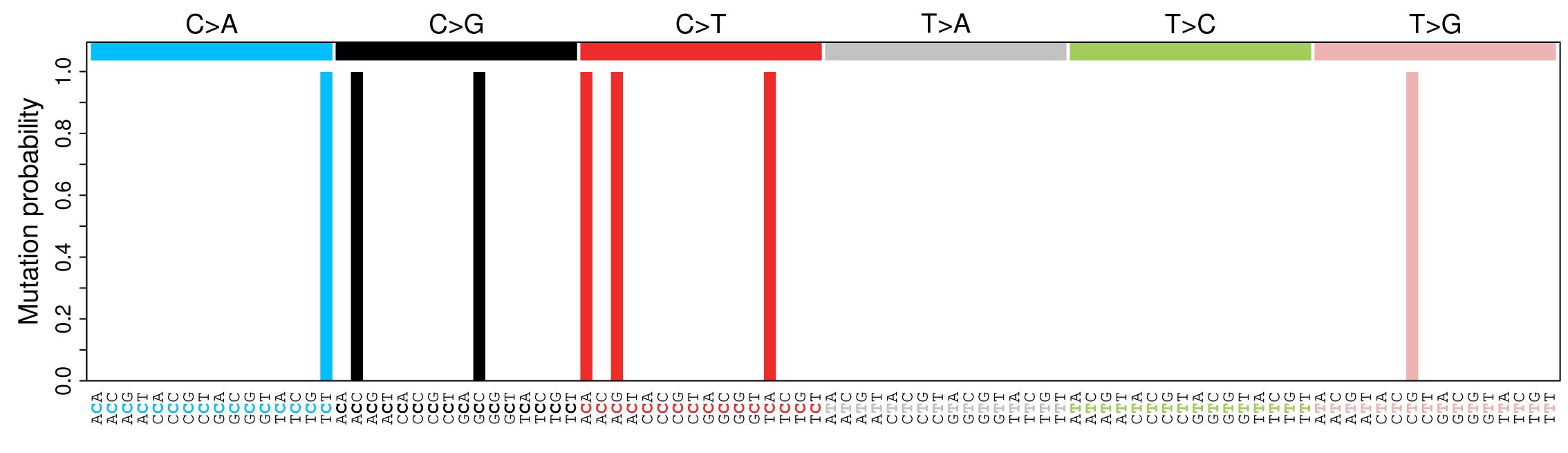
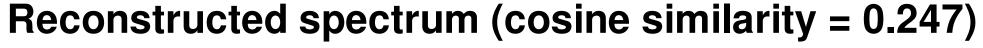
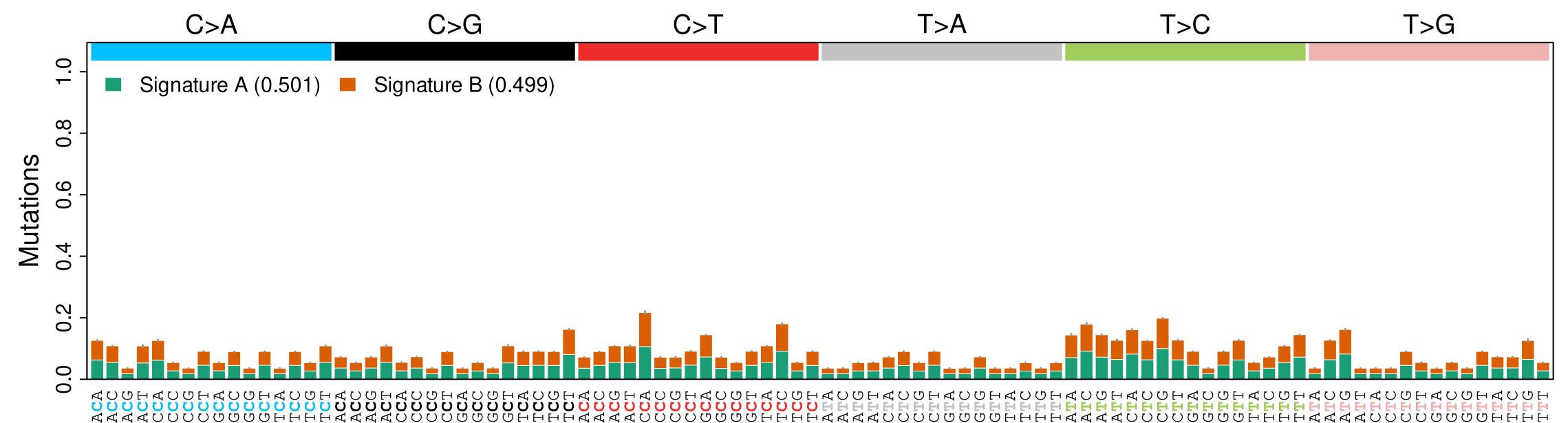
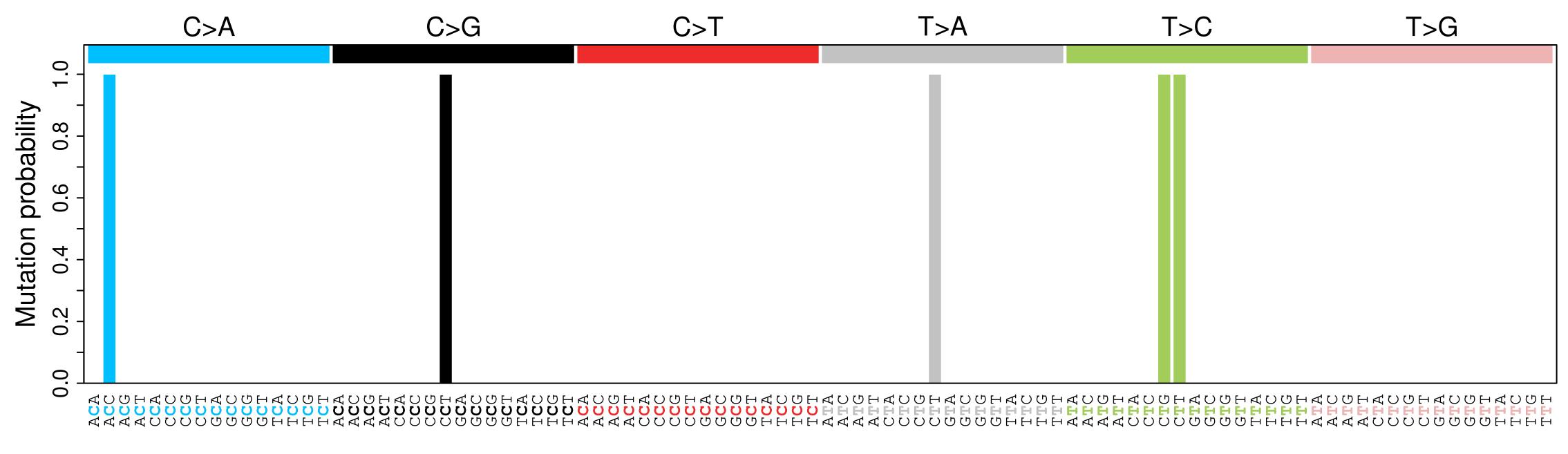
CATD0414a

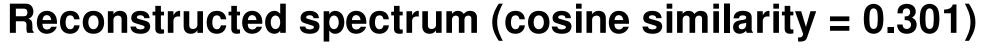


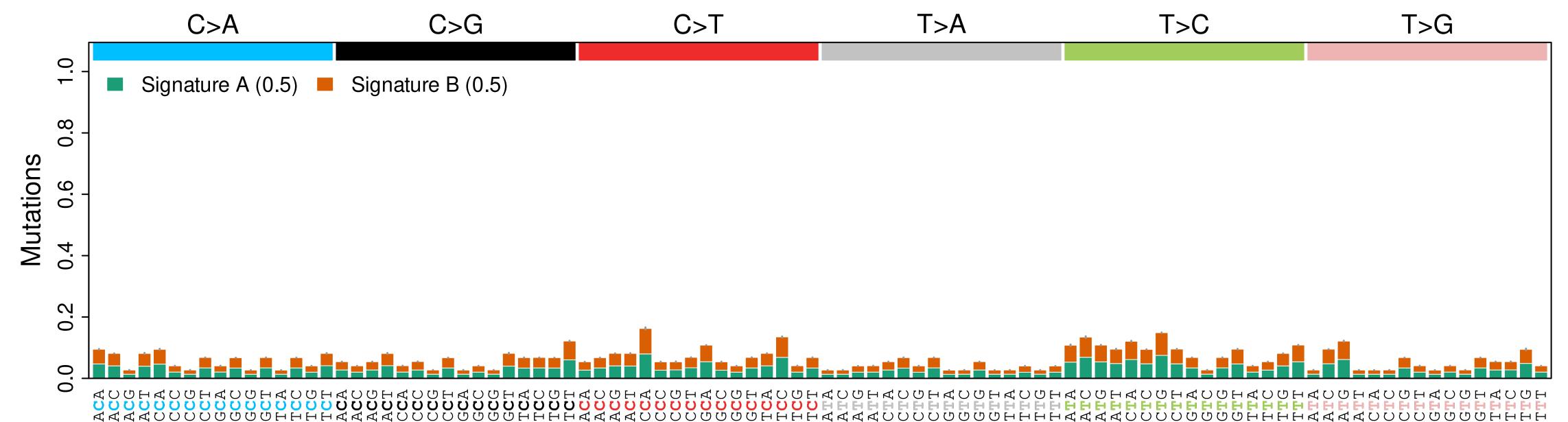




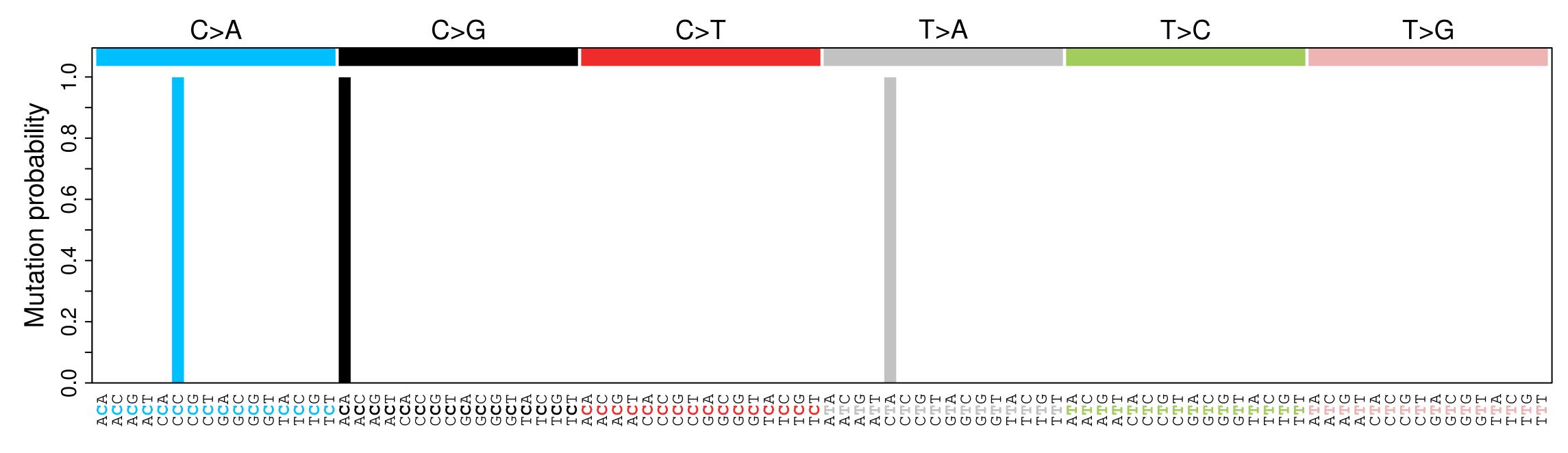
CATD0105a

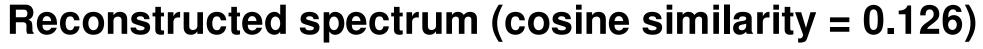


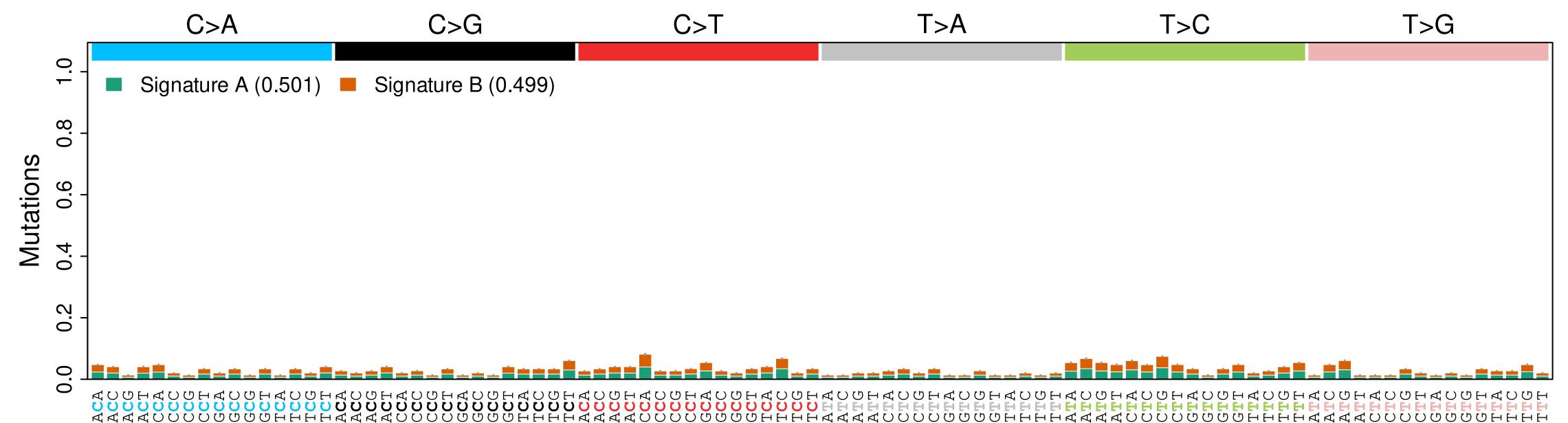






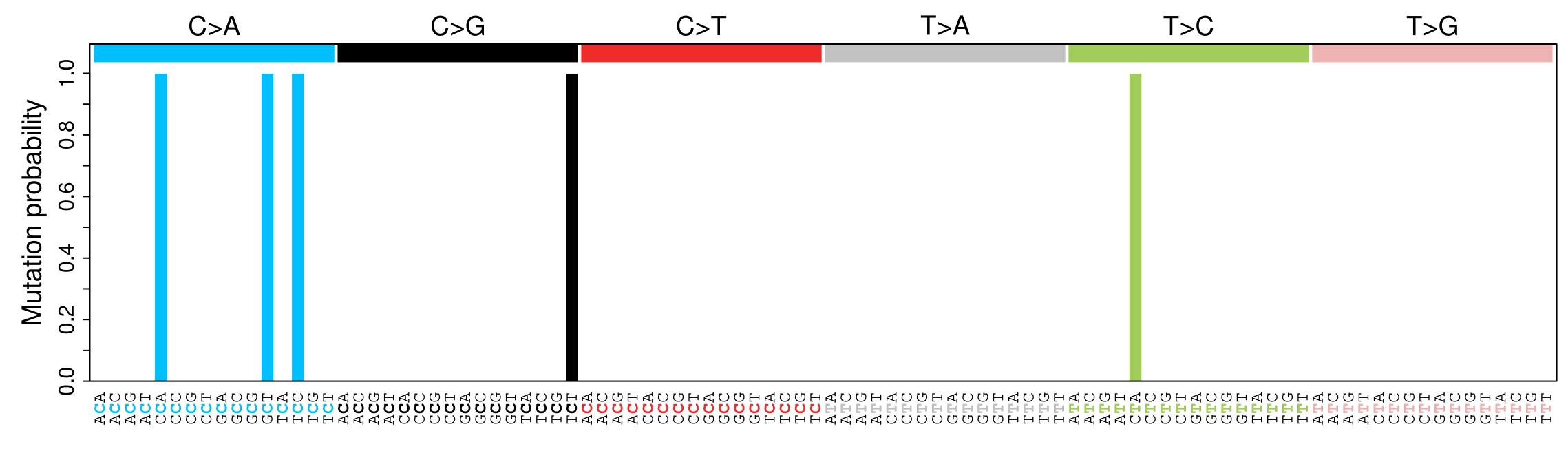




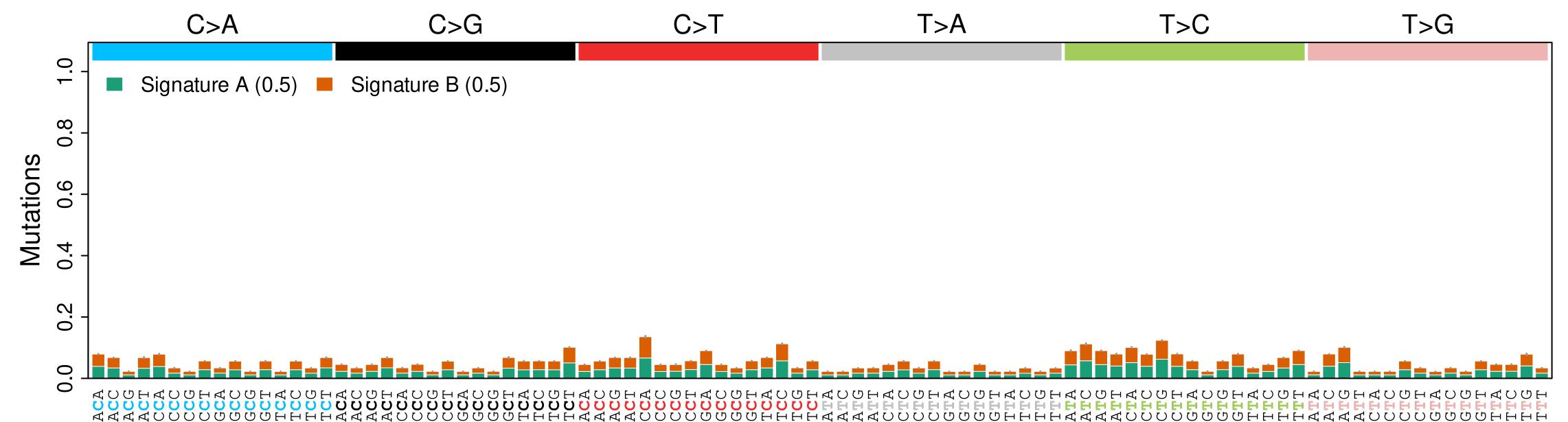


CATD0090a (7 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.275)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.497) Signature B (0.503) 5 Mutations 2 0

CATD0088a



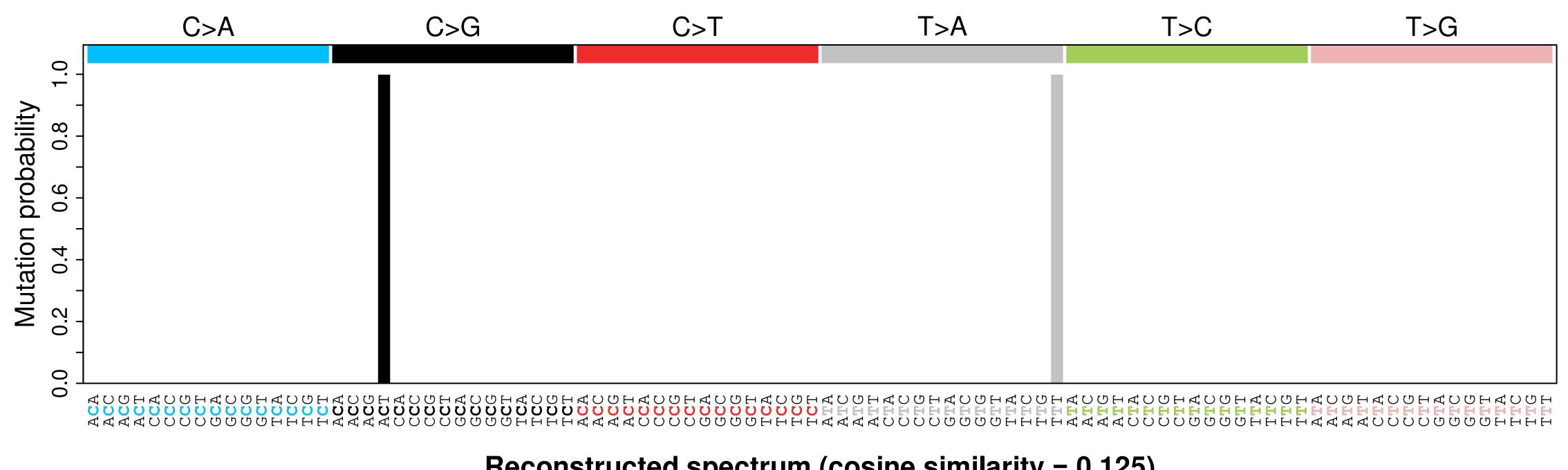
Reconstructed spectrum (cosine similarity = 0.308)



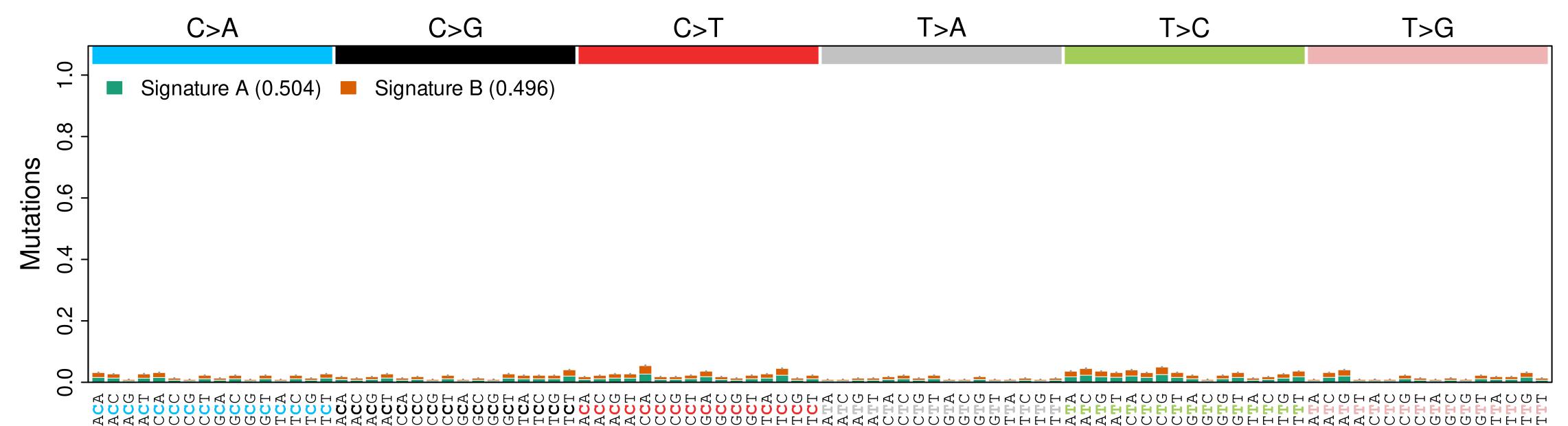
CATD0102a (7 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.239)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.504) Signature B (0.496) 5 Mutations

