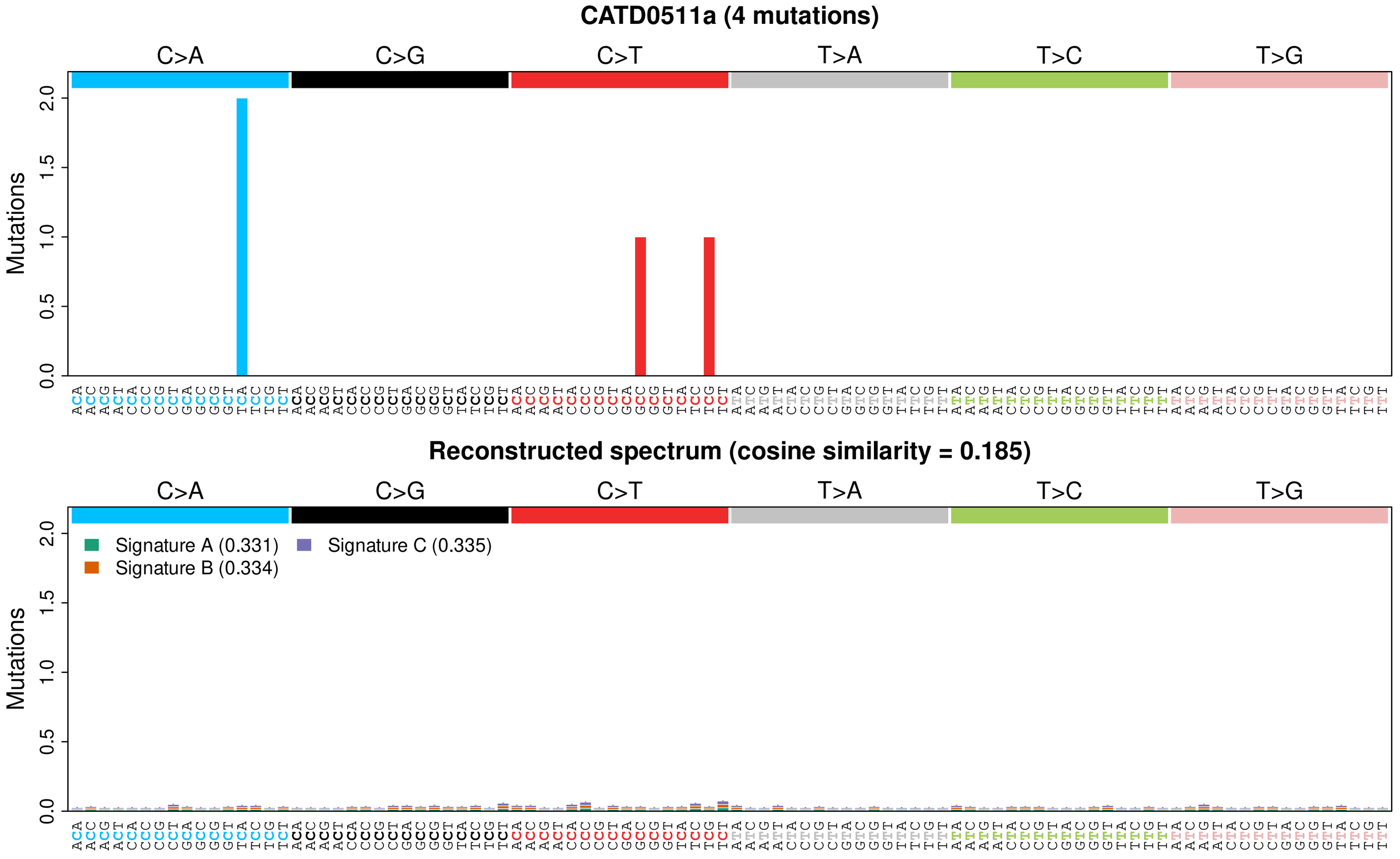
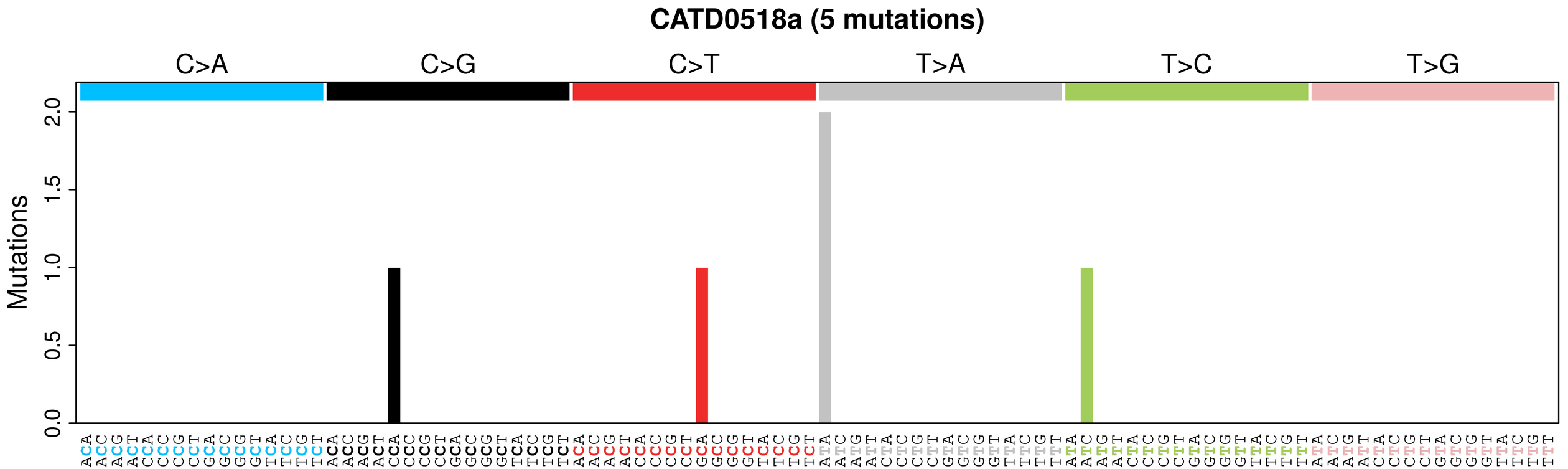
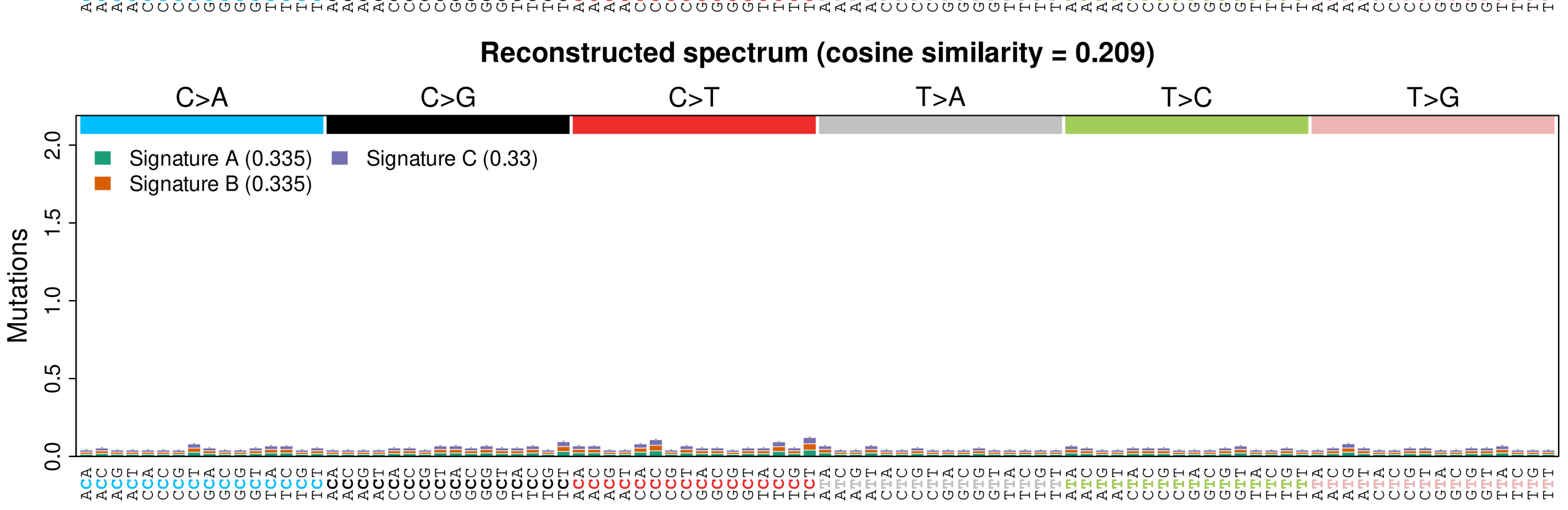
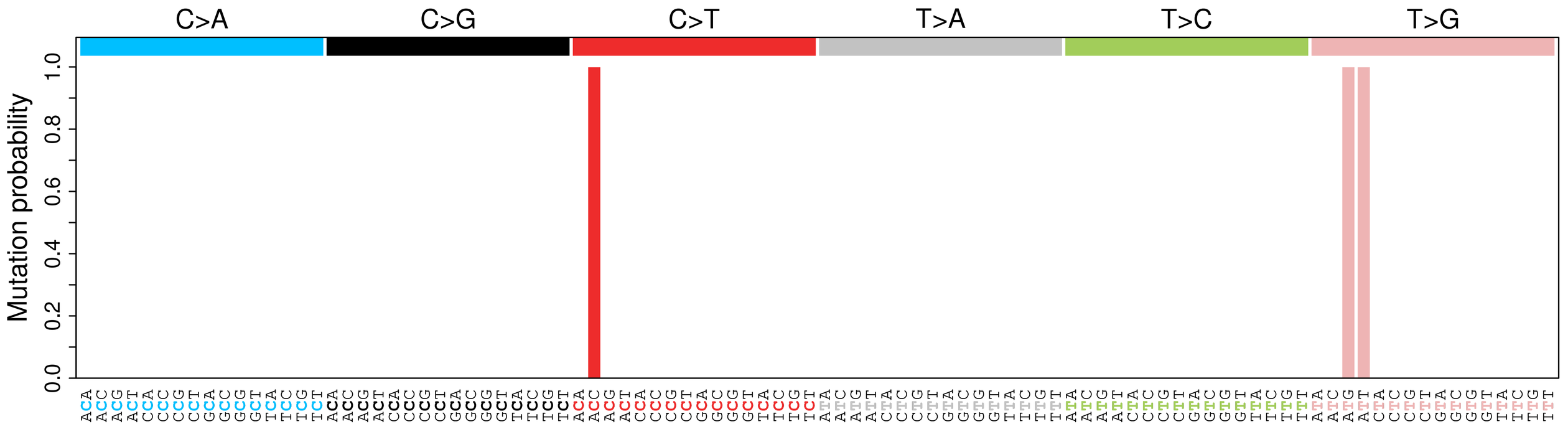

CATD0511a (4 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0
Reconstructed spectrum (cosine similarity = 0.185)
Signature A (0.331)
Signature B (0.334)
Signature C (0.335)

