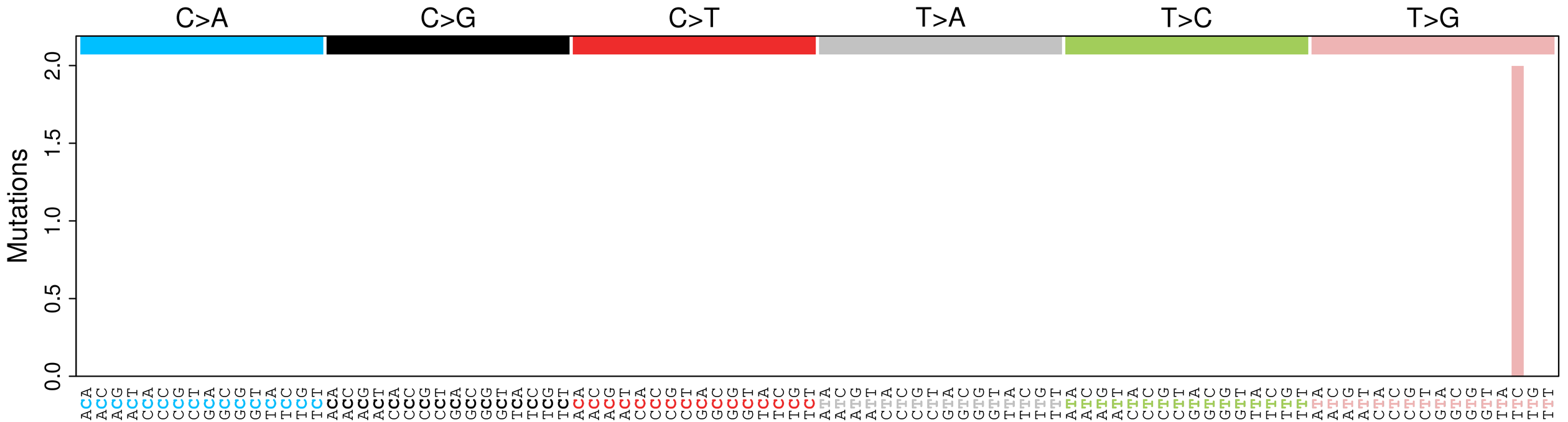
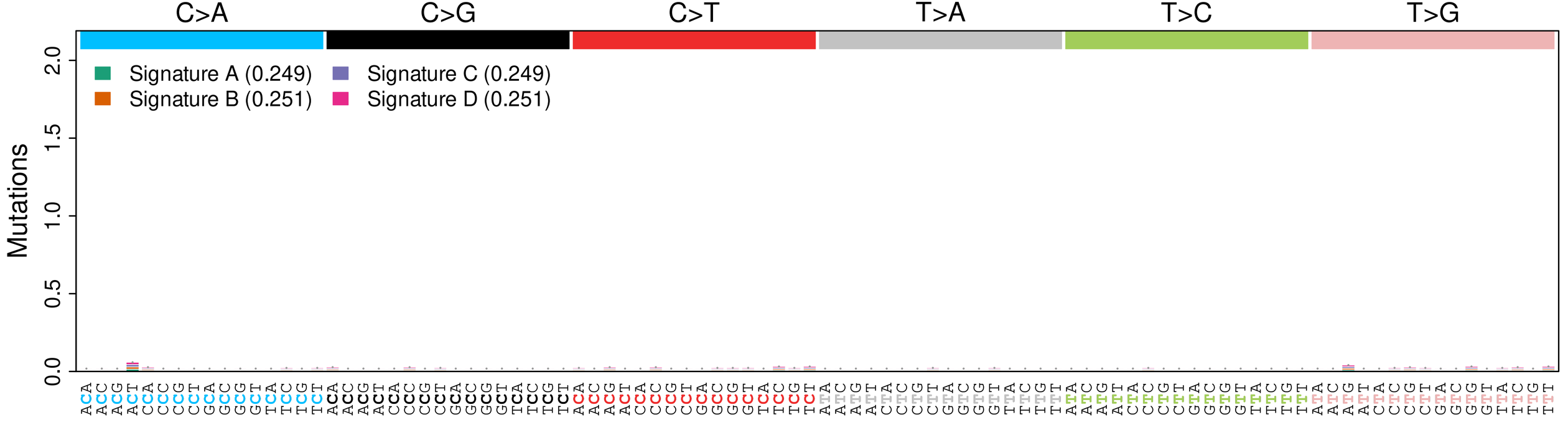
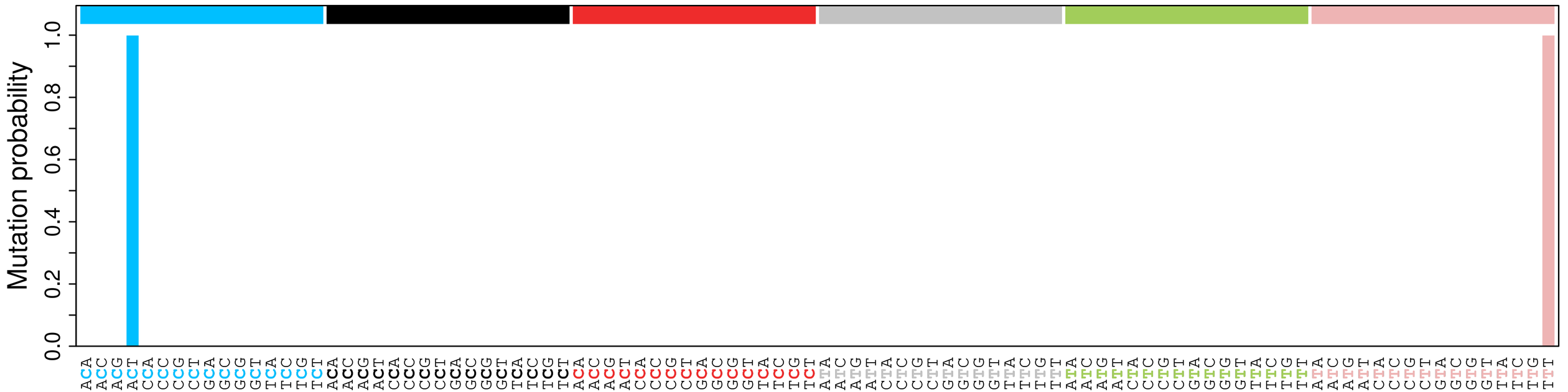
CATD0161a (2 mutations)



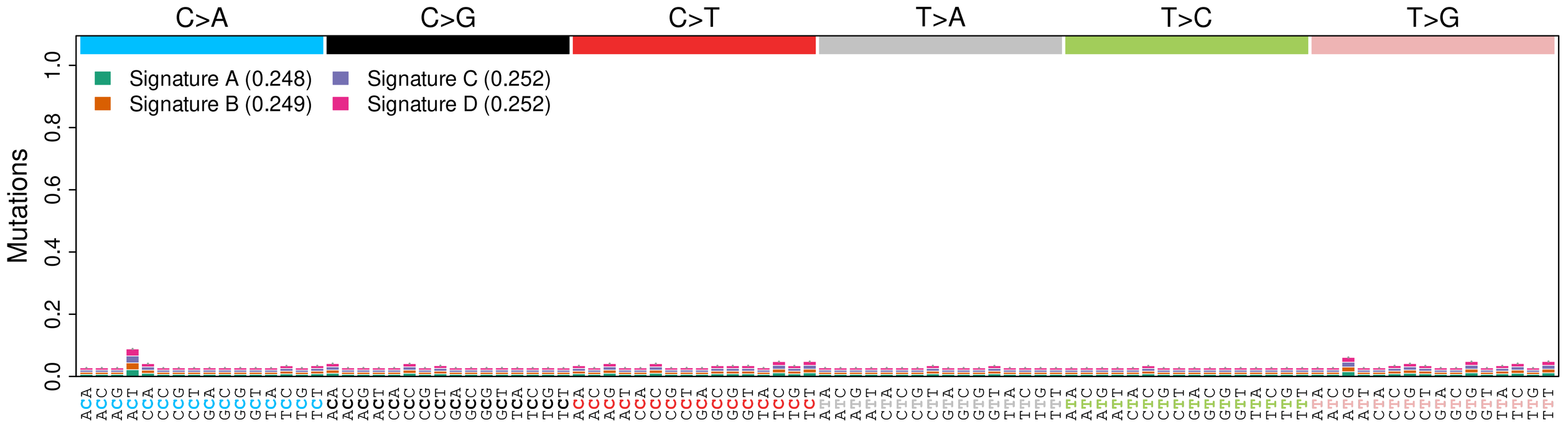
Reconstructed spectrum (cosine similarity = 0.13)



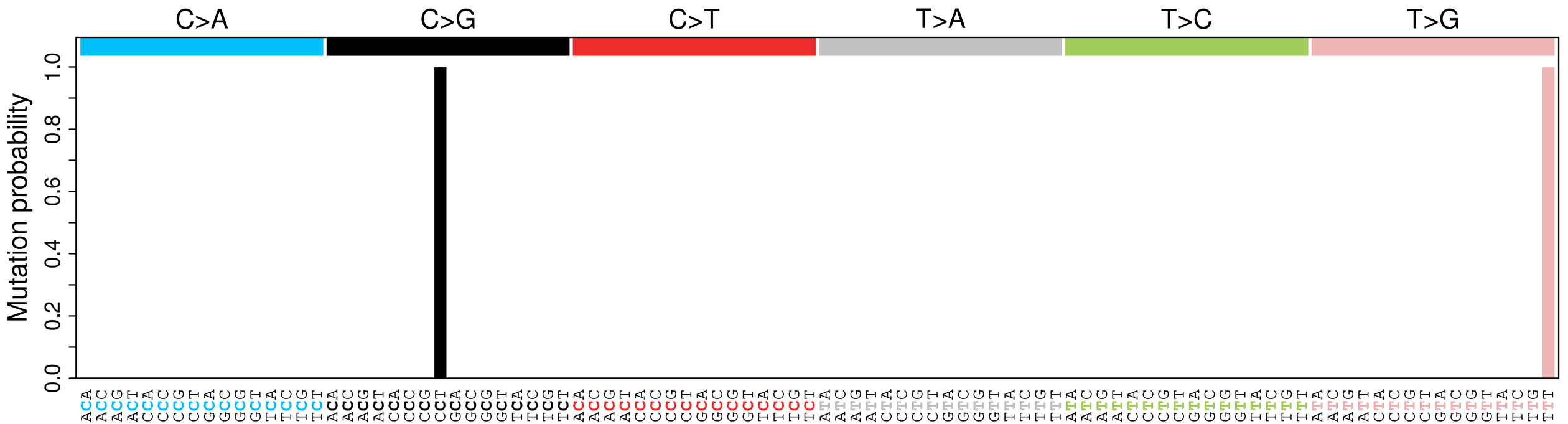
CATD0371a



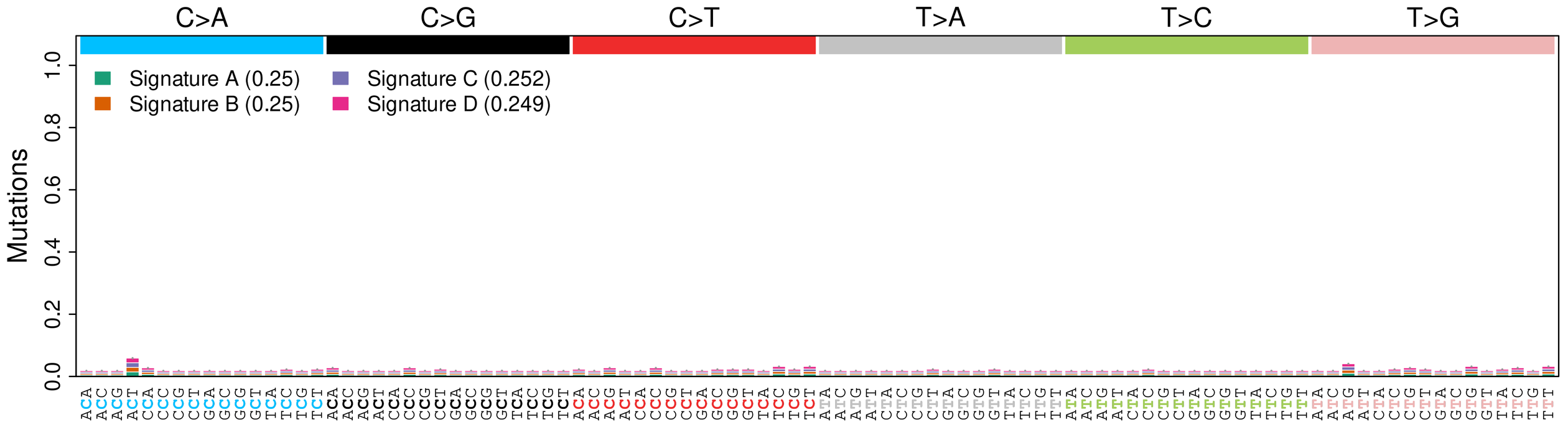
Reconstructed spectrum (cosine similarity = 0.303)

