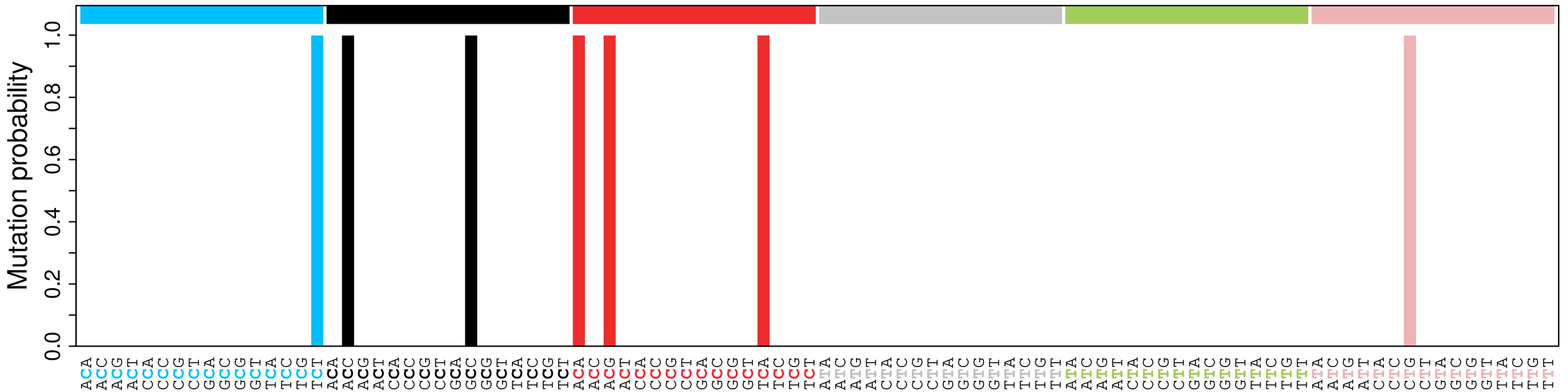
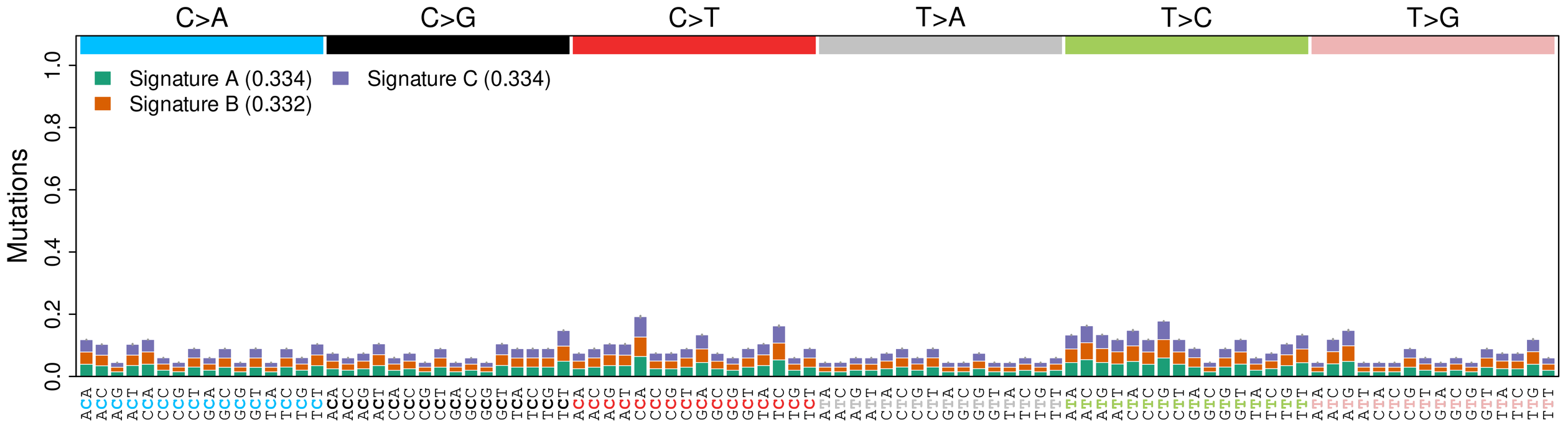
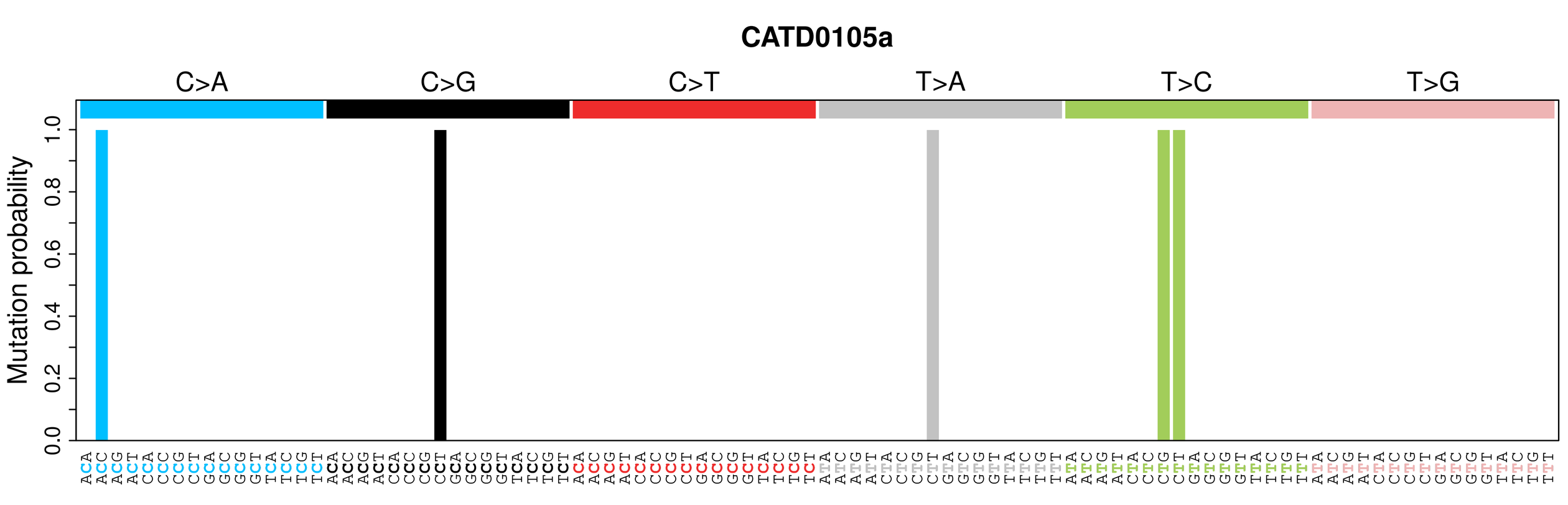
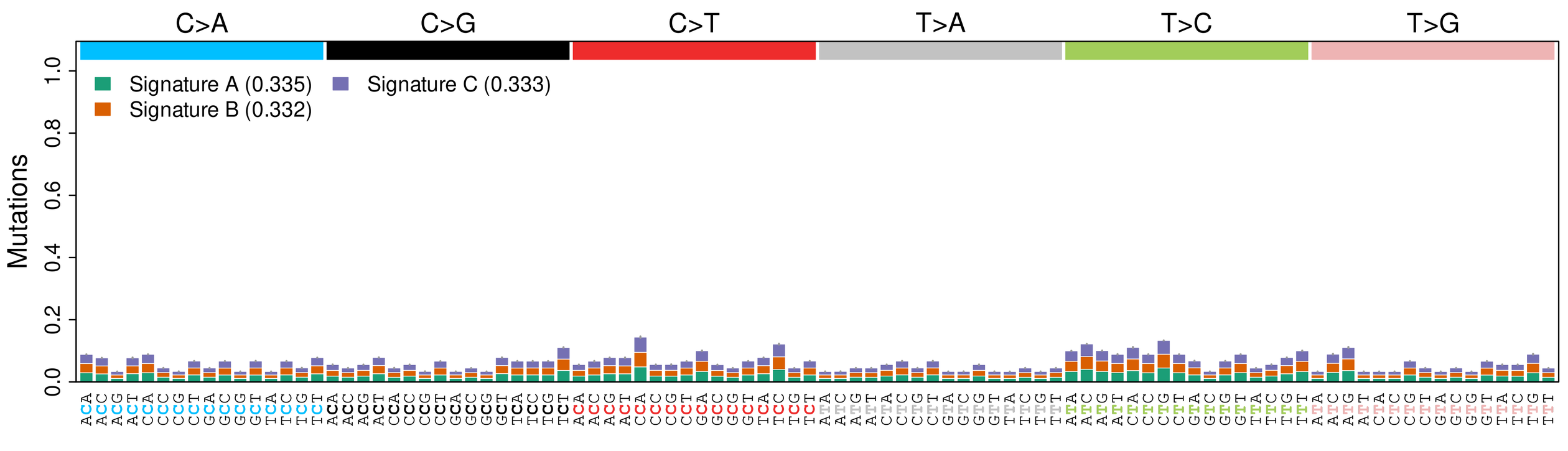
CATD0414a



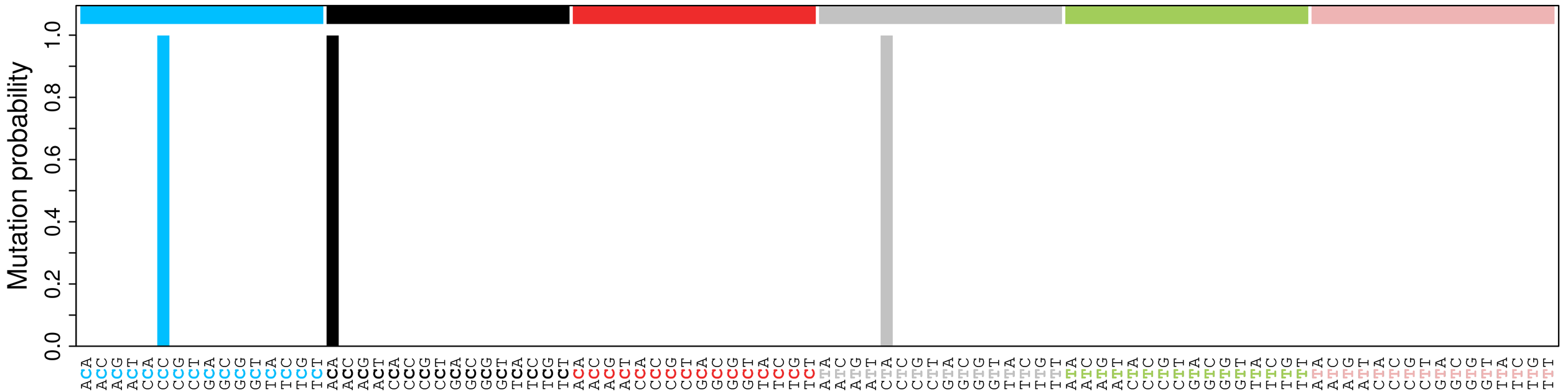
Reconstructed spectrum (cosine similarity = 0.255)



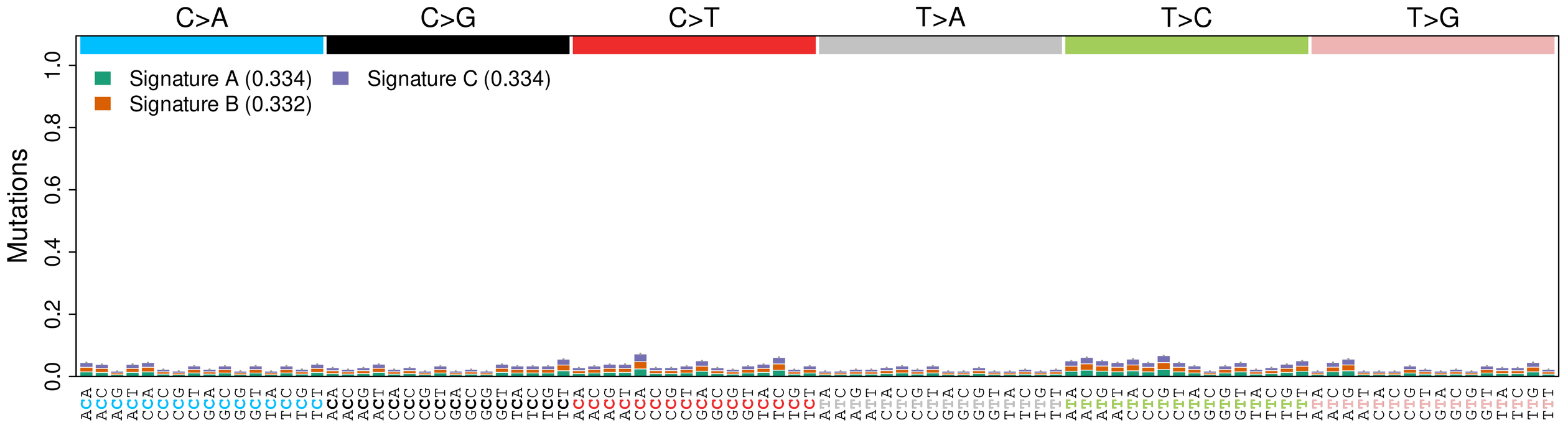

CATD0105a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0

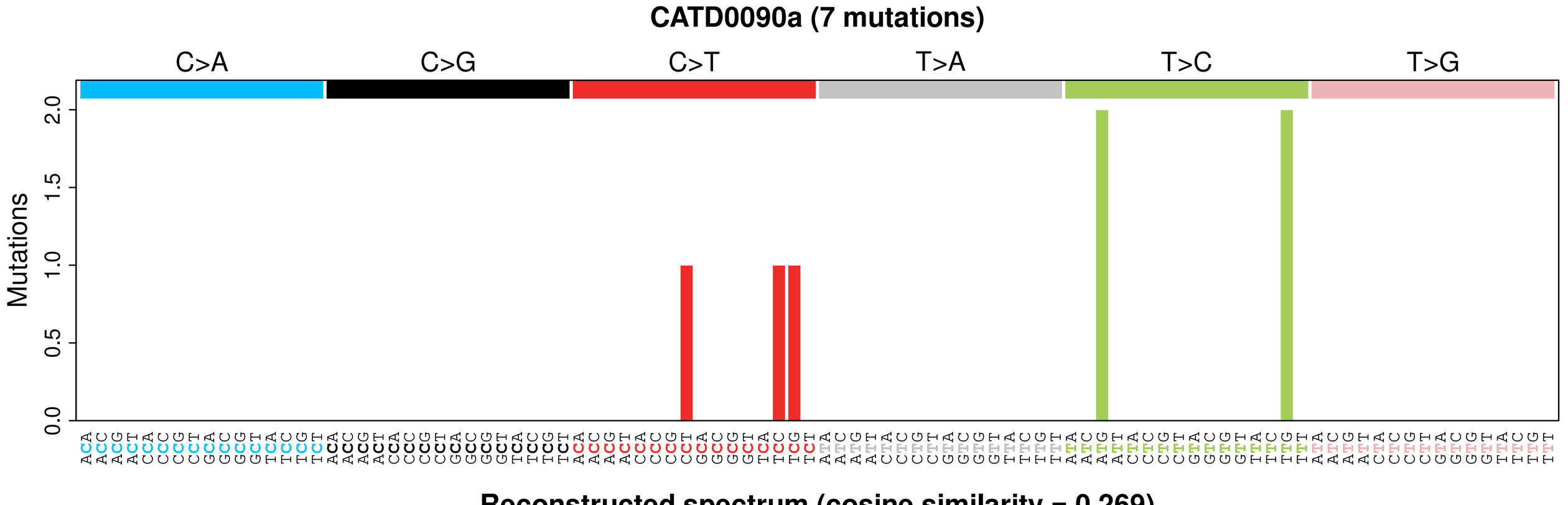

Reconstructed spectrum (cosine similarity = 0.293)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.335)
Signature B (0.332)
Signature C (0.333)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

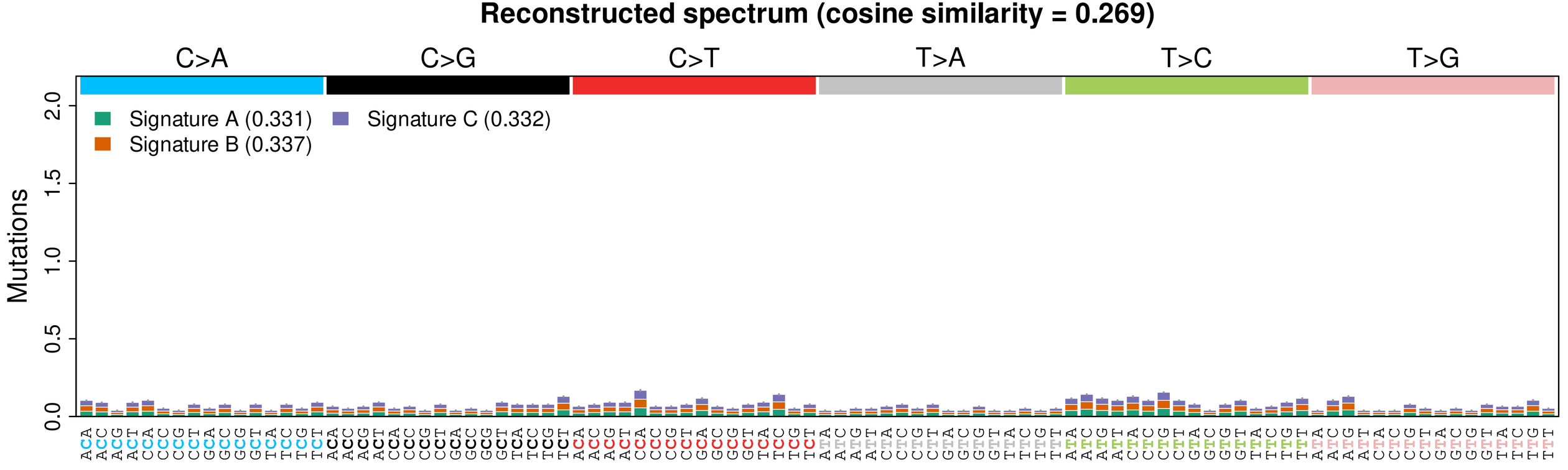
CATD189a

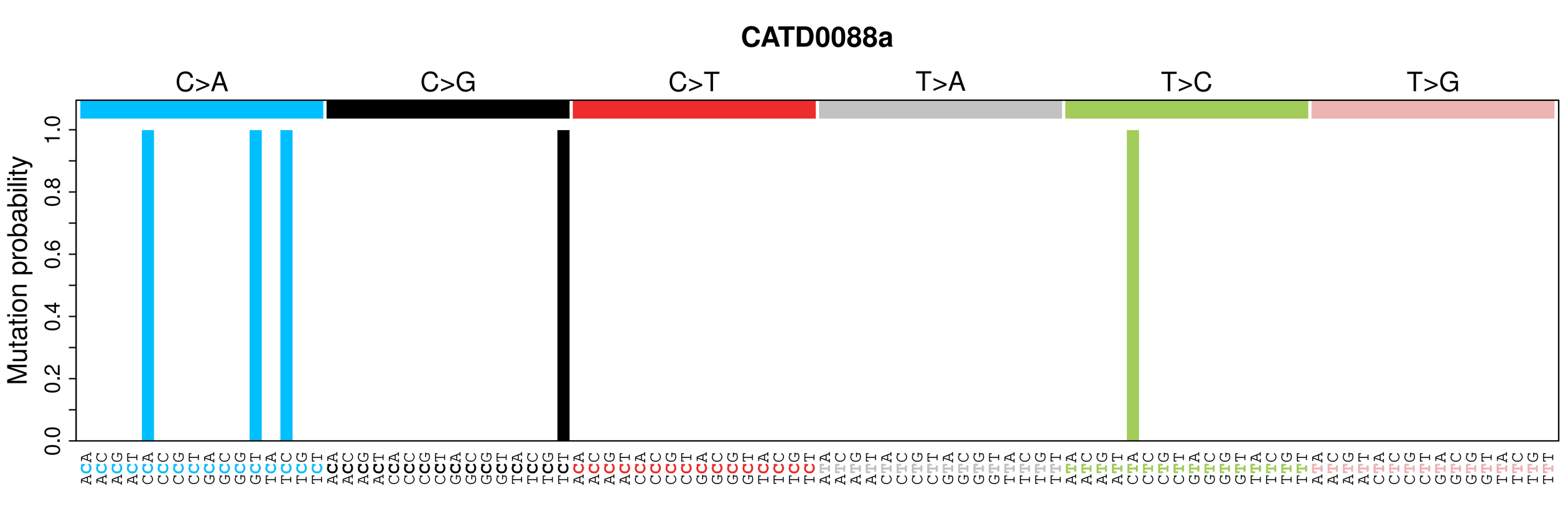


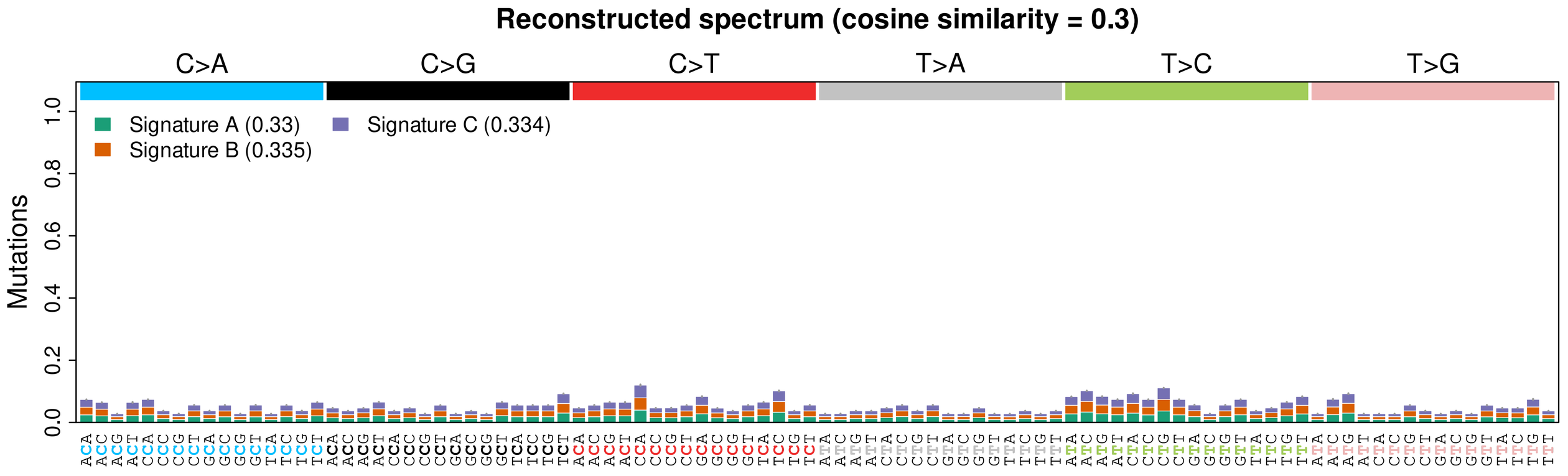
Reconstructed spectrum (cosine similarity = 0.136)

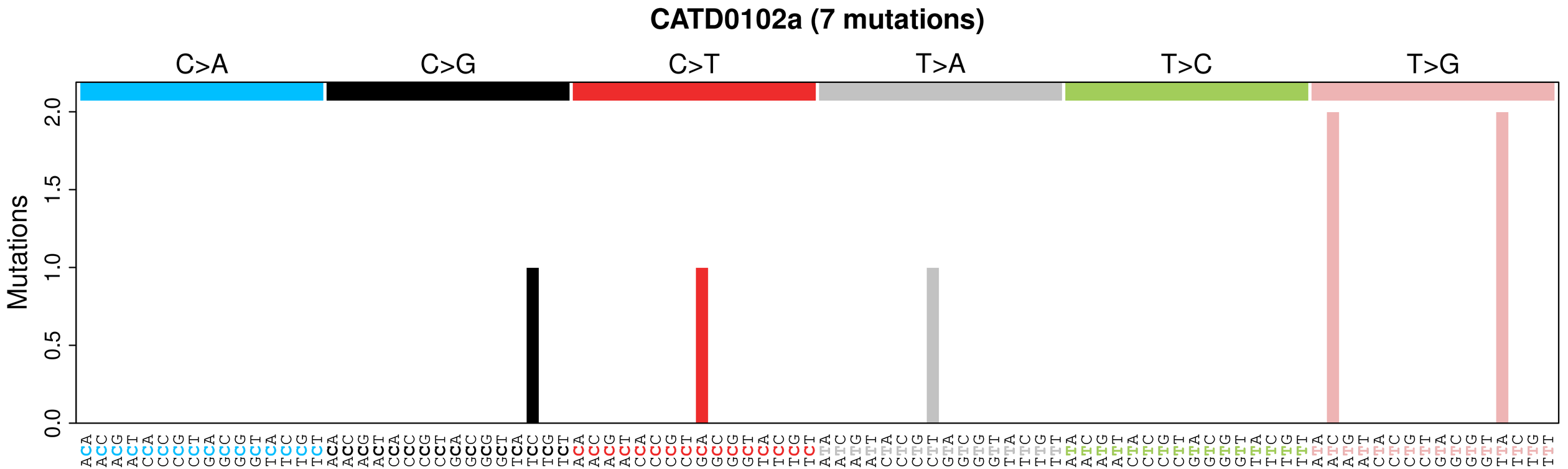


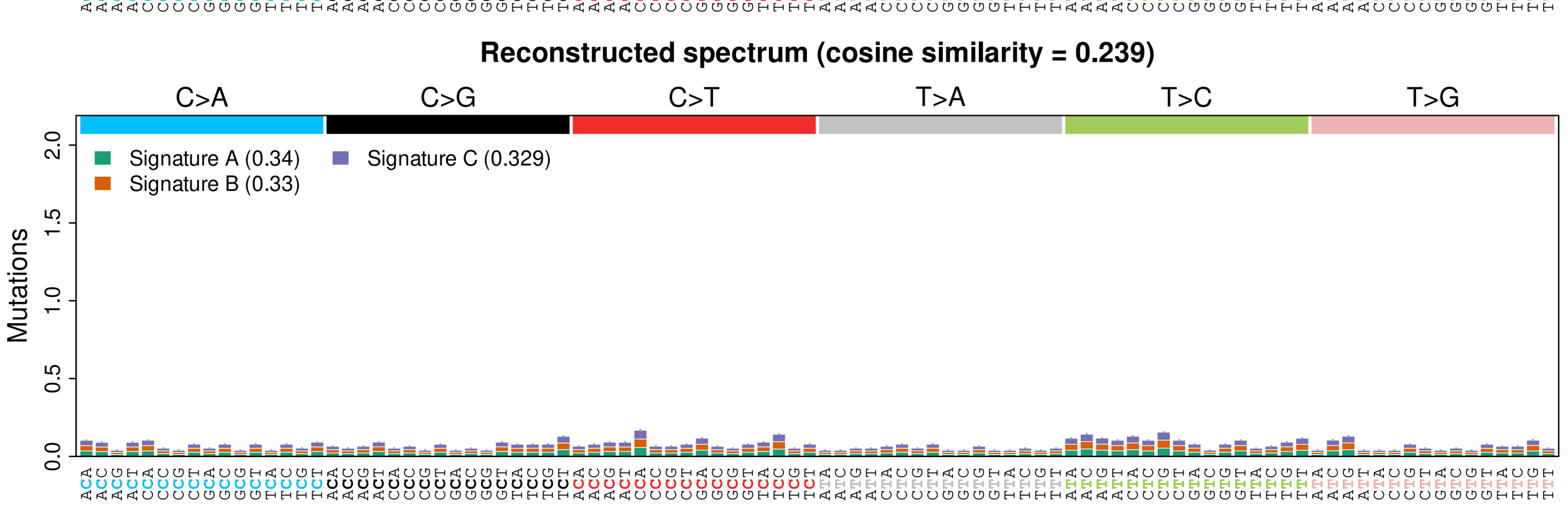

CATD0090a (7 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.269)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.331)
Signature B (0.337)
Signature C (0.332)
Mutations
0.0
0.5
1.0
1.5
2.0

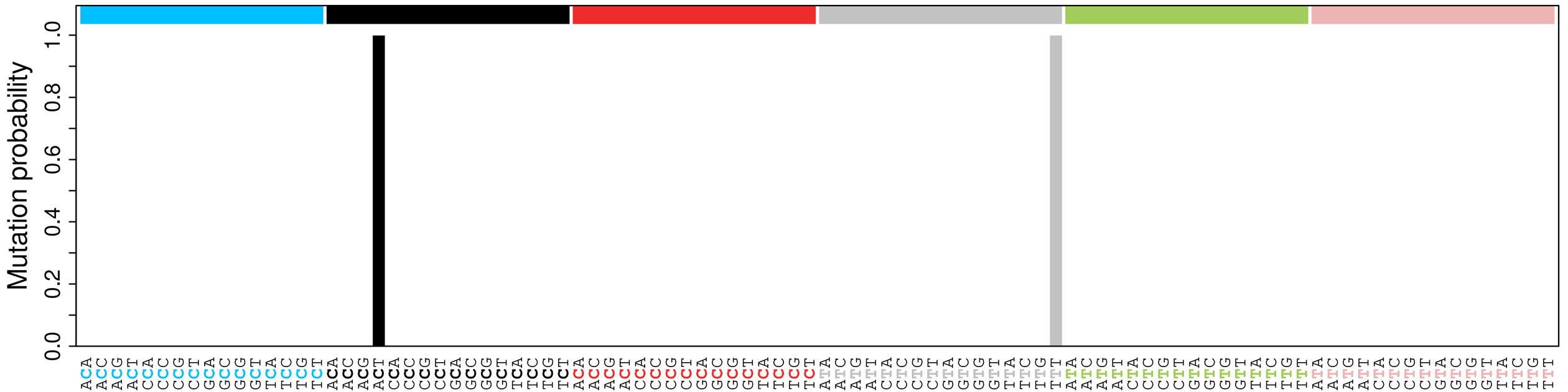

CATD0088a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0


Reconstructed spectrum (cosine similarity = 0.3)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.33)
Signature B (0.335)
Signature C (0.334)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

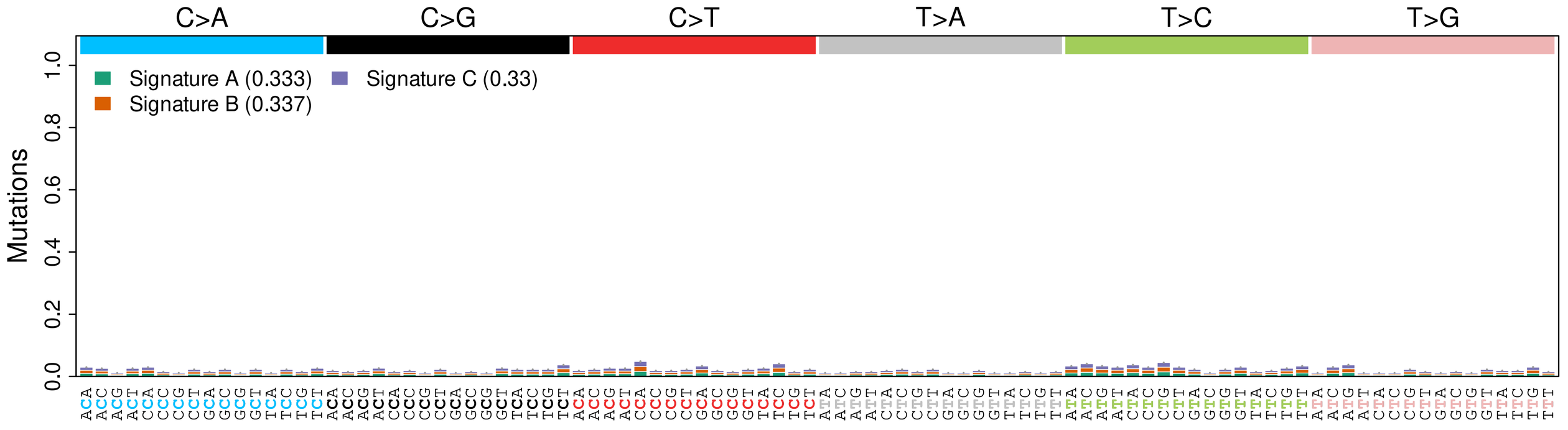

CATD0102a (7 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.239)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.34)
Signature B (0.33)
Signature C (0.329)
Mutations
0.0
0.5
1.0
1.5
2.0