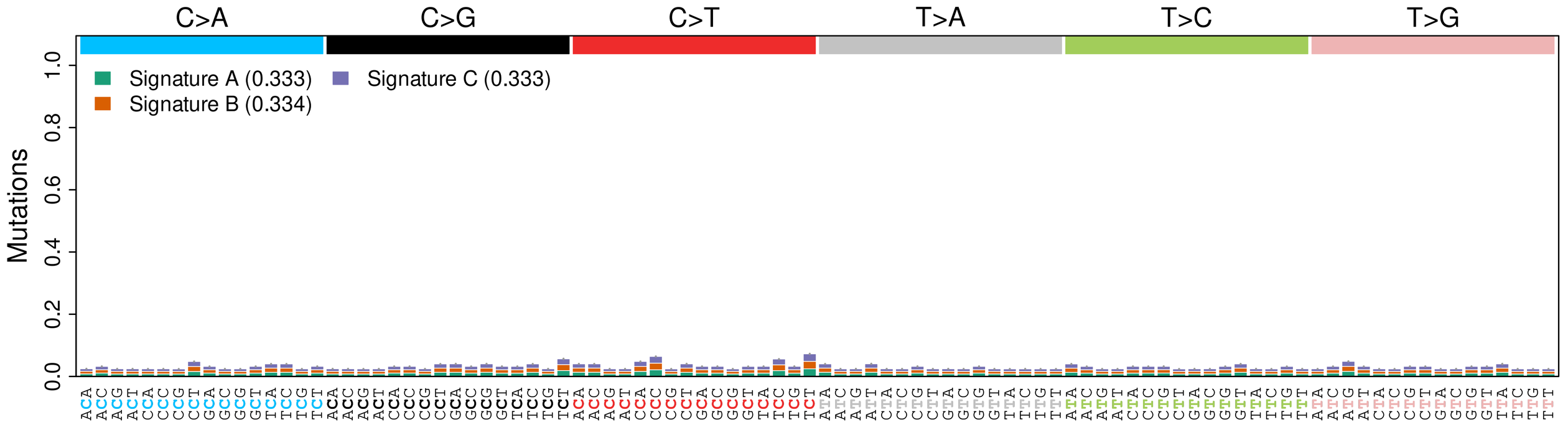

CATD0518a (5 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

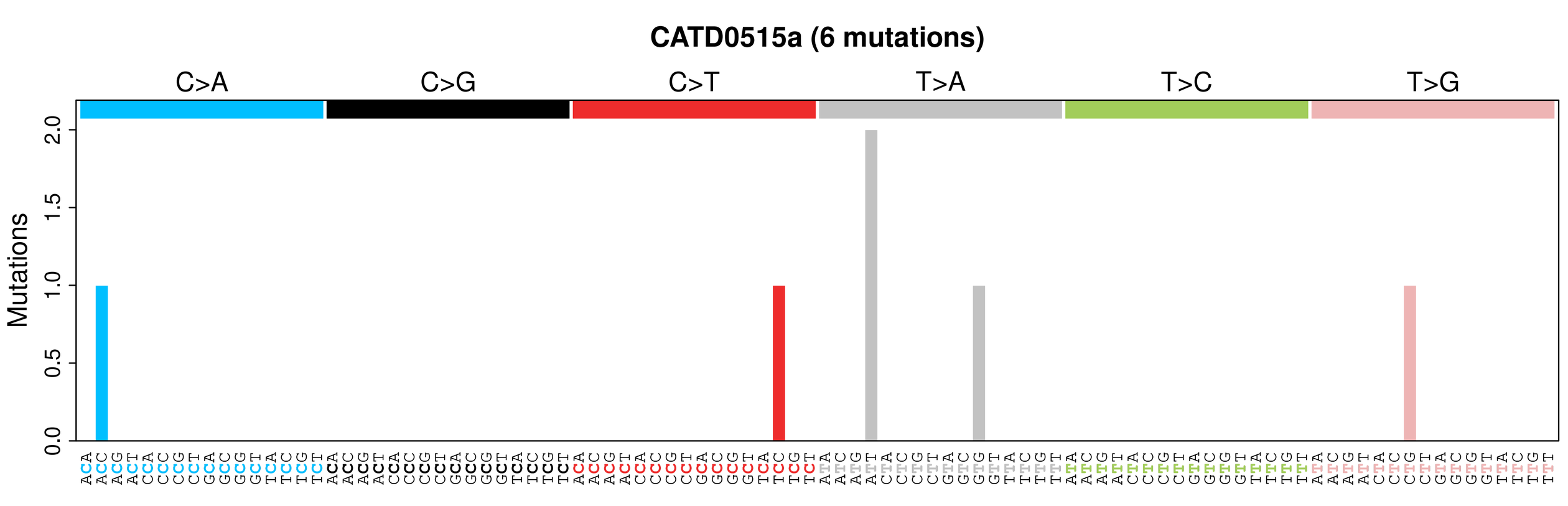

Reconstructed spectrum (cosine similarity = 0.209)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.335)
Signature B (0.335)
Signature C (0.33)
Mutations
0.0
0.5
1.0
1.5
2.0

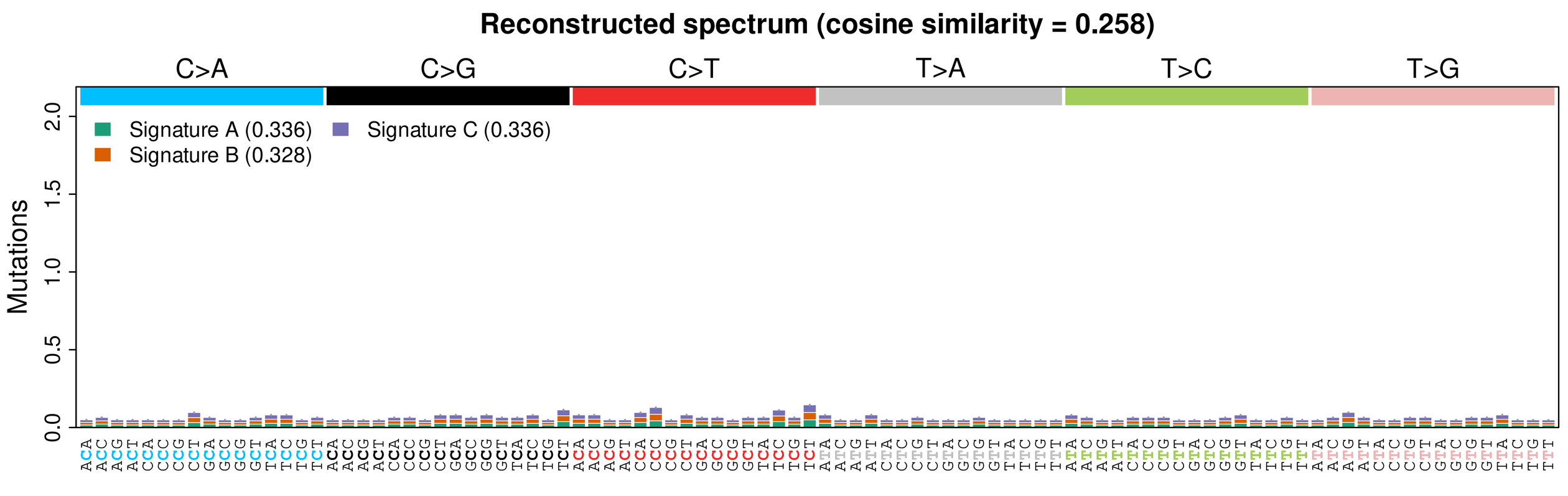
CATD0524a



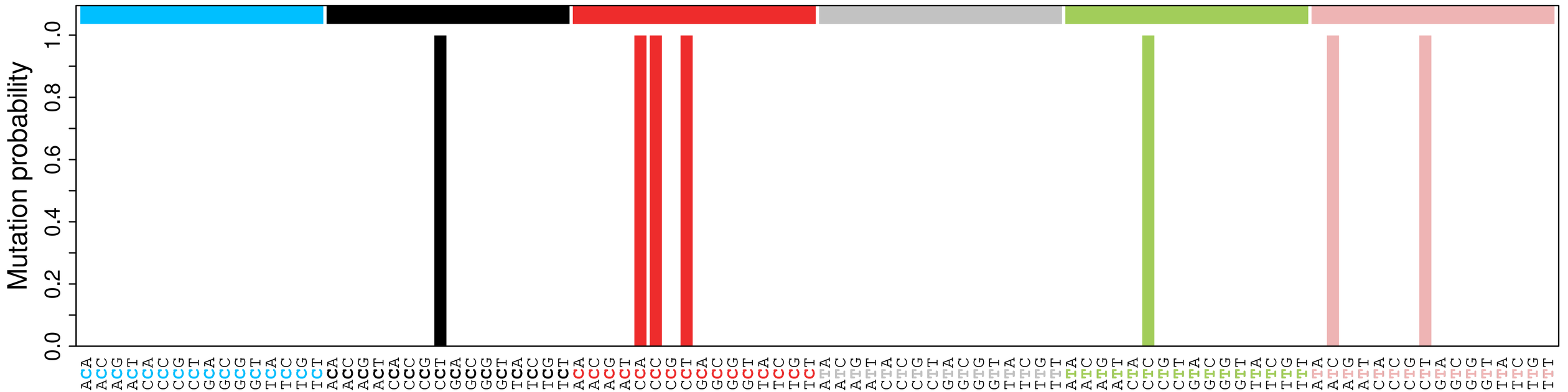
Reconstructed spectrum (cosine similarity = 0.219)



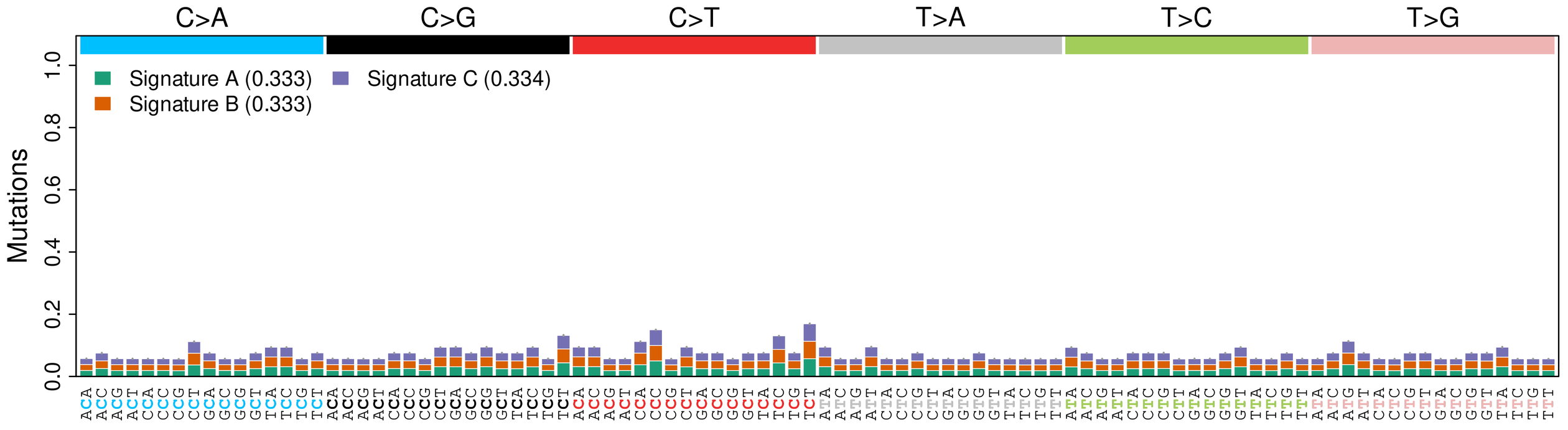

CATD0515a (6 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.258)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.336)
Signature B (0.328)
Signature C (0.336)
Mutations
0.0
0.5
1.0
1.5
2.0

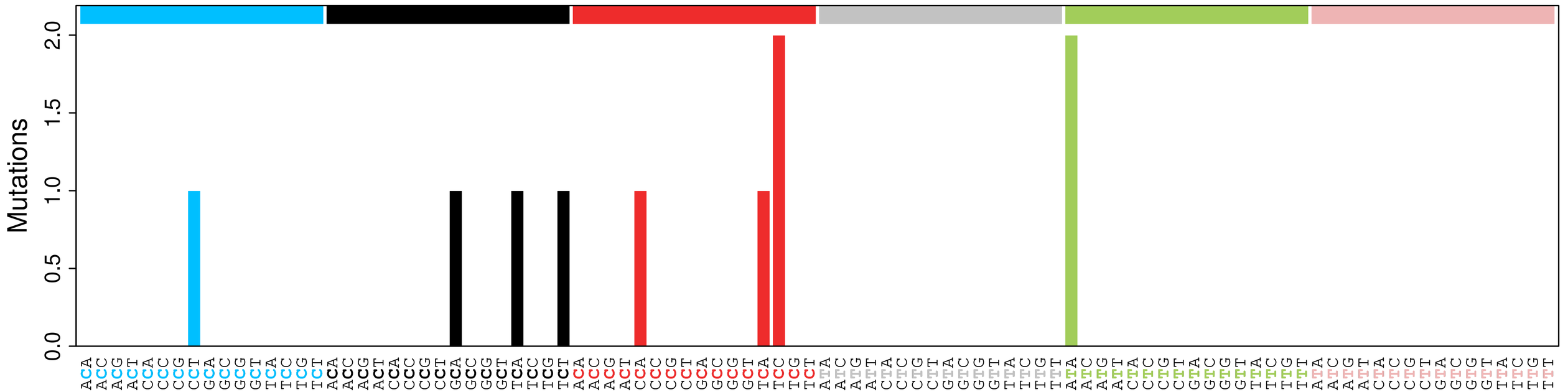
CATD196a



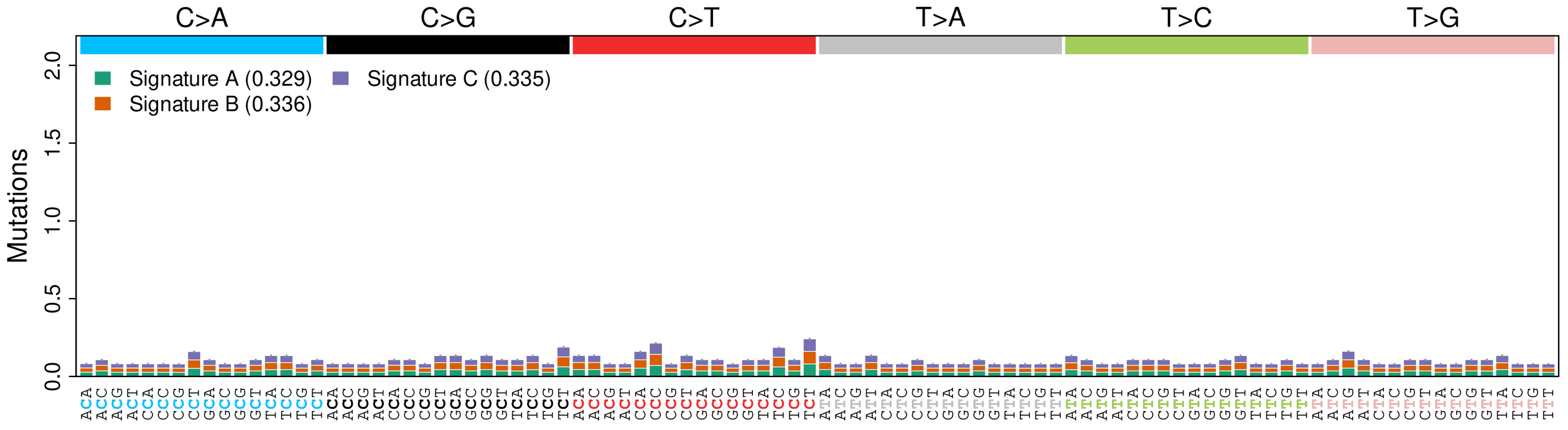
Reconstructed spectrum (cosine similarity = 0.343)