0.5

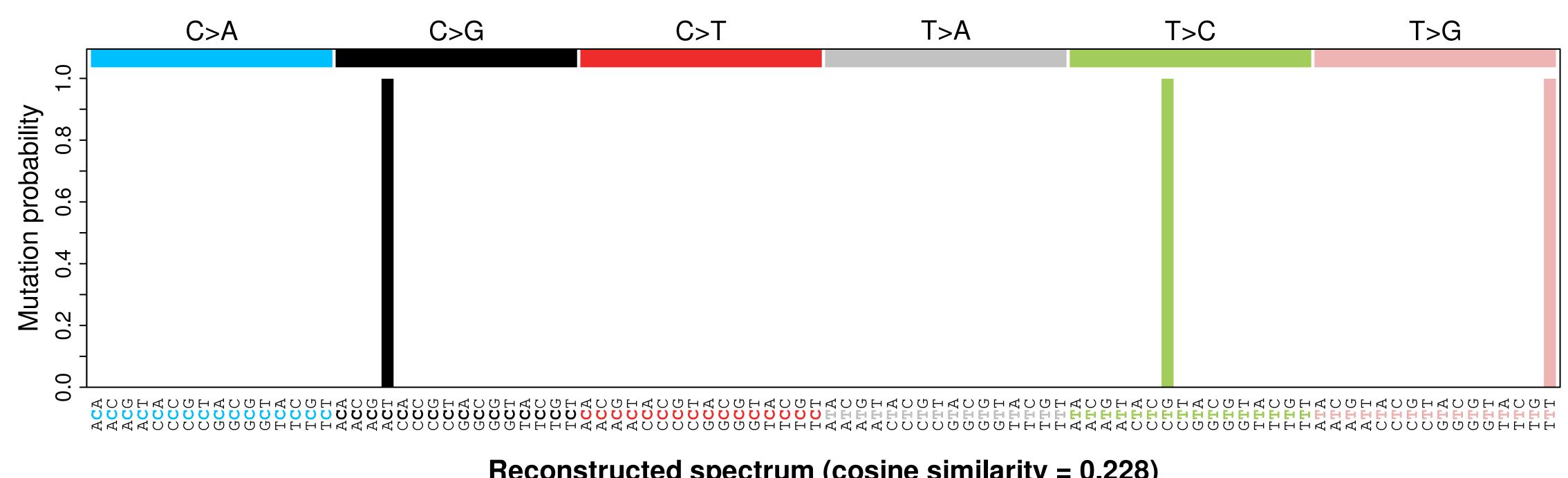


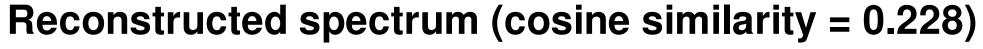


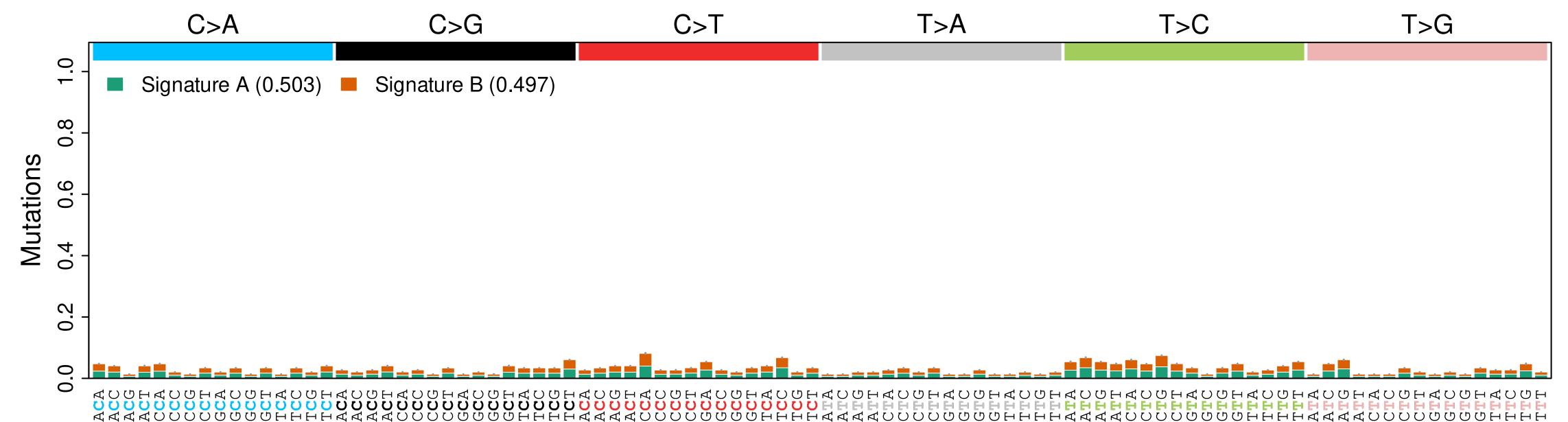




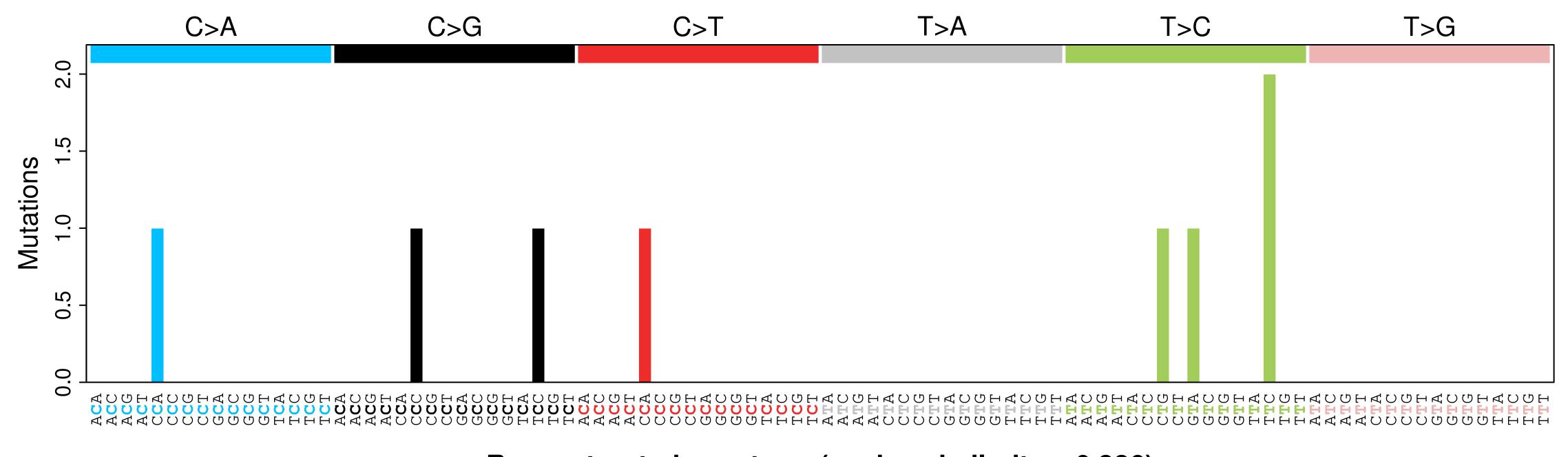


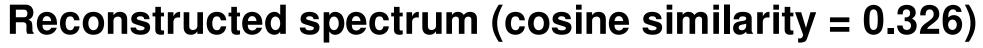


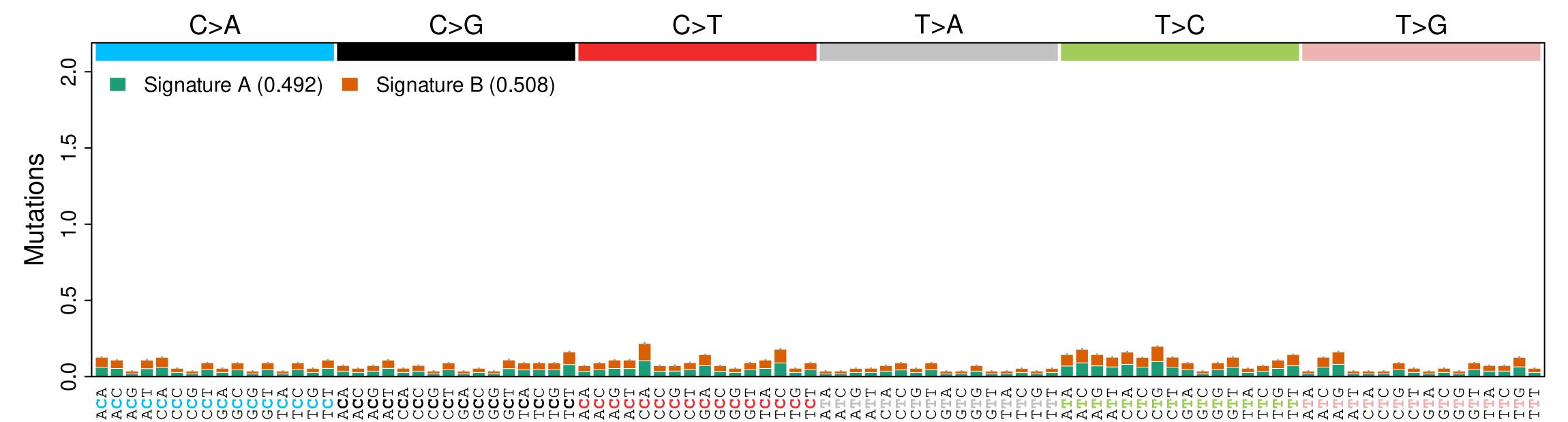




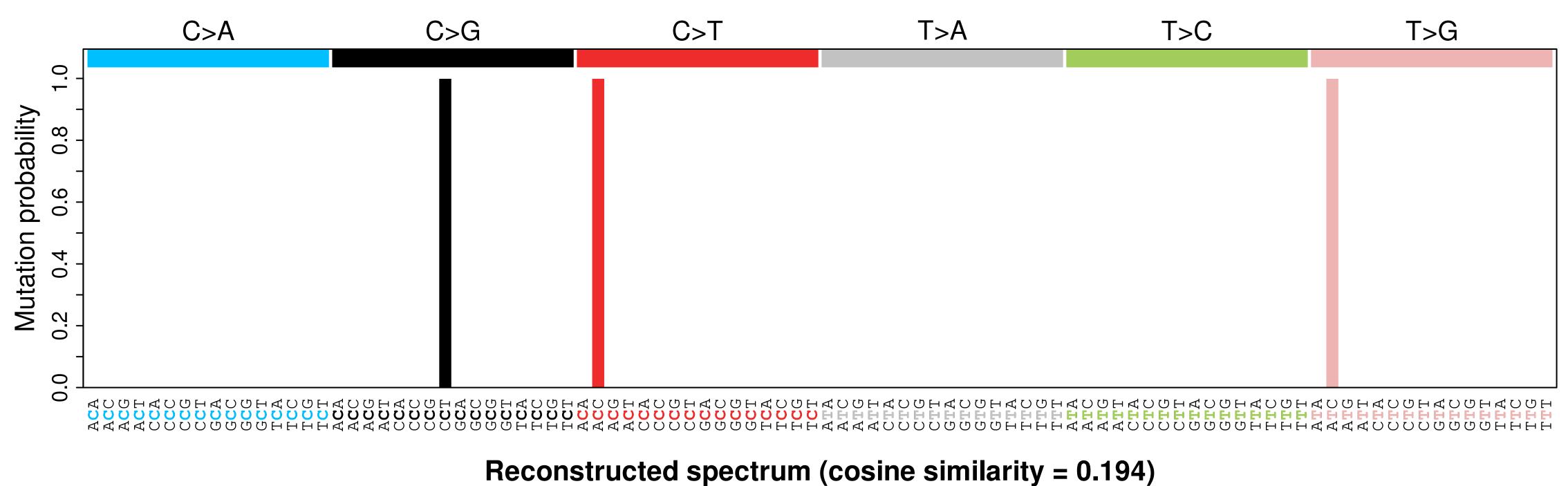
CATD0087a (8 mutations)

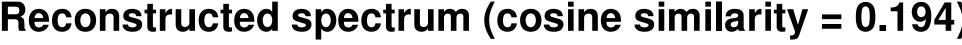


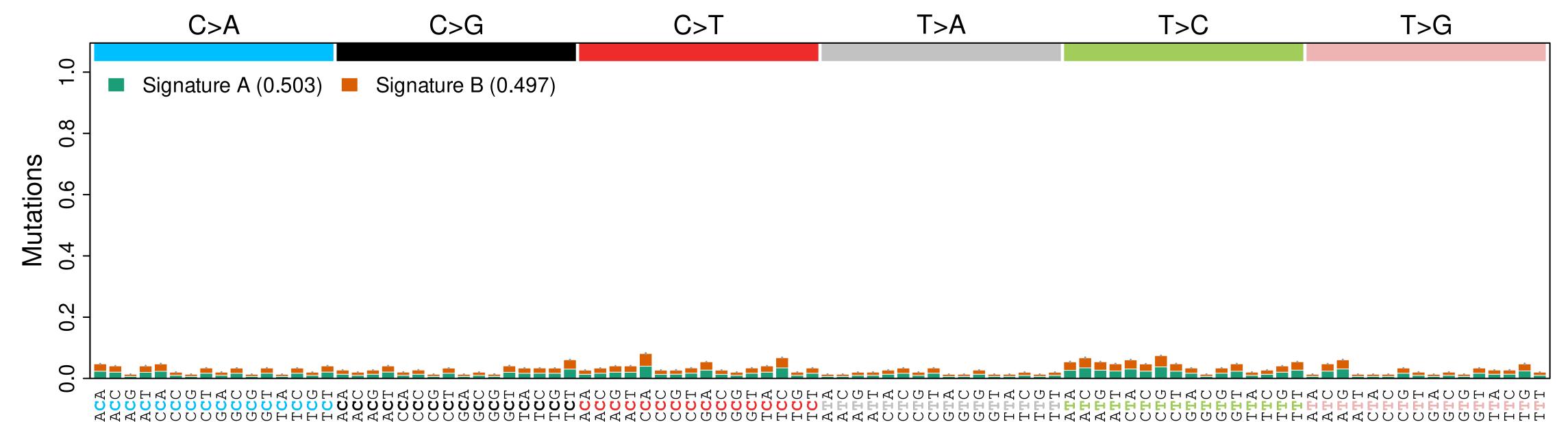




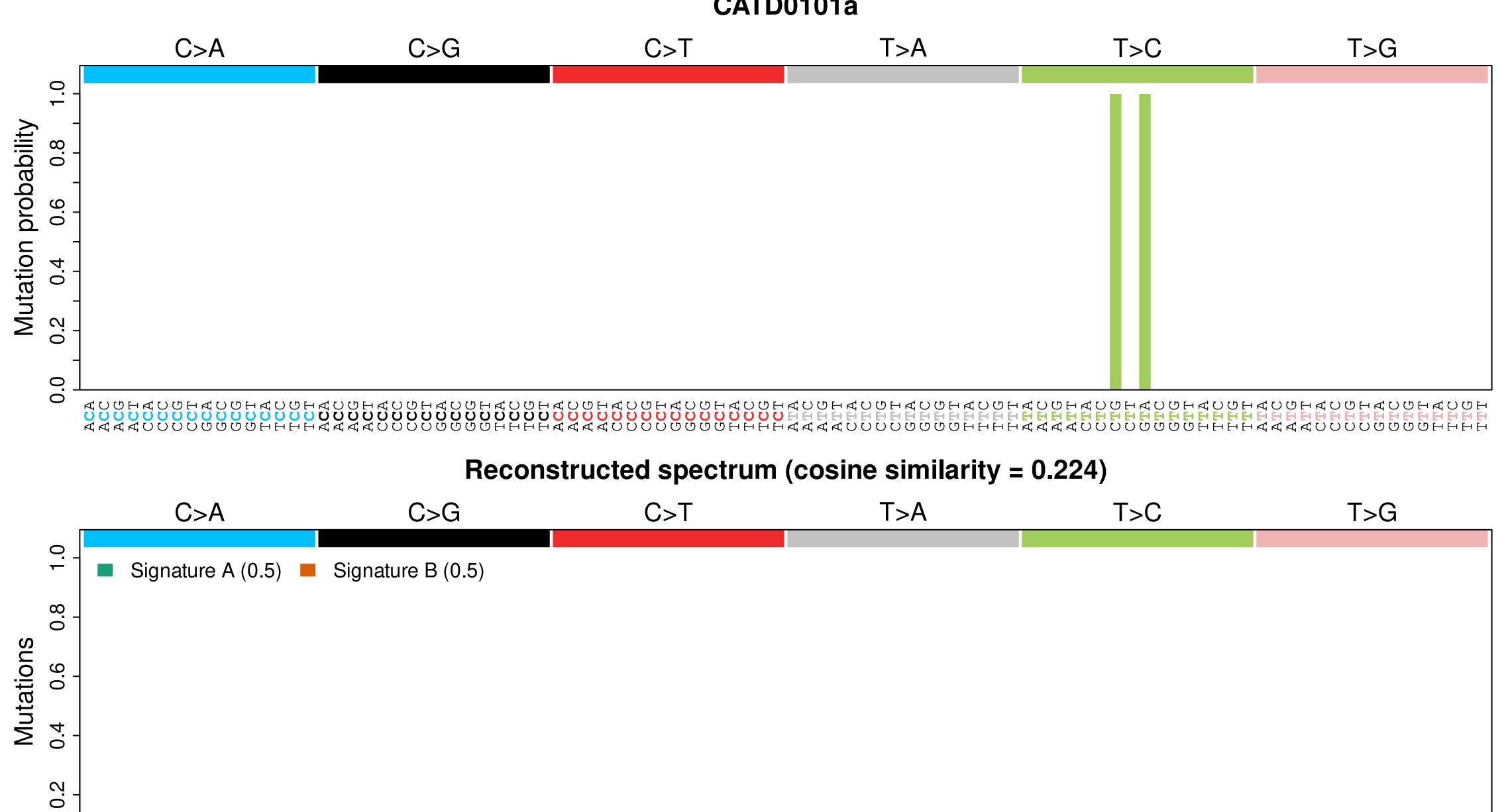


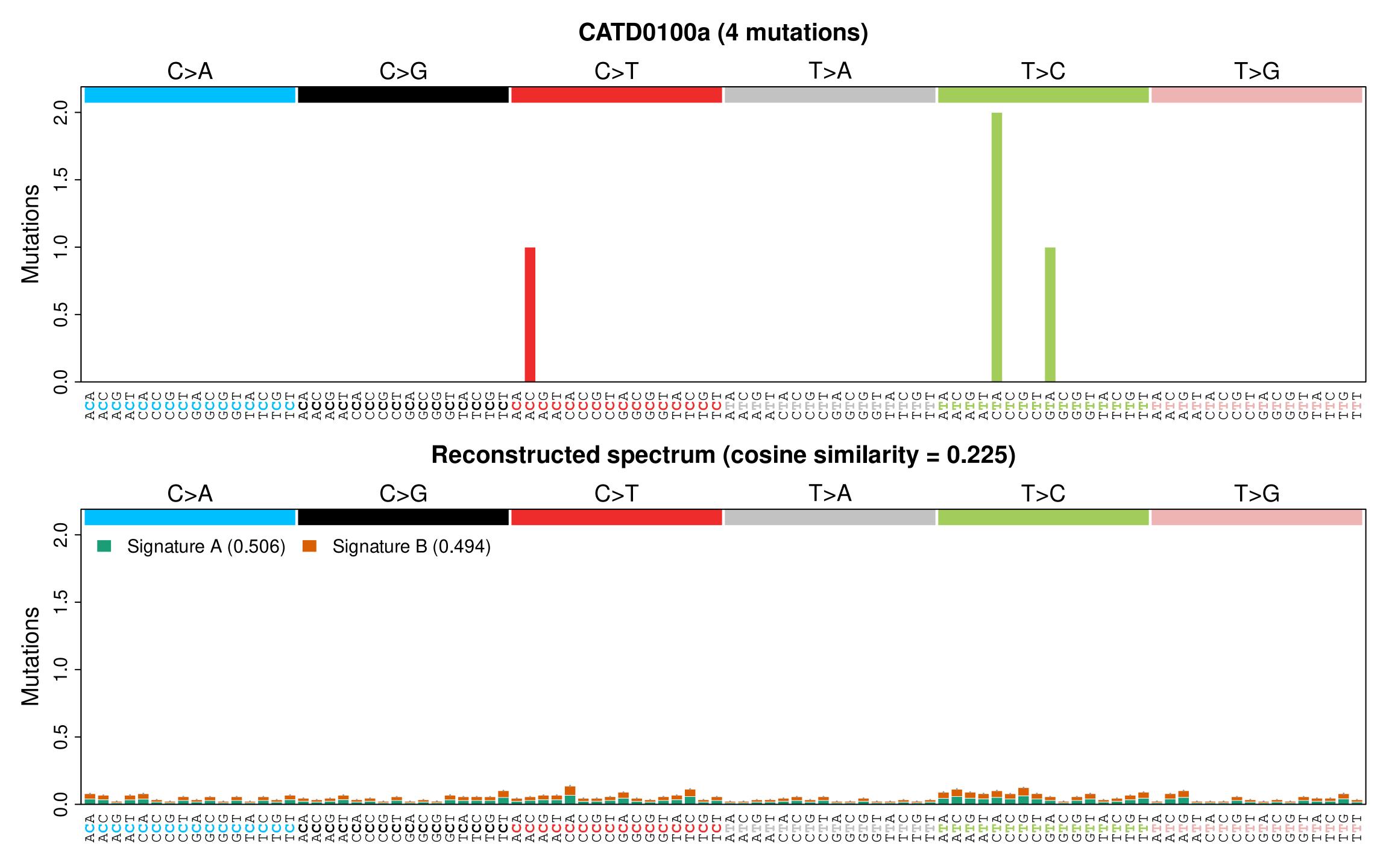




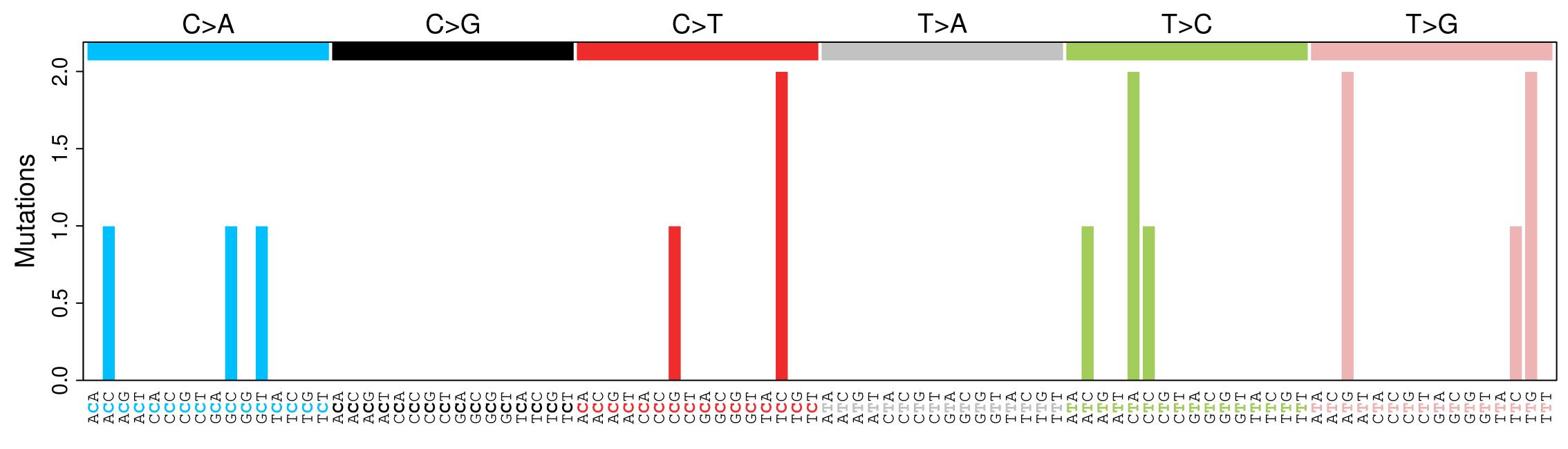




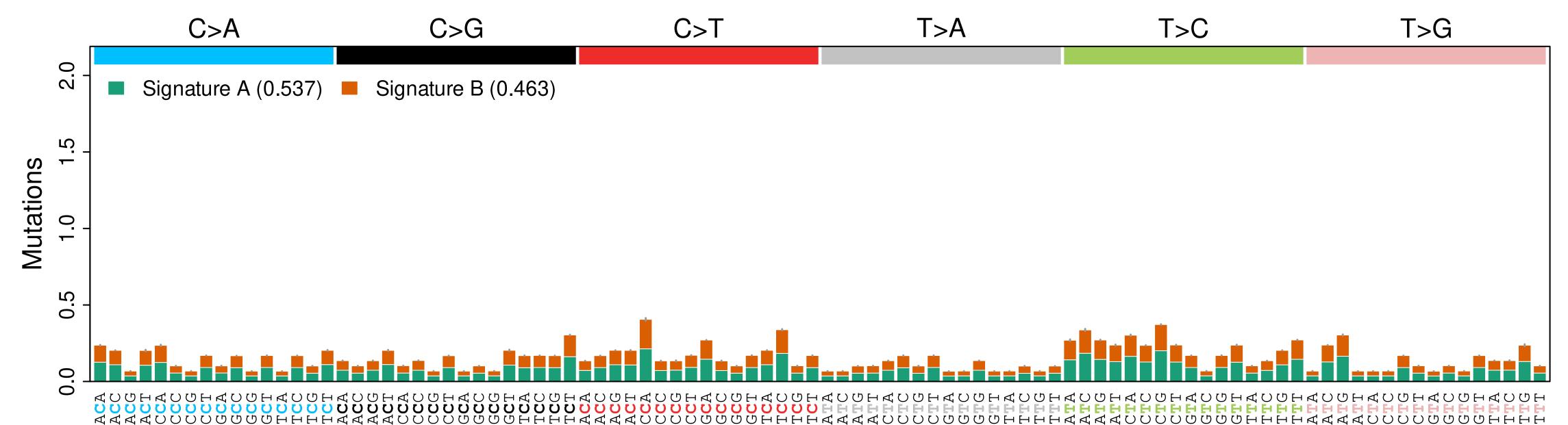




CATD0118a (15 mutations)

