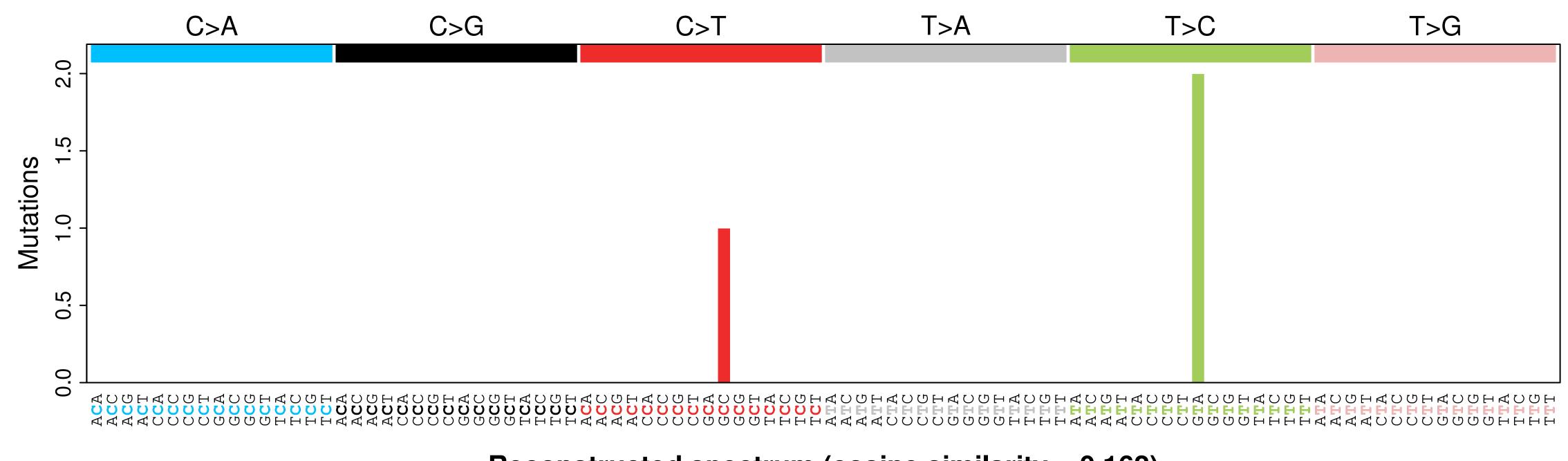
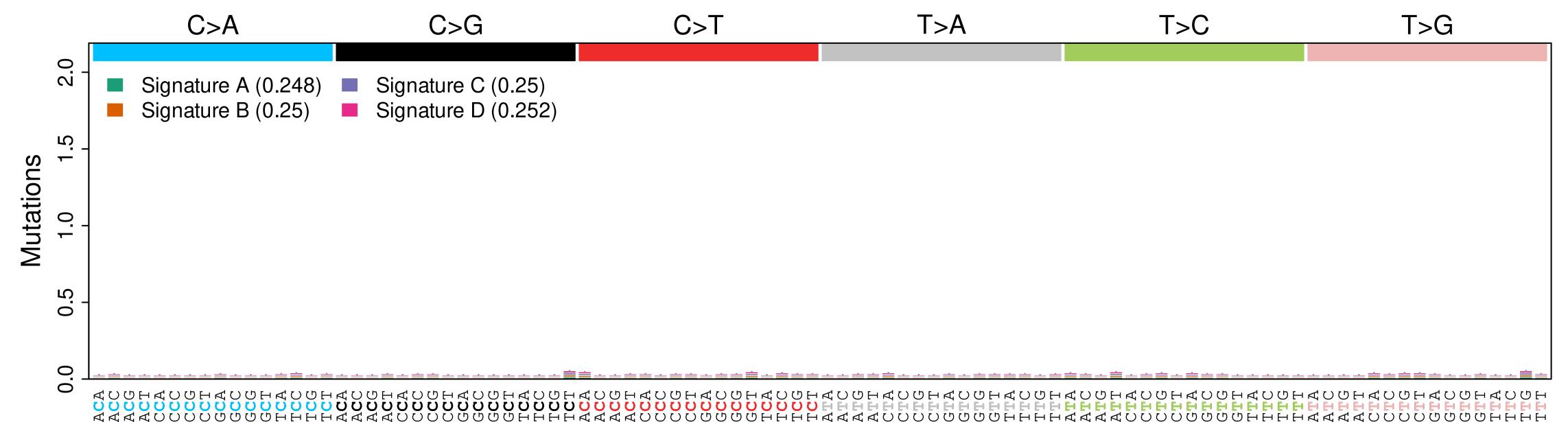


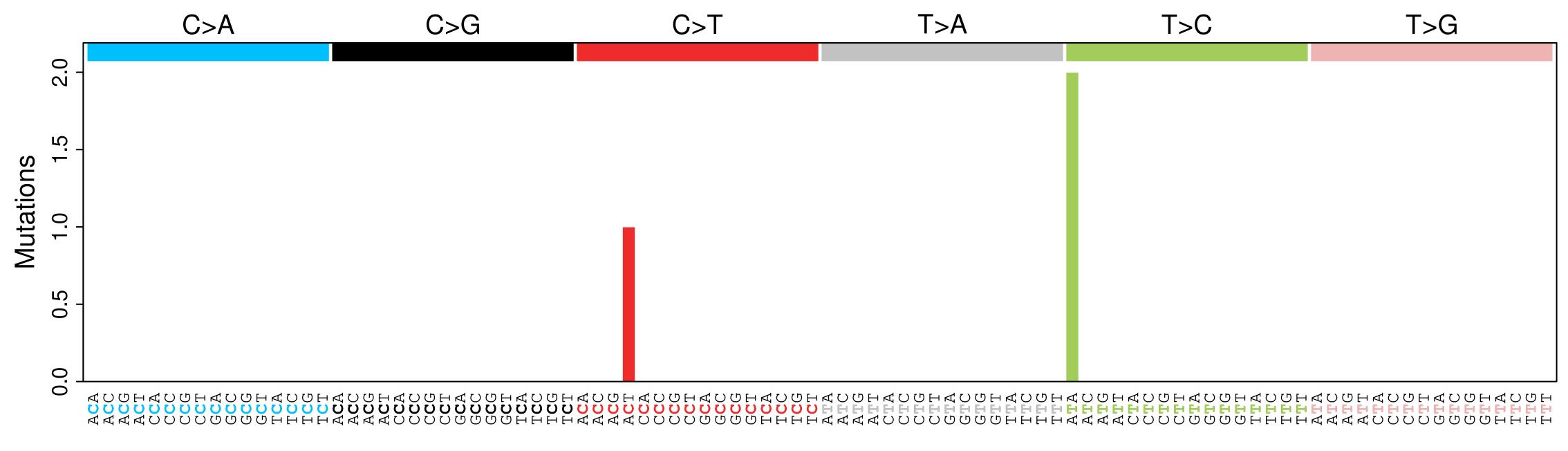
CATD331a (3 mutations)



