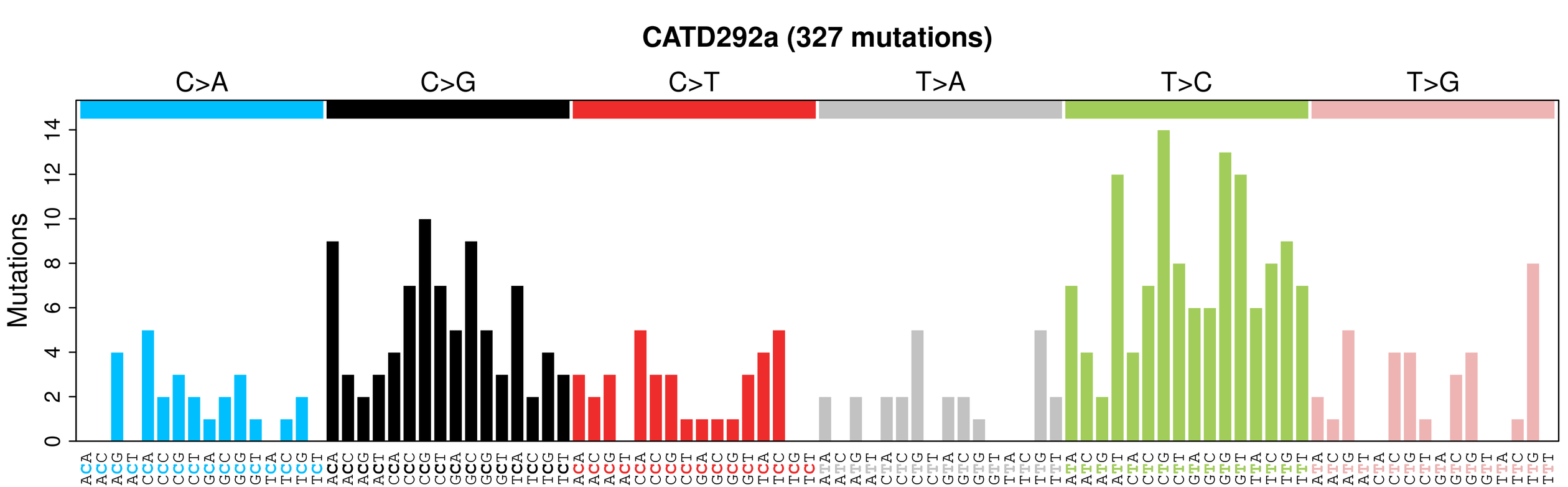
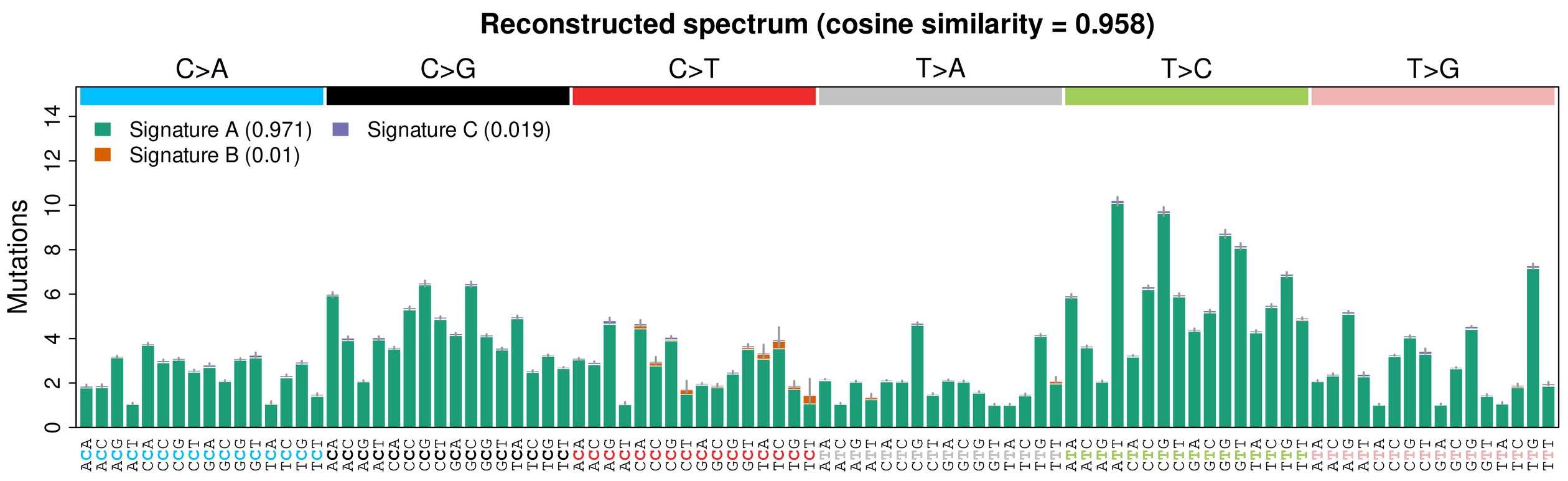
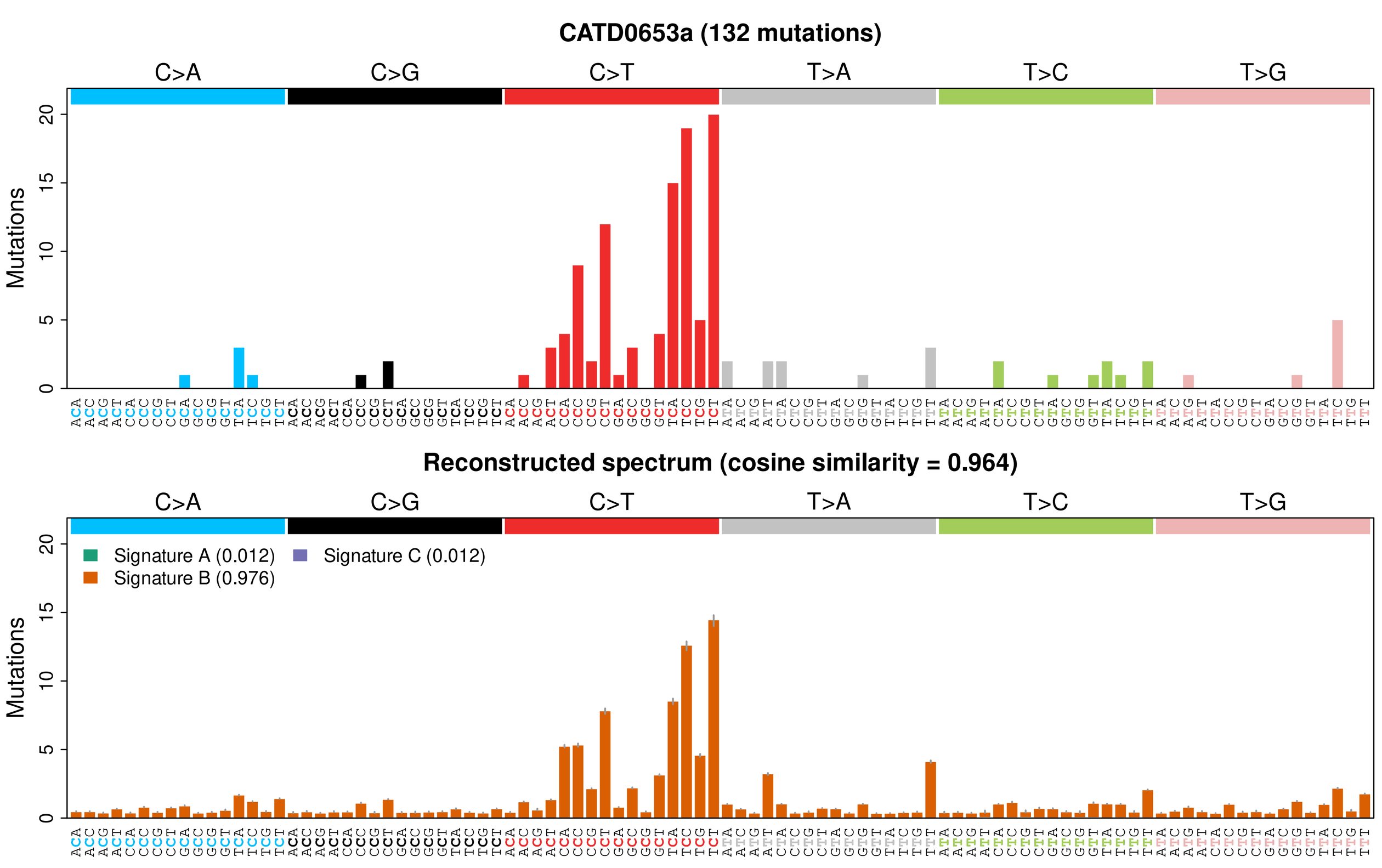
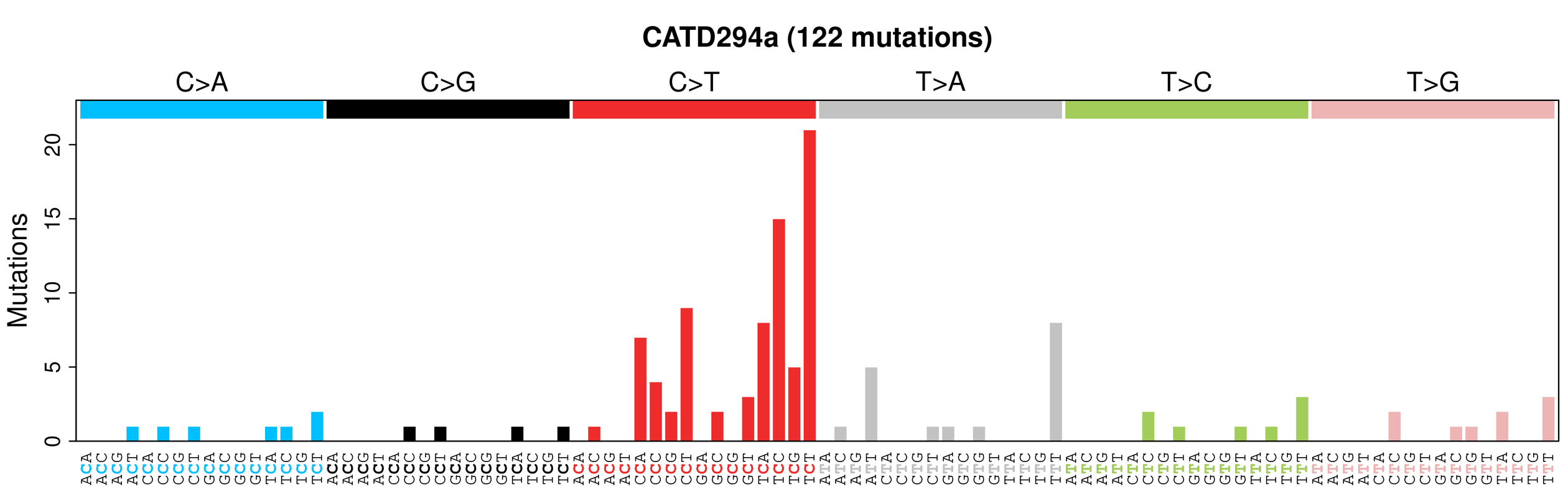
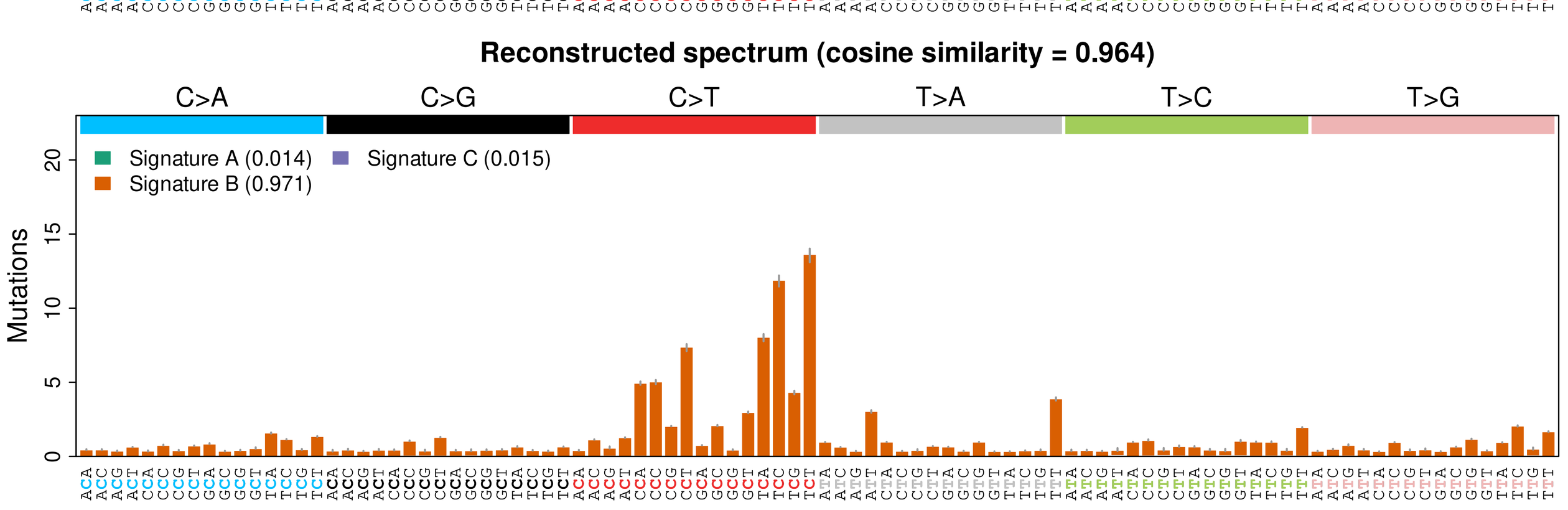
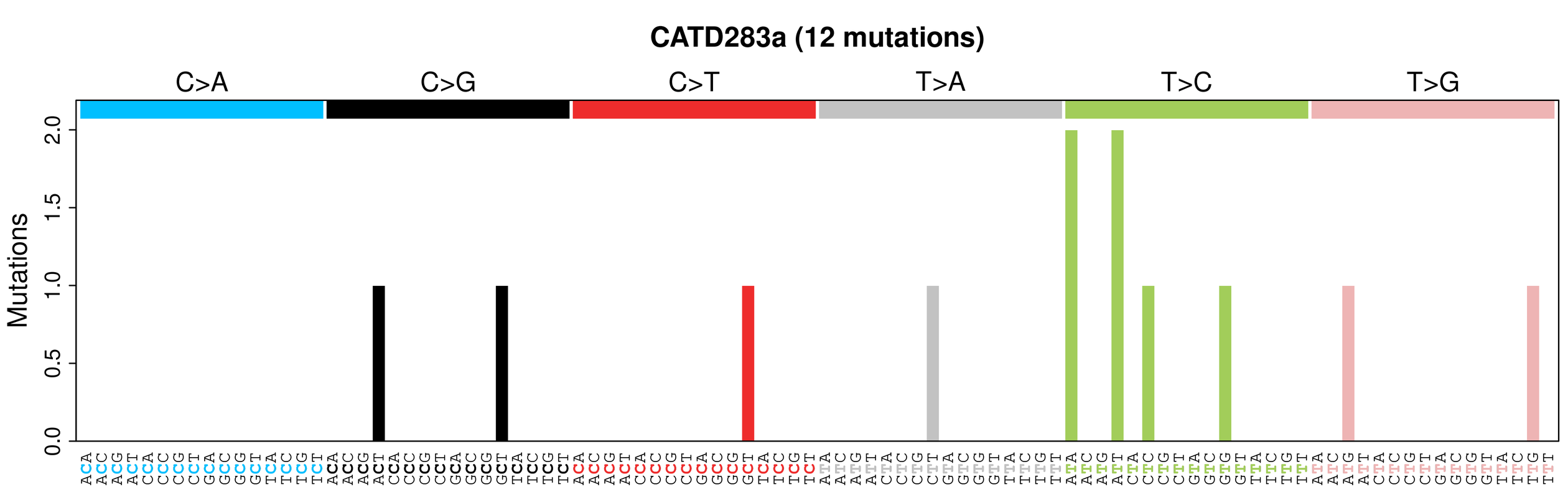

CATD292a (327 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
14

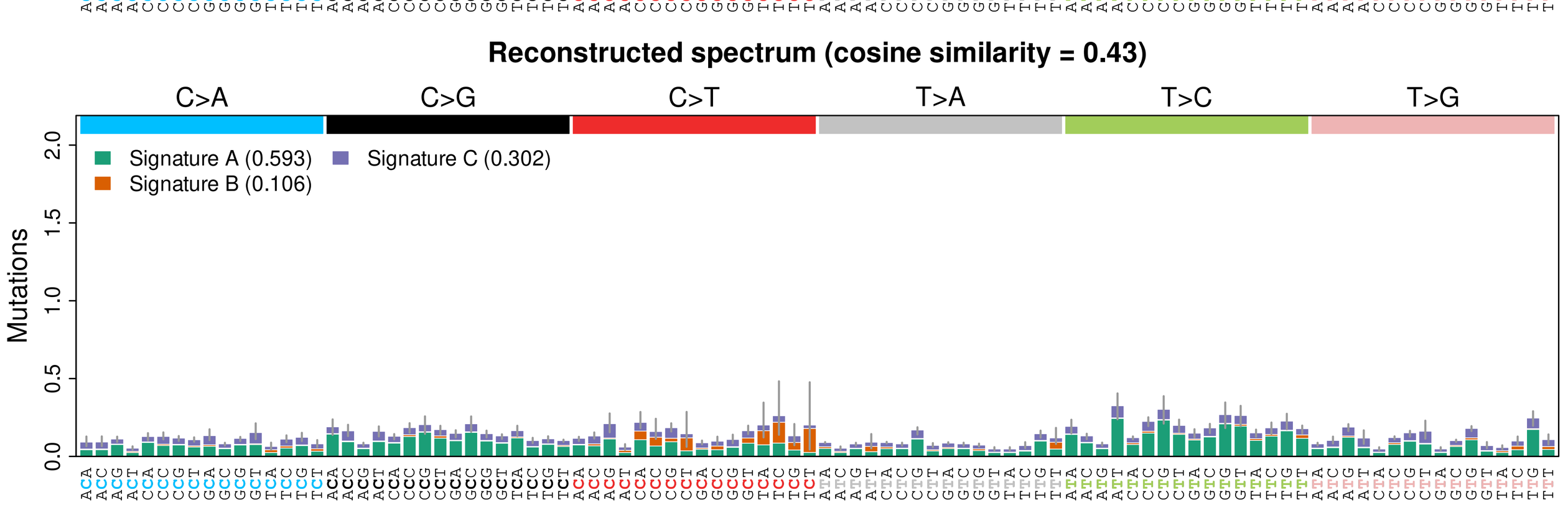

Reconstructed spectrum (cosine similarity = 0.958)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.971)
Signature B (0.01)
Signature C (0.019)
Mutations
0
2
4
6
8
10
12
14


CATD0653a (132 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
Reconstructed spectrum (cosine similarity = 0.964)
Signature A (0.012)
Signature B (0.976)
Signature C (0.012)