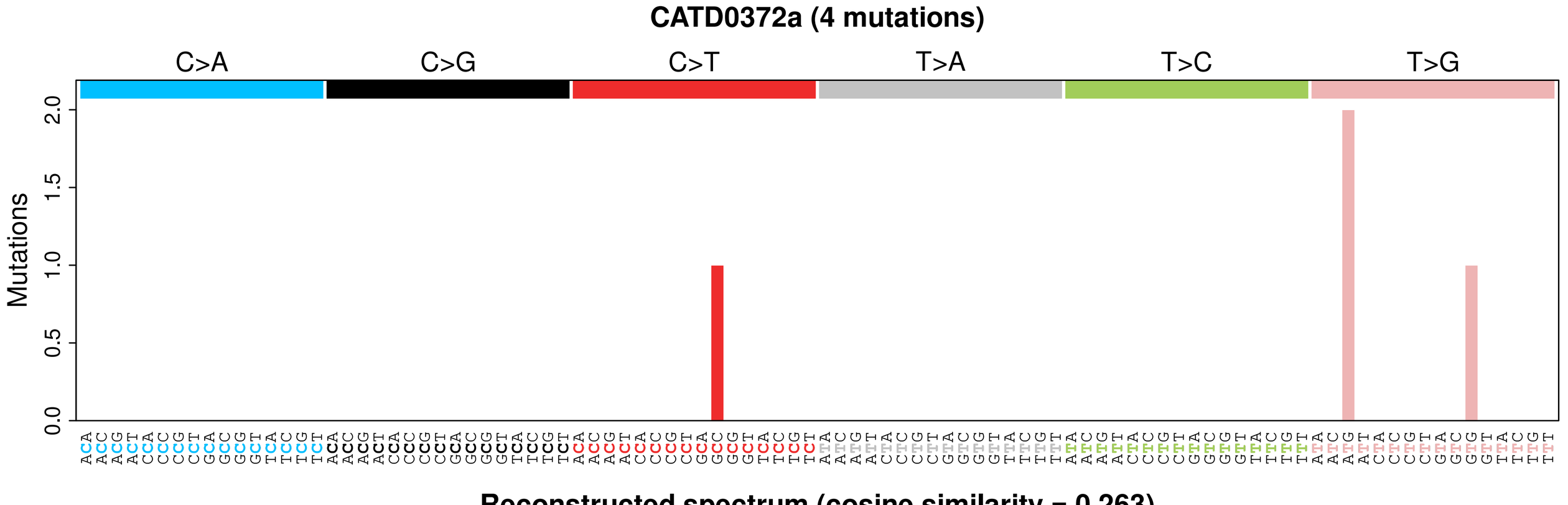


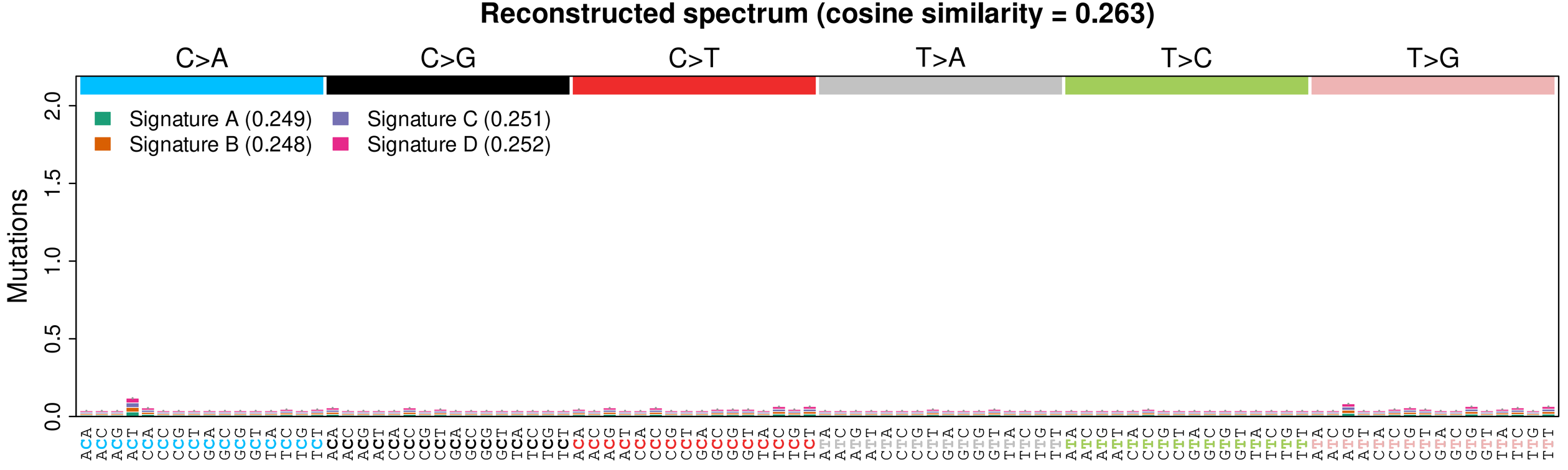
CATD0354a



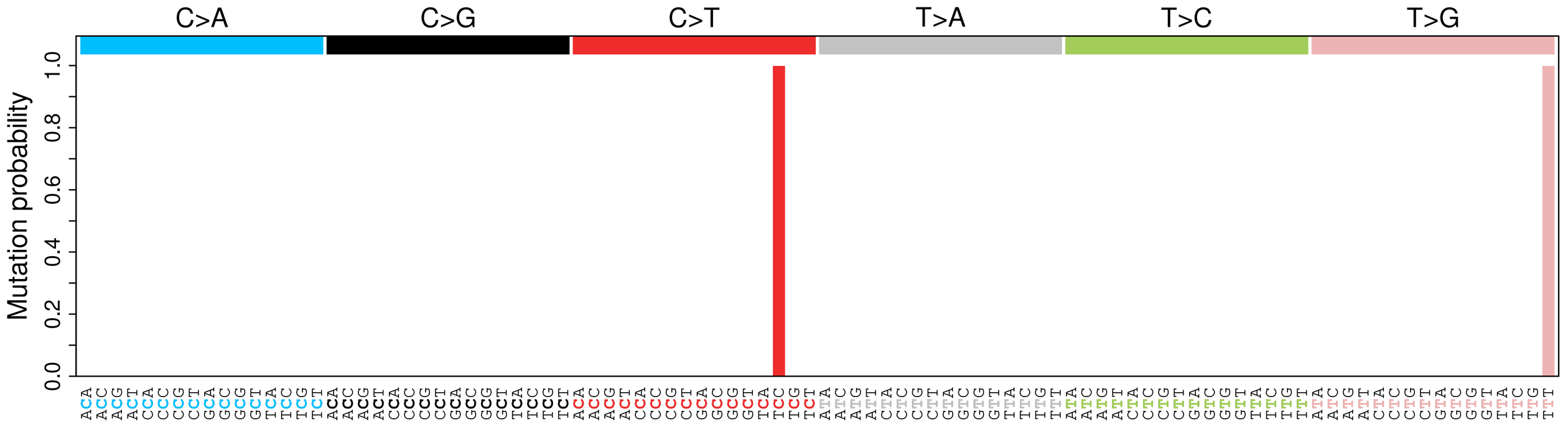
Reconstructed spectrum (cosine similarity = 0.183)



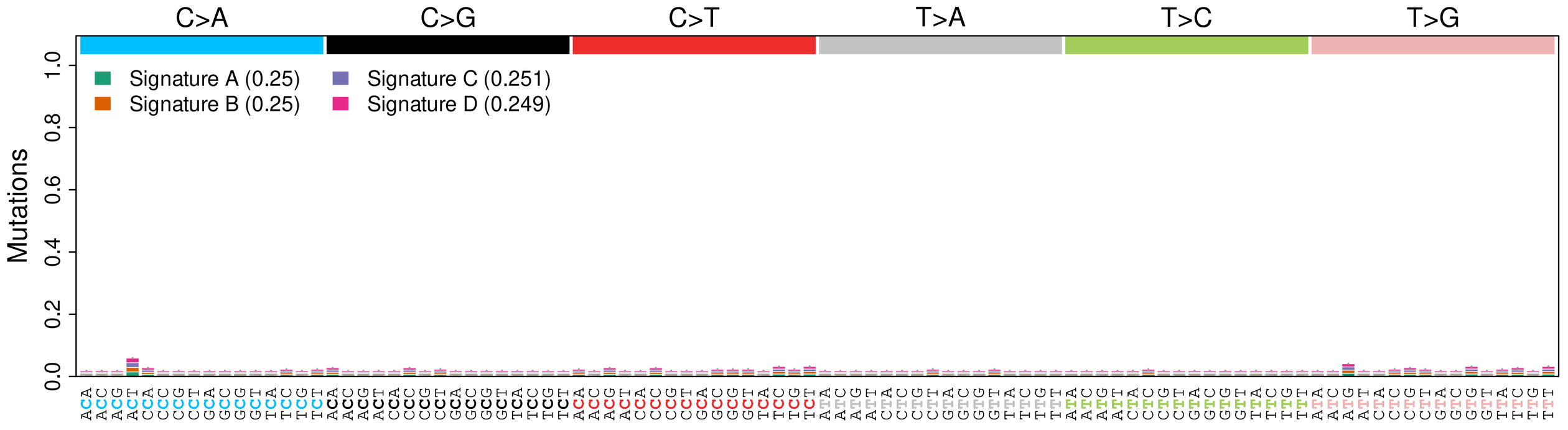

CATD0372a (4 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

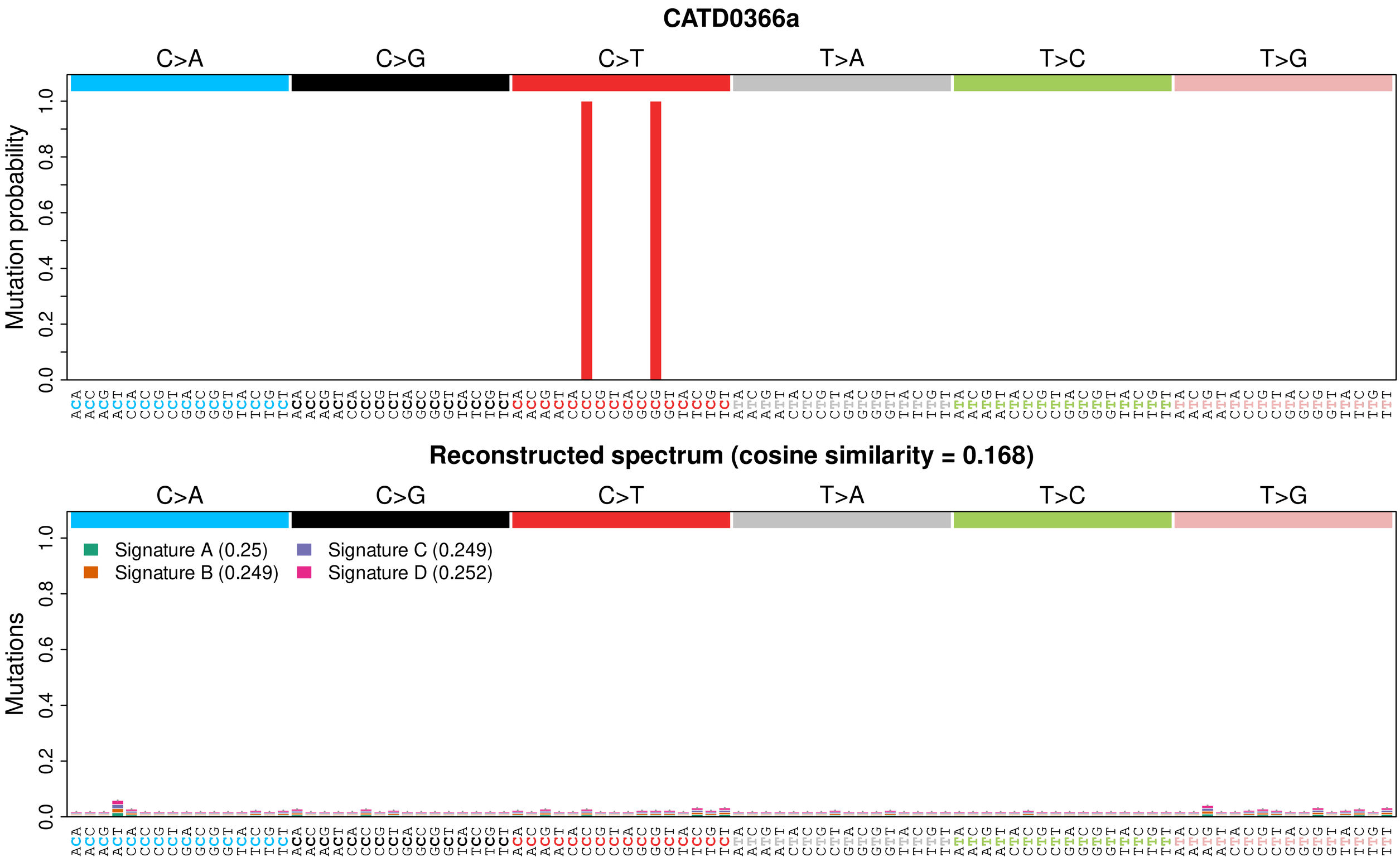

Reconstructed spectrum (cosine similarity = 0.263)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.249)
Signature B (0.248)
Signature C (0.251)
Signature D (0.252)
Mutations
0.0
0.5
1.0
1.5
2.0

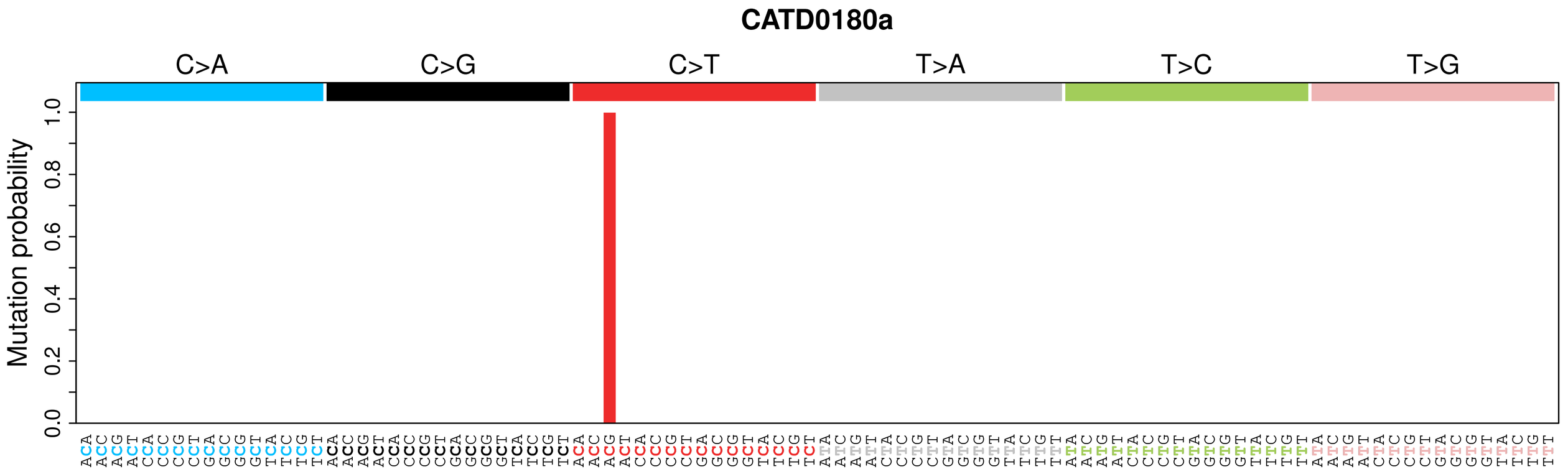
CATD0352a

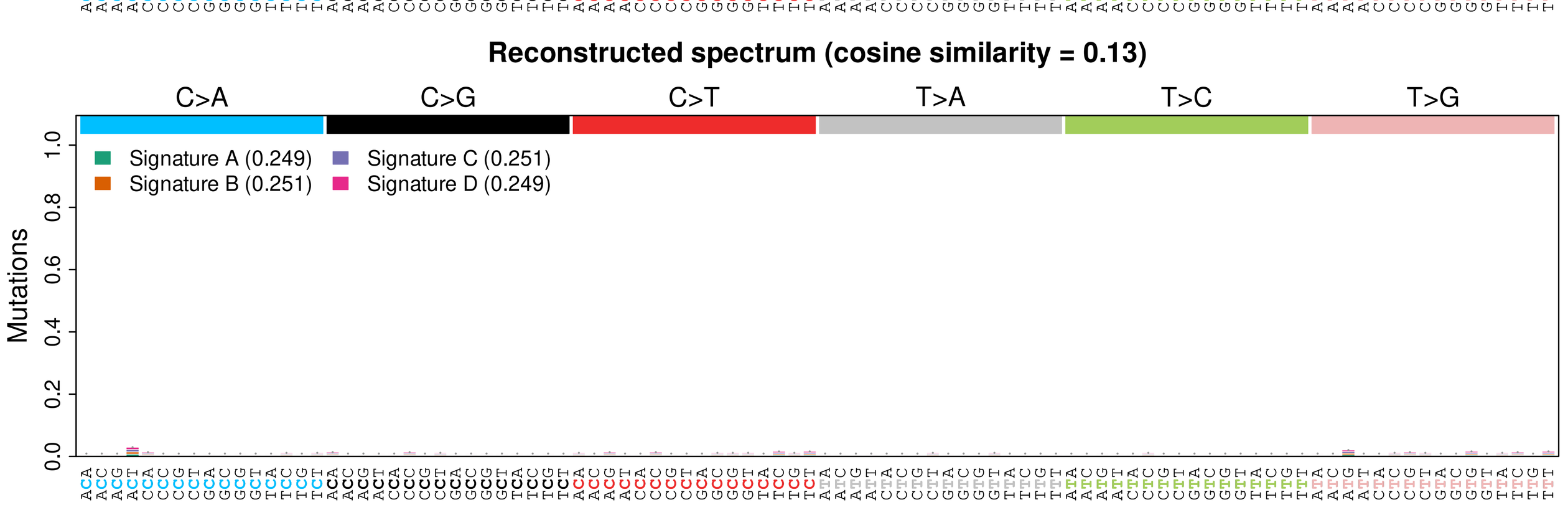


Reconstructed spectrum (cosine similarity = 0.213)