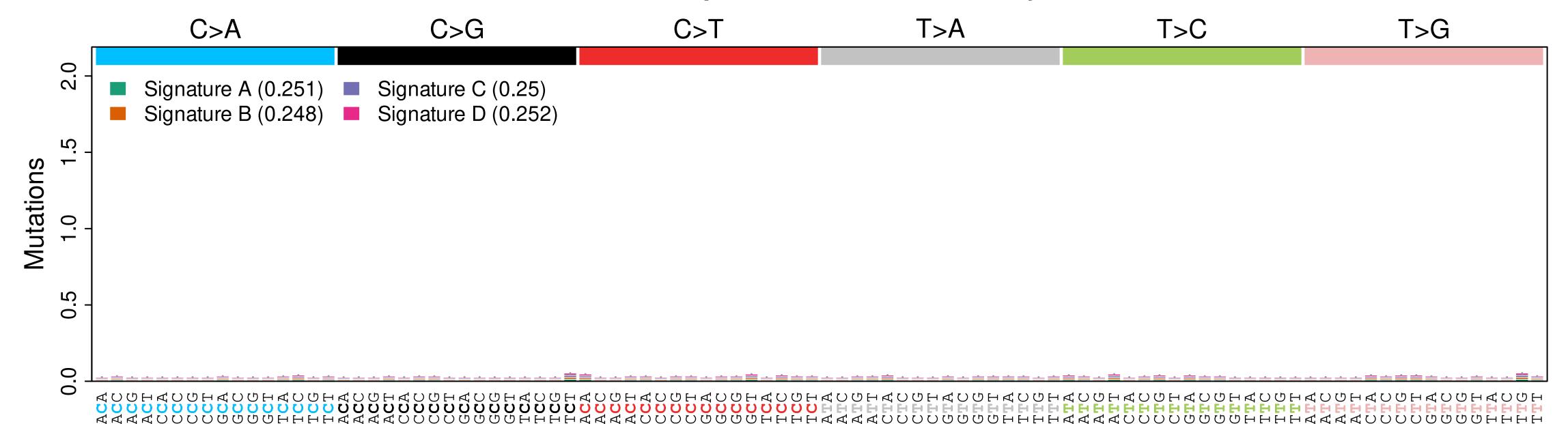
Reconstructed spectrum (cosine similarity = 0.162)



CATD0550a (3 mutations)

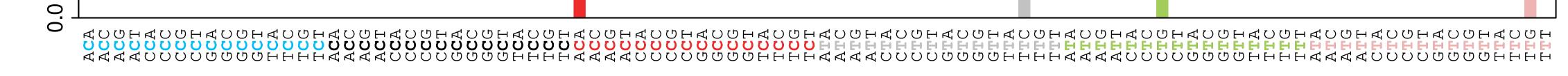


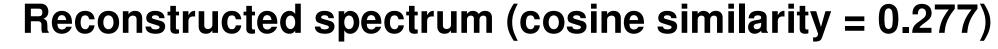
Reconstructed spectrum (cosine similarity = 0.163)