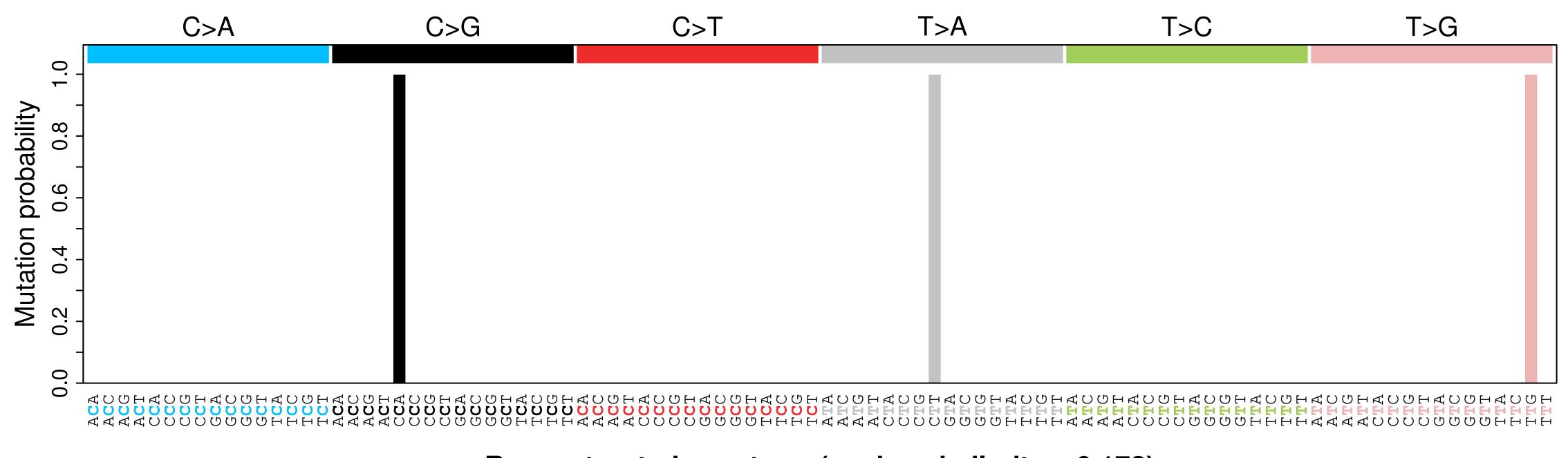


Reconstructed spectrum (cosine similarity = 0.456)

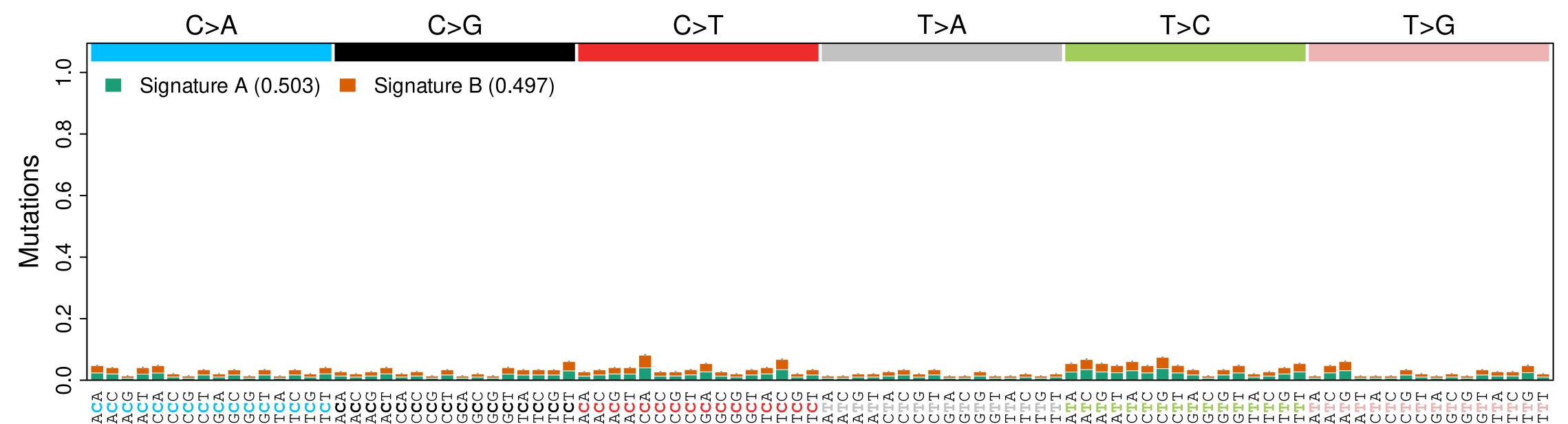


CATD0108a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 1.5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.115)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.5) Signature B (0.5) 5 Mutations 5 0