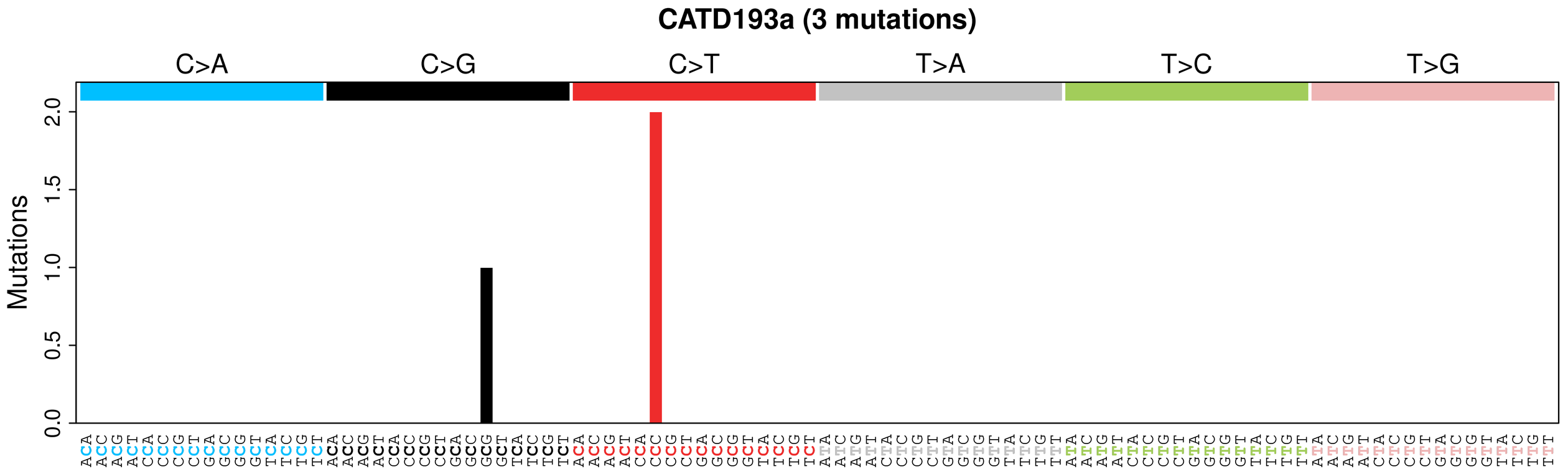


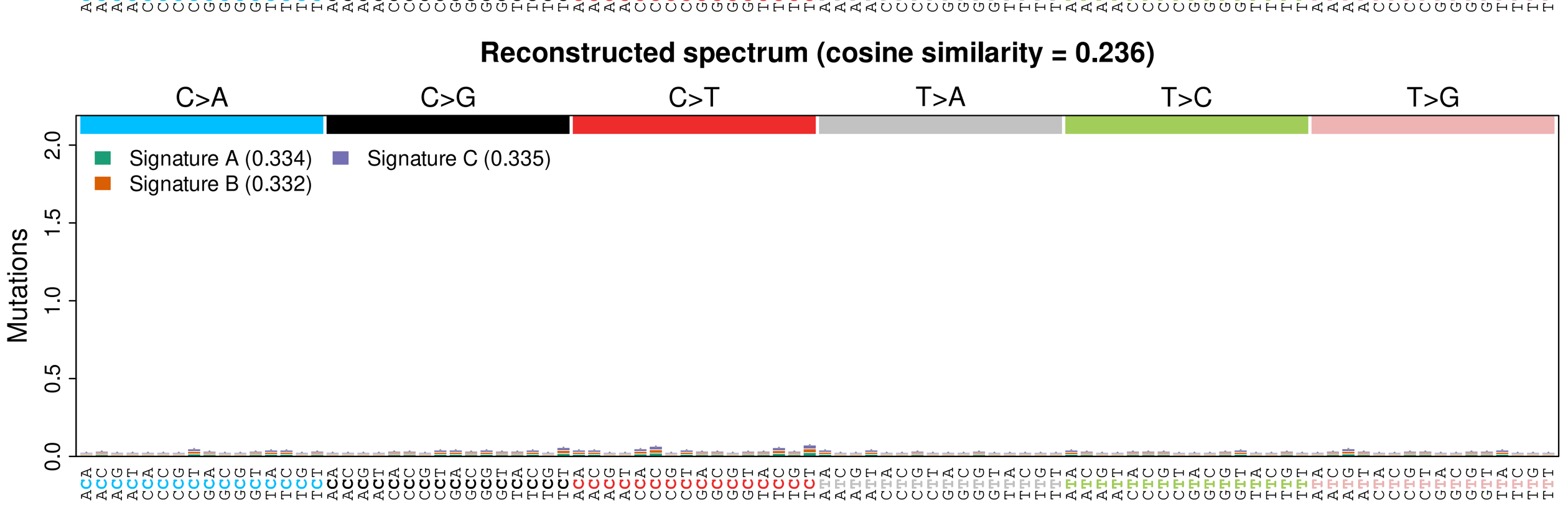
CATD205a (10 mutations)



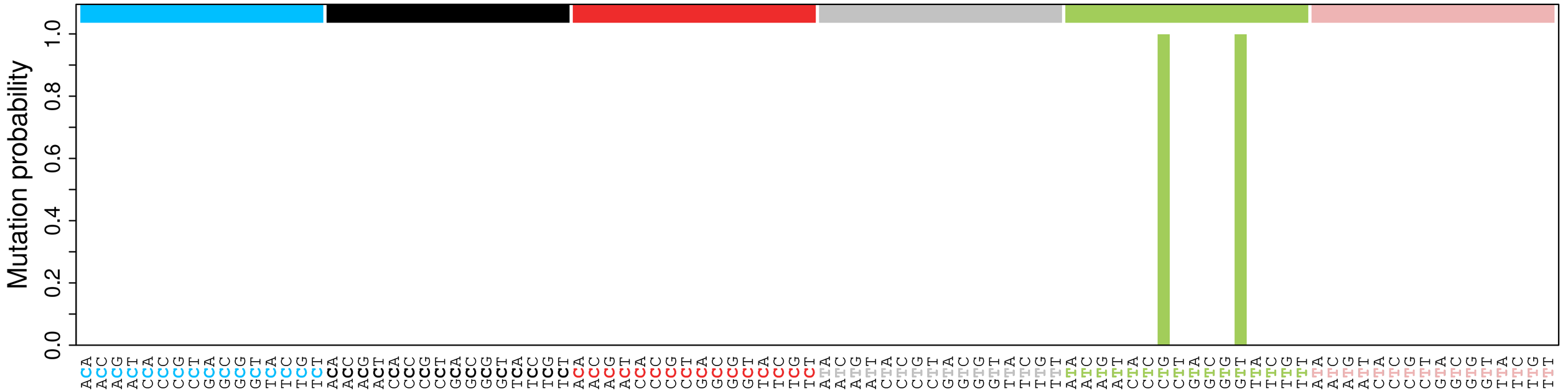
Reconstructed spectrum (cosine similarity = 0.376)



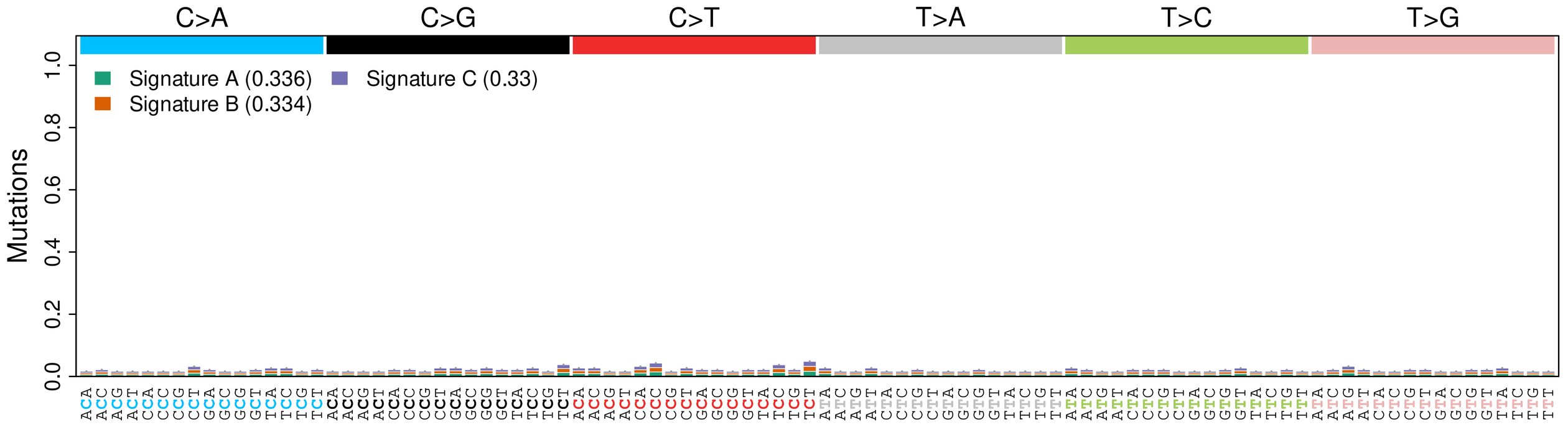

CATD193a (3 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.236)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.334)
Signature B (0.332)
Signature C (0.335)
Mutations
0.0
0.5
1.0
1.5
2.0

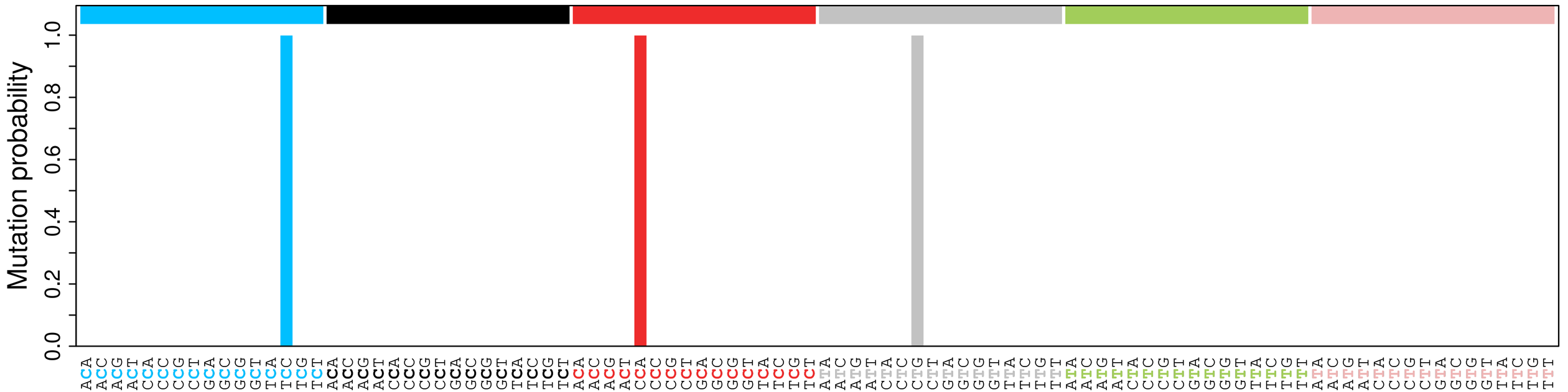
CATD192a



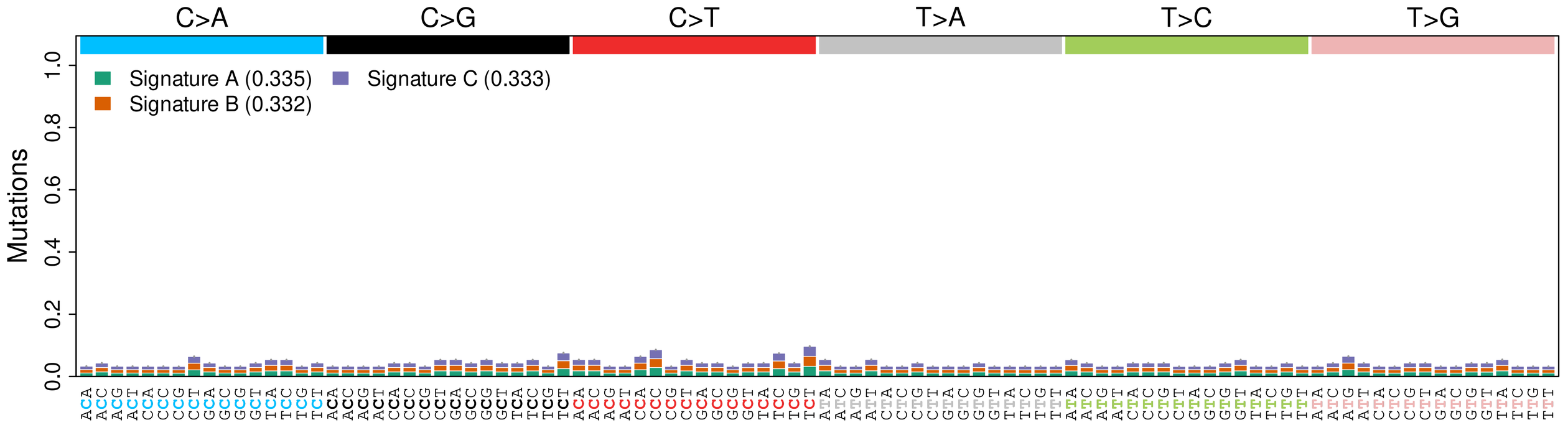
Reconstructed spectrum (cosine similarity = 0.16)