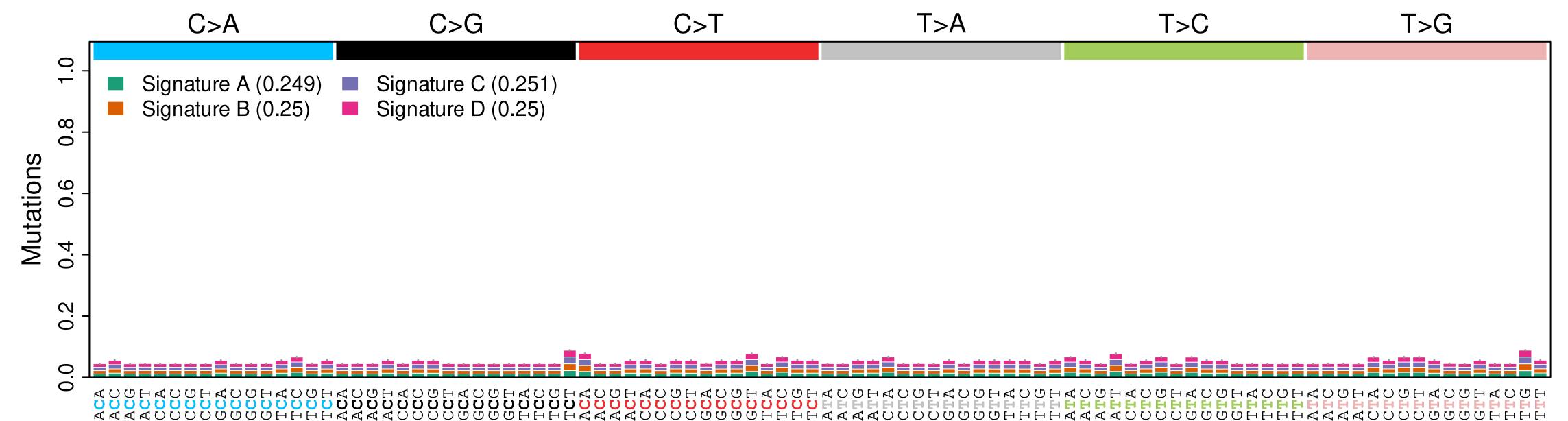


CATD334a T>C T>G C>A C>G C>T T>A 1.0 Mutation probability 0.8 9.0 0.4

0.2

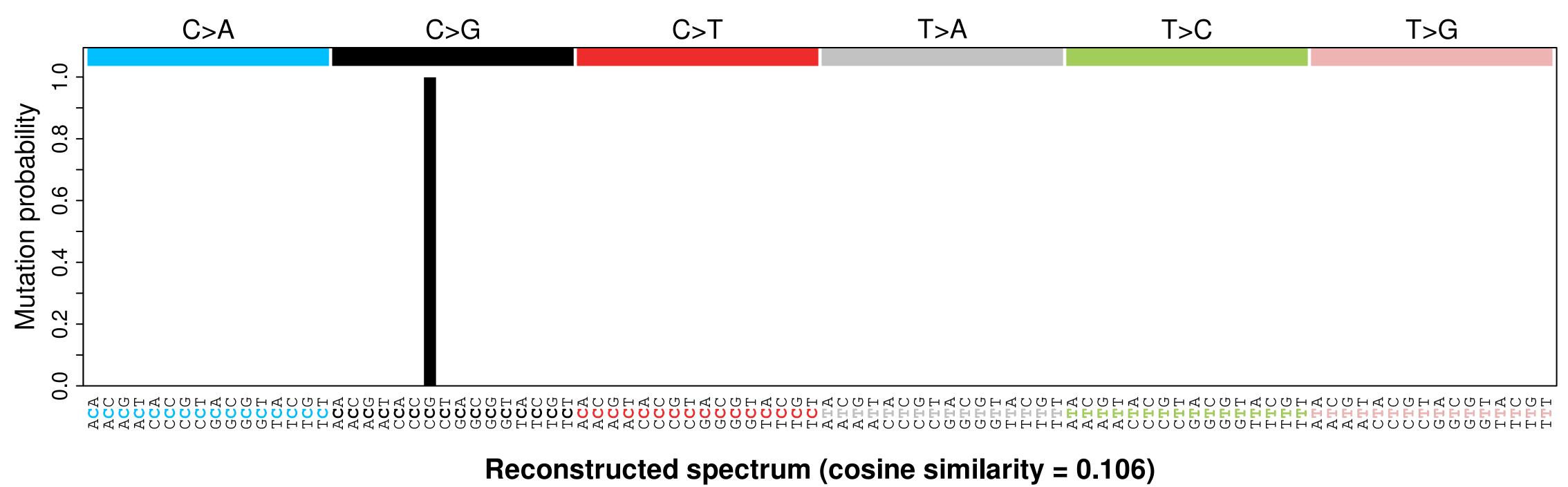




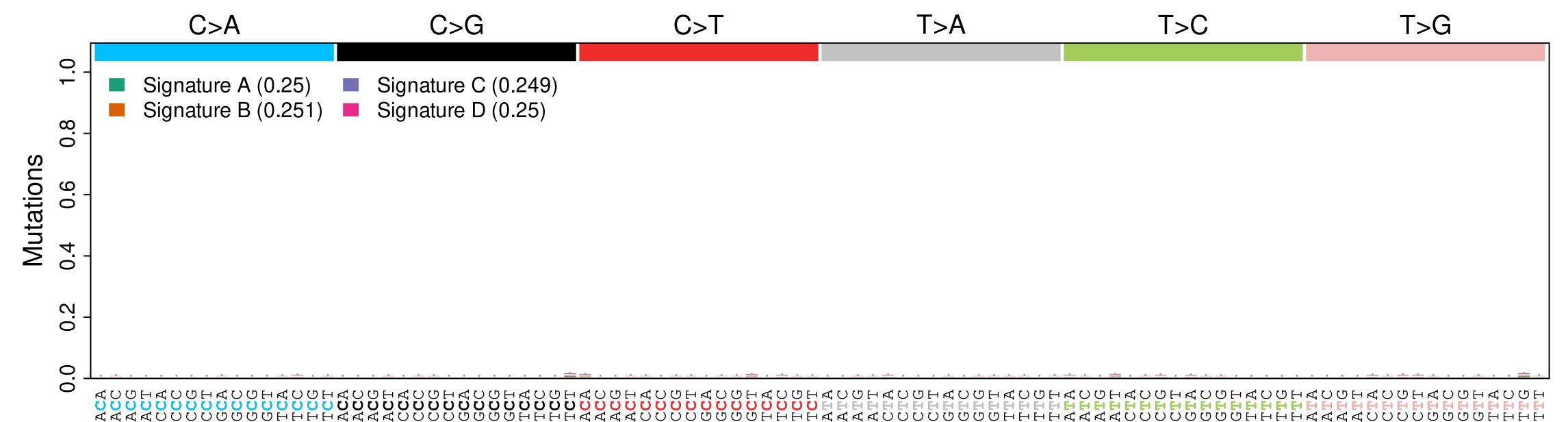


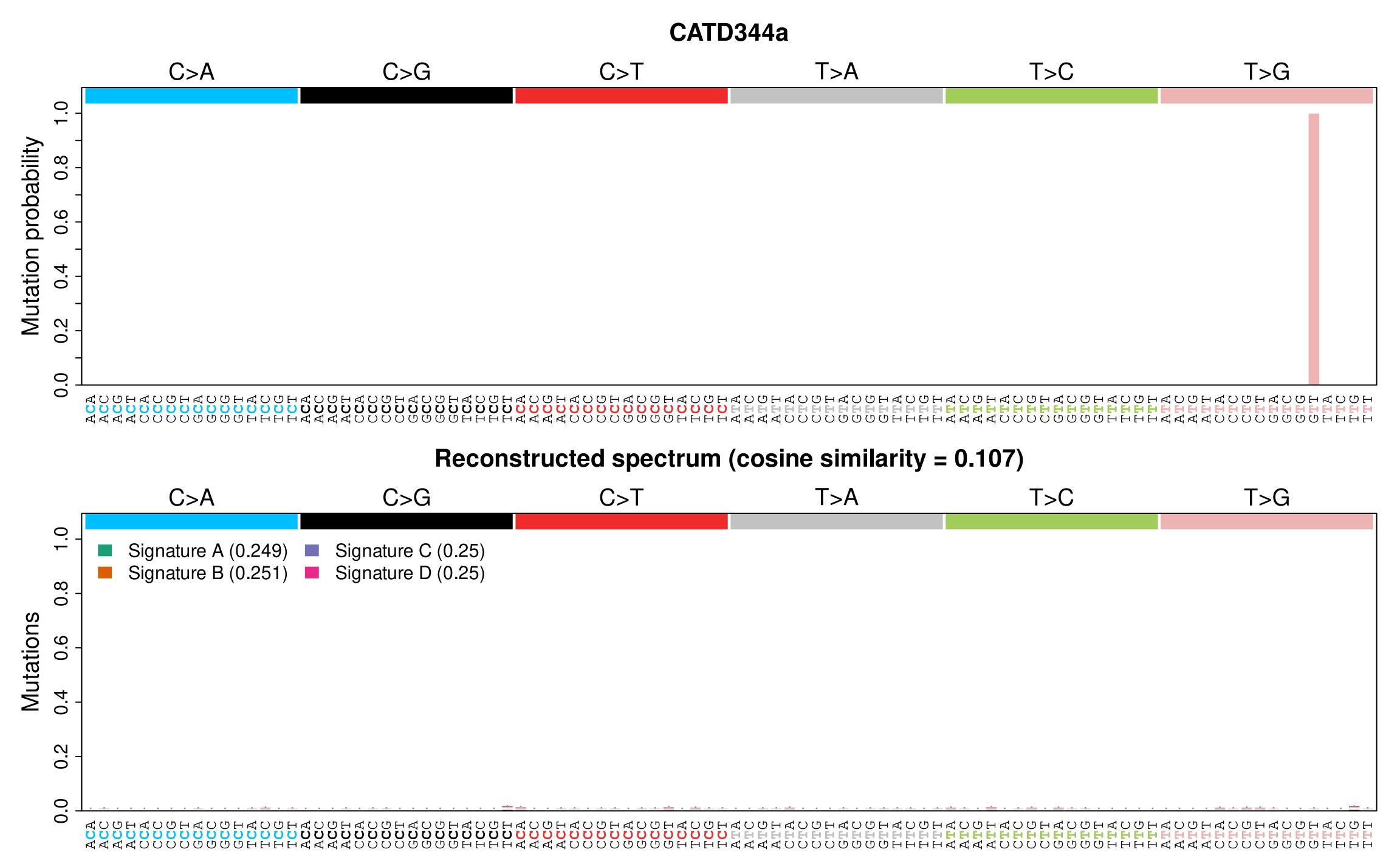
CATD0557a (5 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.242)** T>C T>G C>A C>G T>A C>T 2.0 Signature A (0.25) Signature C (0.249) Signature B (0.249) Signature D (0.252) 5 Mutations 2