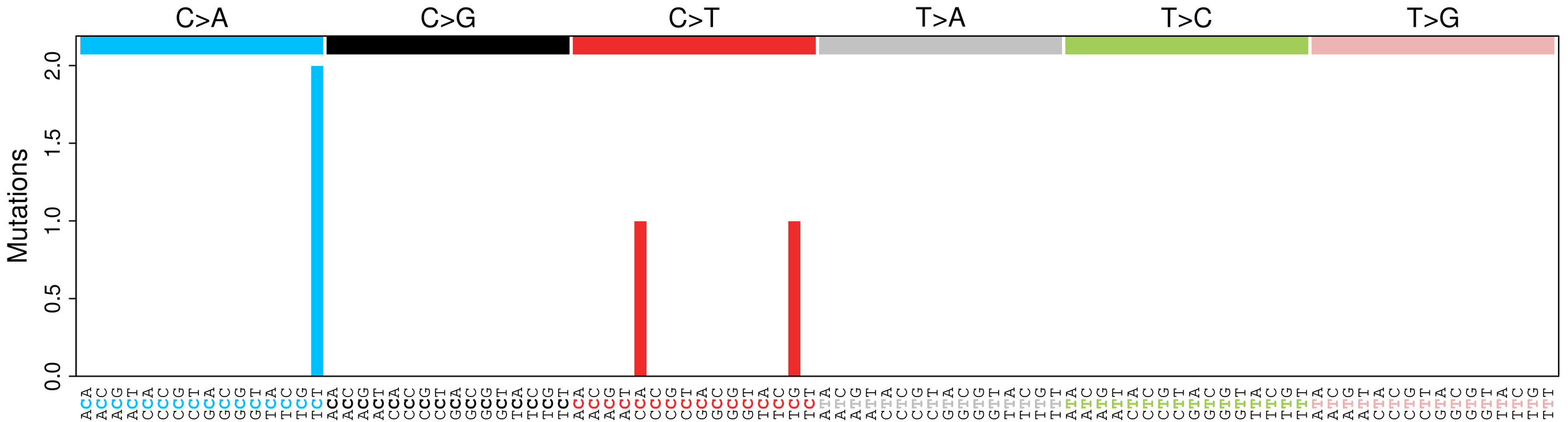

CATD294a (122 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20


Reconstructed spectrum (cosine similarity = 0.964)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.014)
Signature B (0.971)
Signature C (0.015)
Mutations
0
5
10
15
20

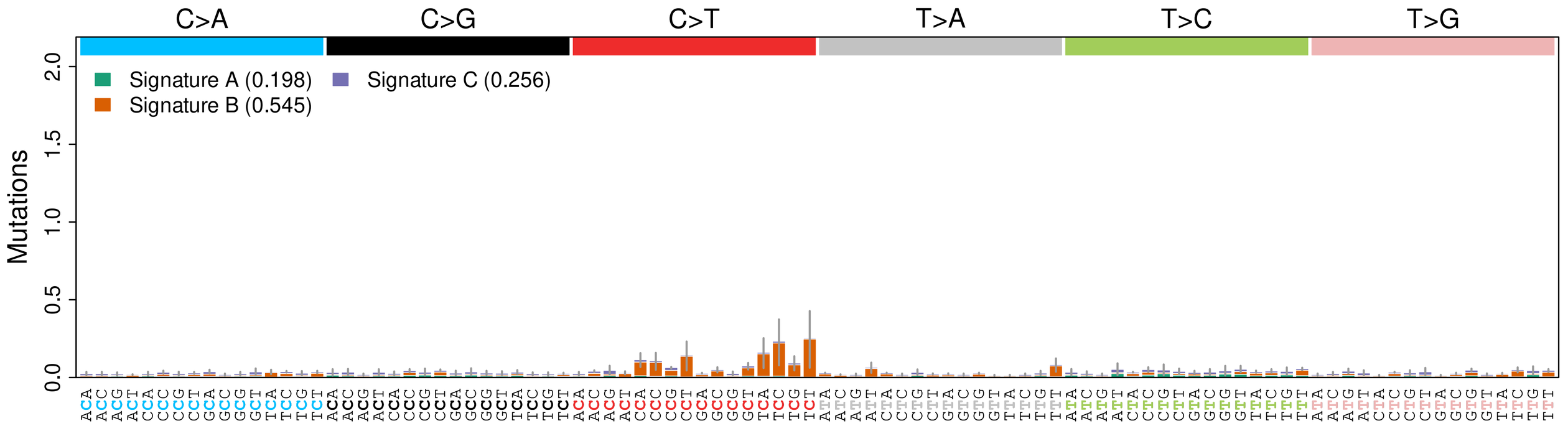

CATD283a (12 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.43)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.593)
Signature B (0.106)
Signature C (0.302)
Mutations
0.0
0.5
1.0
1.5
2.0

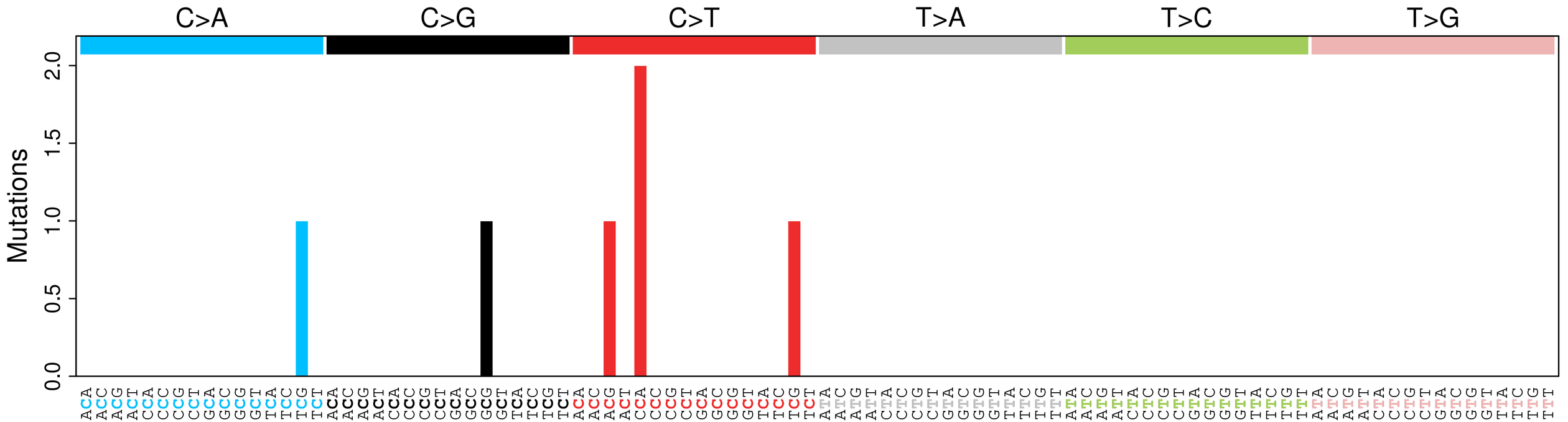
CATD0645a (4 mutations)



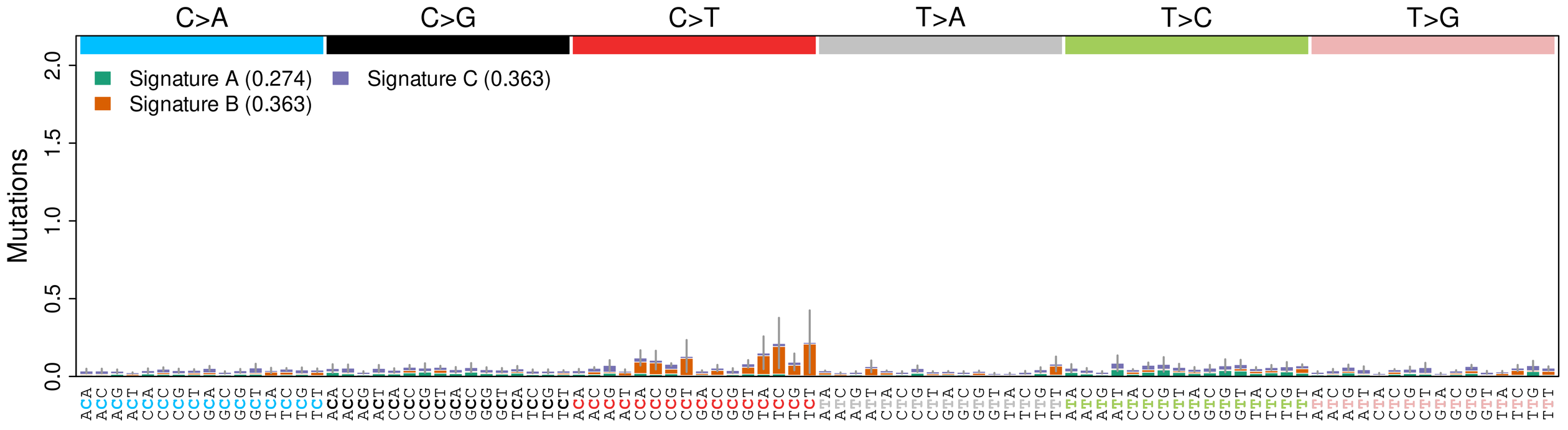
Reconstructed spectrum (cosine similarity = 0.205)

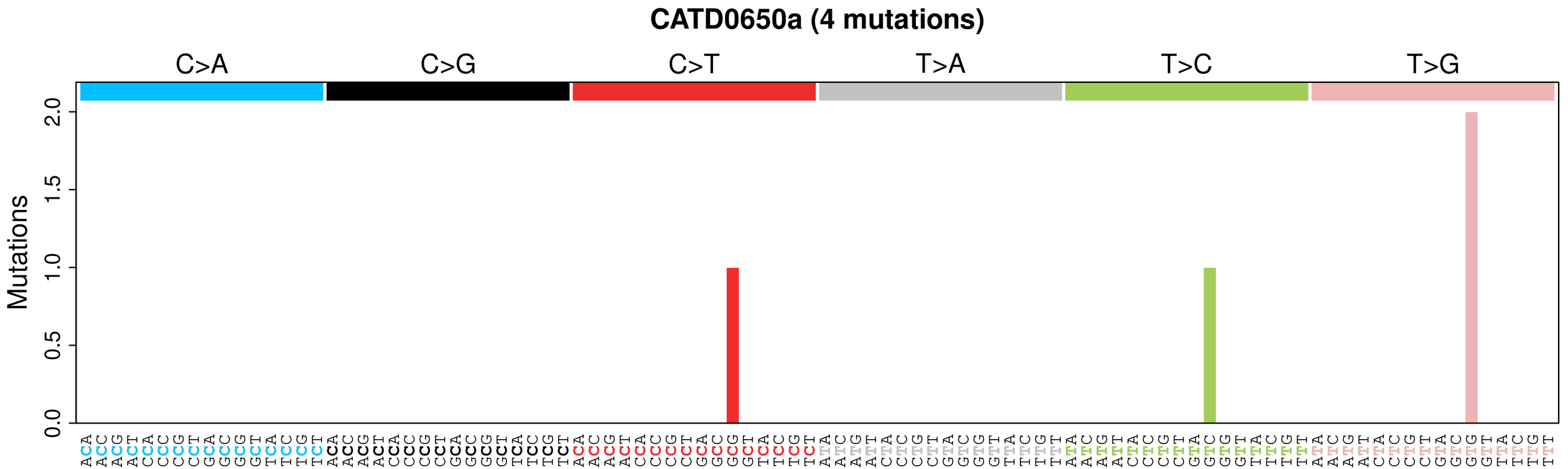


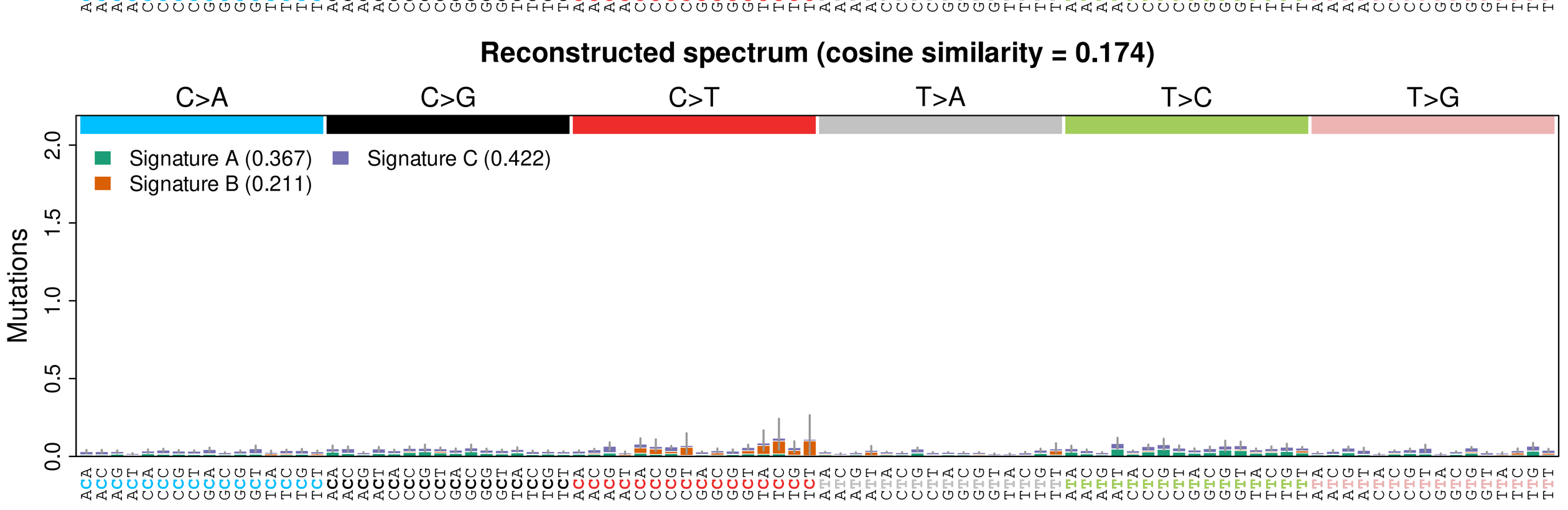
CATD0670a (6 mutations)



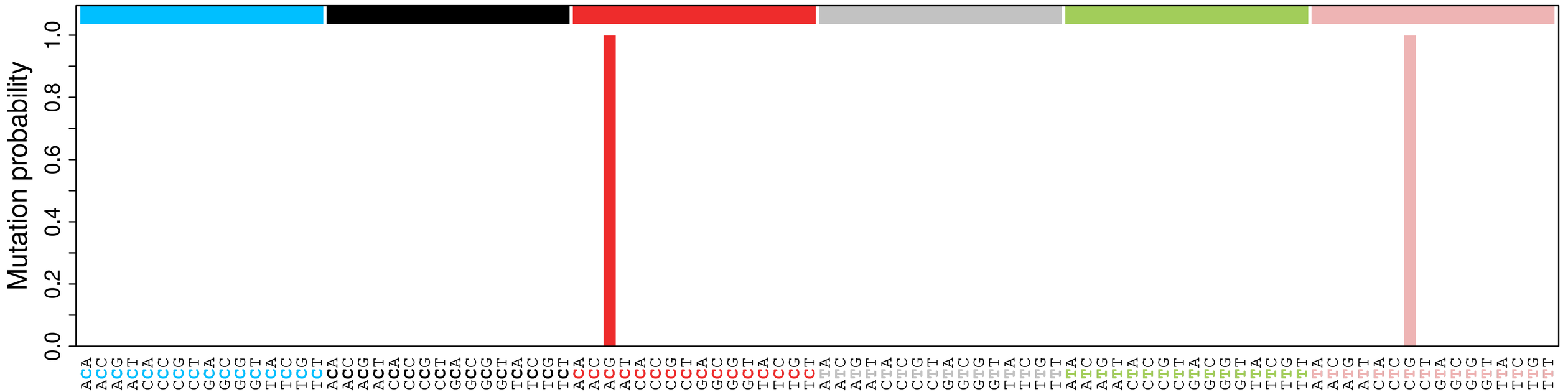
Reconstructed spectrum (cosine similarity = 0.282)



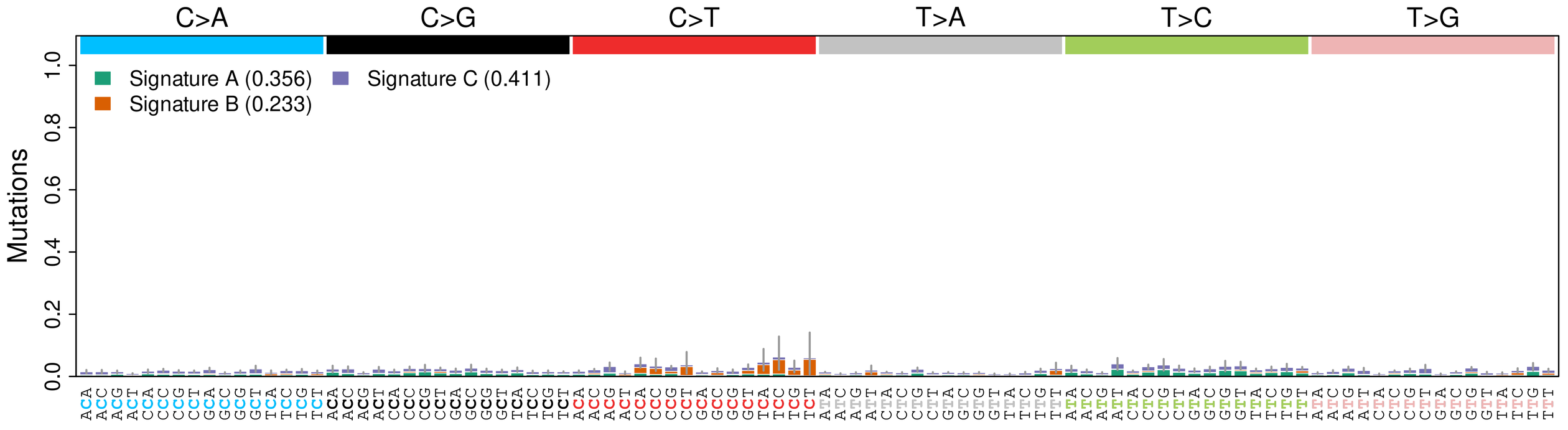

CATD0650a (4 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

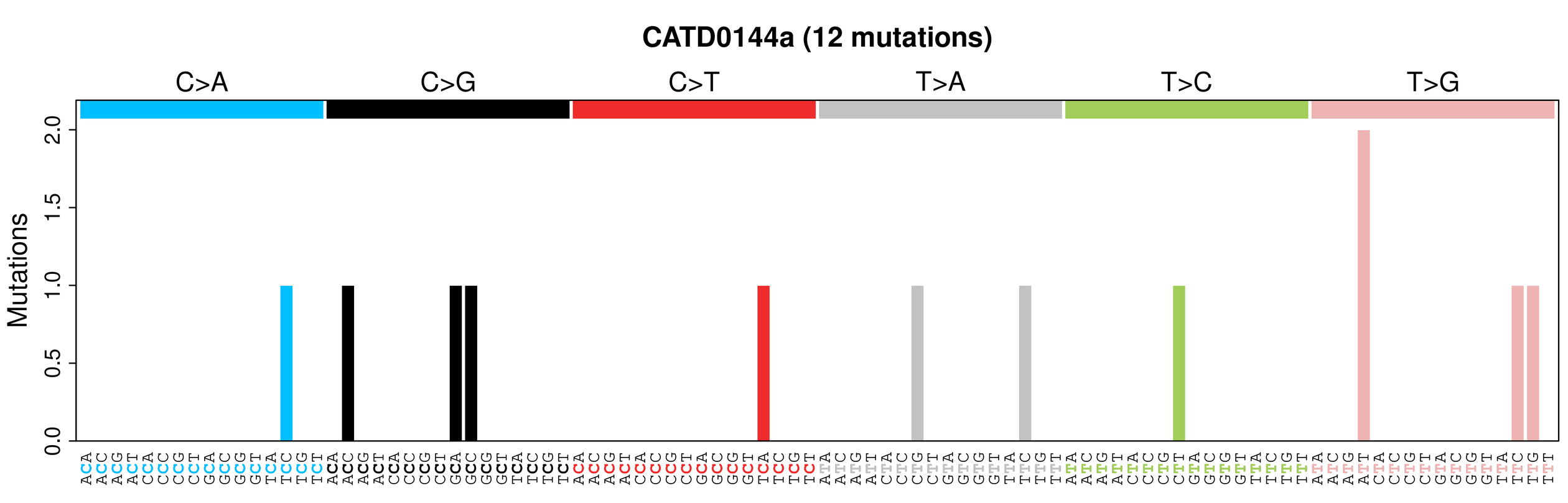

Reconstructed spectrum (cosine similarity = 0.174)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.367)
Signature B (0.211)
Signature C (0.422)
Mutations
0.0
0.5
1.0
1.5
2.0