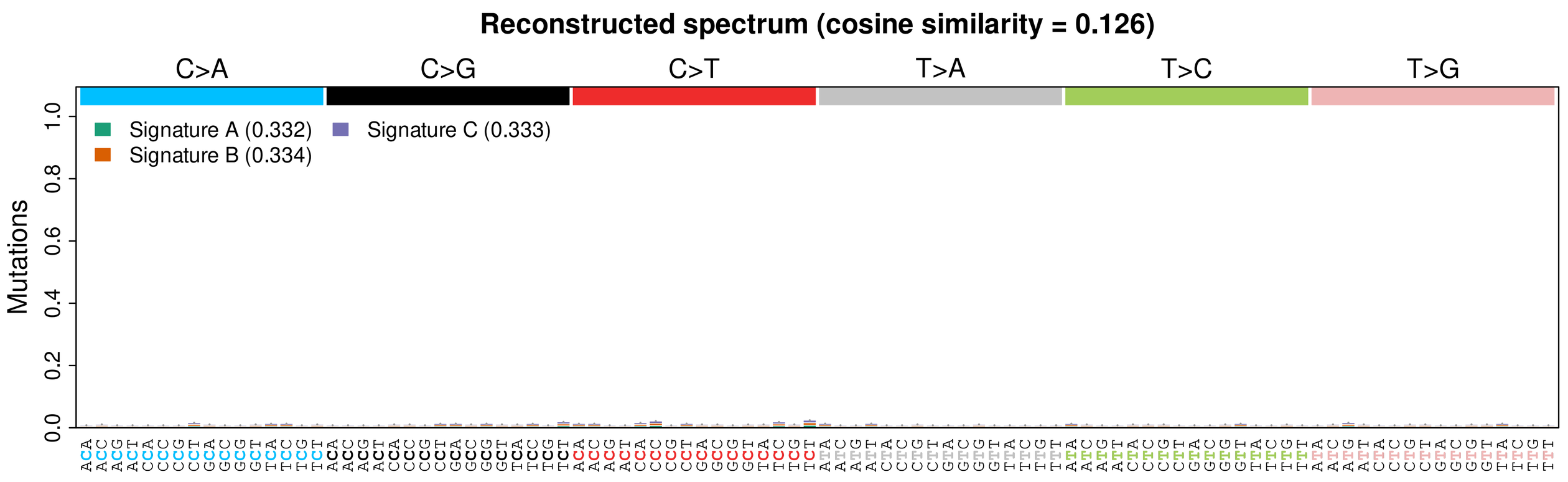
CATD0519a

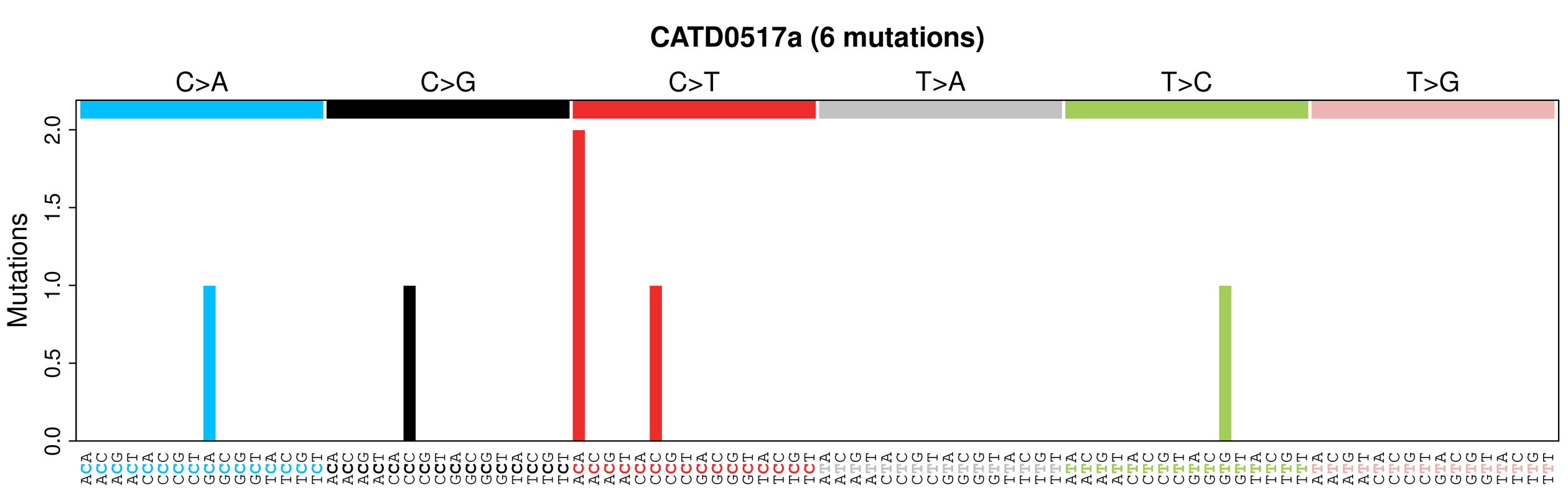


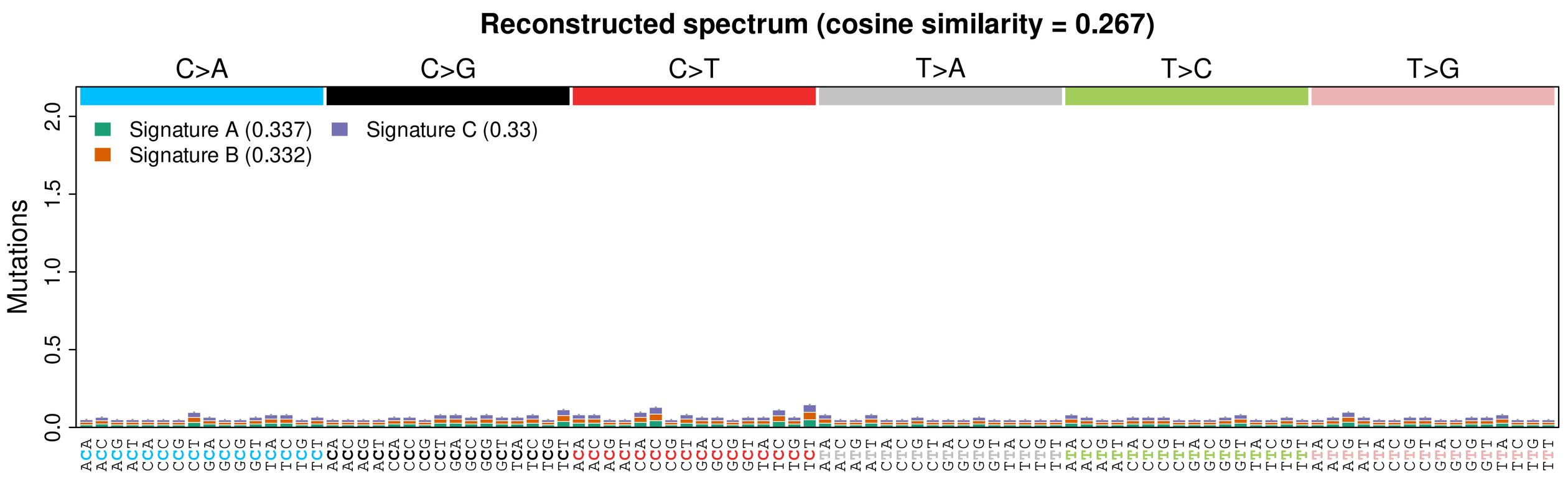
Reconstructed spectrum (cosine similarity = 0.218)



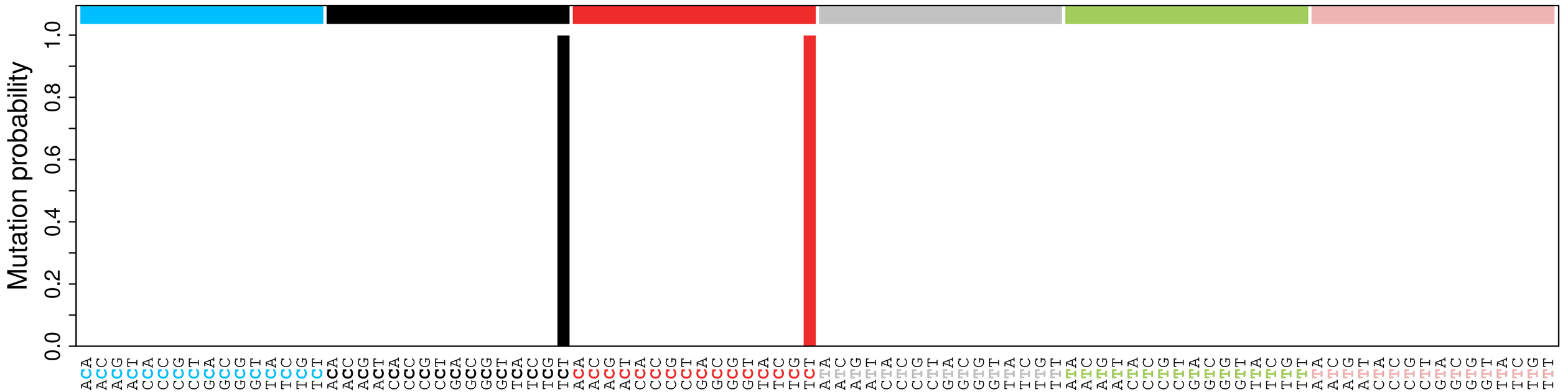
CATD0520a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0


Reconstructed spectrum (cosine similarity = 0.126)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.332)
Signature B (0.334)
Signature C (0.333)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

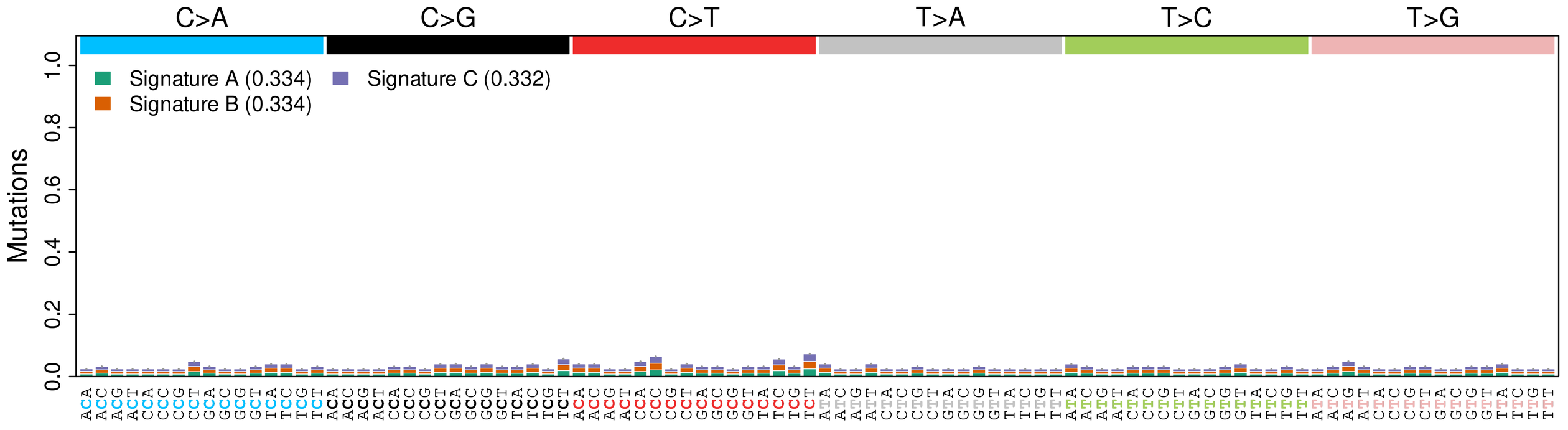

CATD0517a (6 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

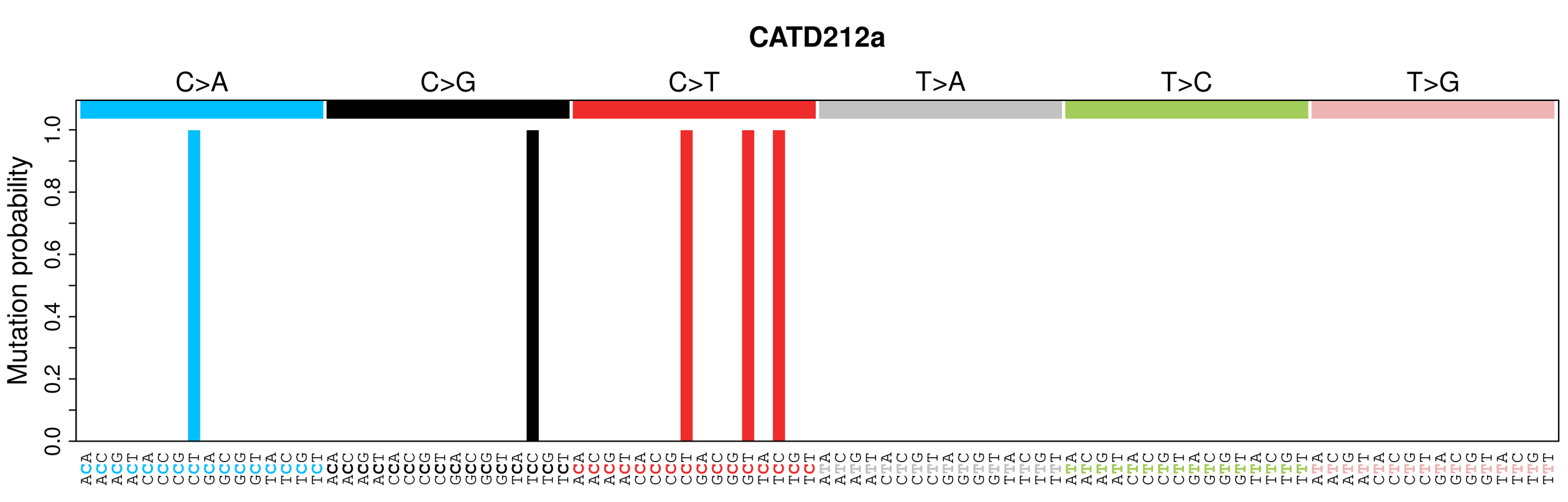

Reconstructed spectrum (cosine similarity = 0.267)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.337)
Signature B (0.332)
Signature C (0.33)
Mutations
0.0
0.5
1.0
1.5
2.0

