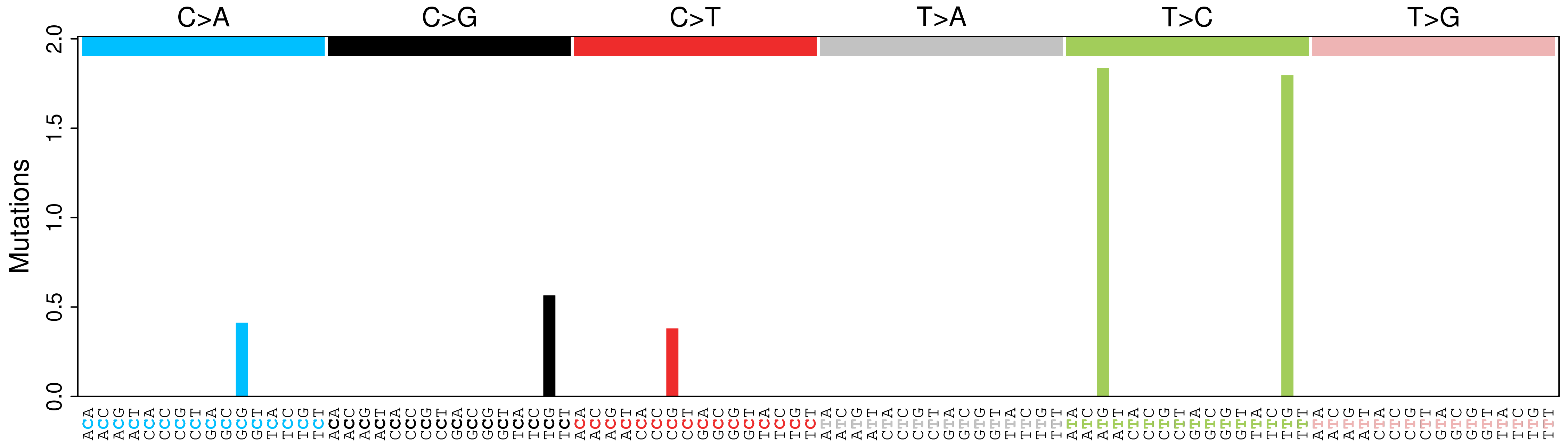
T>G

Mutations

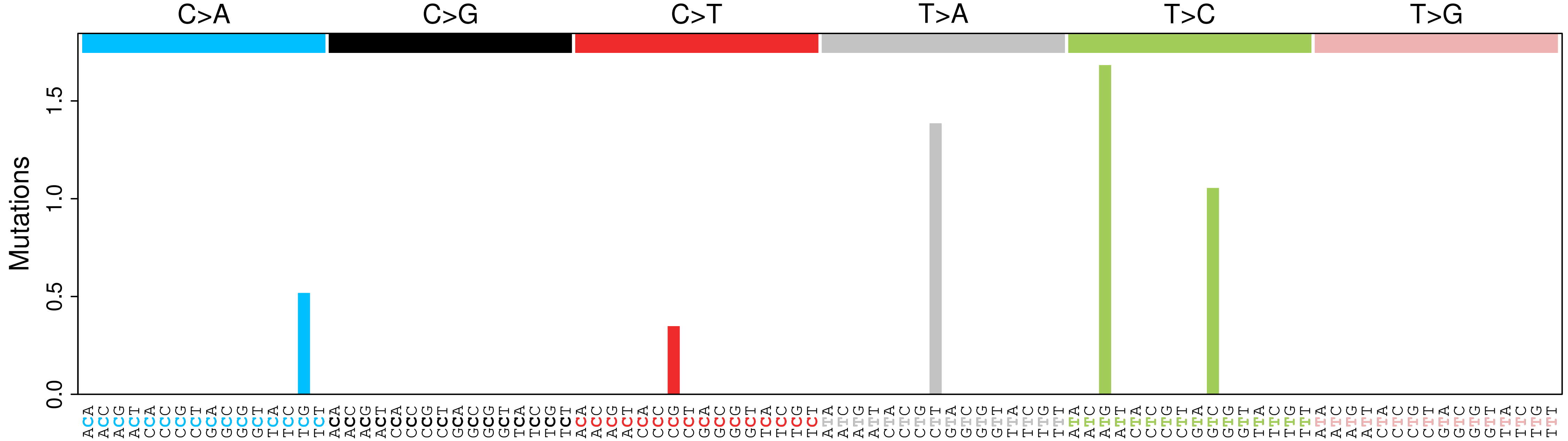
1.2
1.0
0.8
0.6
0.4
0.2
0.0

ACA
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CCT
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GCC
GGG
GCT
TCA