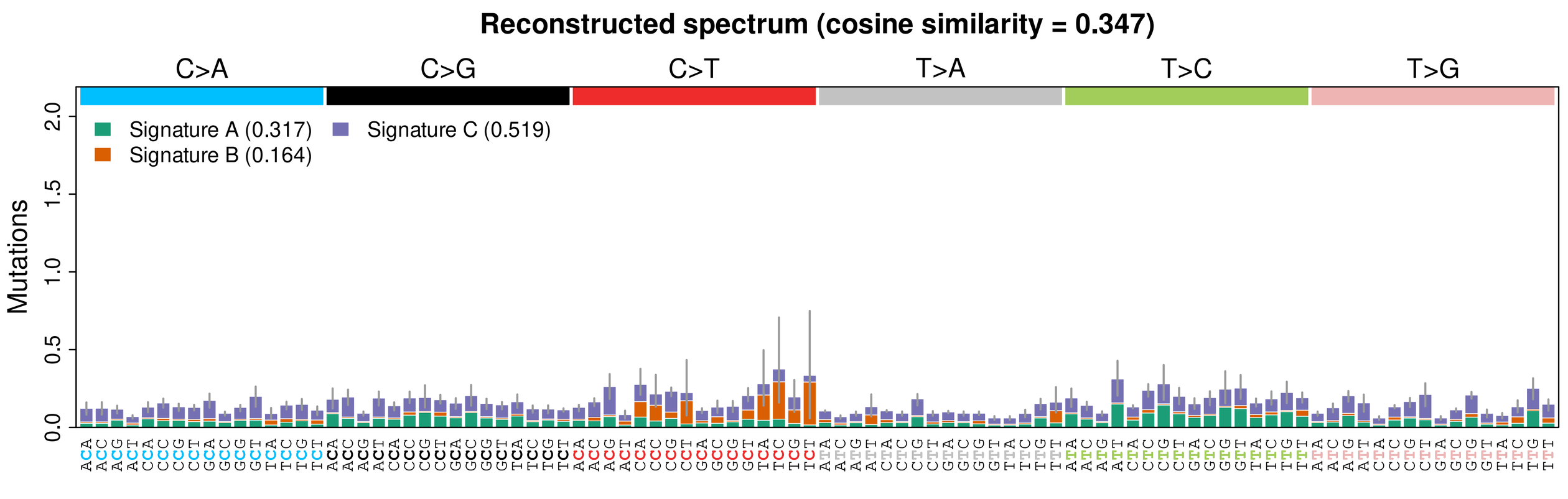
CATD289a

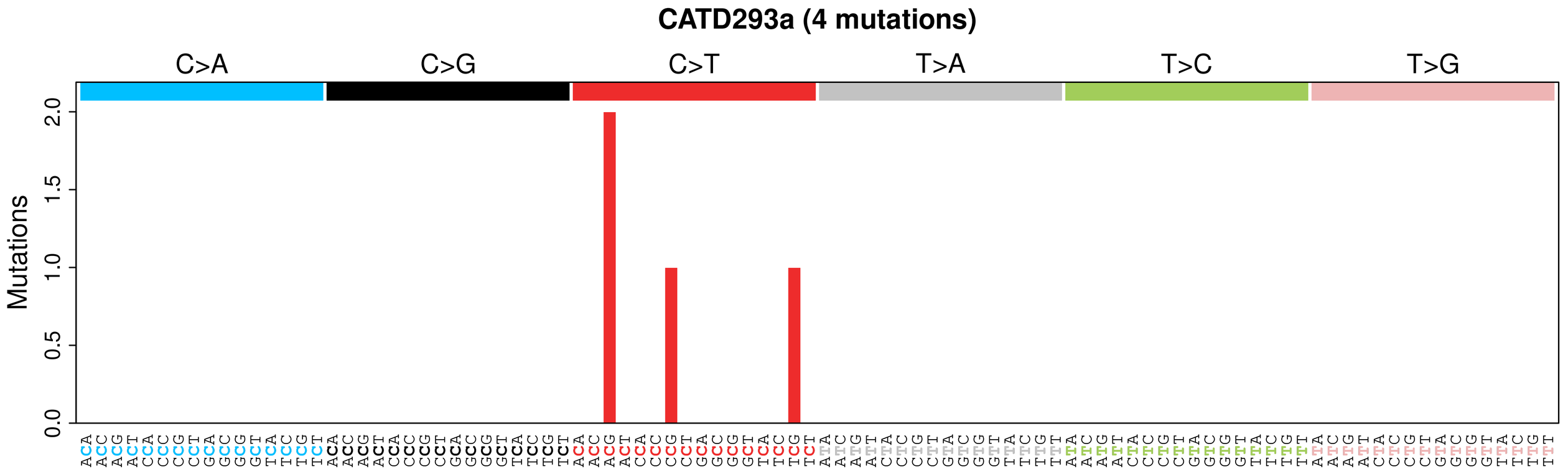


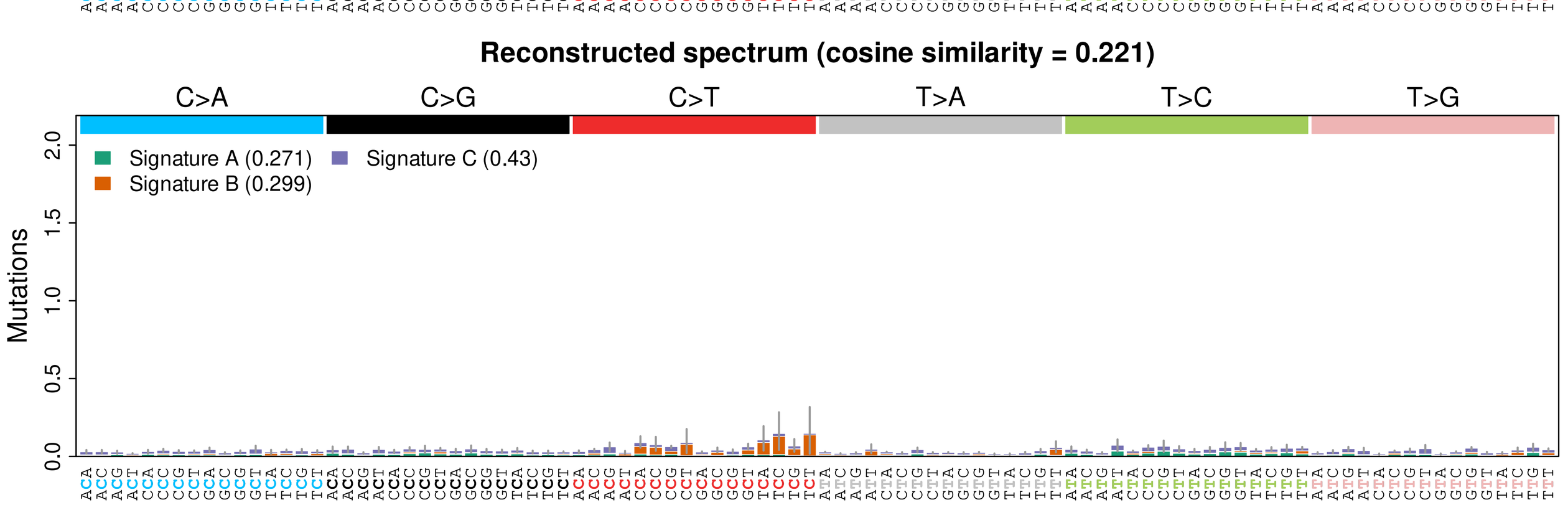
Reconstructed spectrum (cosine similarity = 0.164)

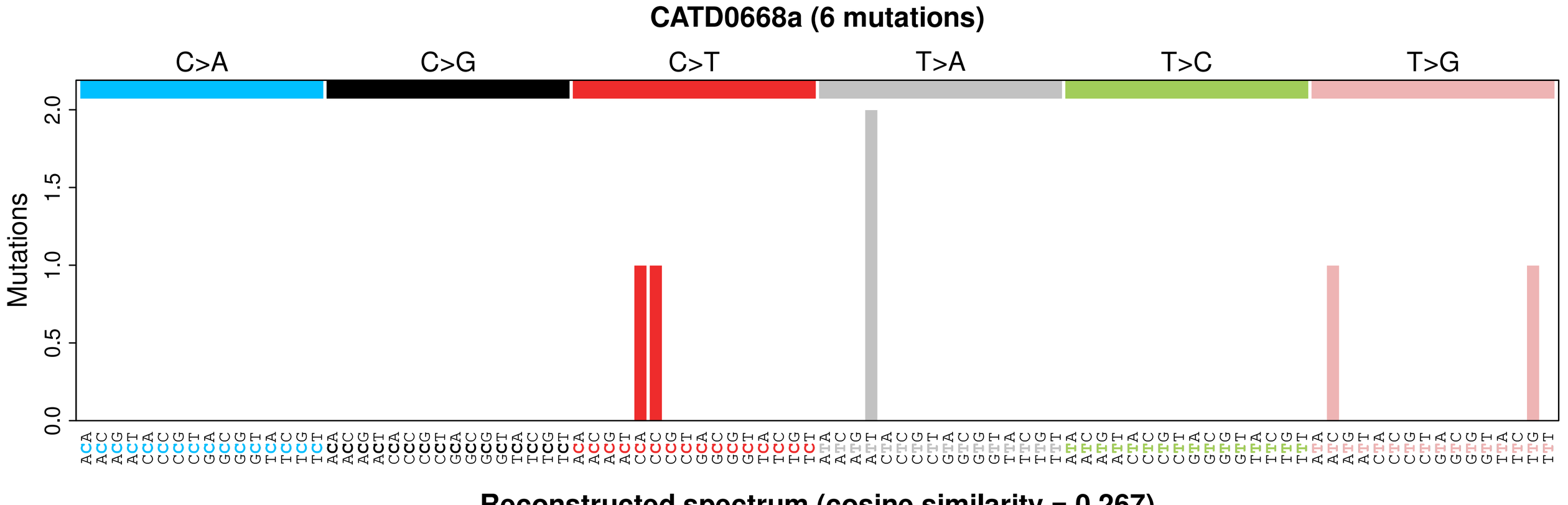


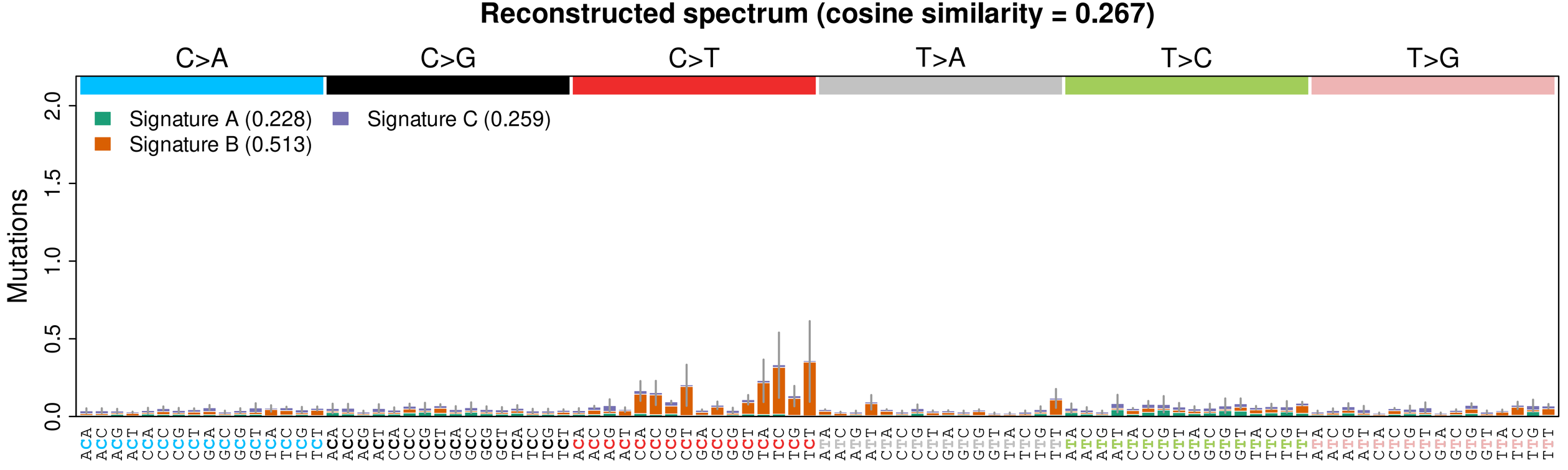

CATD0144a (12 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.347)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.317)
Signature B (0.164)
Signature C (0.519)
Mutations
0.0
0.5
1.0
1.5
2.0

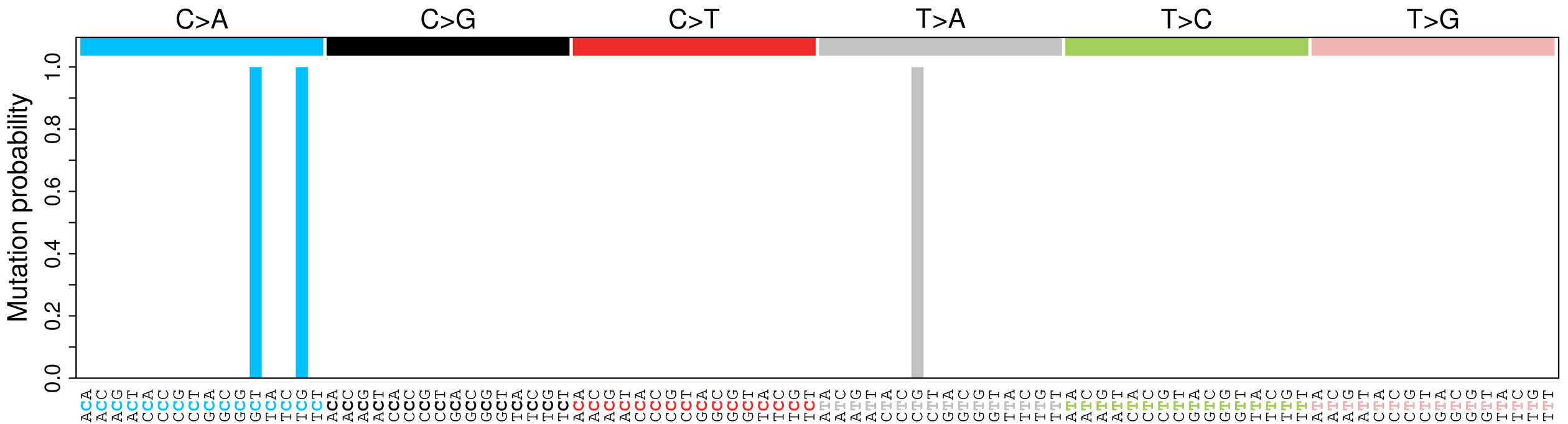

CATD293a (4 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.221)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.271)
Signature B (0.299)
Signature C (0.43)
Mutations
0.0
0.5
1.0
1.5
2.0

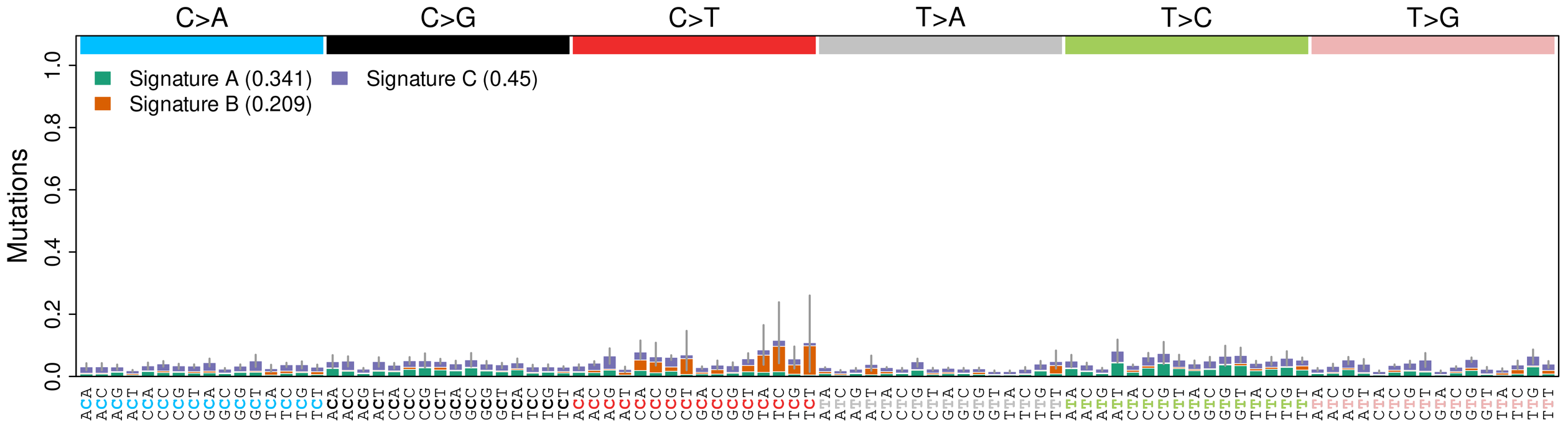

CATD0668a (6 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0


Reconstructed spectrum (cosine similarity = 0.267)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.228)
Signature B (0.513)
Signature C (0.259)
Mutations
0.0
0.5
1.0
1.5
2.0

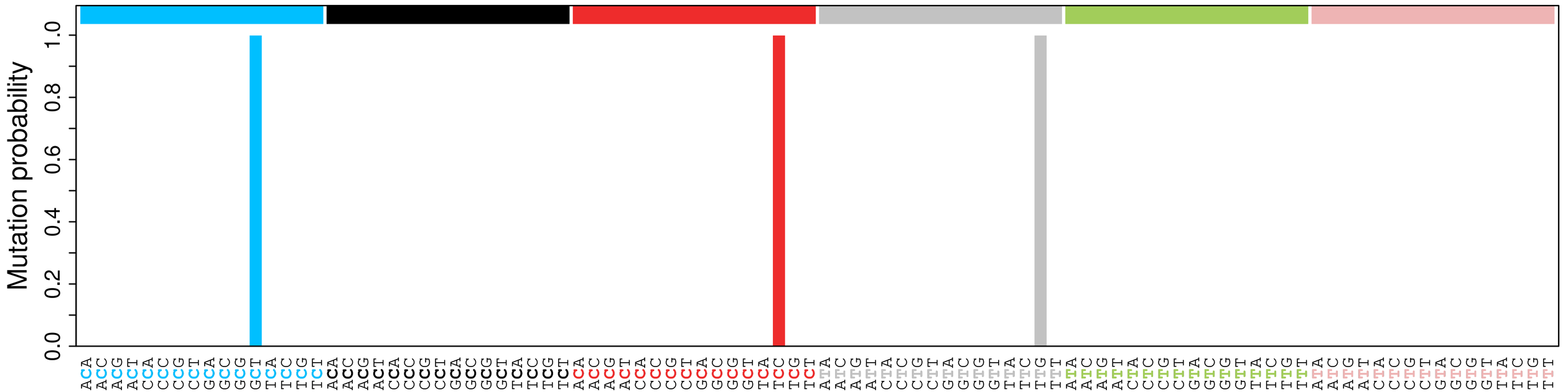
CATD0146a



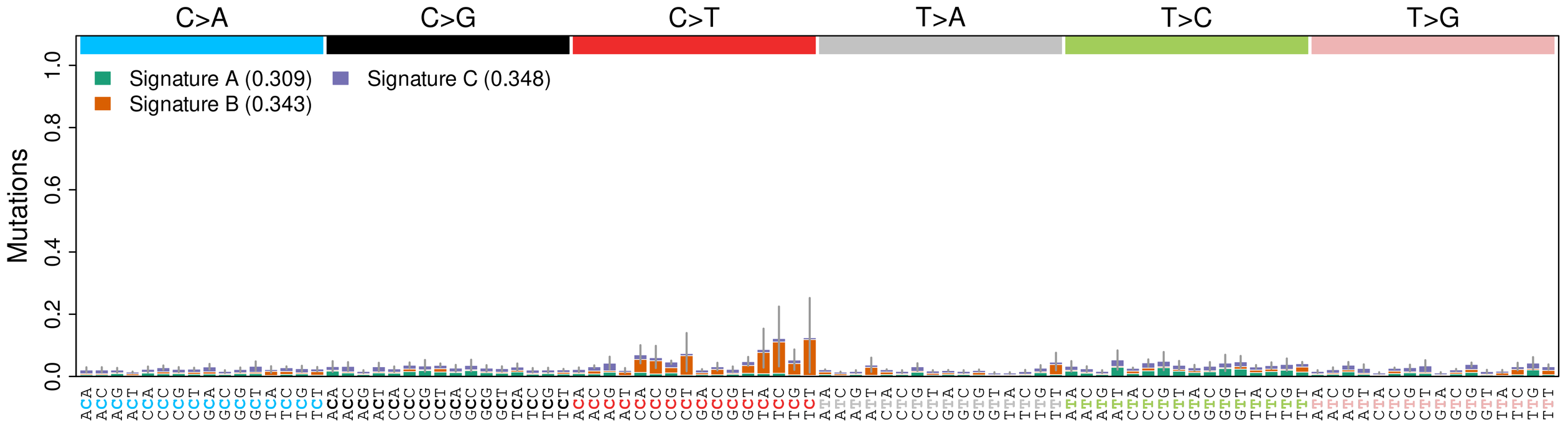
Reconstructed spectrum (cosine similarity = 0.173)