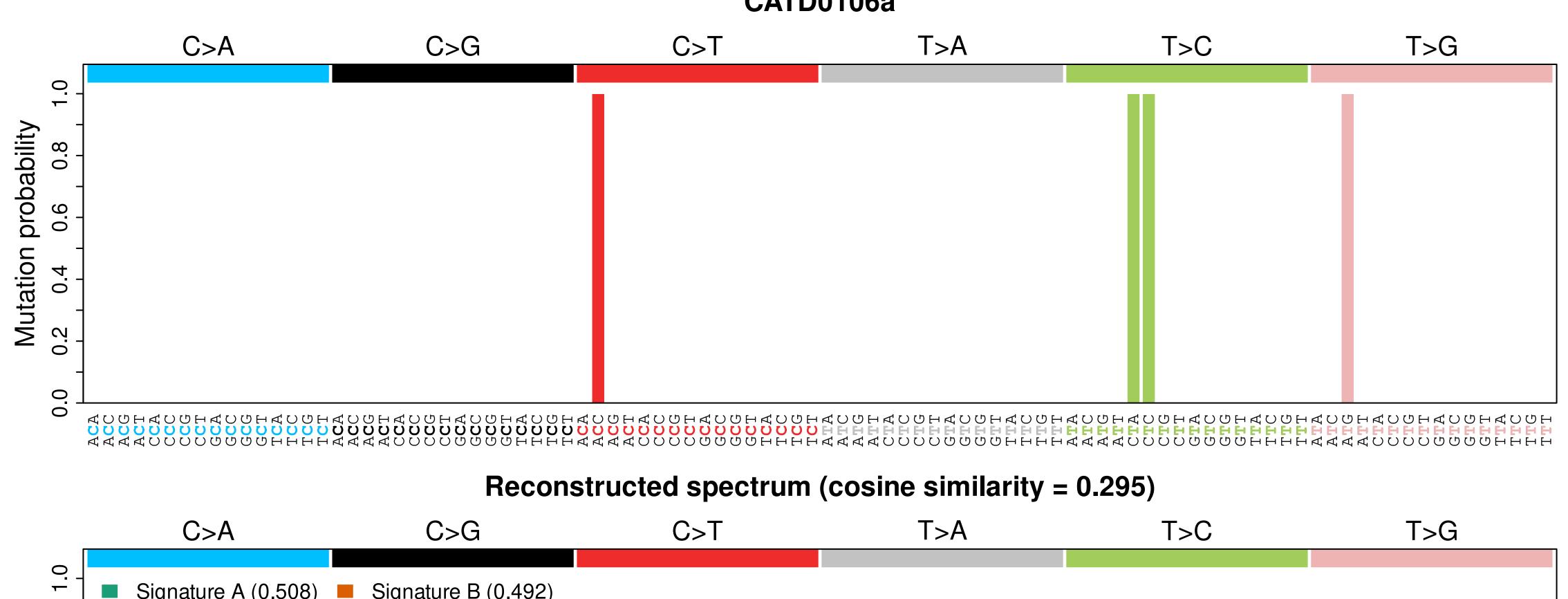


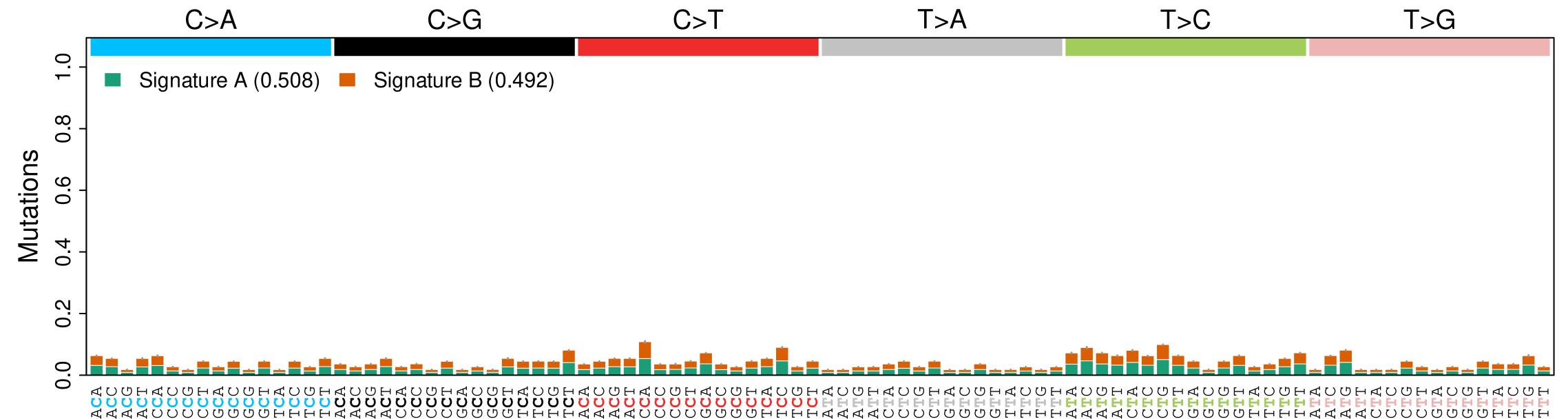




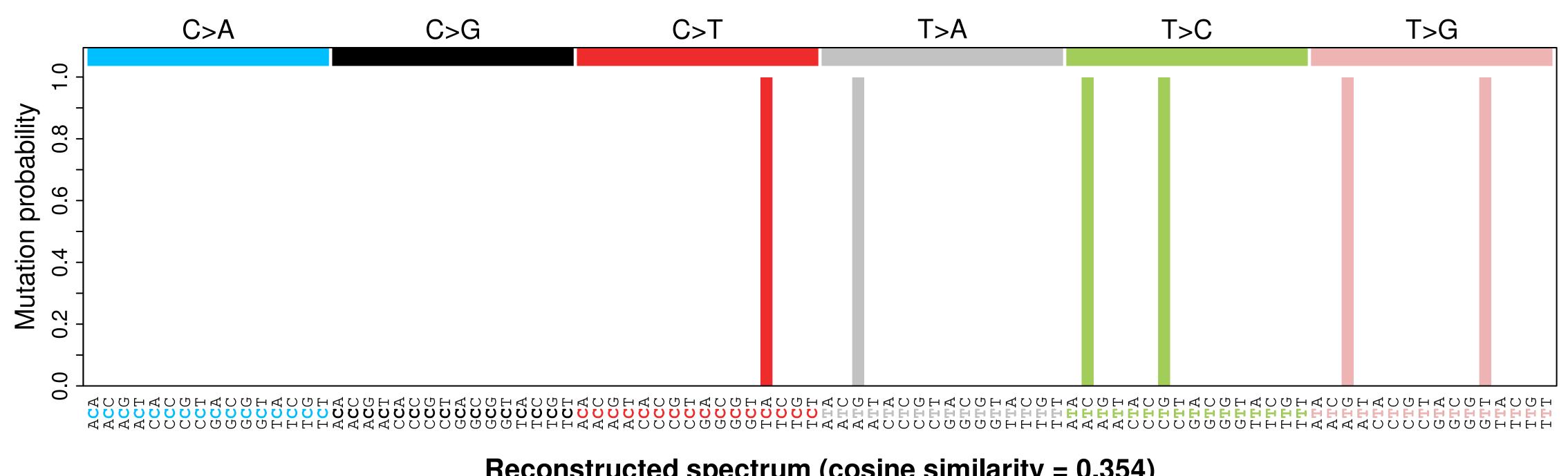


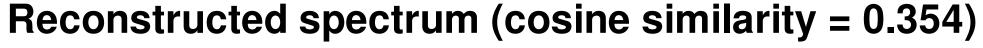
CATD0106a

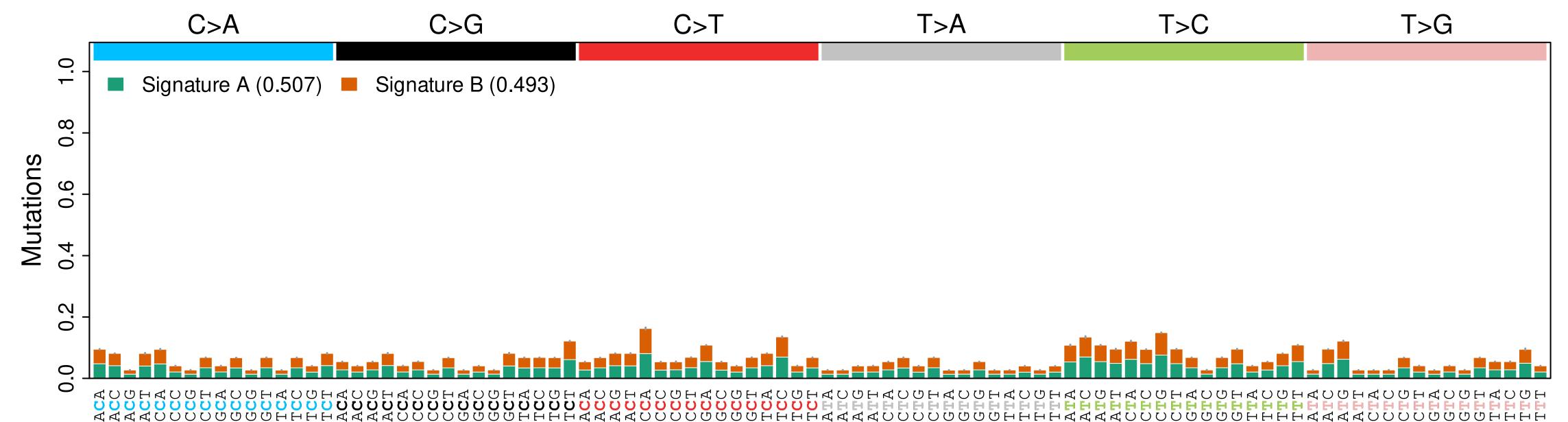




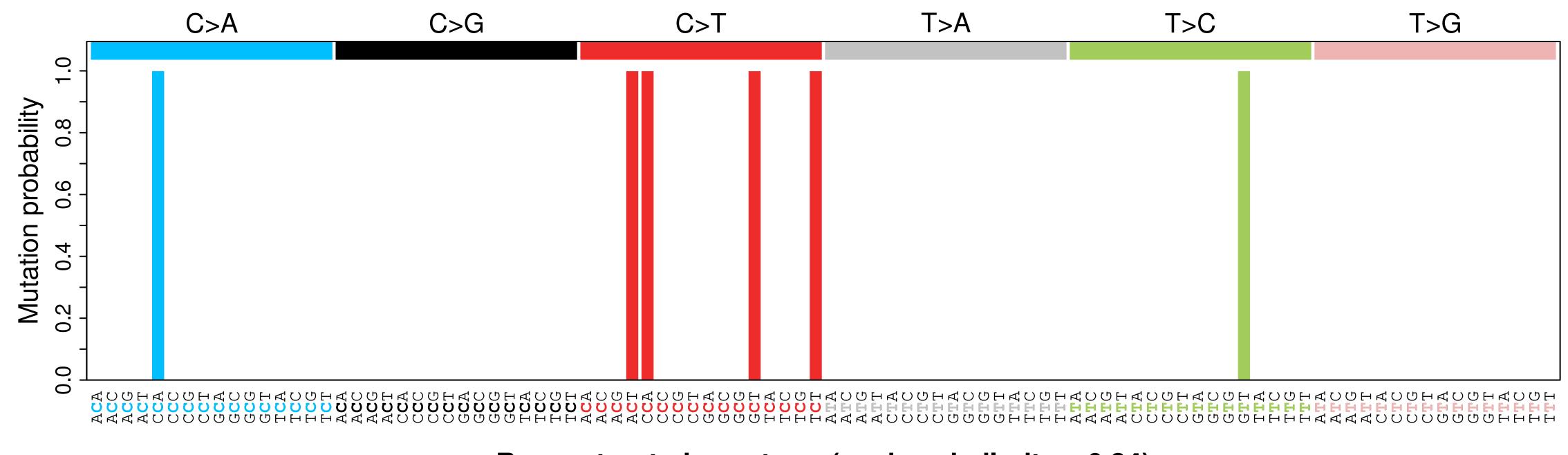
CATD0107a

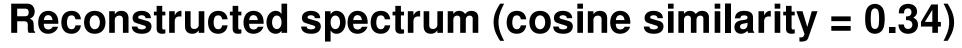


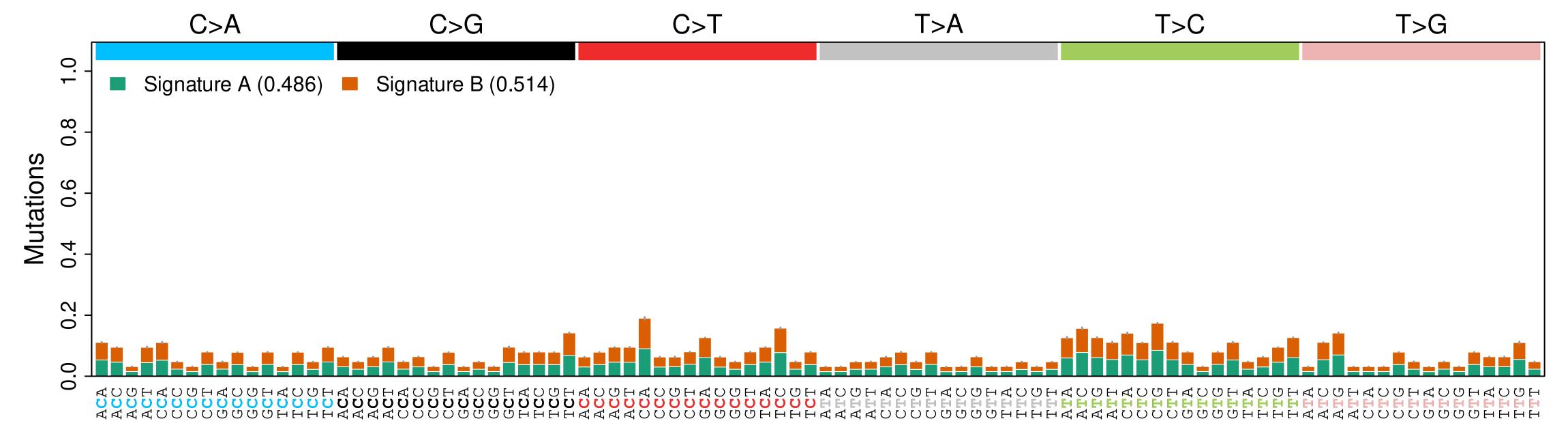




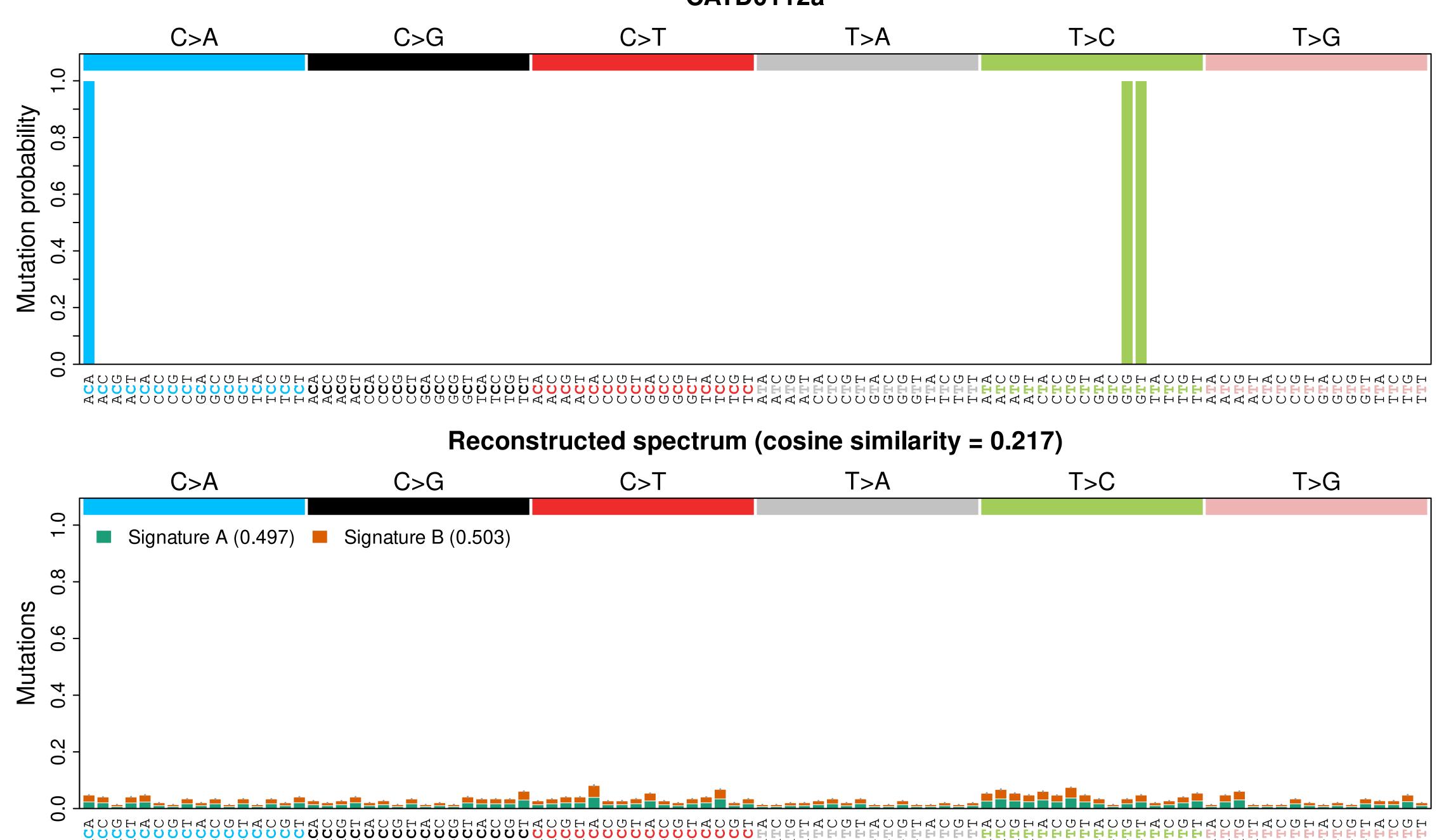
CATD0097a



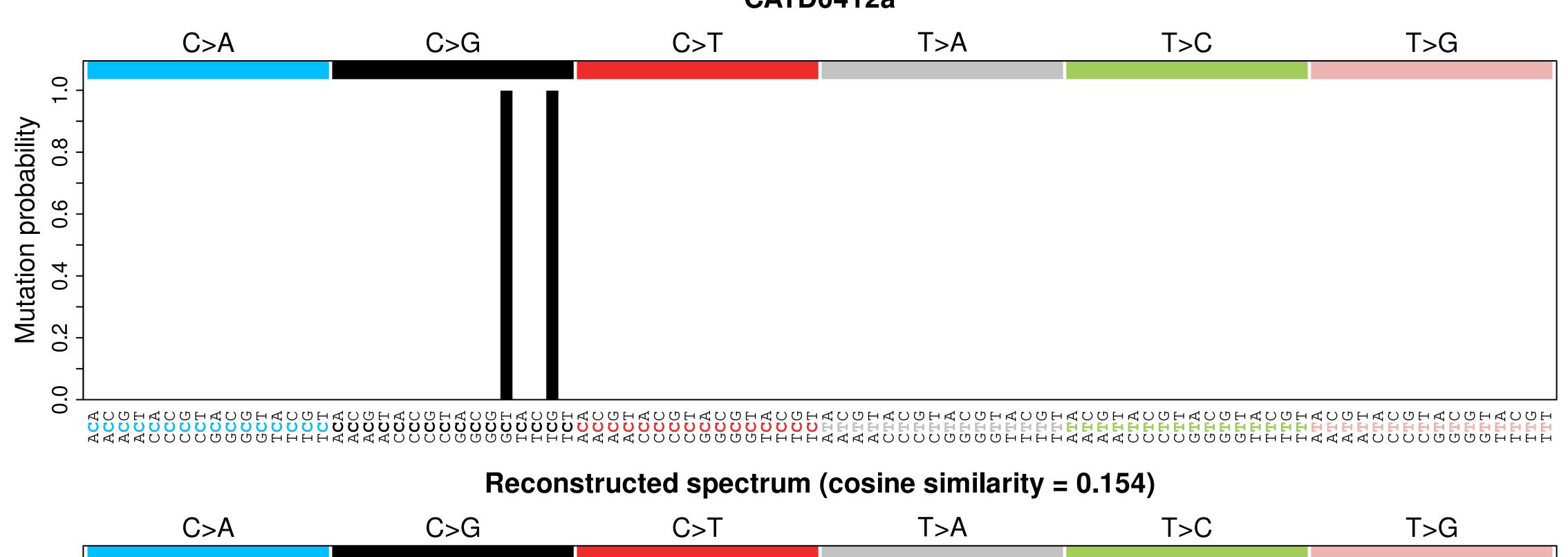


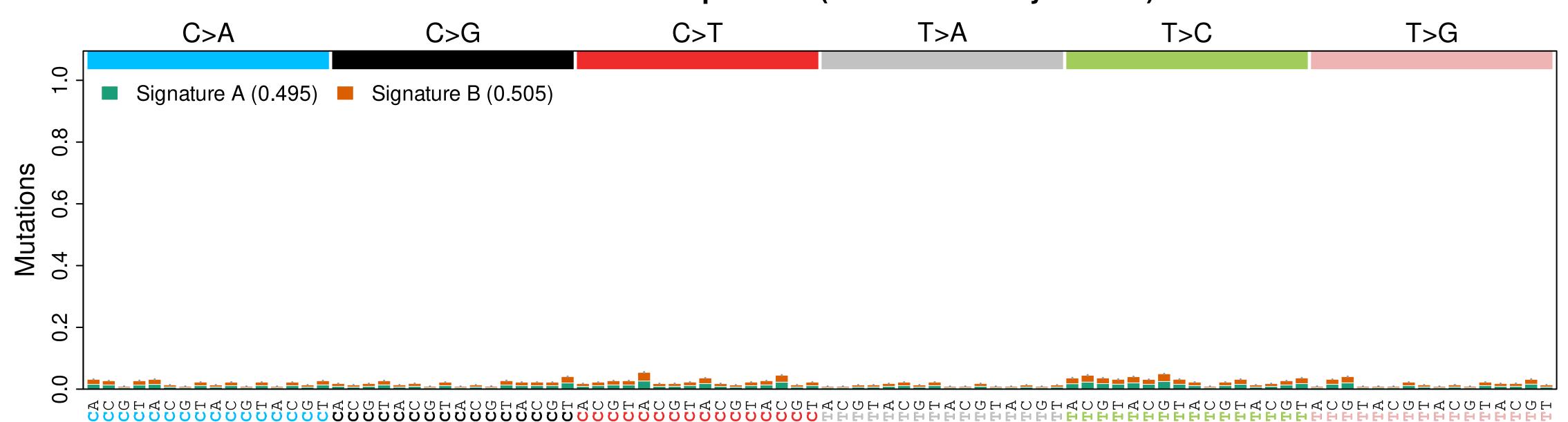




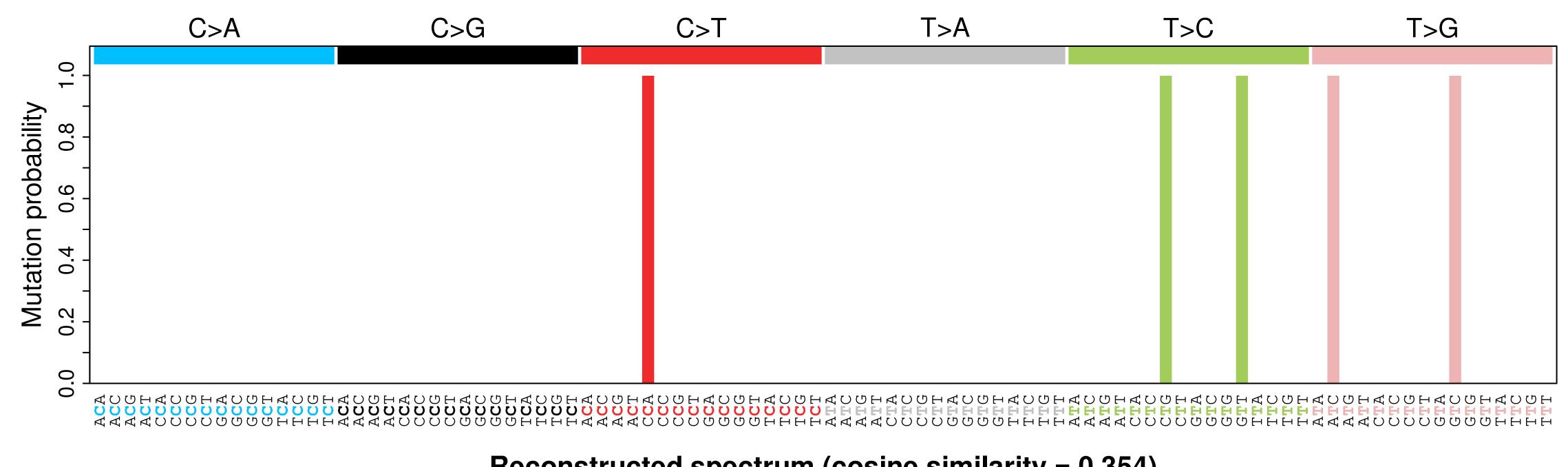




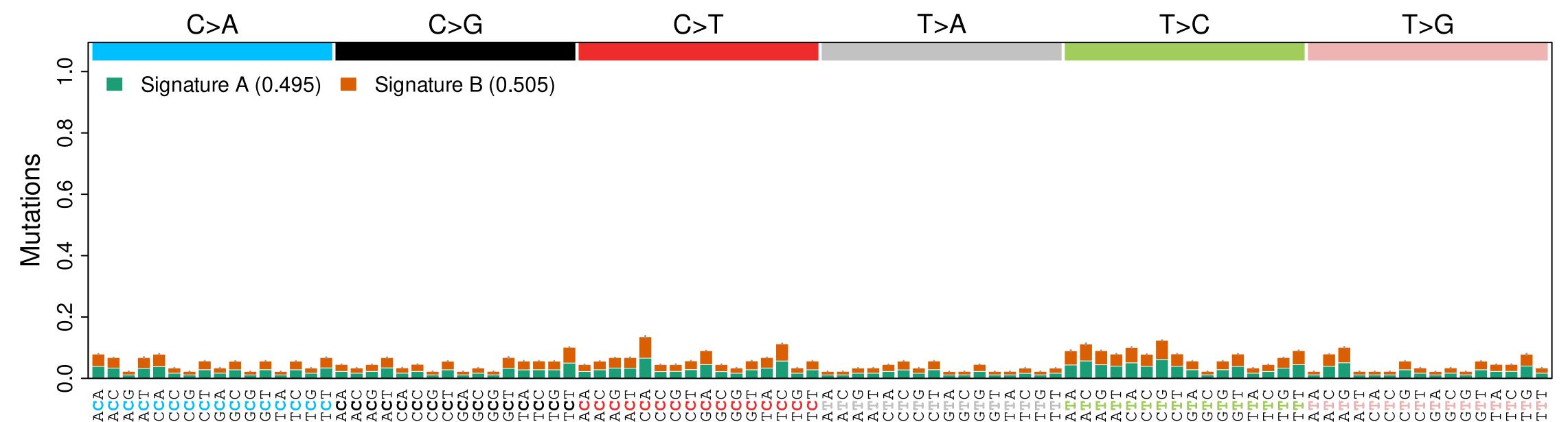




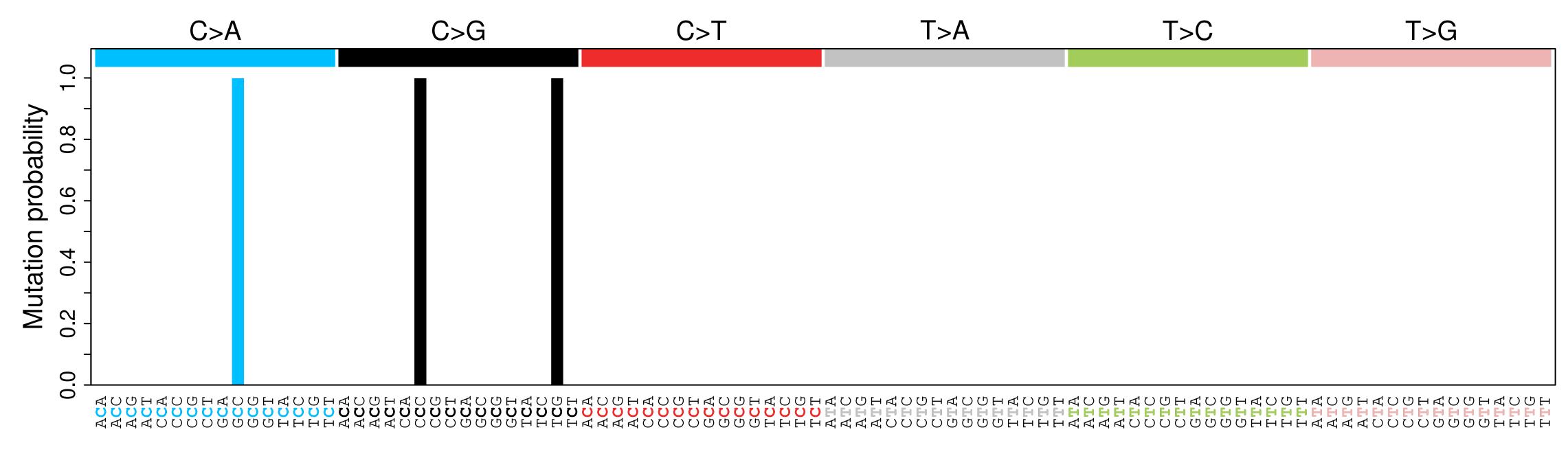
CATD0110a



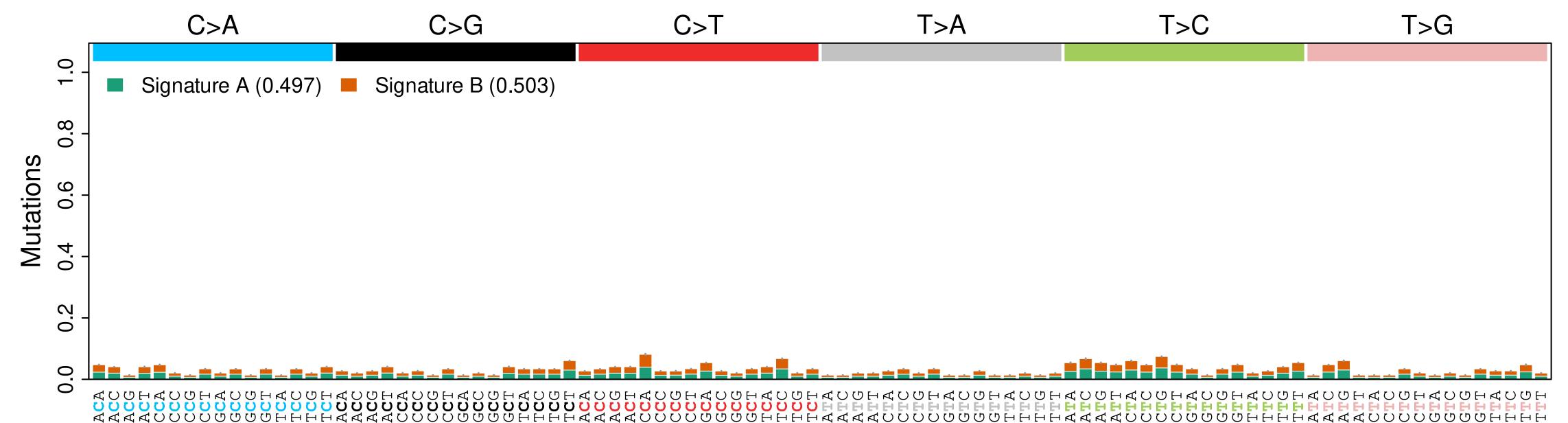
Reconstructed spectrum (cosine similarity = 0.354)



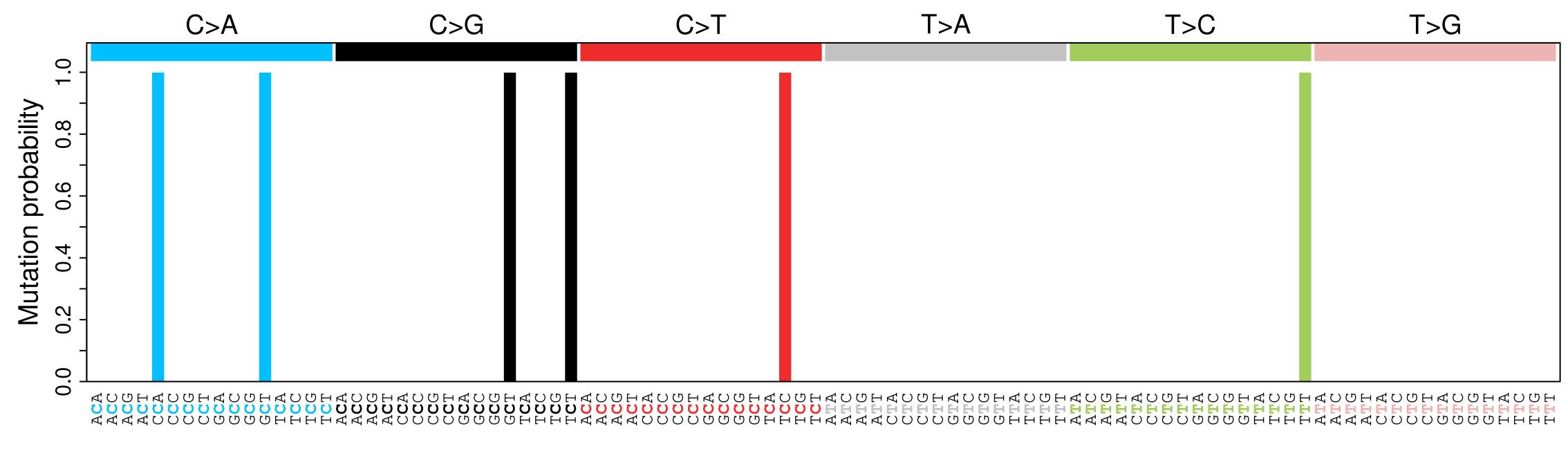
CATD0117a



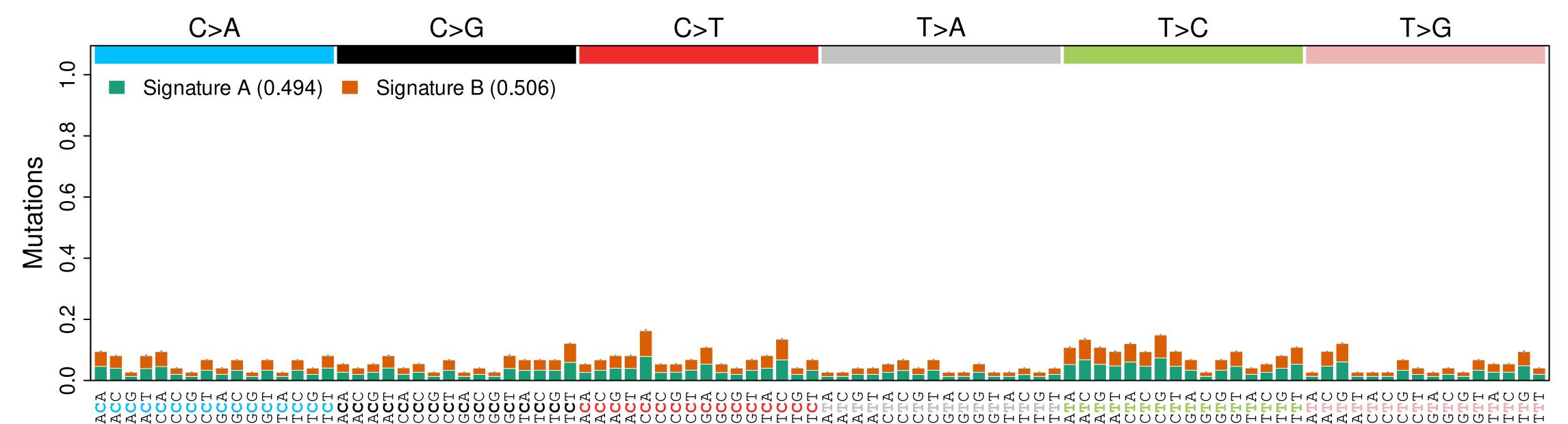
Reconstructed spectrum (cosine similarity = 0.16)



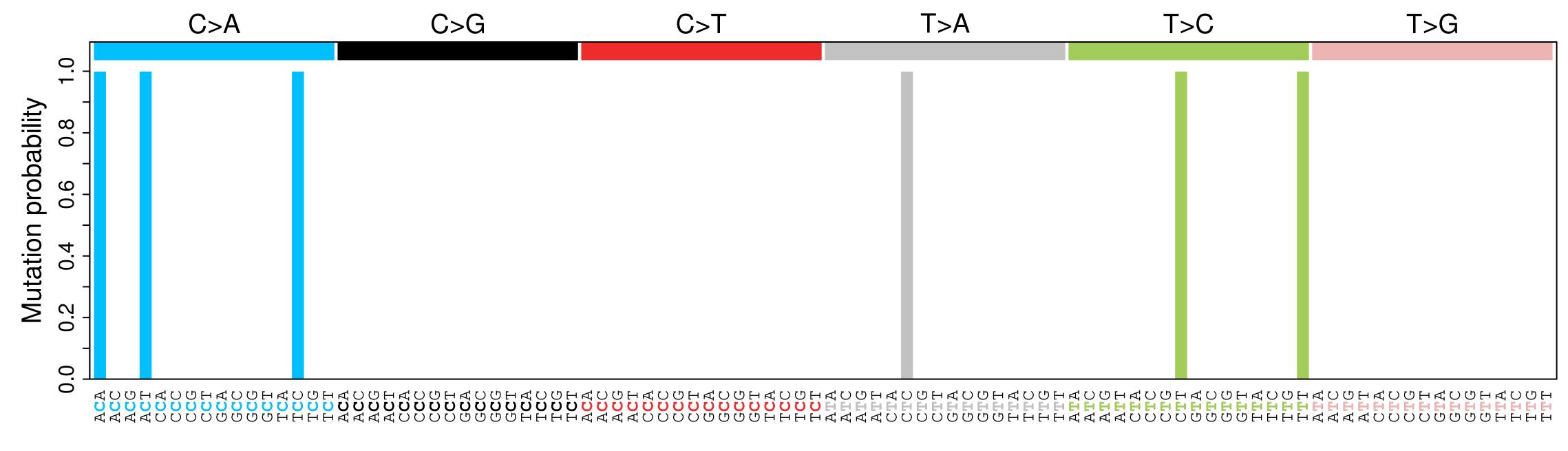
CATD0084a



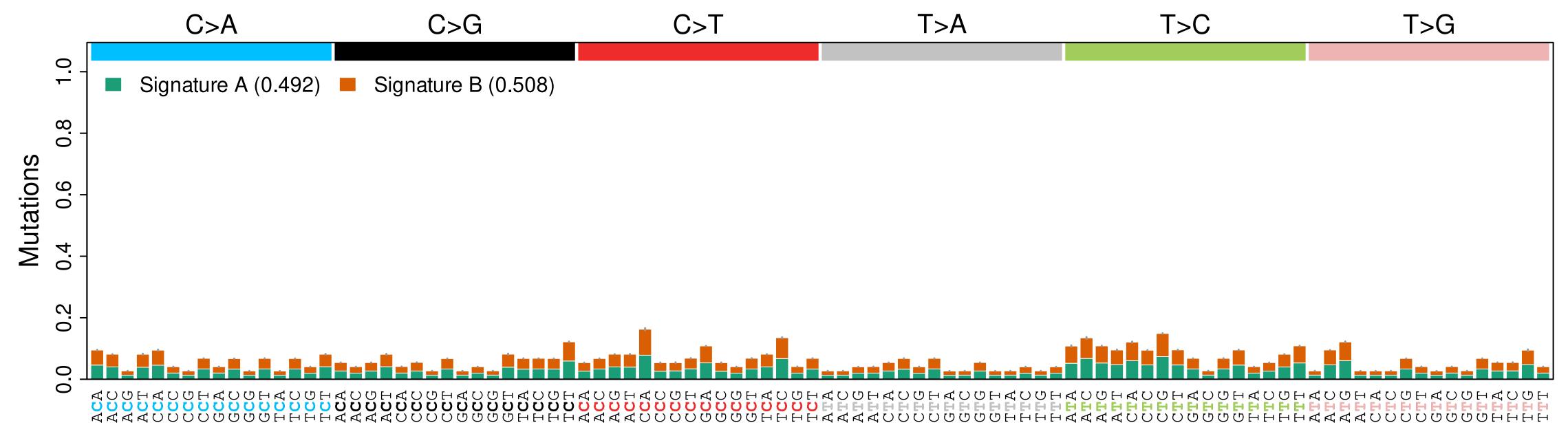
Reconstructed spectrum (cosine similarity = 0.363)