TCC
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TCT
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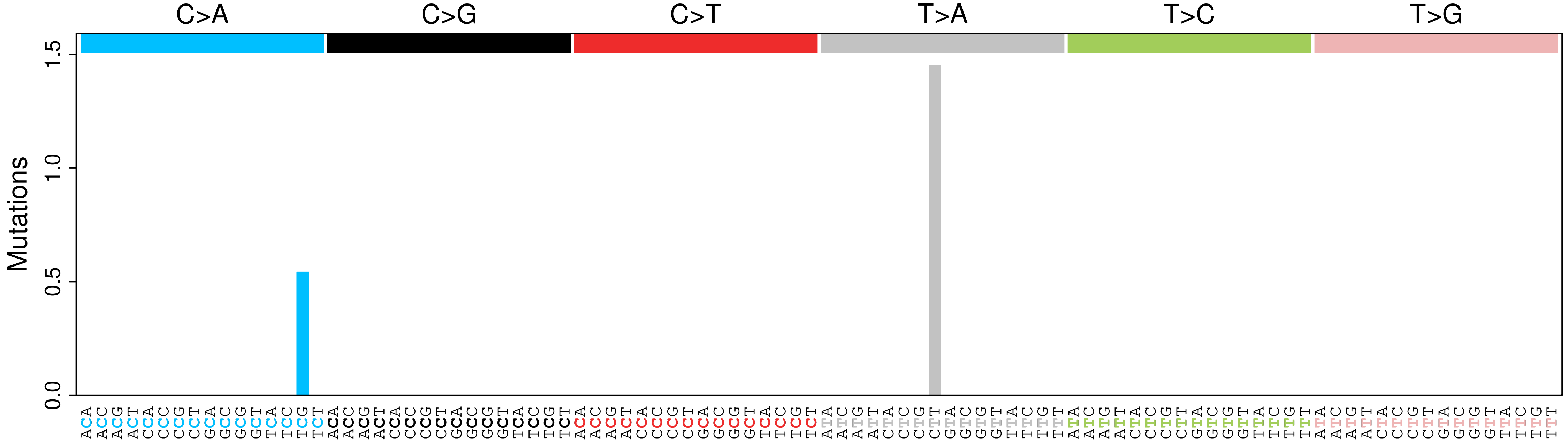
CATD0744a (5 mutations)



CATD0471a (5 mutations)



CATD0741a (2 mutations)



CATD0739a (3 mutations)