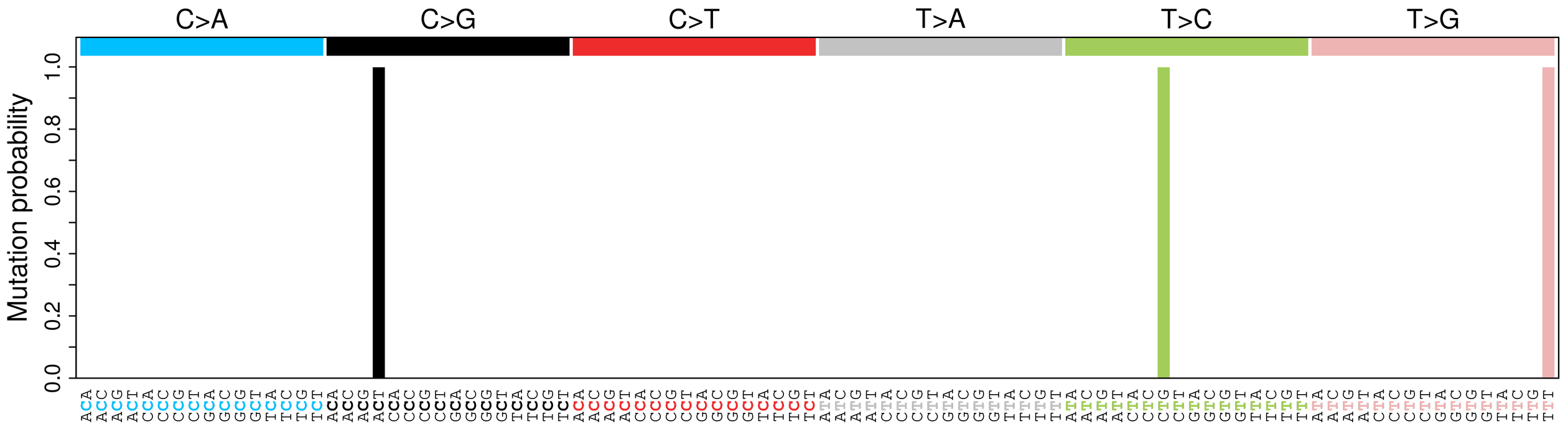
CATD0400a



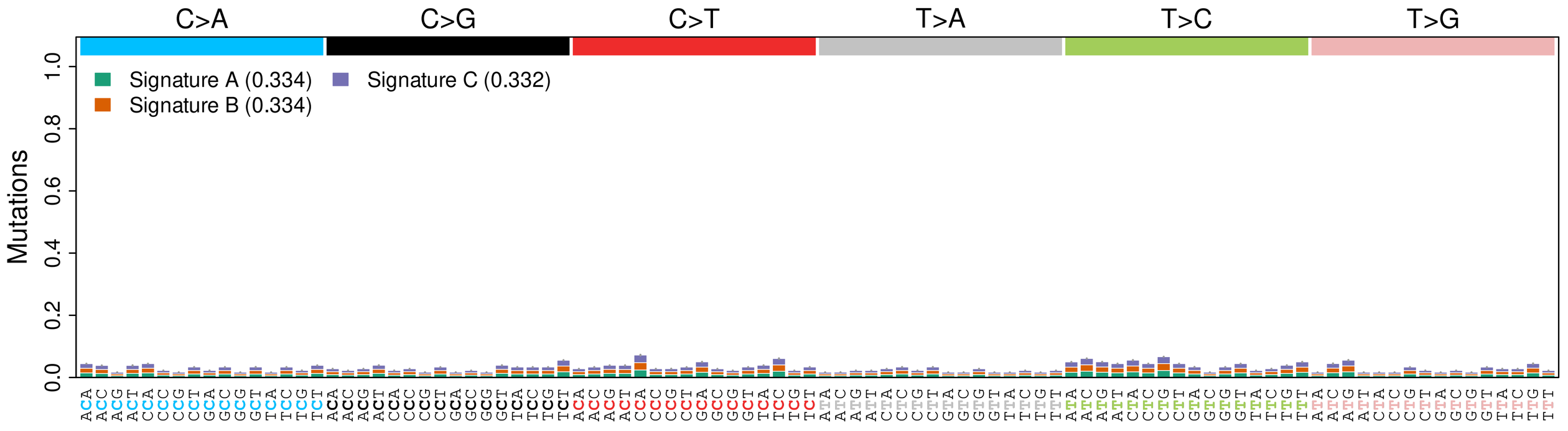
Reconstructed spectrum (cosine similarity = 0.132)

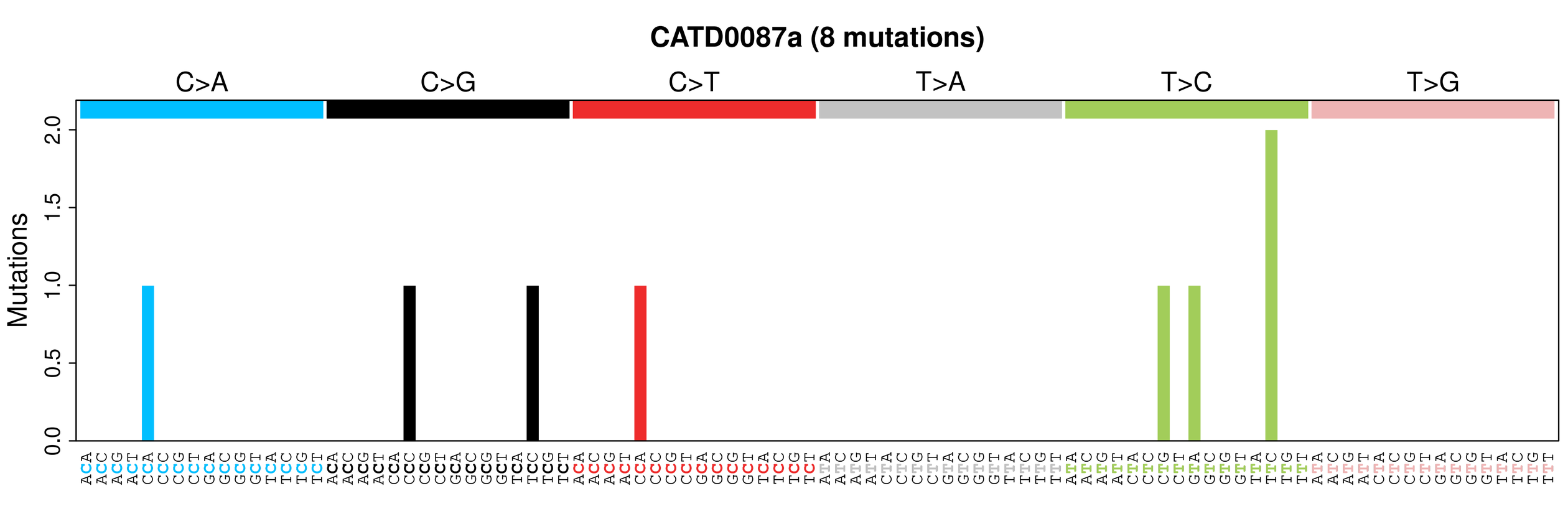


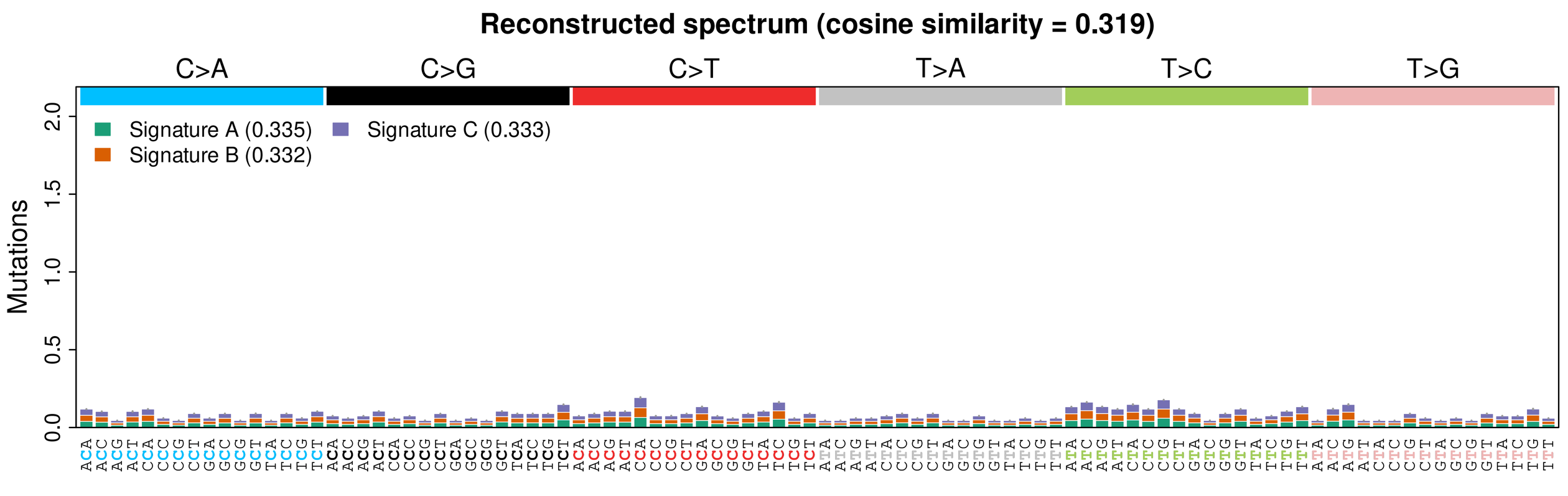
CATD0095a



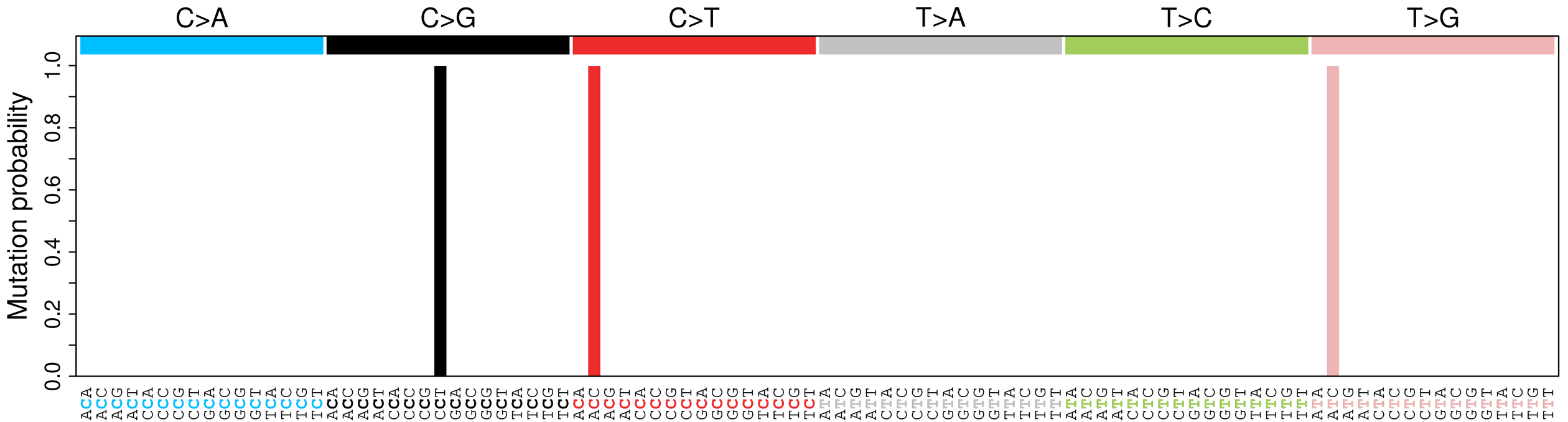
Reconstructed spectrum (cosine similarity = 0.224)



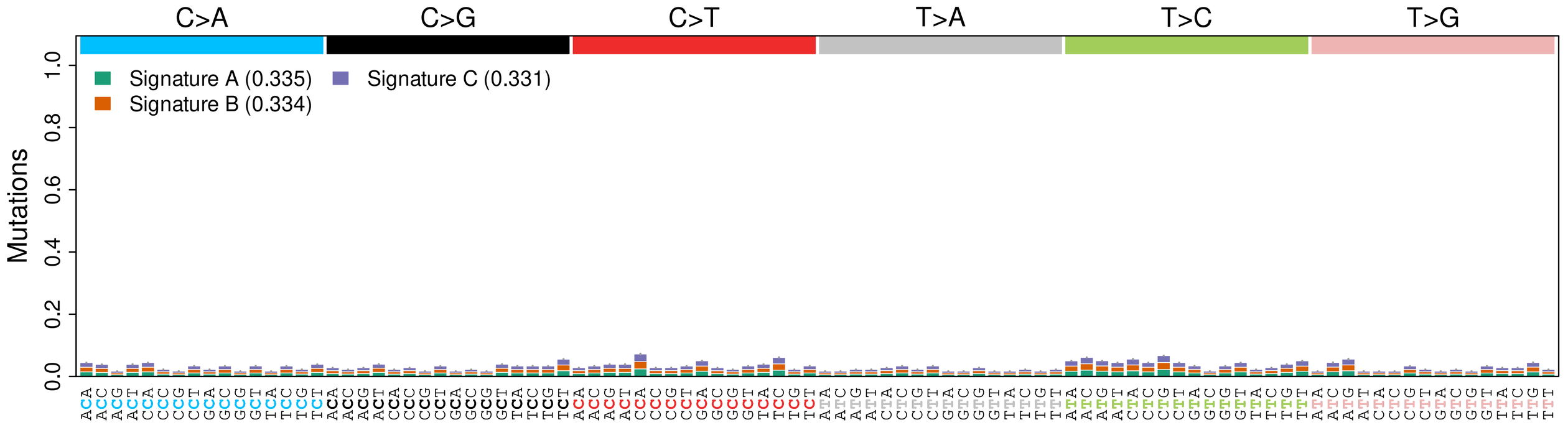

CATD0087a (8 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.319)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.335)
Signature B (0.332)
Signature C (0.333)
Mutations
0.0
0.5
1.0
1.5
2.0

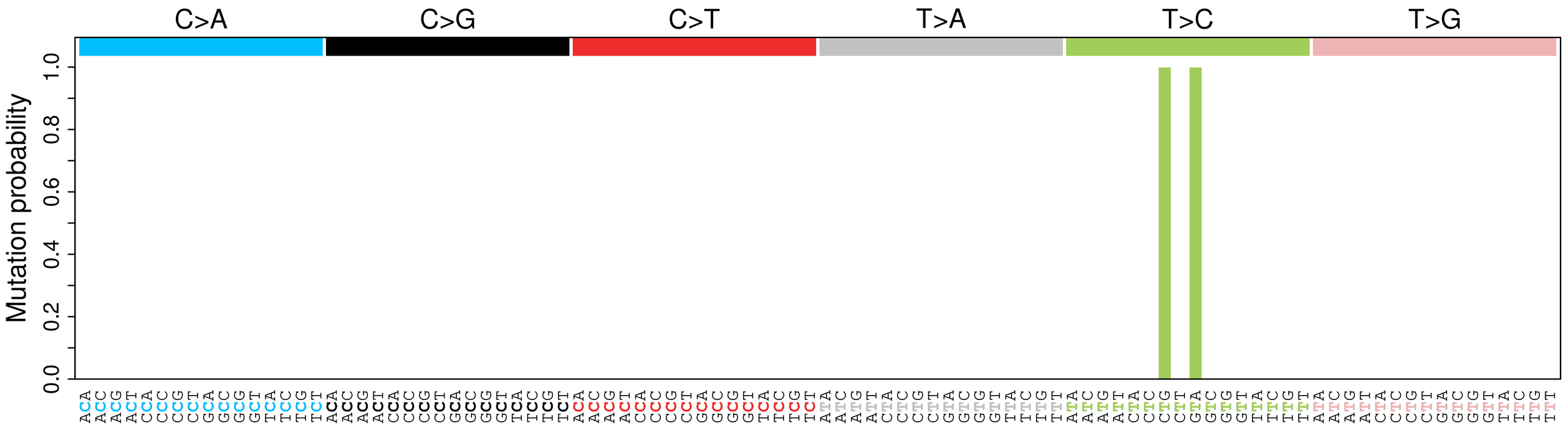
CATD0410a



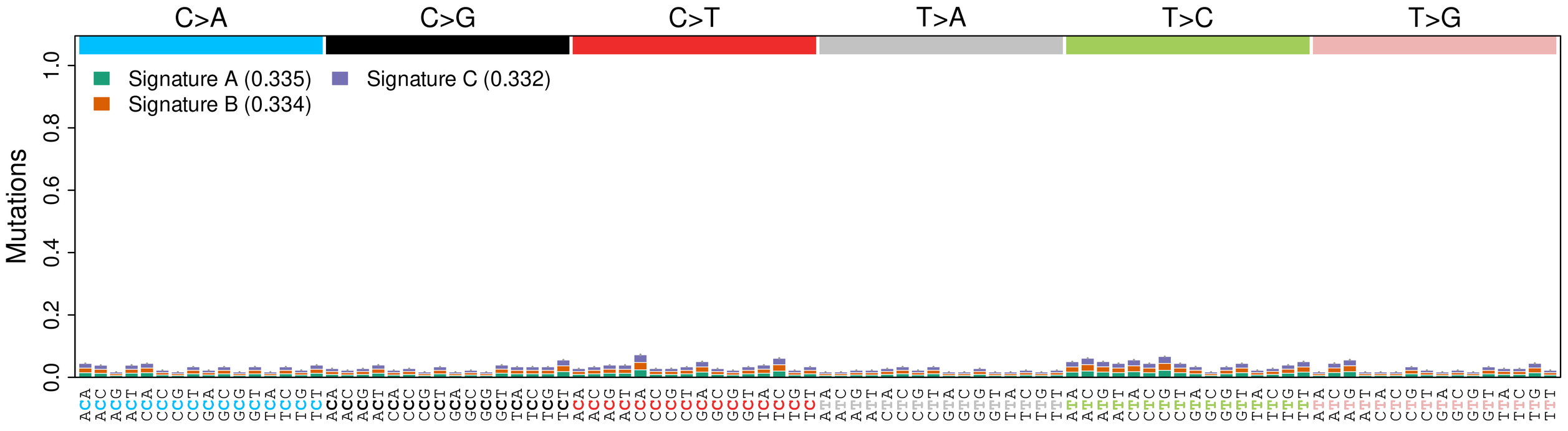
Reconstructed spectrum (cosine similarity = 0.194)

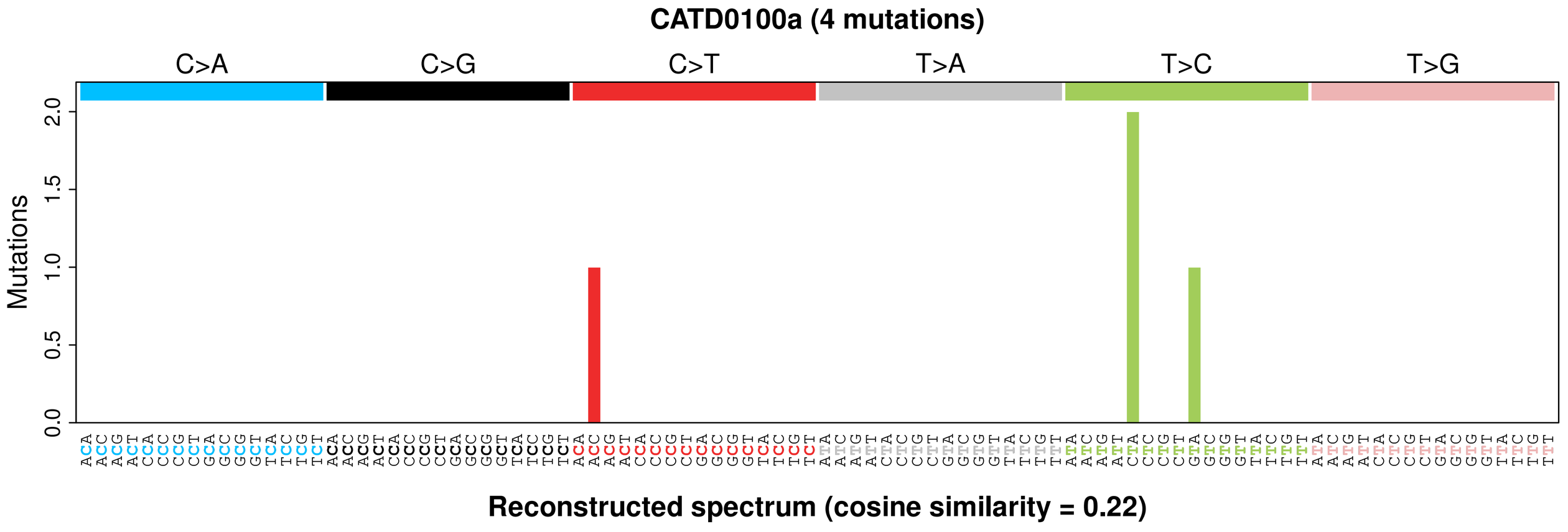


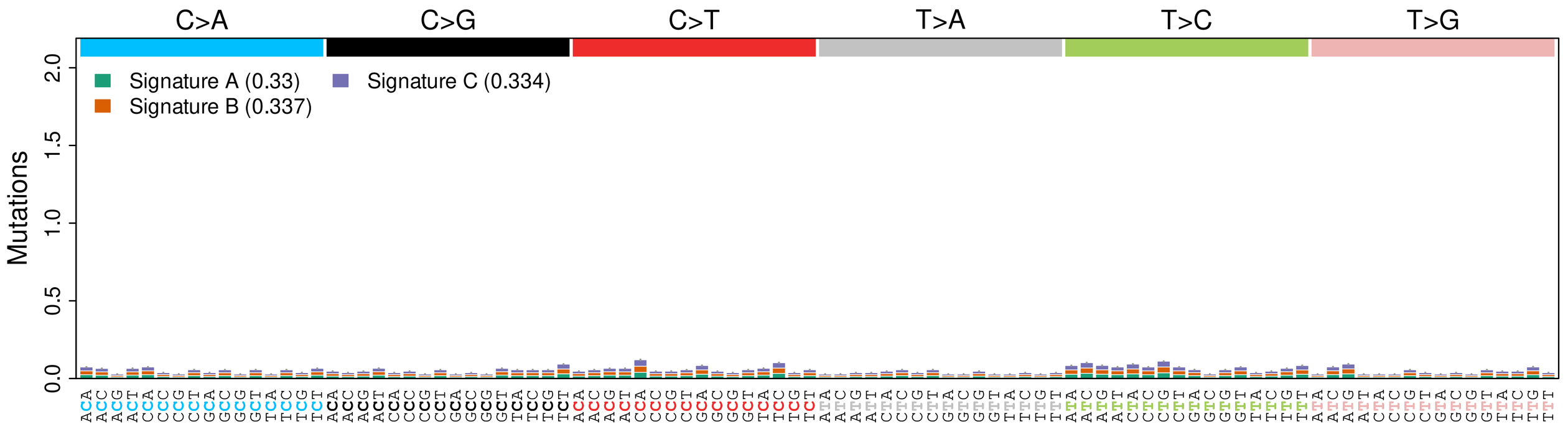
CATD0101a

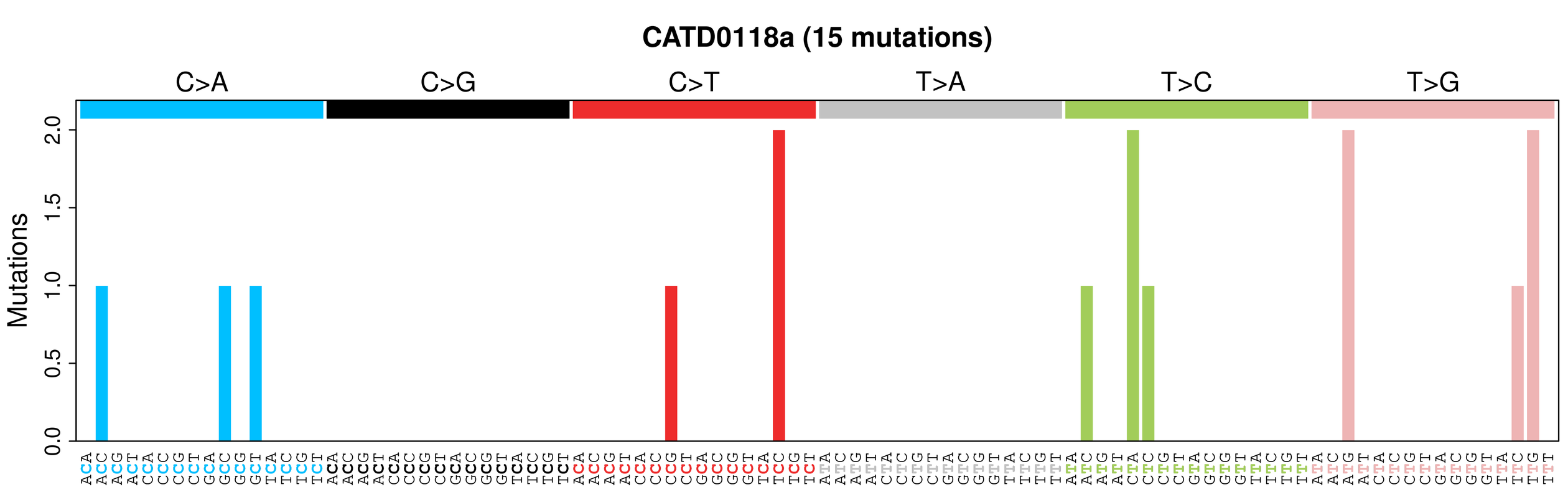


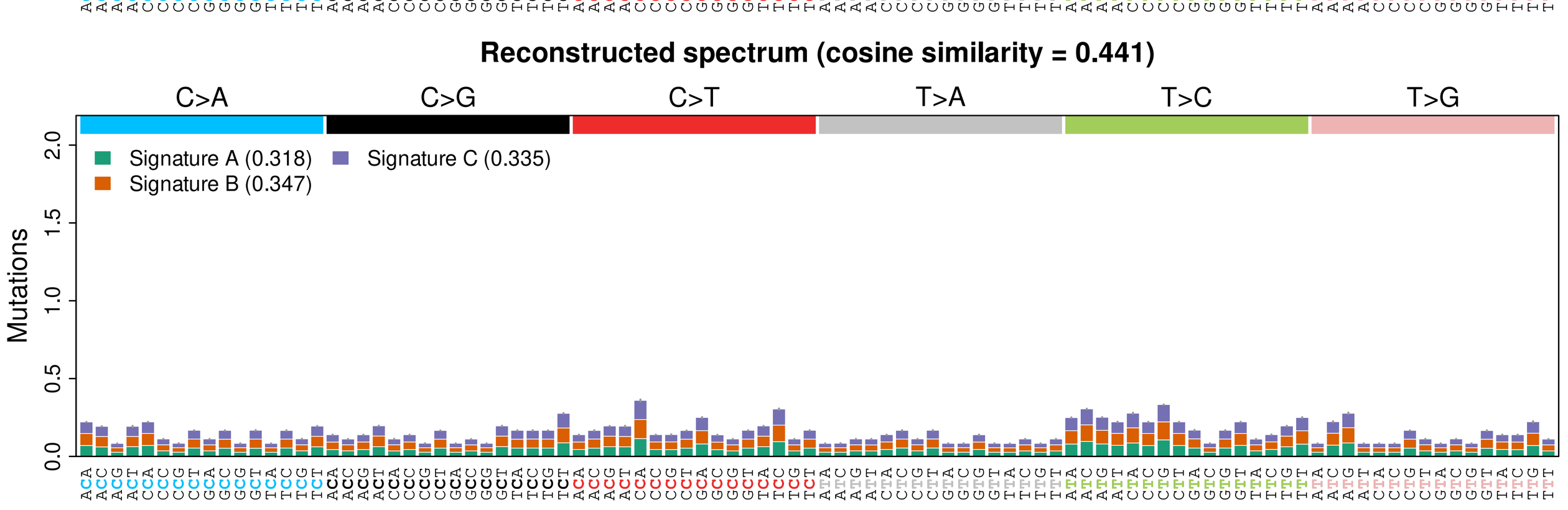
Reconstructed spectrum (cosine similarity = 0.214)

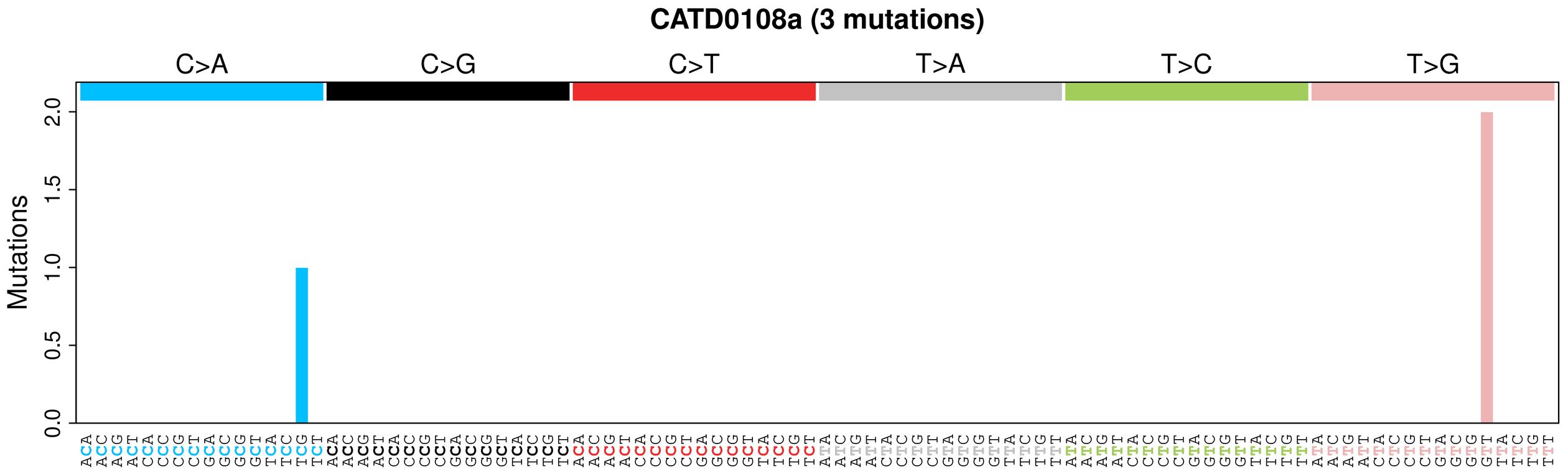


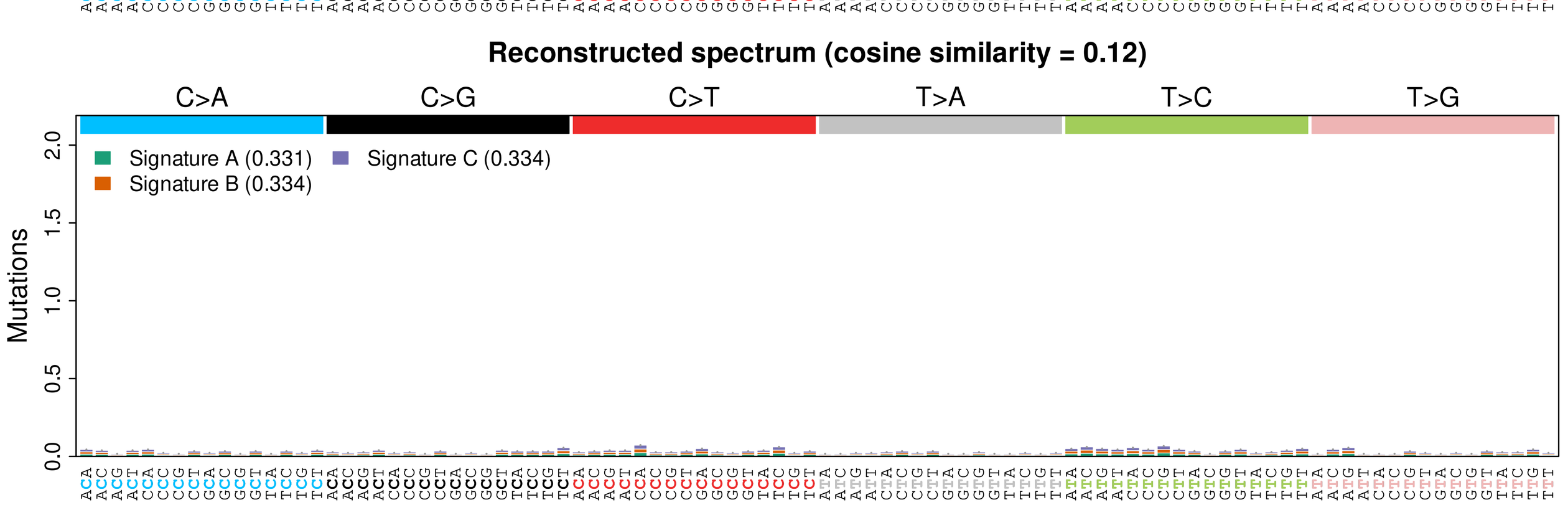

CATD0100a (4 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.22)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.33)
Signature B (0.337)
Signature C (0.334)
Mutations
0.0
0.5
1.0
1.5
2.0