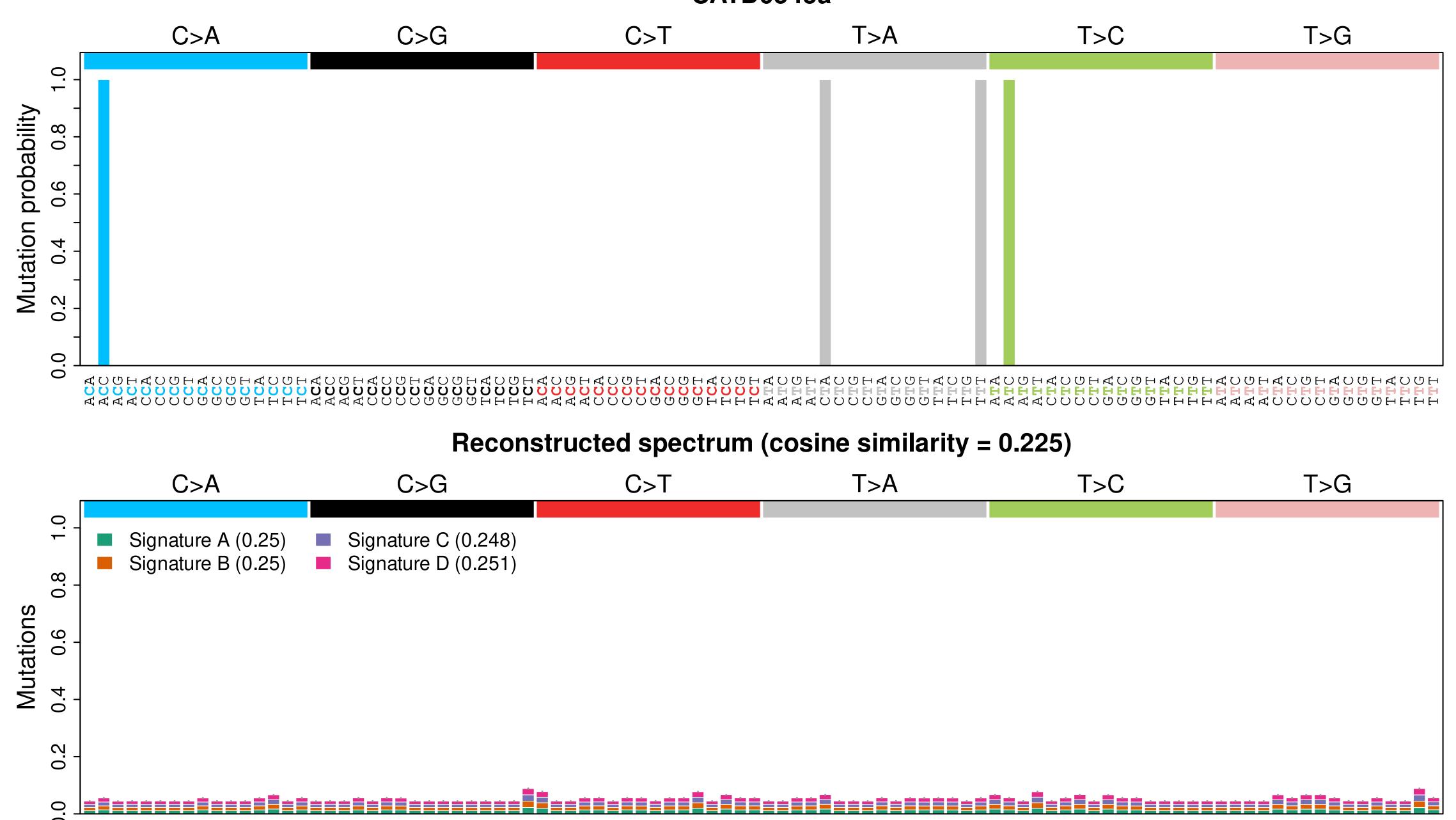




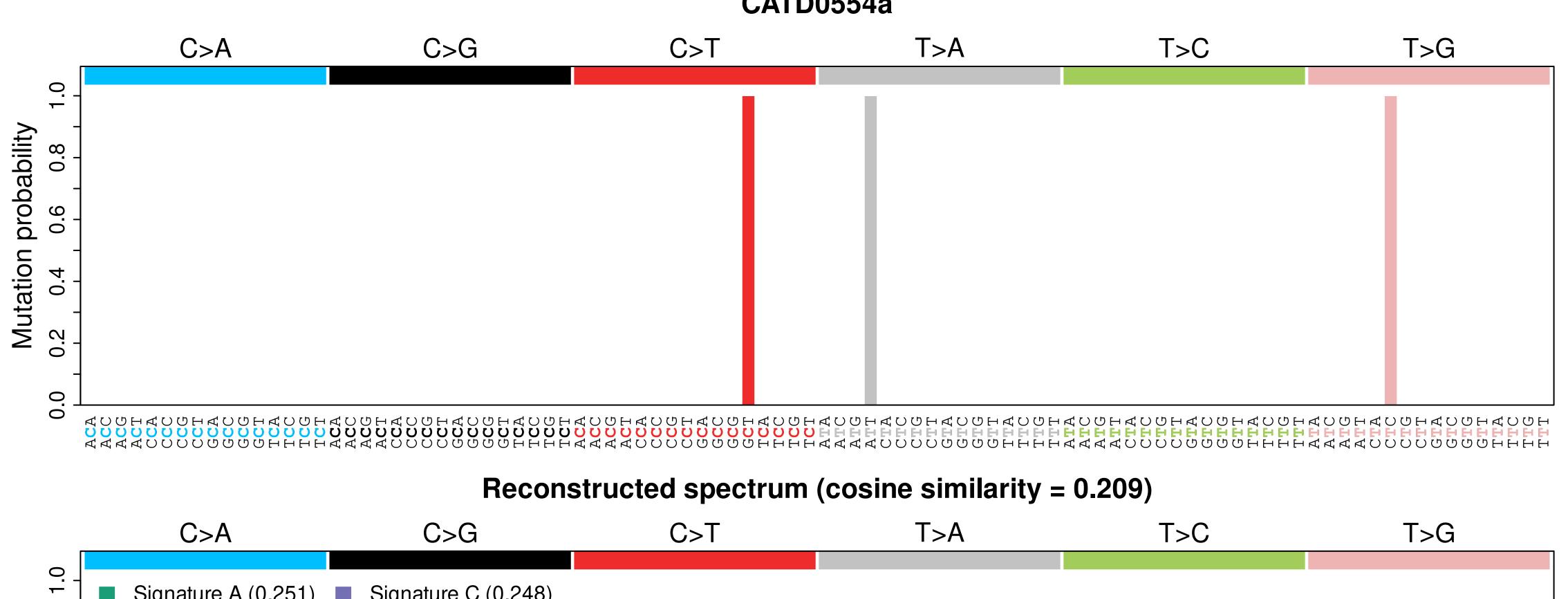


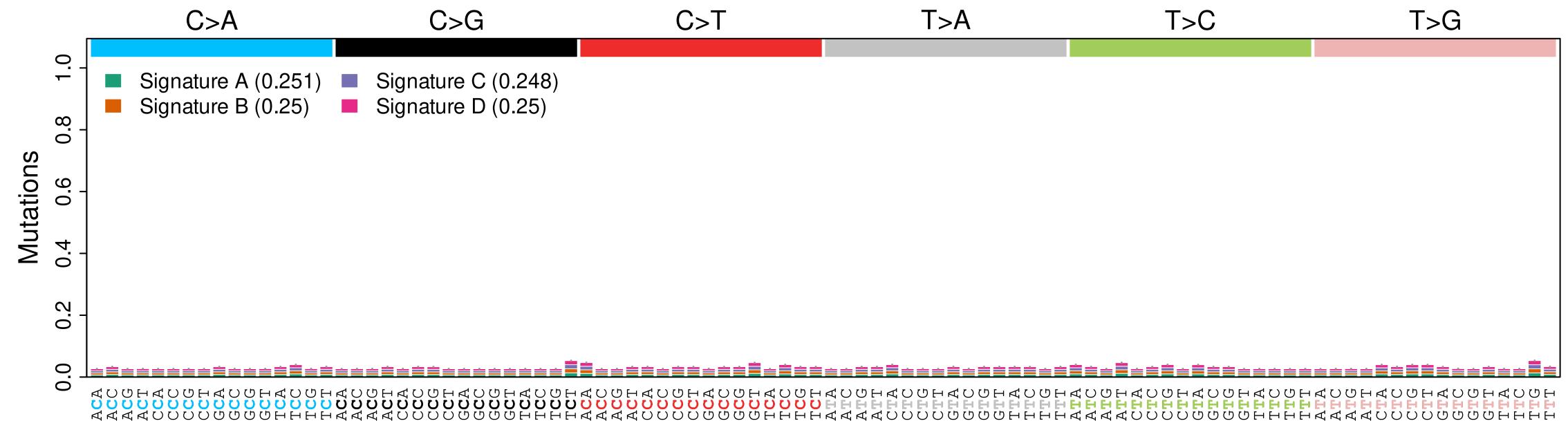