$C > A$

$C > G$

$C > T$

T > A

$T > C$

T > G

Mutations

1.5

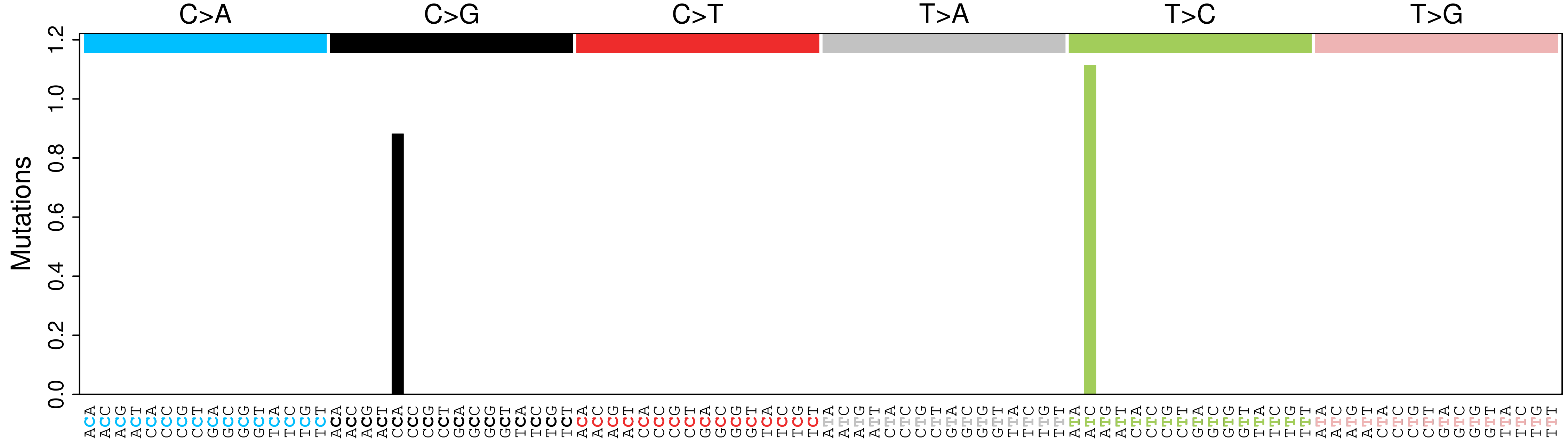
1.0

0.

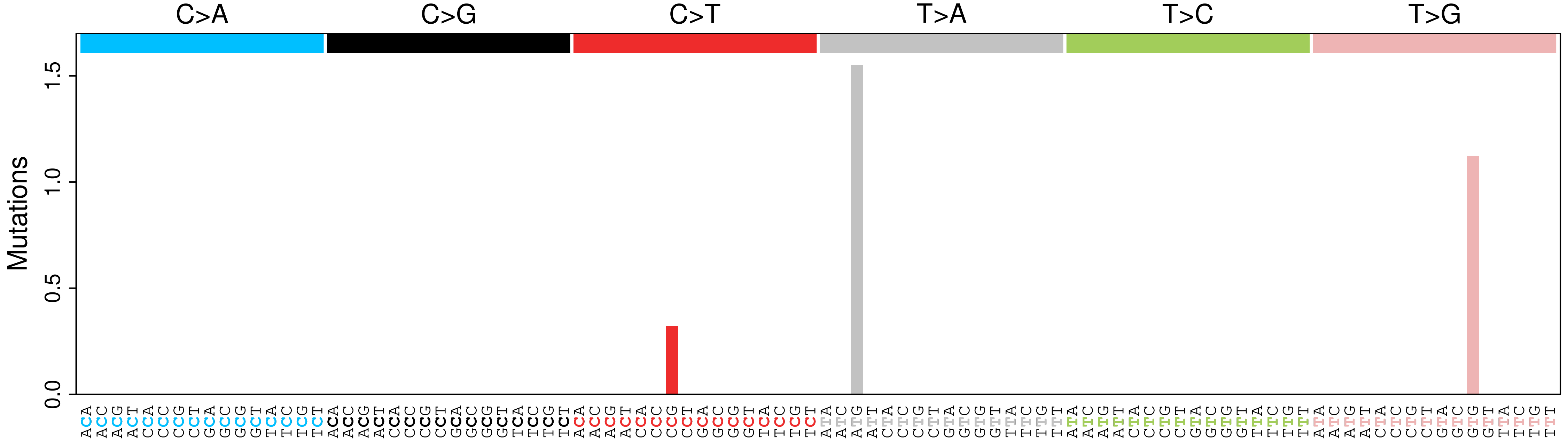
0

[illegible]