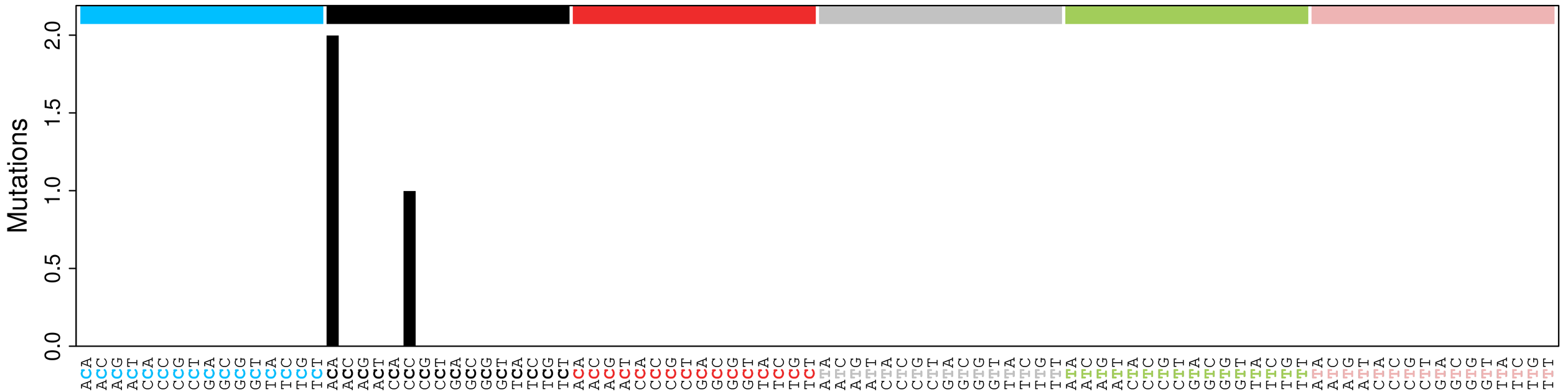



CATD0366a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0
Reconstructed spectrum (cosine similarity = 0.168)
Signature A (0.25)
Signature B (0.249)
Signature C (0.249)
Signature D (0.252)
Mutations

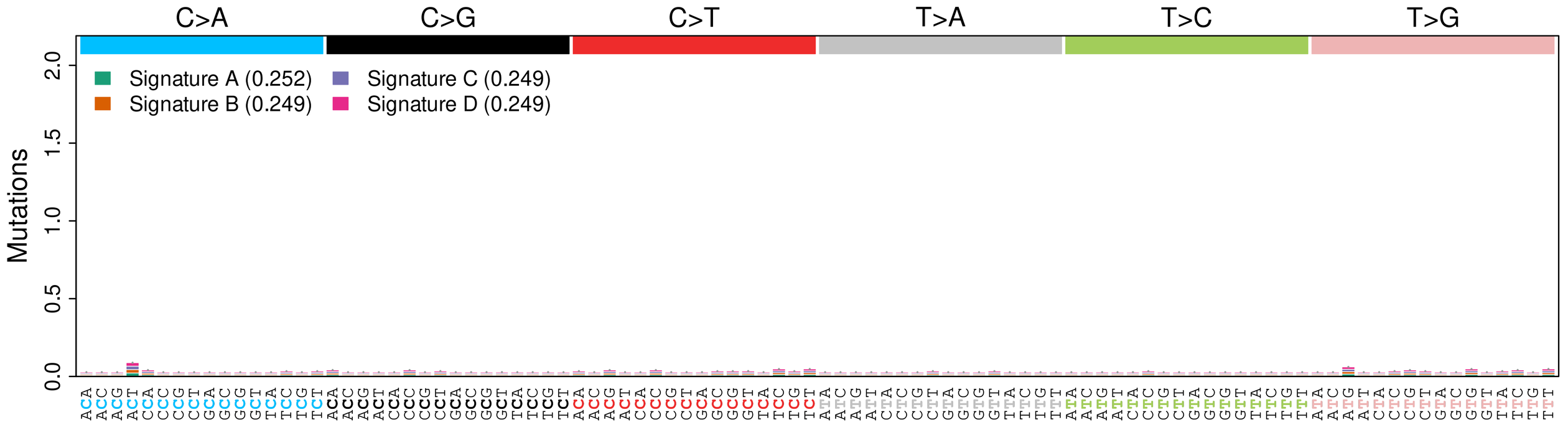

CATD0180a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0

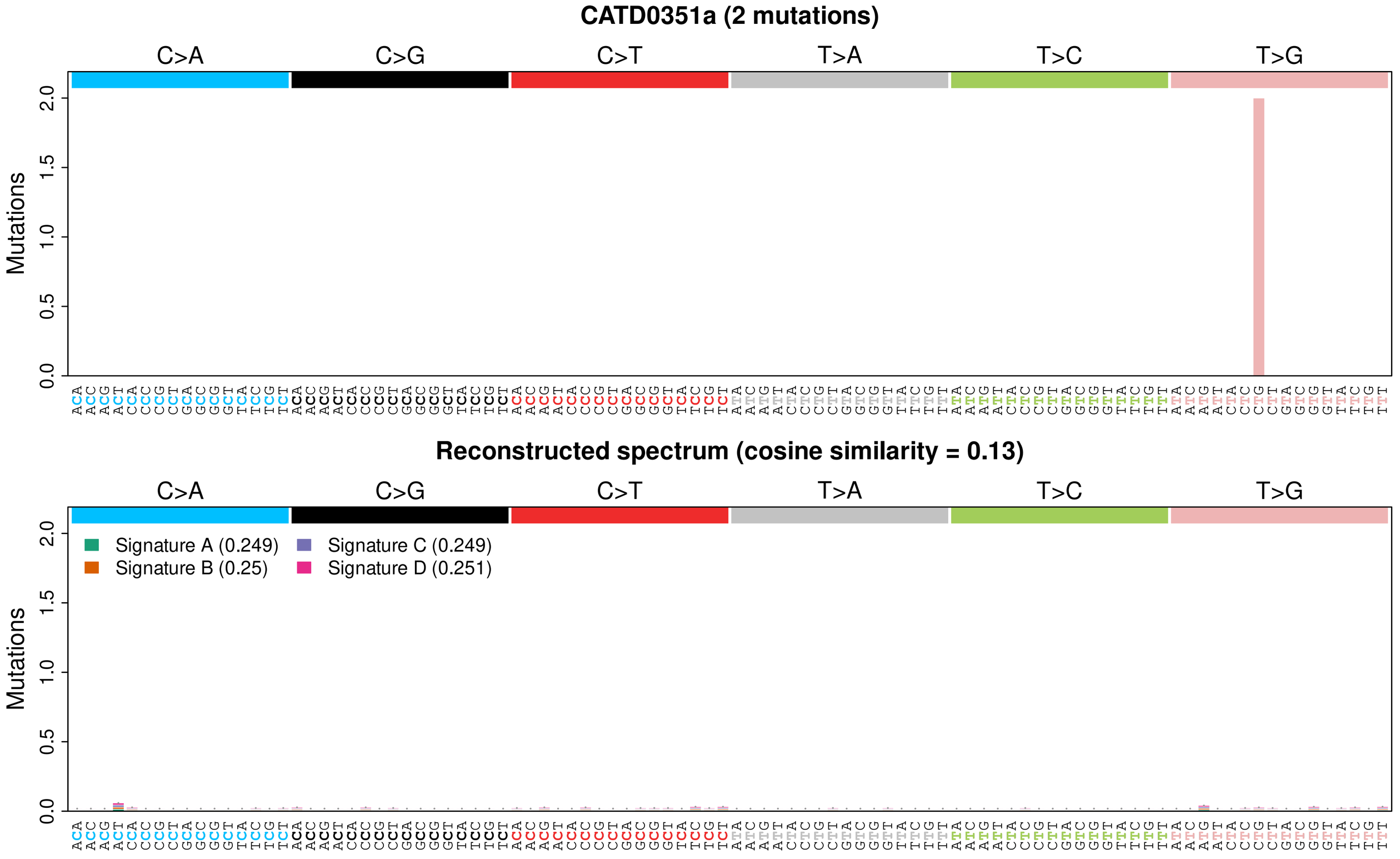

Reconstructed spectrum (cosine similarity = 0.13)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.249)
Signature B (0.251)
Signature C (0.251)
Signature D (0.249)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

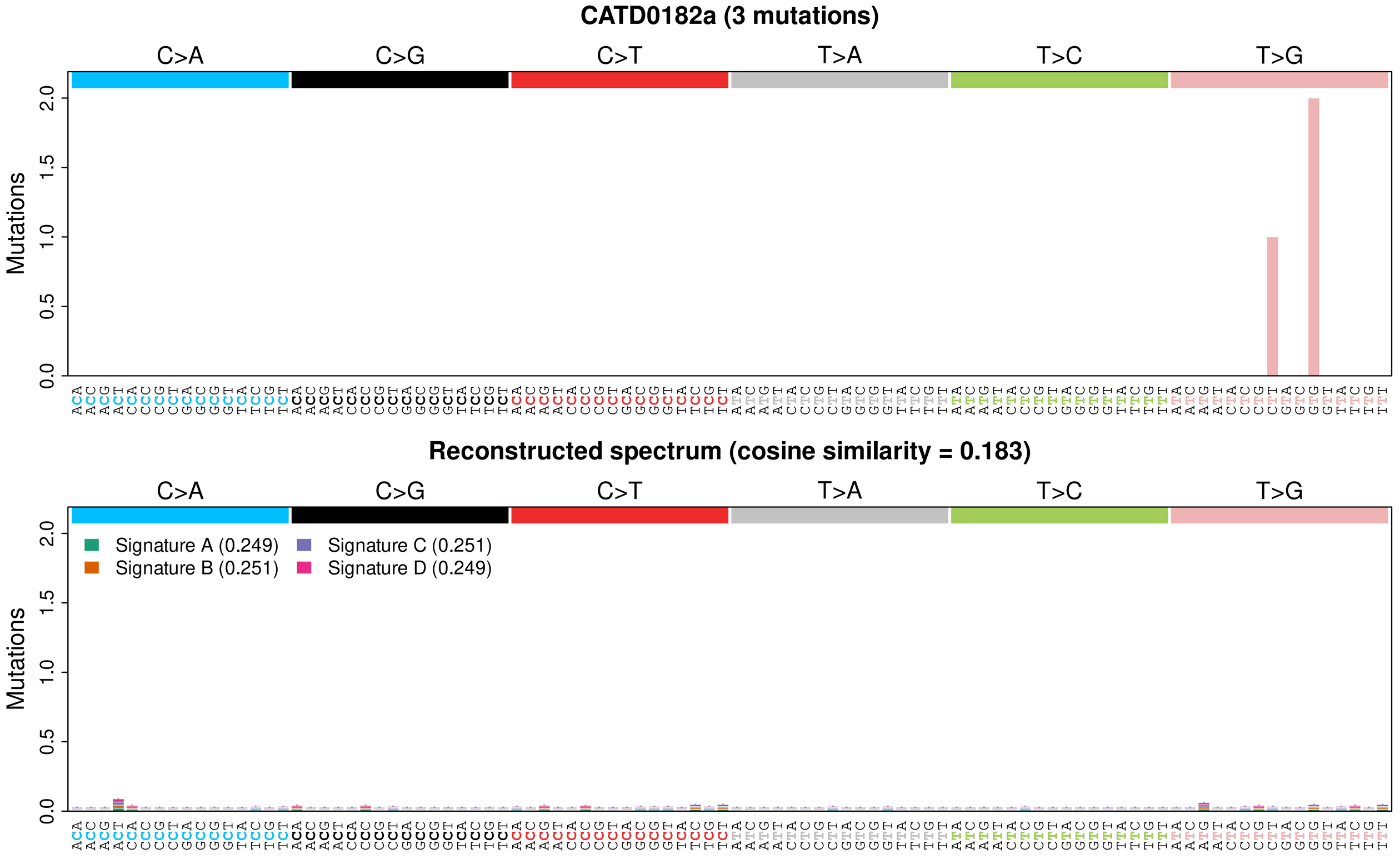
CATD0375a (3 mutations)

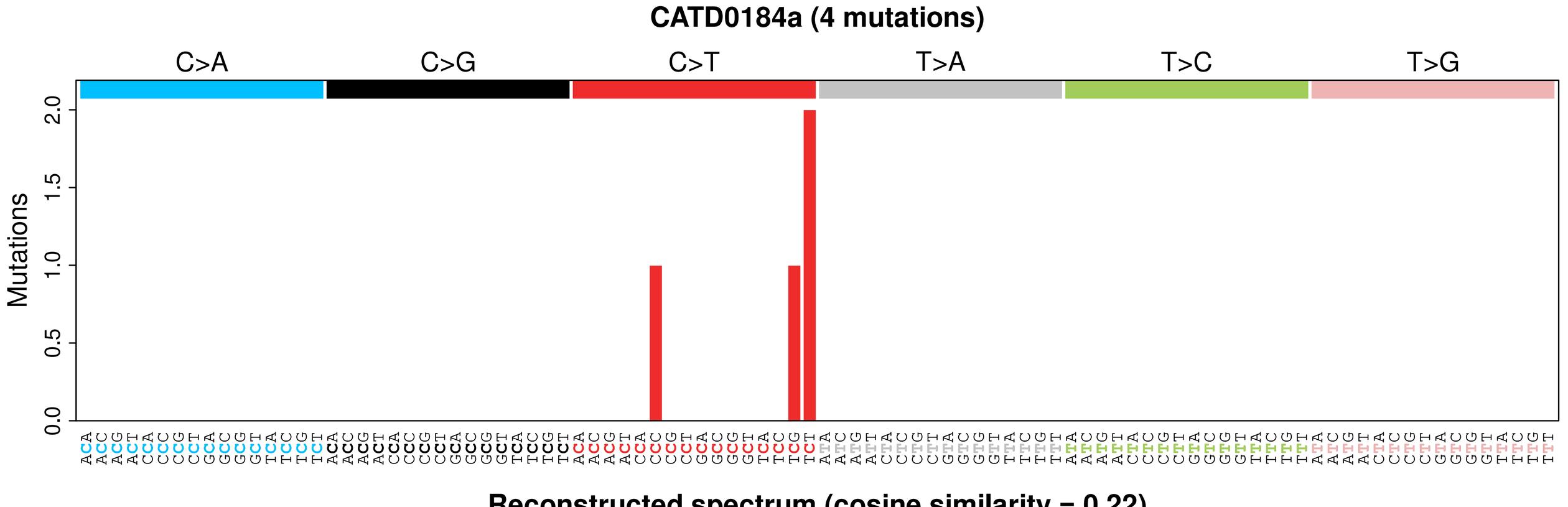


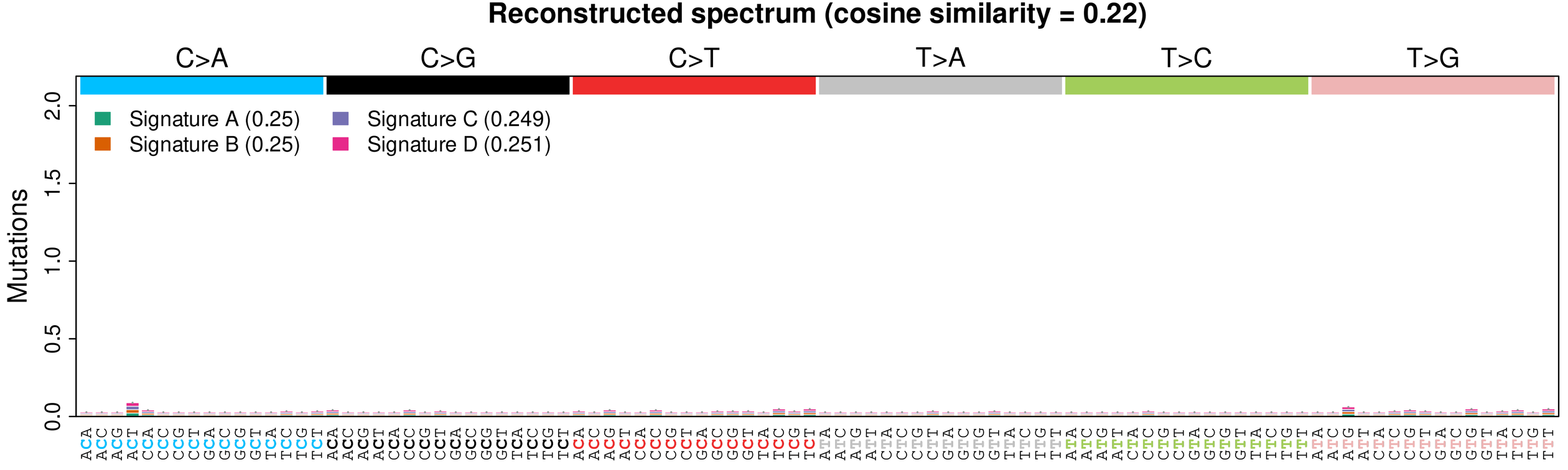
Reconstructed spectrum (cosine similarity = 0.174)