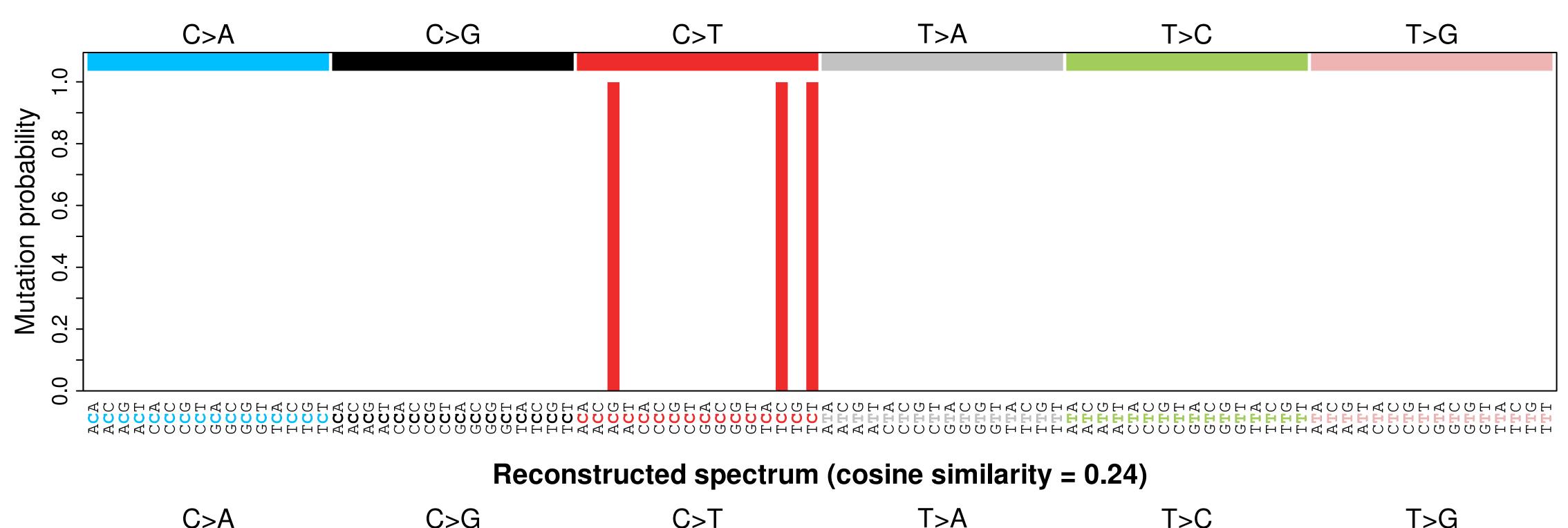
CATD0081a

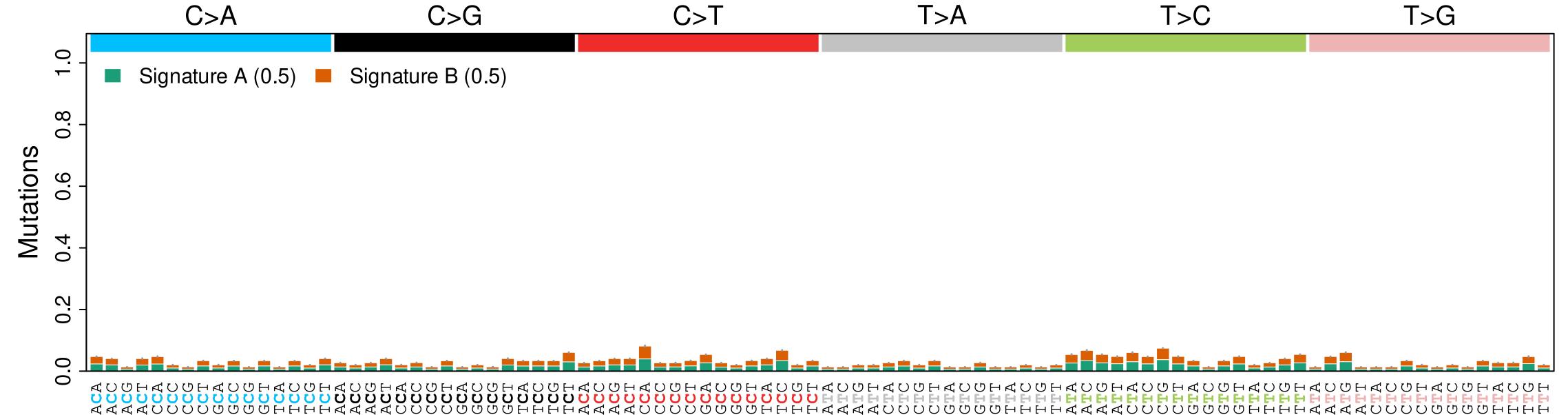


Reconstructed spectrum (cosine similarity = 0.307)



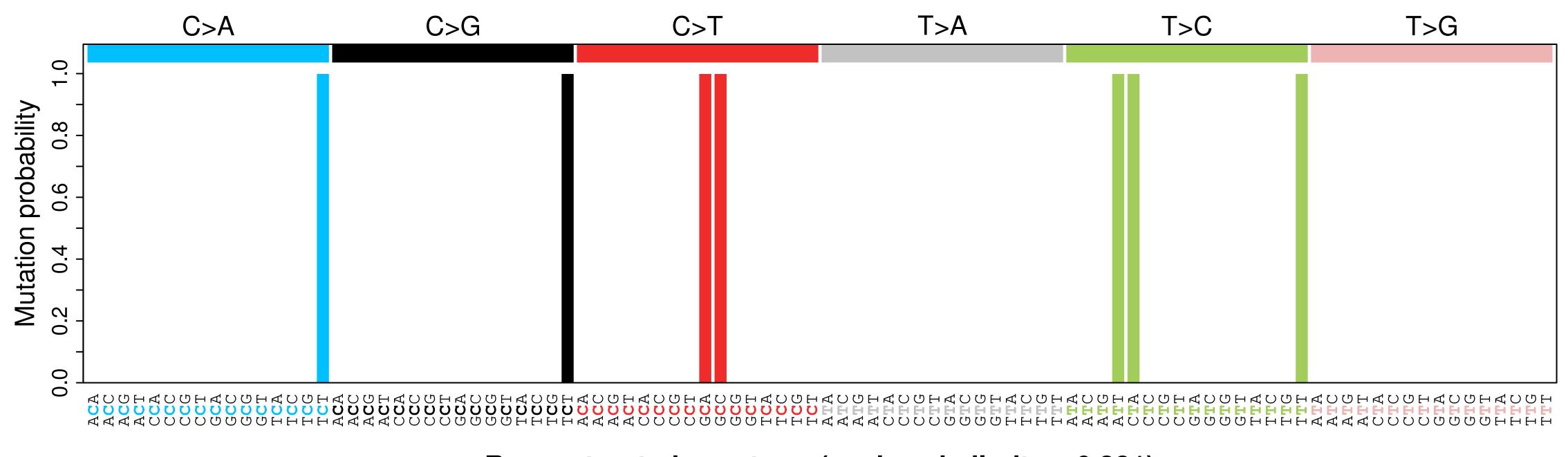


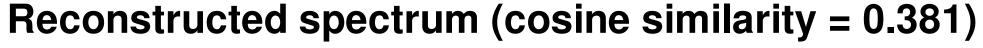


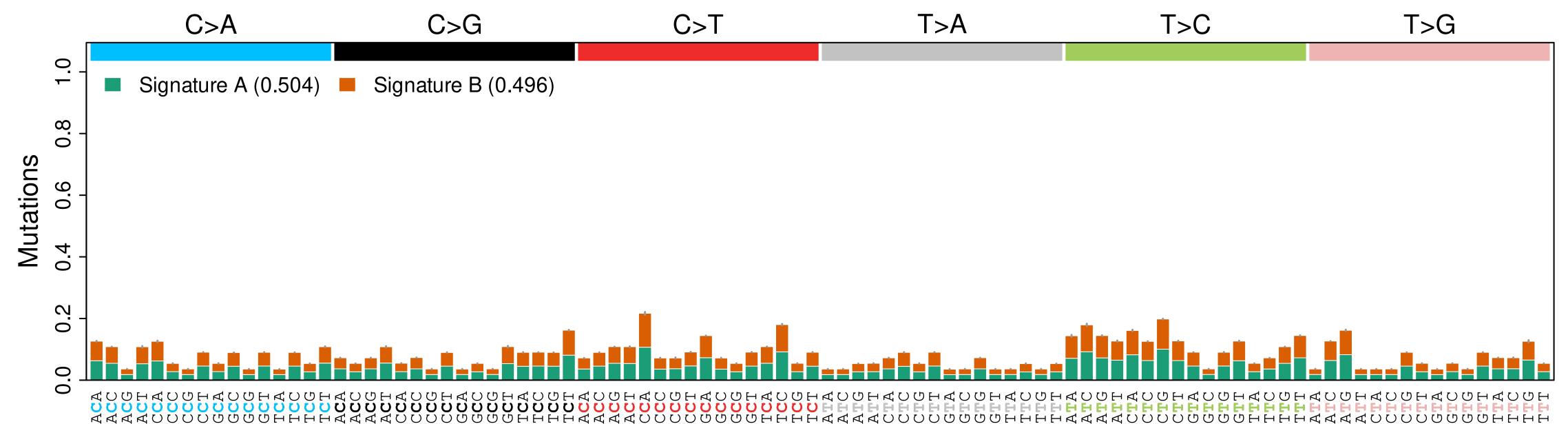


CATD0111a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.314)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.512) Signature B (0.488) 5 Mutations 2

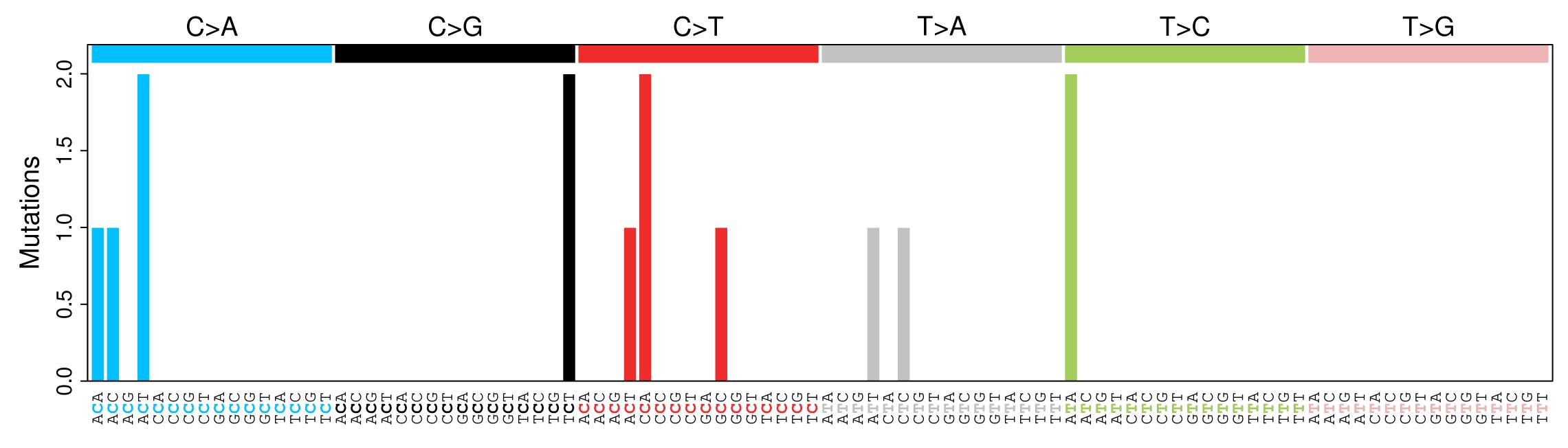
CATD0114a



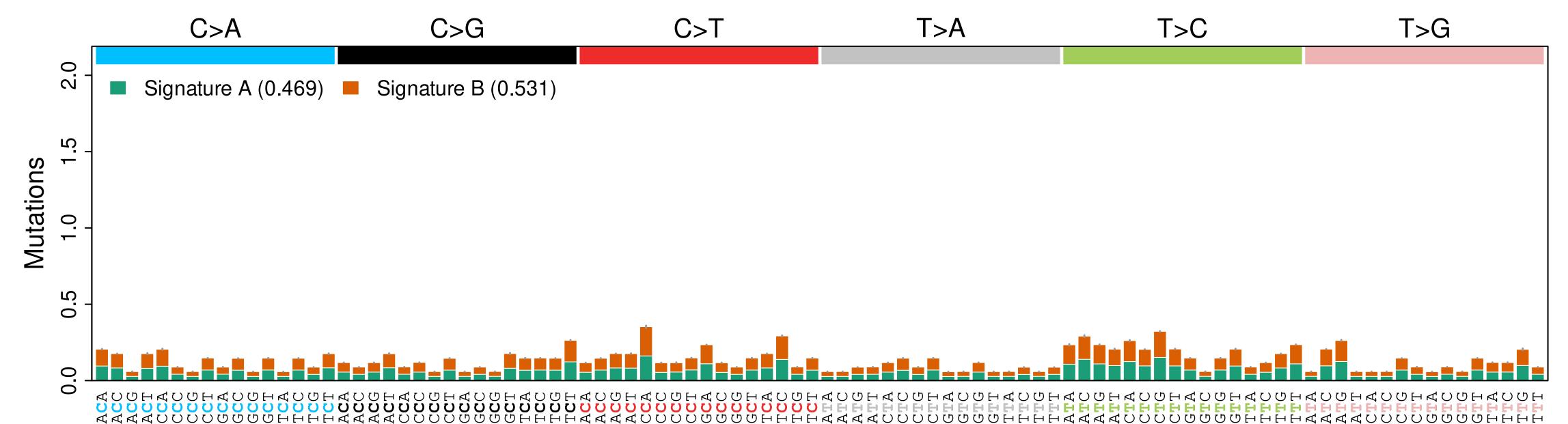




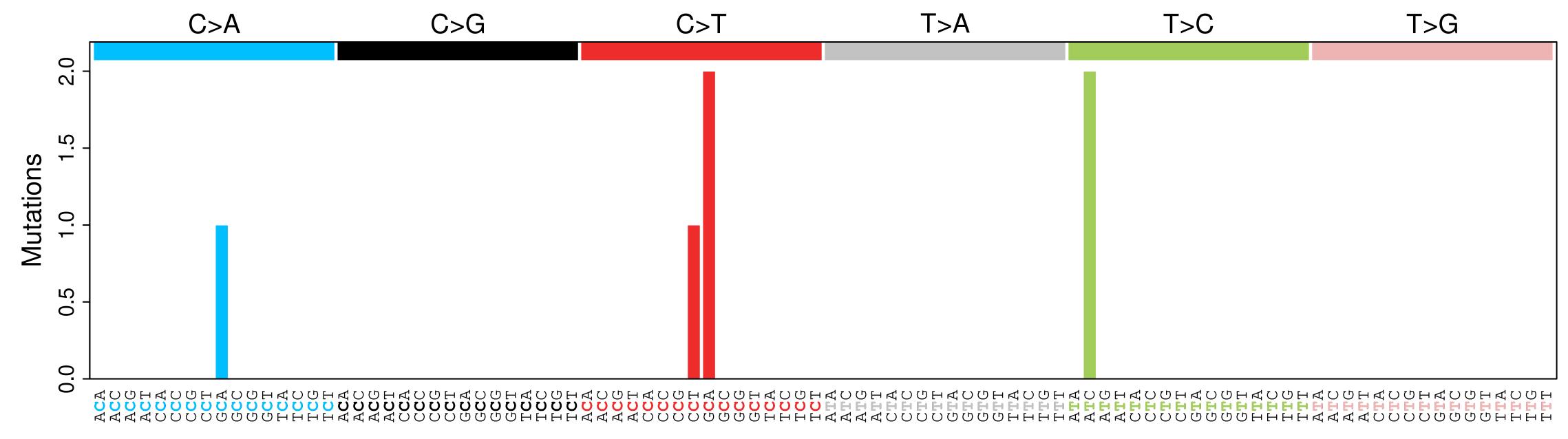
CATD0103a (14 mutations)



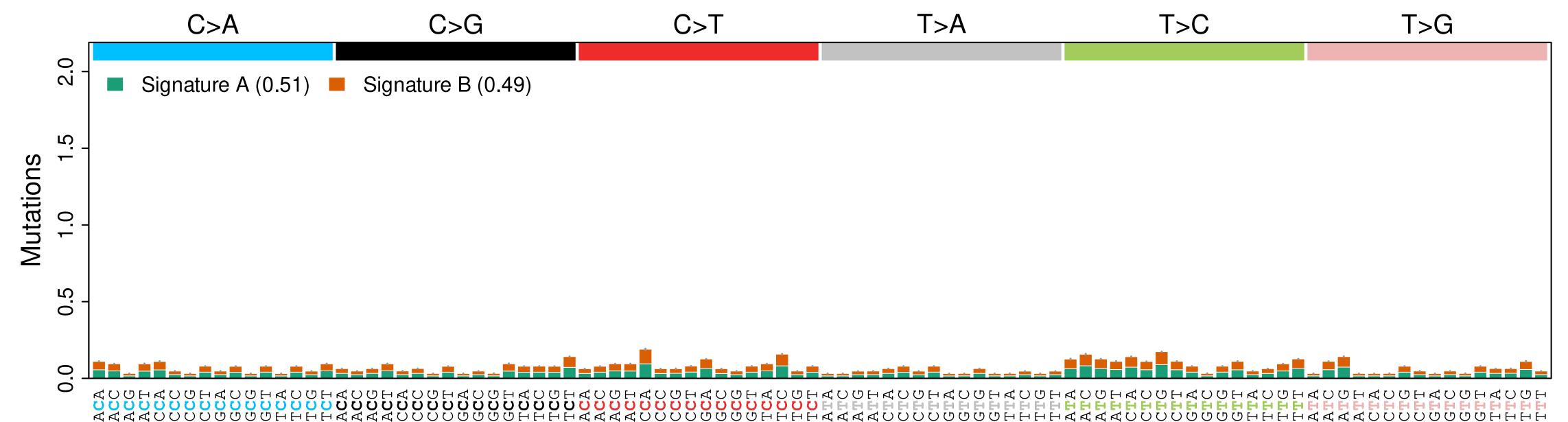
Reconstructed spectrum (cosine similarity = 0.426)



CATD0099a (6 mutations)

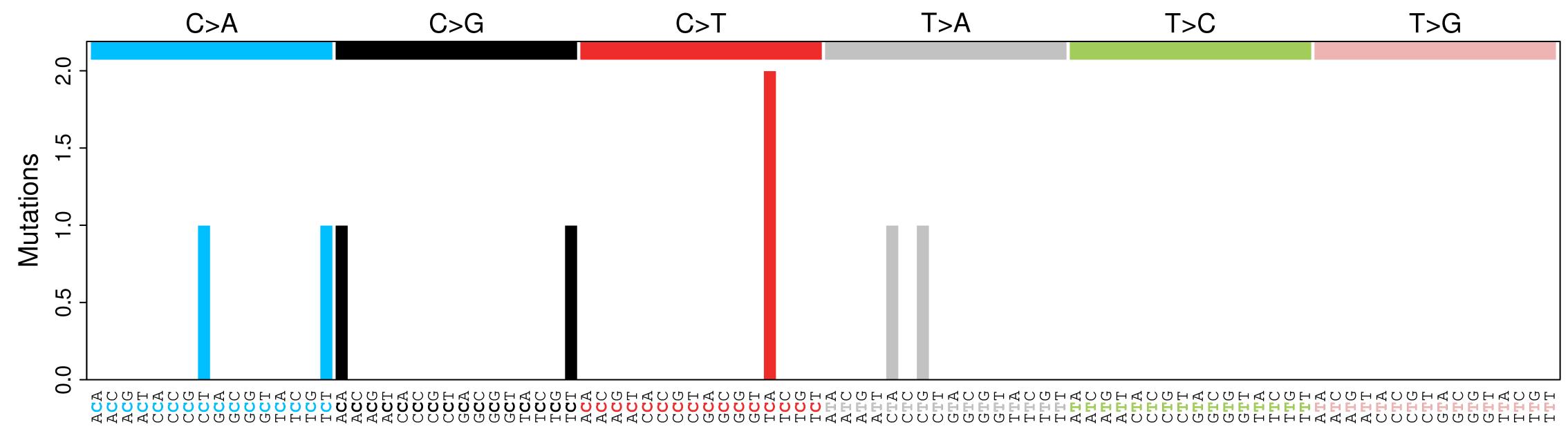


Reconstructed spectrum (cosine similarity = 0.275)

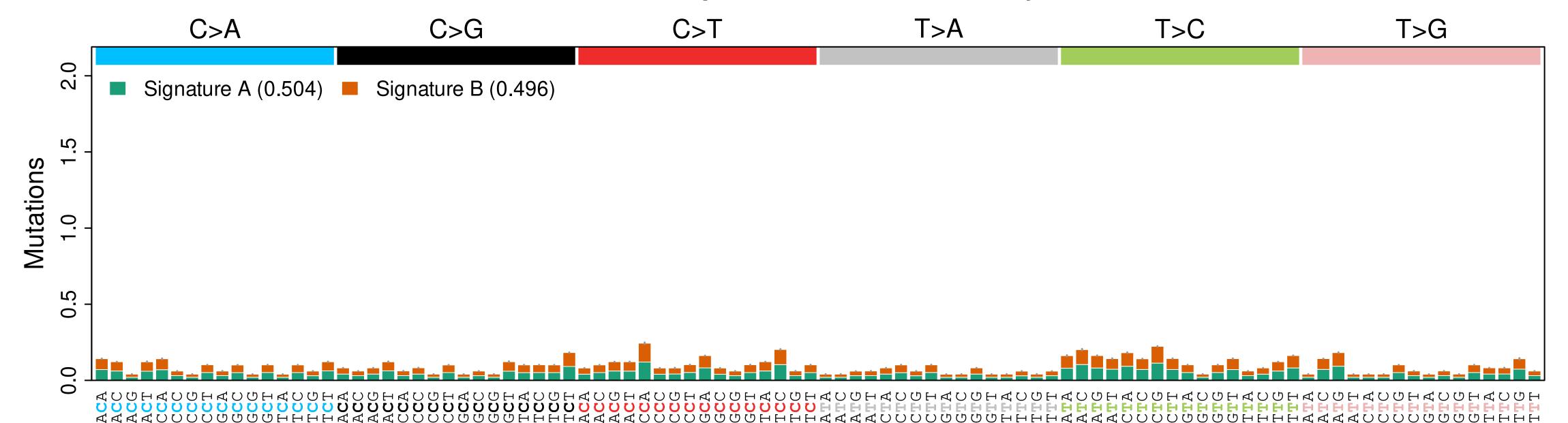


CATD0091a (5 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.0 **Reconstructed spectrum (cosine similarity = 0.276)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.499) Signature B (0.501) 5 Mutations 2 0

