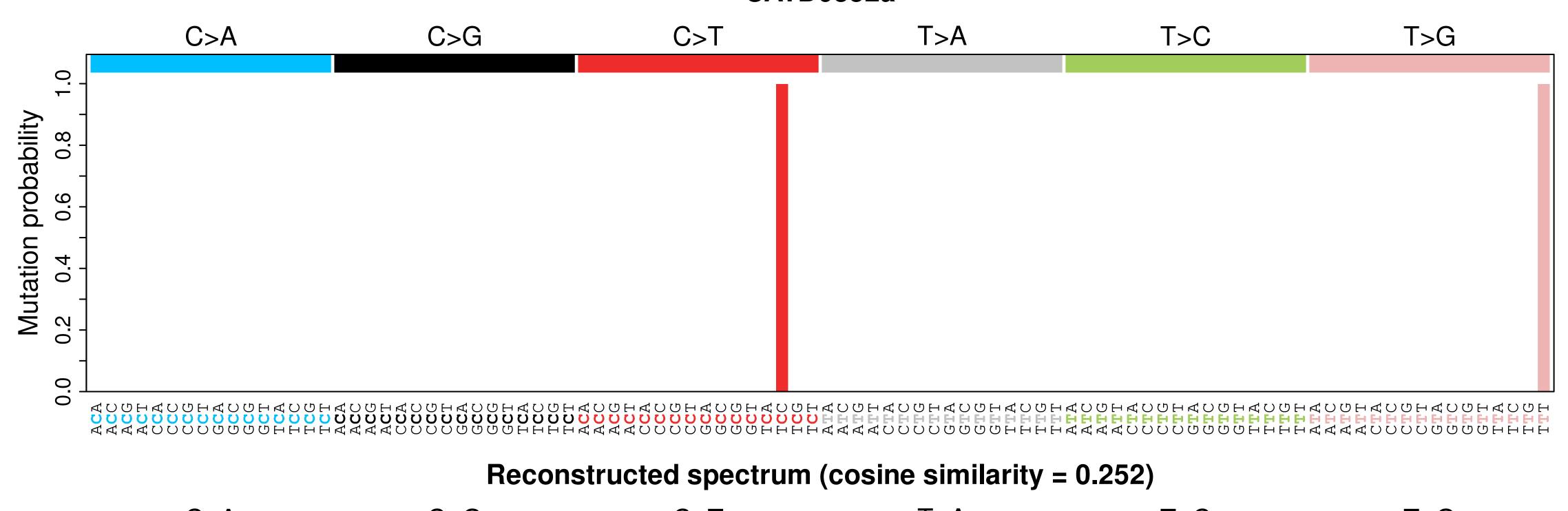
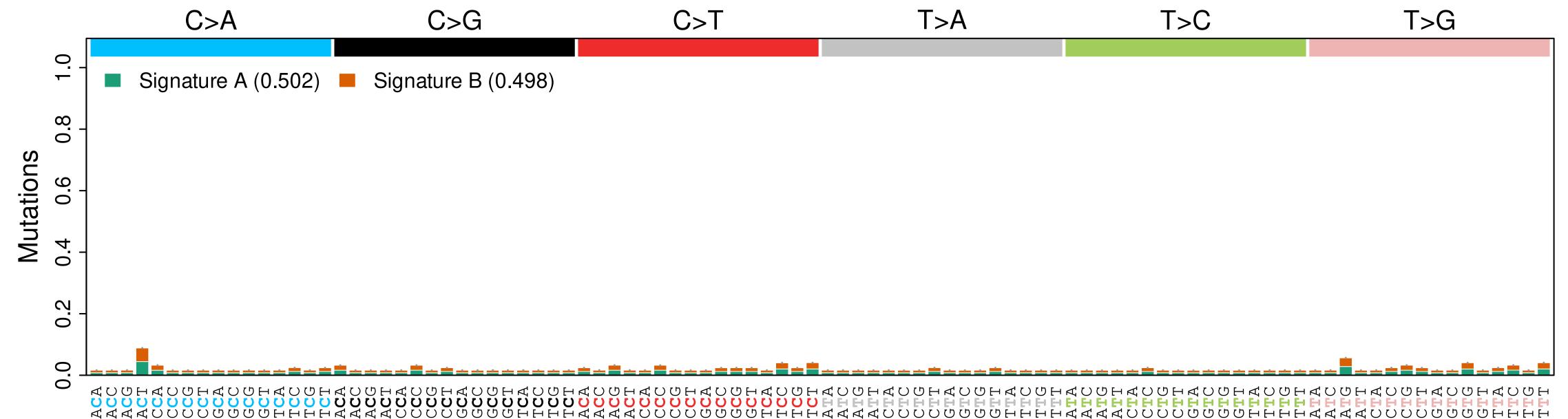


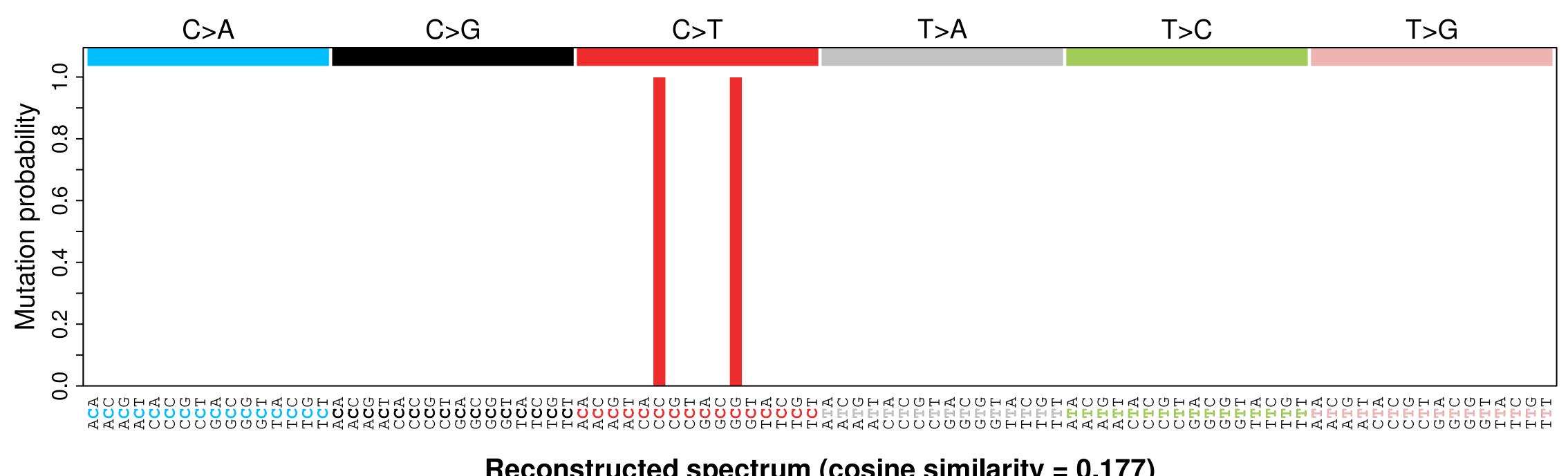