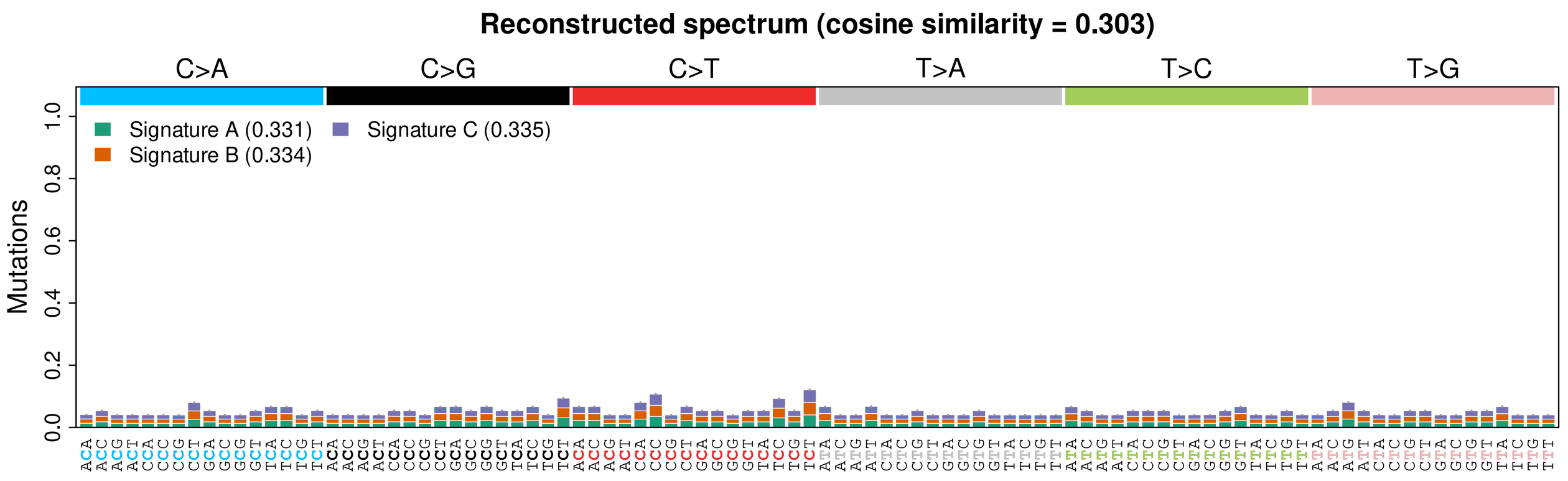
CATD210a



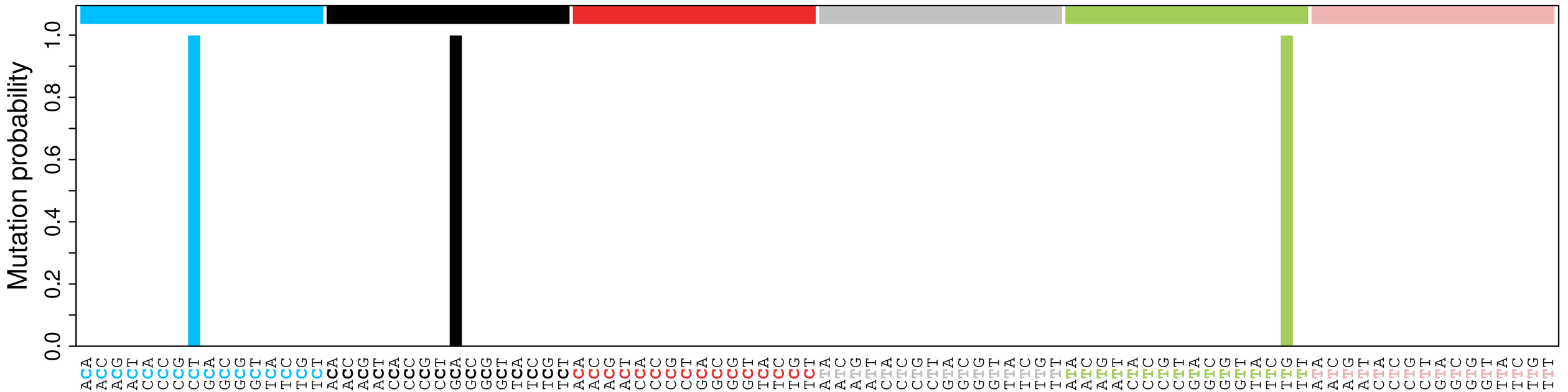
Reconstructed spectrum (cosine similarity = 0.285)



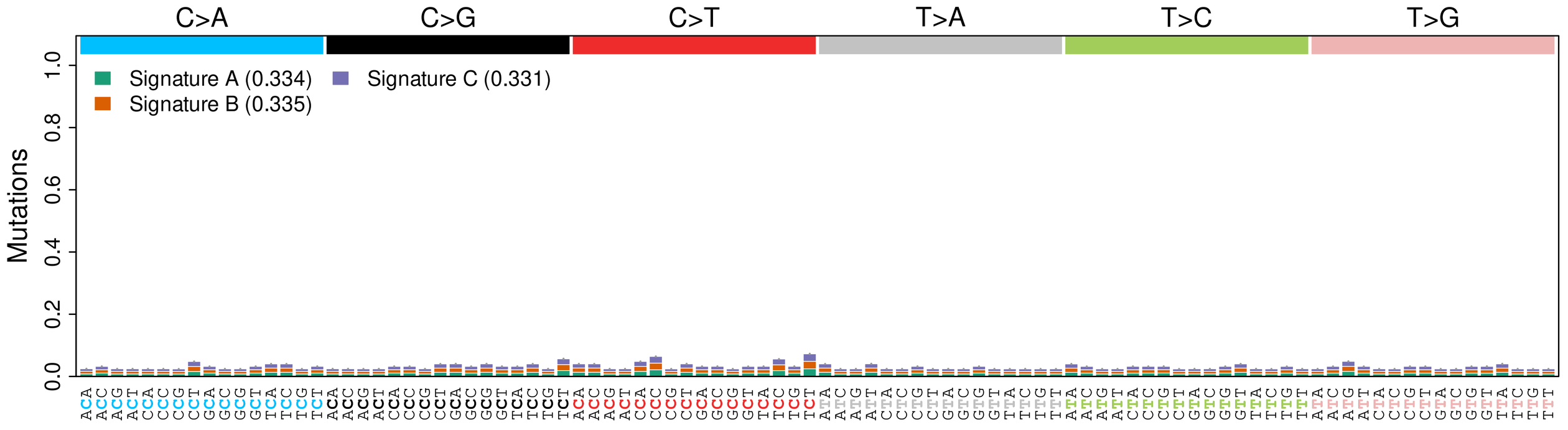

CATD212a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0

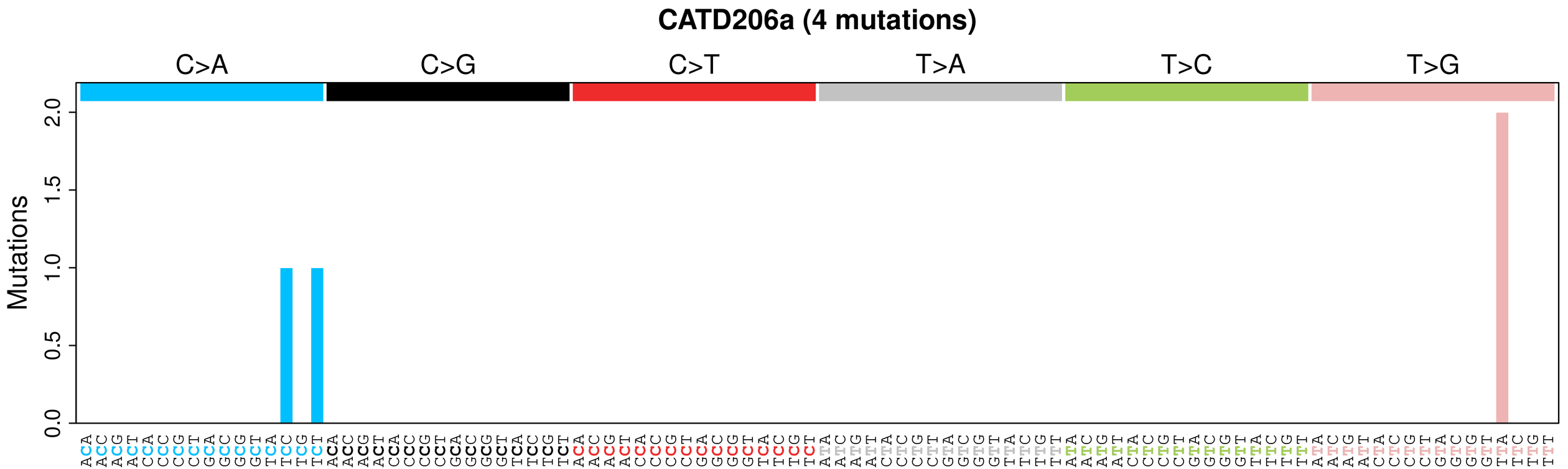

Reconstructed spectrum (cosine similarity = 0.303)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.331)
Signature B (0.334)
Signature C (0.335)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

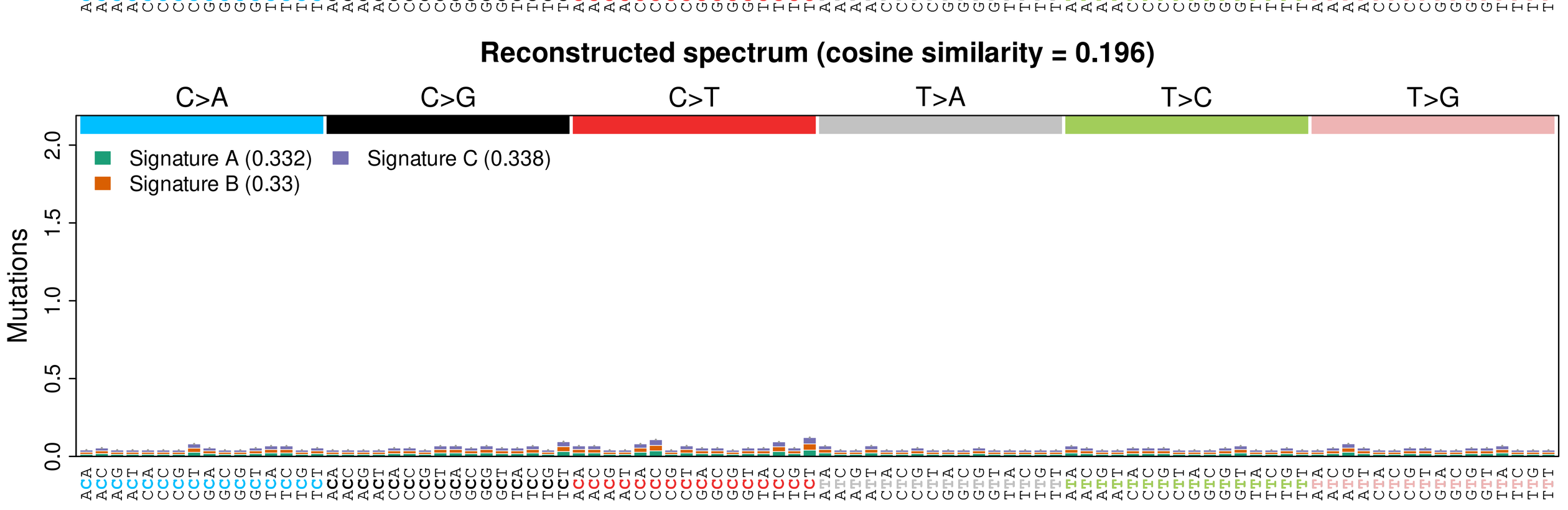
CATD209a



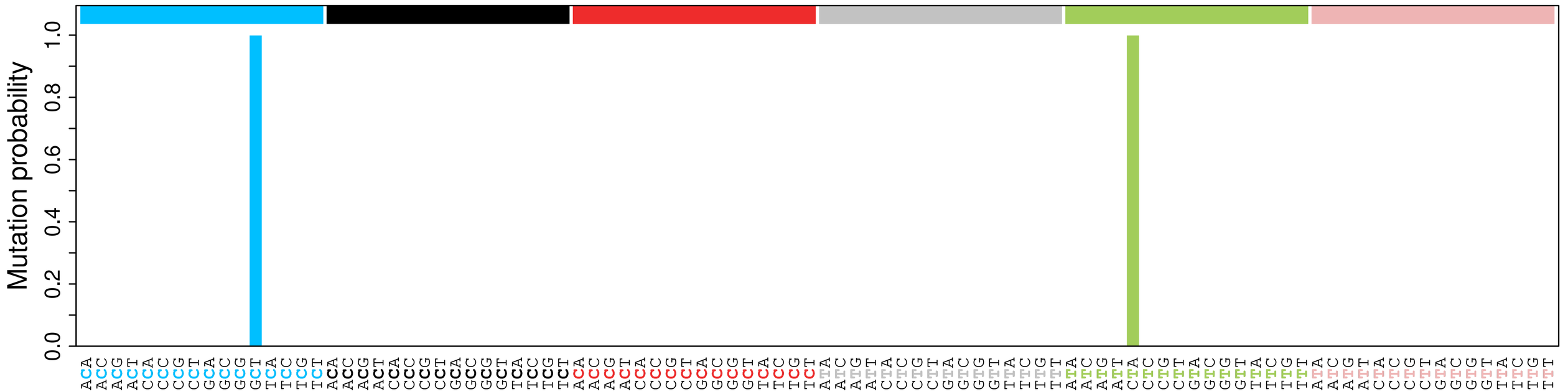
Reconstructed spectrum (cosine similarity = 0.218)