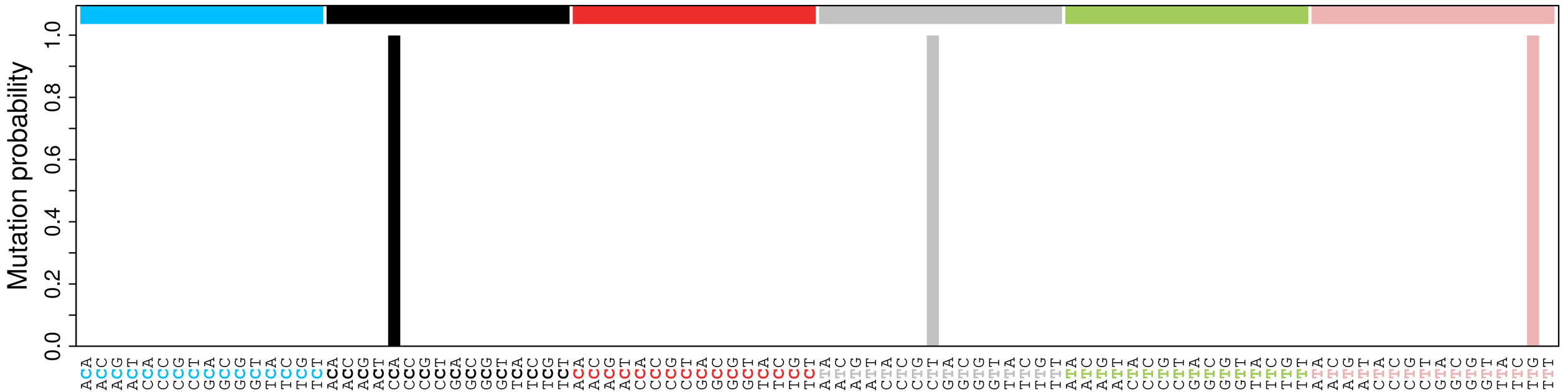

CATD0118a (15 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.441)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.318)
Signature B (0.347)
Signature C (0.335)
Mutations
0.0
0.5
1.0
1.5
2.0

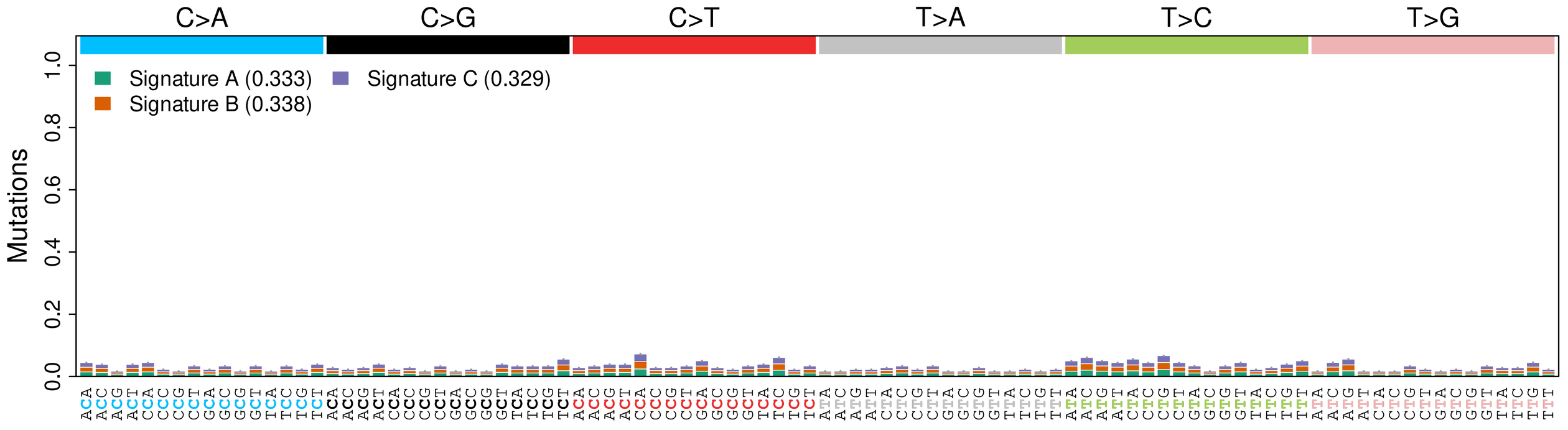

CATD0108a (3 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

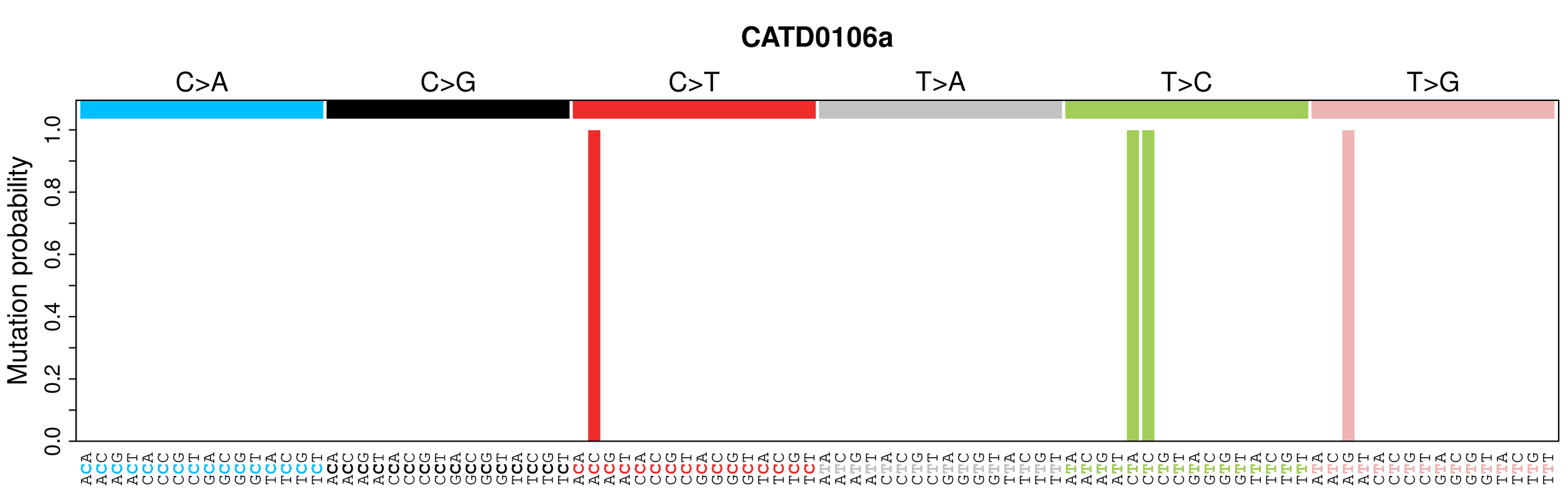

Reconstructed spectrum (cosine similarity = 0.12)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.331)
Signature B (0.334)
Signature C (0.334)
Mutations
0.0
0.5
1.0
1.5
2.0

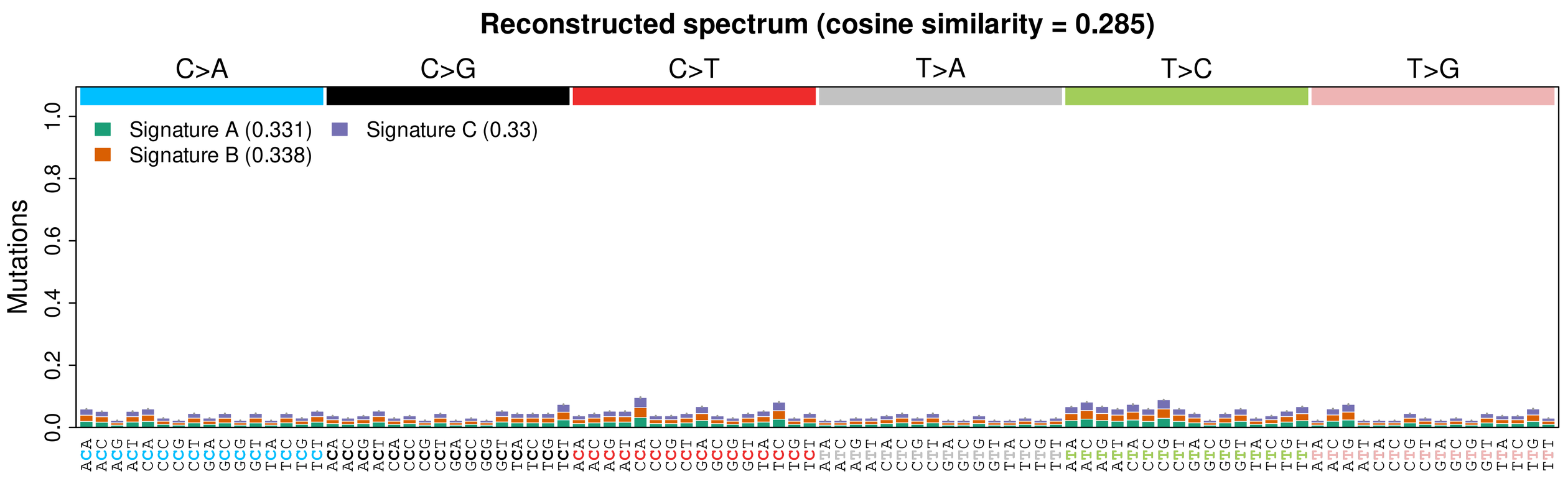
CATD0082a



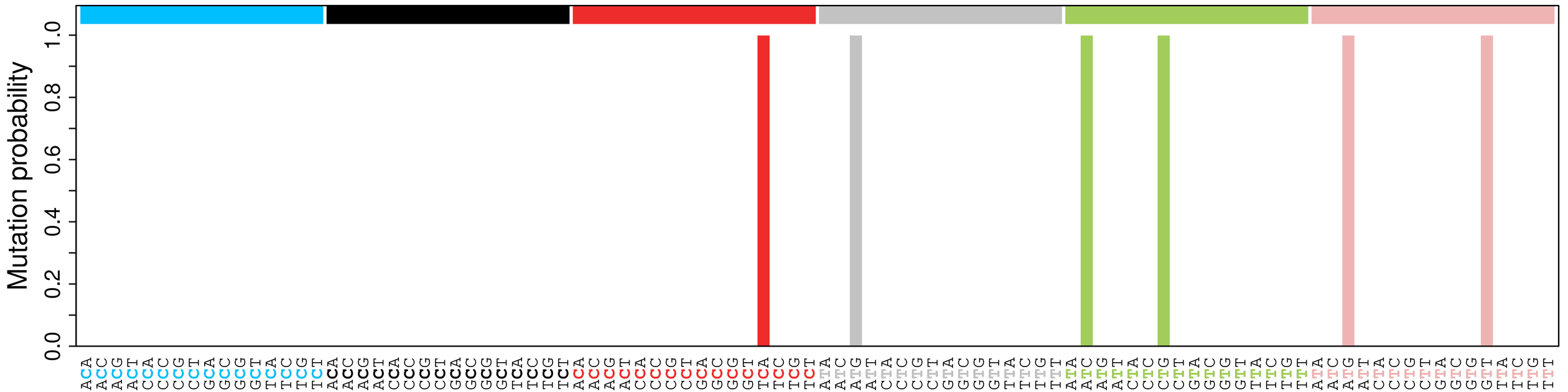
Reconstructed spectrum (cosine similarity = 0.175)



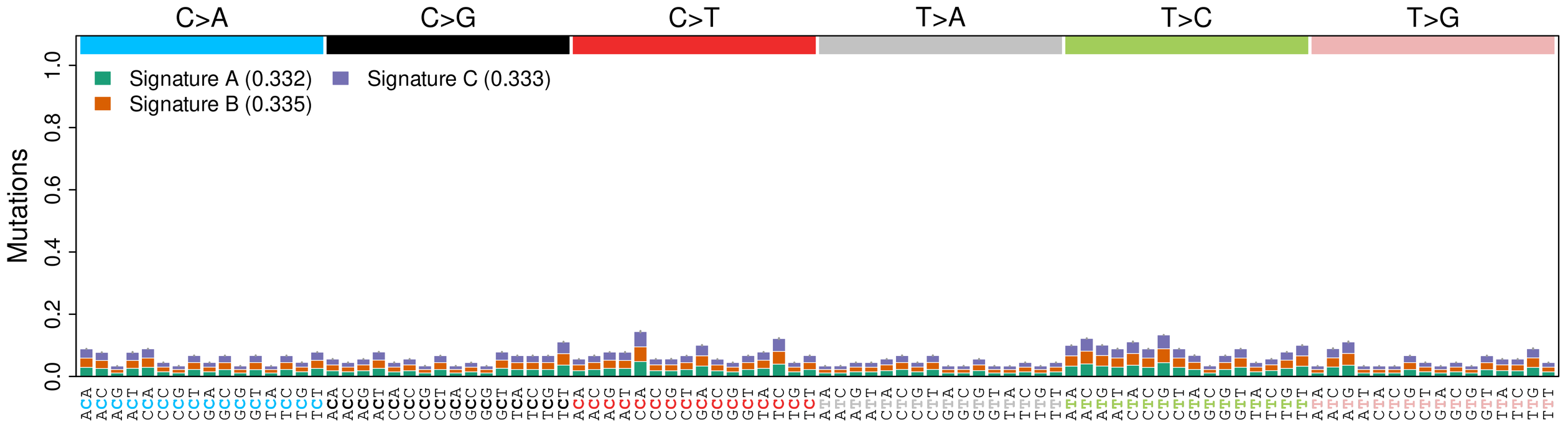

CATD0106a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0

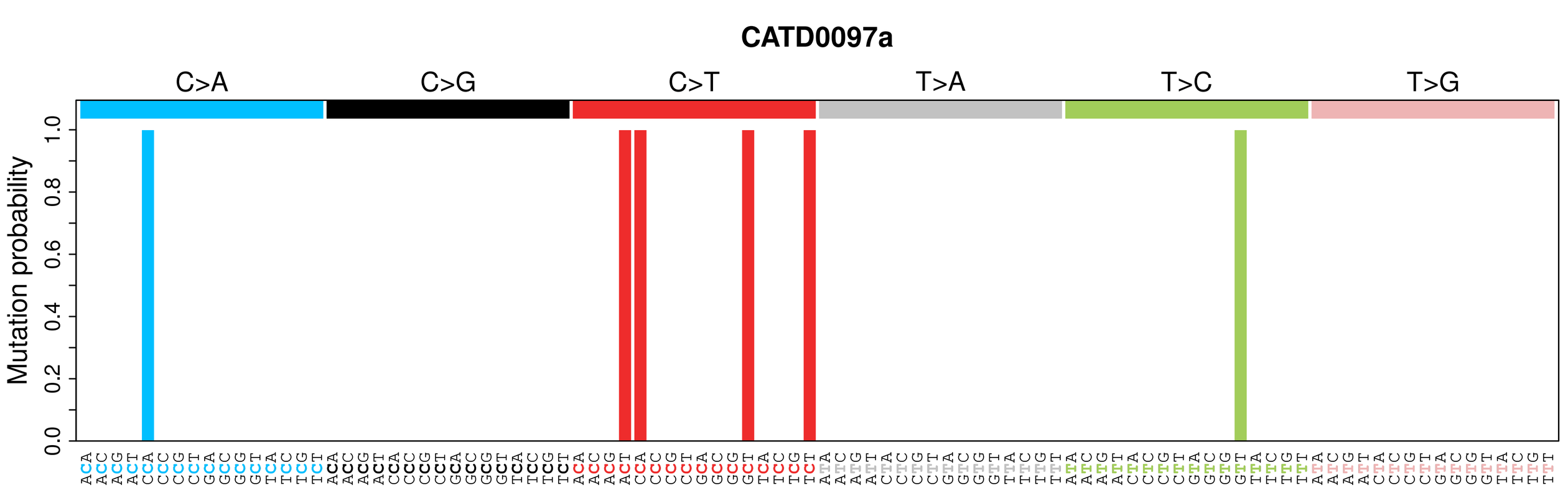

Reconstructed spectrum (cosine similarity = 0.285)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.331)
Signature B (0.338)
Signature C (0.33)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

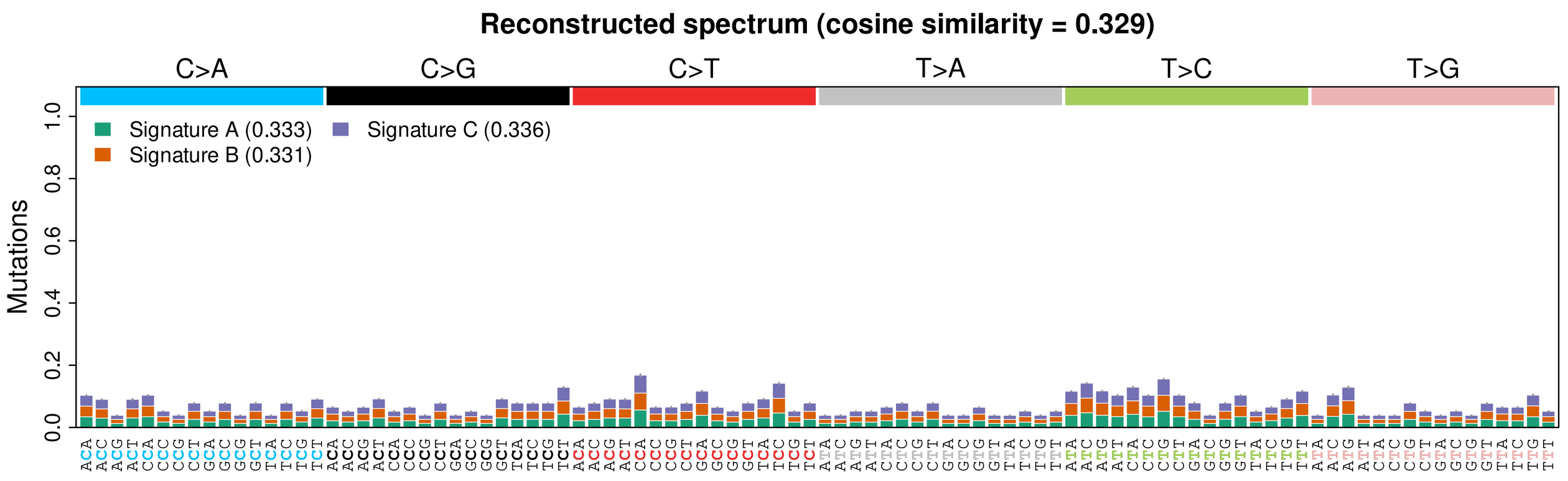
CATD0107a



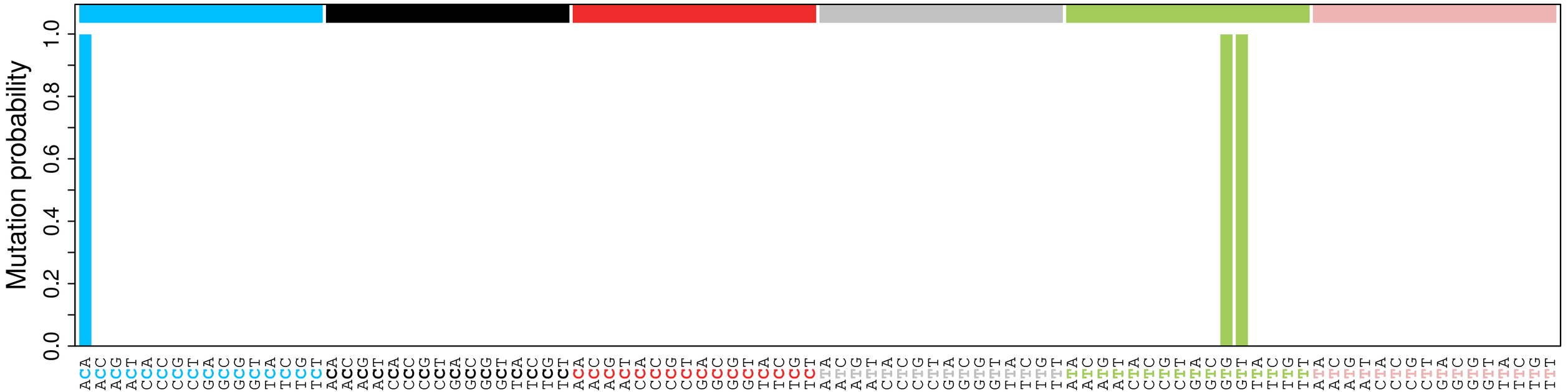
Reconstructed spectrum (cosine similarity = 0.343)



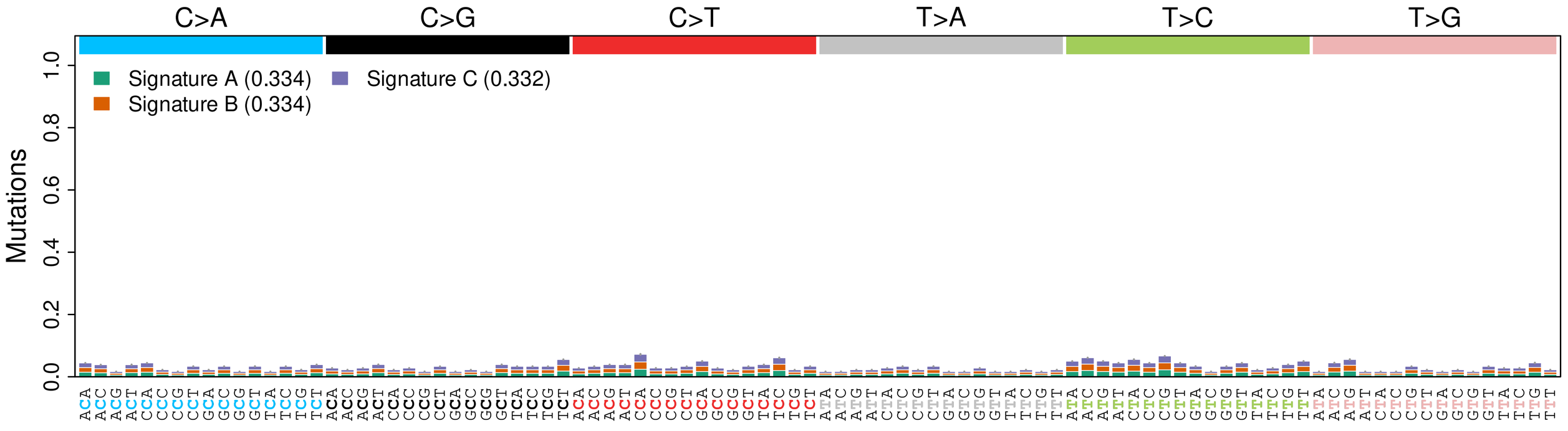

CATD0097a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0


Reconstructed spectrum (cosine similarity = 0.329)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.333)
Signature B (0.331)
Signature C (0.336)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

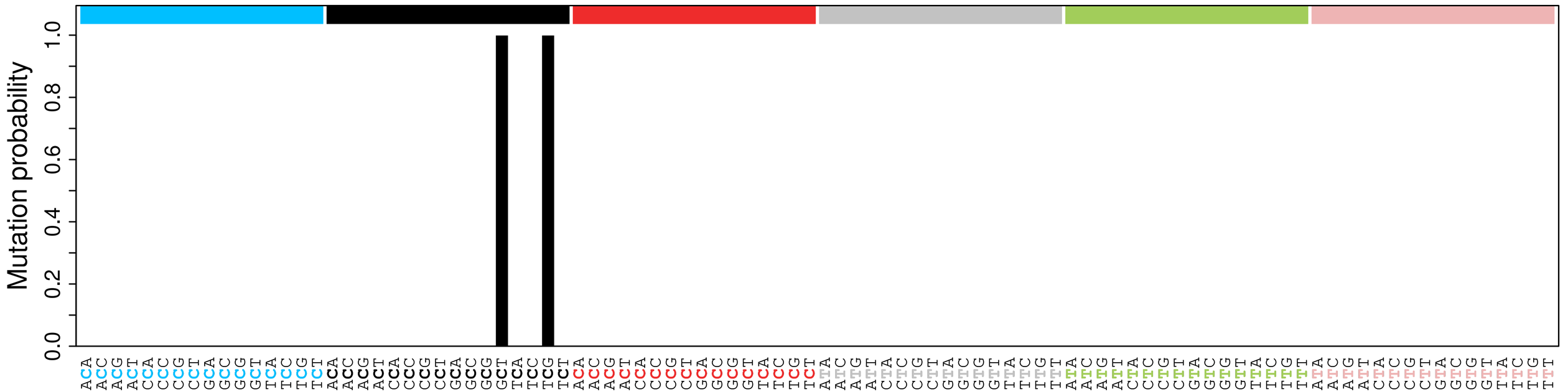
CATD0112a



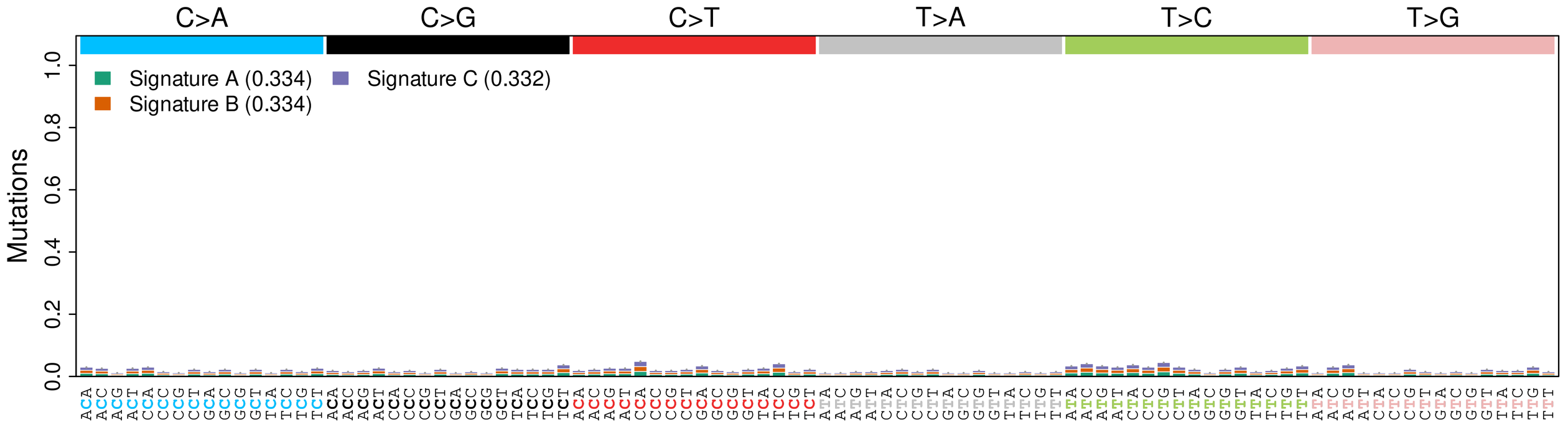
Reconstructed spectrum (cosine similarity = 0.213)



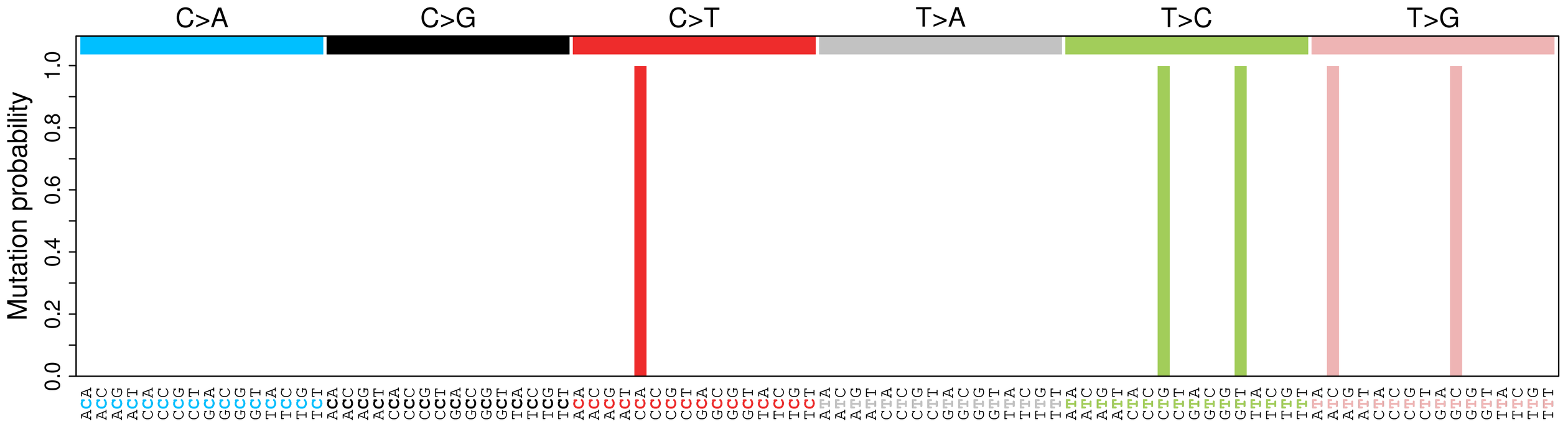
CATD0412a



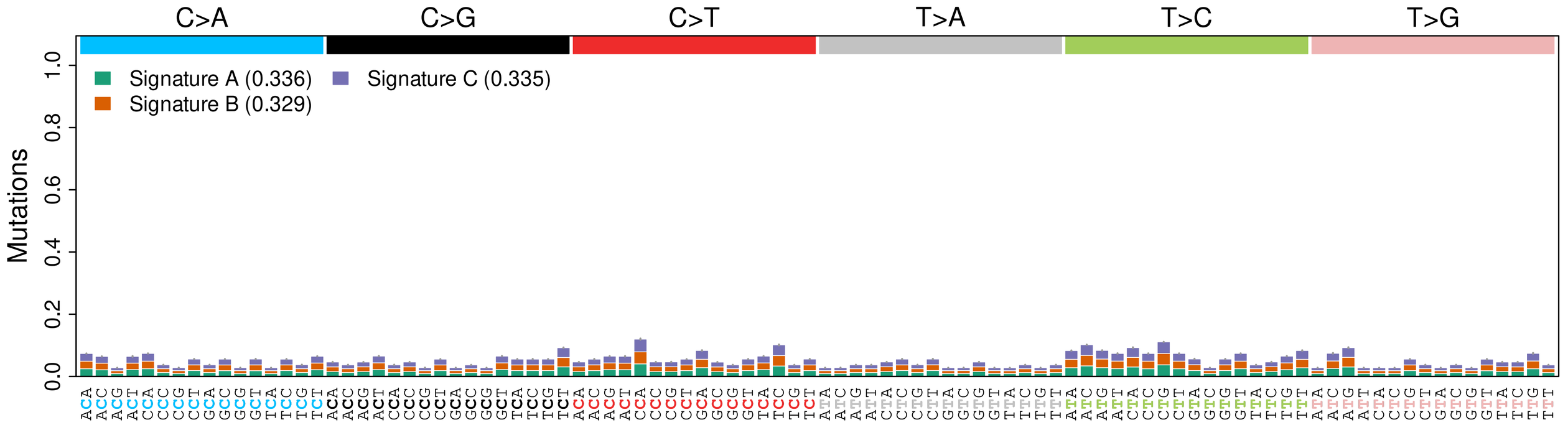
Reconstructed spectrum (cosine similarity = 0.155)