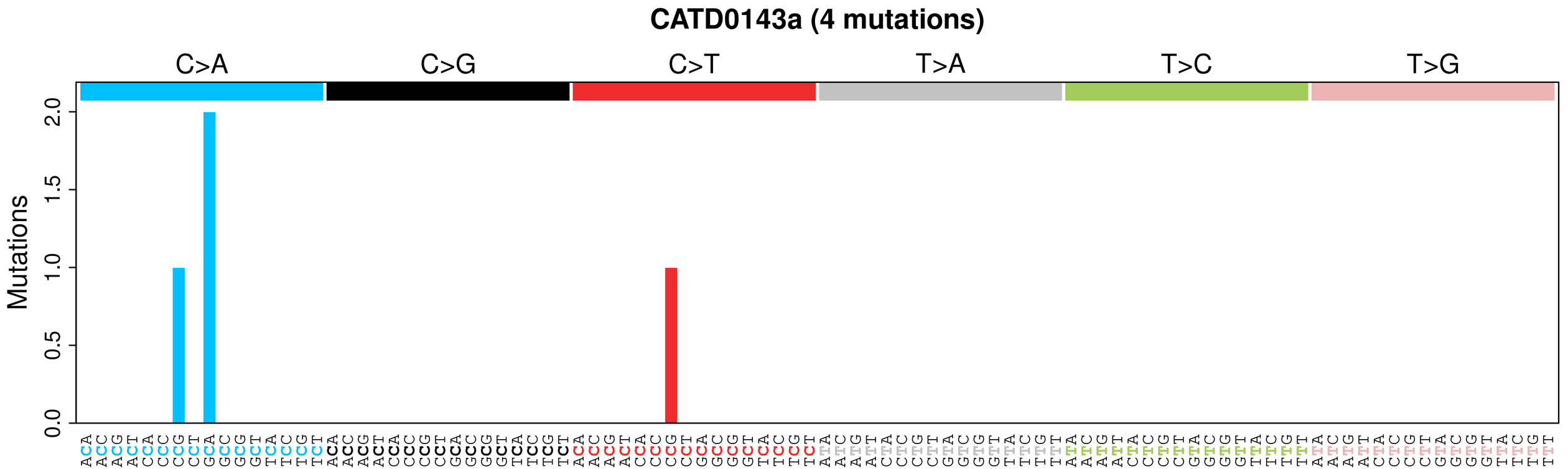


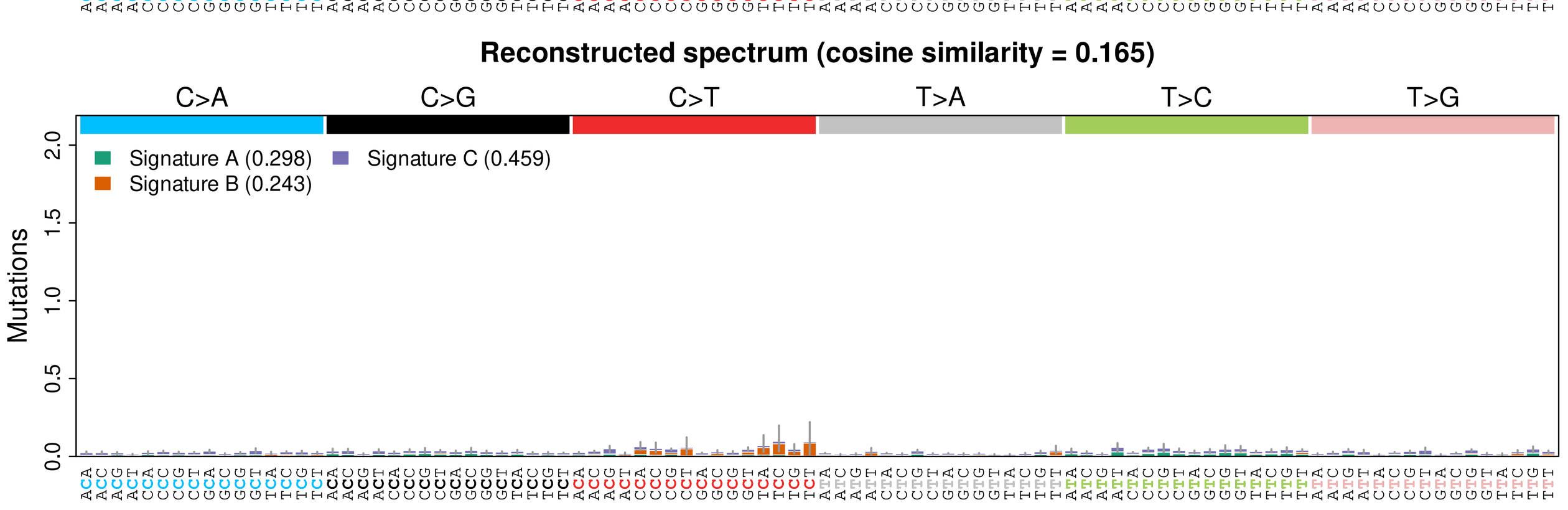
CATD0641a



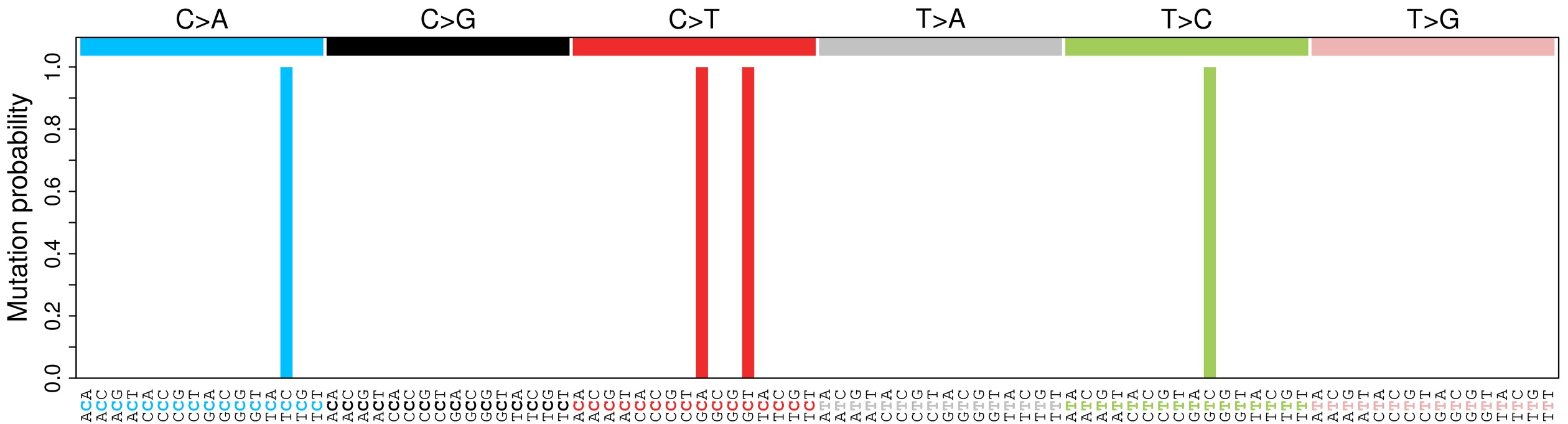
Reconstructed spectrum (cosine similarity = 0.291)



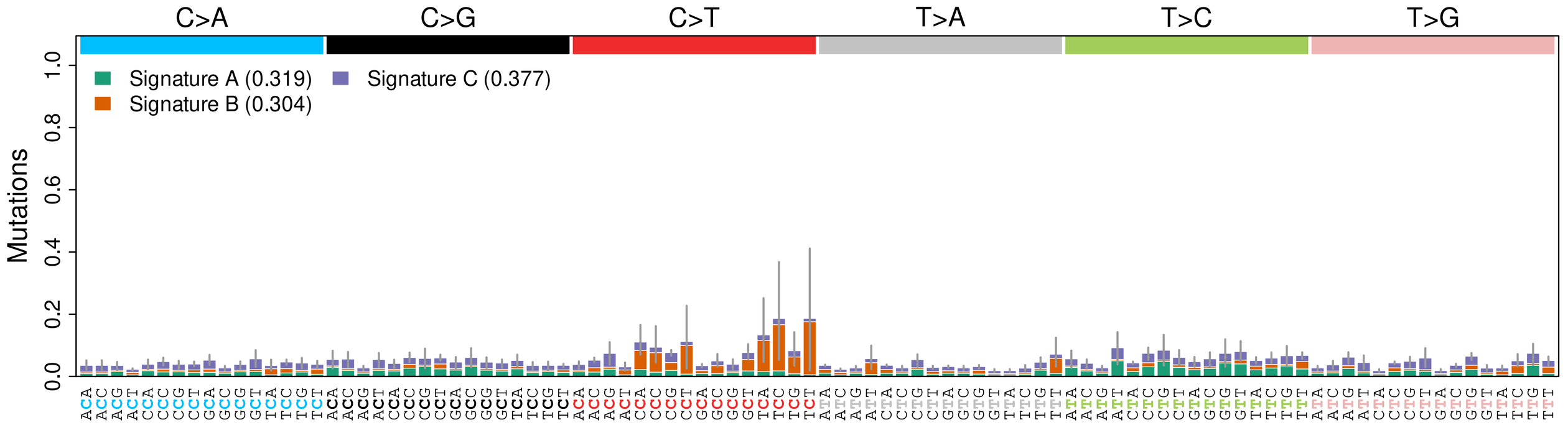

CATD0143a (4 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

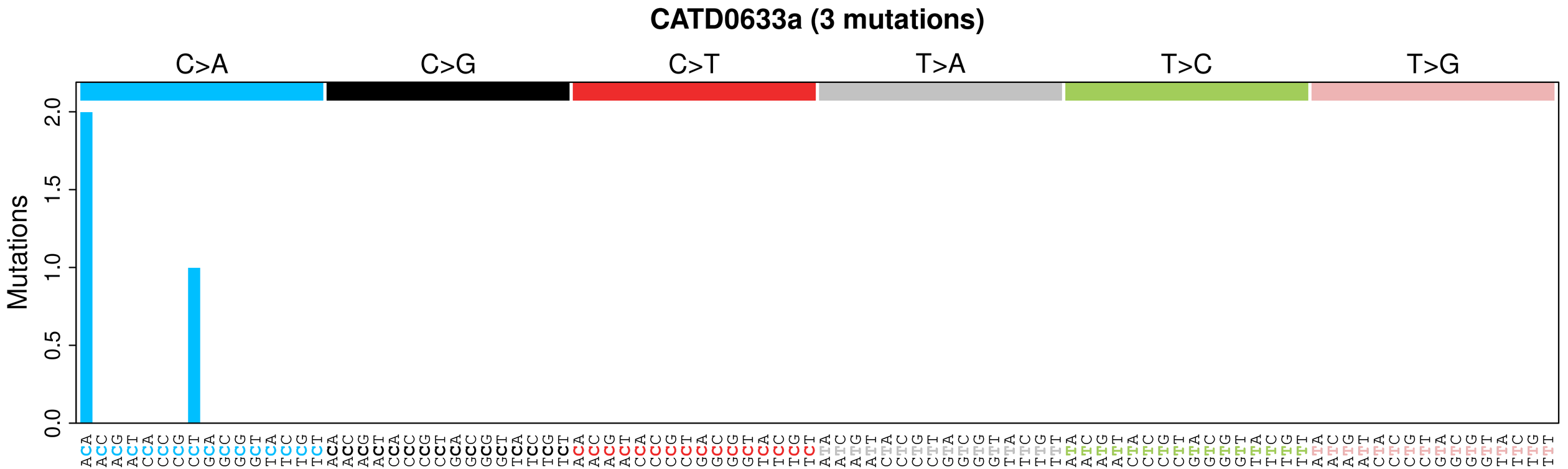

Reconstructed spectrum (cosine similarity = 0.165)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.298)
Signature B (0.243)
Signature C (0.459)
Mutations
0.0
0.5
1.0
1.5
2.0

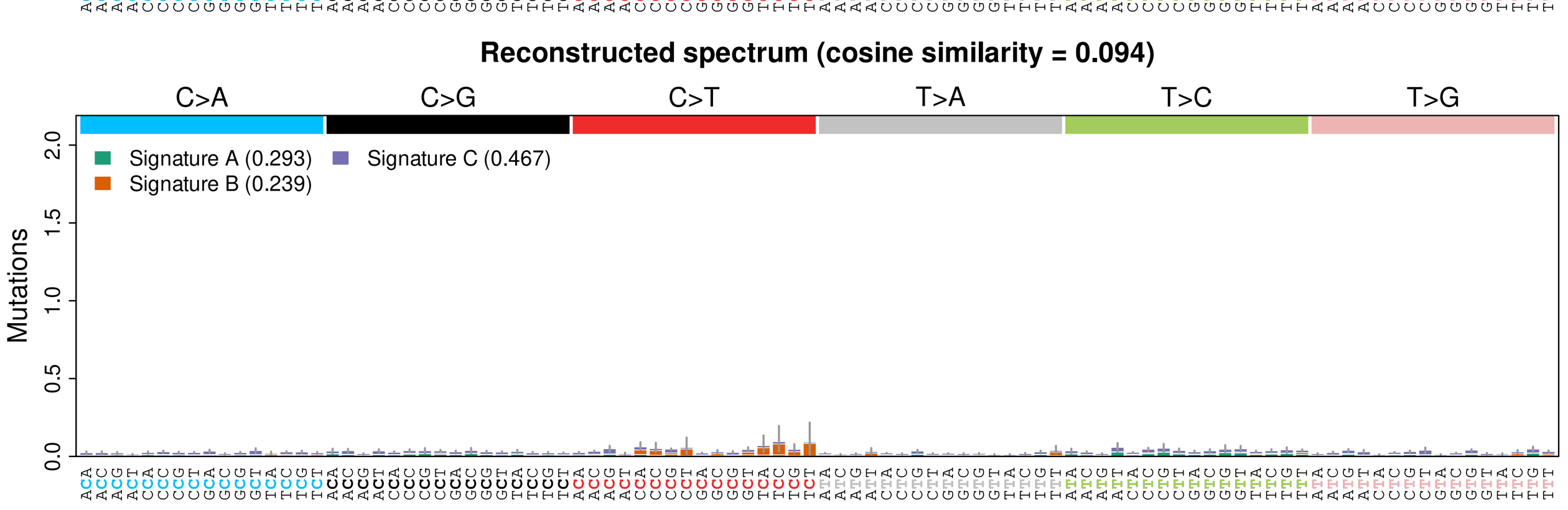
CATD0632a



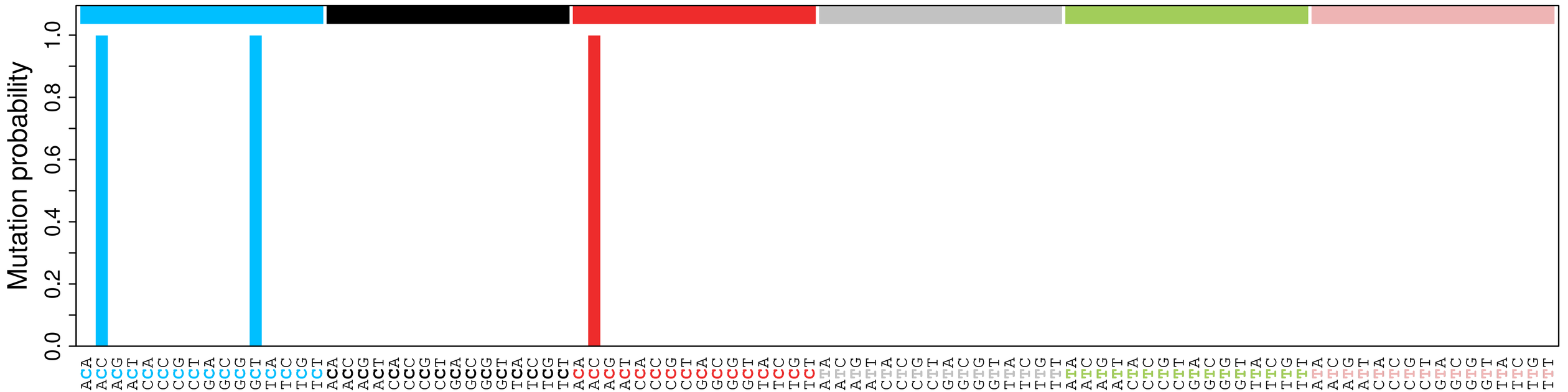
Reconstructed spectrum (cosine similarity = 0.183)



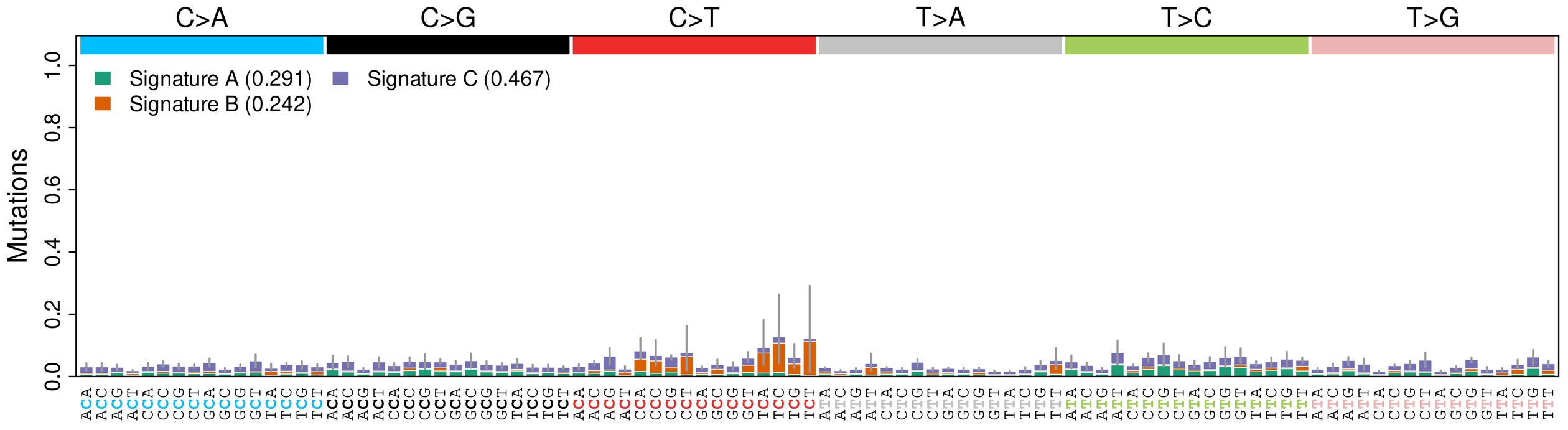

CATD0633a (3 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

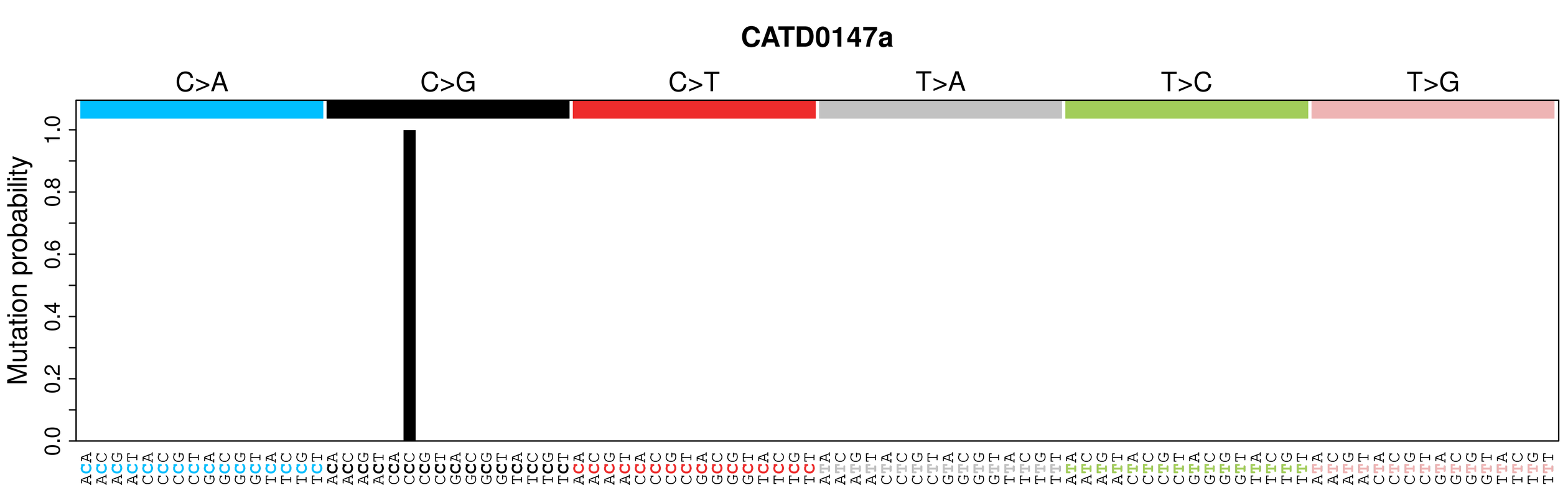

Reconstructed spectrum (cosine similarity = 0.094)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.293)
Signature B (0.239)
Signature C (0.467)
Mutations
0.0
0.5
1.0
1.5
2.0