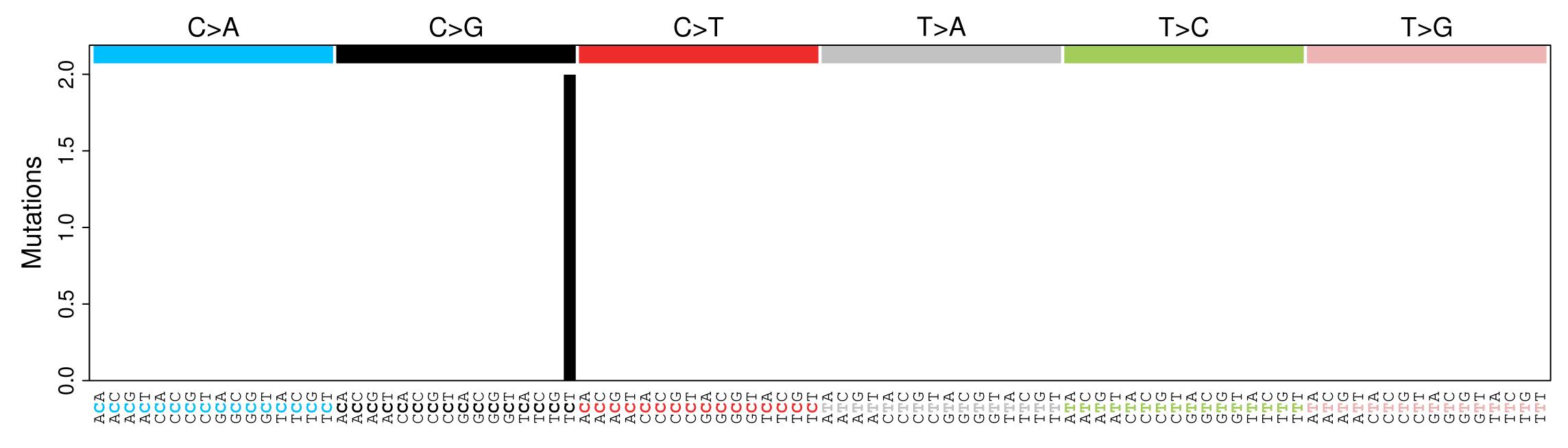




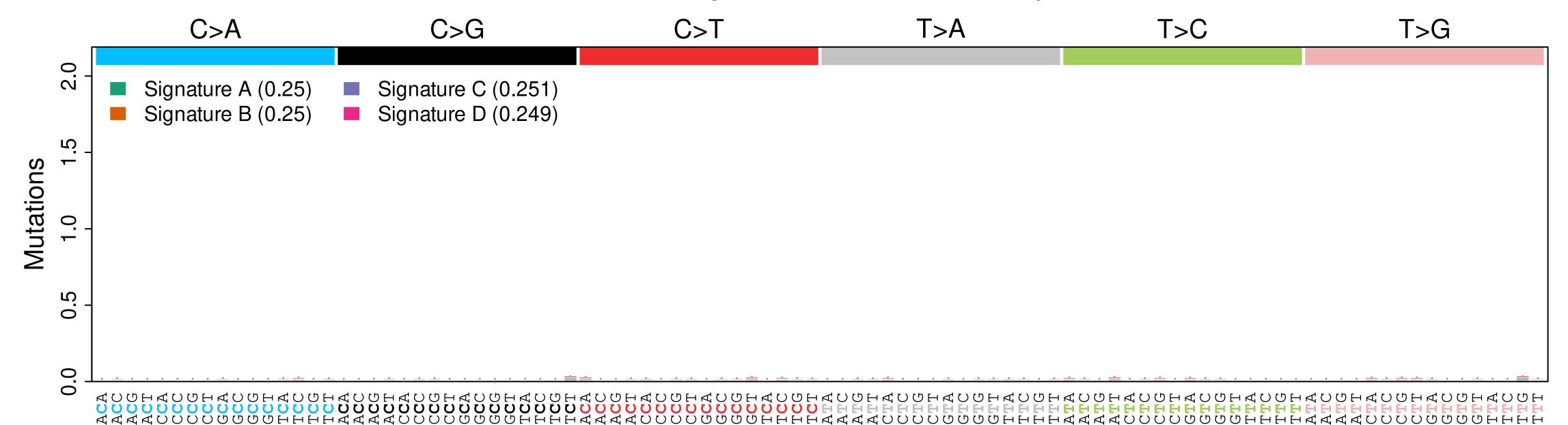




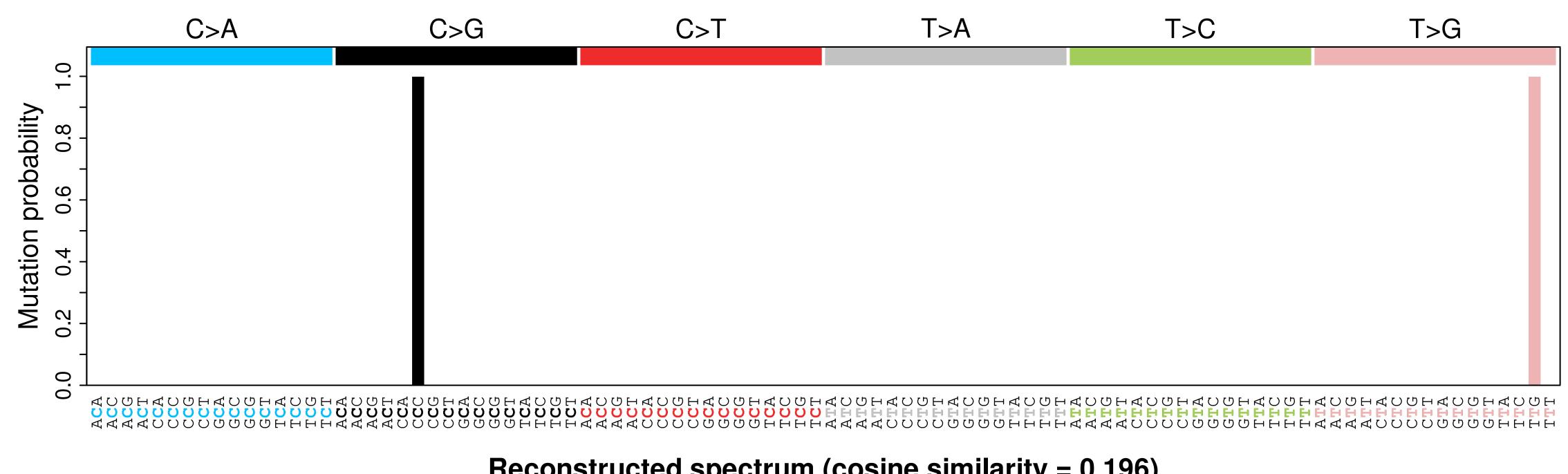
CATD0541a (2 mutations)