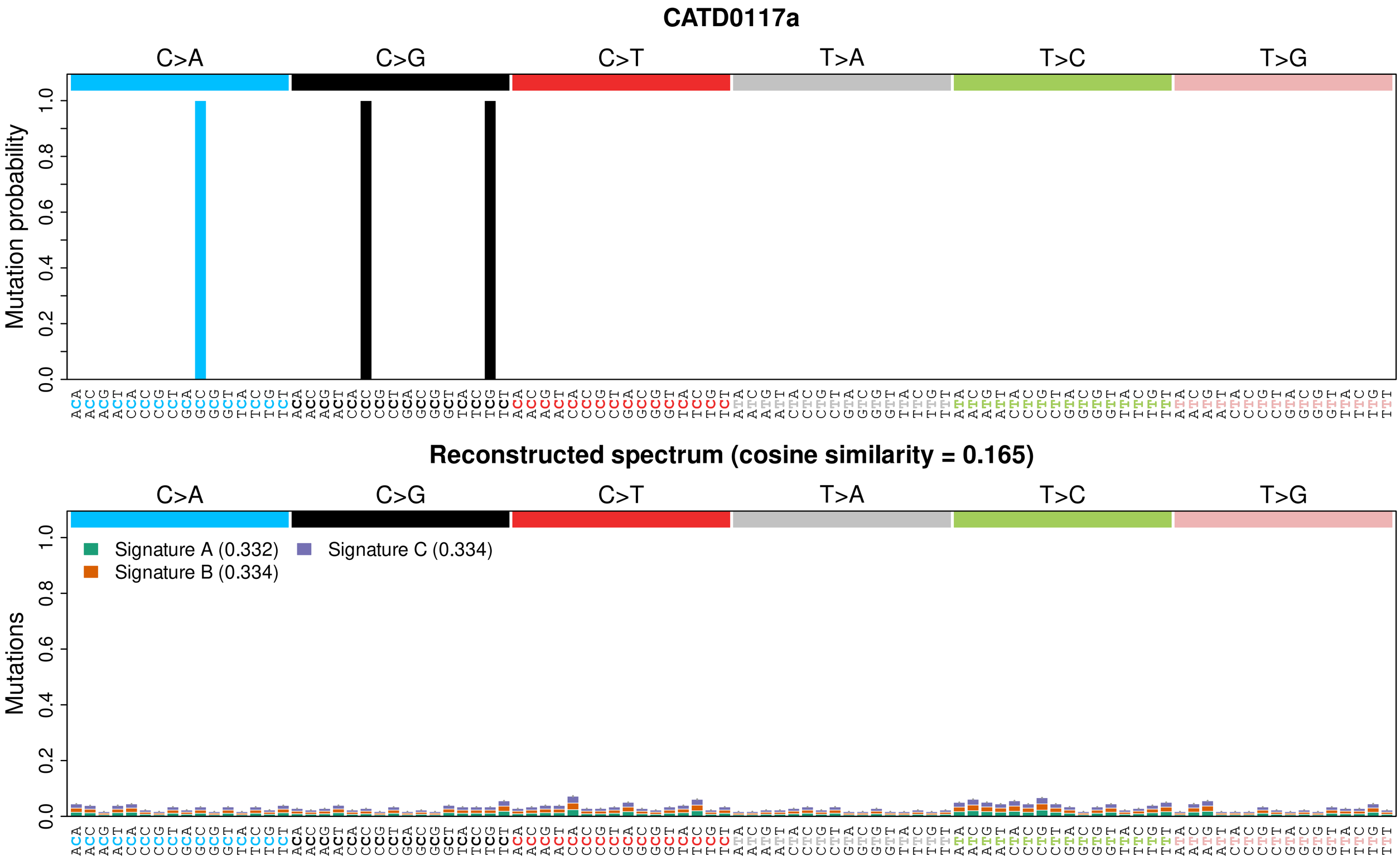


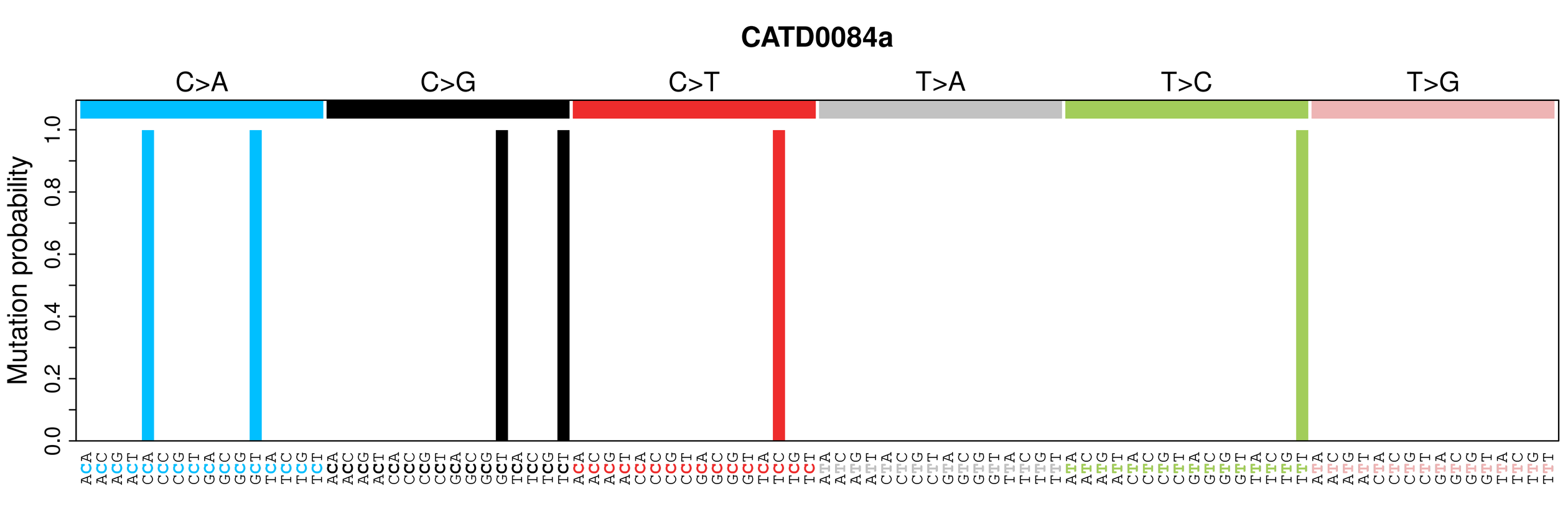
CATD0110a

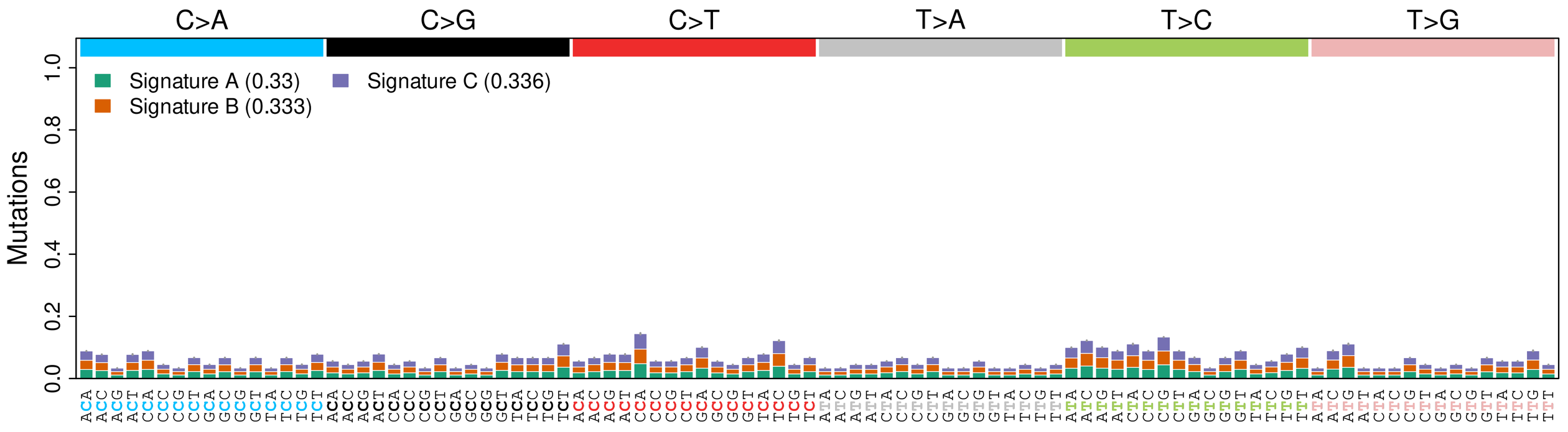


Reconstructed spectrum (cosine similarity = 0.338)

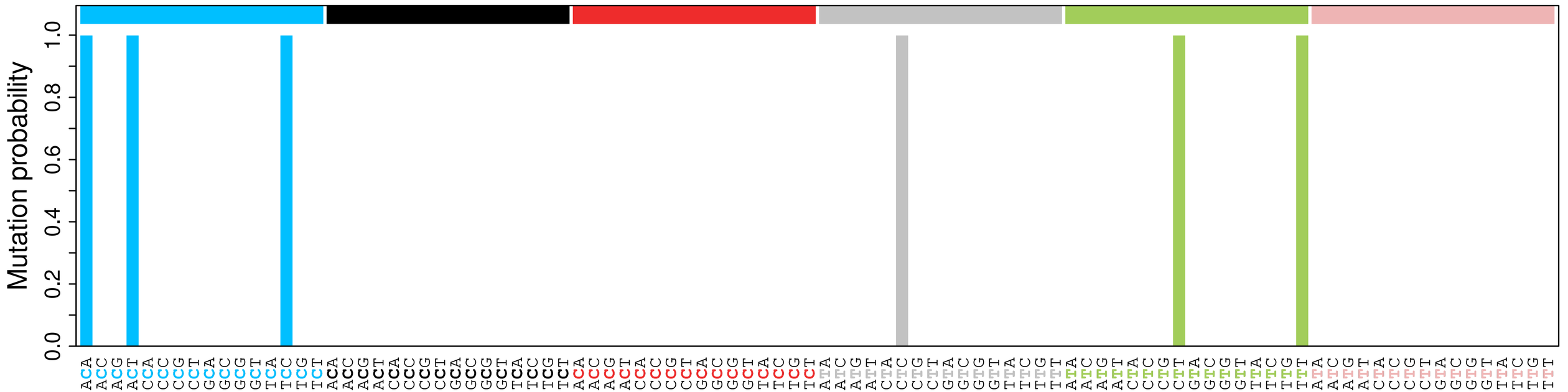



CATD0117a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0
Reconstructed spectrum (cosine similarity = 0.165)
Signature A (0.332)
Signature B (0.334)
Signature C (0.334)
Mutations

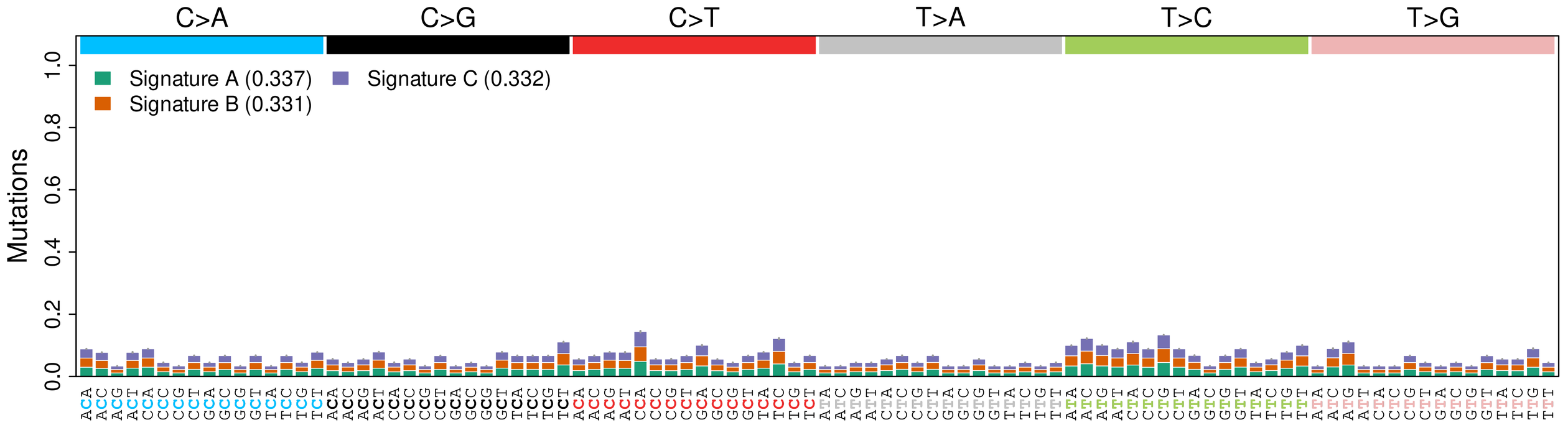

CATD0084a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0


Reconstructed spectrum (cosine similarity = 0.349)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.33)
Signature B (0.333)
Signature C (0.336)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

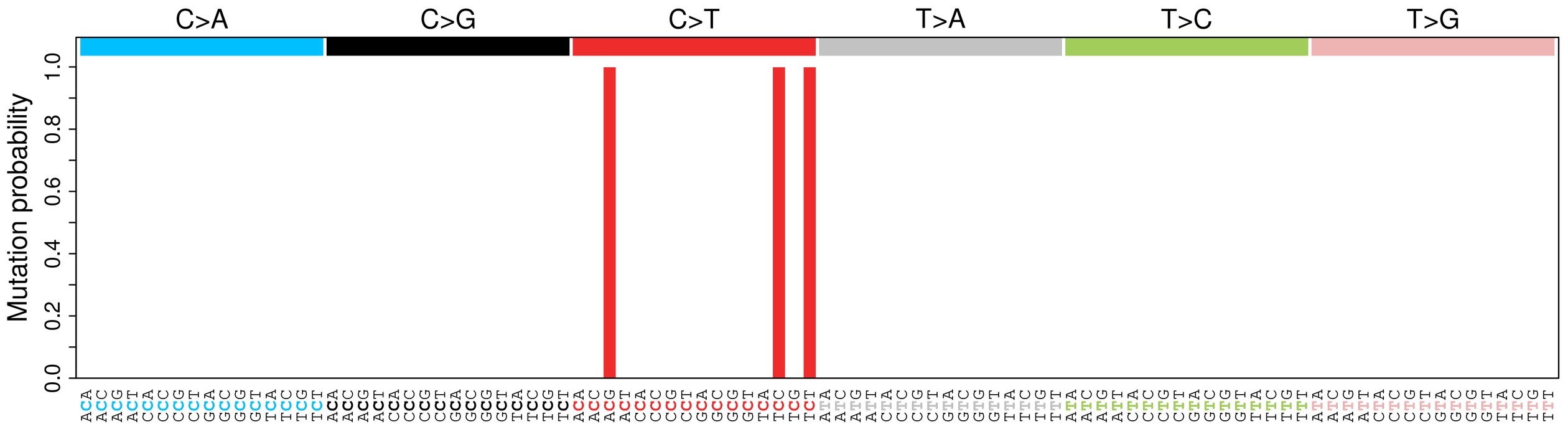
CATD0081a



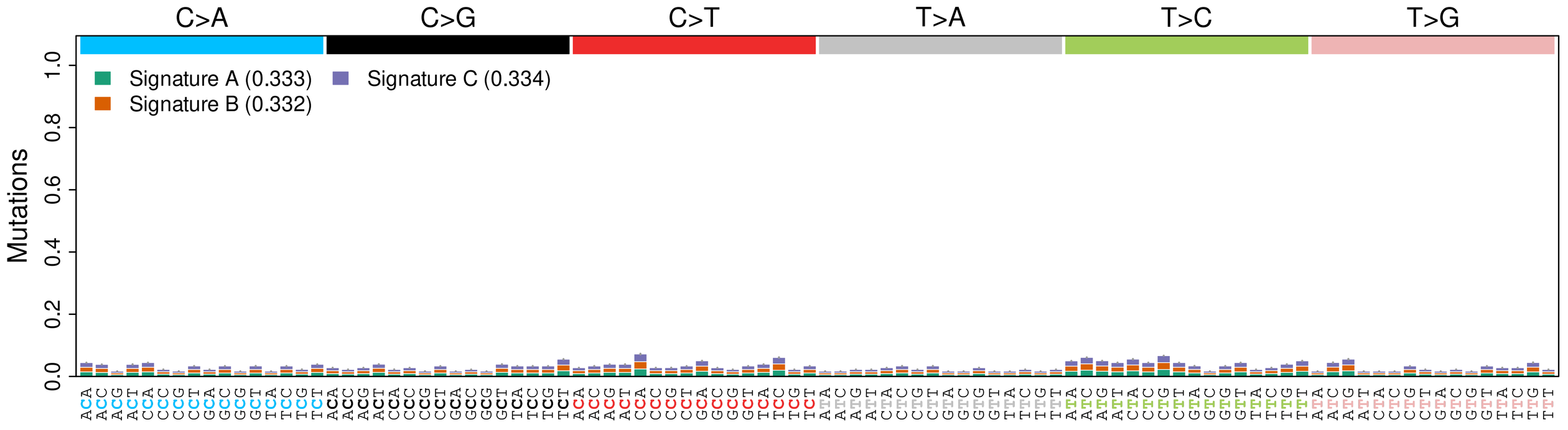
Reconstructed spectrum (cosine similarity = 0.301)

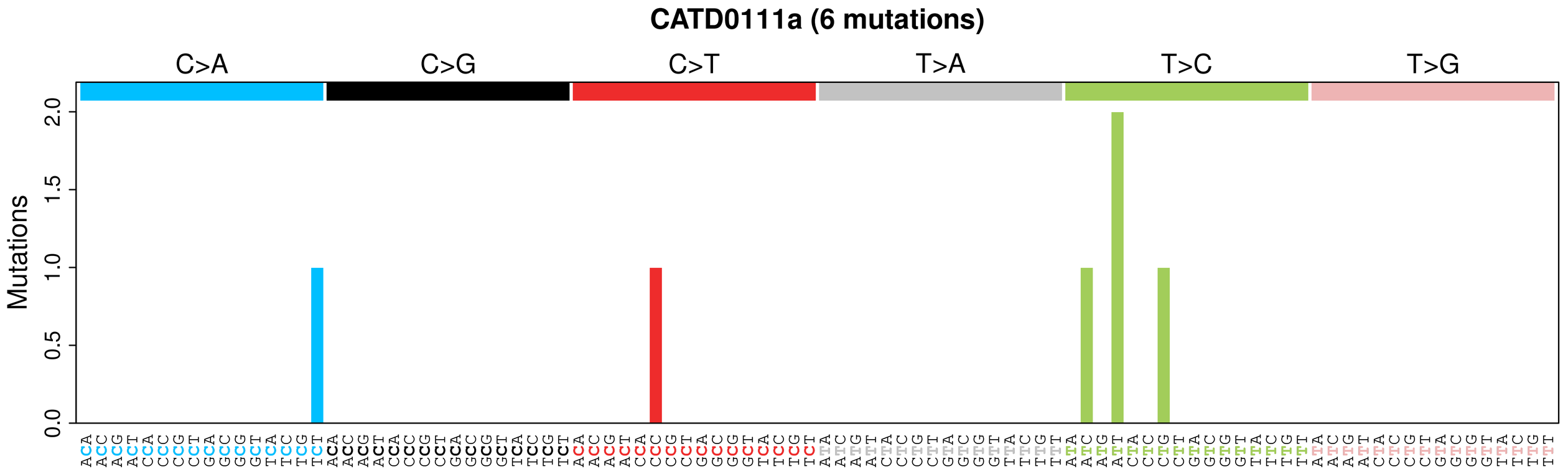


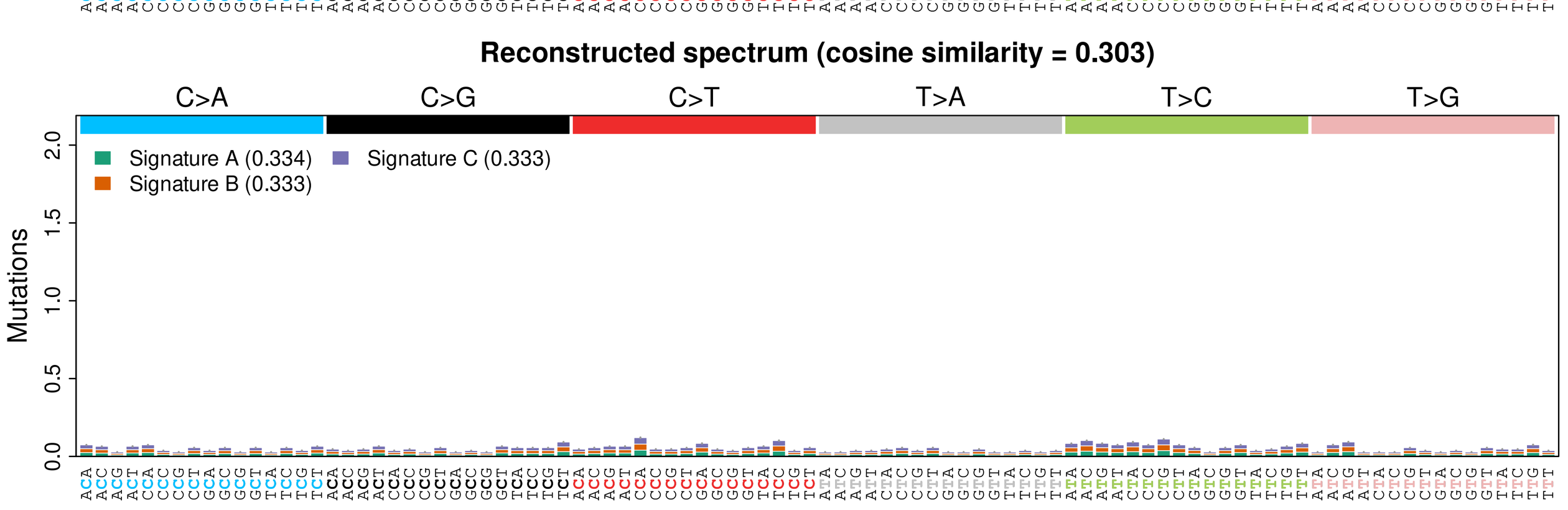
CATD0092a

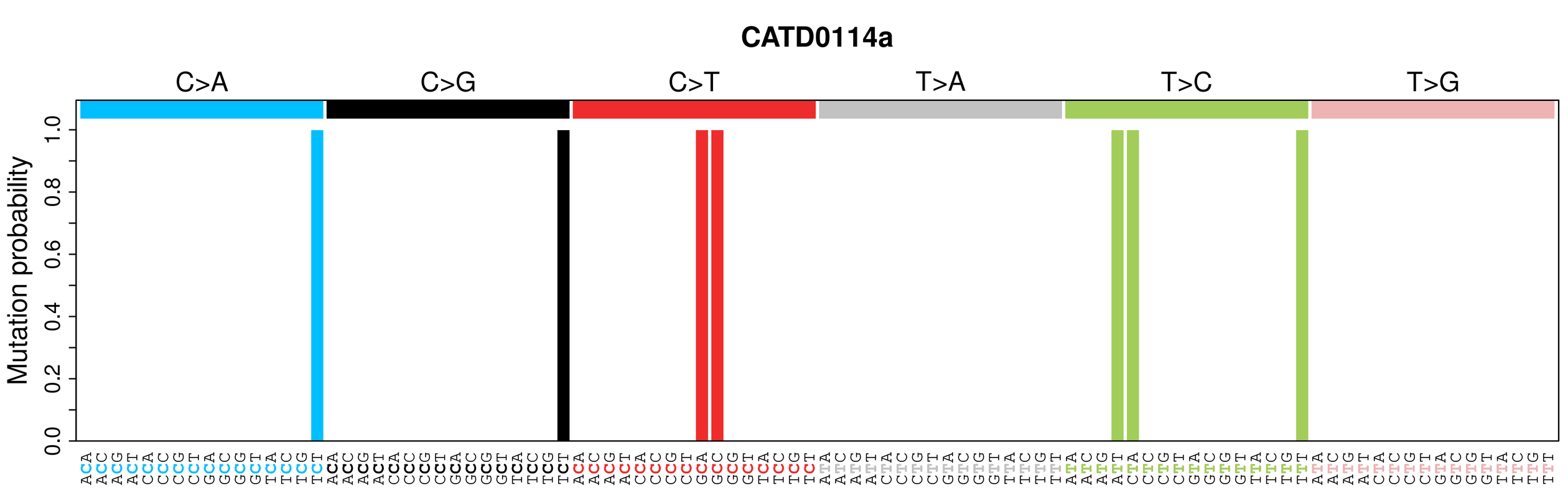


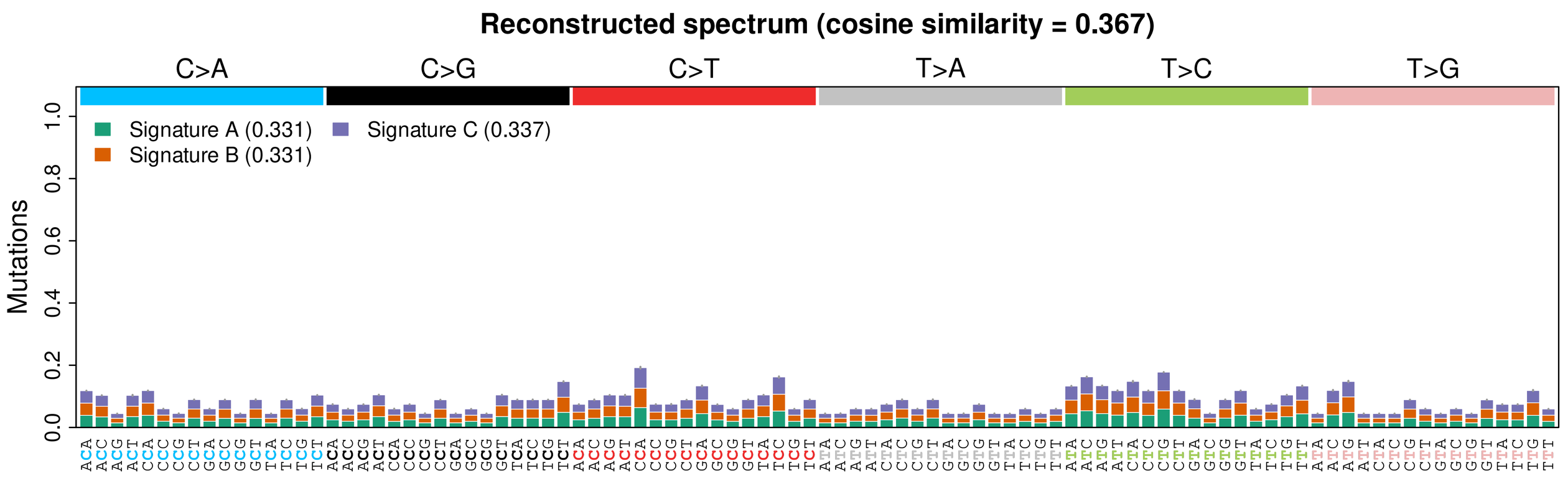
Reconstructed spectrum (cosine similarity = 0.233)

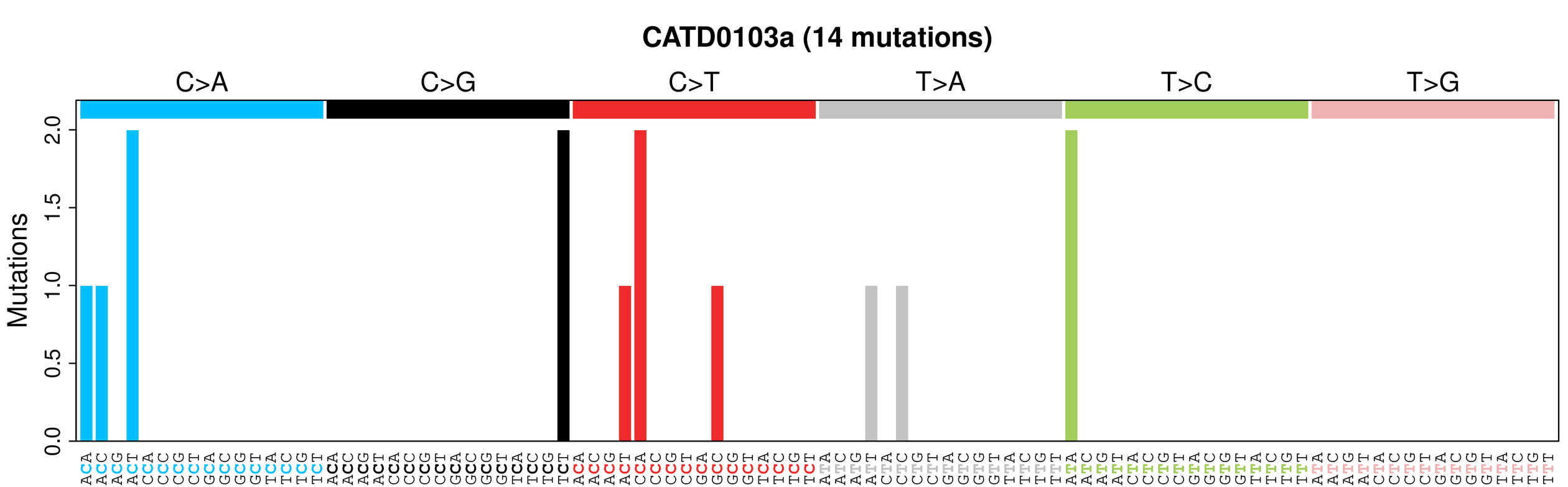


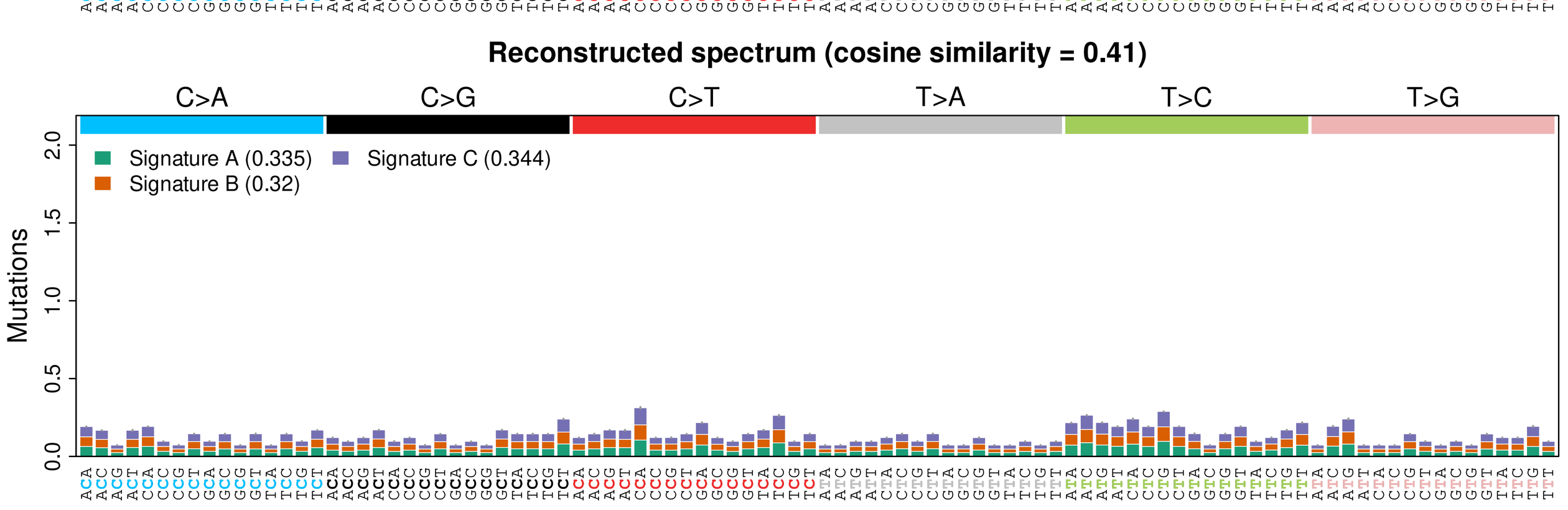

CATD0111a (6 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

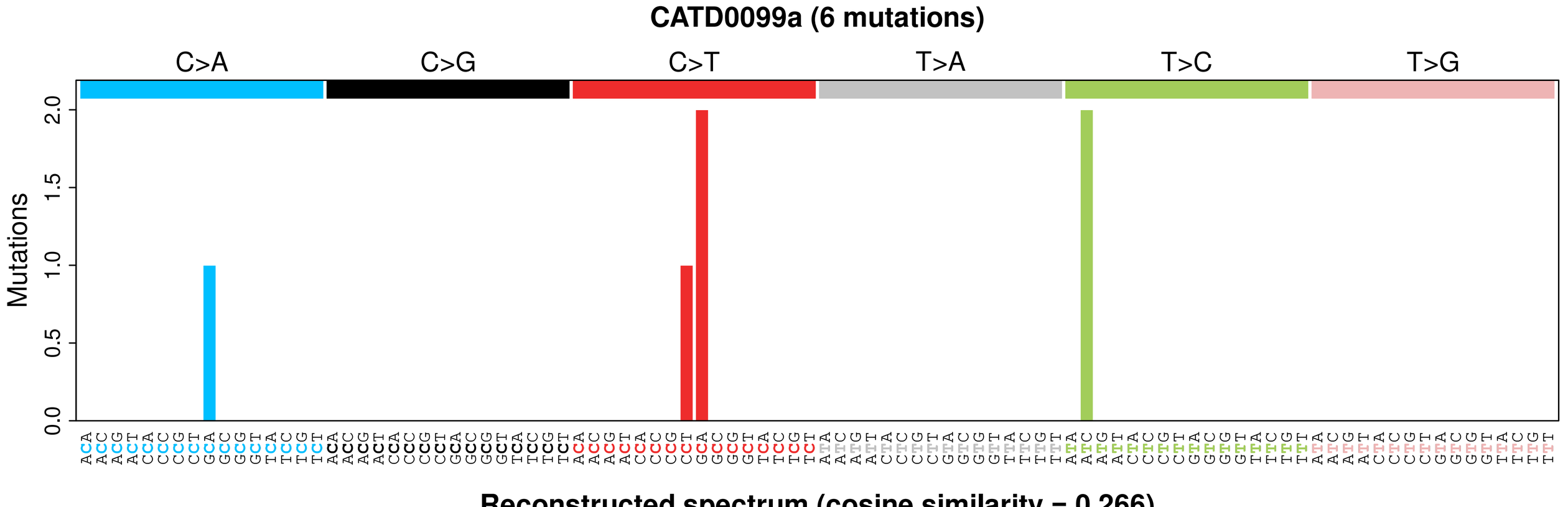

Reconstructed spectrum (cosine similarity = 0.303)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.334)
Signature B (0.333)
Signature C (0.333)
Mutations
0.0
0.5
1.0
1.5
2.0