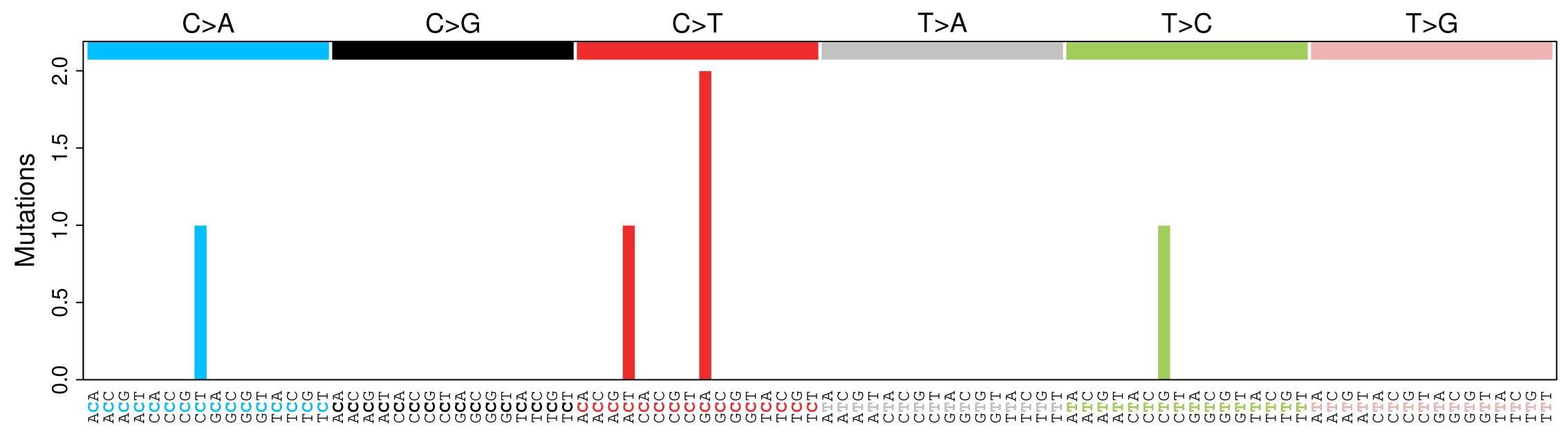
CATD0086a (8 mutations)



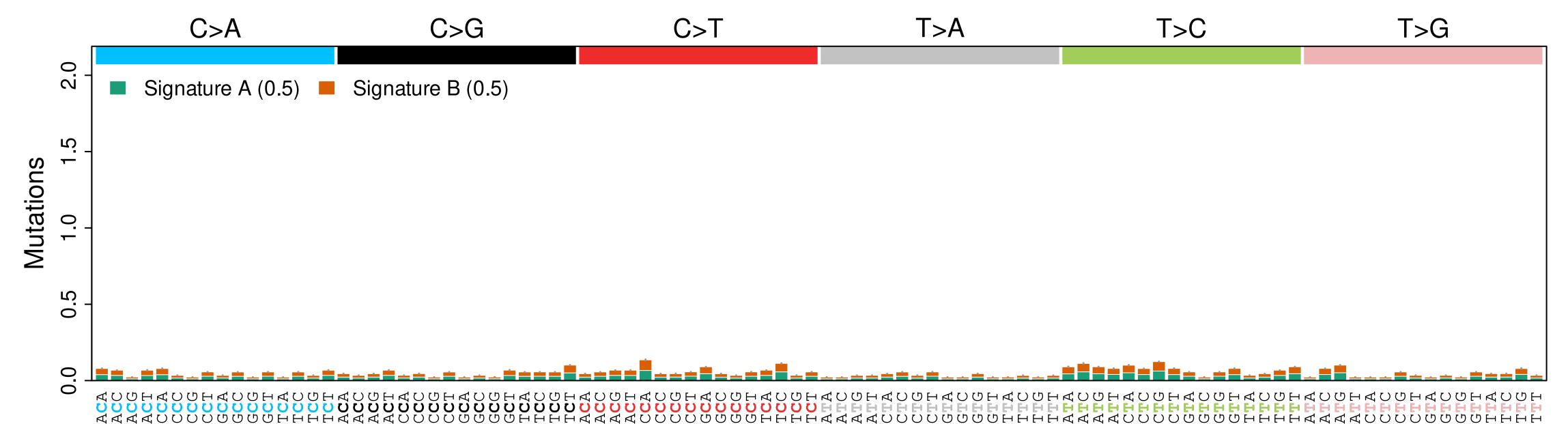
Reconstructed spectrum (cosine similarity = 0.269)



CATD0405a (5 mutations)

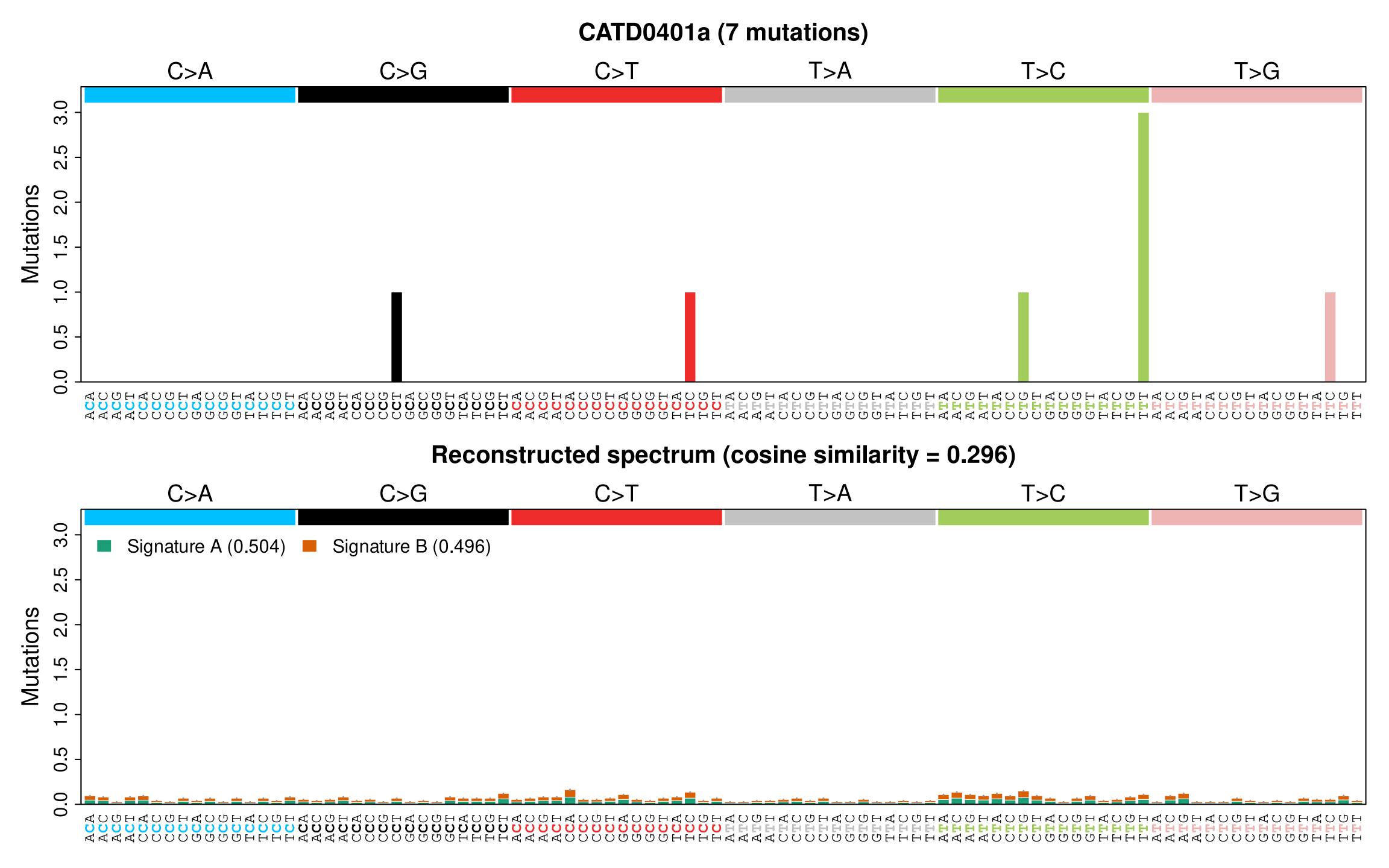


Reconstructed spectrum (cosine similarity = 0.284)

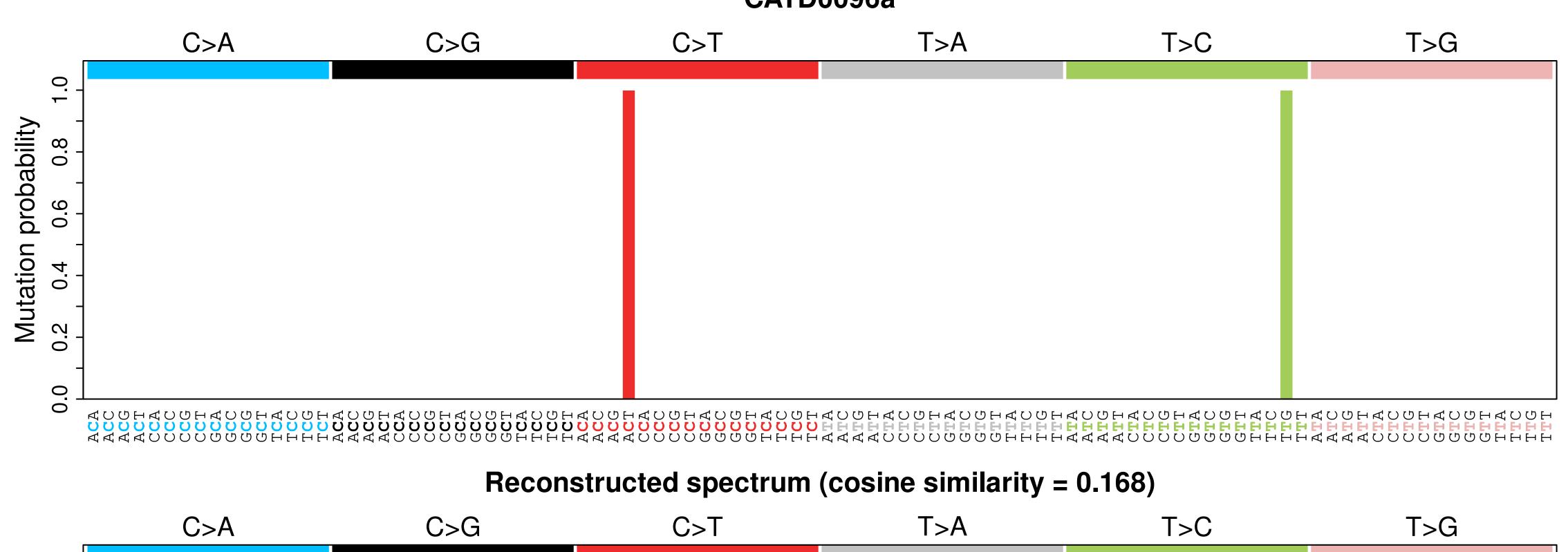


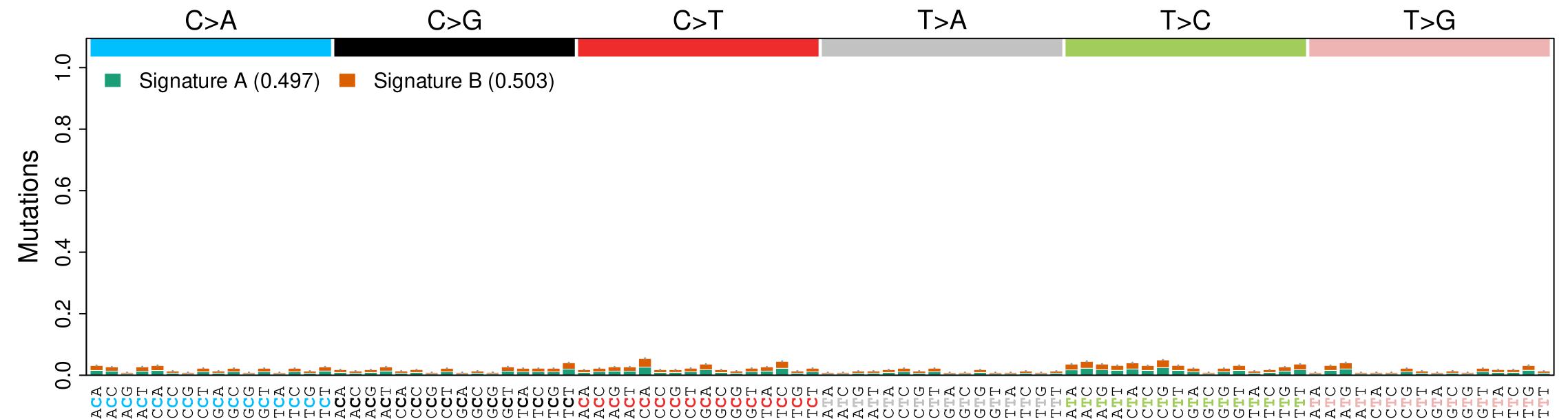
CATD188a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.275)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.487) Signature B (0.513) 5 Mutations

0.5

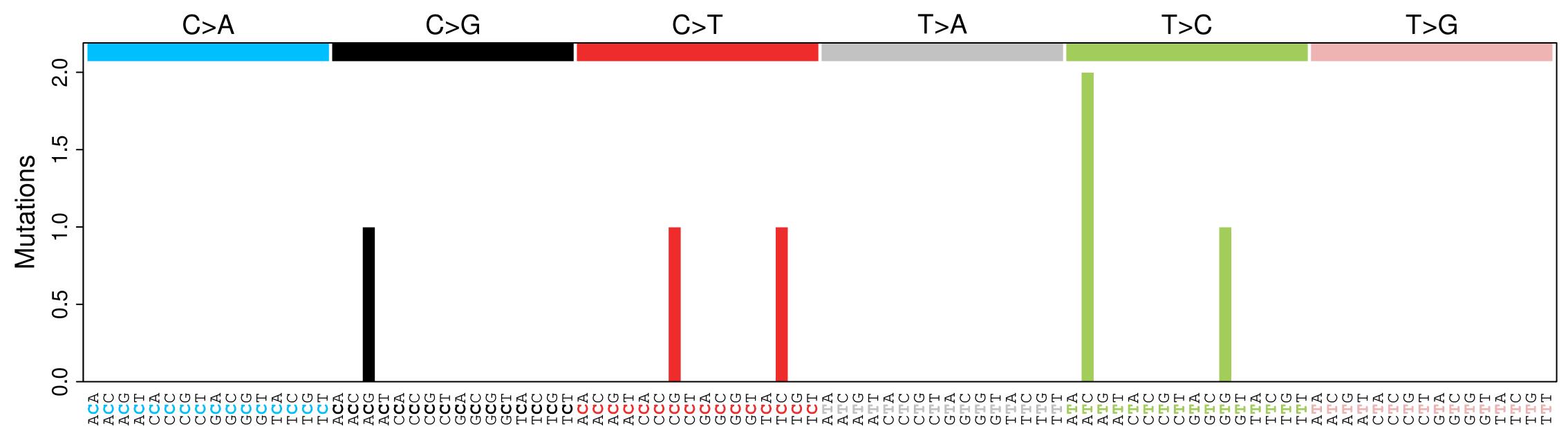




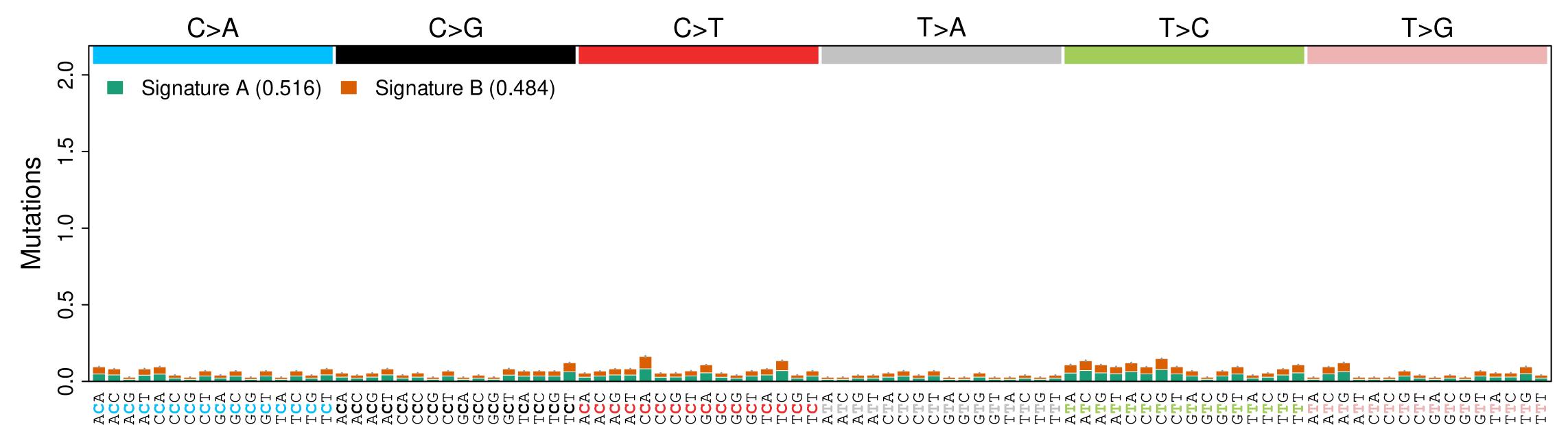




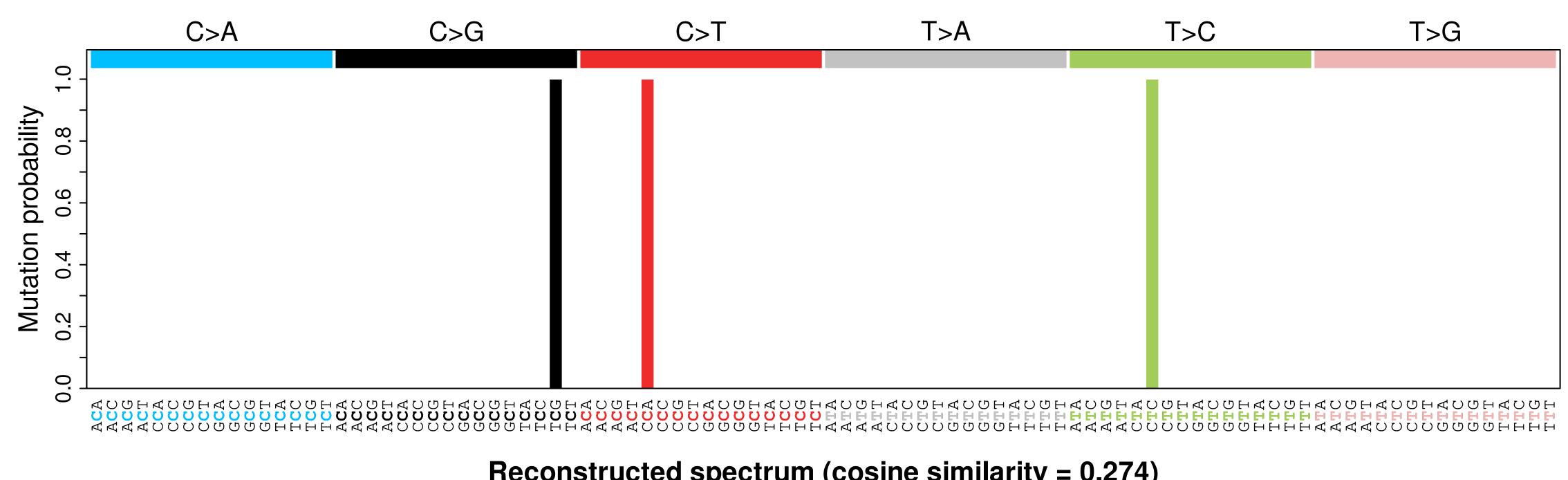
CATD0411a (6 mutations) C>G C>T T>A

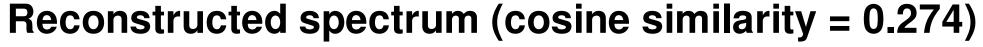


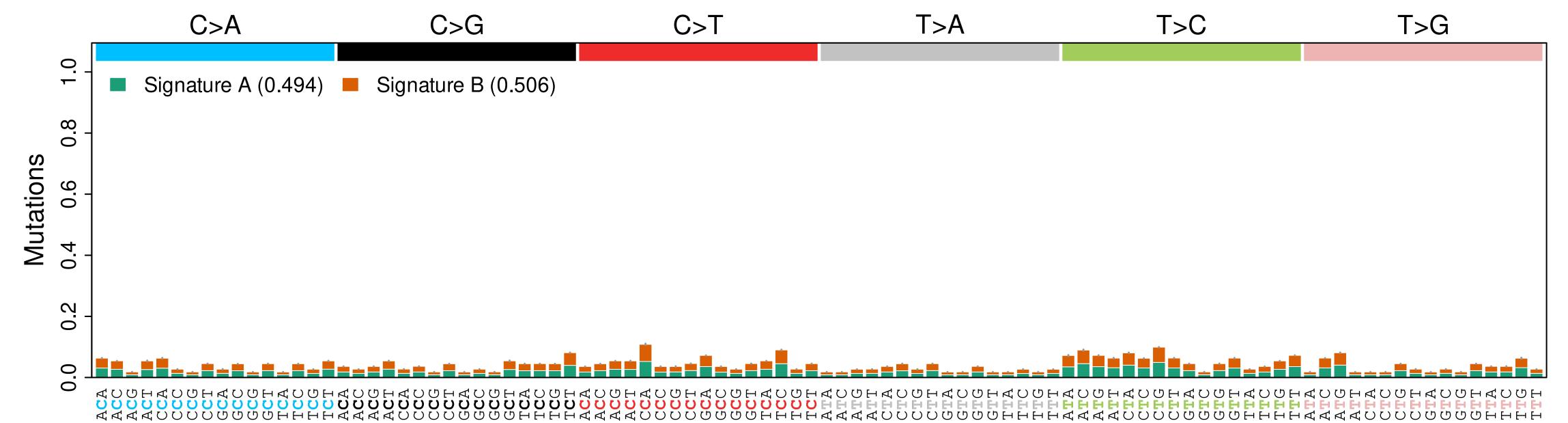
Reconstructed spectrum (cosine similarity = 0.3)