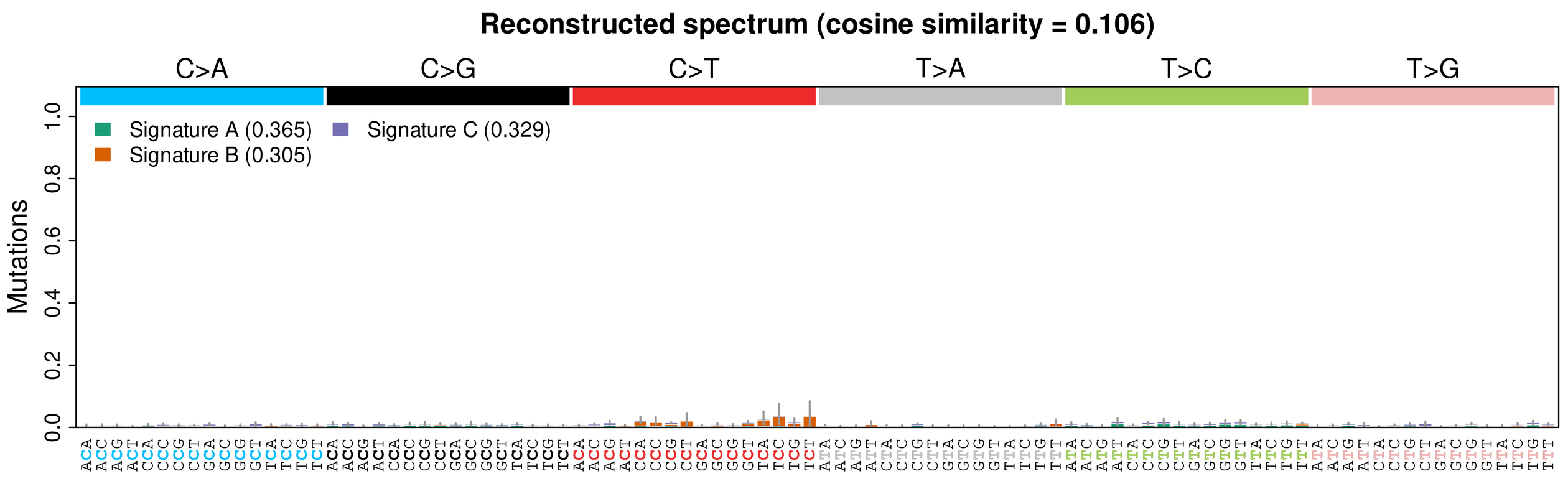
CATD0157a



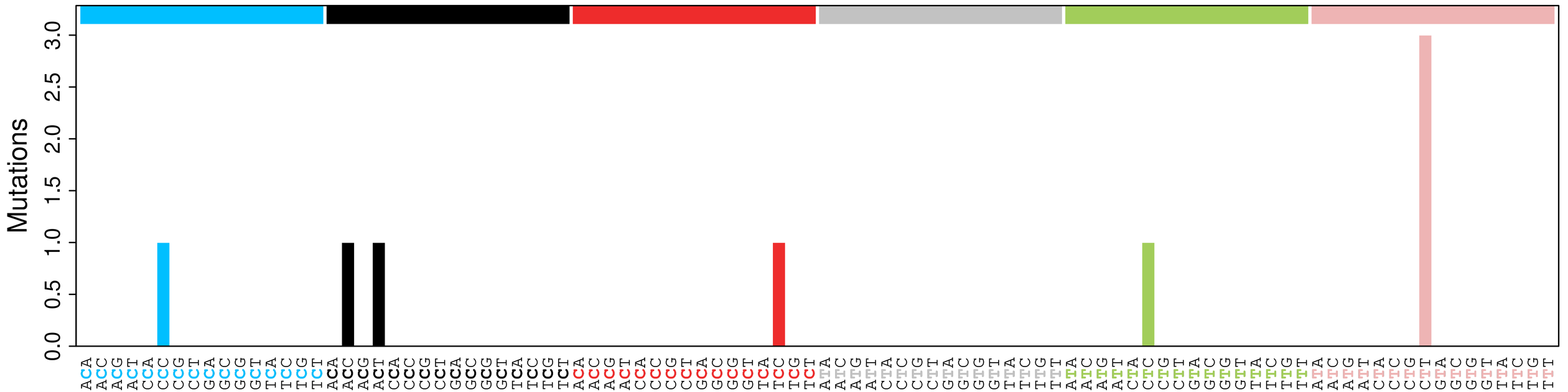
Reconstructed spectrum (cosine similarity = 0.158)



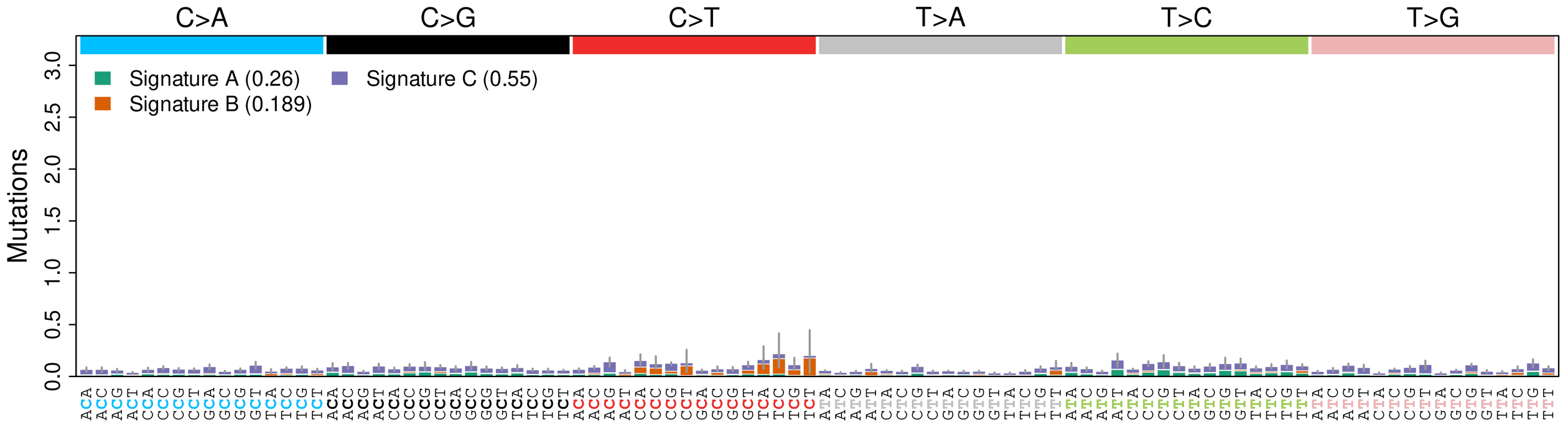

CATD0147a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0

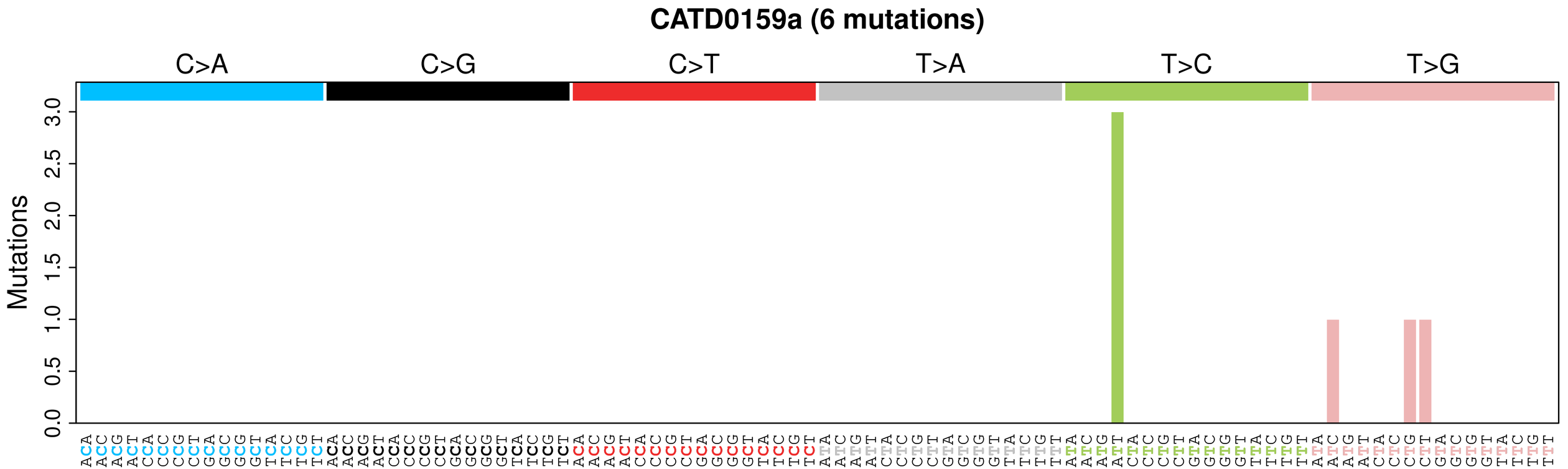

Reconstructed spectrum (cosine similarity = 0.106)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.365)
Signature B (0.305)
Signature C (0.329)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0

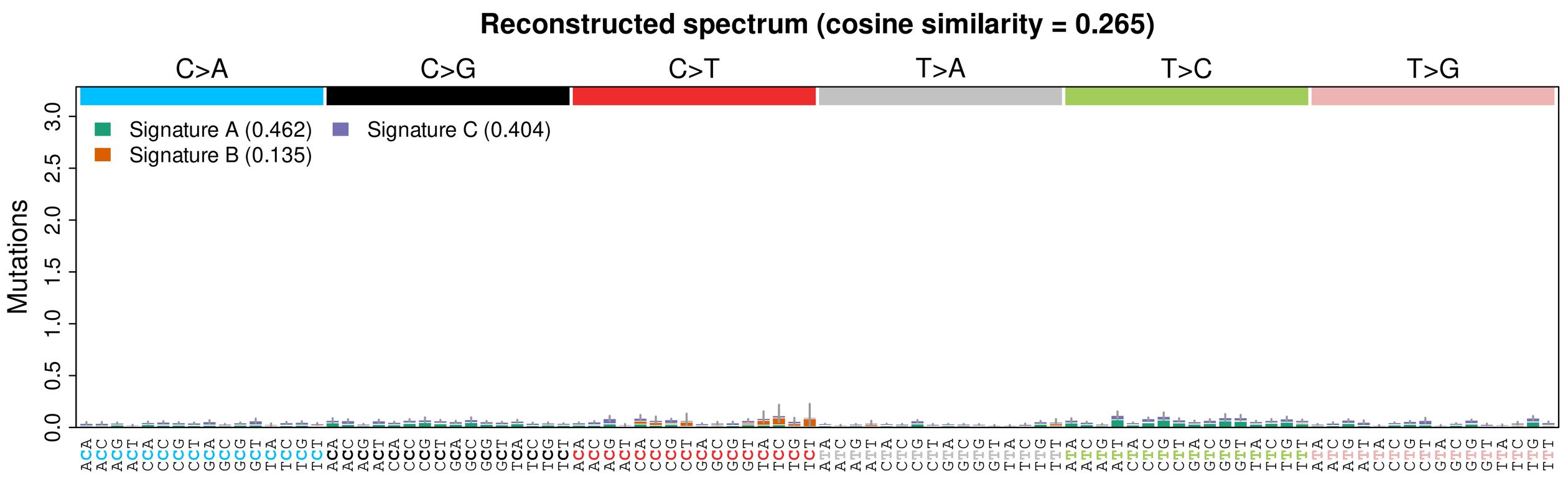
CATD0145a (8 mutations)



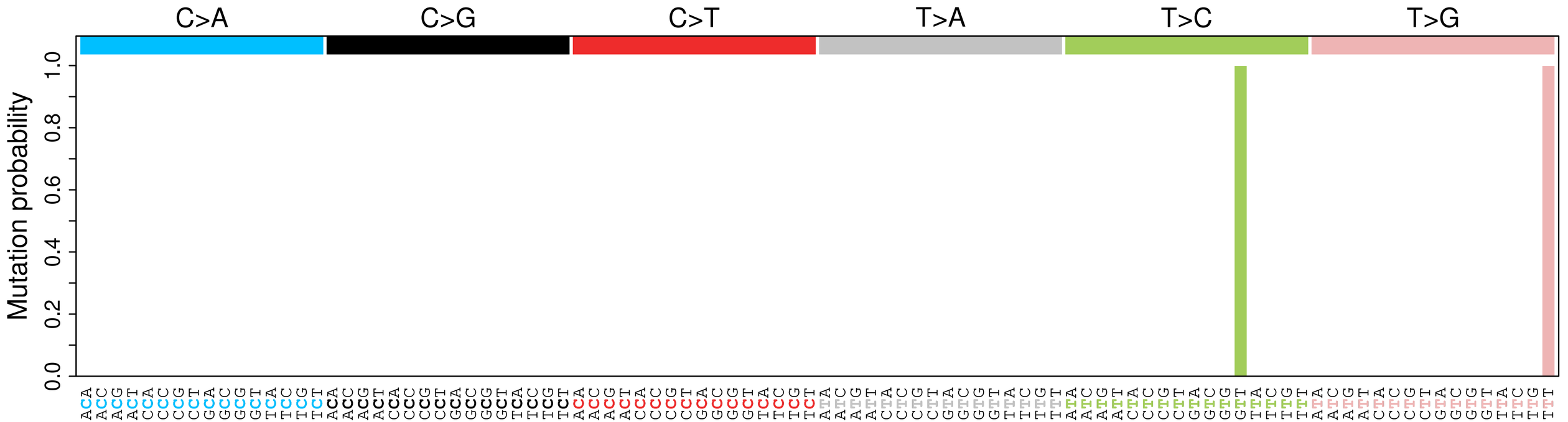
Reconstructed spectrum (cosine similarity = 0.292)



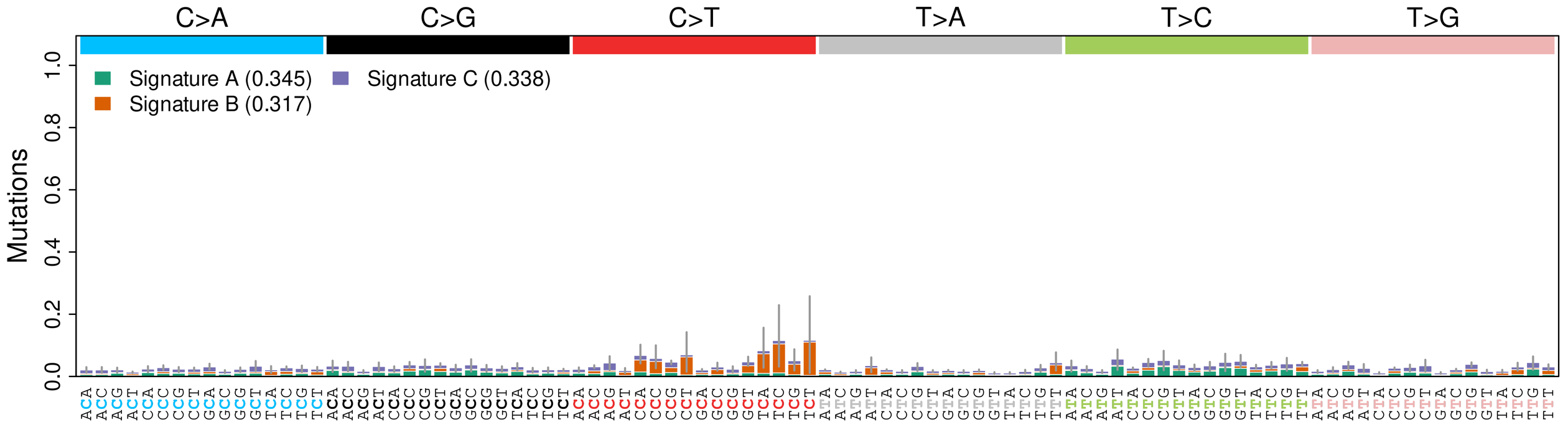

CATD0159a (6 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0
2.5
3.0


Reconstructed spectrum (cosine similarity = 0.265)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.462)
Signature B (0.135)
Signature C (0.404)
Mutations
0.0
0.5
1.0
1.5
2.0
2.5
3.0

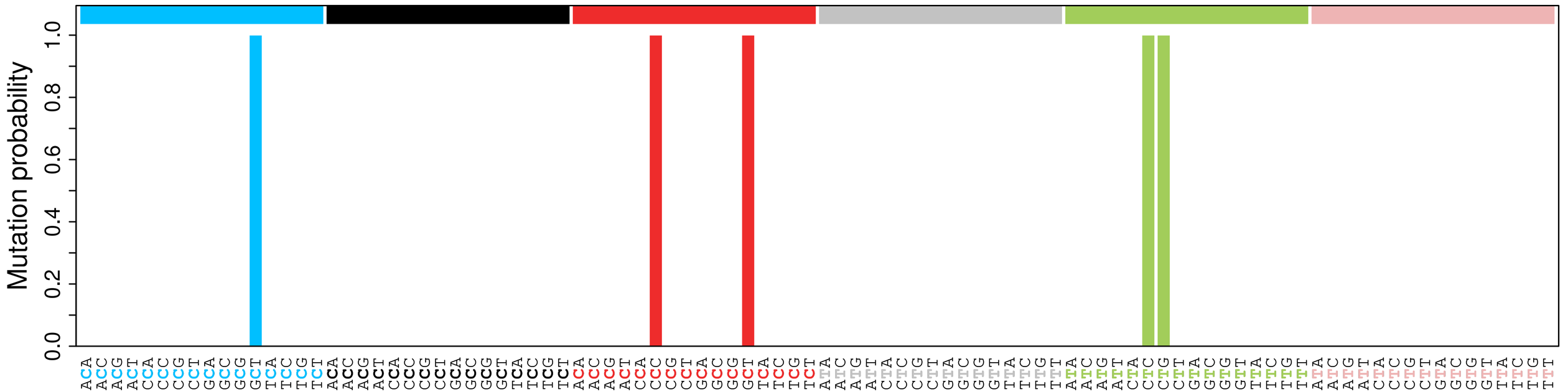
CATD0148a



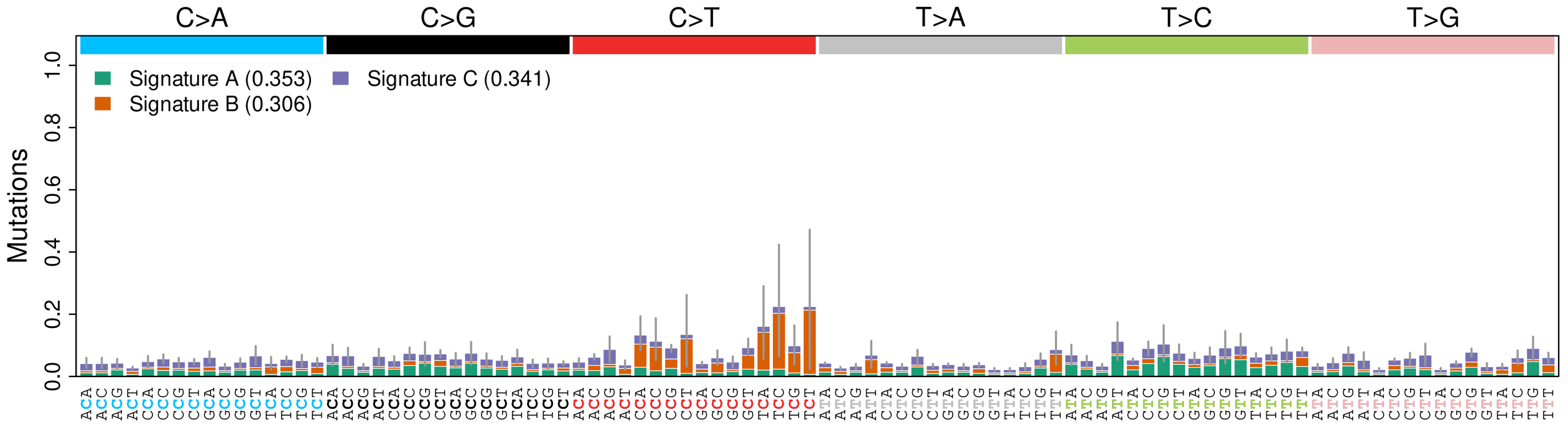
Reconstructed spectrum (cosine similarity = 0.158)