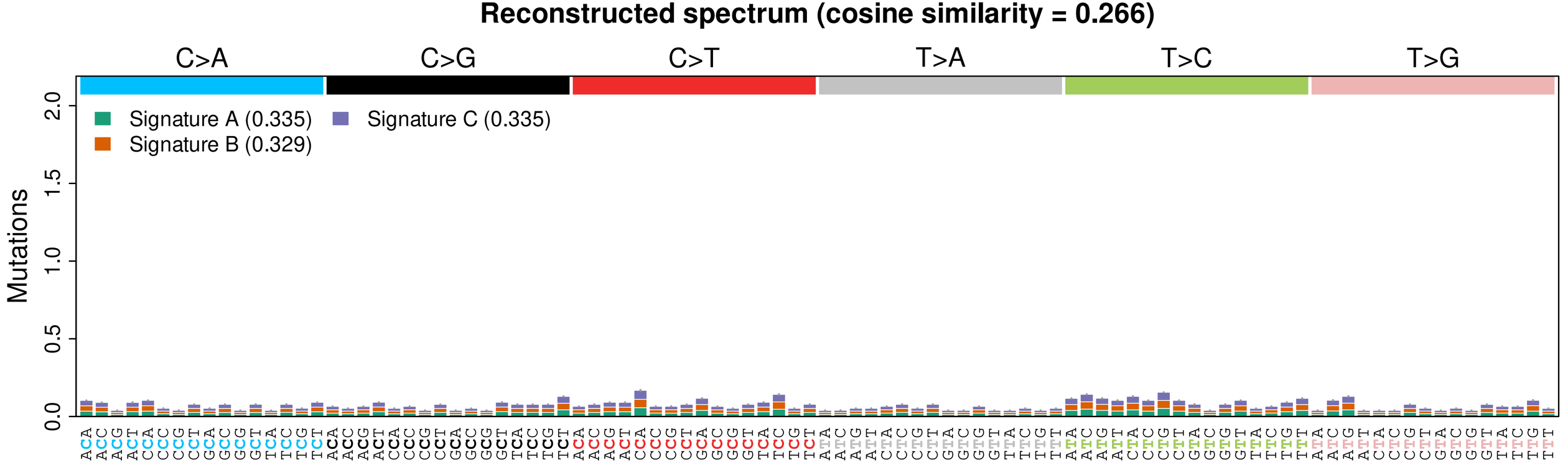

CATD0114a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0

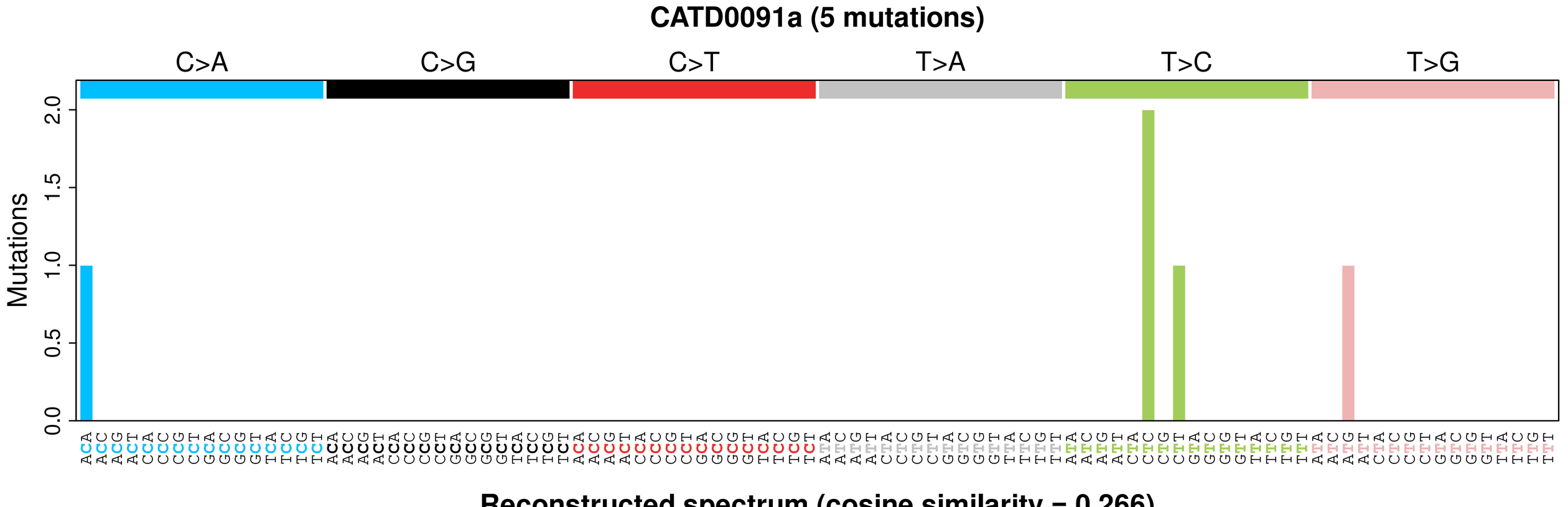

Reconstructed spectrum (cosine similarity = 0.367)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.331)
Signature B (0.331)
Signature C (0.337)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

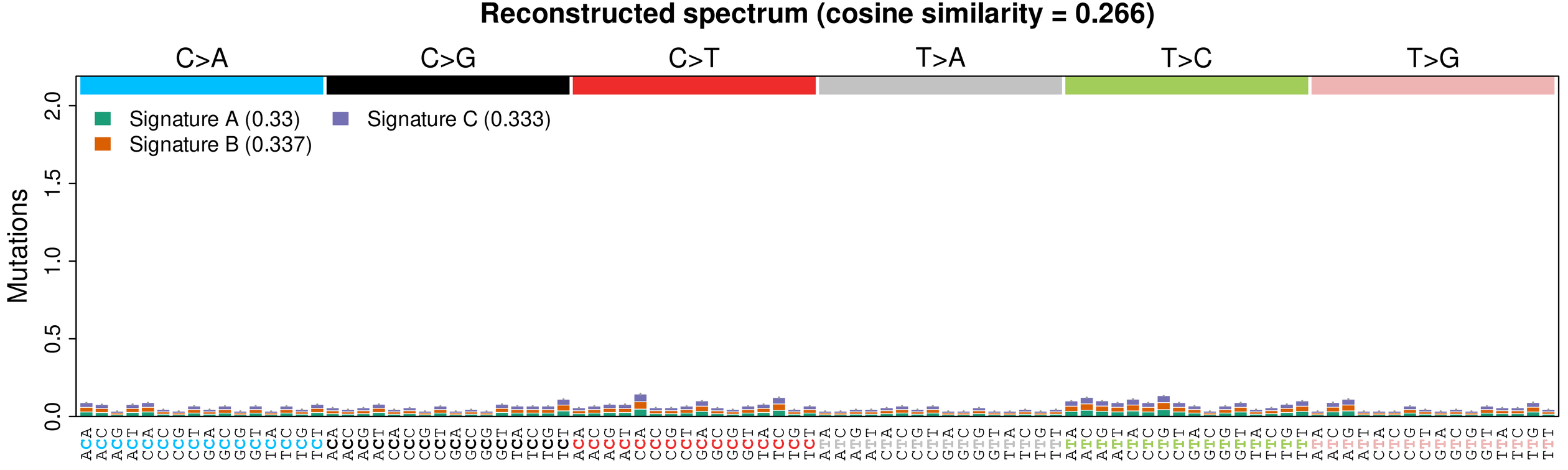

CATD0103a (14 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

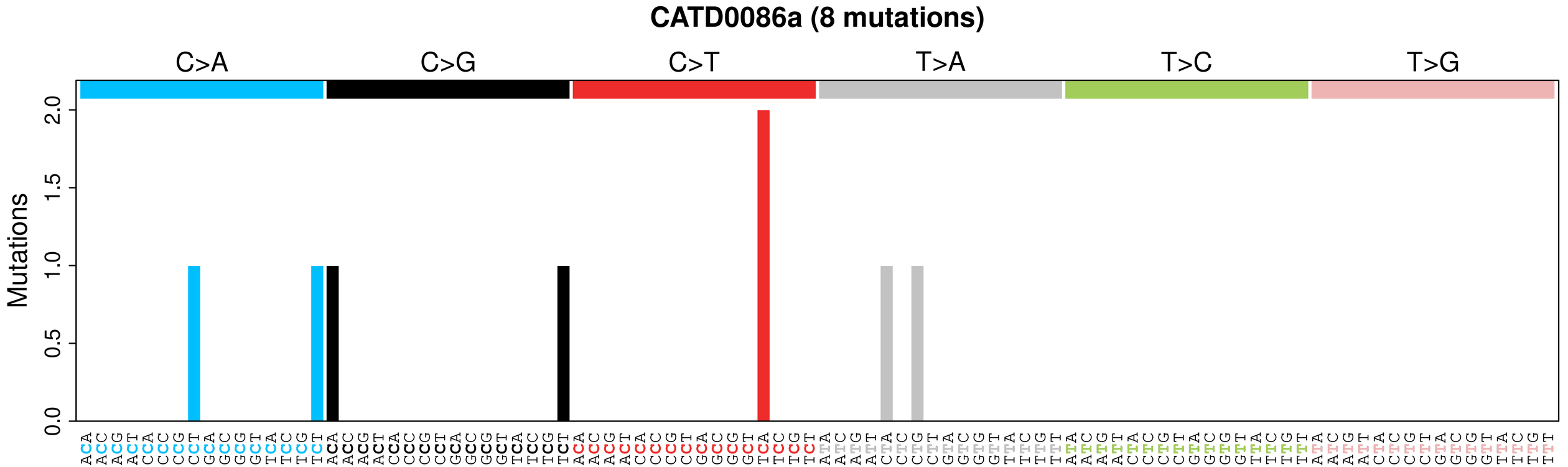

Reconstructed spectrum (cosine similarity = 0.41)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.335)
Signature B (0.32)
Signature C (0.344)
Mutations
0.0
0.5
1.0
1.5
2.0

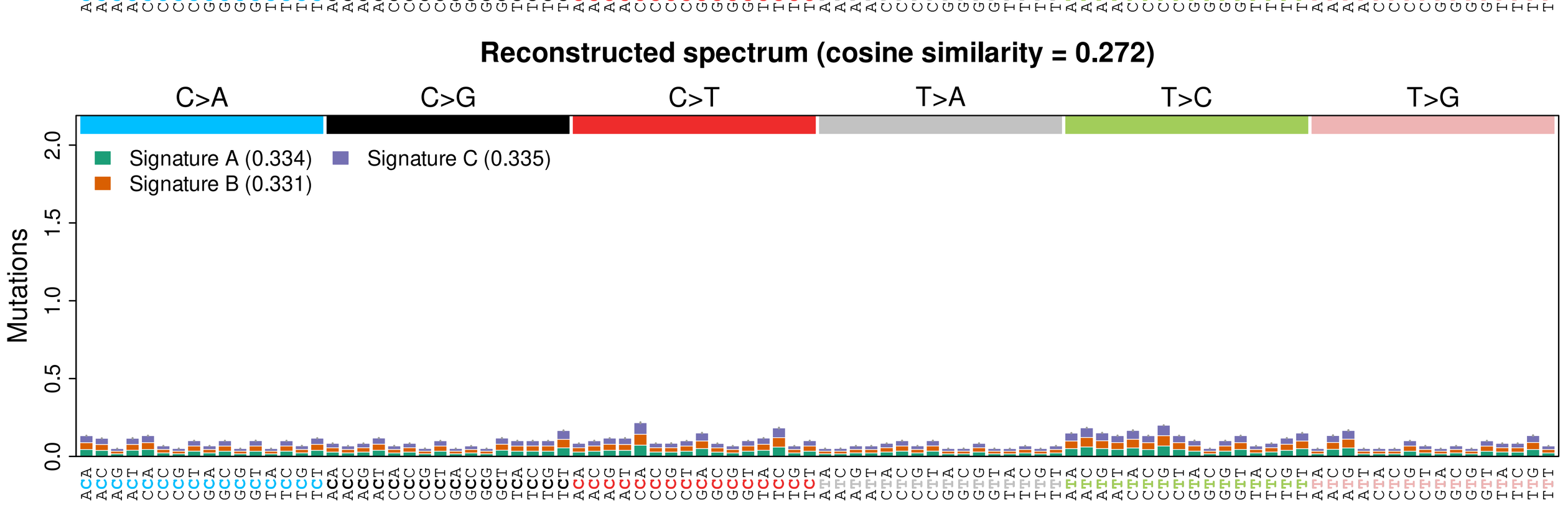

CATD0099a (6 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

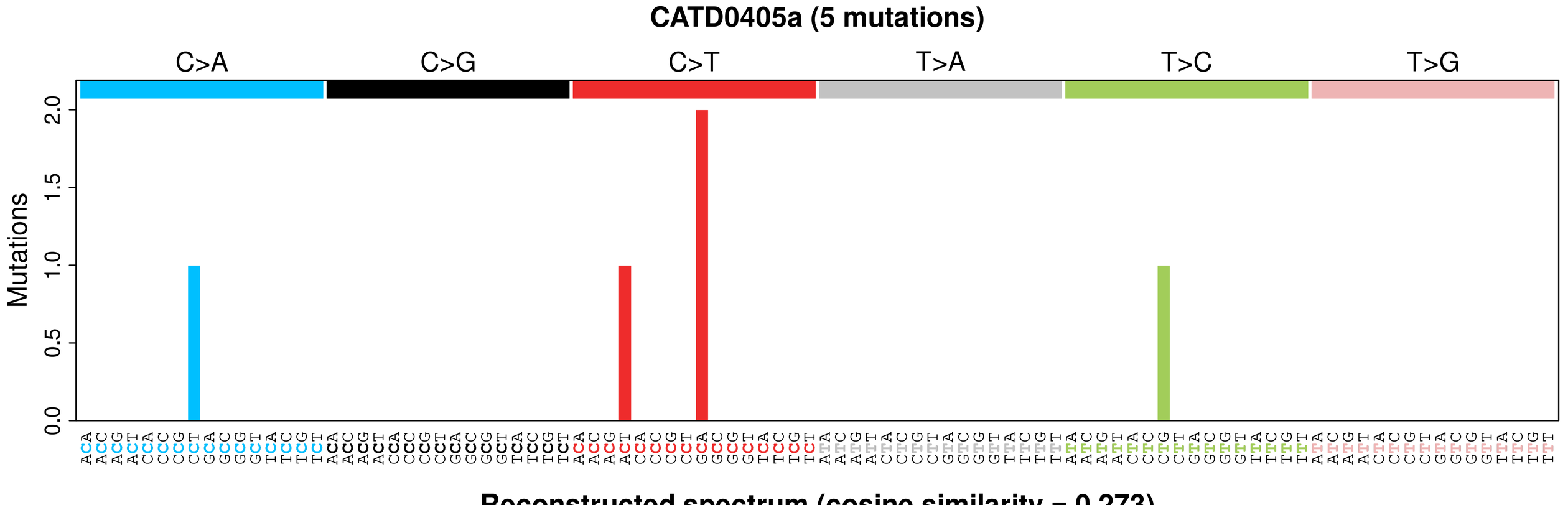

Reconstructed spectrum (cosine similarity = 0.266)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.335)
Signature B (0.329)
Signature C (0.335)
Mutations
0.0
0.5
1.0
1.5
2.0

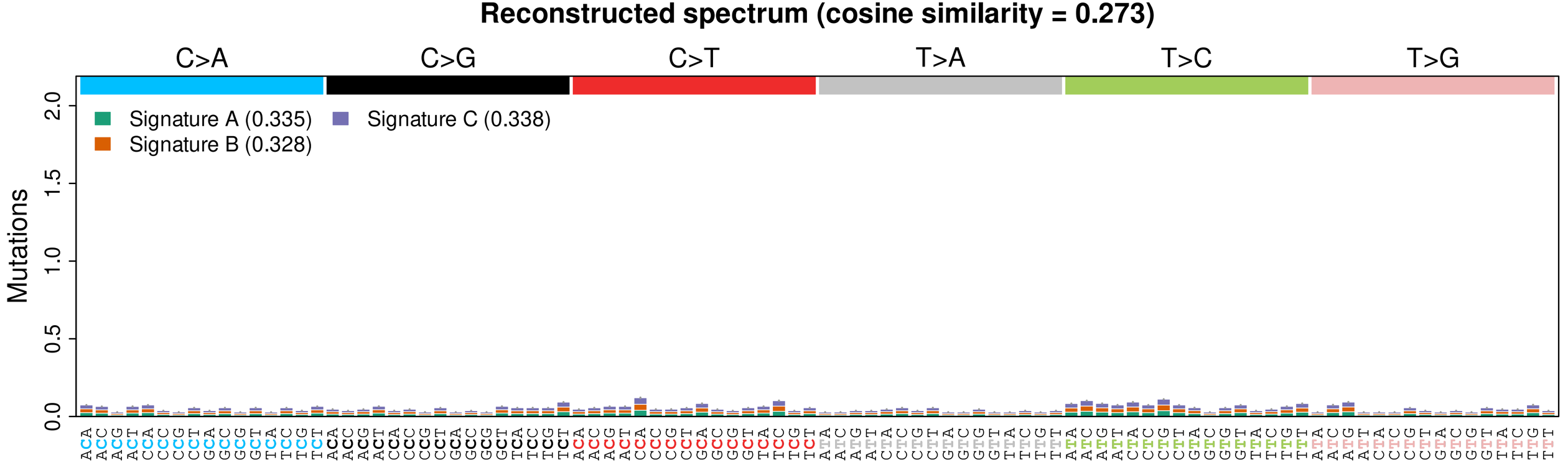

CATD0091a (5 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

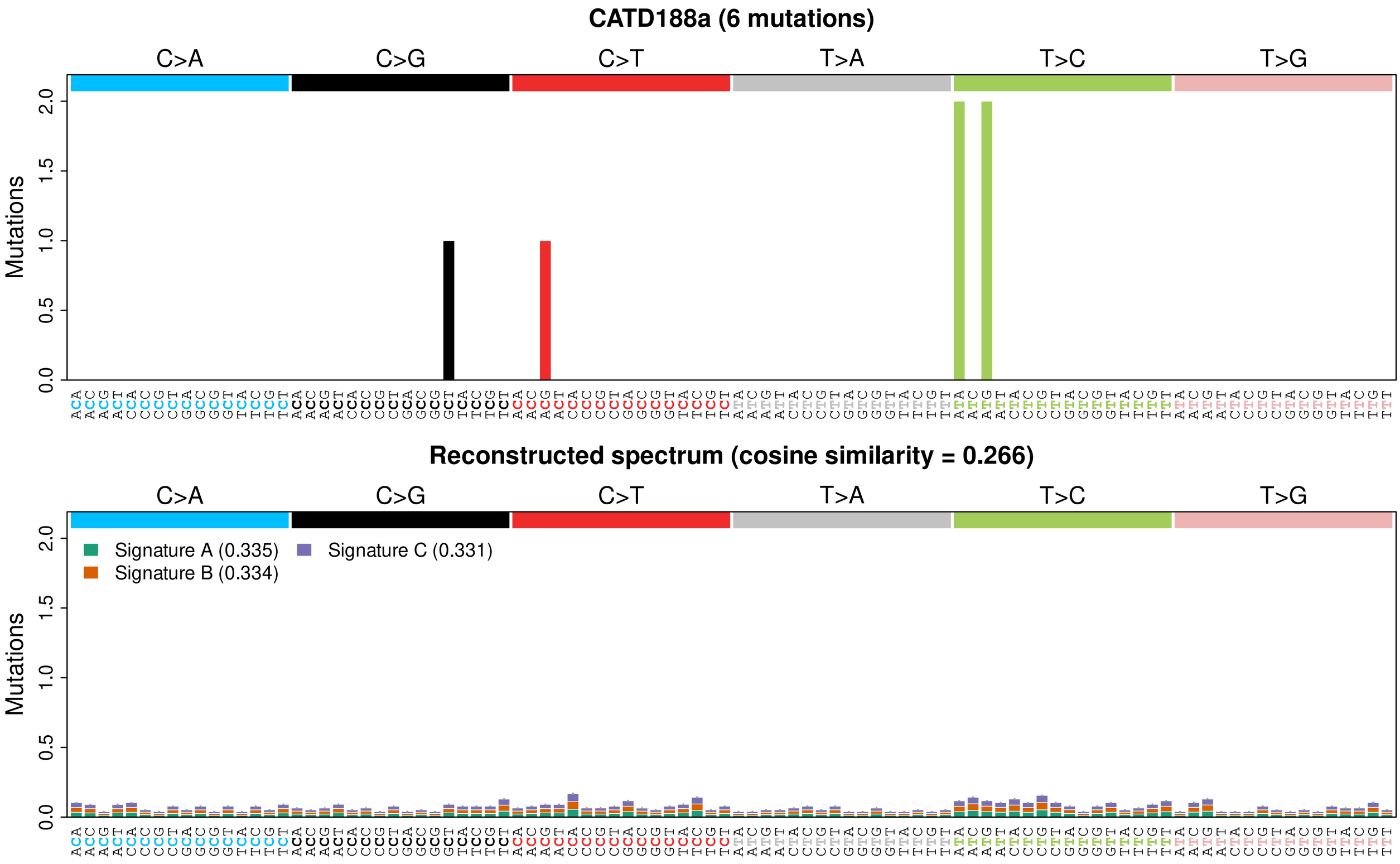

Reconstructed spectrum (cosine similarity = 0.266)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.33)
Signature B (0.337)
Signature C (0.333)
Mutations
0.0
0.5
1.0
1.5
2.0

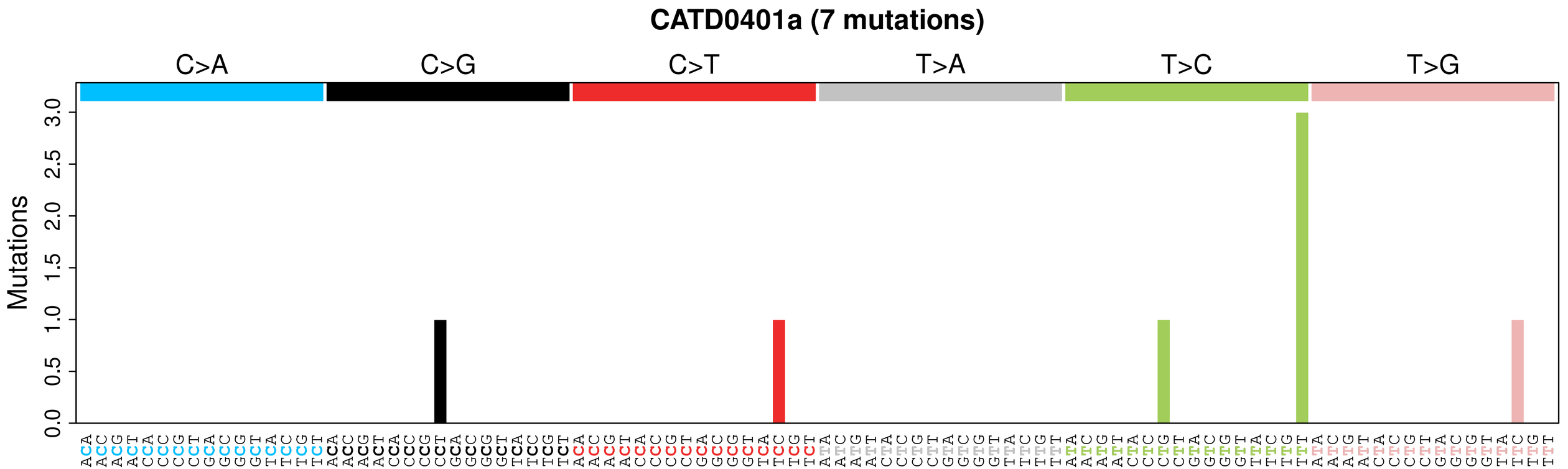

CATD0086a (8 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

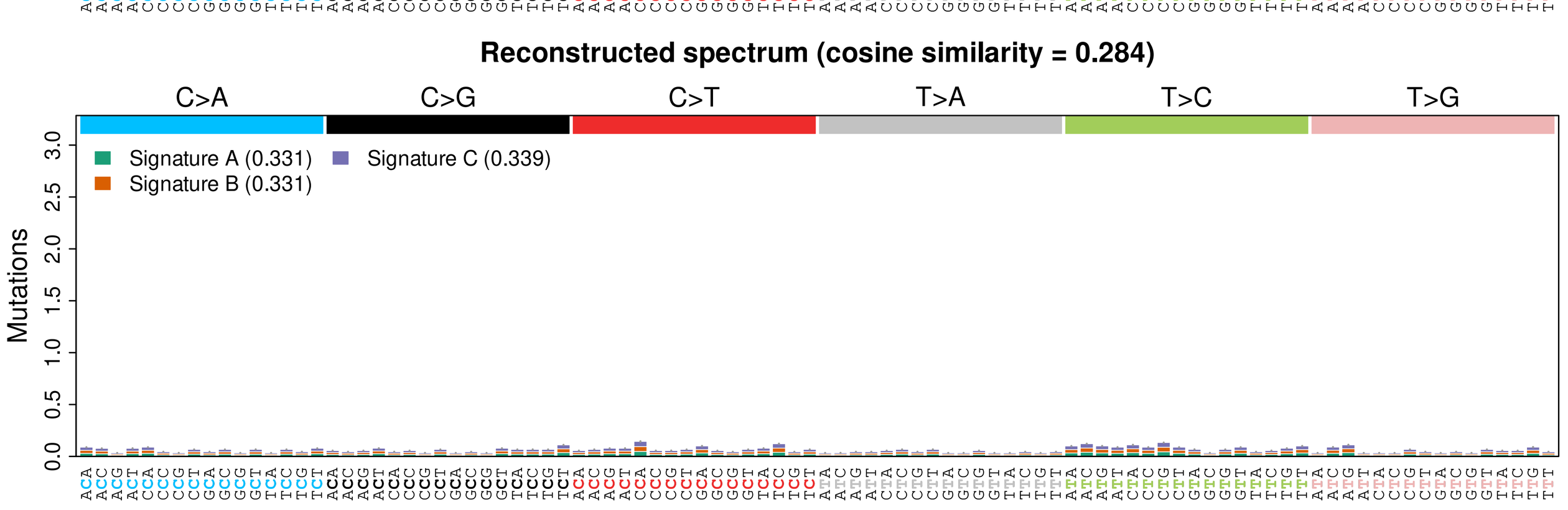

Reconstructed spectrum (cosine similarity = 0.272)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.334)
Signature B (0.331)
Signature C (0.335)
Mutations
0.0
0.5
1.0
1.5
2.0