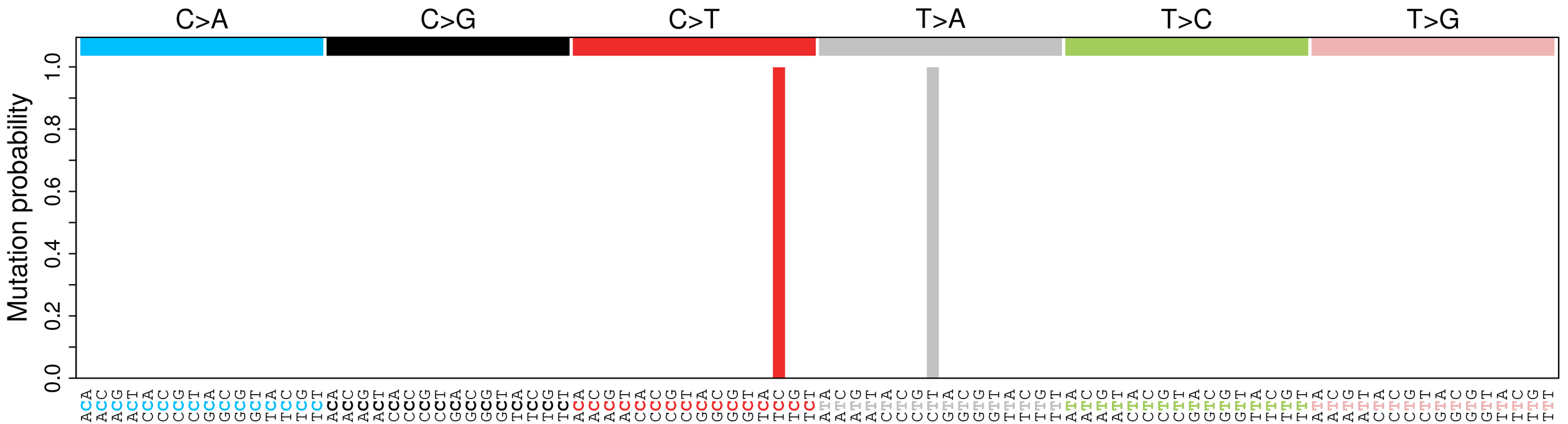

CATD0351a (2 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0
Reconstructed spectrum (cosine similarity = 0.13)
Signature A (0.249)
Signature B (0.25)
Signature C (0.249)
Signature D (0.251)


CATD0182a (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 = 0.183)
Signature A (0.249)
Signature B (0.251)
Signature C (0.251)
Signature D (0.249)

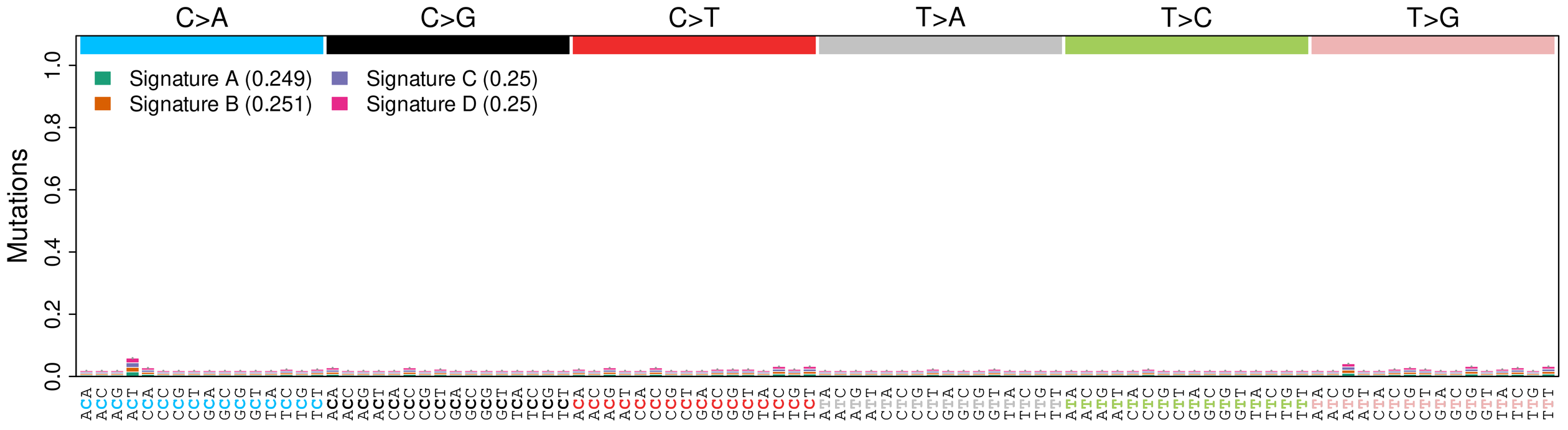

CATD0184a (4 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.22)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.25)
Signature B (0.25)
Signature C (0.249)
Signature D (0.251)
Mutations
0.0
0.5
1.0
1.5
2.0

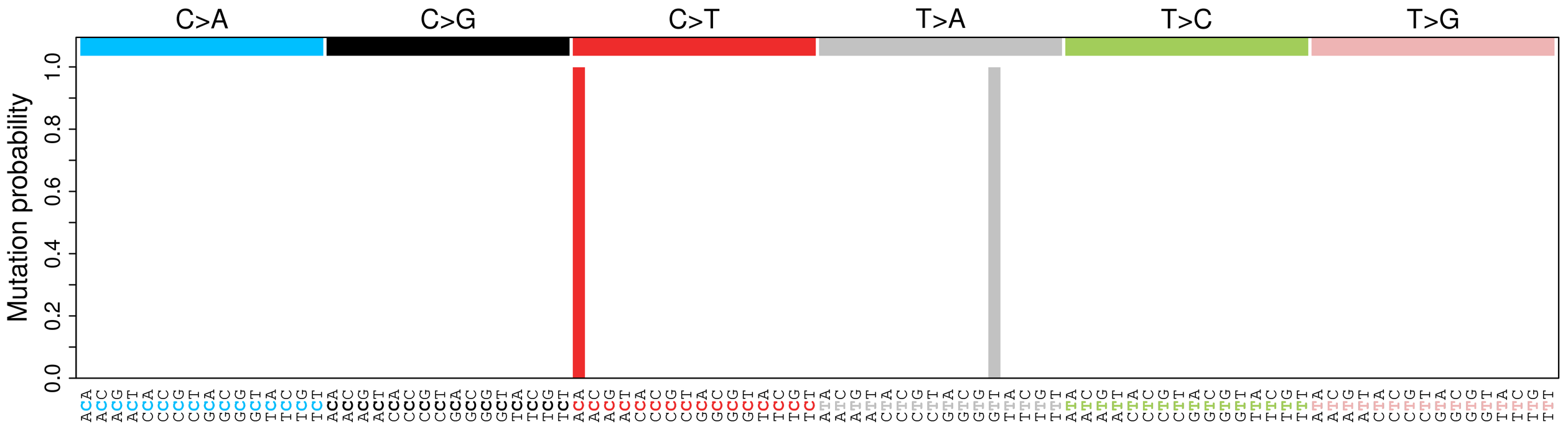
CATD0179a



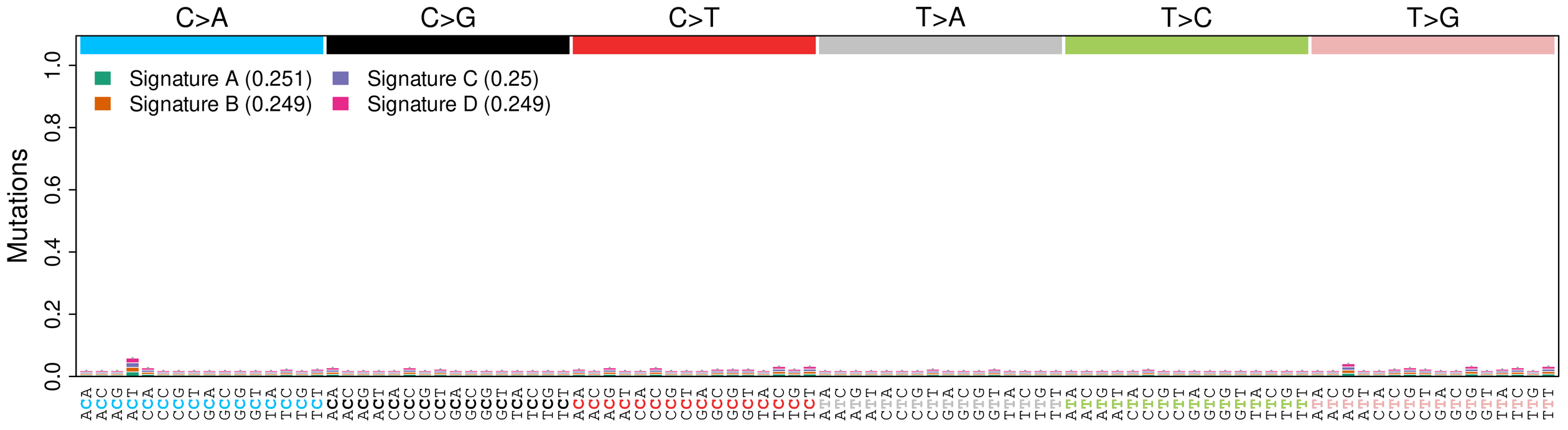
Reconstructed spectrum (cosine similarity = 0.183)



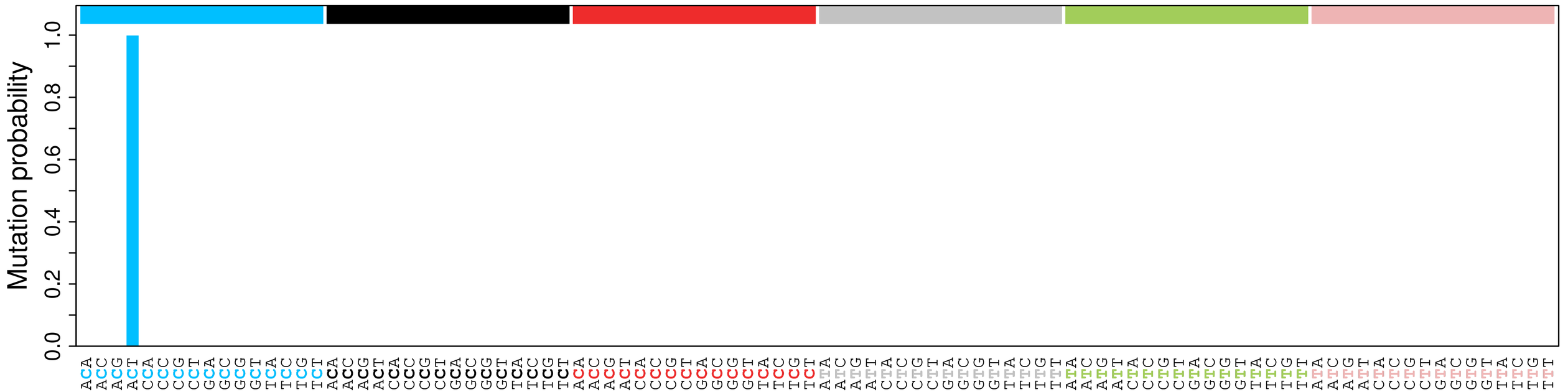
CATD0370a



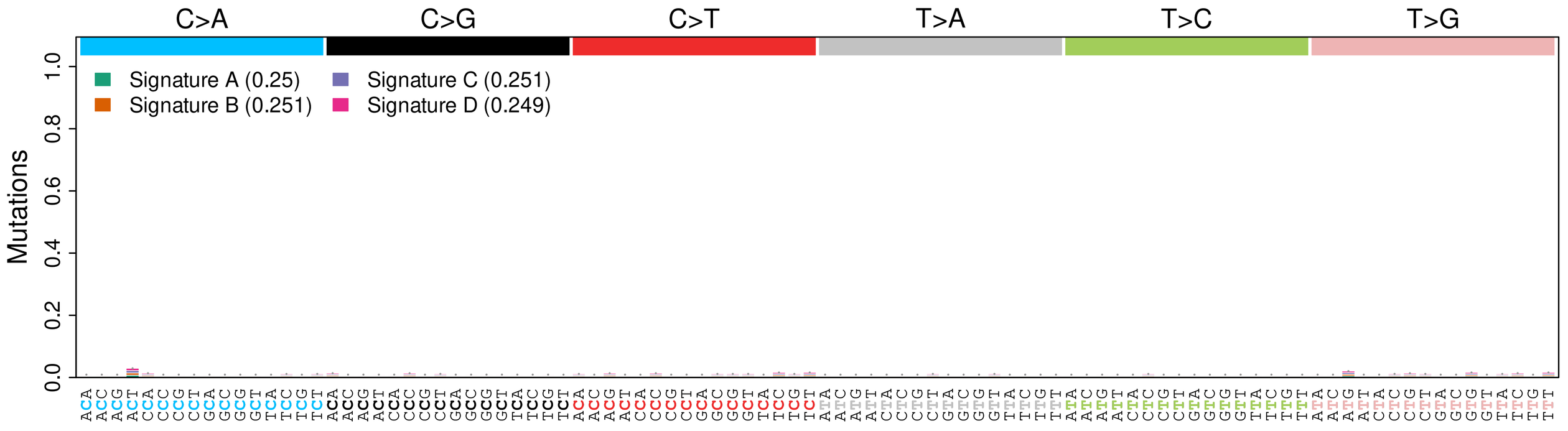
Reconstructed spectrum (cosine similarity = 0.153)