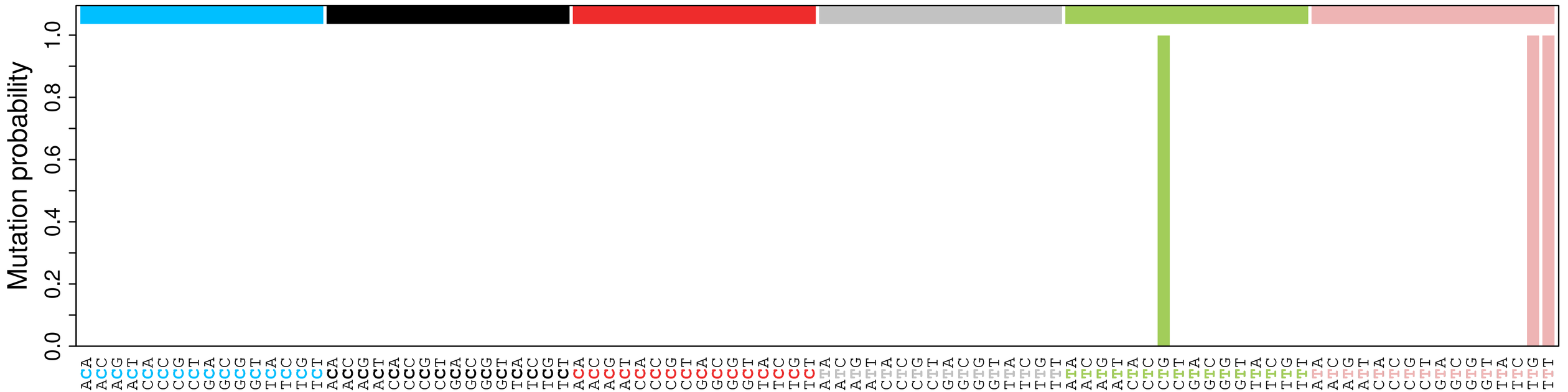
CATD0153a



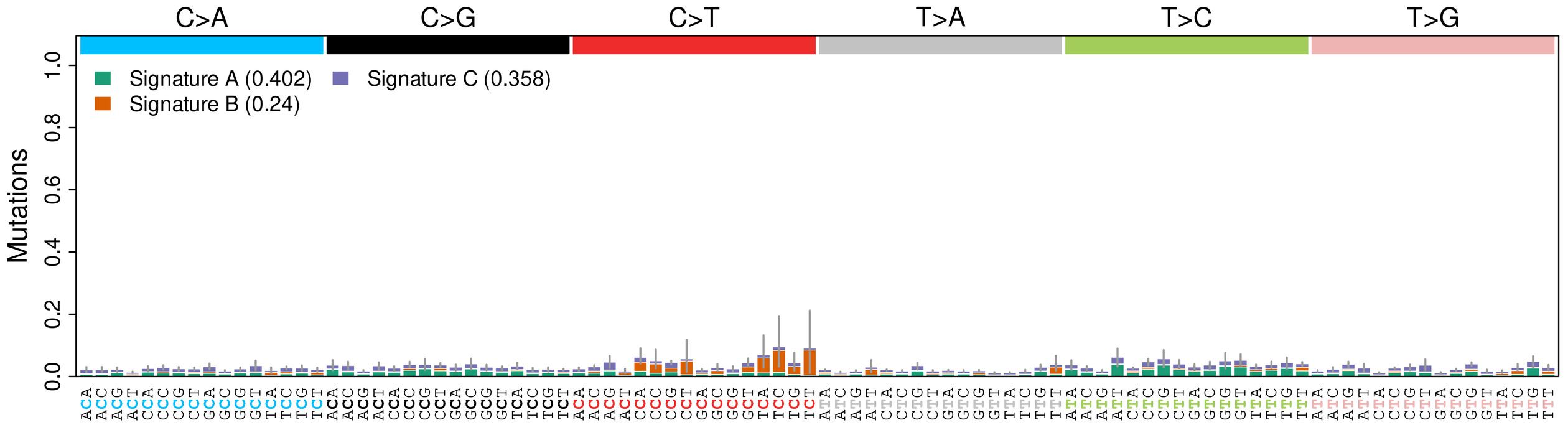
Reconstructed spectrum (cosine similarity = 0.296)



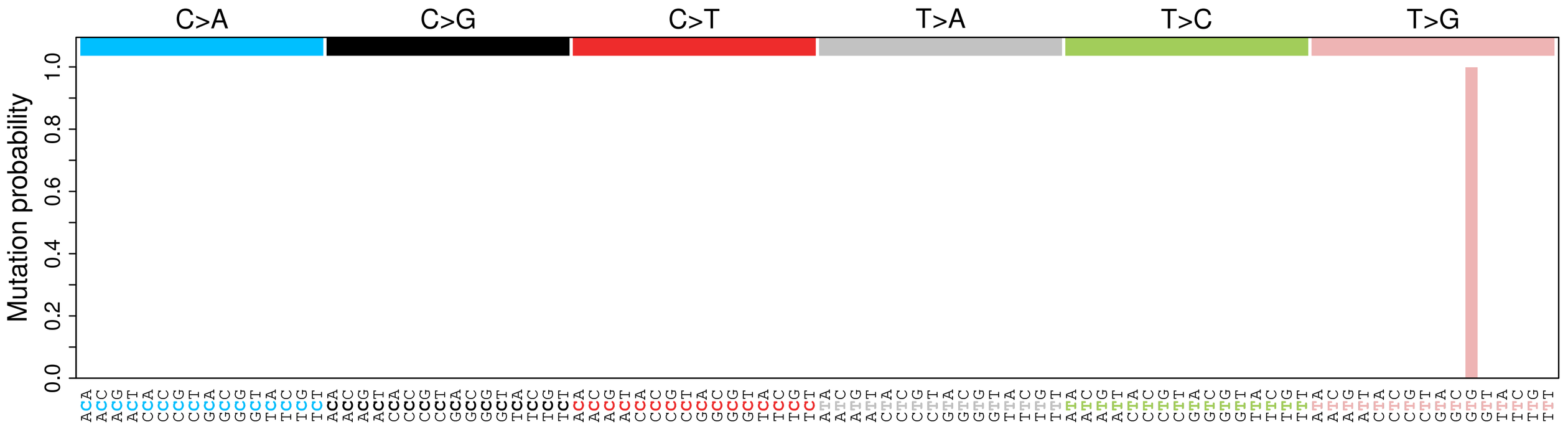
CATD0635a



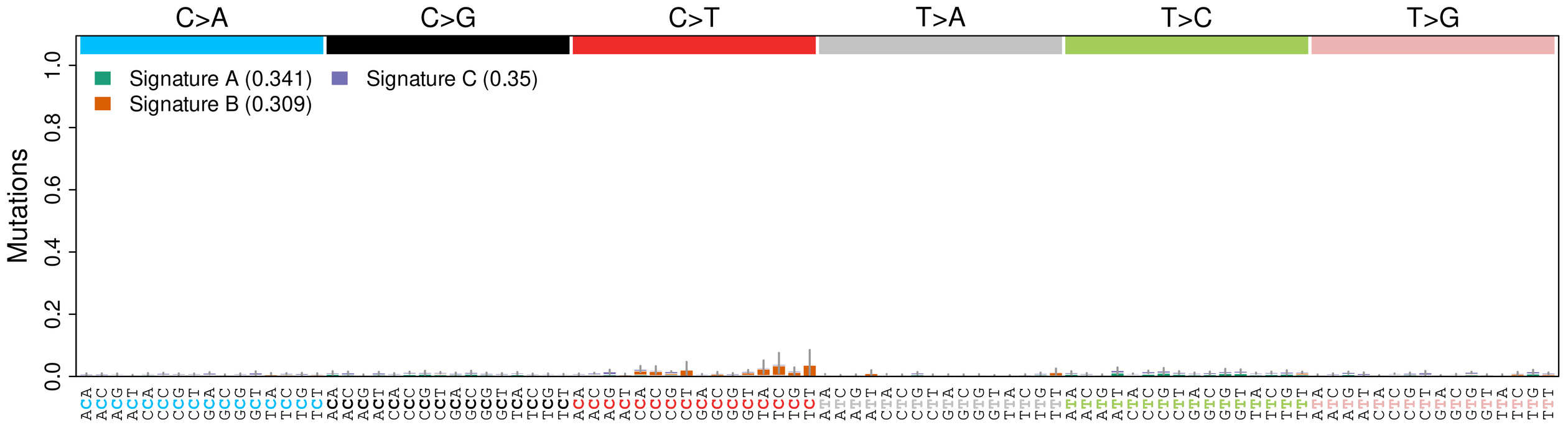
Reconstructed spectrum (cosine similarity = 0.227)

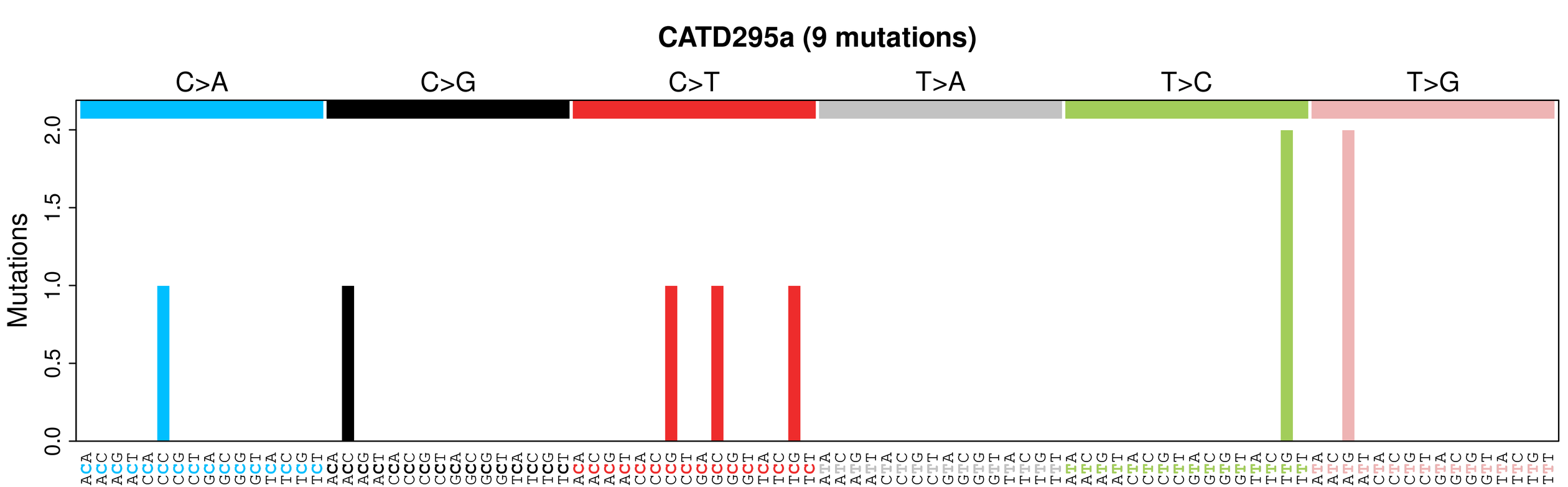


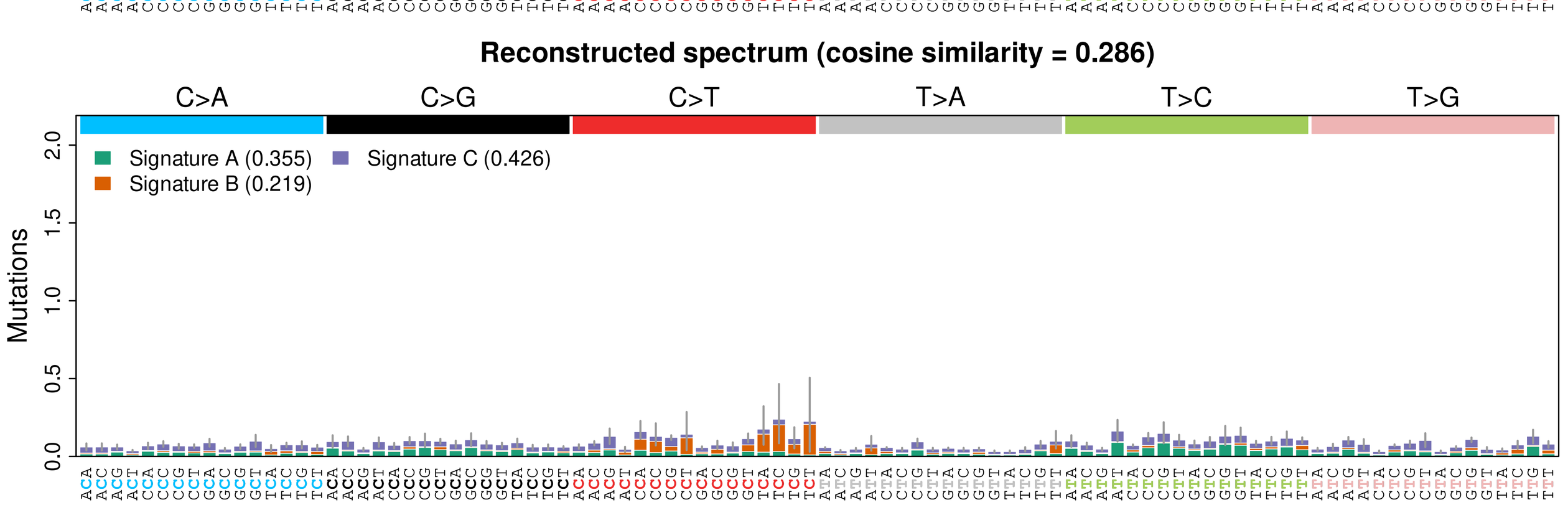
CATD0646a



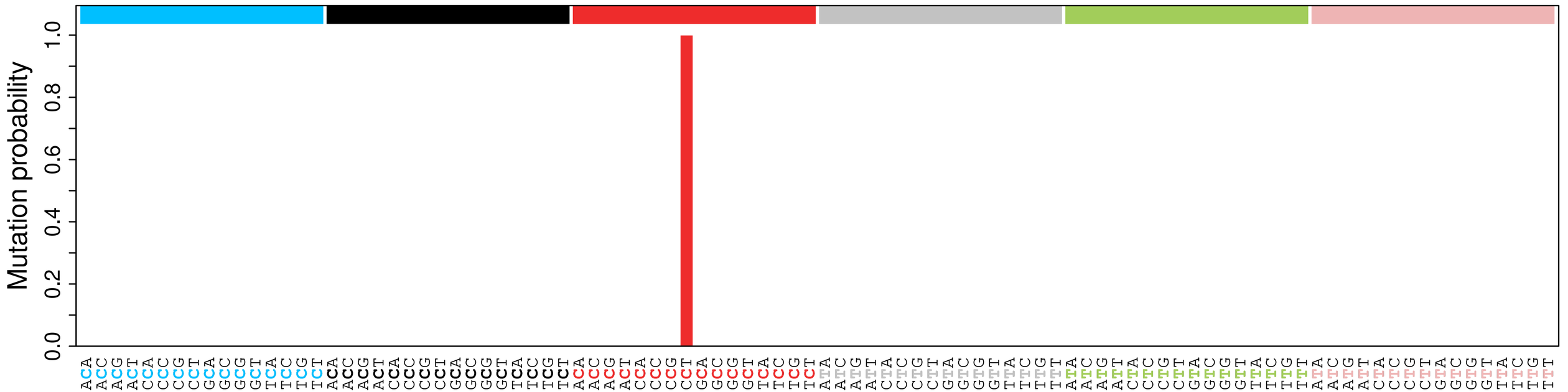
Reconstructed spectrum (cosine similarity = 0.11)



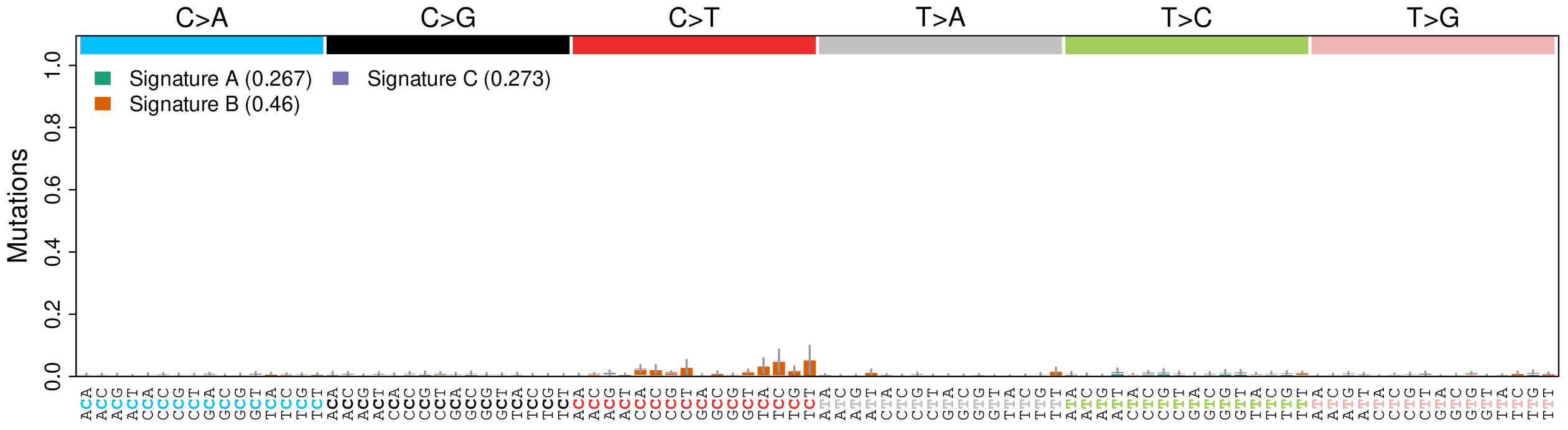

CATD295a (9 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0.0
0.5
1.0
1.5
2.0