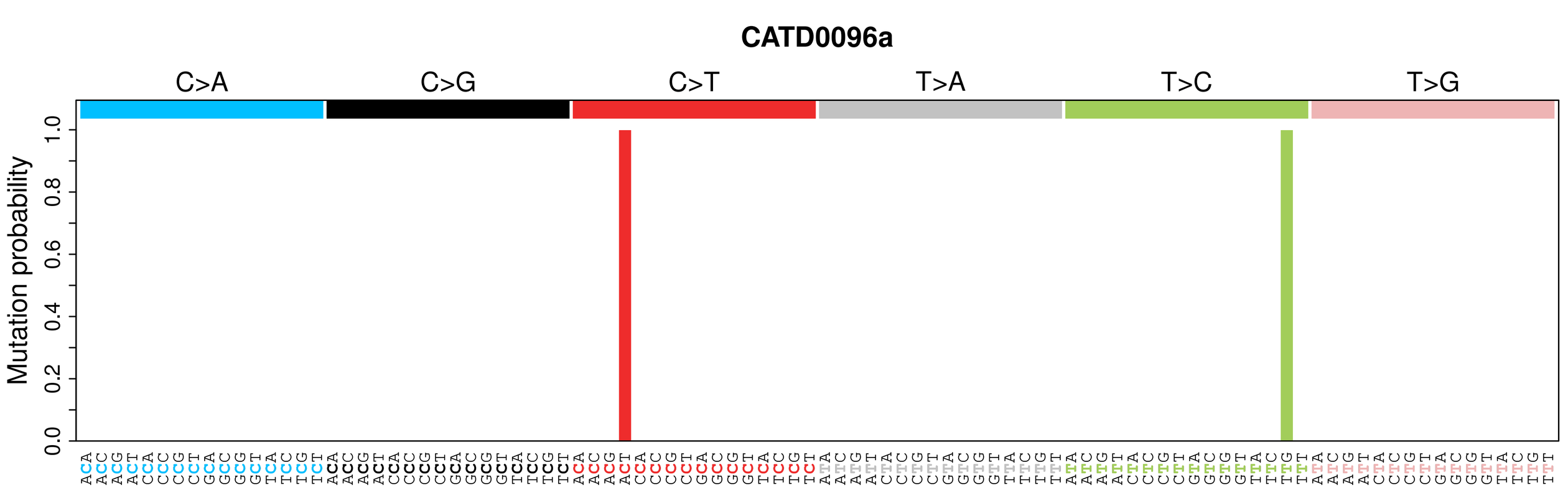

CATD0405a (5 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

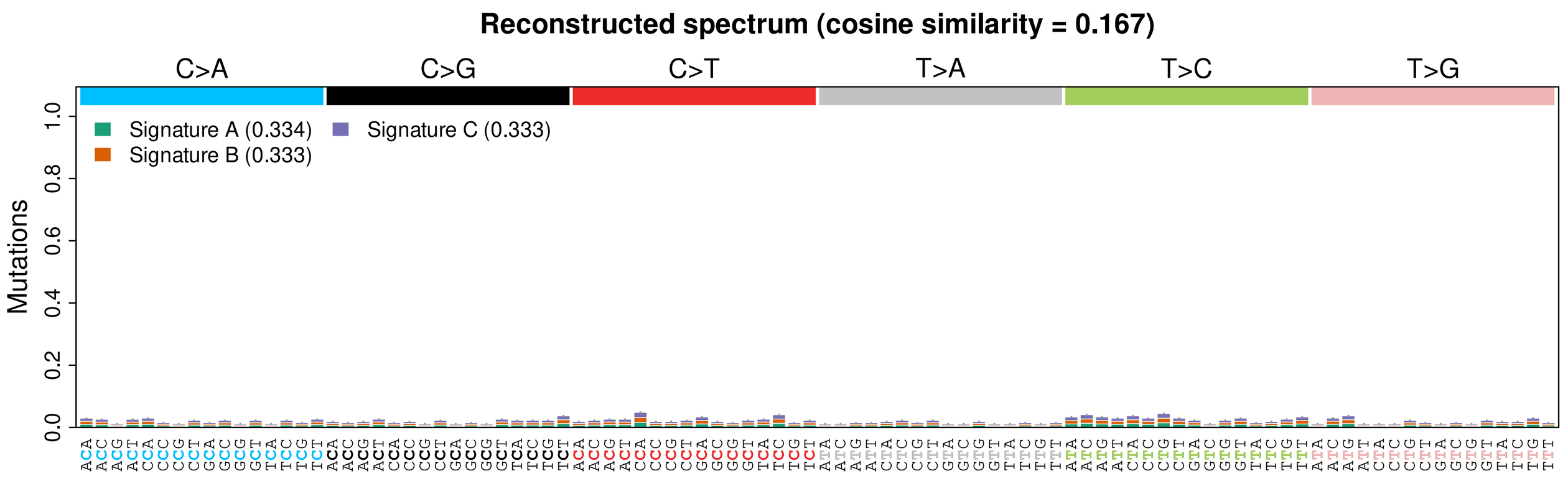

Reconstructed spectrum (cosine similarity = 0.273)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.335)
Signature B (0.328)
Signature C (0.338)
Mutations
0.0
0.5
1.0
1.5
2.0

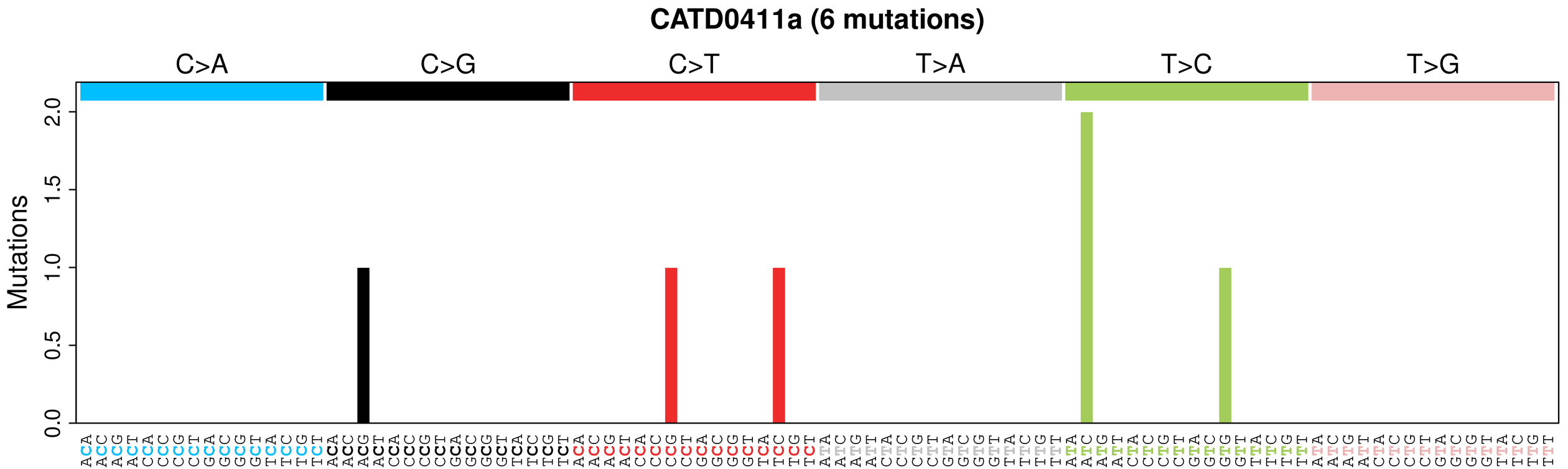

CATD188a (6 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0
Reconstructed spectrum (cosine similarity = 0.266)
Signature A (0.335)
Signature B (0.334)
Signature C (0.331)

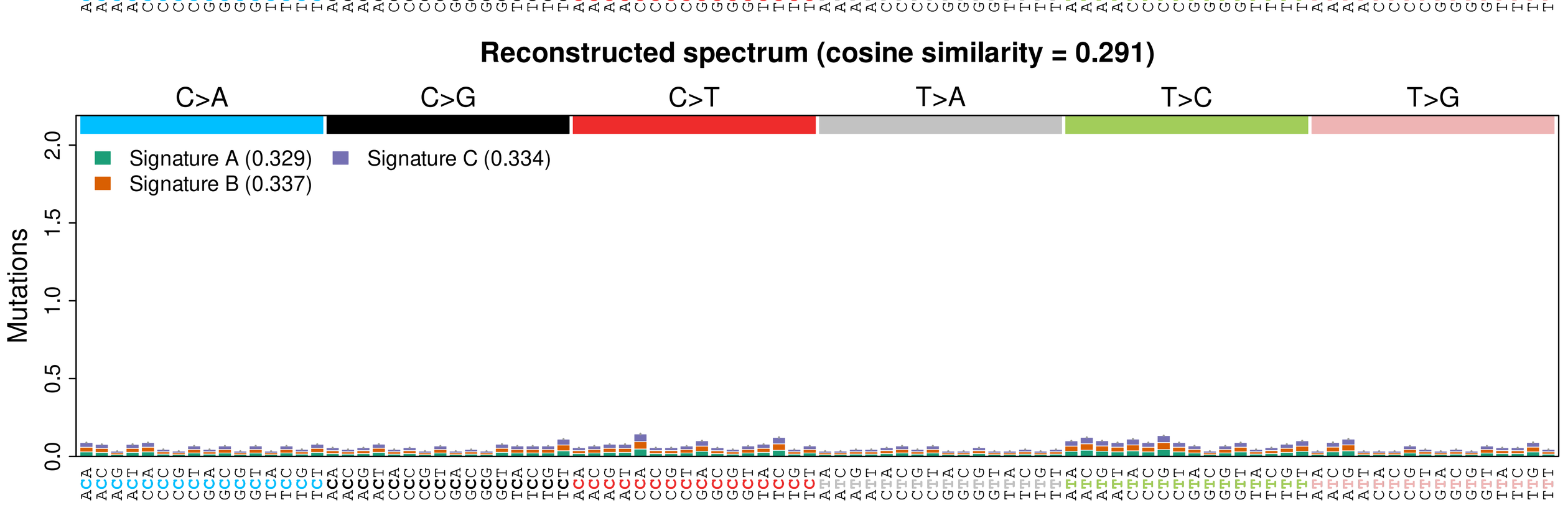

CATD0401a (7 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0
2.5
3.0


Reconstructed spectrum (cosine similarity = 0.284)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.331)
Signature B (0.331)
Signature C (0.339)
Mutations
0.0
0.5
1.0
1.5
2.0
2.5
3.0

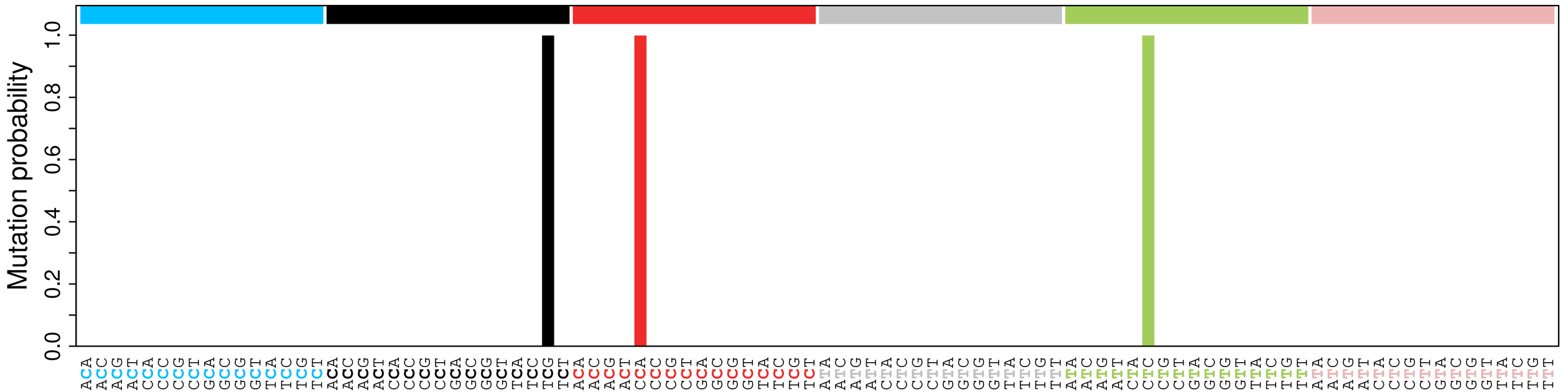

CATD0096a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0


Reconstructed spectrum (cosine similarity = 0.167)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.334)
Signature B (0.333)
Signature C (0.333)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

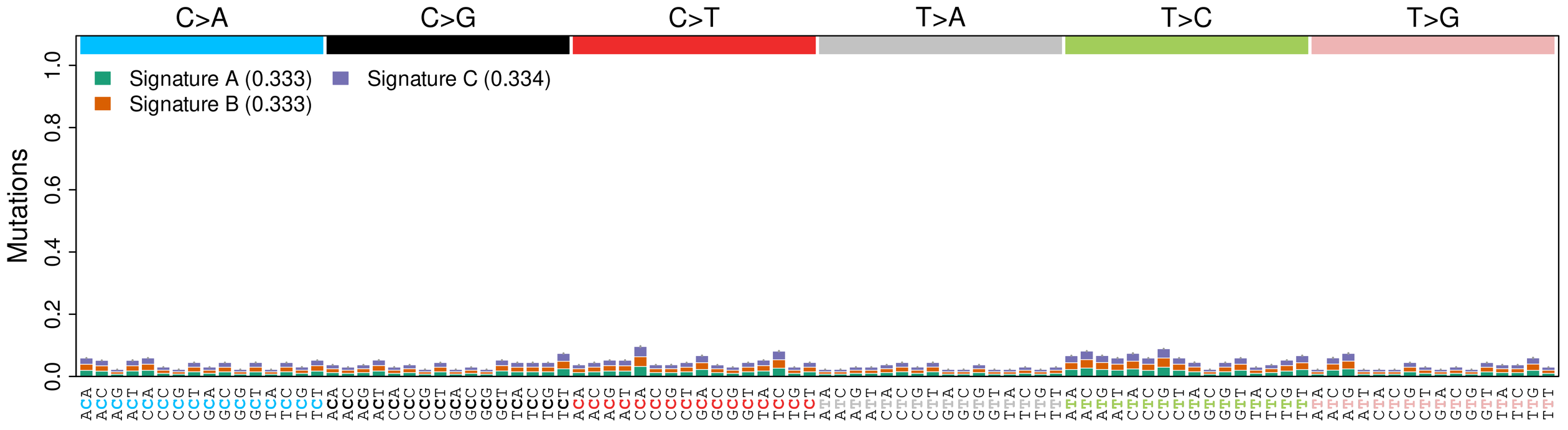

CATD0411a (6 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.291)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.329)
Signature B (0.337)
Signature C (0.334)
Mutations
0.0
0.5
1.0
1.5
2.0

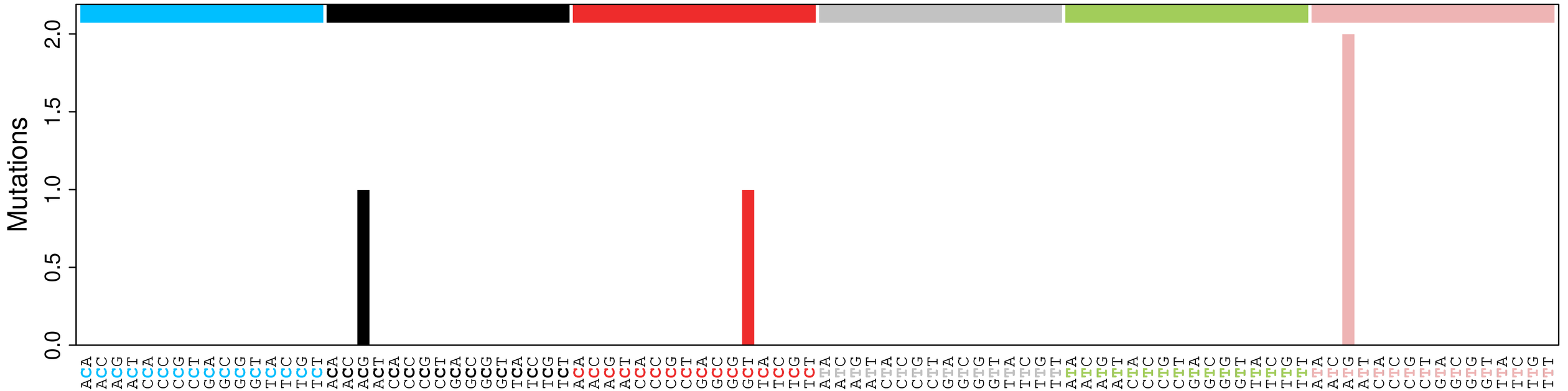
CATD0113a



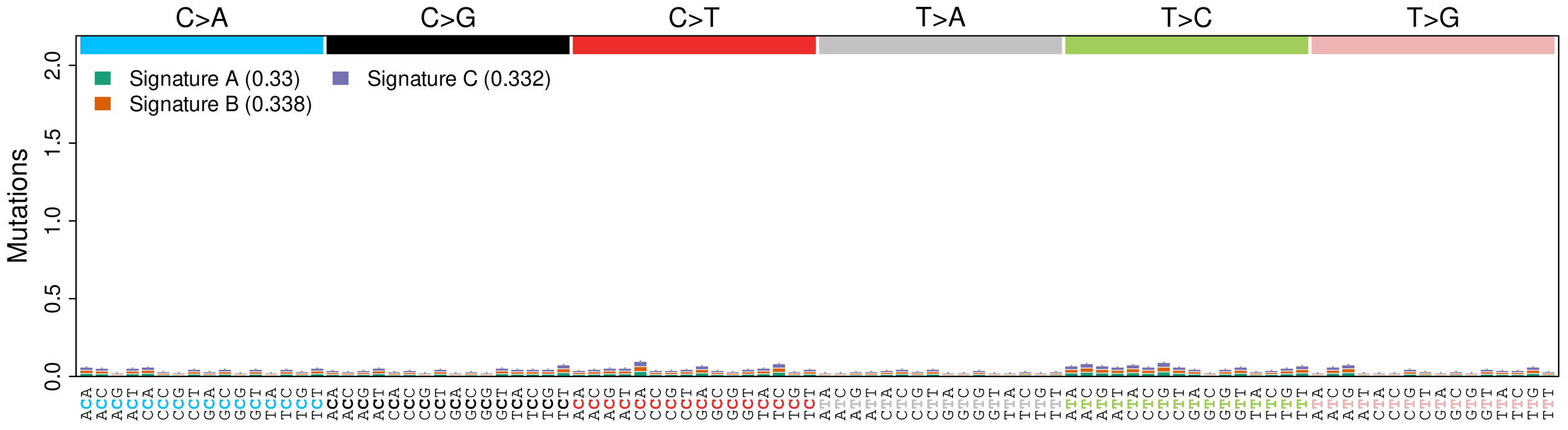
Reconstructed spectrum (cosine similarity = 0.261)



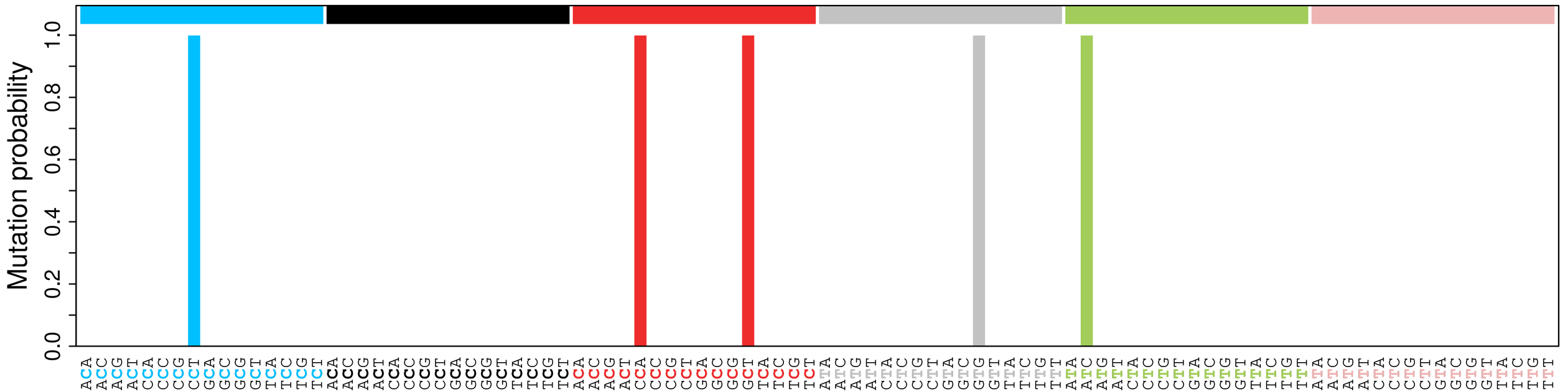
CATD0403a (4 mutations)



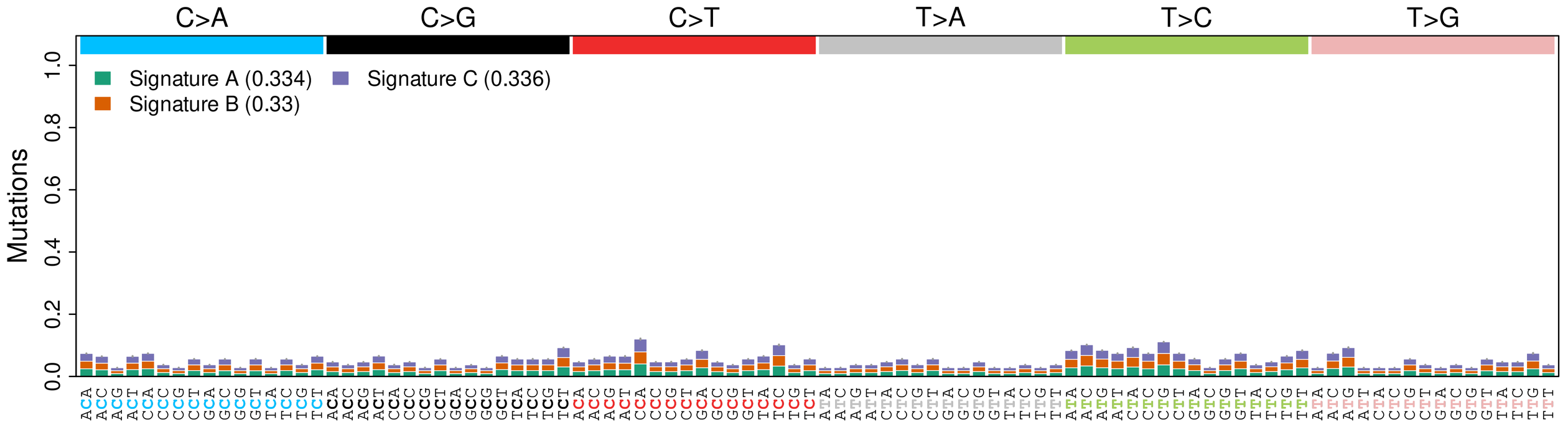
Reconstructed spectrum (cosine similarity = 0.212)

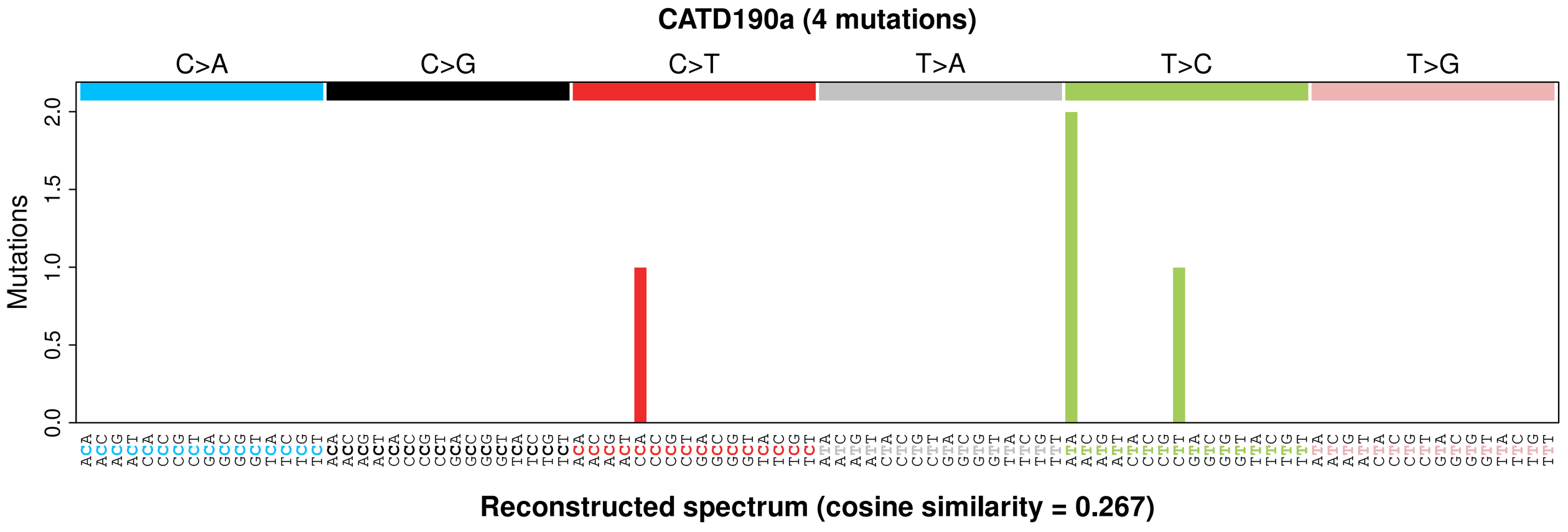


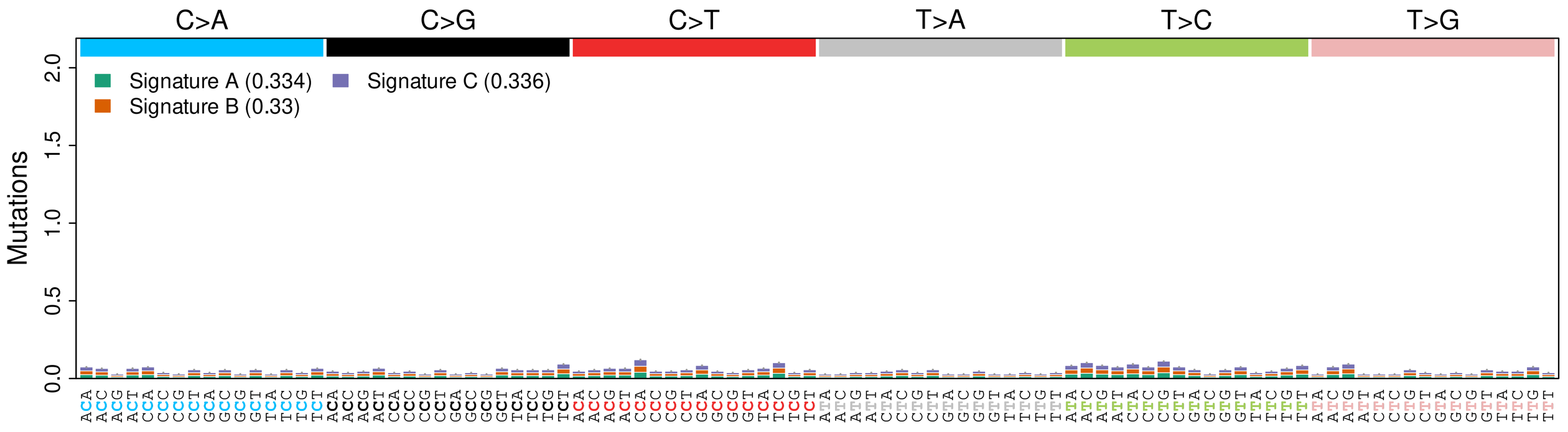
CATD0085a

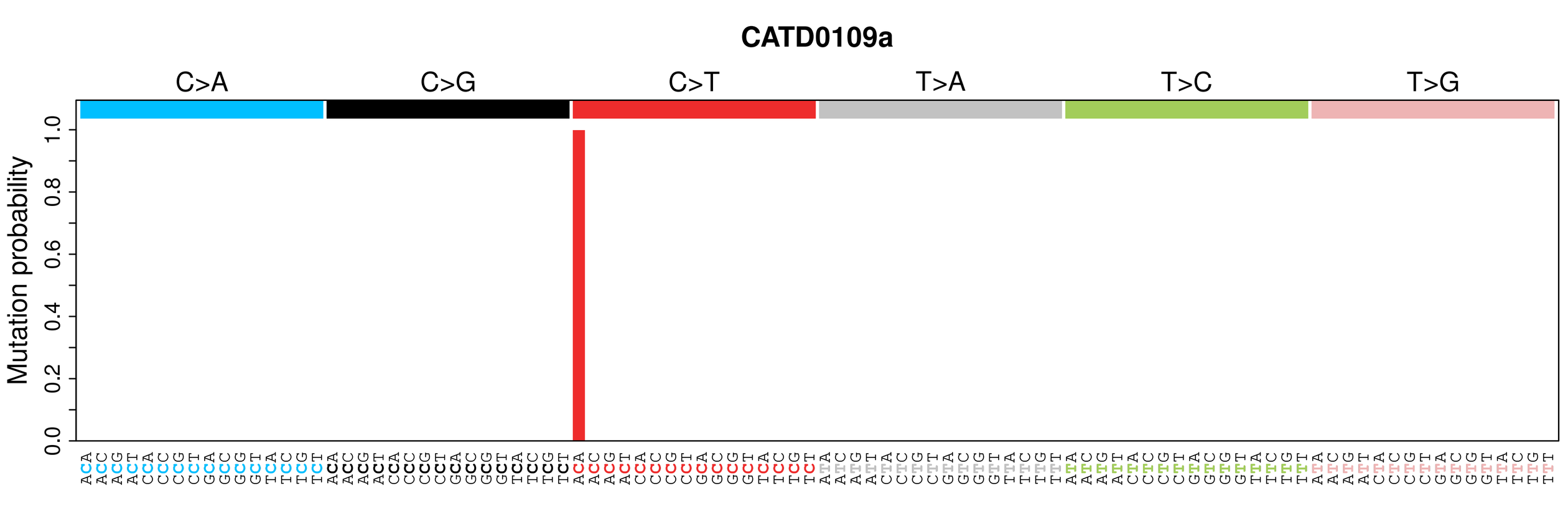


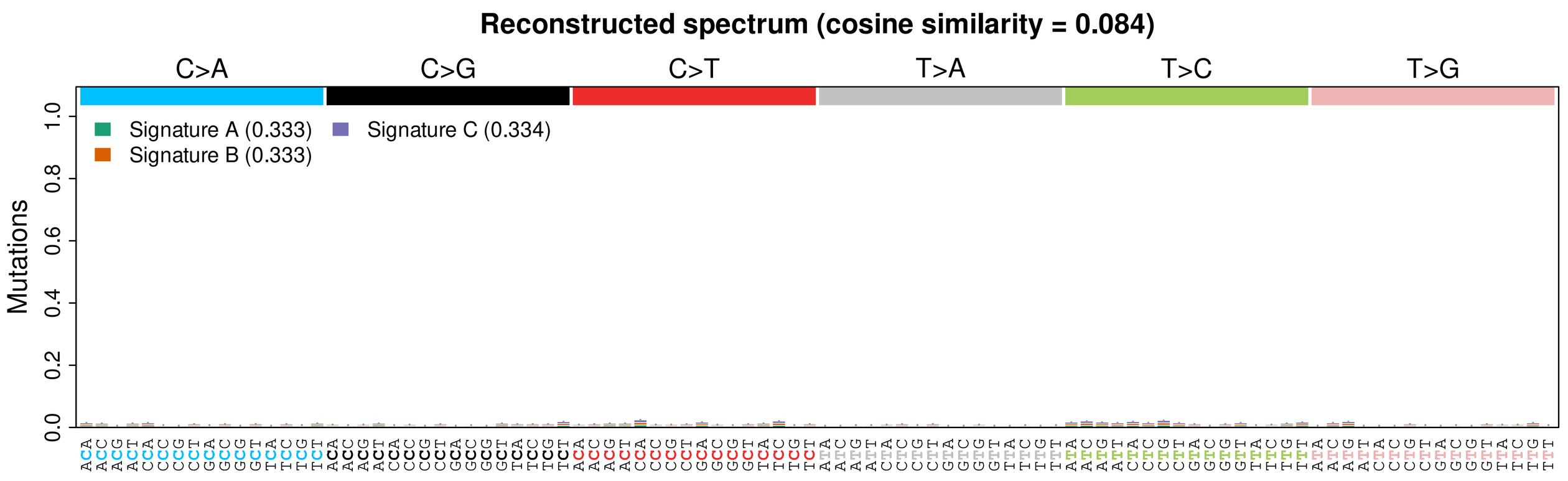
Reconstructed spectrum (cosine similarity = 0.308)