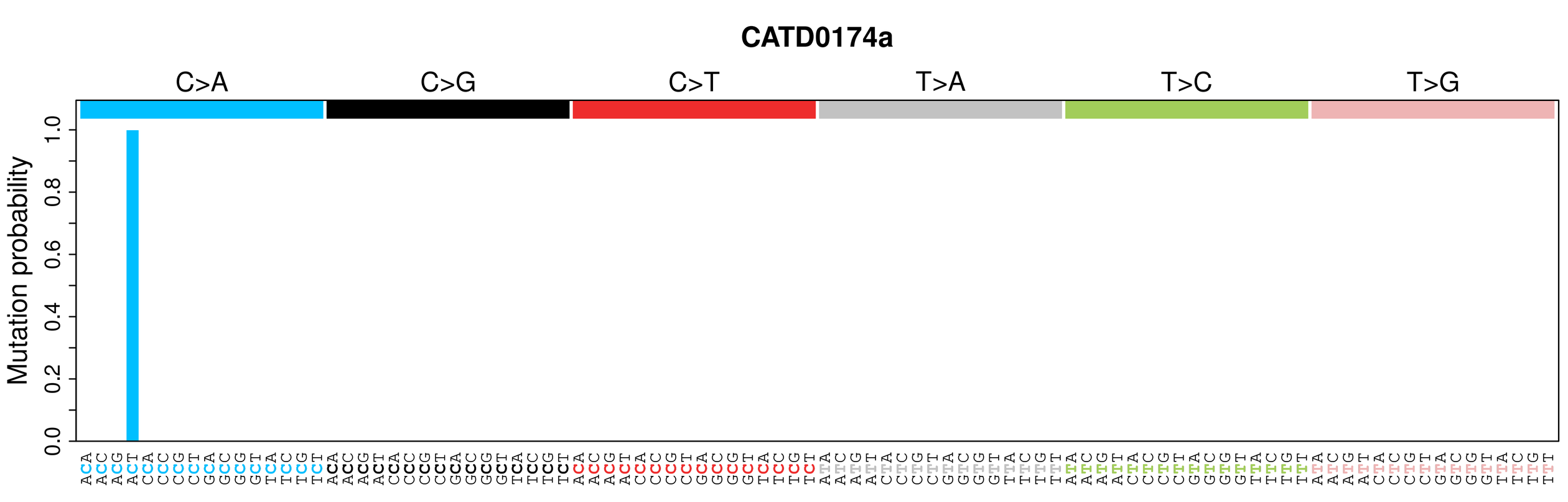


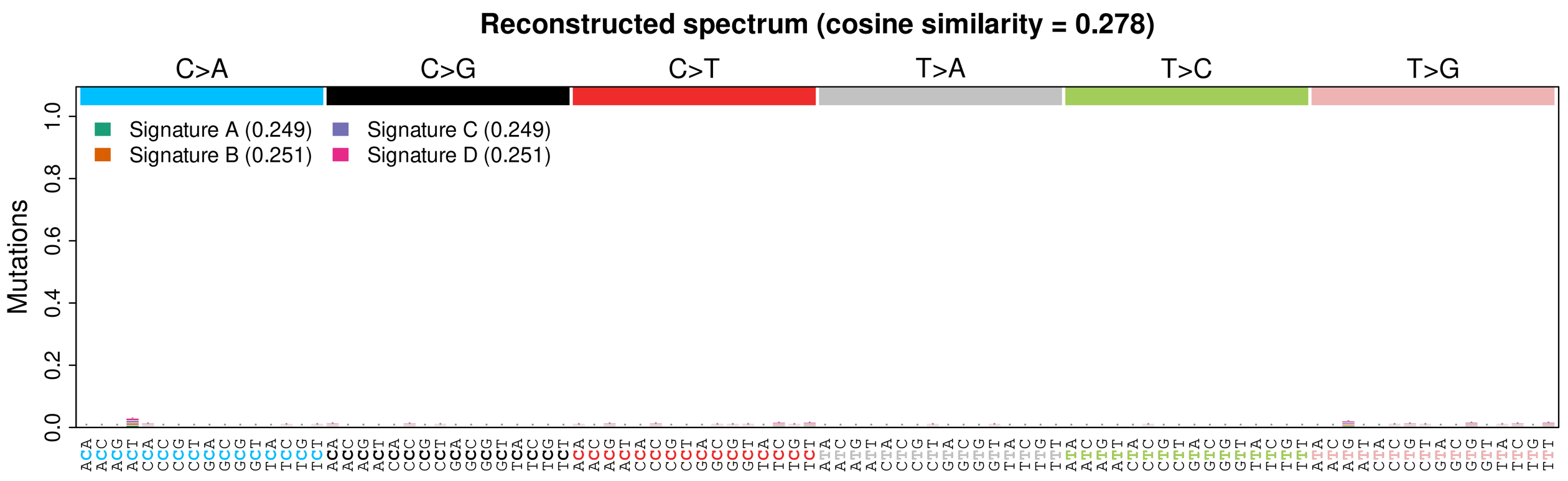
CATD0167a

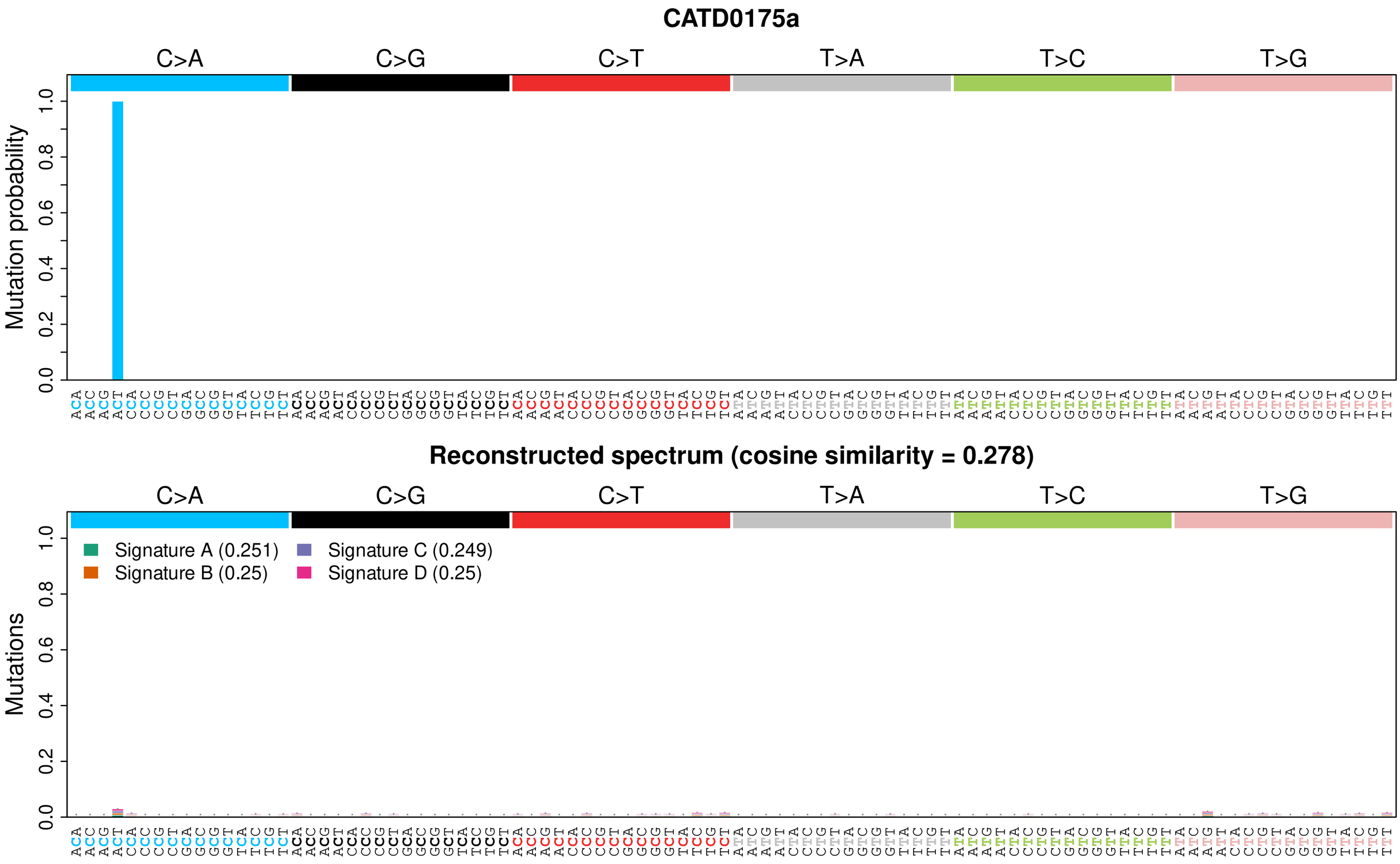


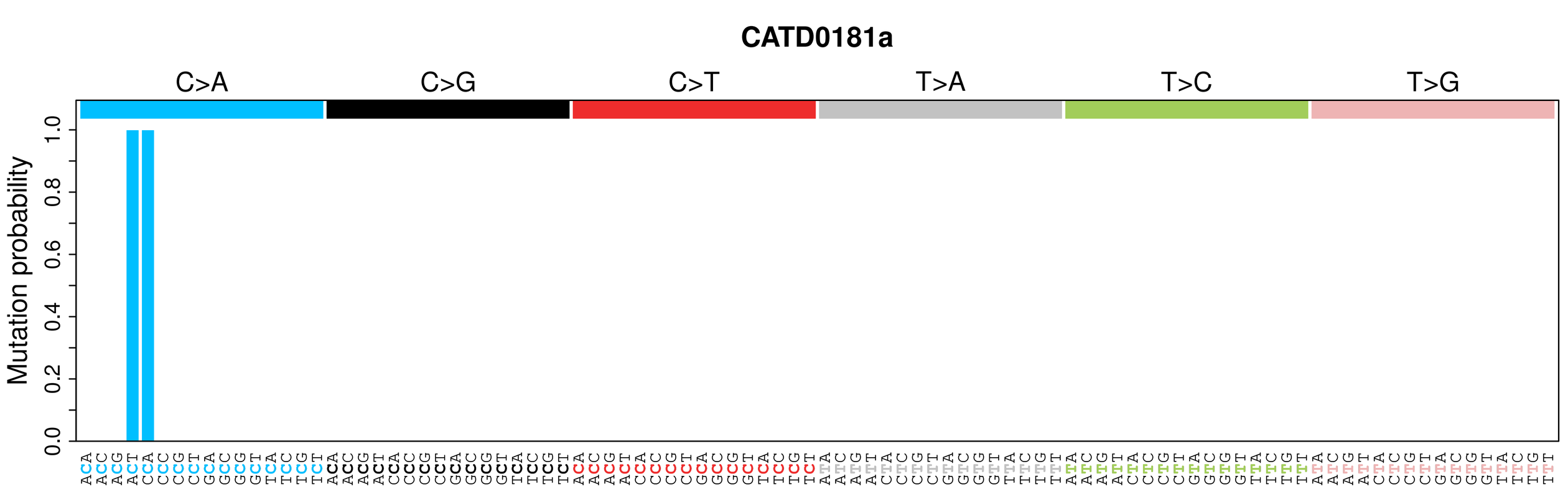
Reconstructed spectrum (cosine similarity = 0.278)

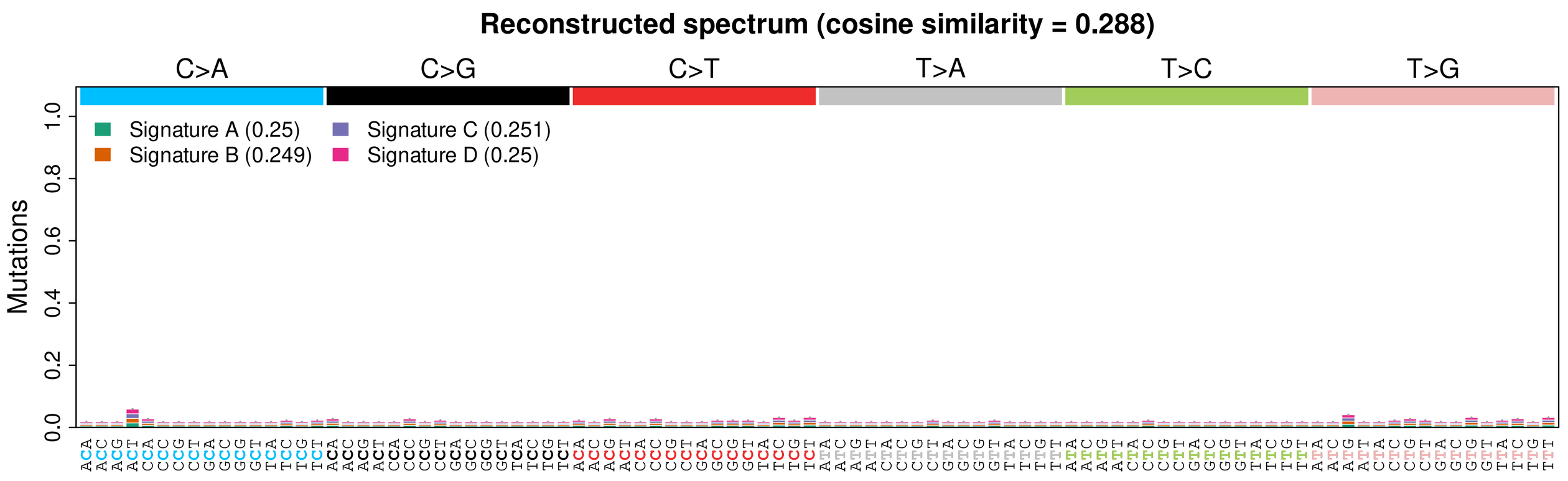



CATD0174a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0

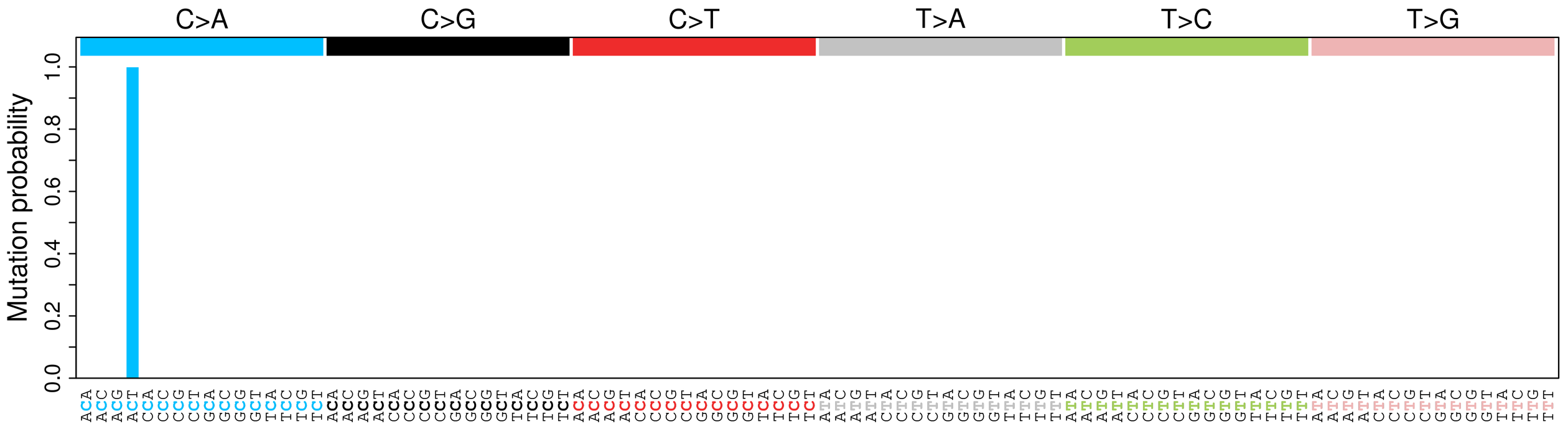

Reconstructed spectrum (cosine similarity = 0.278)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.249)
Signature B (0.251)
Signature C (0.249)
Signature D (0.251)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0