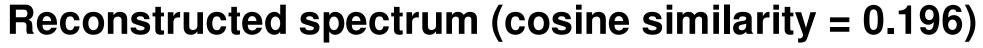


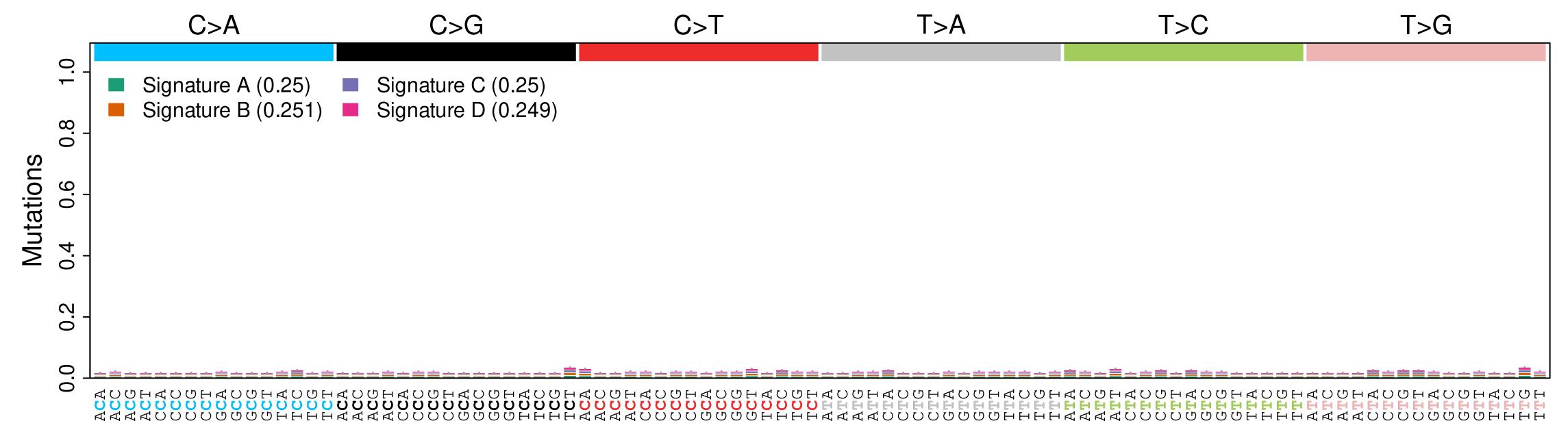


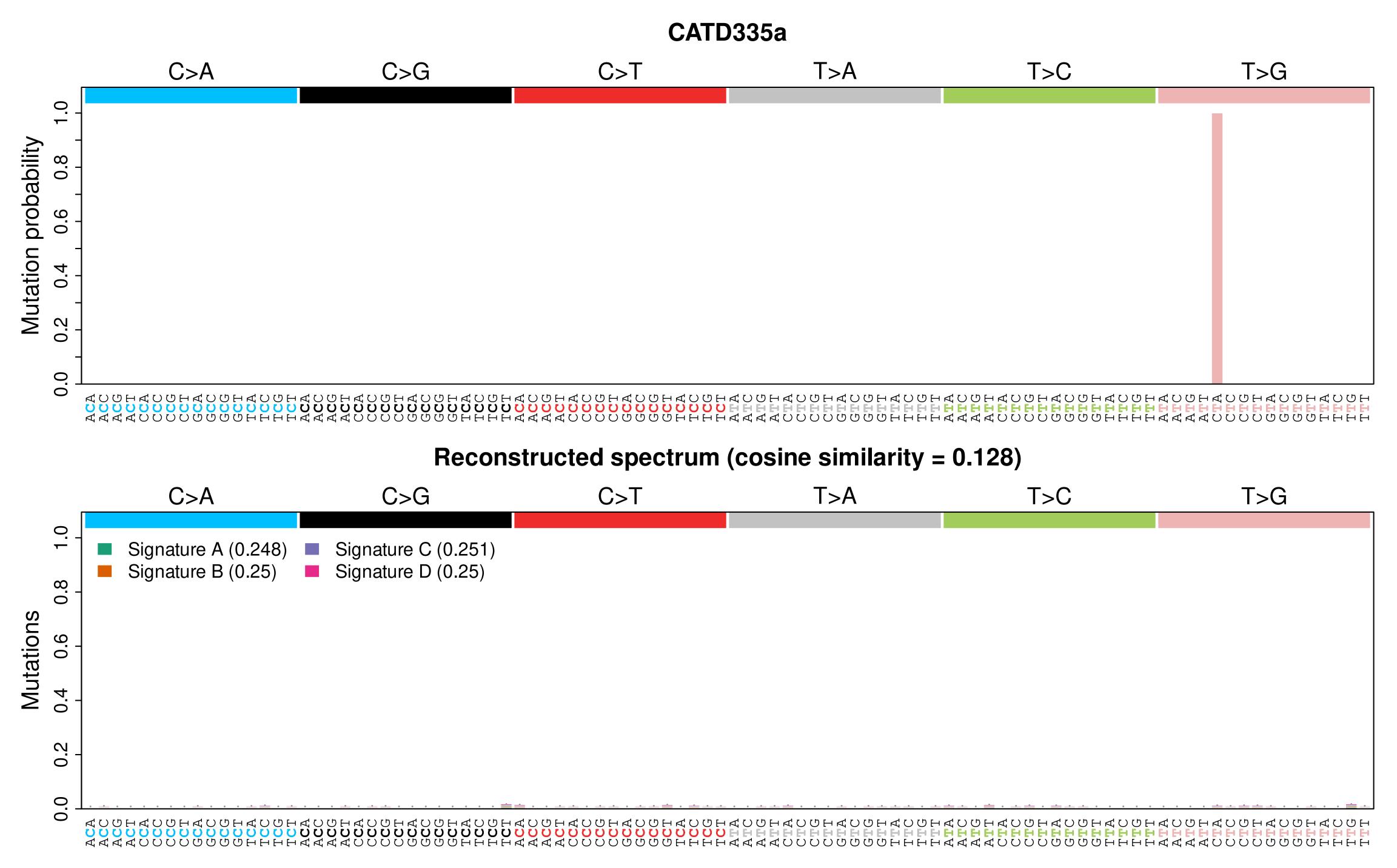