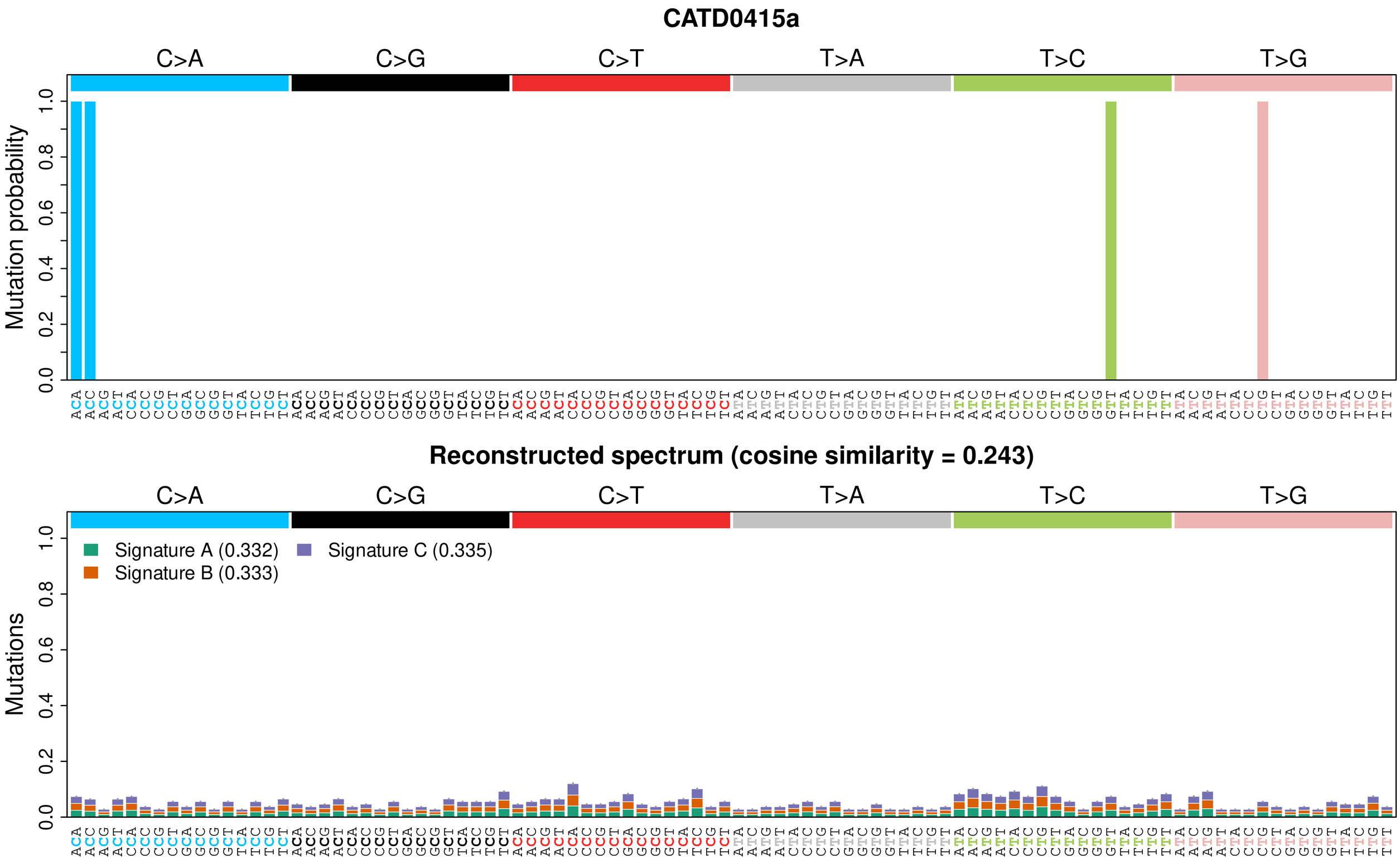



CATD190a (4 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

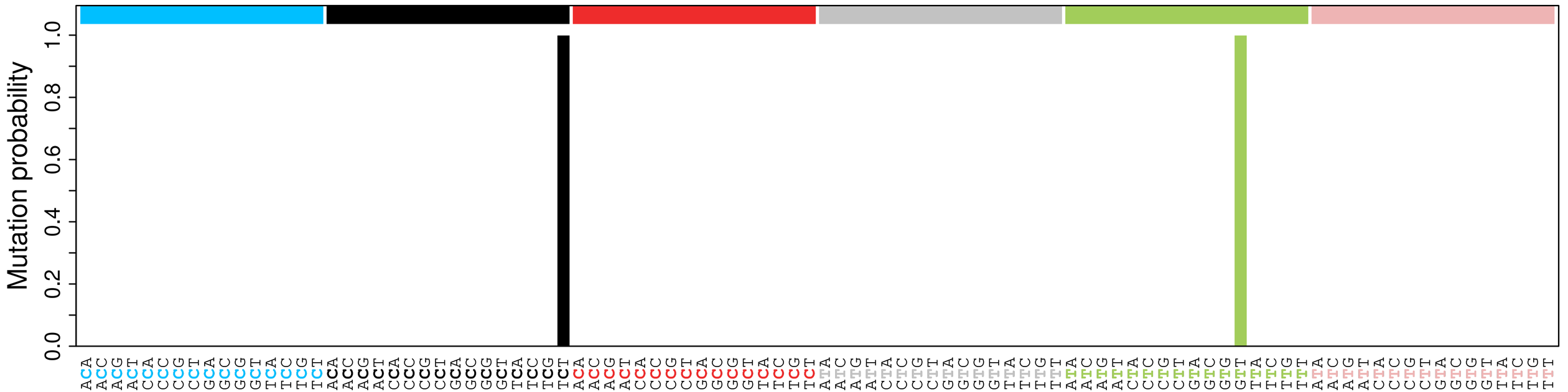

Reconstructed spectrum (cosine similarity = 0.267)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.334)
Signature B (0.33)
Signature C (0.336)
Mutations
0.0
0.5
1.0
1.5
2.0


CATD0109a
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

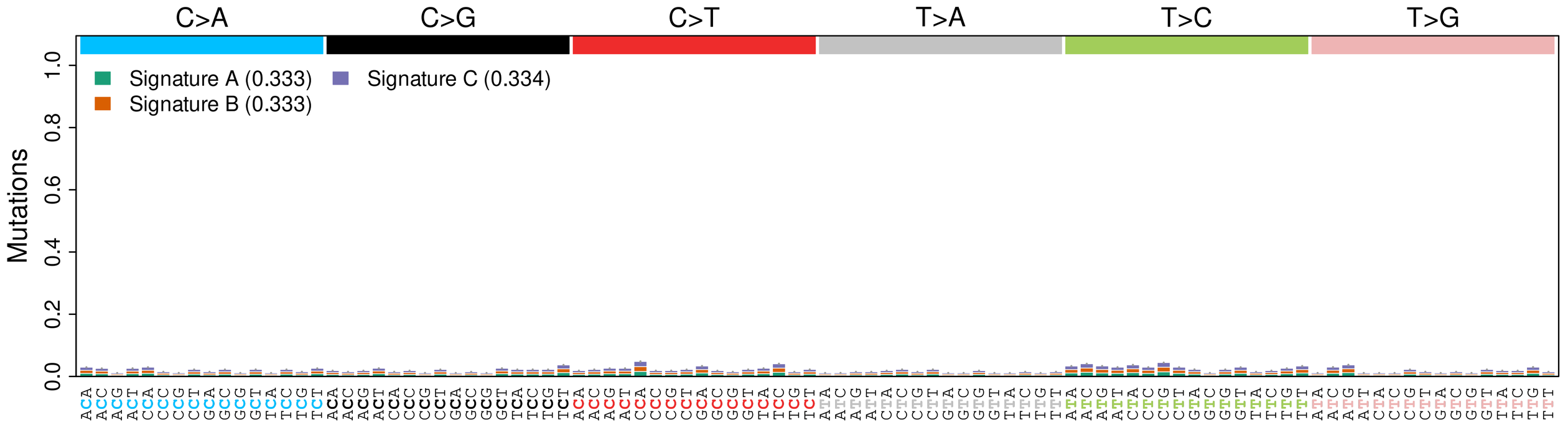

Reconstructed spectrum (cosine similarity = 0.084)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.333)
Signature B (0.333)
Signature C (0.334)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0


CATD0415a
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 = 0.243)
Signature A (0.332)
Signature B (0.333)
Signature C (0.335)
Mutations

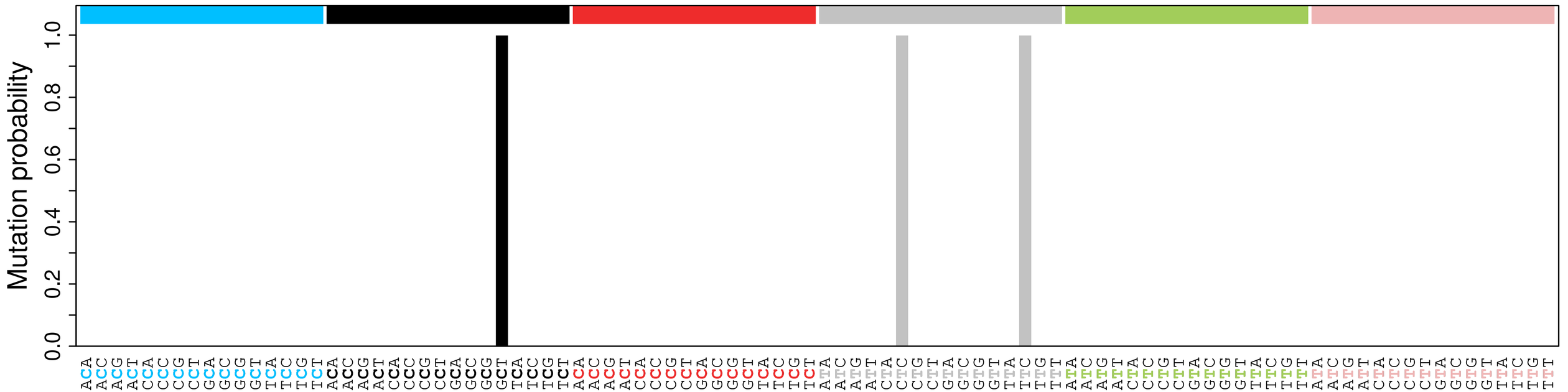
CATD191a



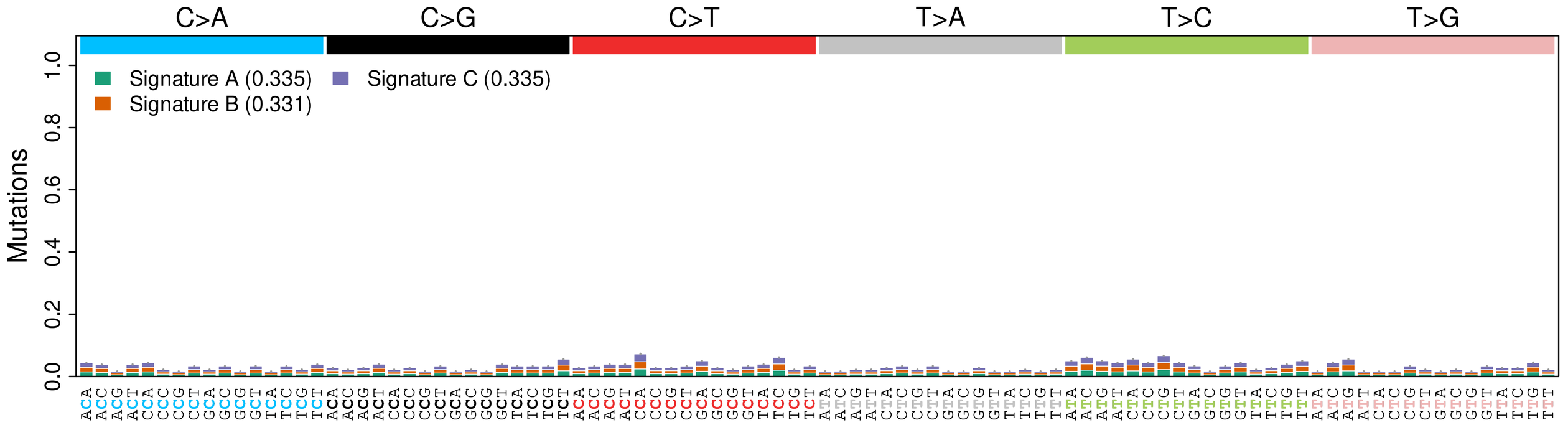
Reconstructed spectrum (cosine similarity = 0.213)

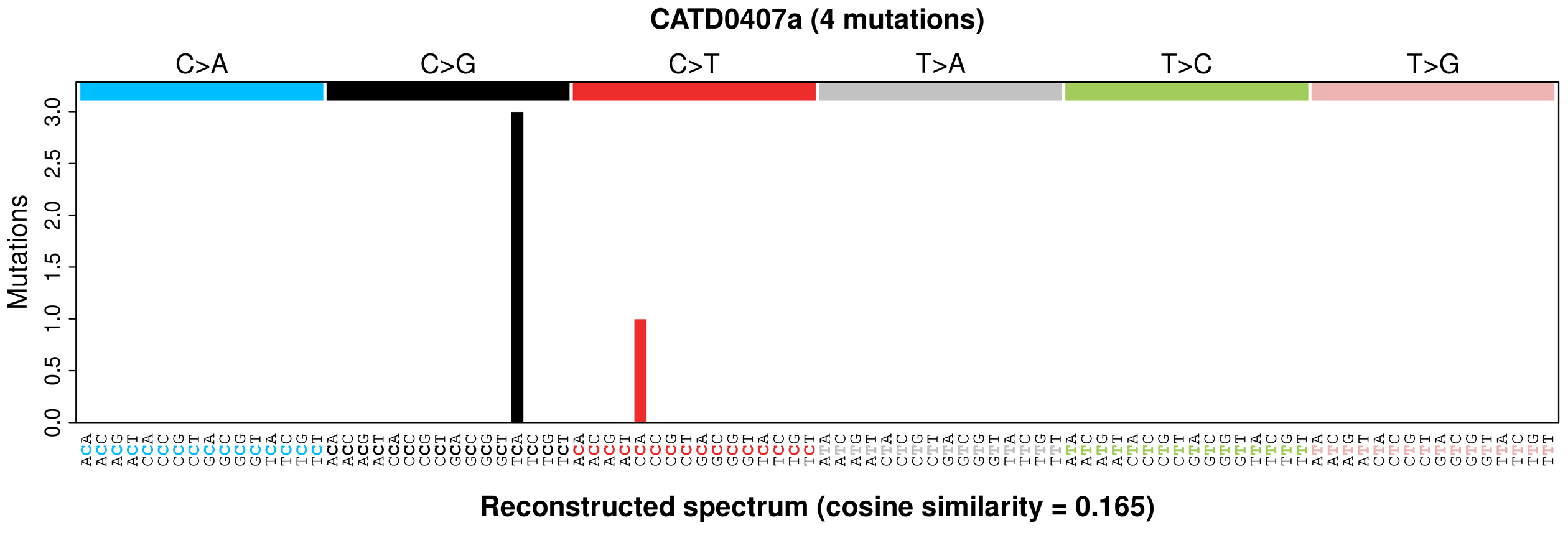


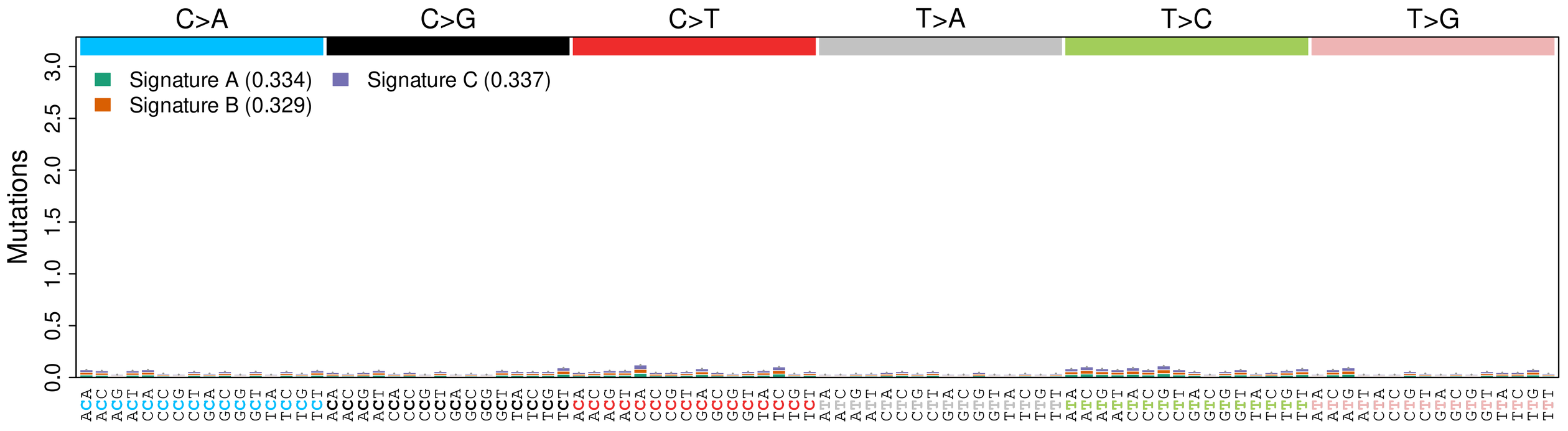
CATD0093a

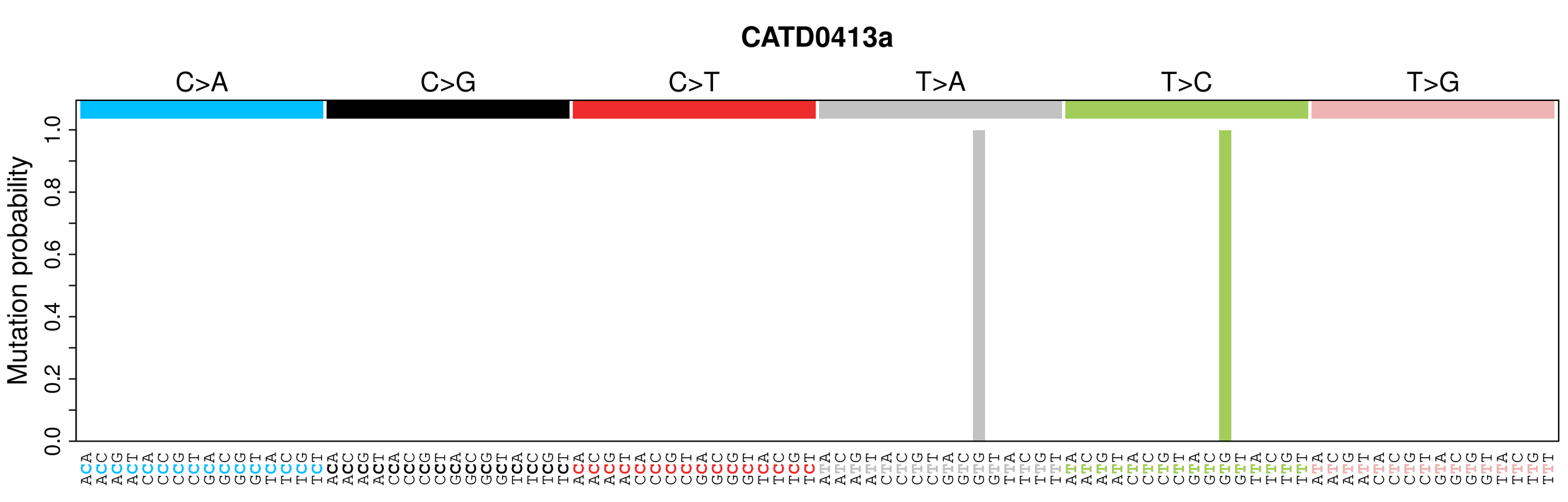


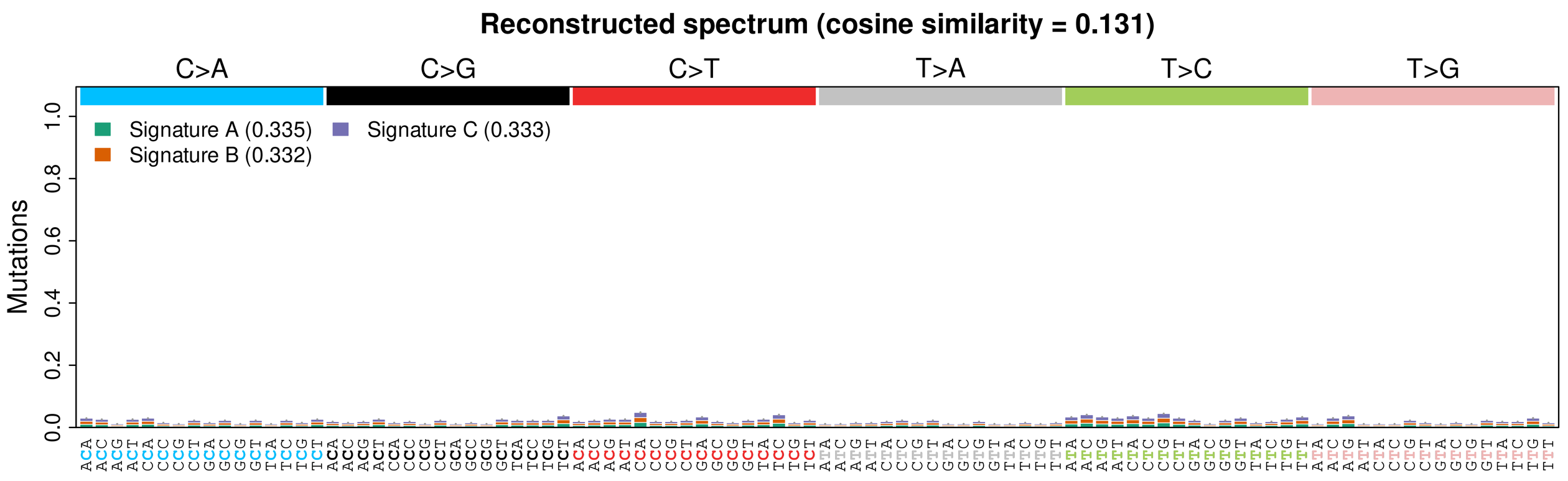
Reconstructed spectrum (cosine similarity = 0.166)



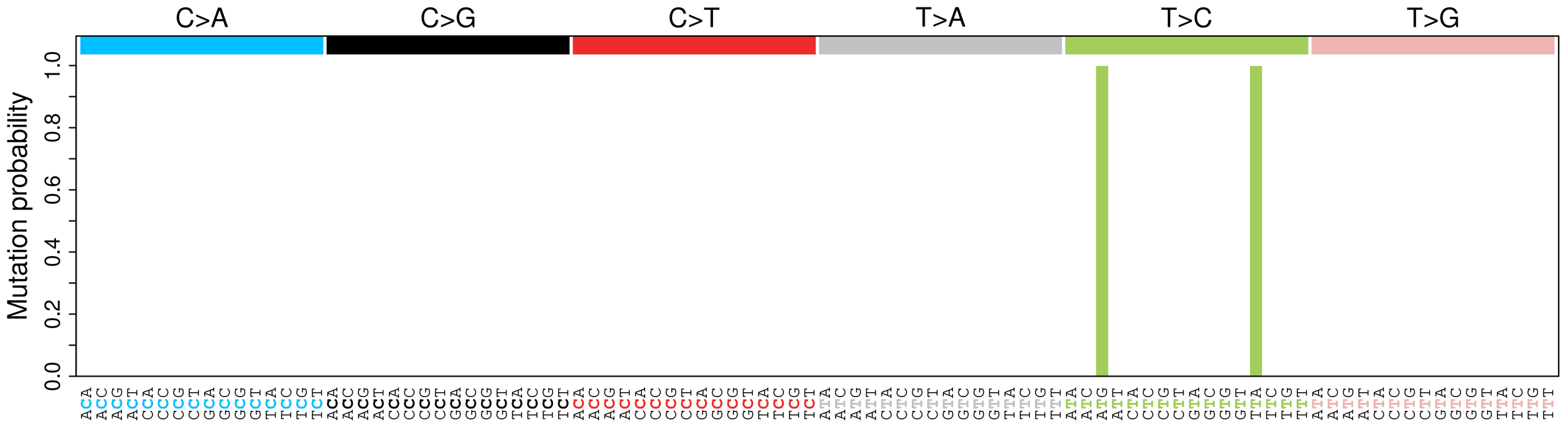

CATD0407a (4 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0
2.5
3.0


Reconstructed spectrum (cosine similarity = 0.165)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.334)
Signature B (0.329)
Signature C (0.337)
Mutations
0.0
0.5
1.0
1.5
2.0
2.5
3.0

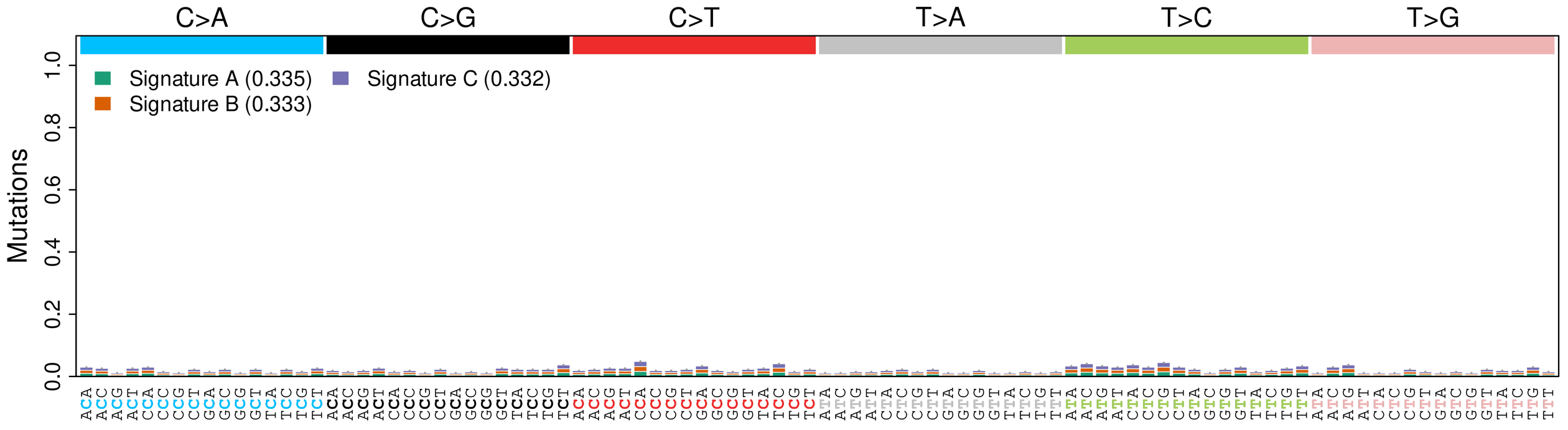

CATD0413a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0

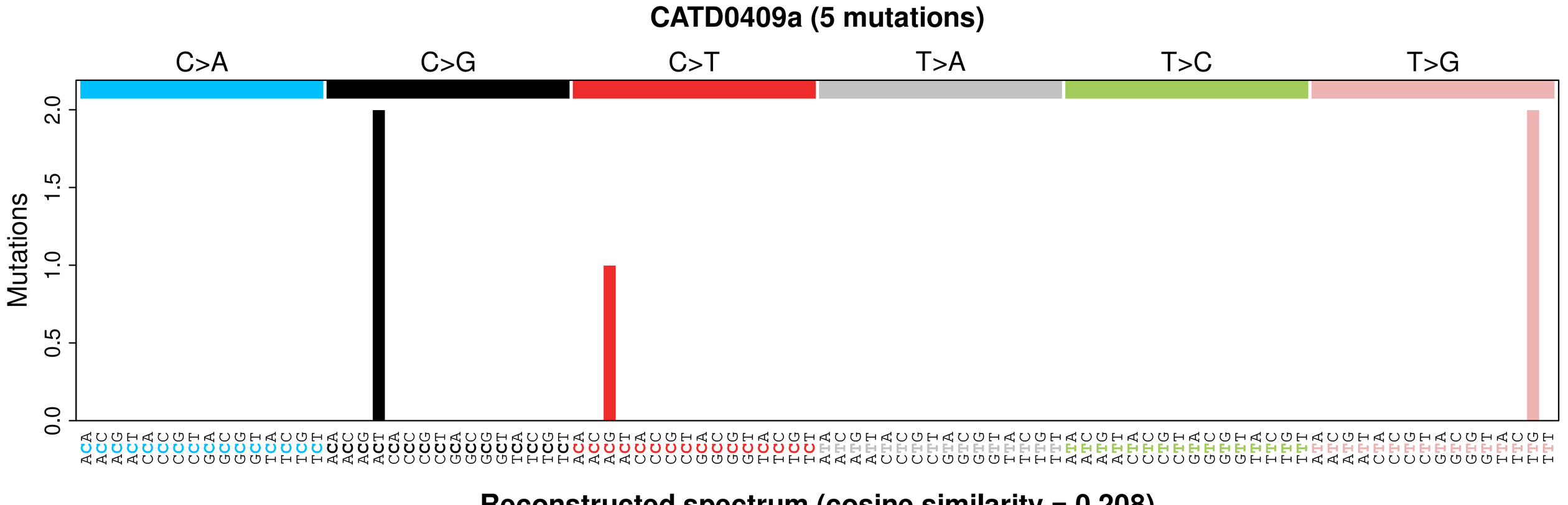

Reconstructed spectrum (cosine similarity = 0.131)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.335)
Signature B (0.332)
Signature C (0.333)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

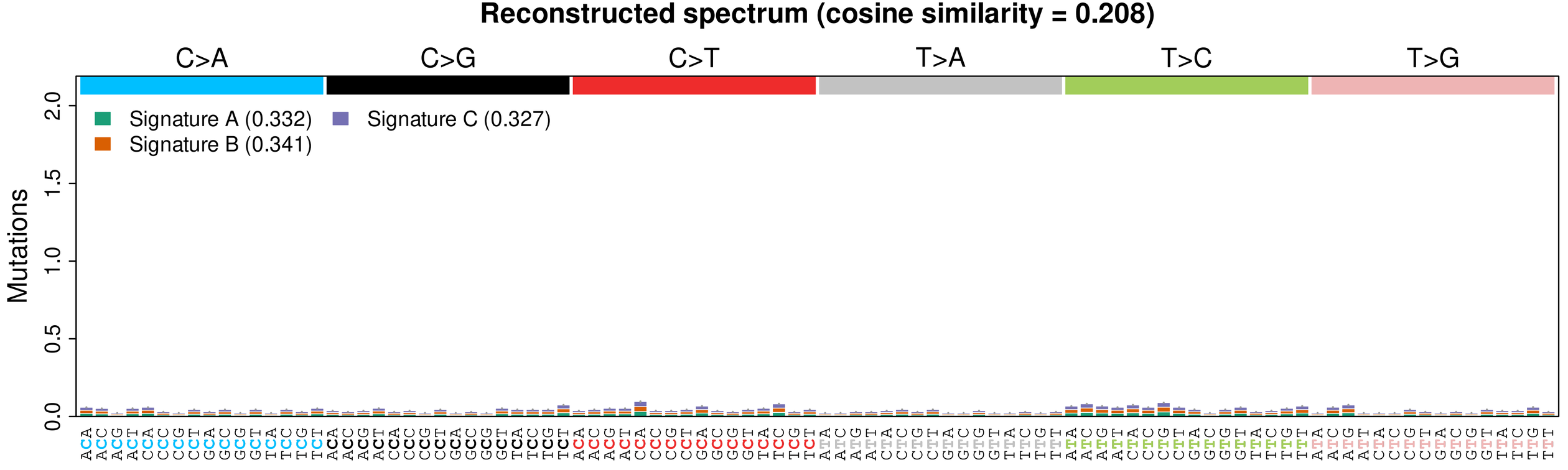
CATD0104a

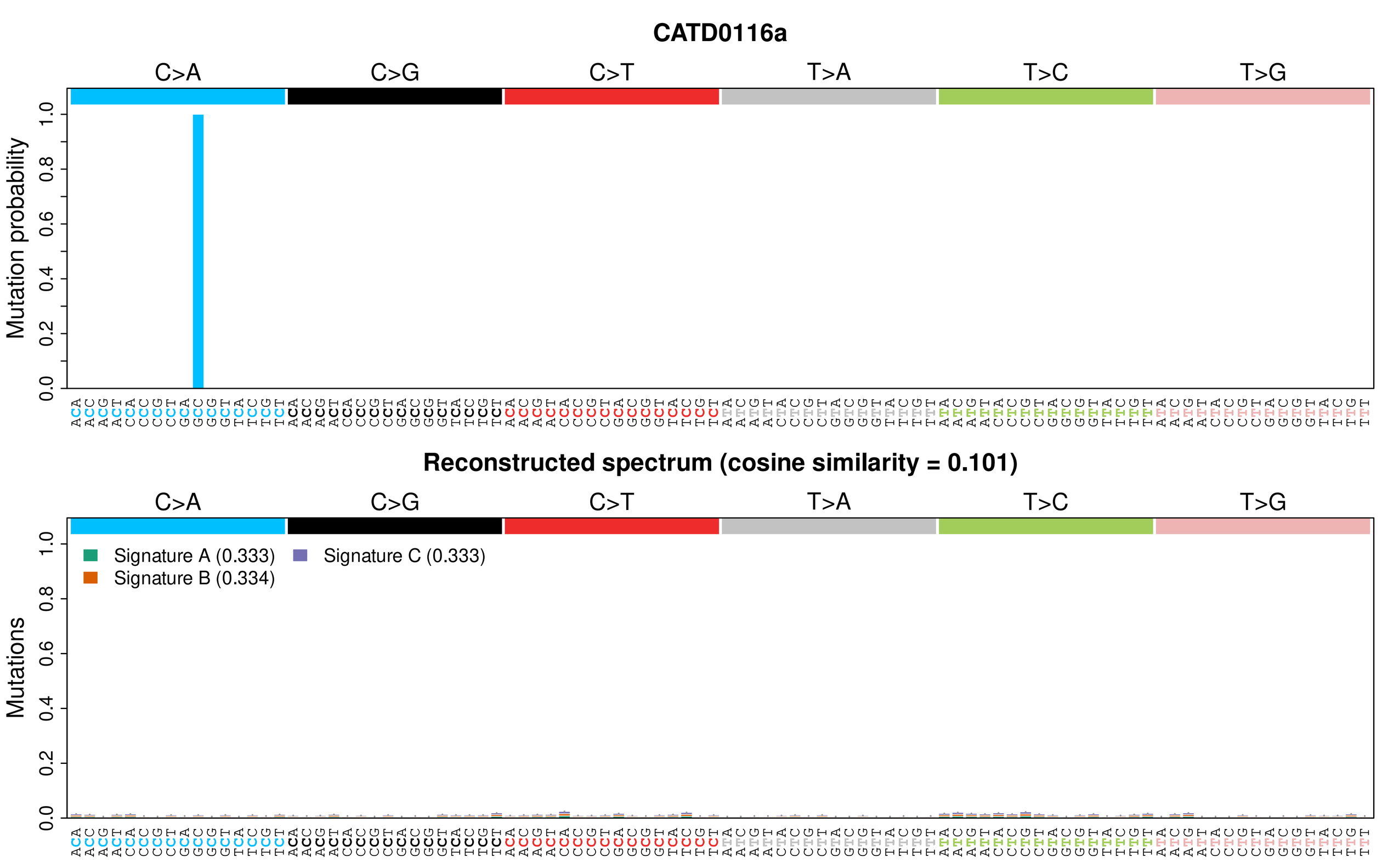


Reconstructed spectrum (cosine similarity = 0.155)