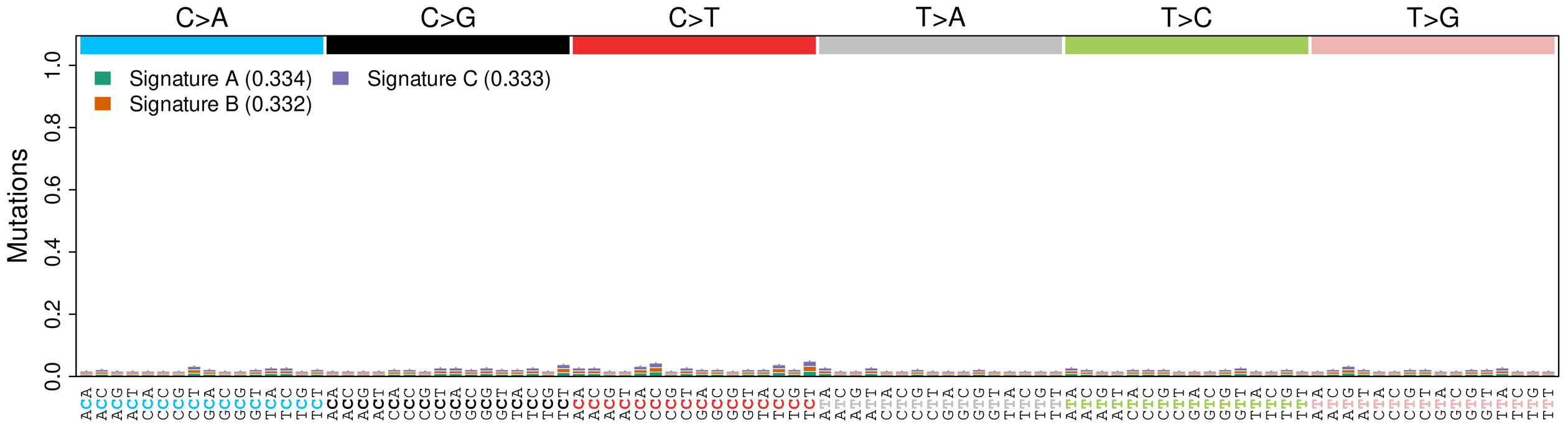

CATD206a (4 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

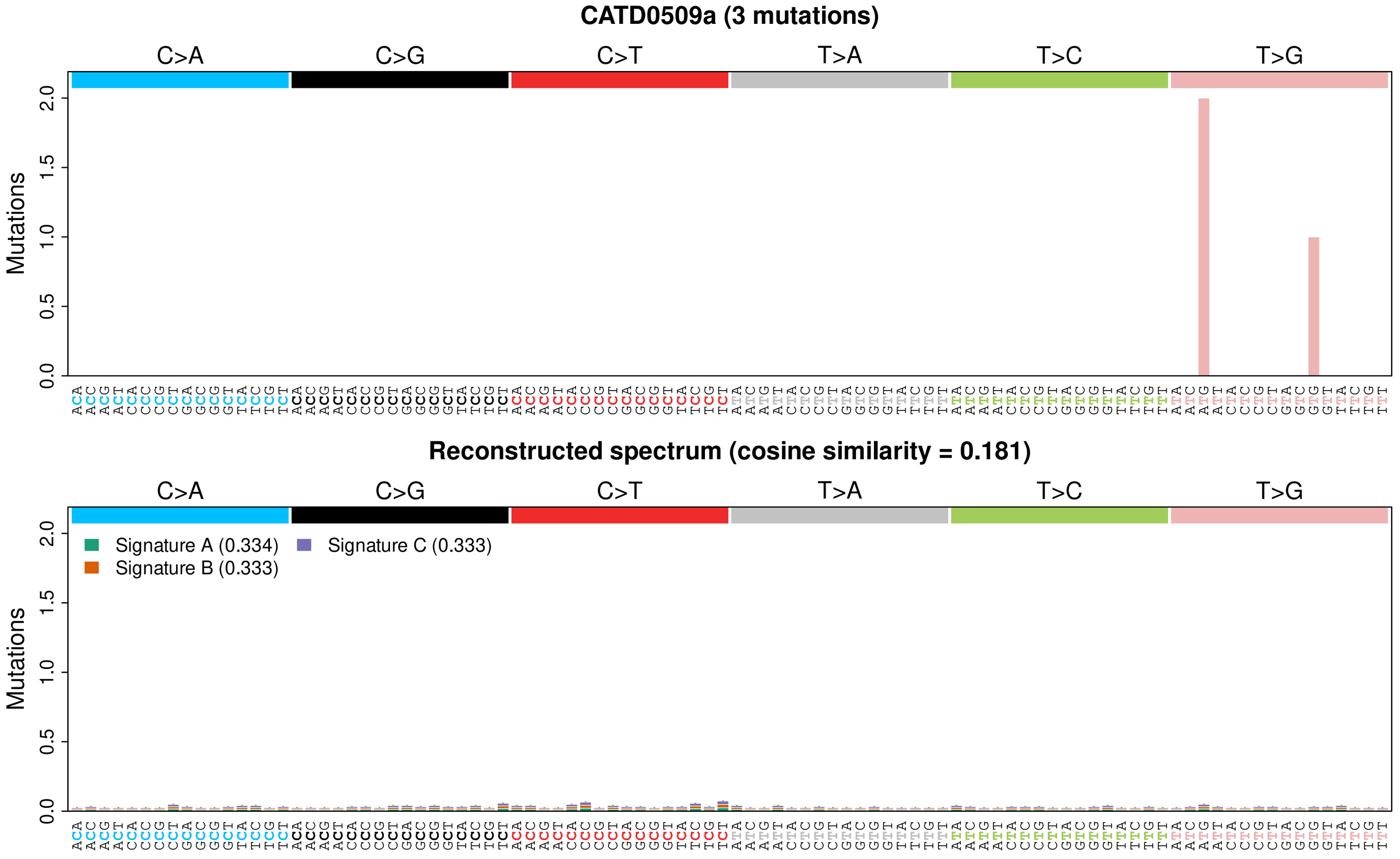

Reconstructed spectrum (cosine similarity = 0.196)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.332)
Signature B (0.33)
Signature C (0.338)
Mutations
0.0
0.5
1.0
1.5
2.0

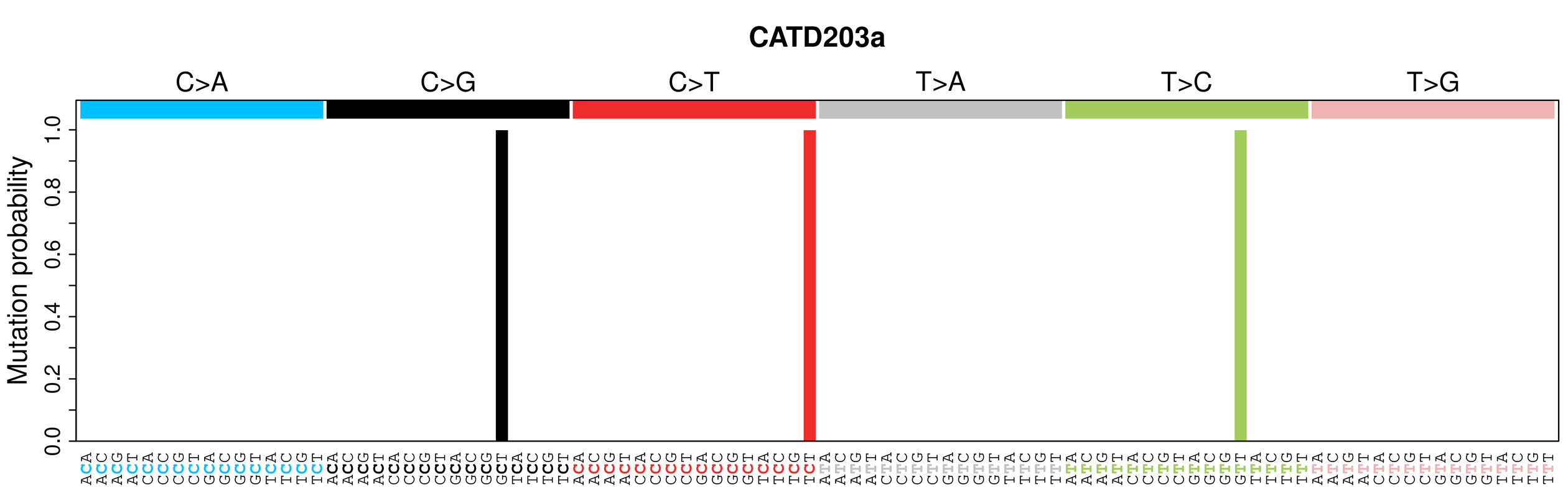
CATD0513a

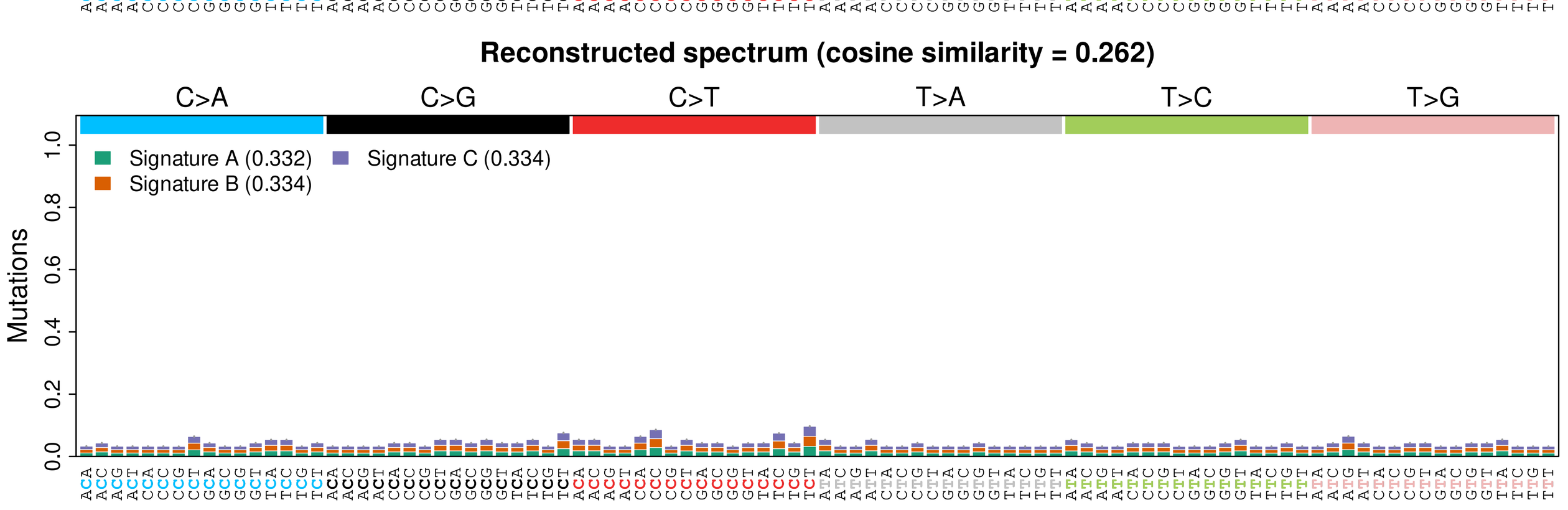


Reconstructed spectrum (cosine similarity = 0.143)

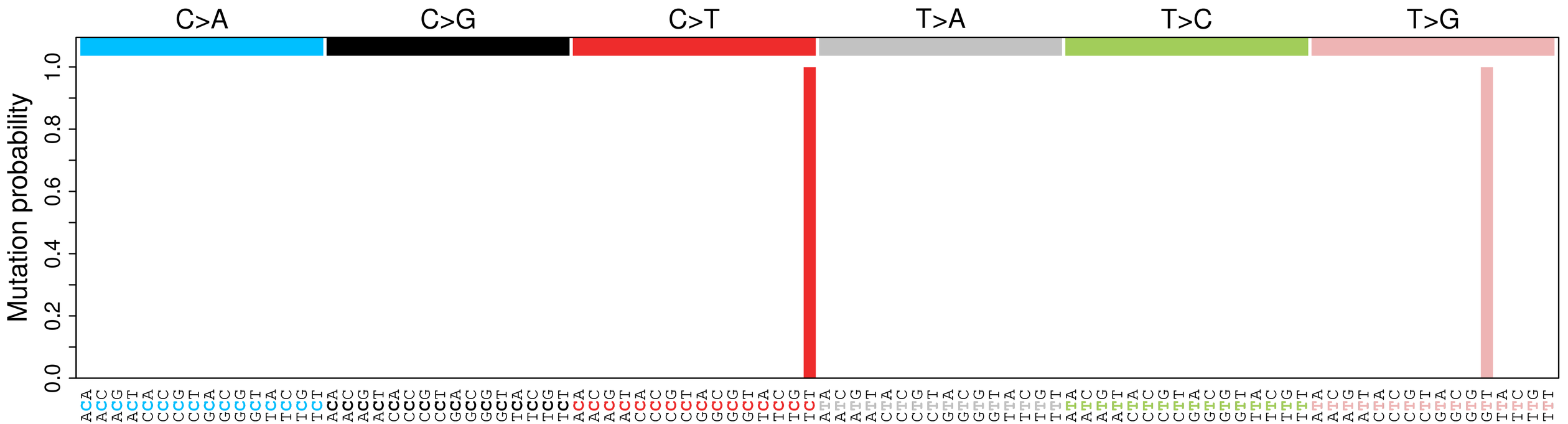



CATD0509a (3 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0
Reconstructed spectrum (cosine similarity = 0.181)
Signature A (0.334)
Signature B (0.333)
Signature C (0.333)