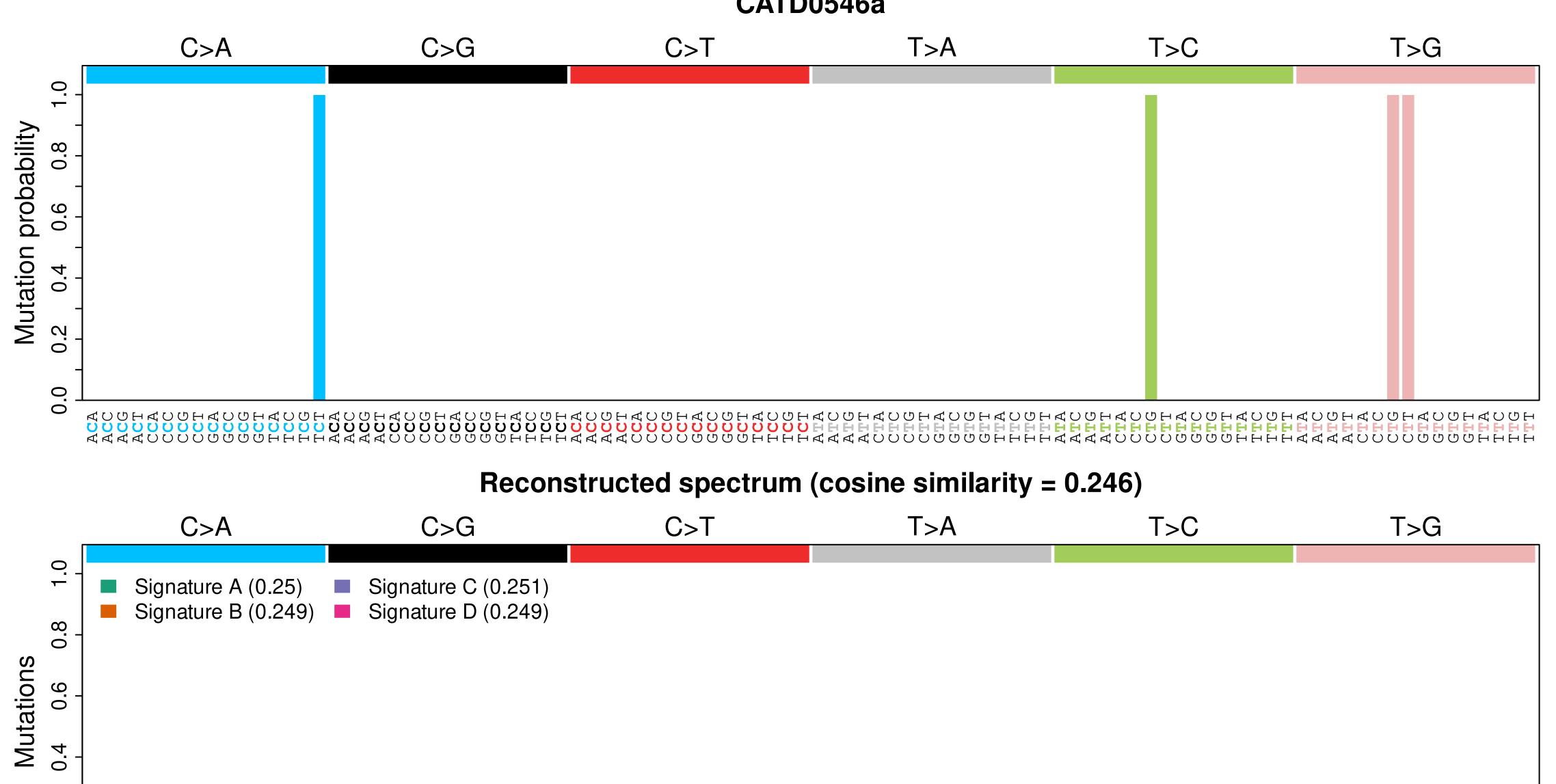






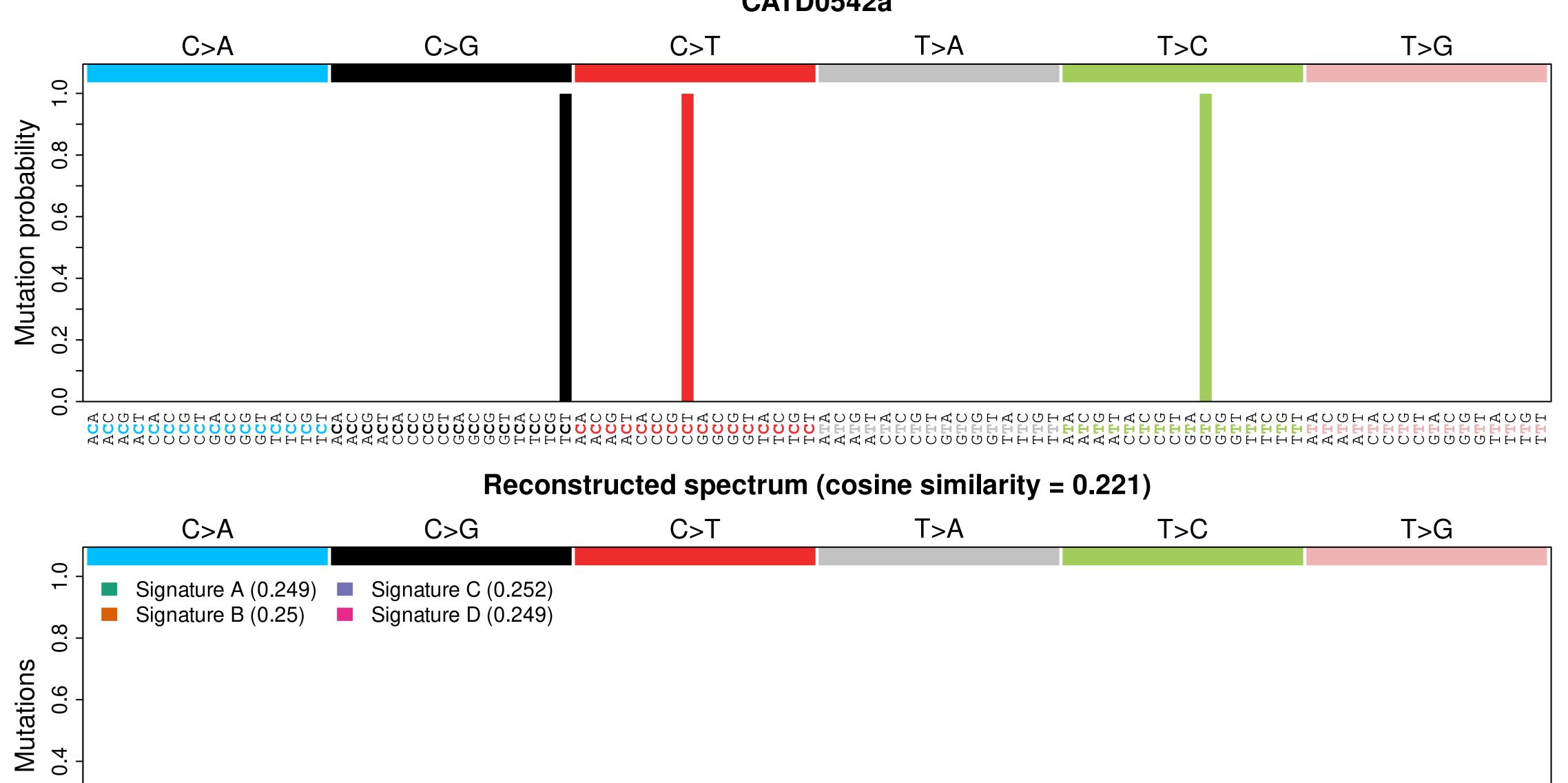