CATD0113a

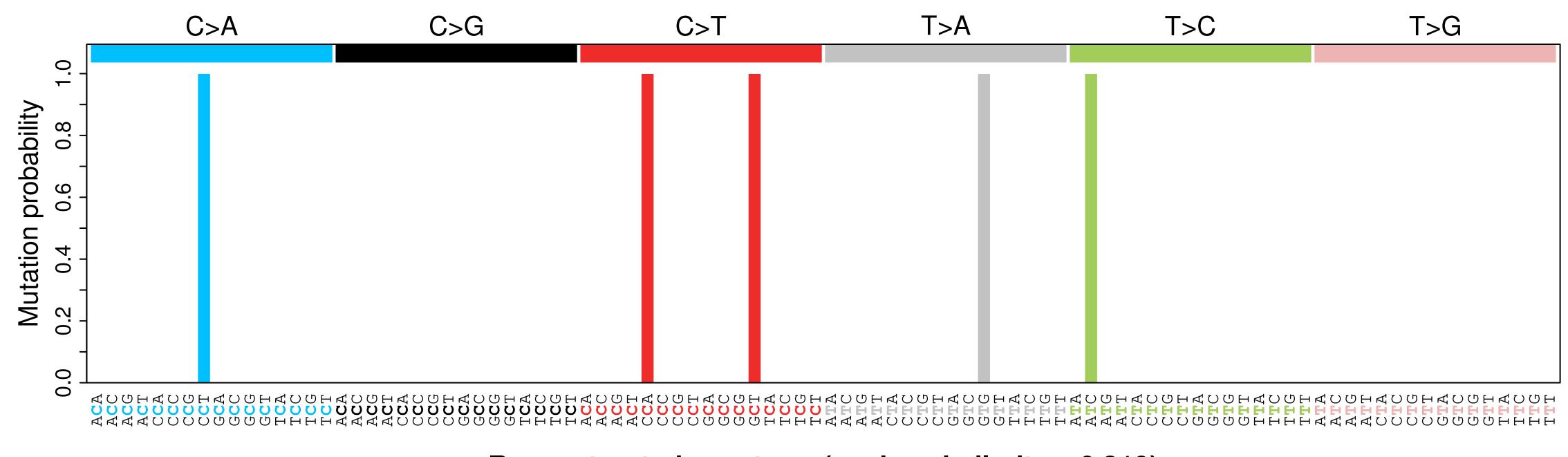


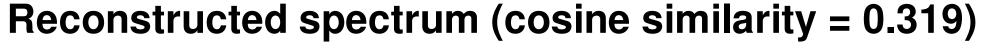


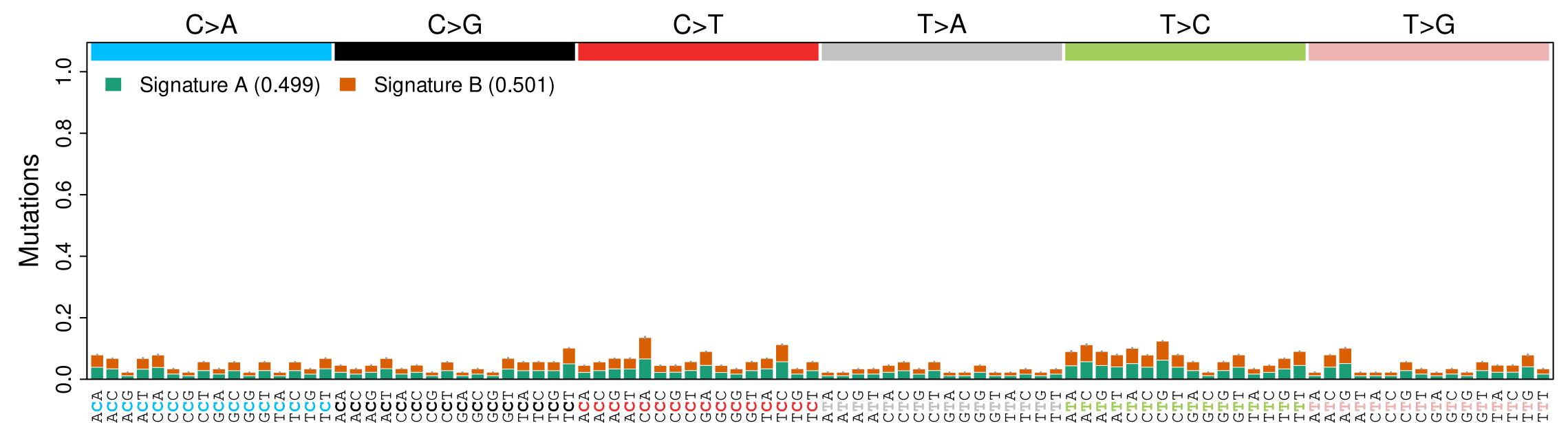


CATD0403a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.218)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.504) Signature B (0.496) 5 Mutations 2 0

CATD0085a

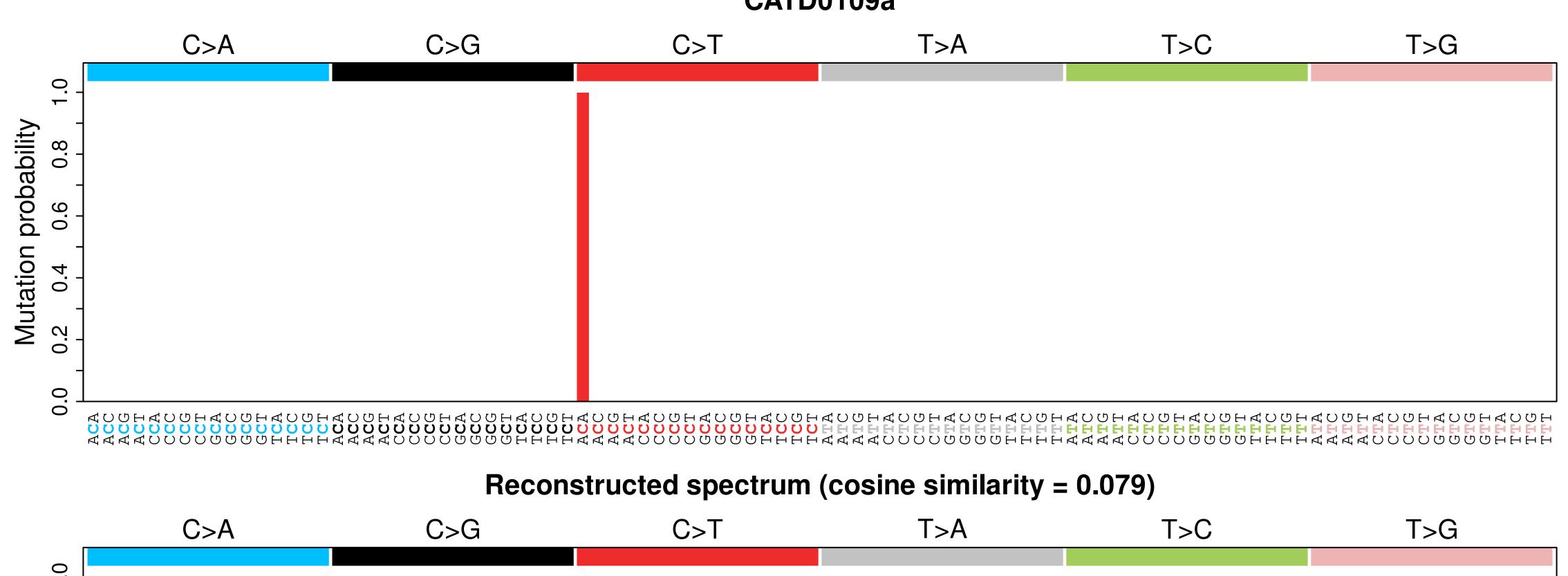


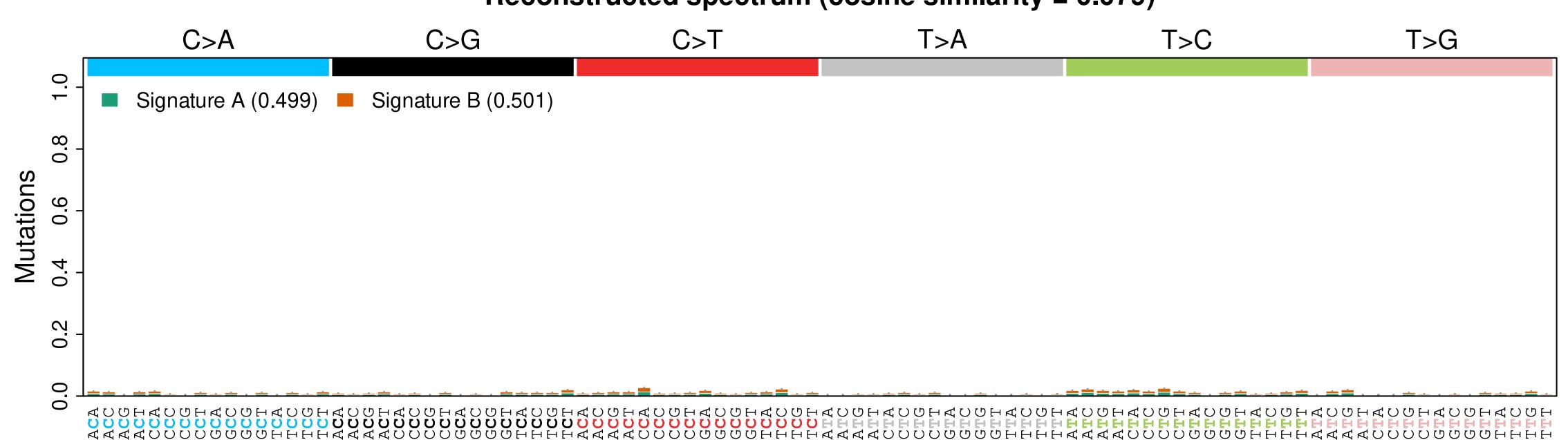




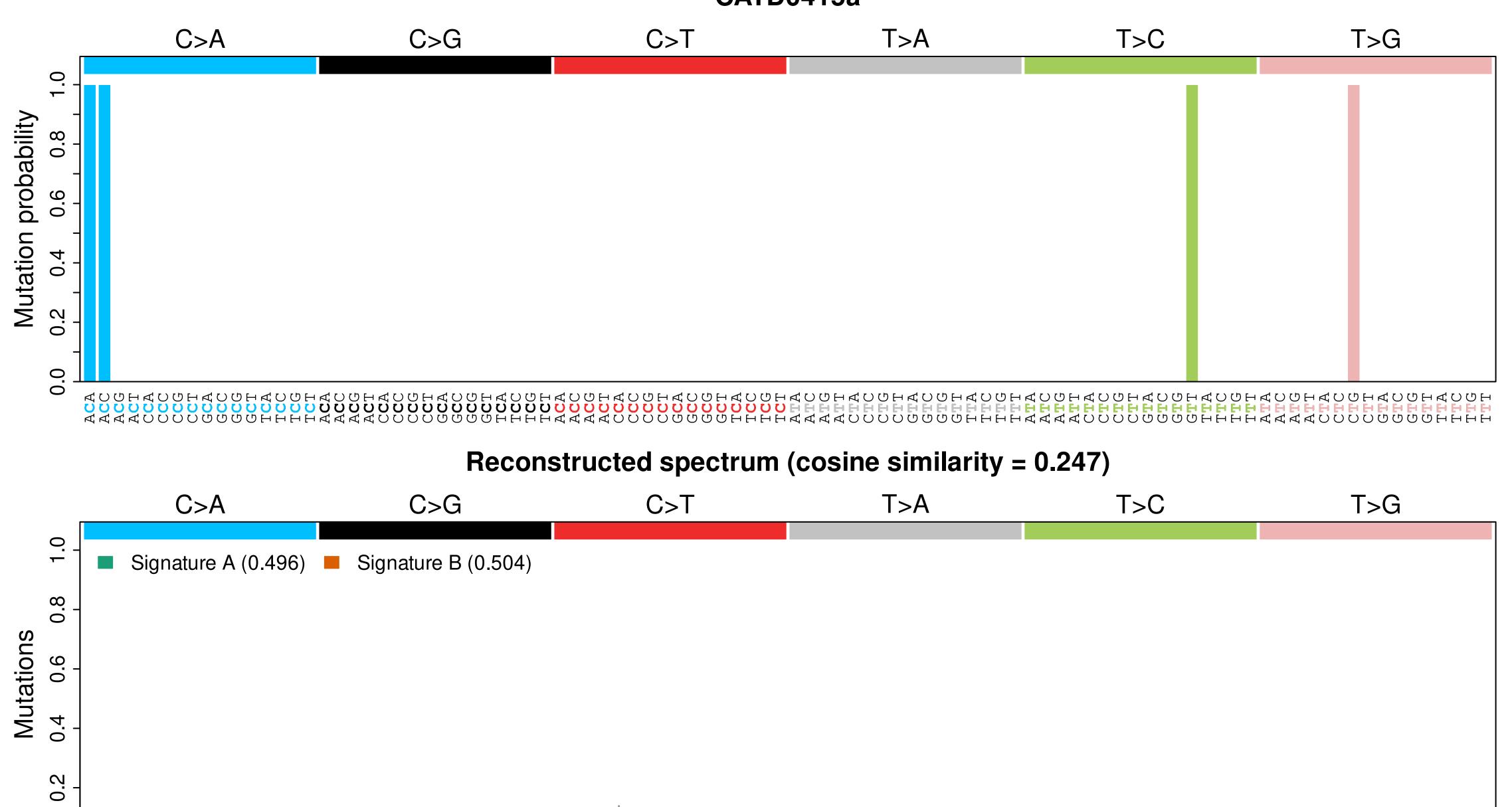
CATD190a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.283)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.487) Signature B (0.513) 5 Mutations 2 0