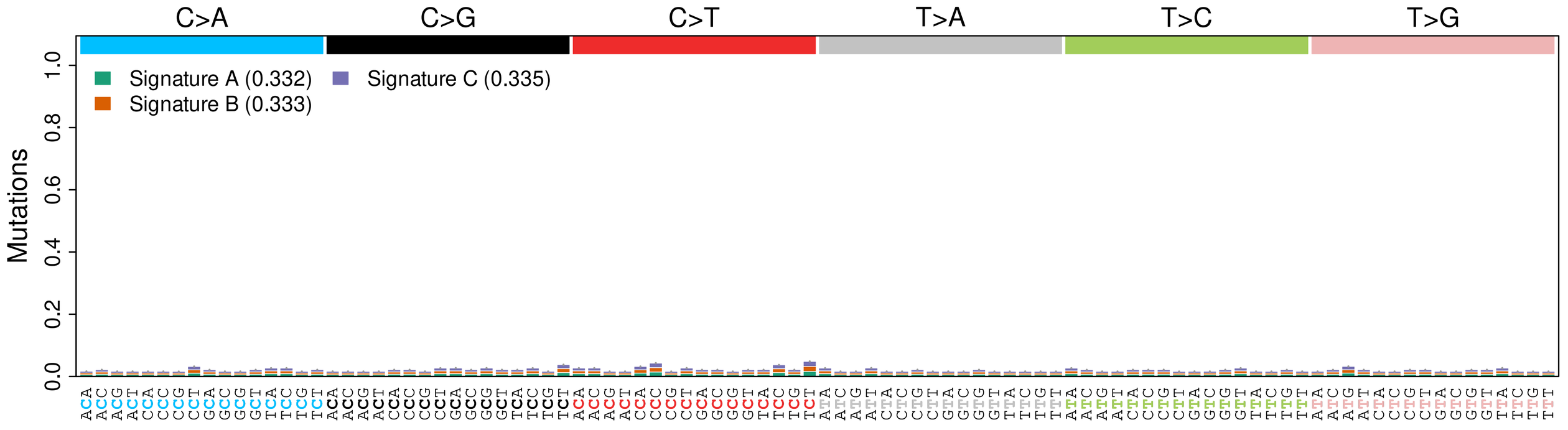

CATD203a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0

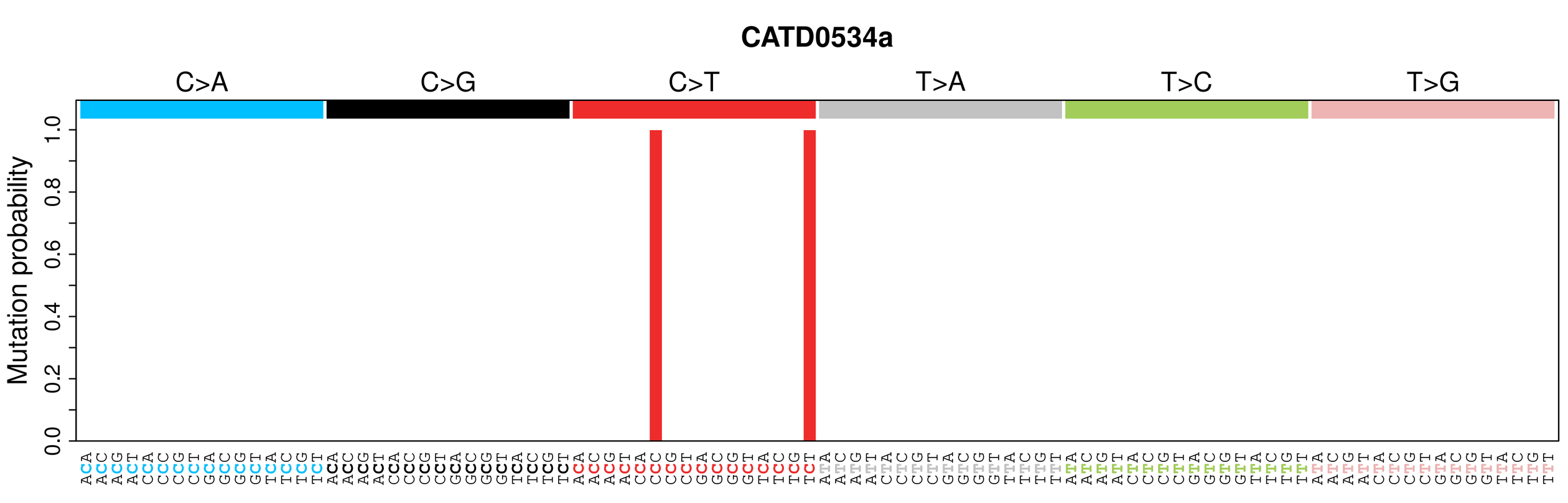

Reconstructed spectrum (cosine similarity = 0.262)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.332)
Signature B (0.334)
Signature C (0.334)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

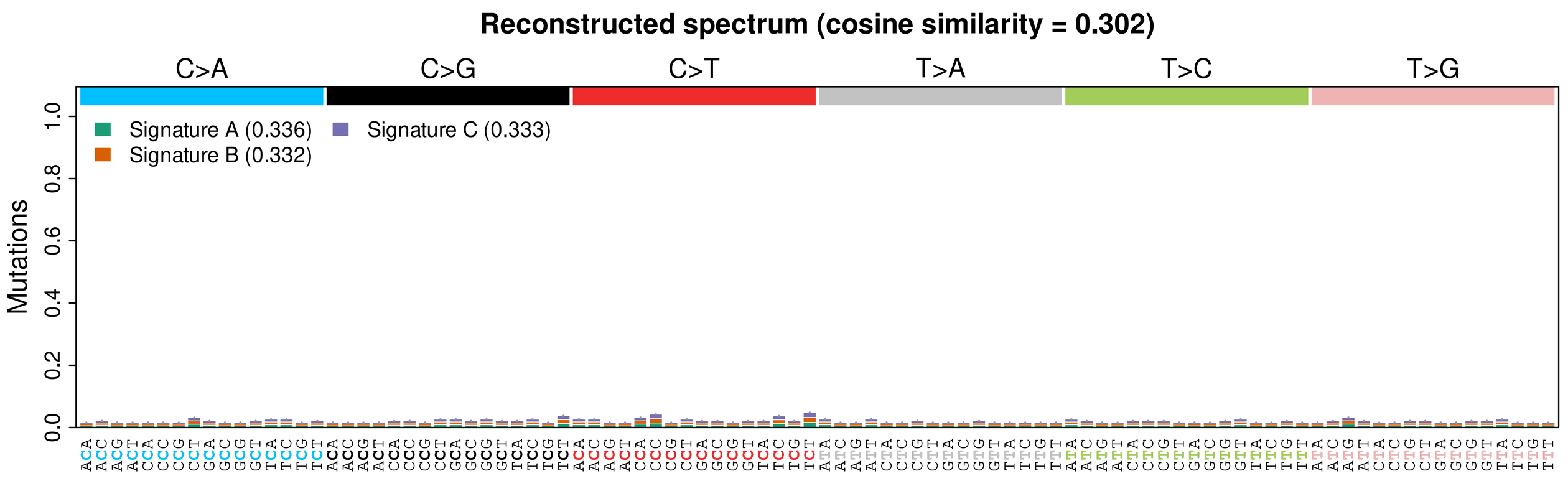
CATD0533a



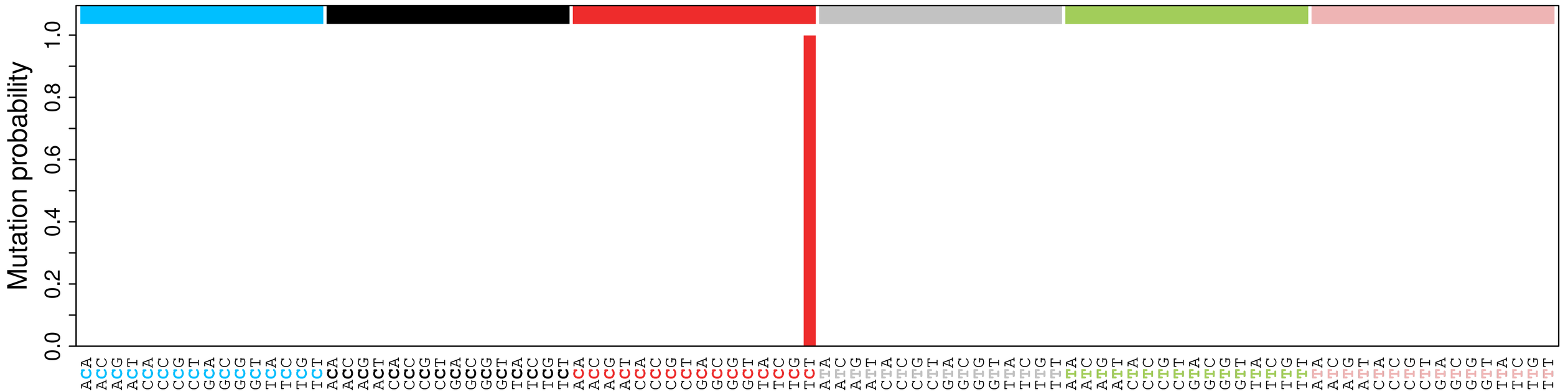
Reconstructed spectrum (cosine similarity = 0.232)



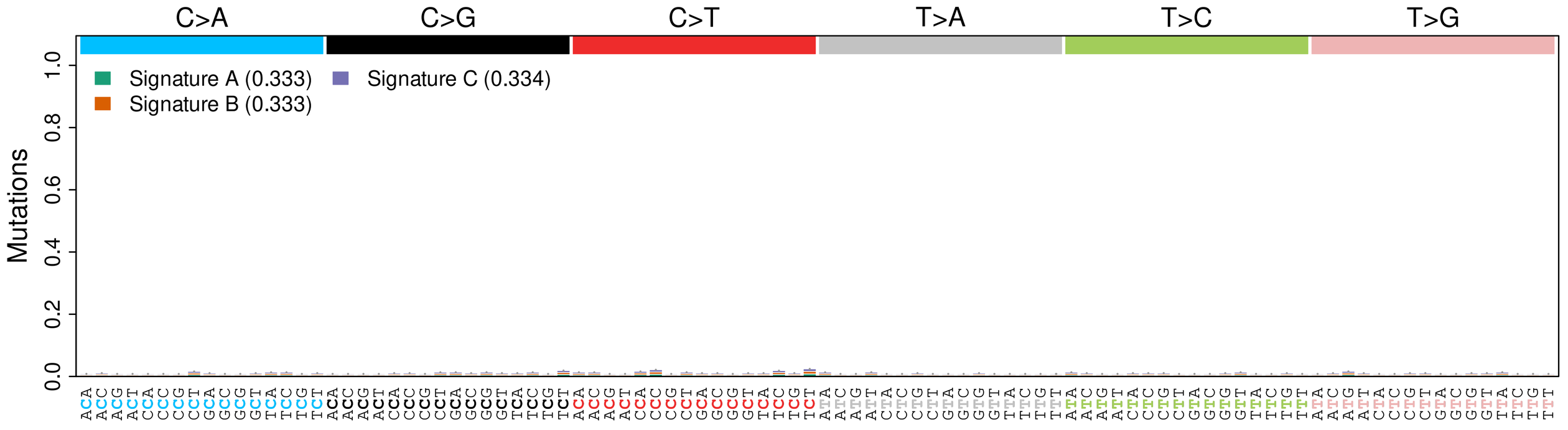

CATD0534a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0


Reconstructed spectrum (cosine similarity = 0.302)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.336)
Signature B (0.332)
Signature C (0.333)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

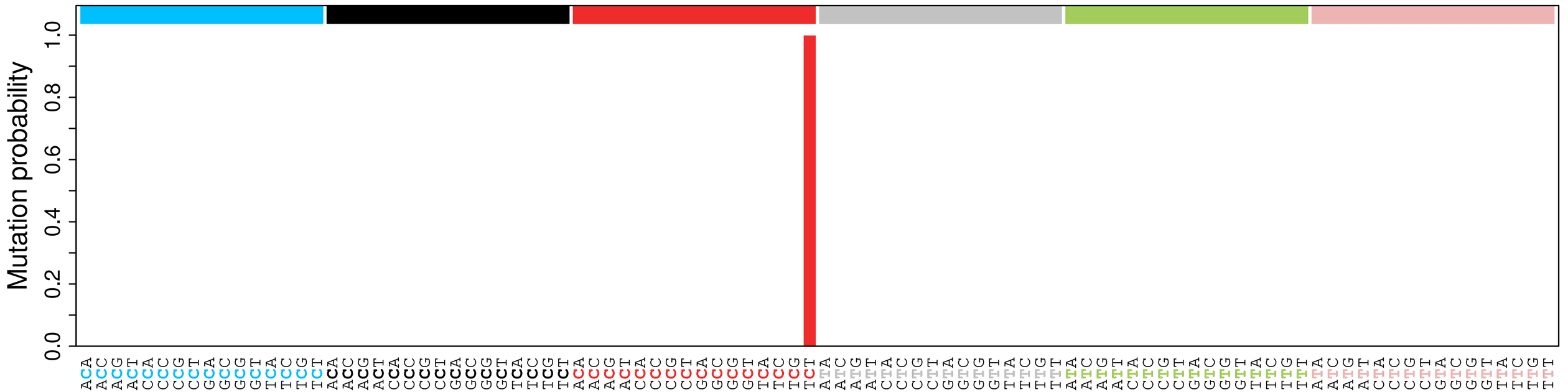
CATD199a



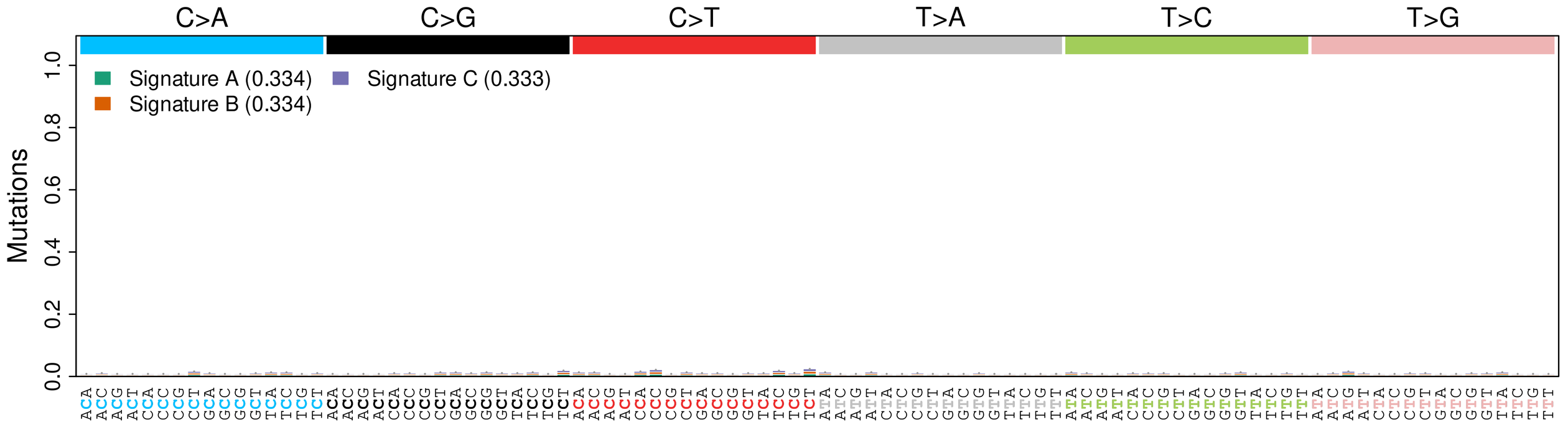
Reconstructed spectrum (cosine similarity = 0.227)