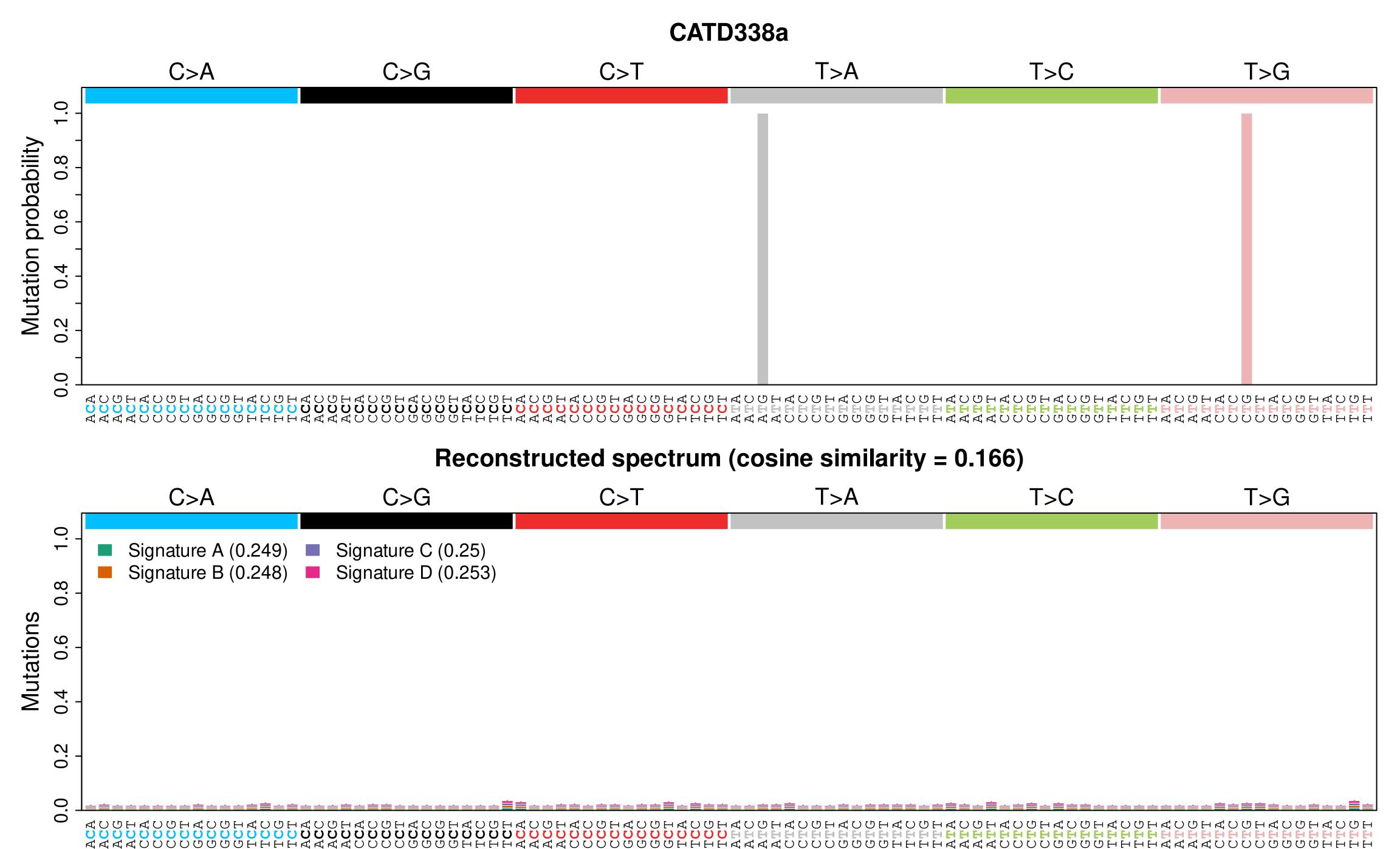


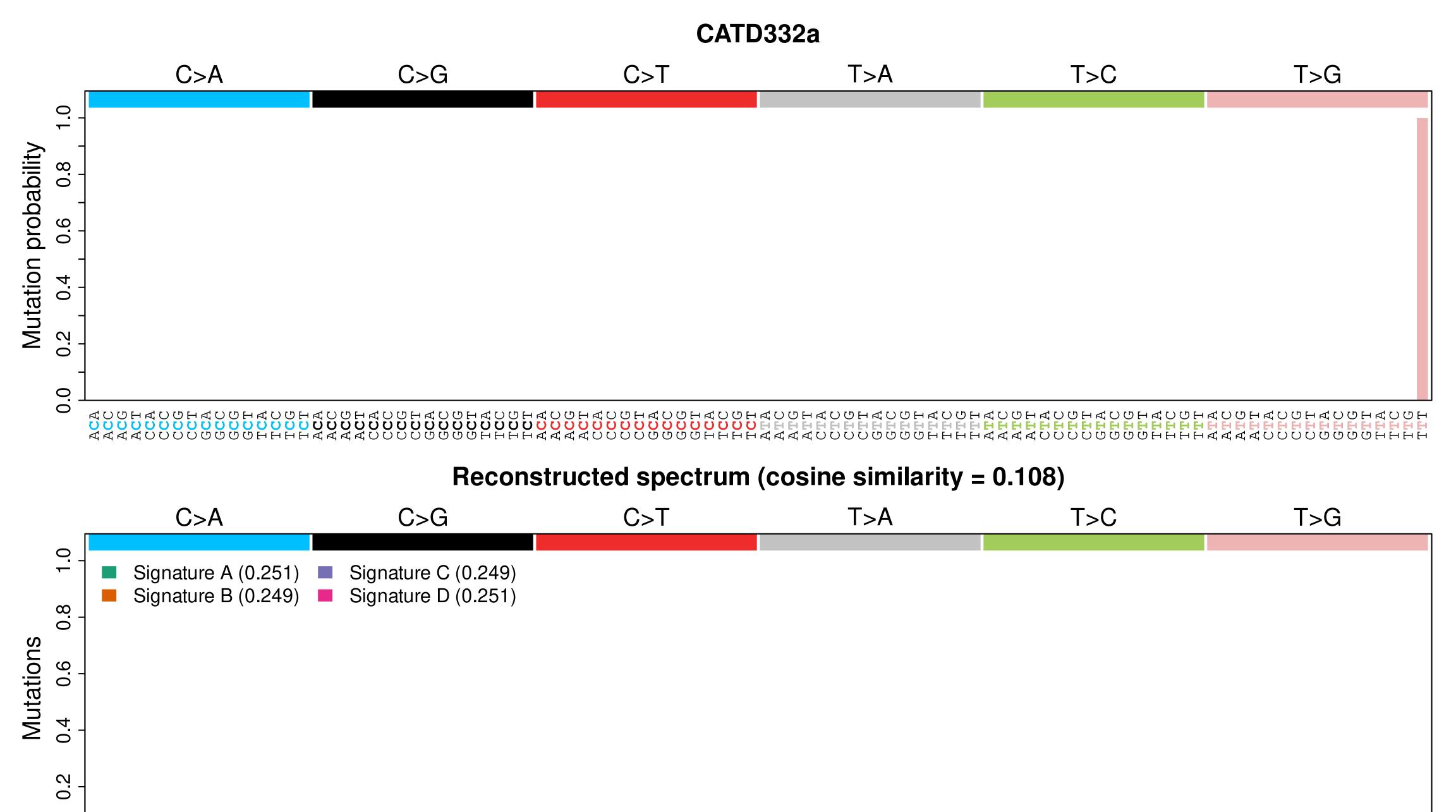
 \mathcal{O} 0





 \mathcal{O} 0





0.0