CATD0175a
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 = 0.278)
Signature A (0.251)
Signature B (0.25)
Signature C (0.249)
Signature D (0.25)
Mutations

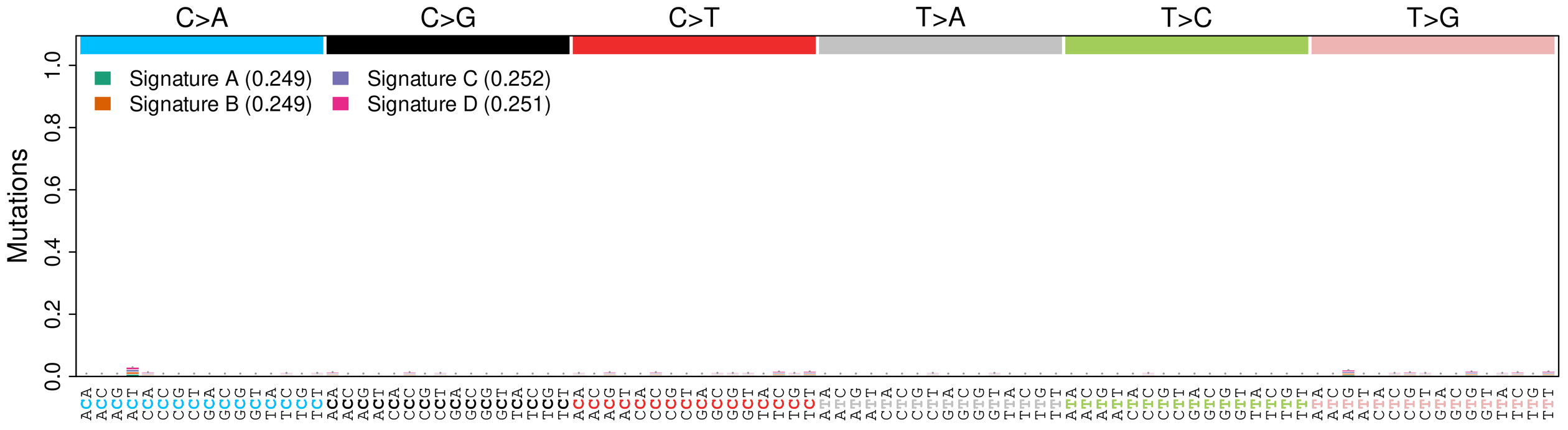

CATD0181a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0


Reconstructed spectrum (cosine similarity = 0.288)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.25)
Signature B (0.249)
Signature C (0.251)
Signature D (0.25)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

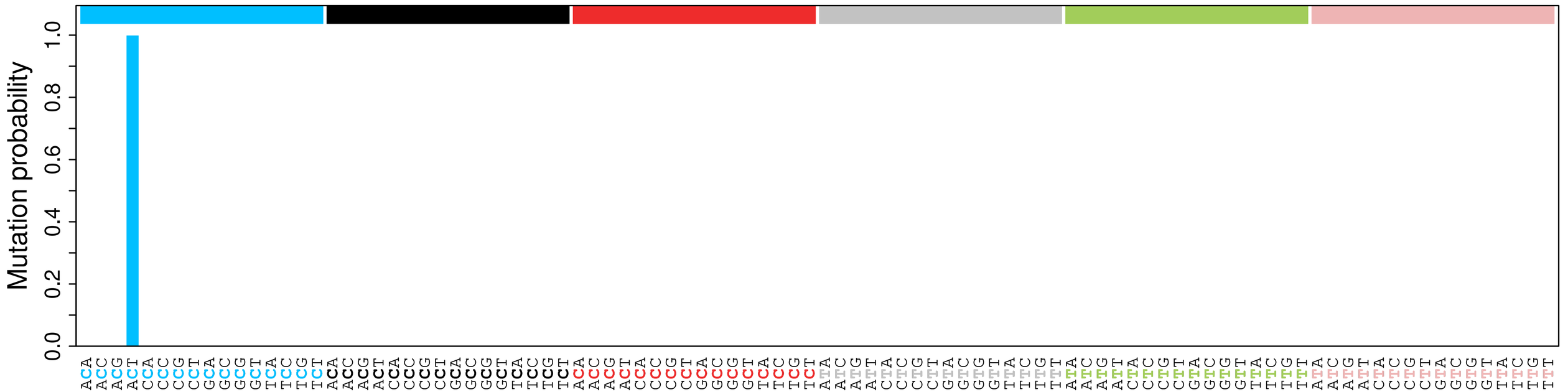
CATD0355a



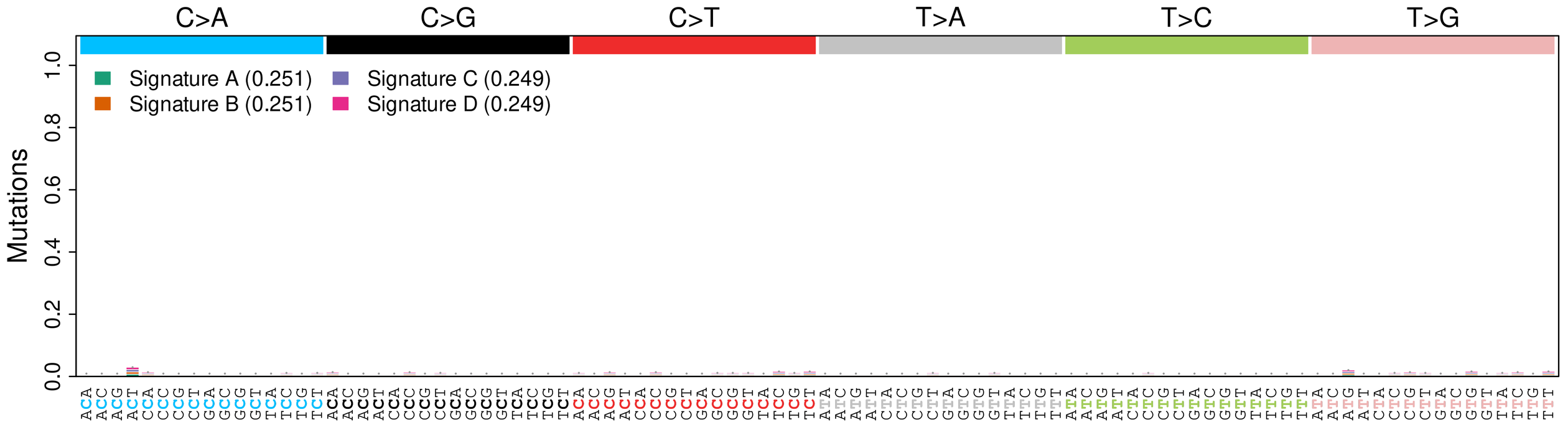
Reconstructed spectrum (cosine similarity = 0.278)

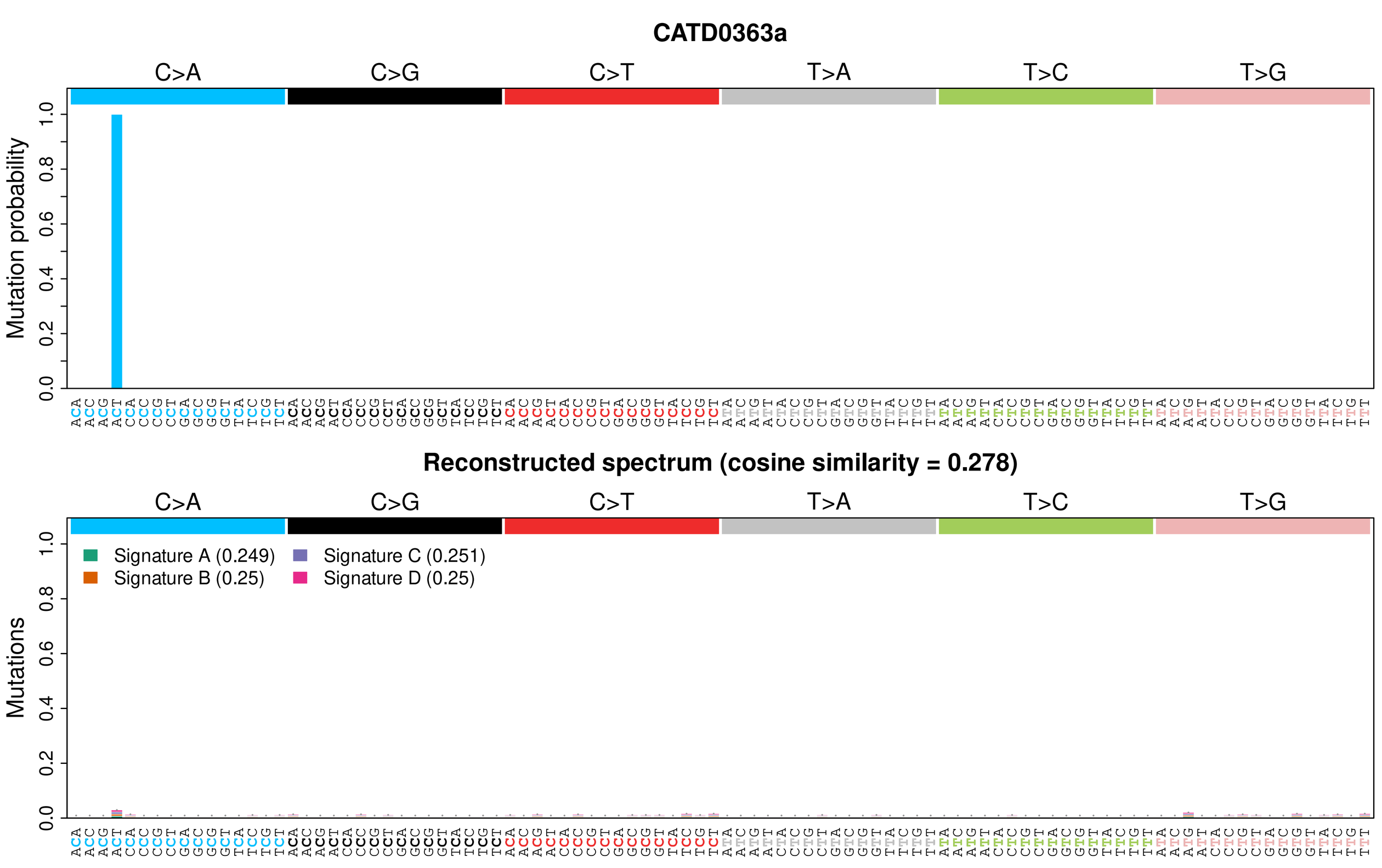


CATD0362a

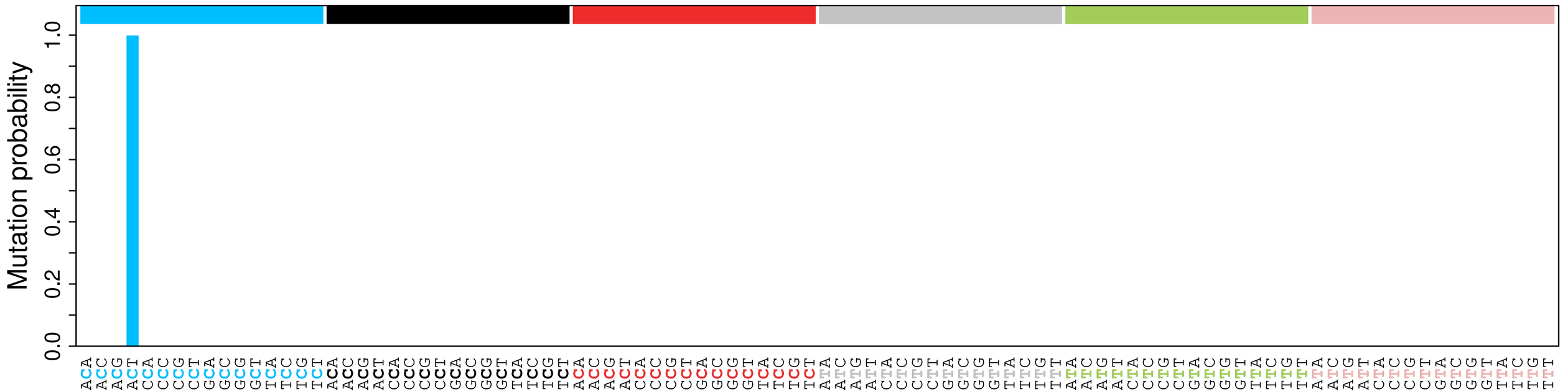


Reconstructed spectrum (cosine similarity = 0.278)

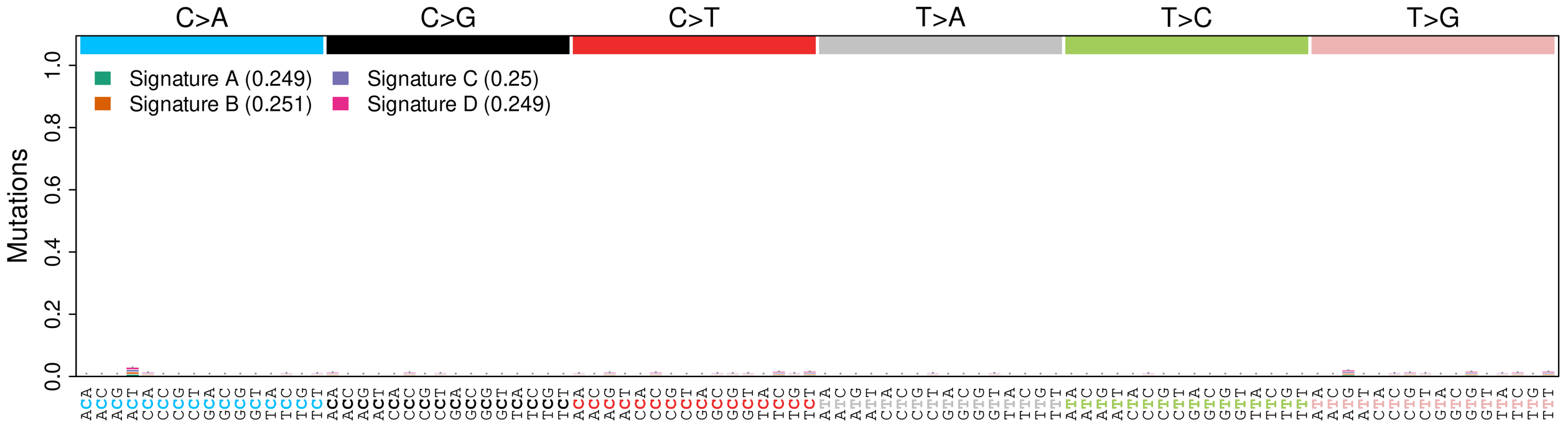



CATD0363a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0
Reconstructed spectrum (cosine similarity = 0.278)
Signature A (0.249)
Signature B (0.25)
Signature C (0.251)
Signature D (0.25)
Mutations