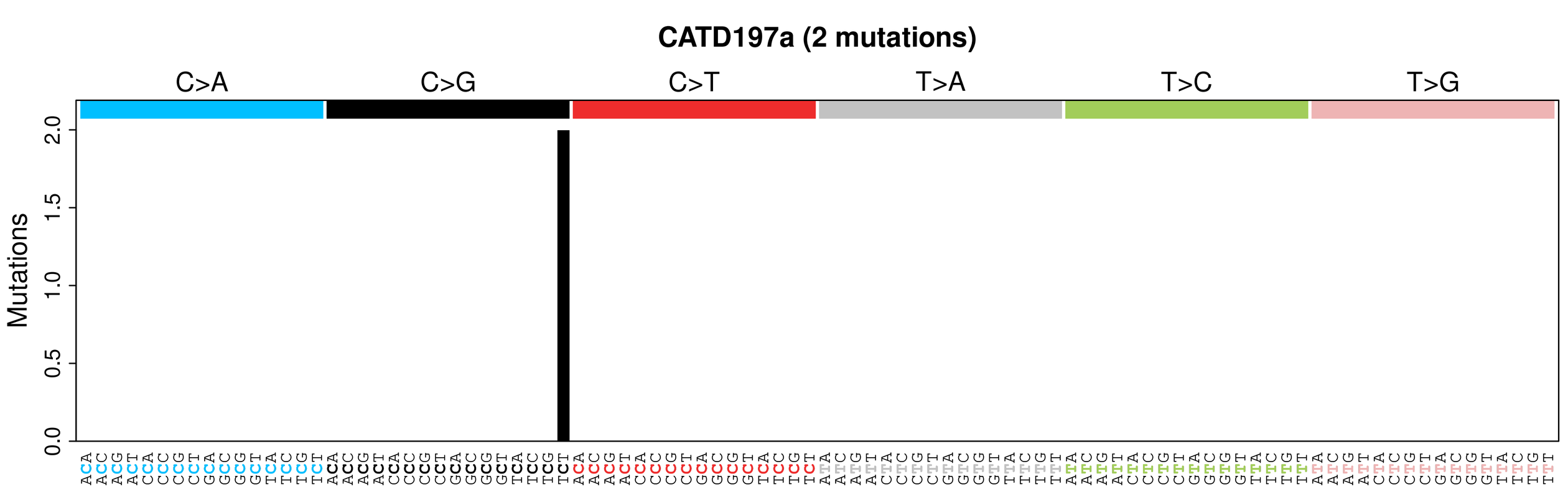


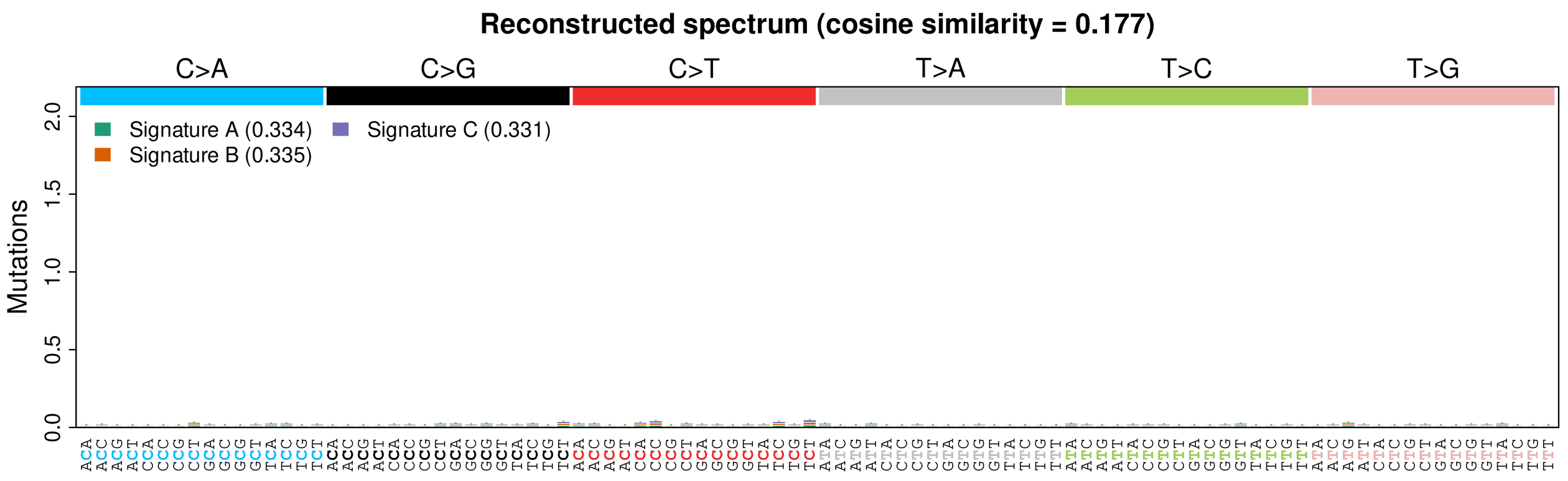
CATD207a



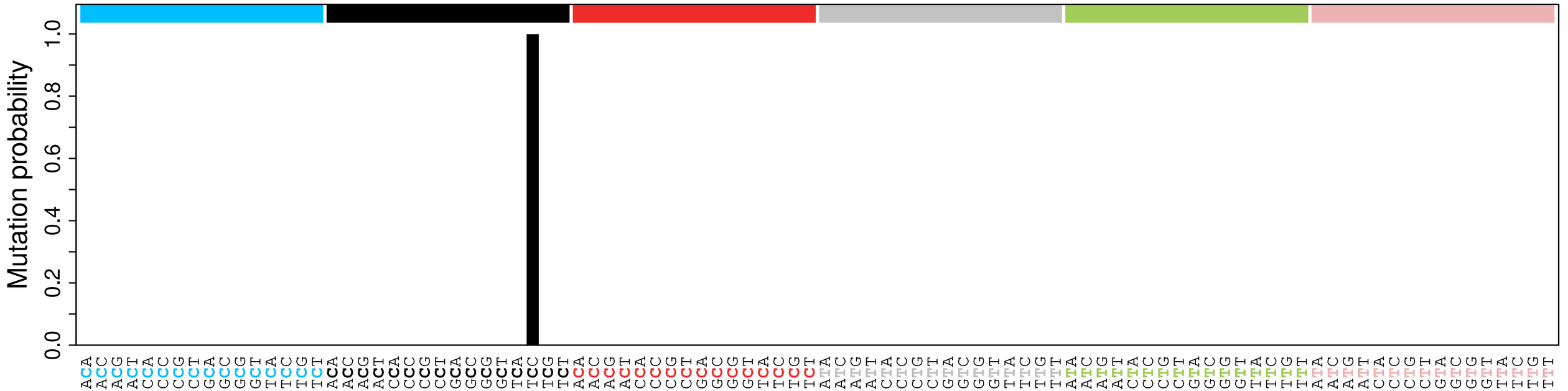
Reconstructed spectrum (cosine similarity = 0.227)



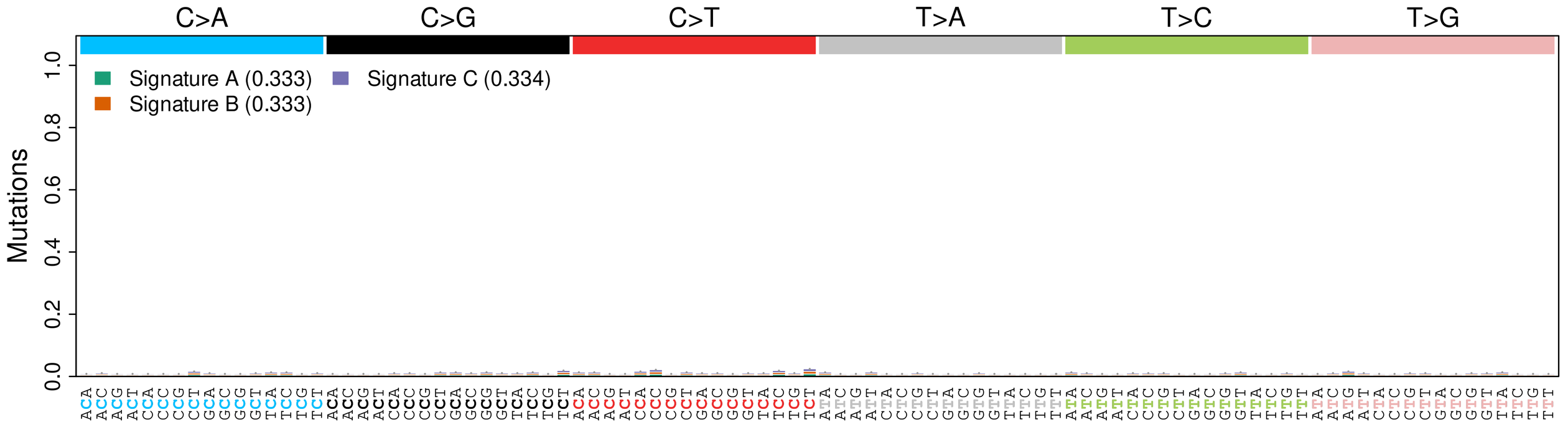

CATD197a (2 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.177)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.334)
Signature B (0.335)
Signature C (0.331)
Mutations
0.0
0.5
1.0
1.5
2.0

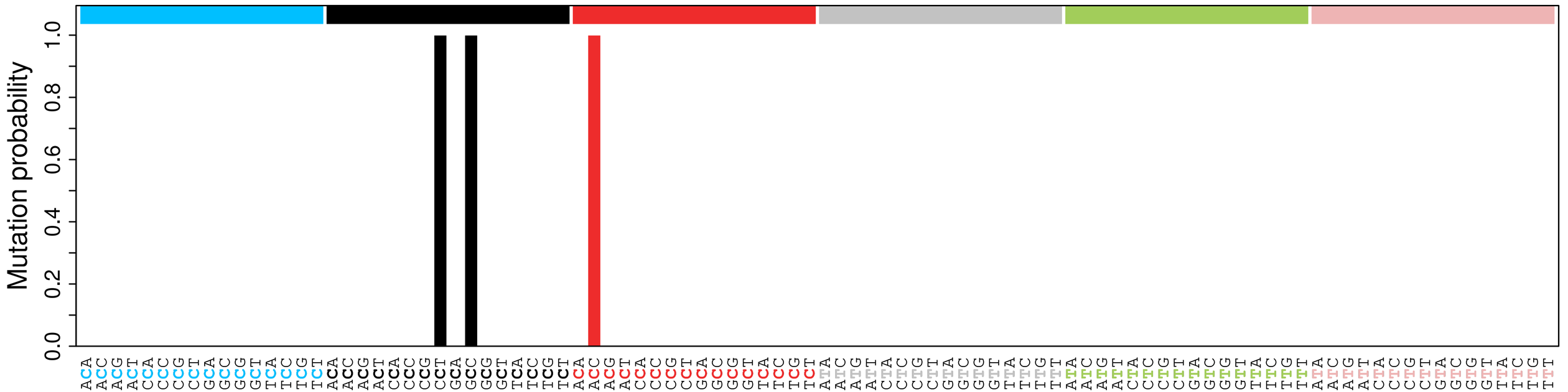
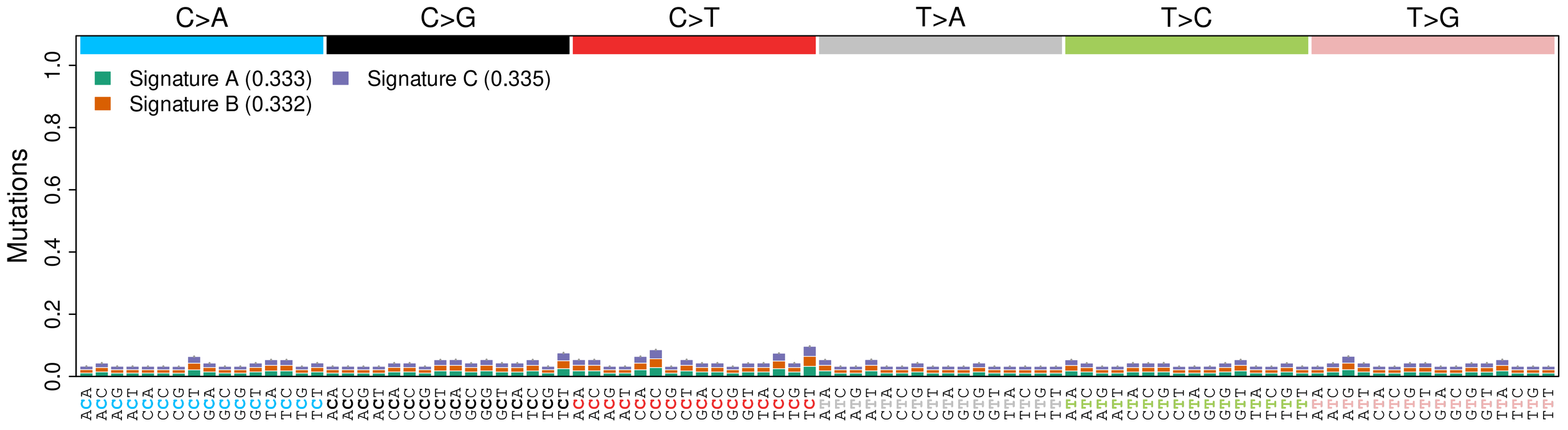
CATD0512a



Reconstructed spectrum (cosine similarity = 0.126)



CATD200a



Reconstructed spectrum (cosine similarity = 0.204)