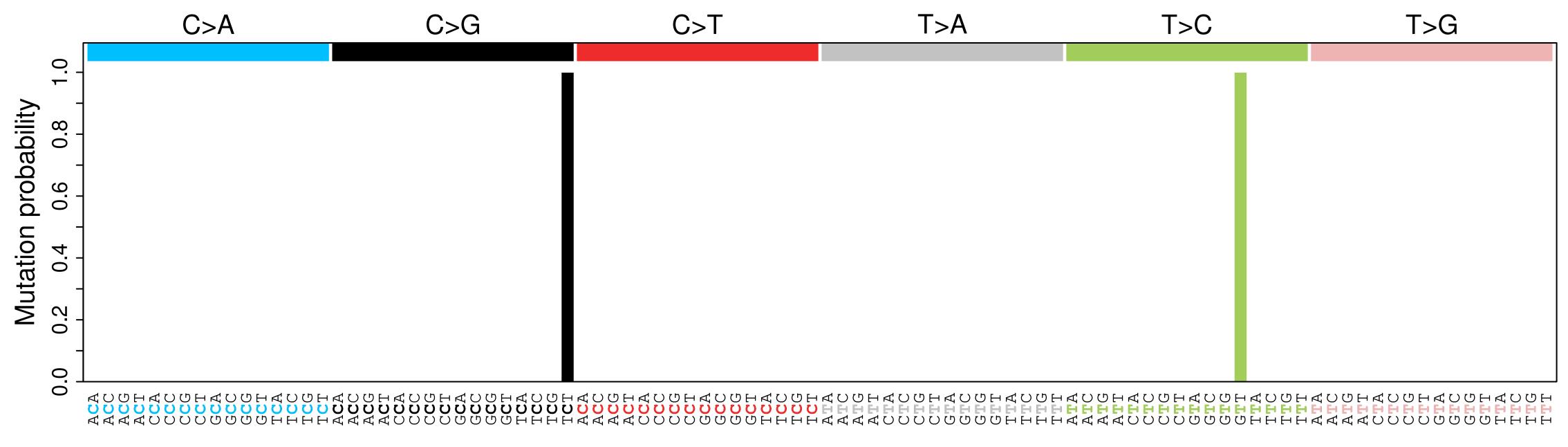


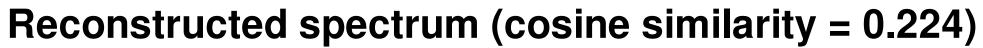


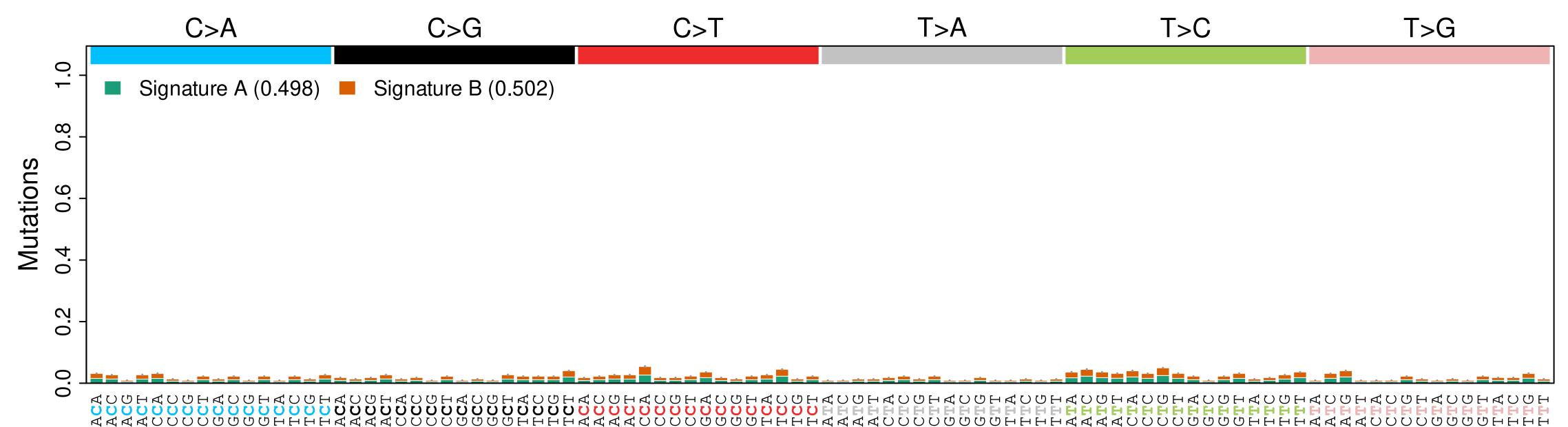
CATD0415a



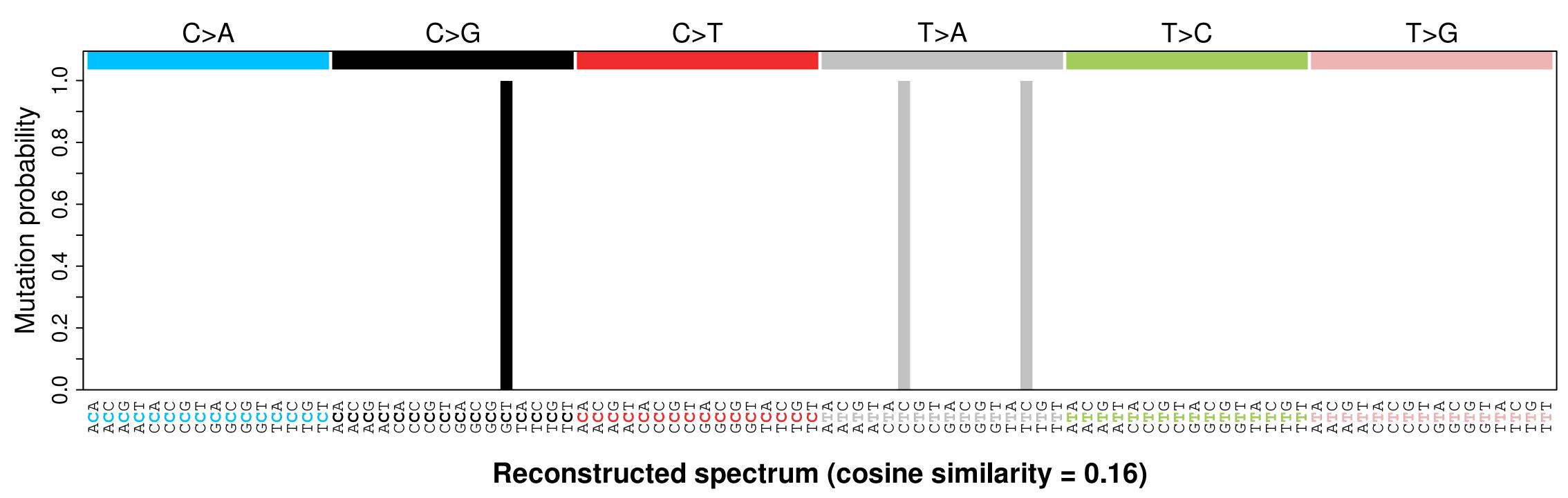


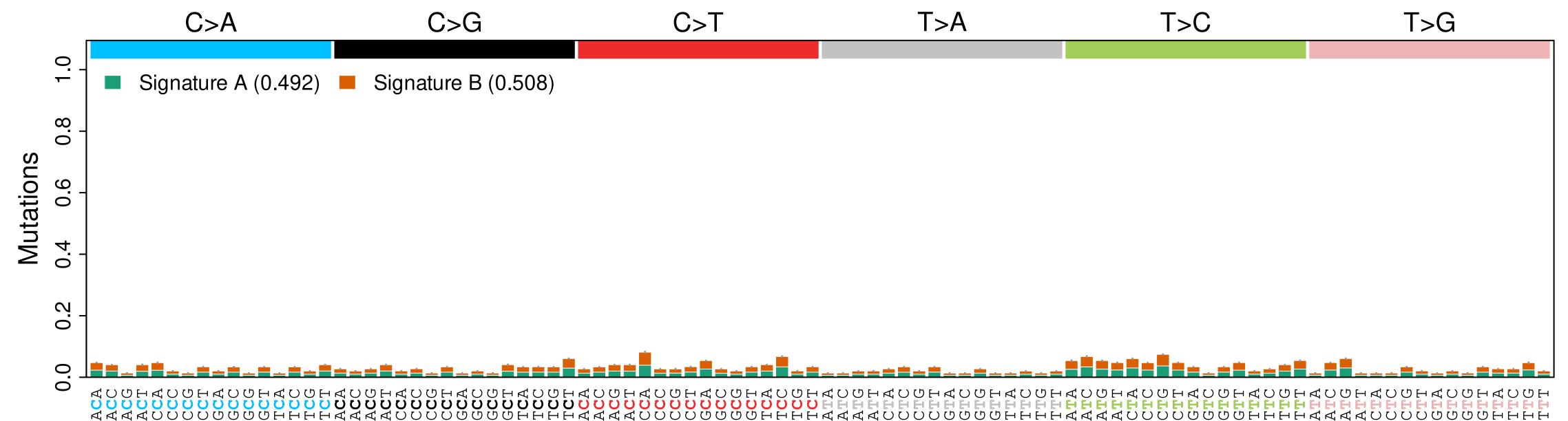




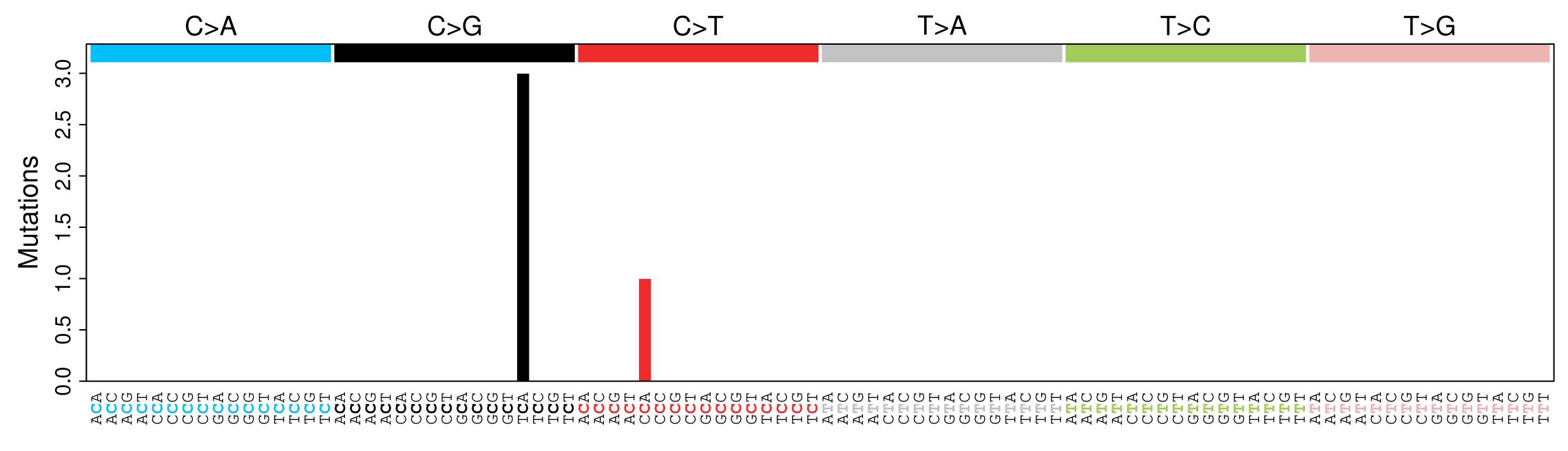




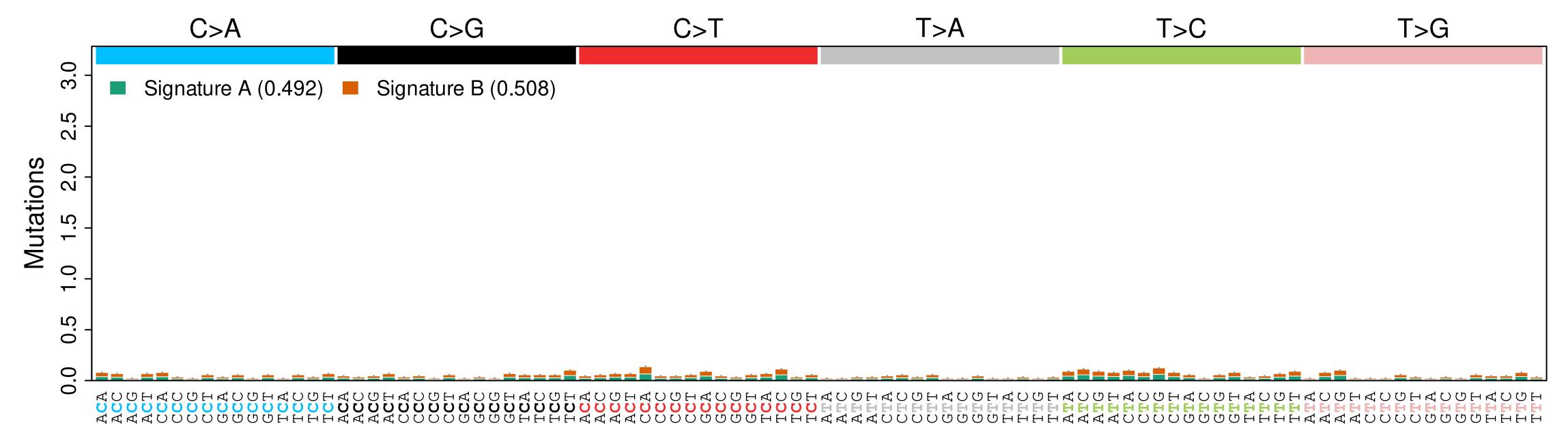




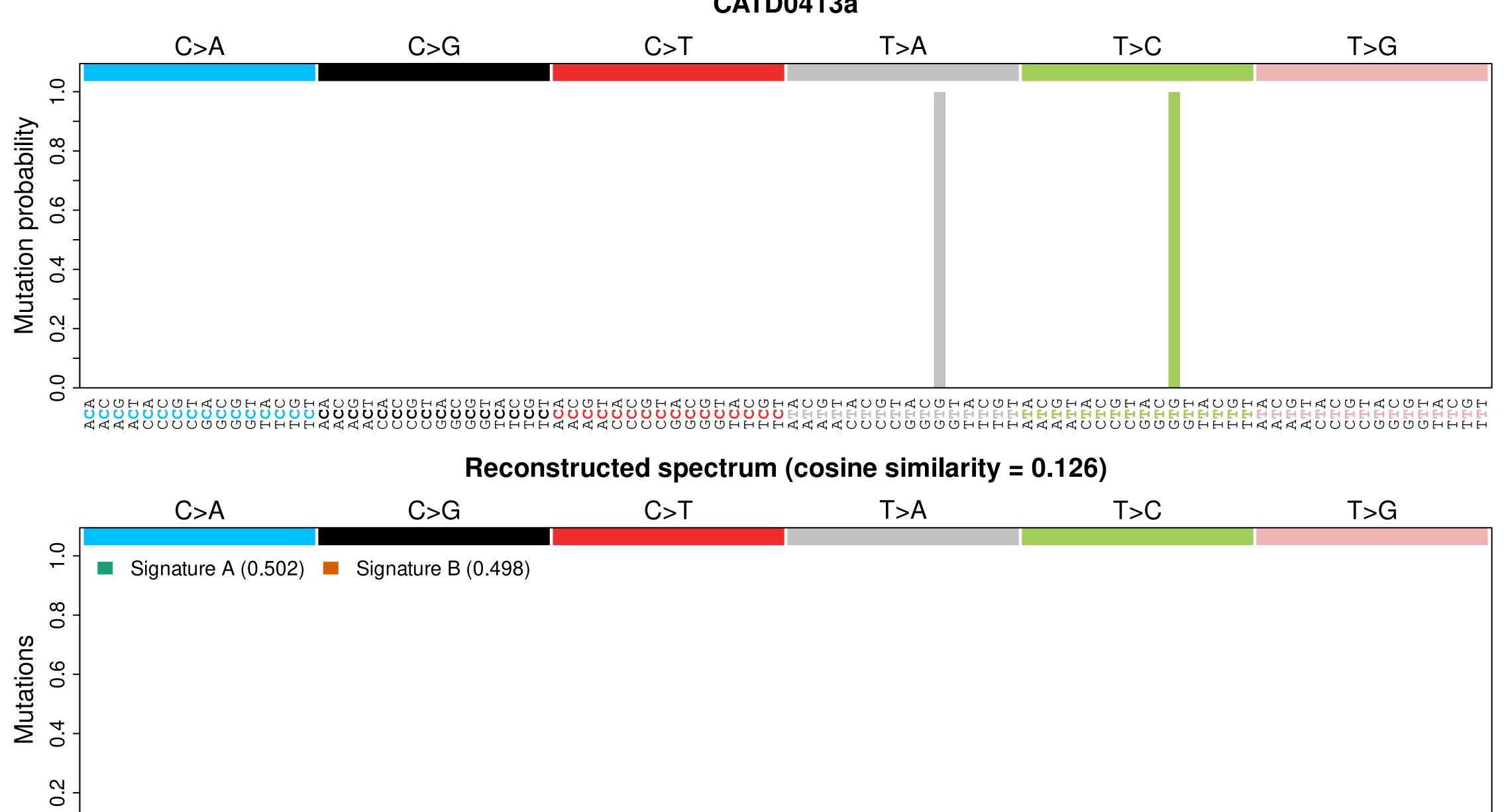
CATD0407a (4 mutations)



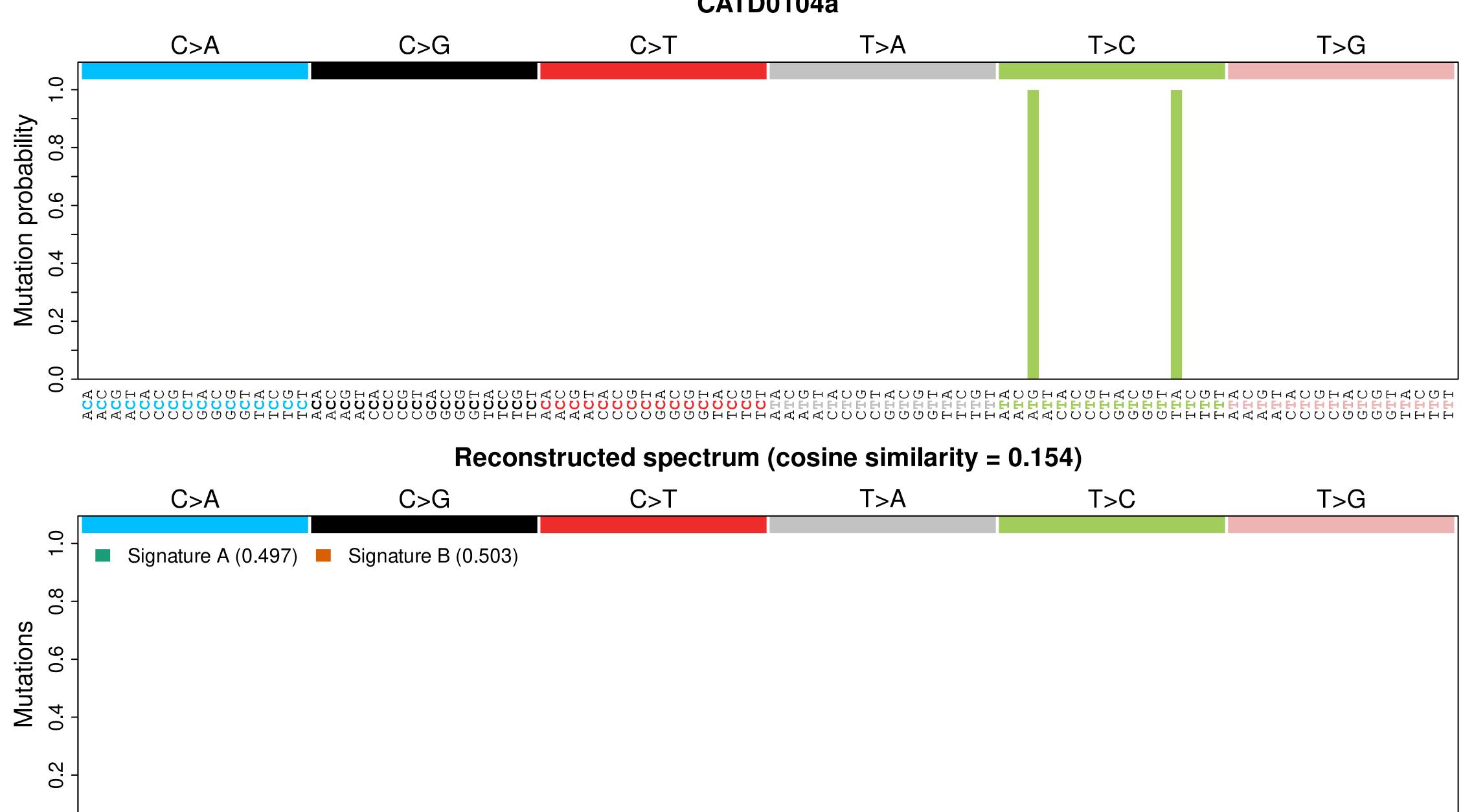
Reconstructed spectrum (cosine similarity = 0.169)



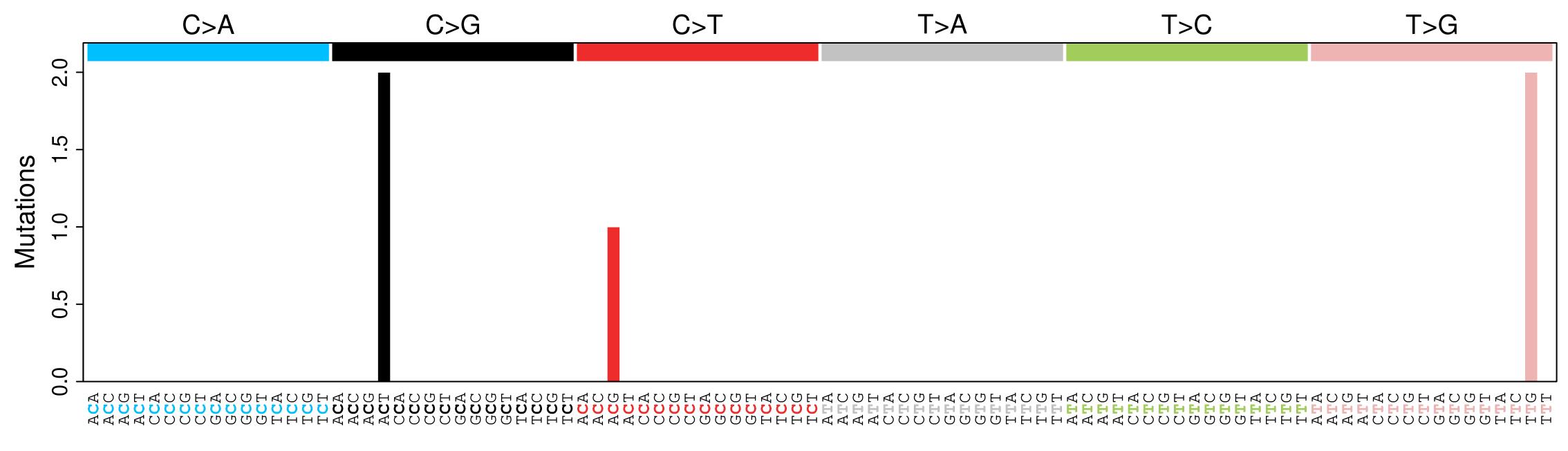




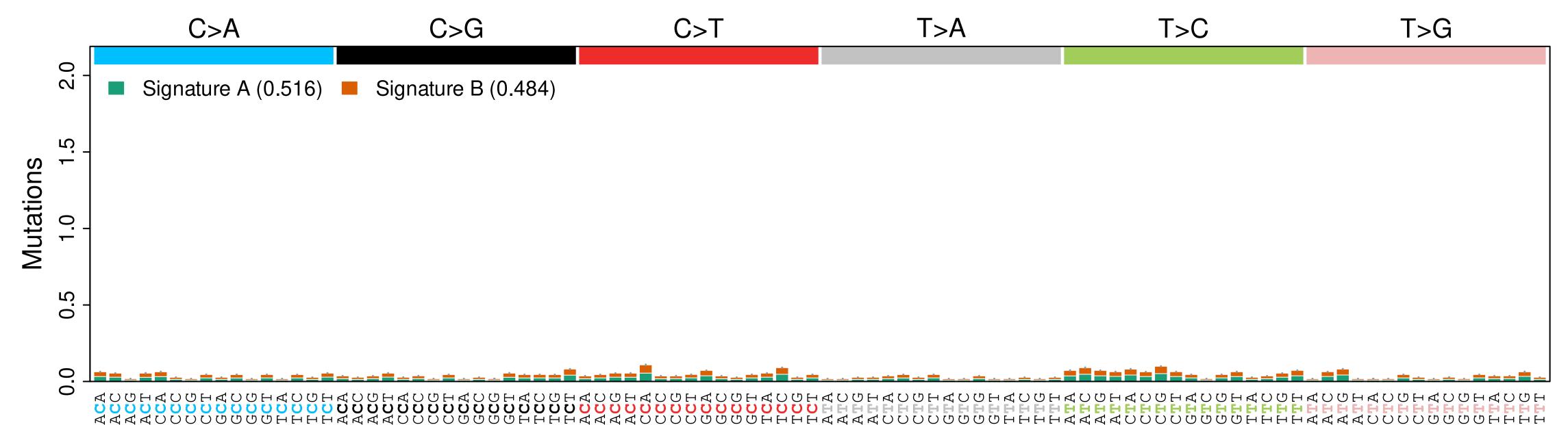




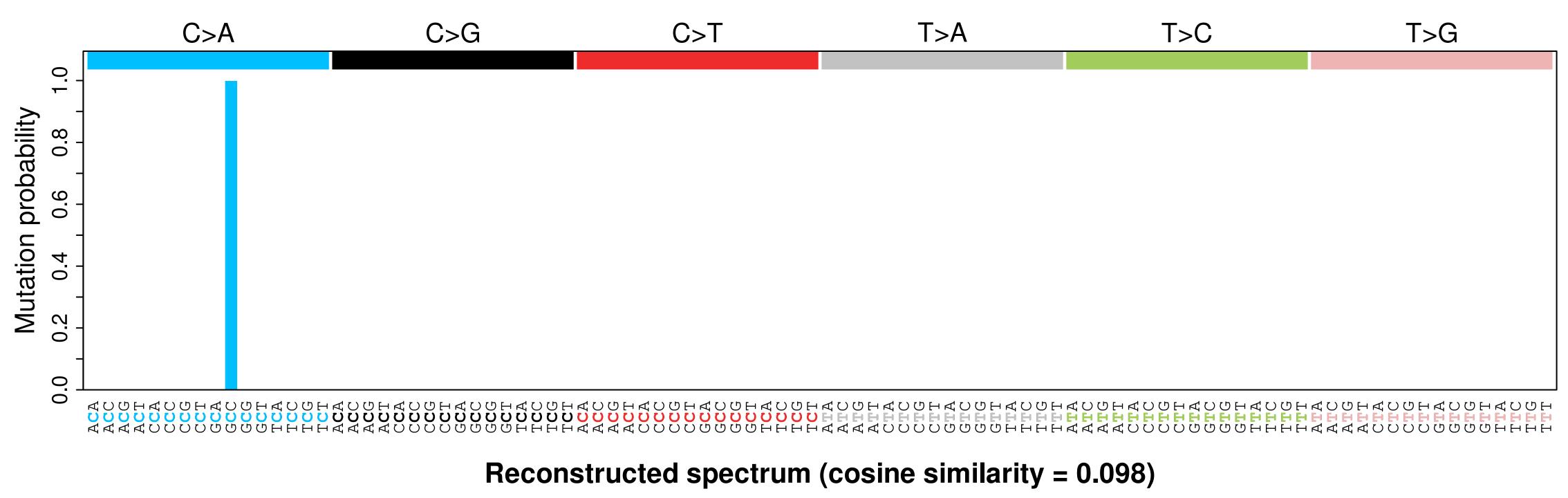
CATD0409a (5 mutations)

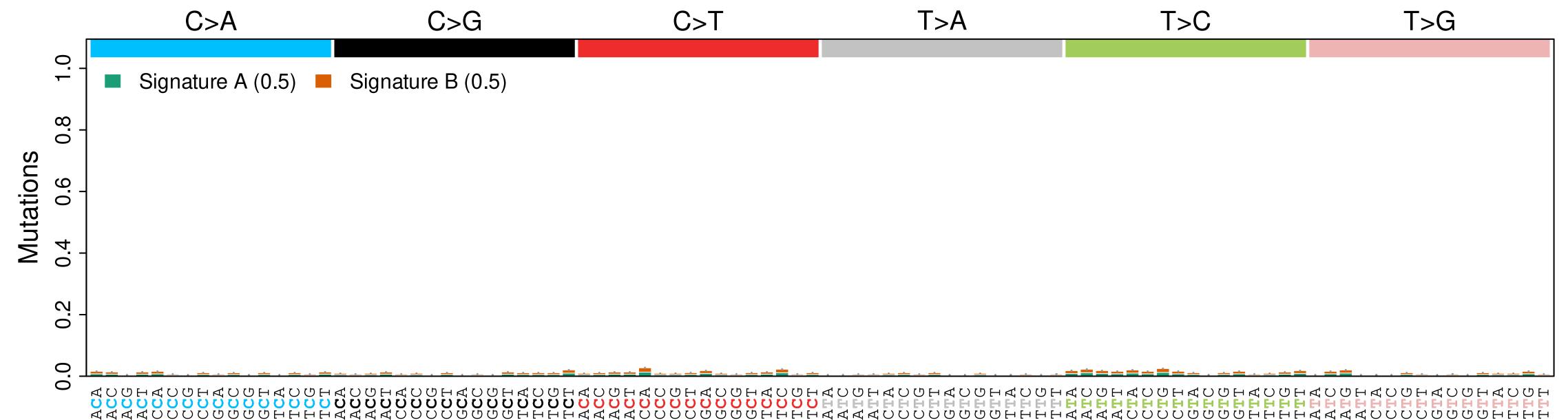




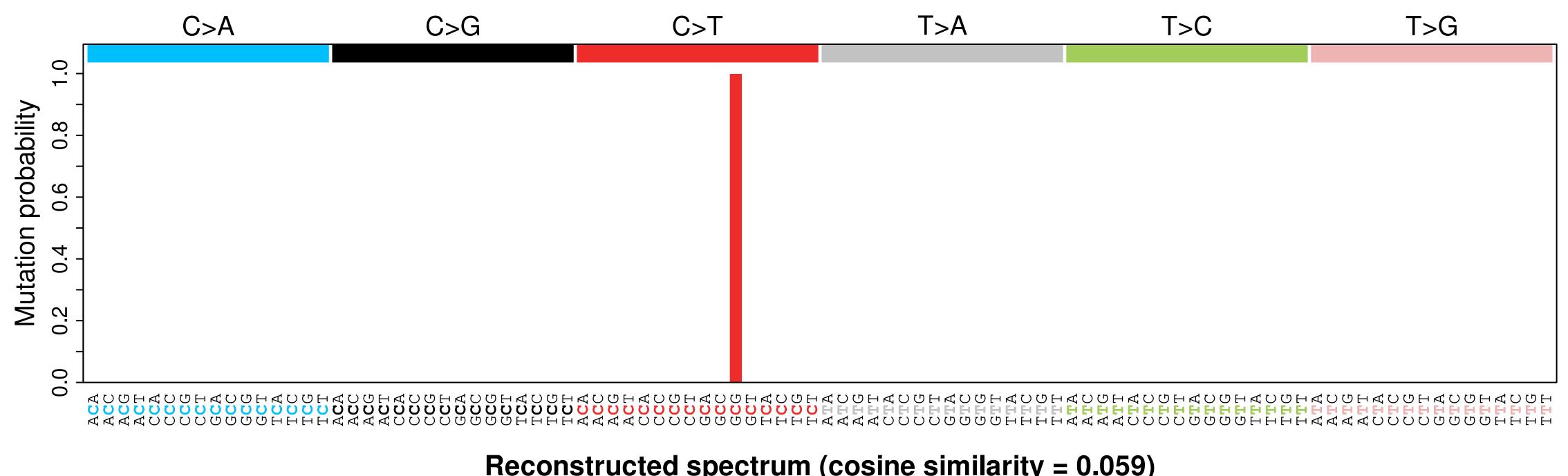


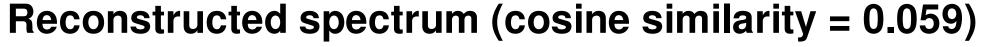


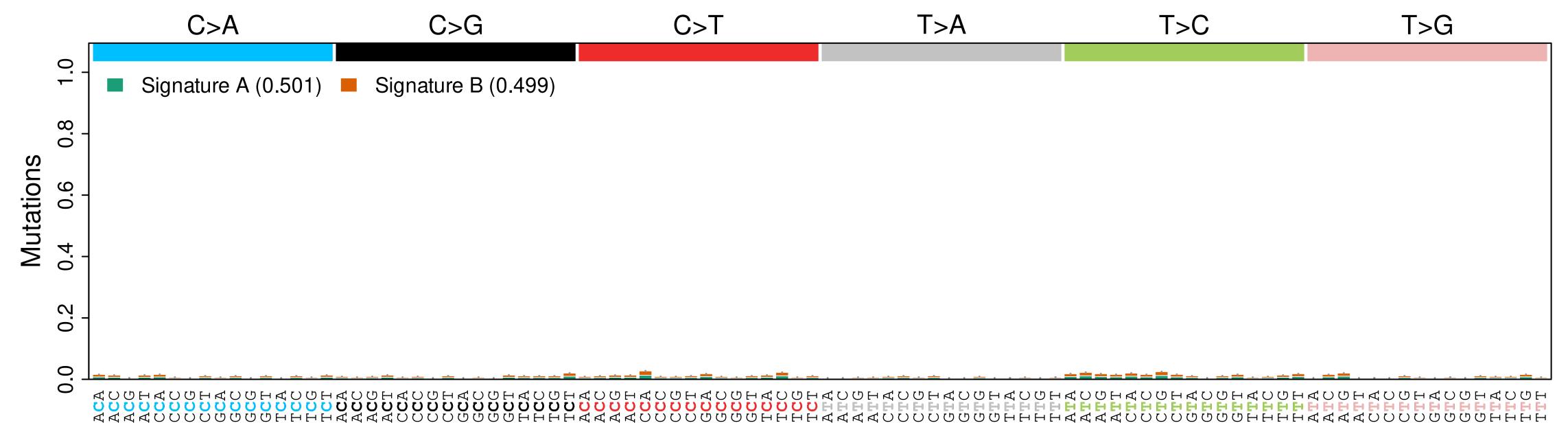












CATD0089a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.212)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.506) Signature B (0.494) 5 Mutations 5 0 0