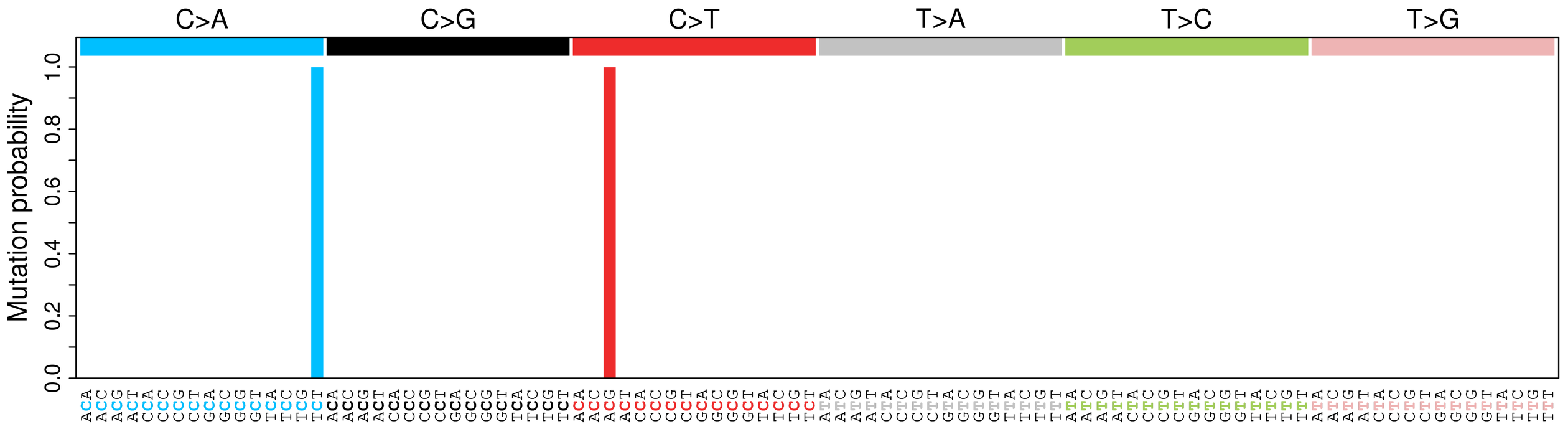
CATD0365a



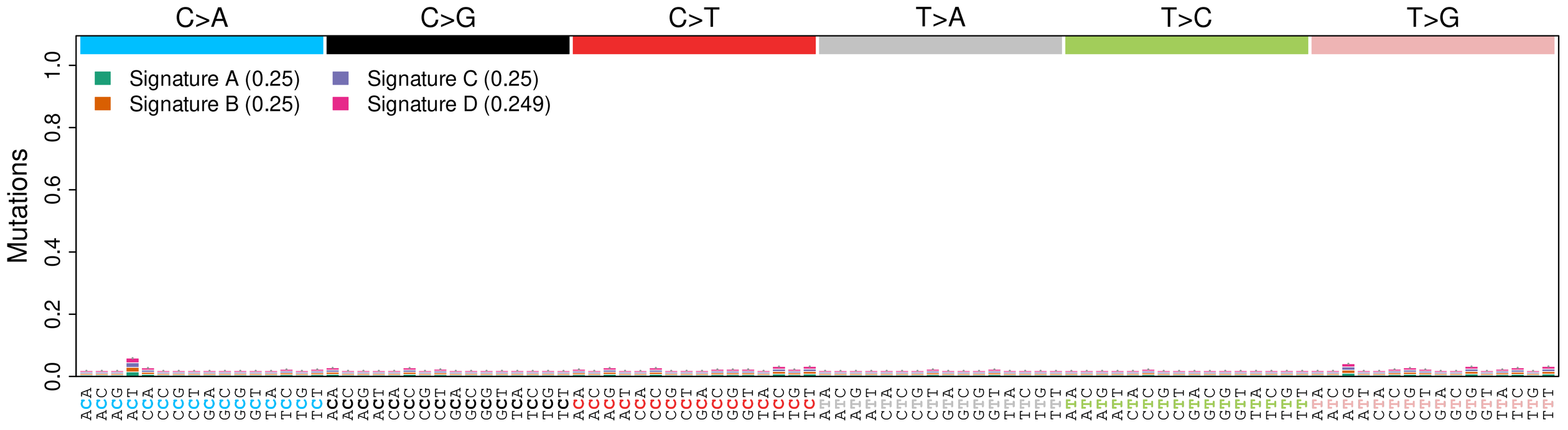
Reconstructed spectrum (cosine similarity = 0.278)

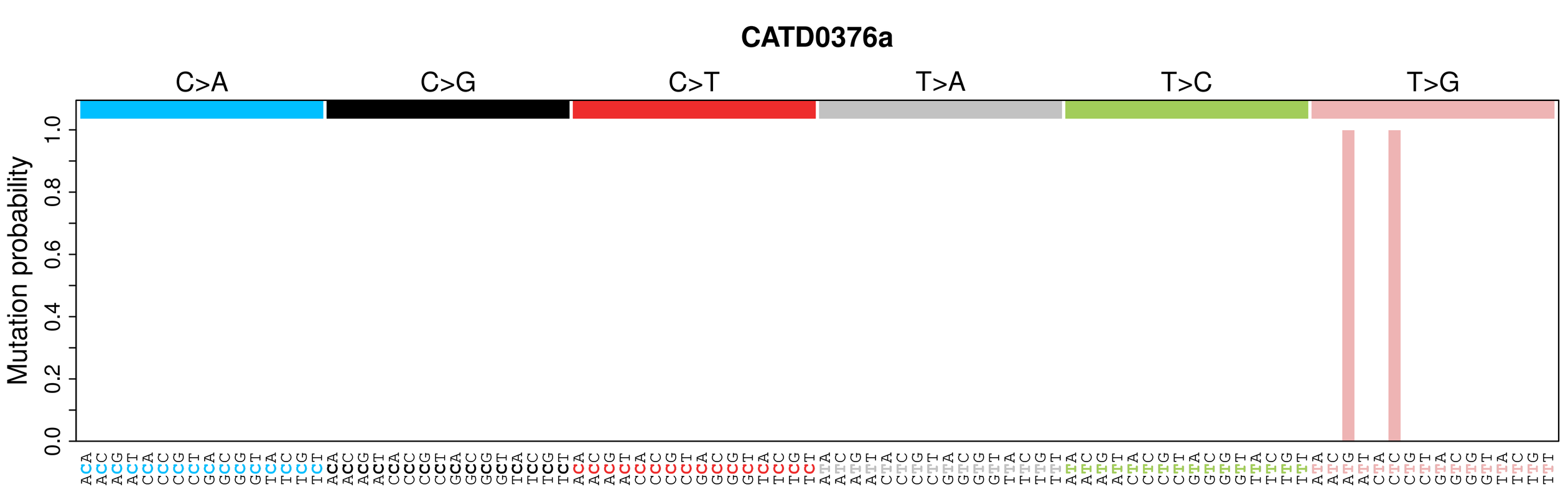


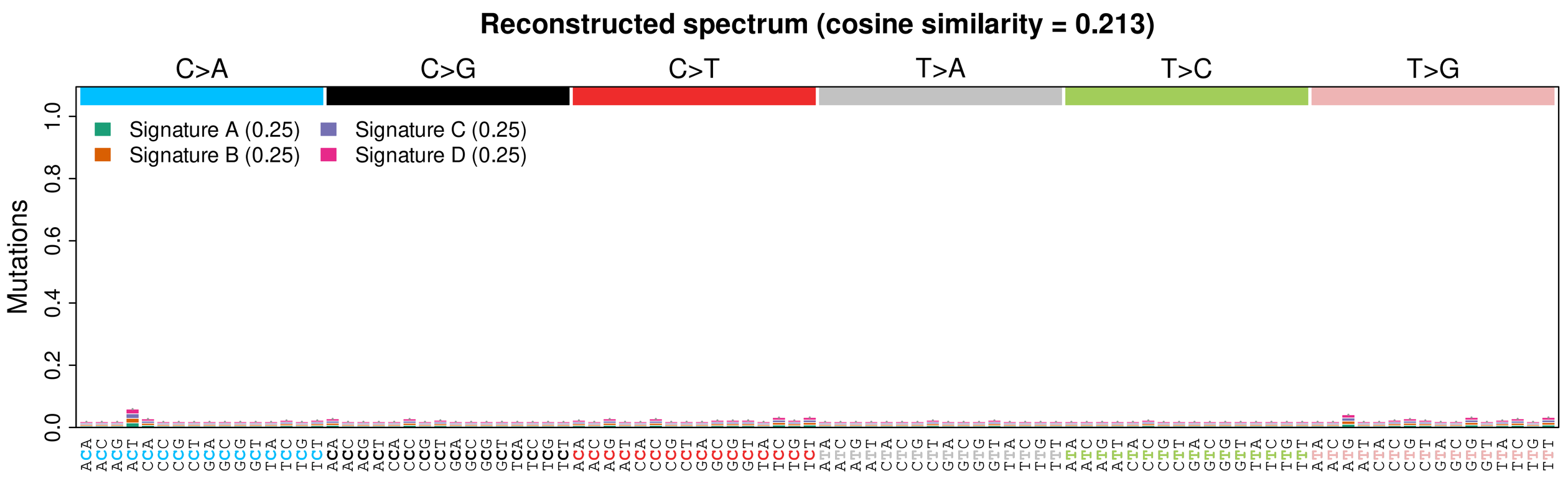
CATD0177a



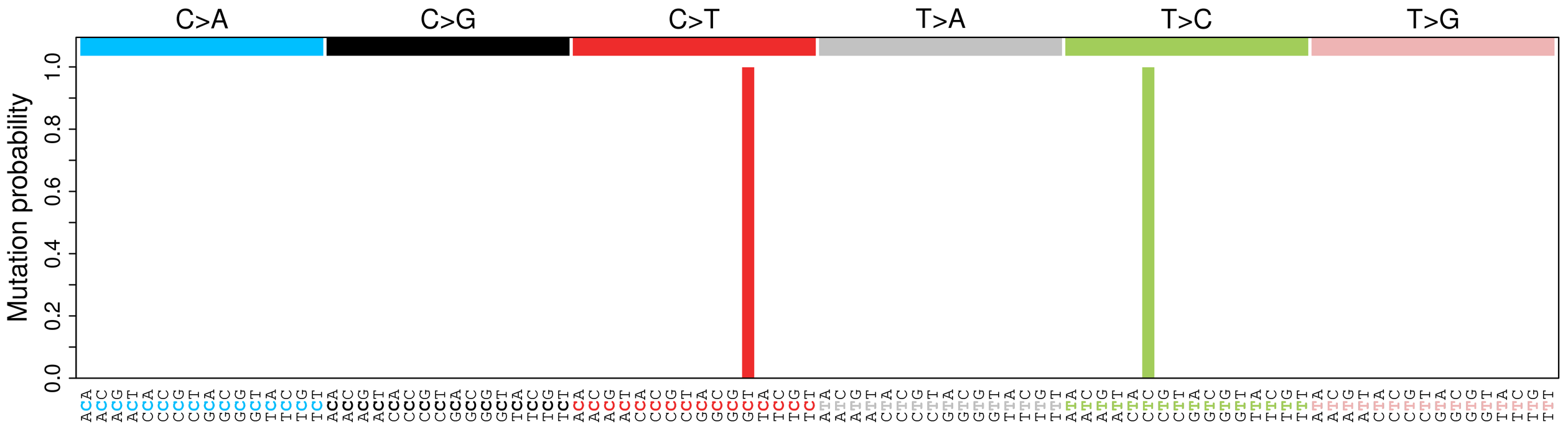
Reconstructed spectrum (cosine similarity = 0.168)



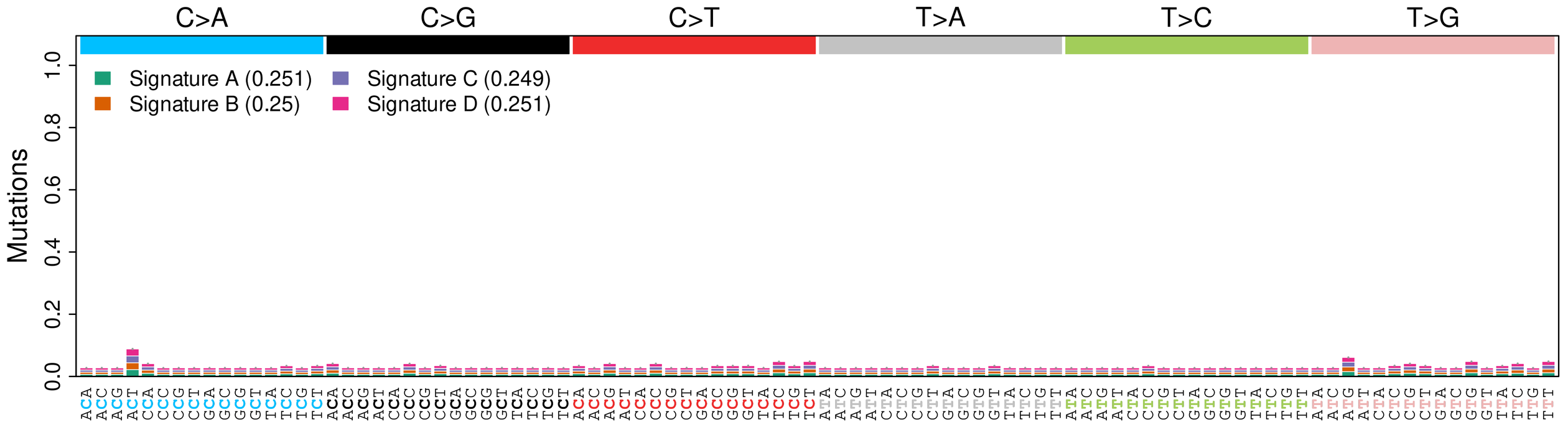

CATD0376a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0


Reconstructed spectrum (cosine similarity = 0.213)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.25)
Signature B (0.25)
Signature C (0.25)
Signature D (0.25)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

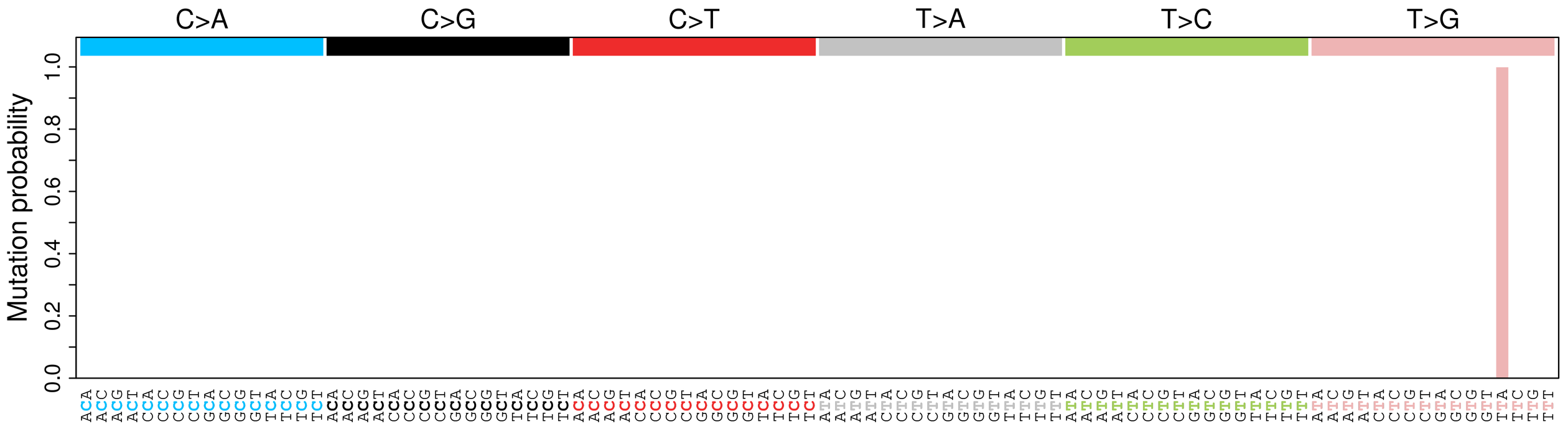
CATD0367a



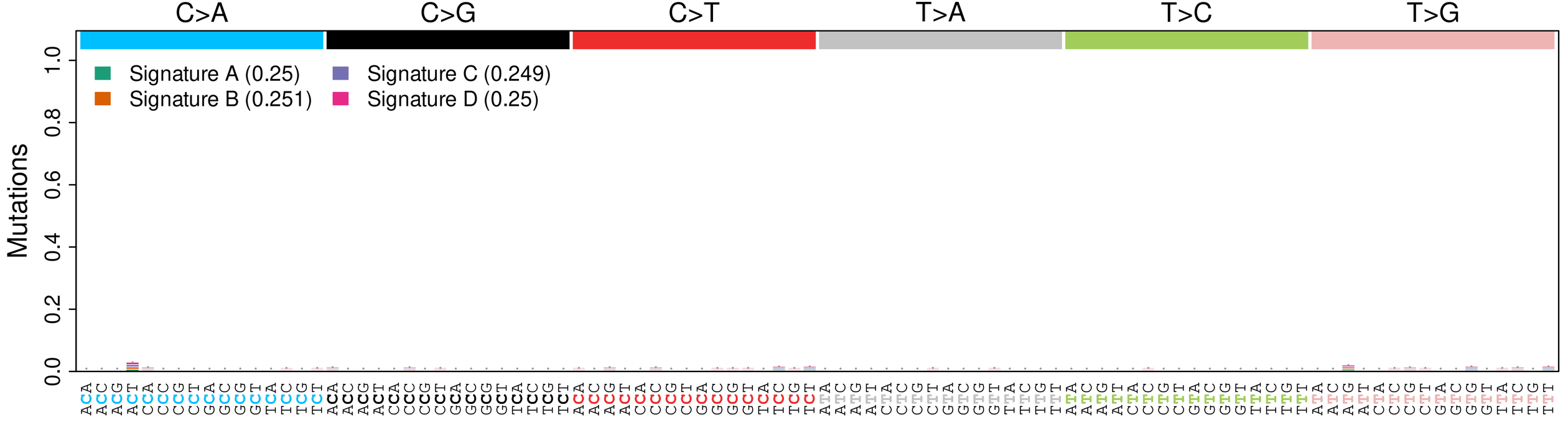
Reconstructed spectrum (cosine similarity = 0.153)