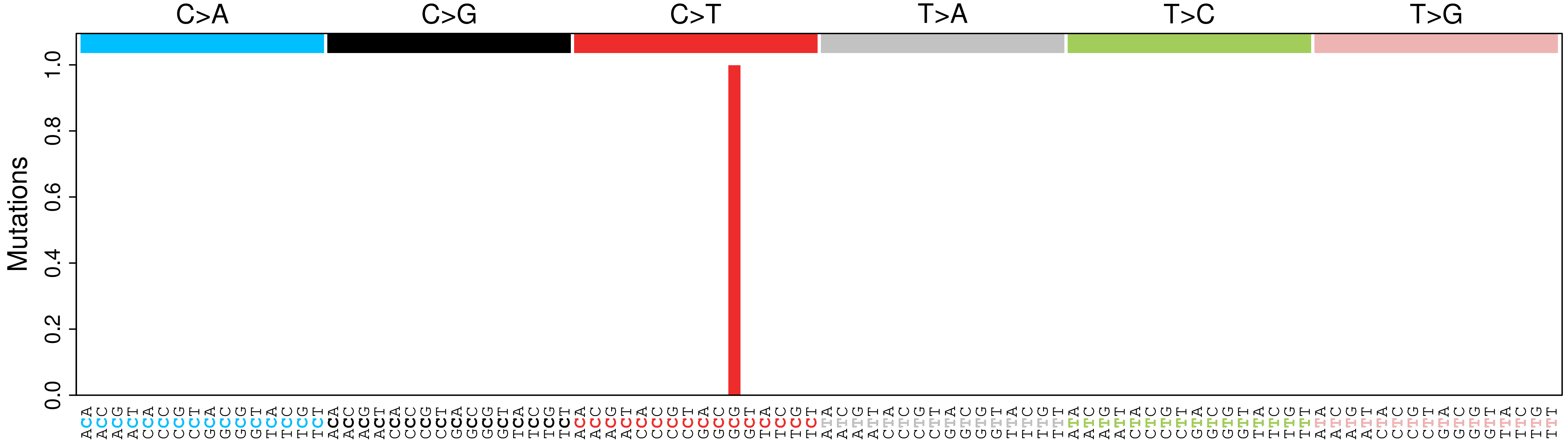
CATD0738a (2 mutations)



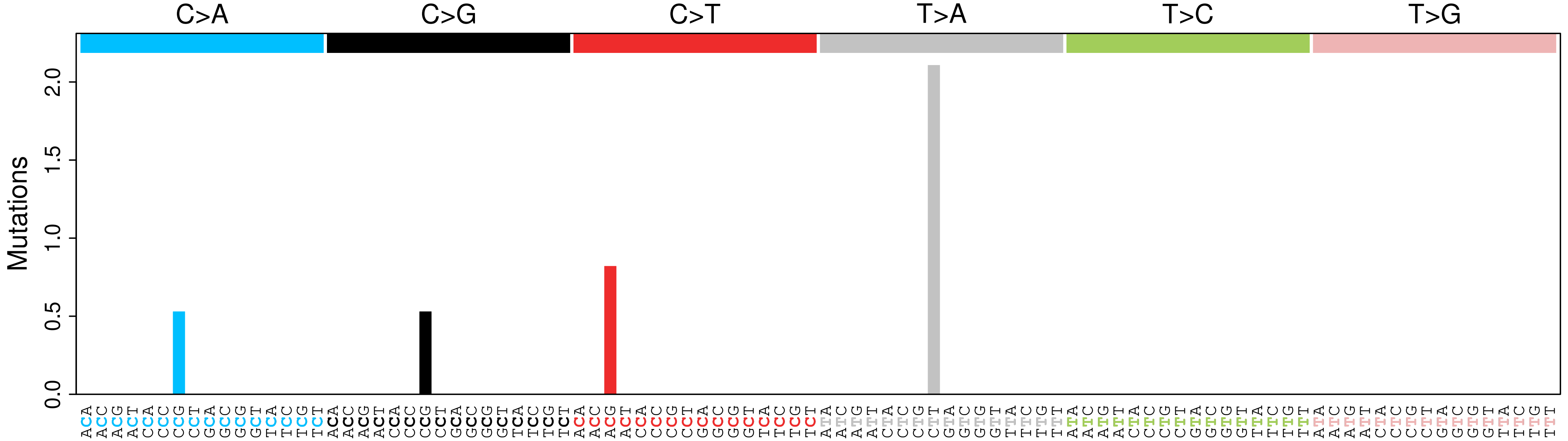
CATD0692a (3 mutations)



CATD0497a (1 mutations)



CATD0498a (4 mutations)



CATD0699a (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
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CATD0695a (1 mutations)