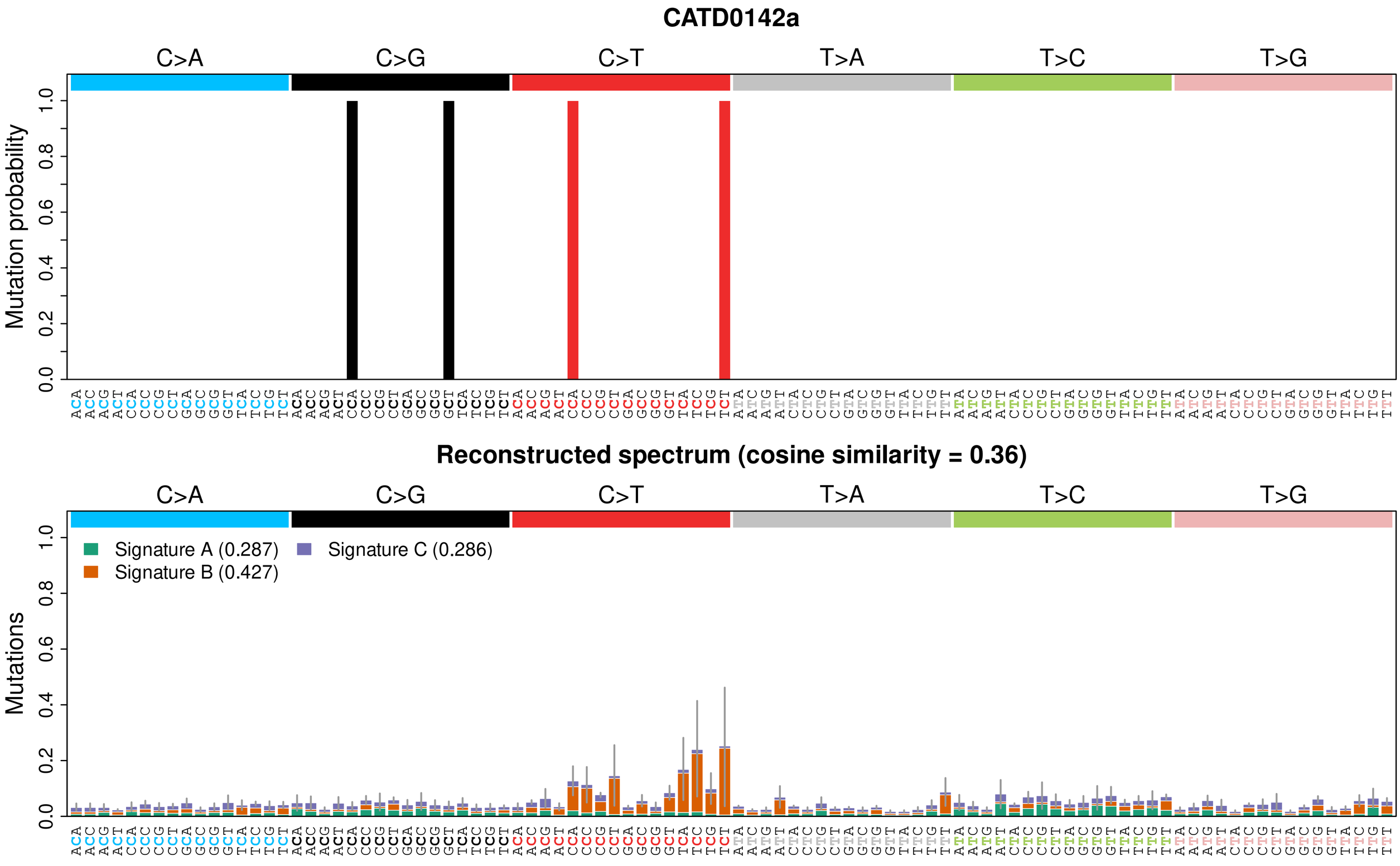

Reconstructed spectrum (cosine similarity = 0.286)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.355)
Signature B (0.219)
Signature C (0.426)
Mutations
0.0
0.5
1.0
1.5
2.0

CATD290a

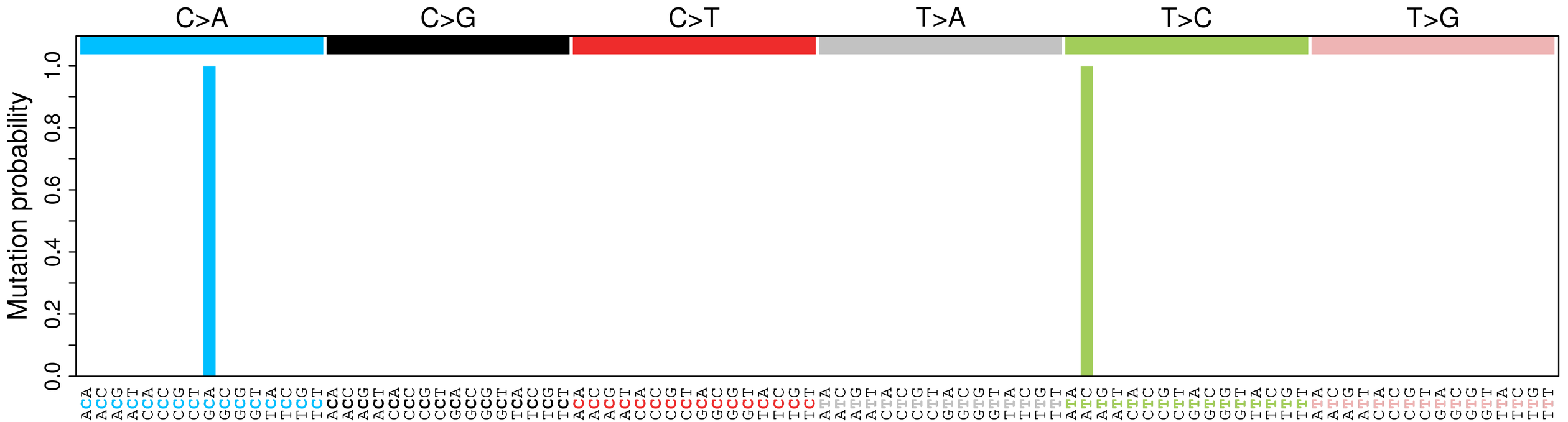


Reconstructed spectrum (cosine similarity = 0.239)

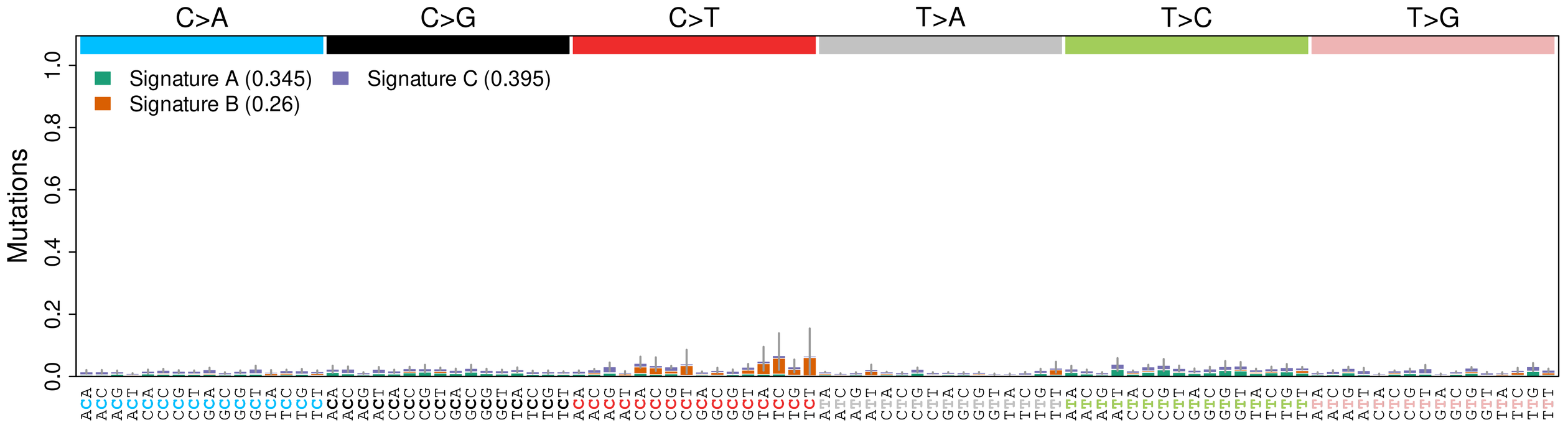



CATD0142a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0
Reconstructed spectrum (cosine similarity = 0.36)
Signature A (0.287)
Signature B (0.427)
Signature C (0.286)
Mutations

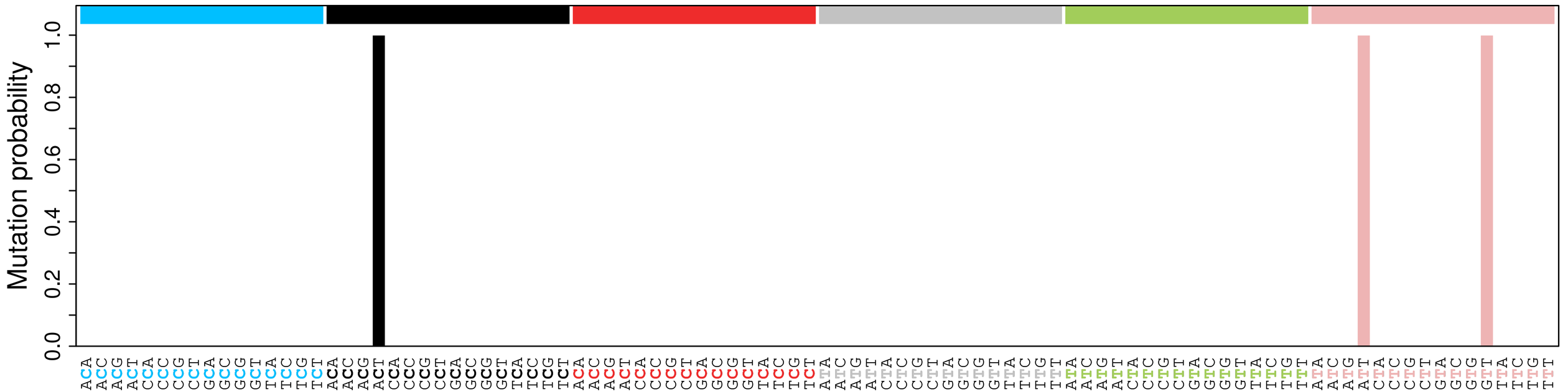
CATD291a



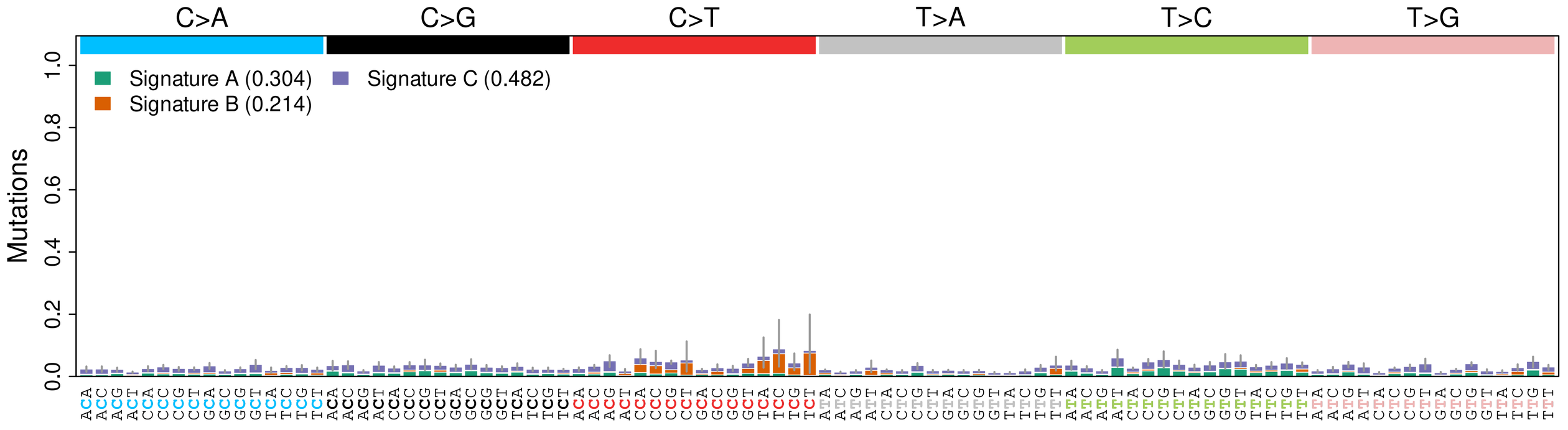
Reconstructed spectrum (cosine similarity = 0.12)



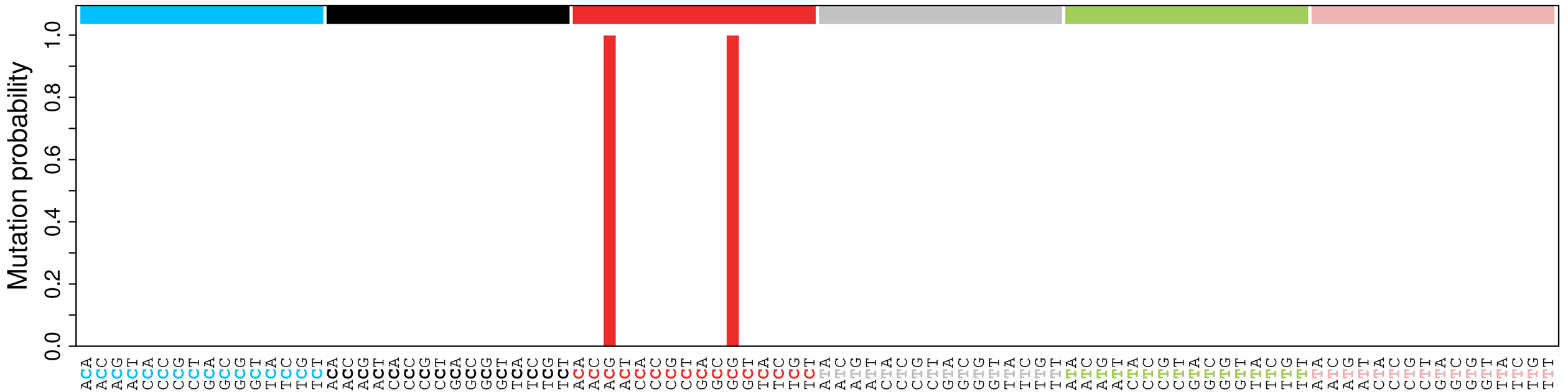
CATD284a



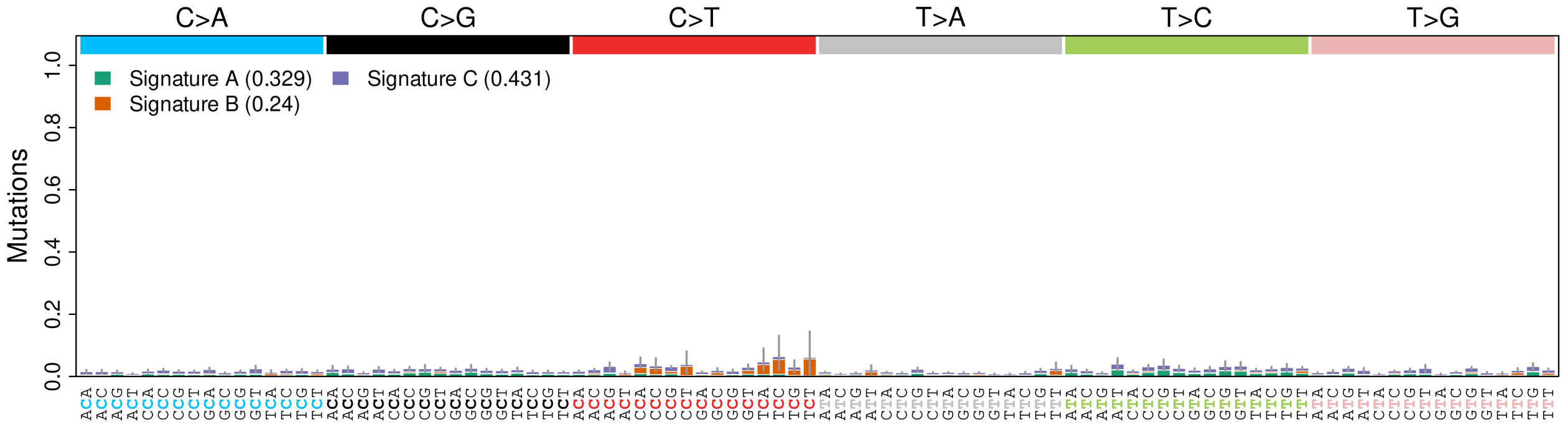
Reconstructed spectrum (cosine similarity = 0.143)



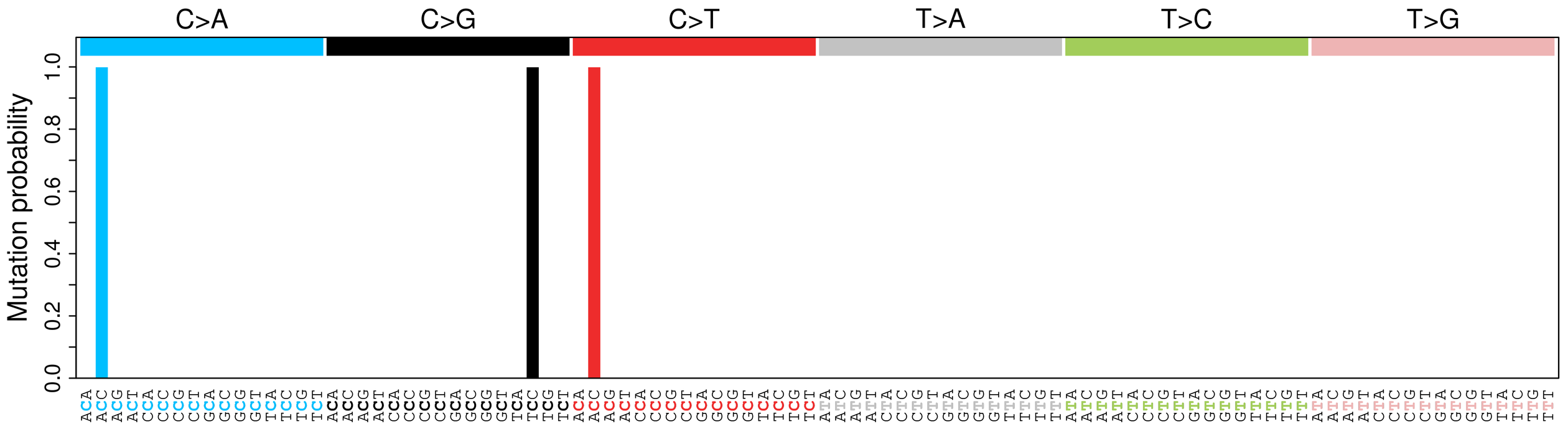
CATD0150a



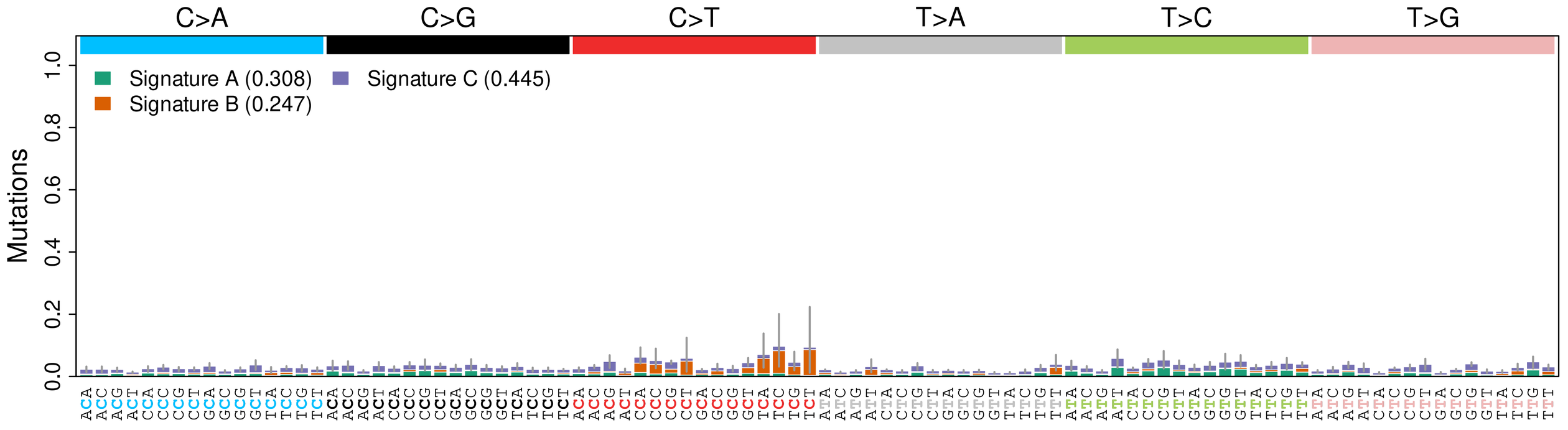
Reconstructed spectrum (cosine similarity = 0.151)