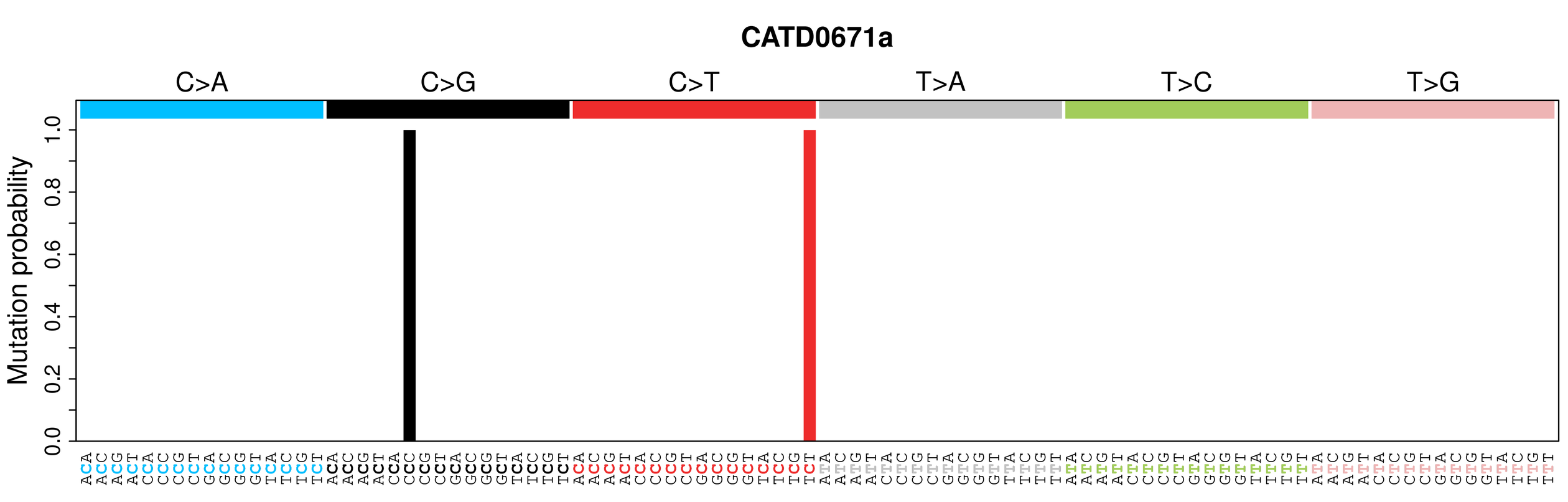


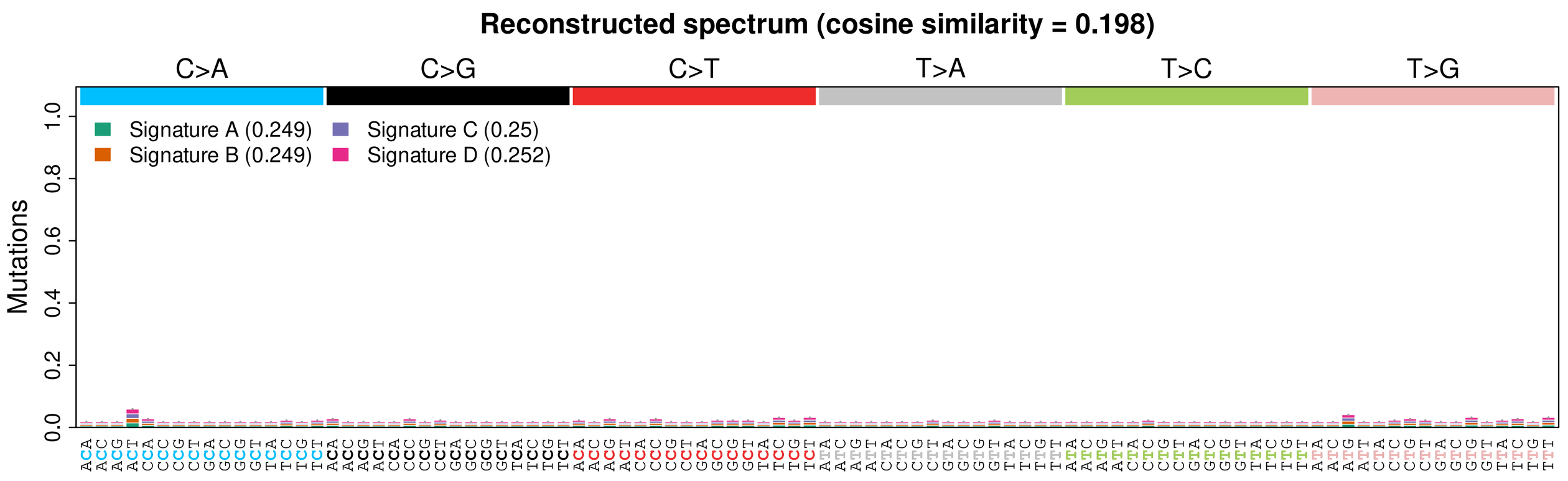
CATD0364a



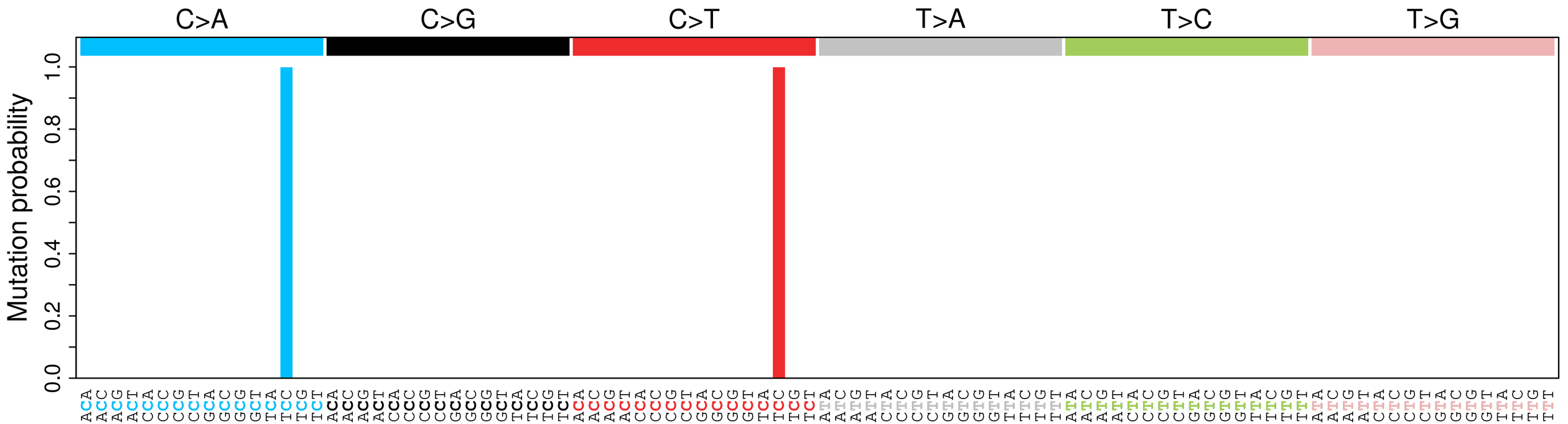
Reconstructed spectrum (cosine similarity = 0.108)



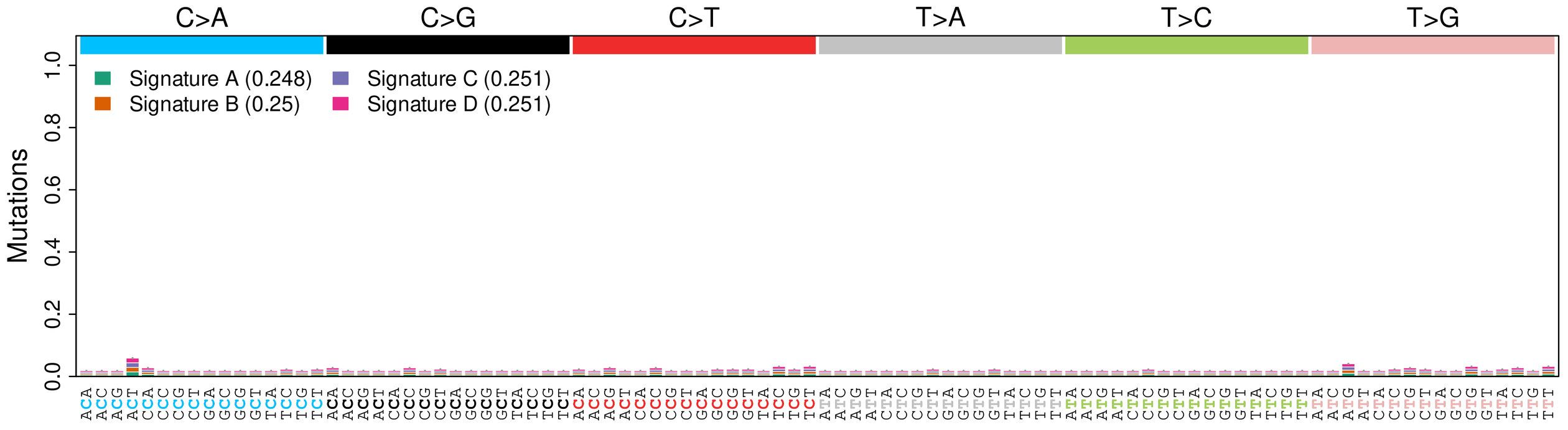

CATD0671a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0

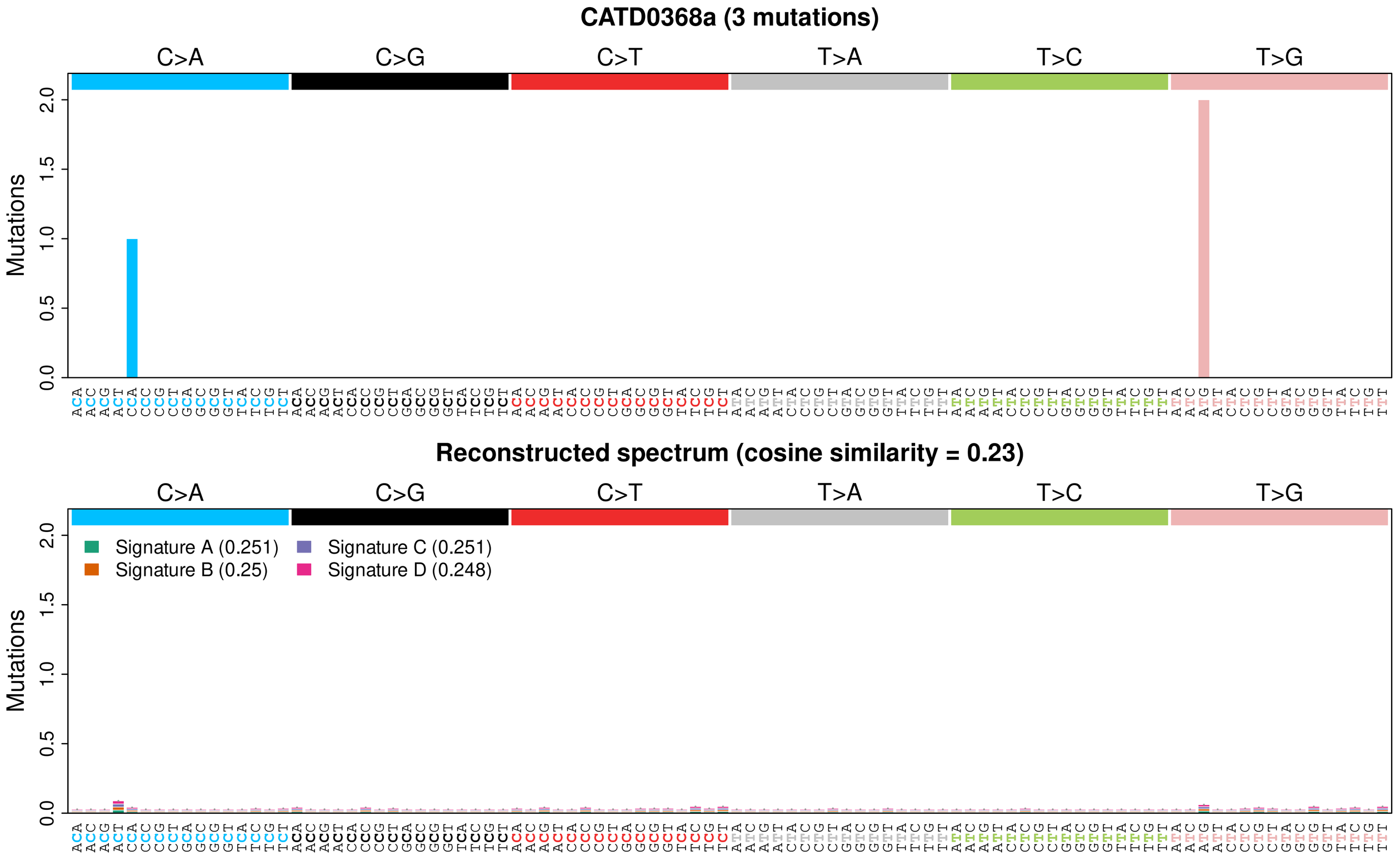

Reconstructed spectrum (cosine similarity = 0.198)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.249)
Signature B (0.249)
Signature C (0.25)
Signature D (0.252)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

CATD0163a



Reconstructed spectrum (cosine similarity = 0.182)




CATD0368a (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 = 0.23)
Signature A (0.251)
Signature B (0.25)
Signature C (0.251)
Signature D (0.248)