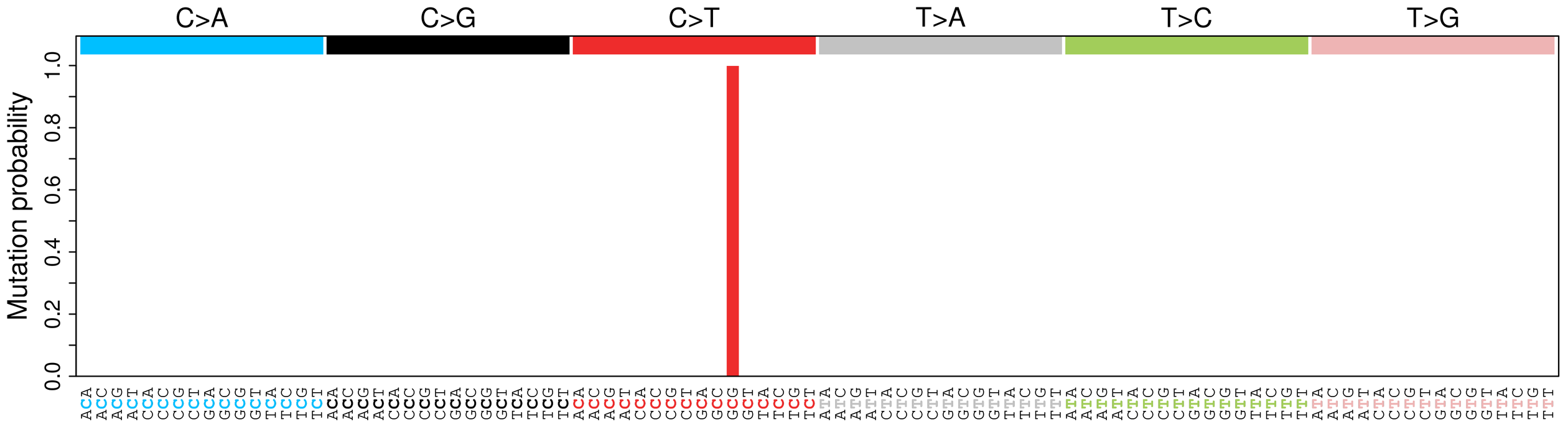



CATD0409a (5 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

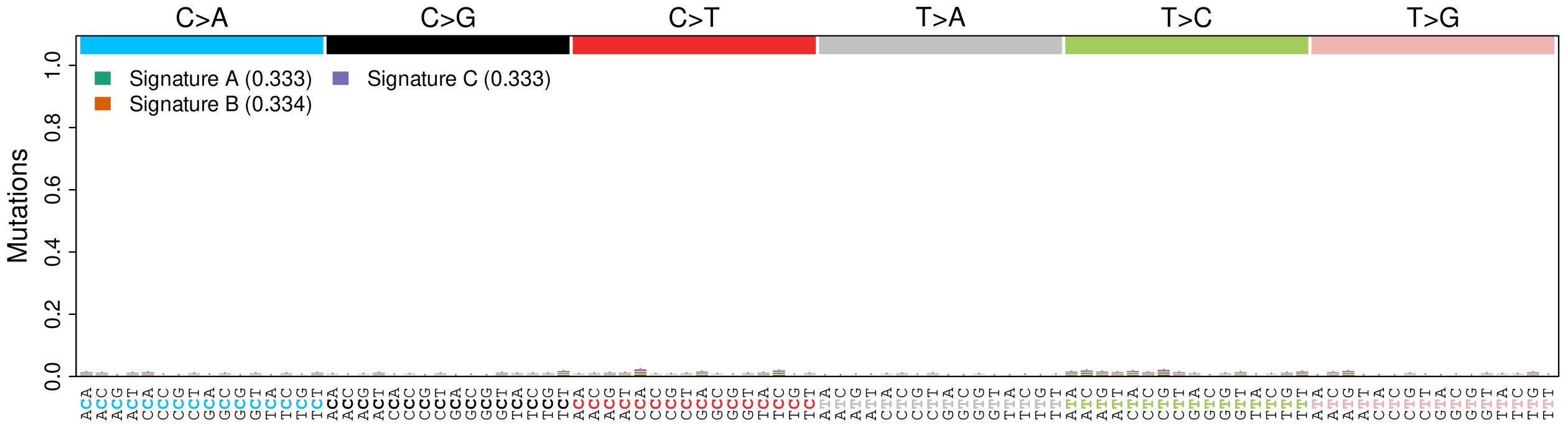

Reconstructed spectrum (cosine similarity = 0.208)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.332)
Signature B (0.341)
Signature C (0.327)
Mutations
0.0
0.5
1.0
1.5
2.0

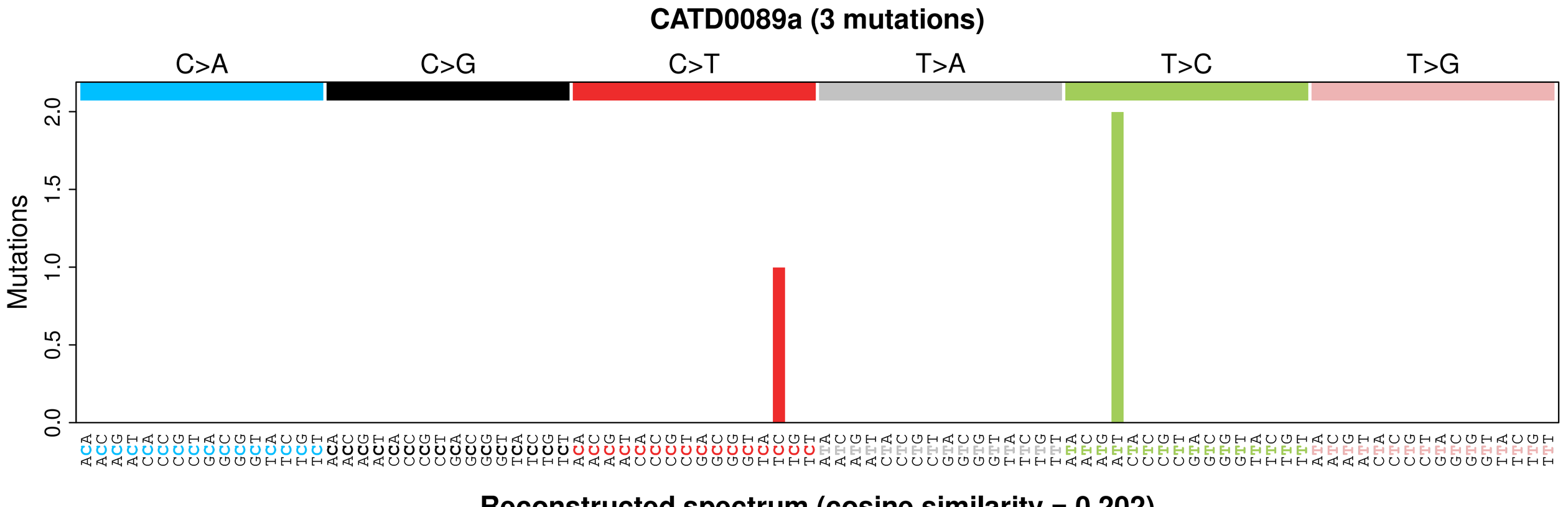

CATD0116a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0
Reconstructed spectrum (cosine similarity = 0.101)
Signature A (0.333)
Signature B (0.334)
Signature C (0.333)
Mutations

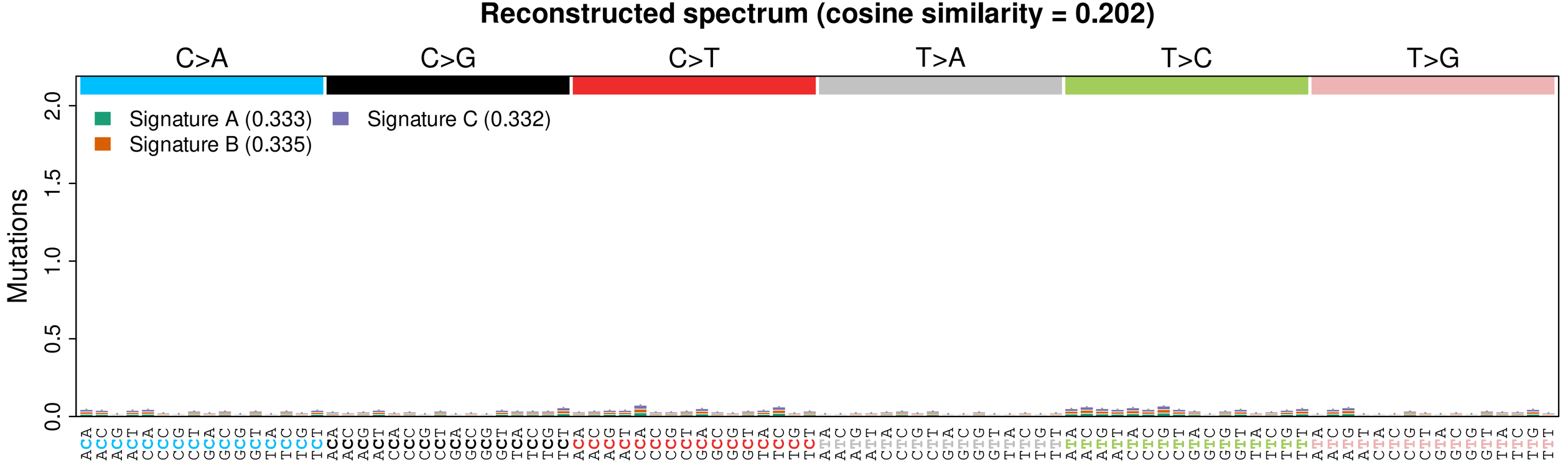
CATD0406a



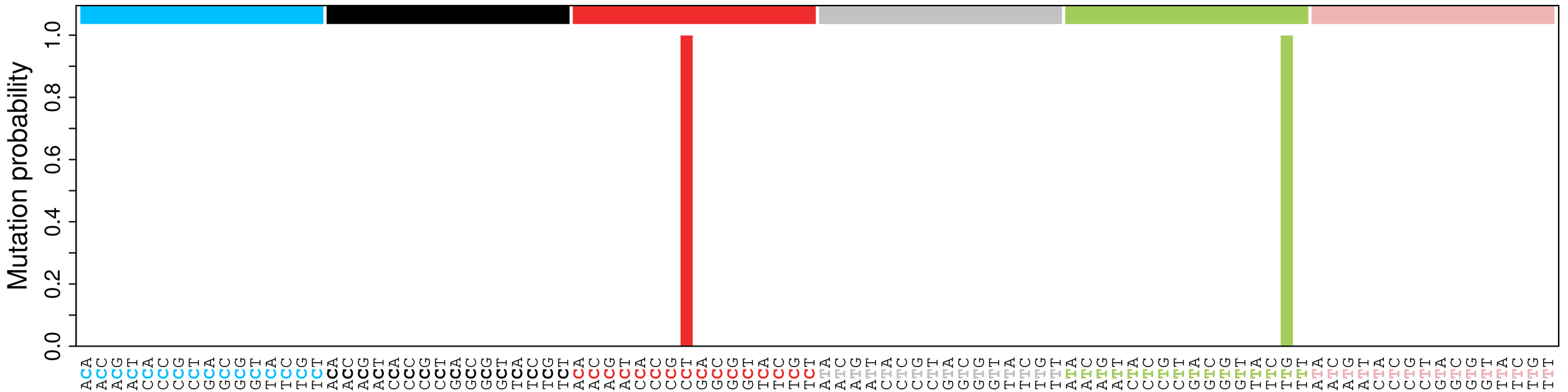
Reconstructed spectrum (cosine similarity = 0.068)



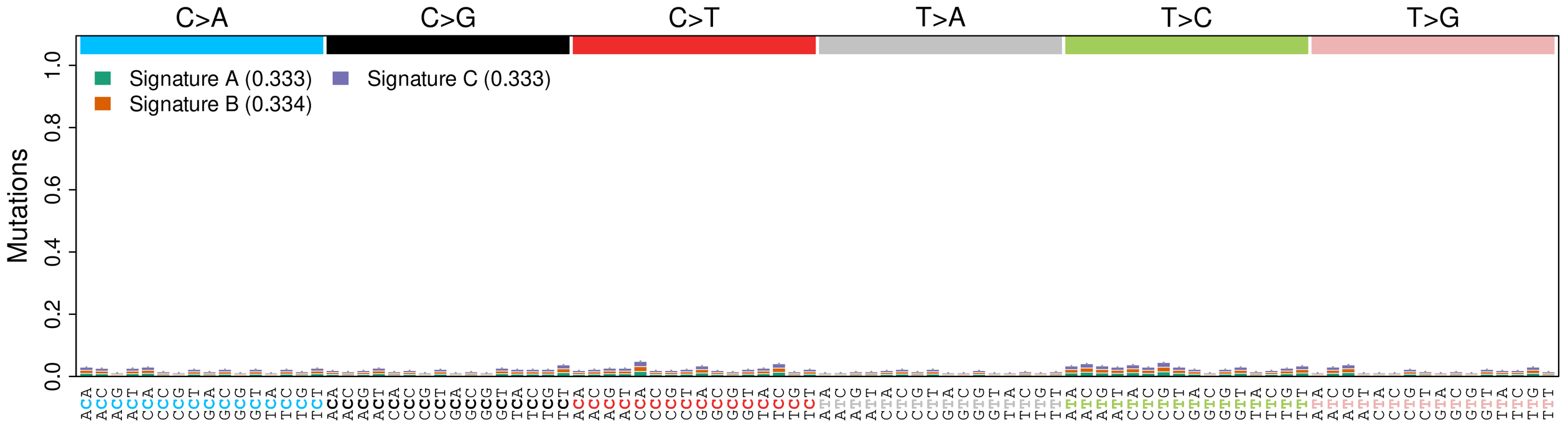

CATD0089a (3 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

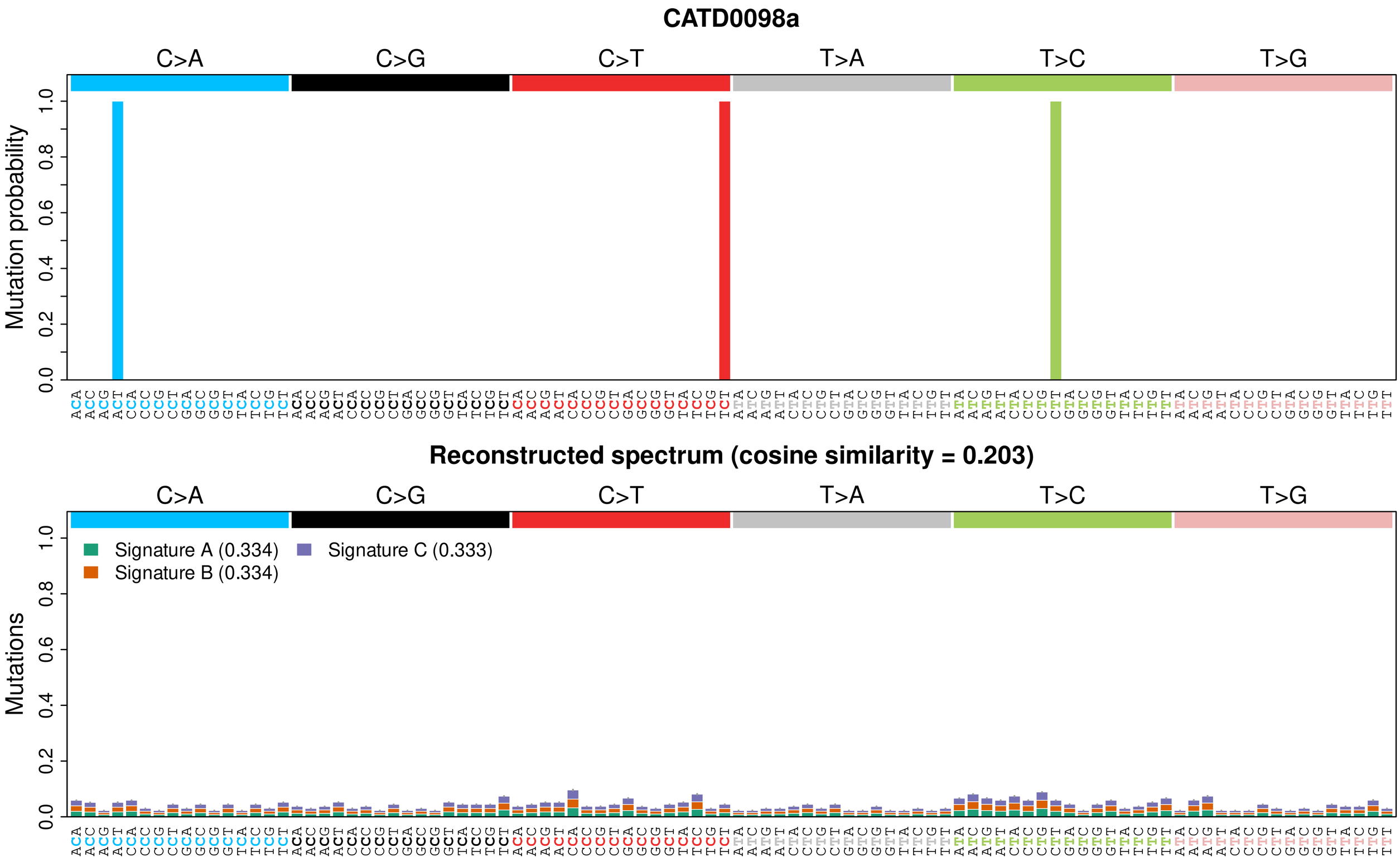

Reconstructed spectrum (cosine similarity = 0.202)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.333)
Signature B (0.335)
Signature C (0.332)
Mutations
0.0
0.5
1.0
1.5
2.0

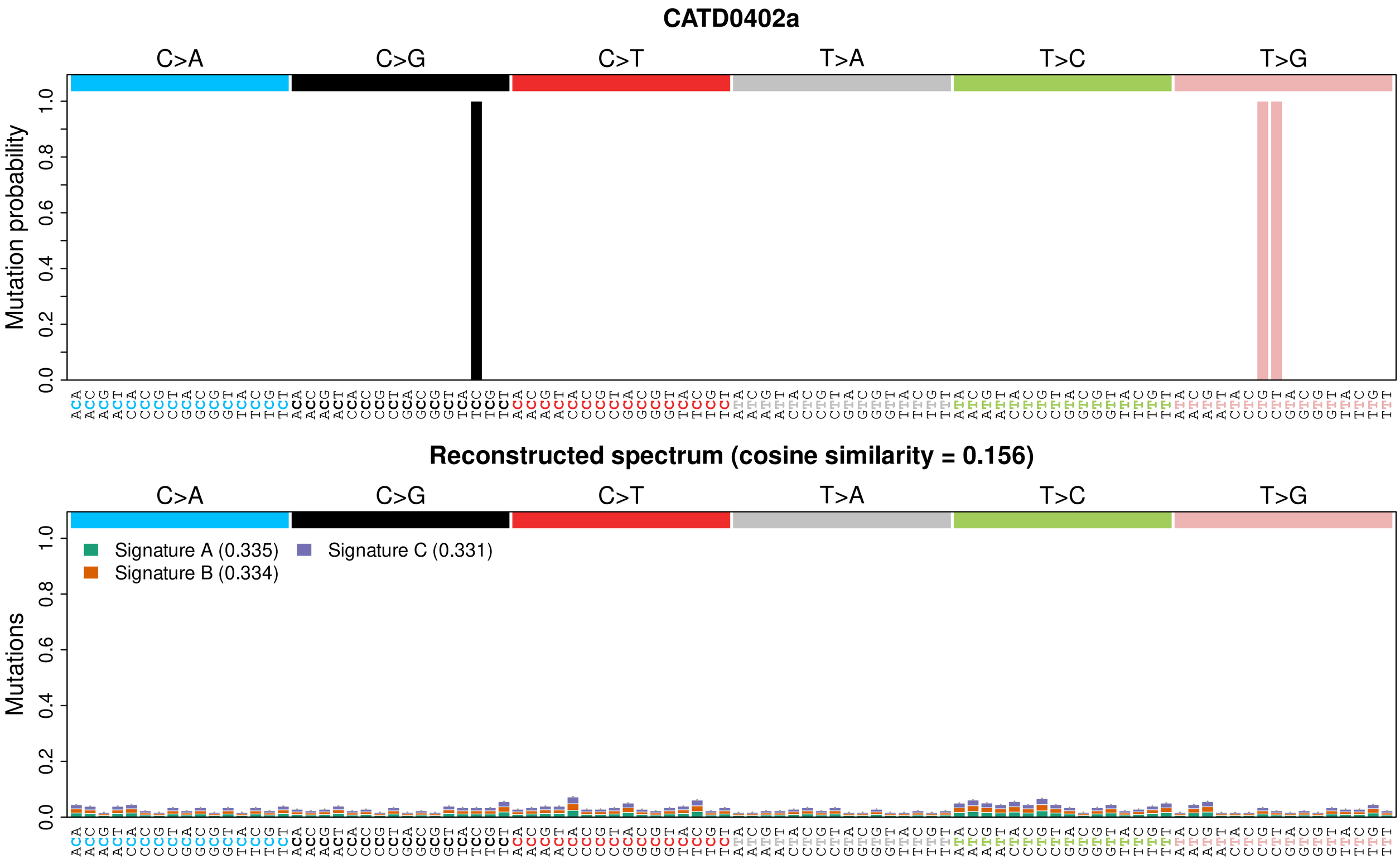
CATD0115a

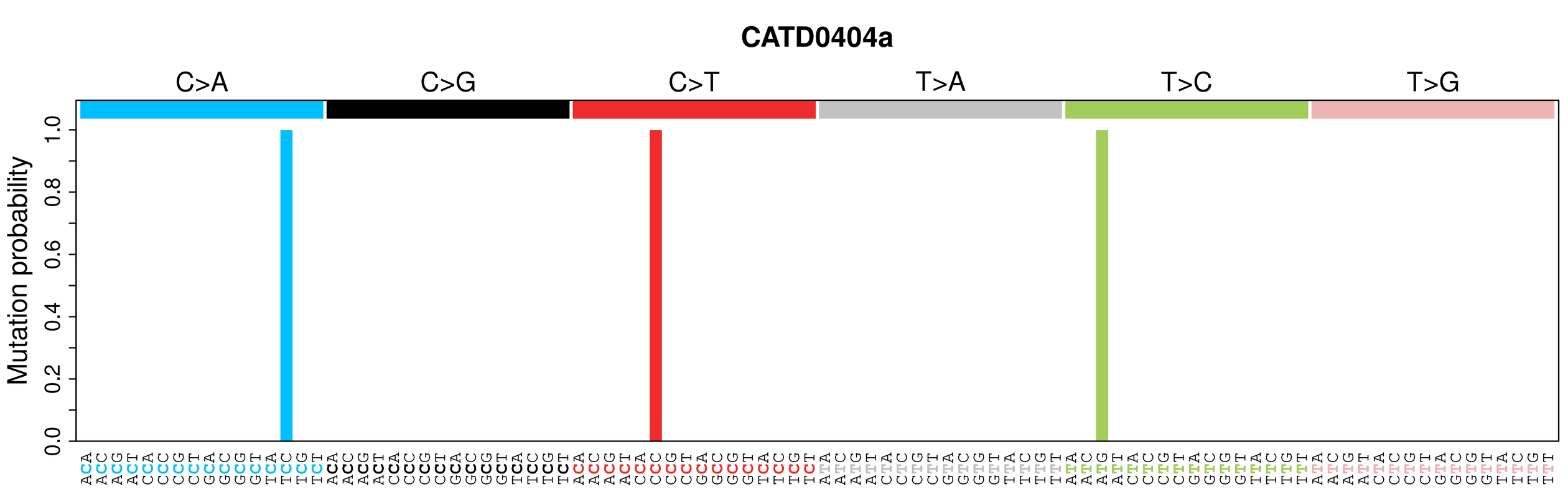


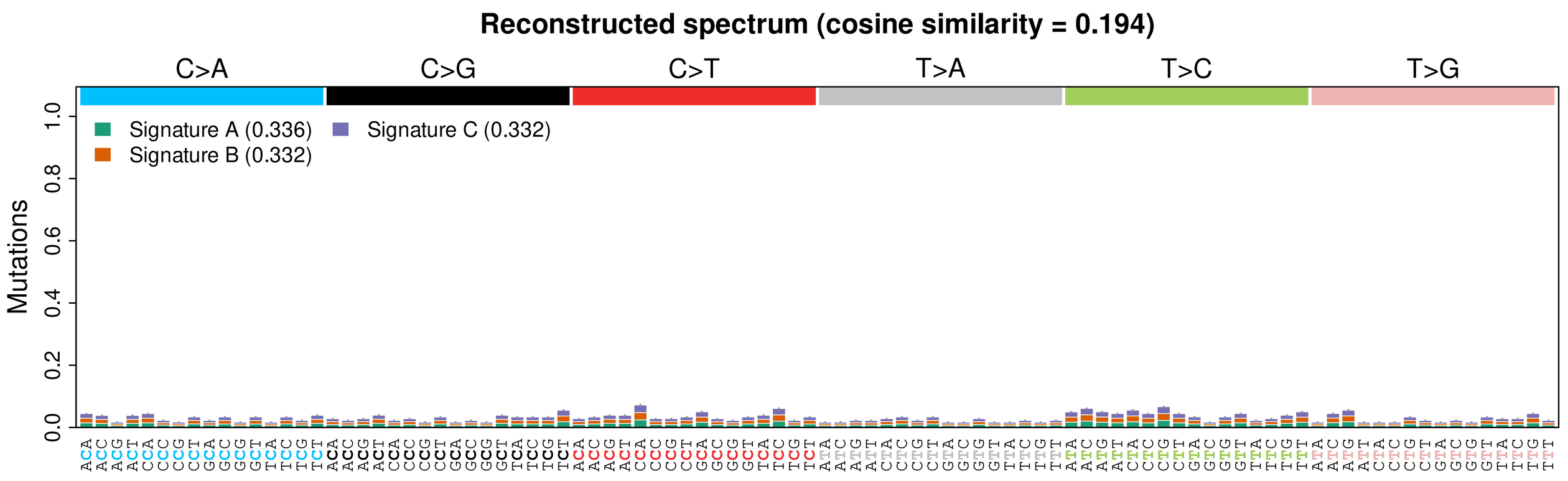
Reconstructed spectrum (cosine similarity = 0.155)

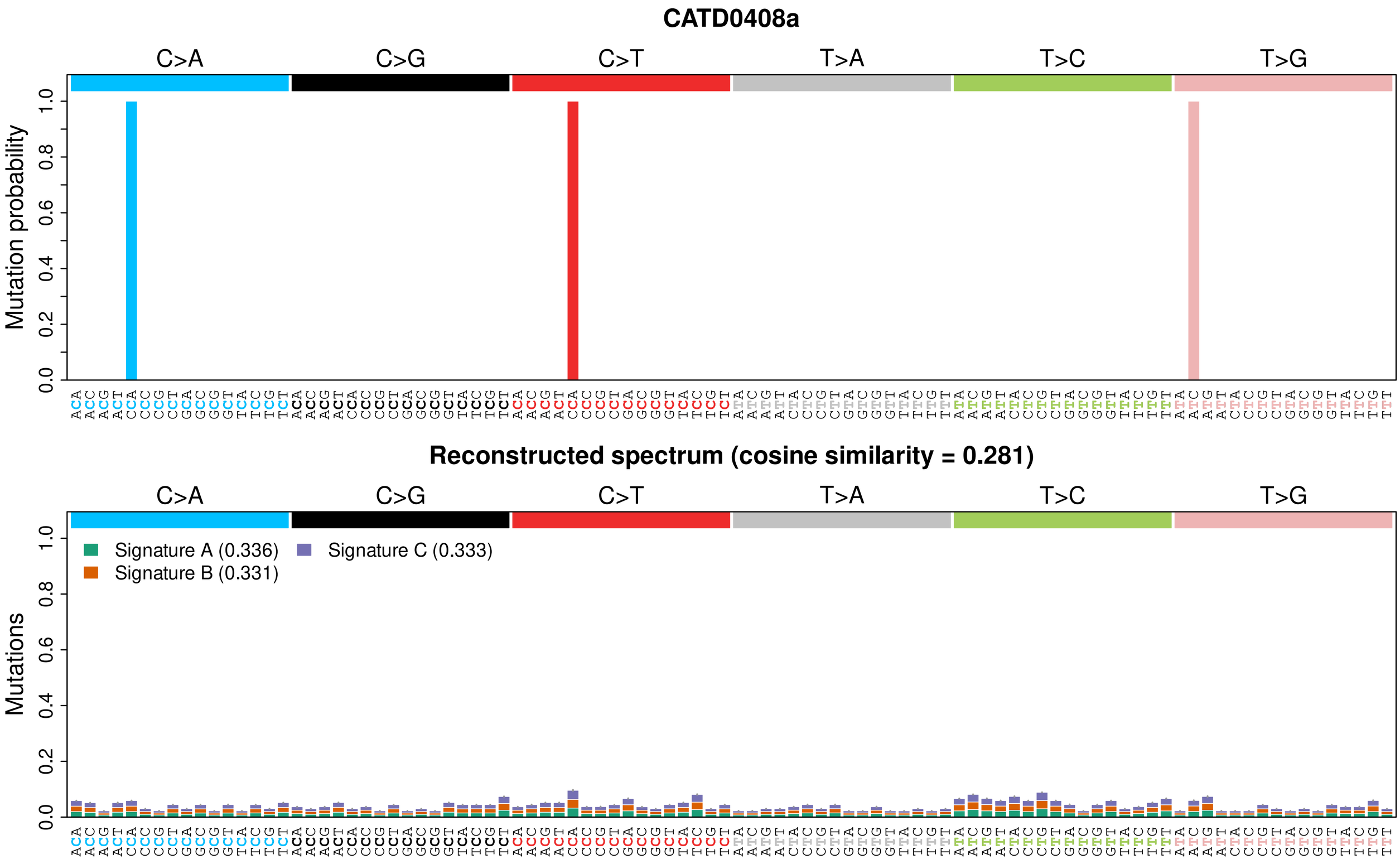



CATD0098a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0
Reconstructed spectrum (cosine similarity = 0.203)
Signature A (0.334)
Signature B (0.334)
Signature C (0.333)
Mutations


CATD0402a
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 = 0.156)
Signature A (0.335)
Signature B (0.334)
Signature C (0.331)
Mutations


CATD0404a
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 = 0.194)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.336)
Signature B (0.332)
Signature C (0.332)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0


CATD0408a
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 = 0.281)
Signature A (0.336)
Signature B (0.331)
Signature C (0.333)
Mutations