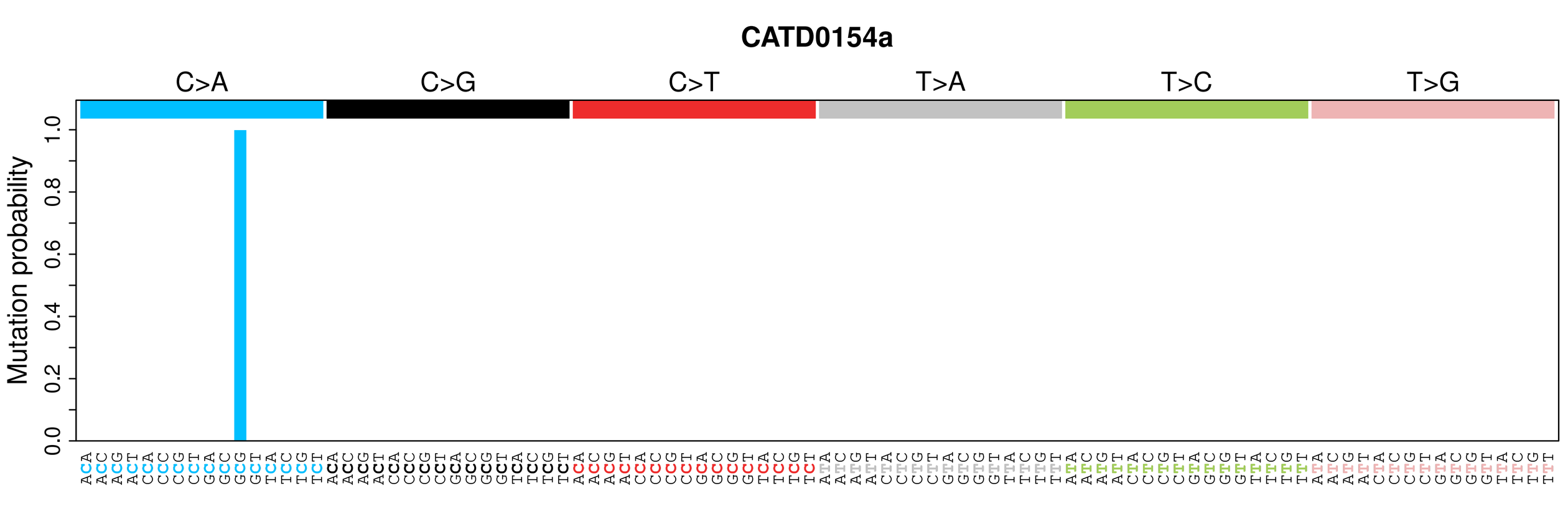


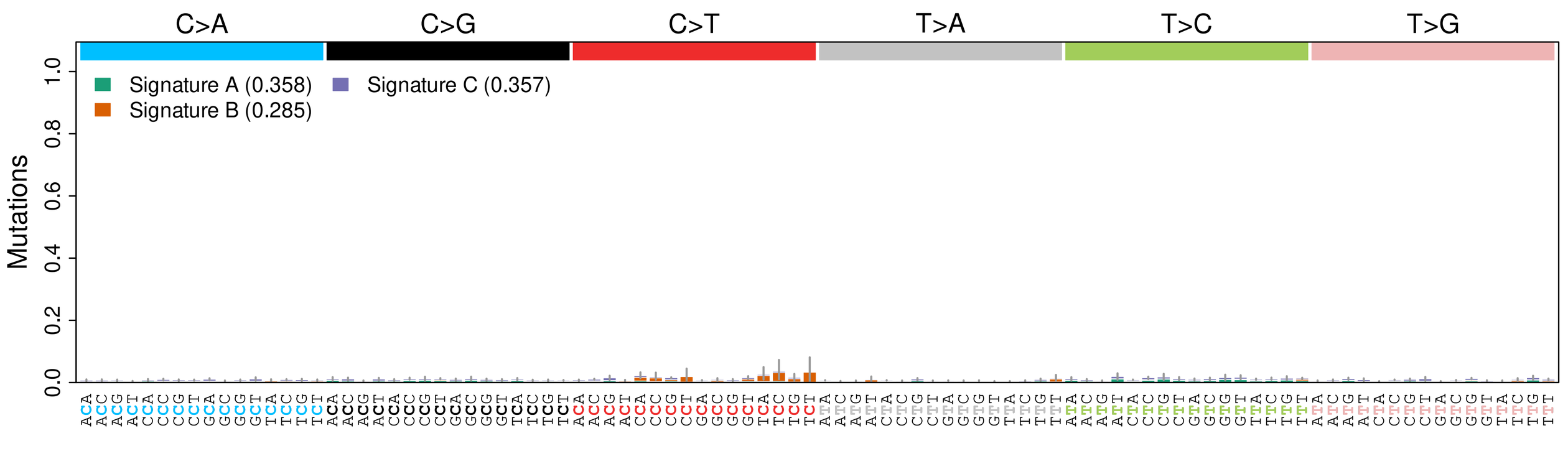
CATD0156a

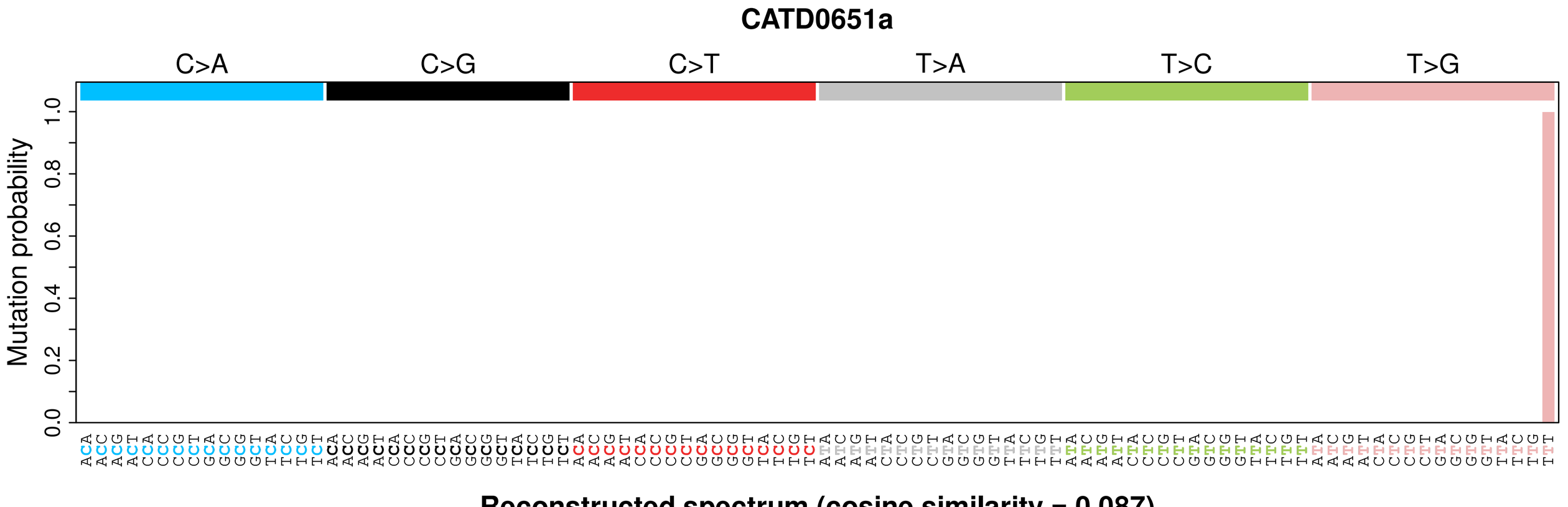


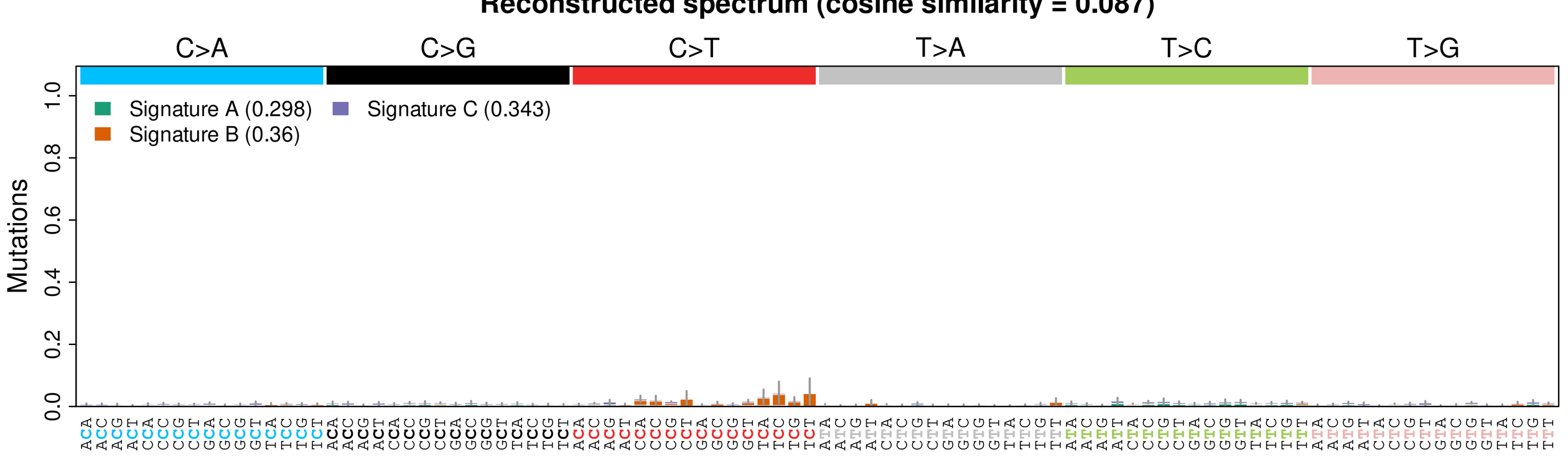
Reconstructed spectrum (cosine similarity = 0.131)

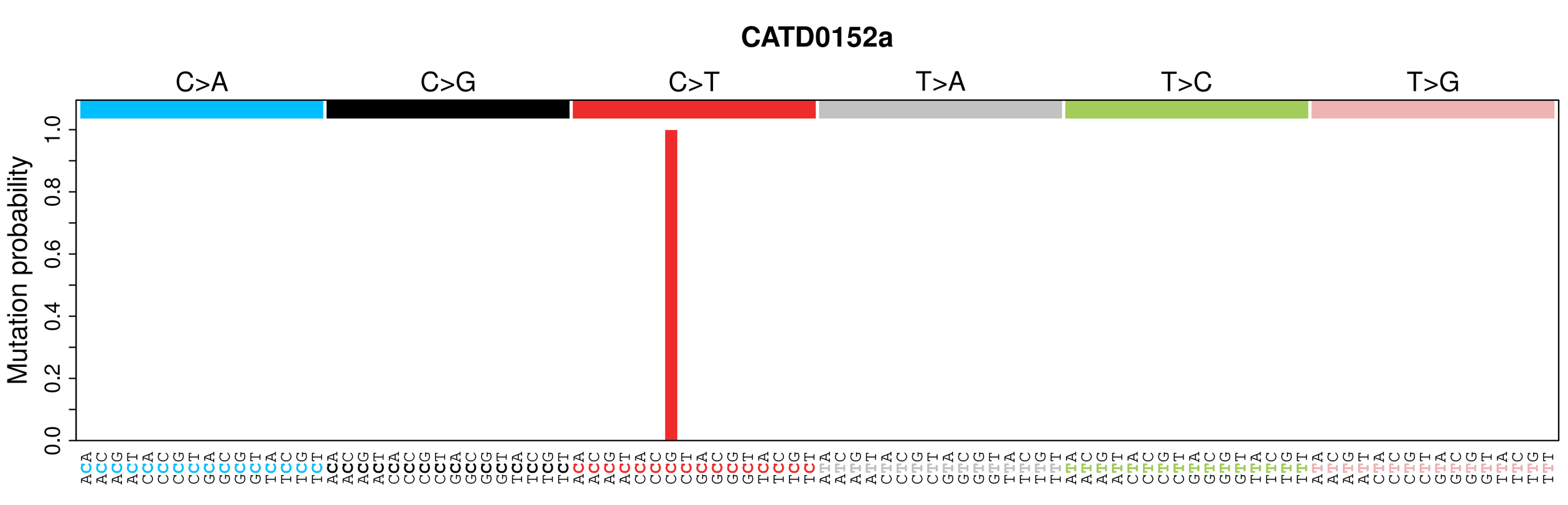


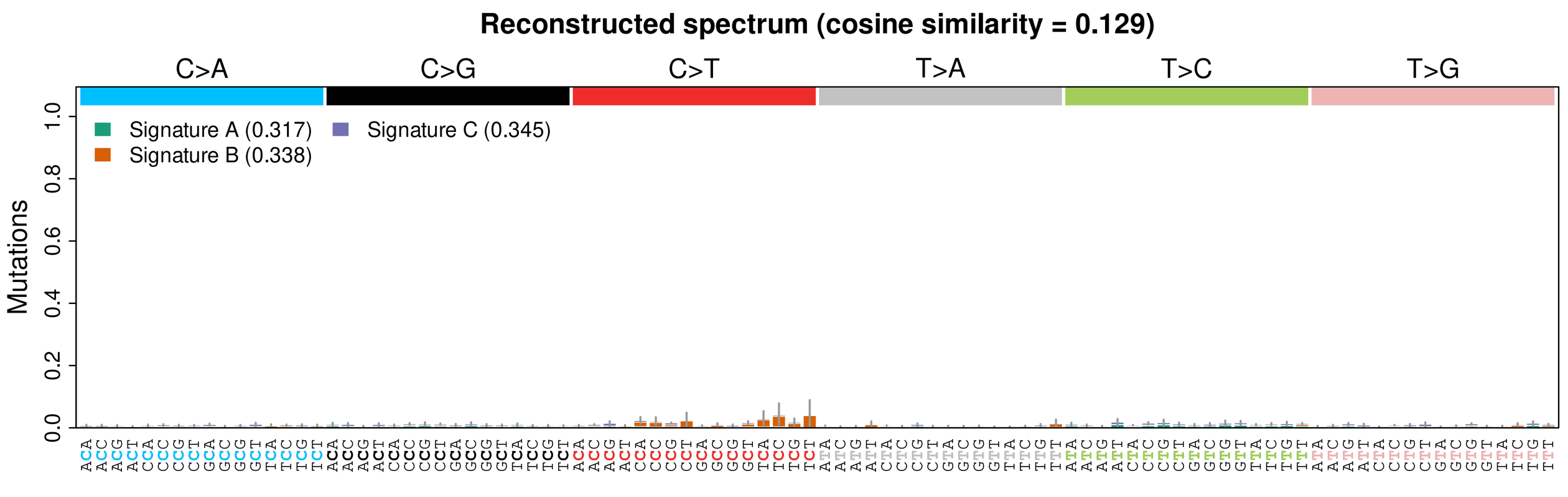

CATD0154a
C>A
C>G
C>T
T>A
T>C
T>G
Mutation probability
0.0
0.2
0.4
0.6
0.8
1.0

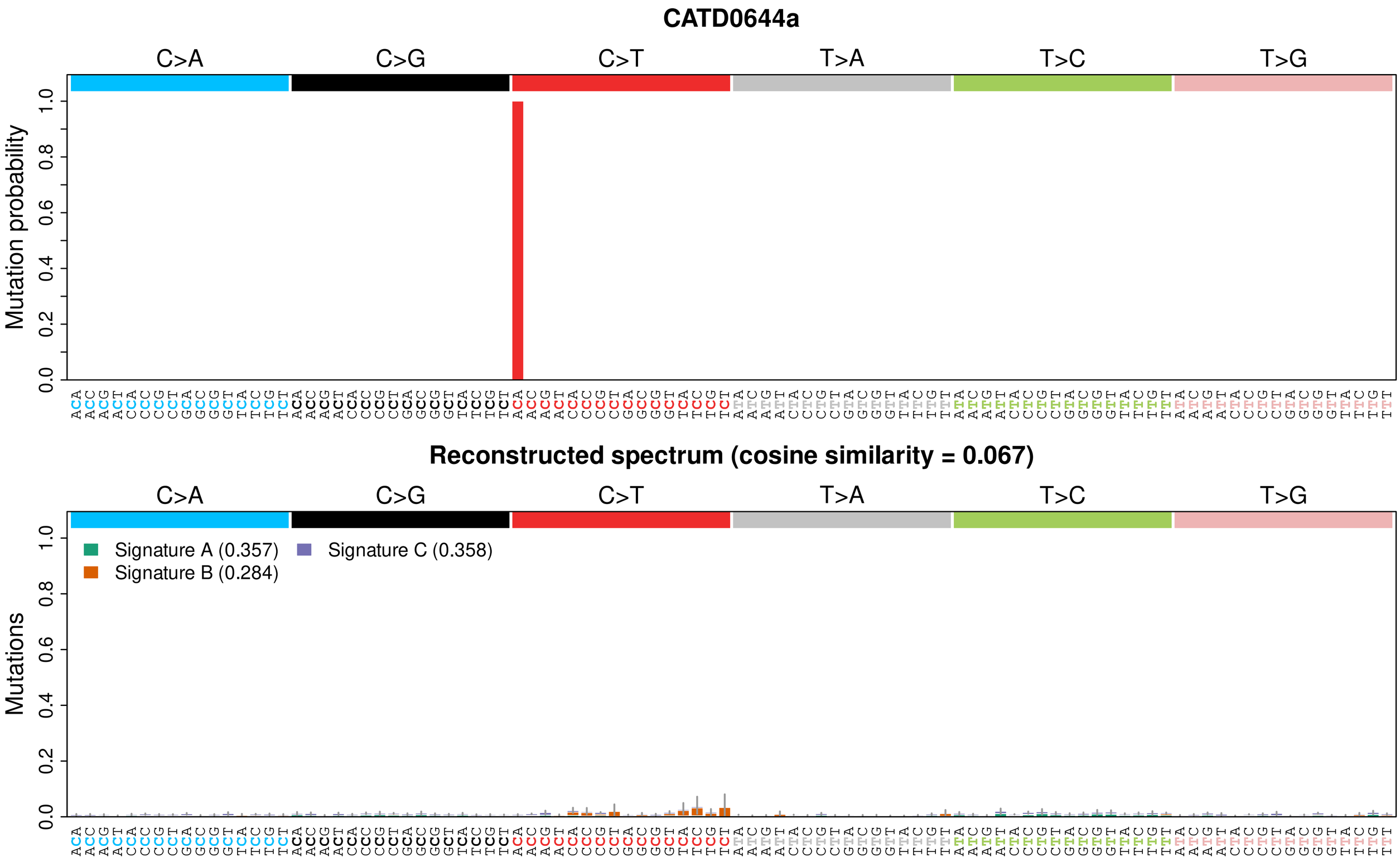

Reconstructed spectrum (cosine similarity = 0.067)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.358)
Signature B (0.285)
Signature C (0.357)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0


CATD0651a
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 = 0.087)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.298)
Signature C (0.343)
Signature B (0.36)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0


CATD0152a
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 = 0.129)
C>A
C>G
C>T
T>A
T>C
T>G
Signature A (0.317)
Signature B (0.338)
Signature C (0.345)
Mutations
0.0
0.2
0.4
0.6
0.8
1.0


CATD0644a
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 = 0.067)
Signature A (0.357)
Signature B (0.284)
Signature C (0.358)
Mutations