CATD0372a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.319)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.498) Signature B (0.502) 5 Mutations 5 0 0



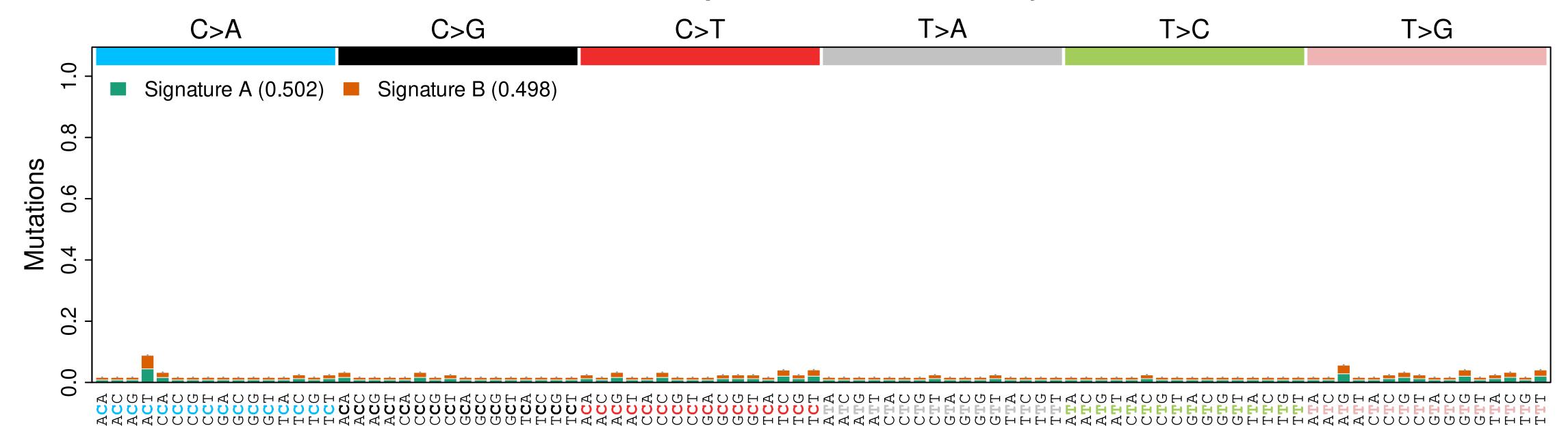




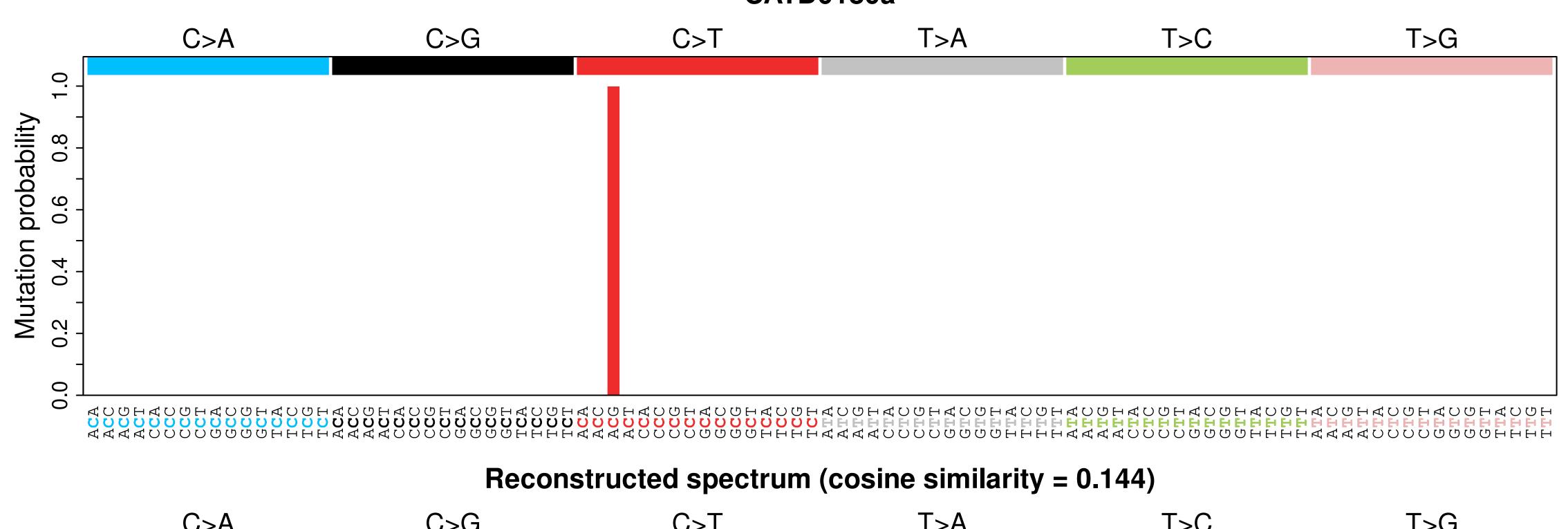


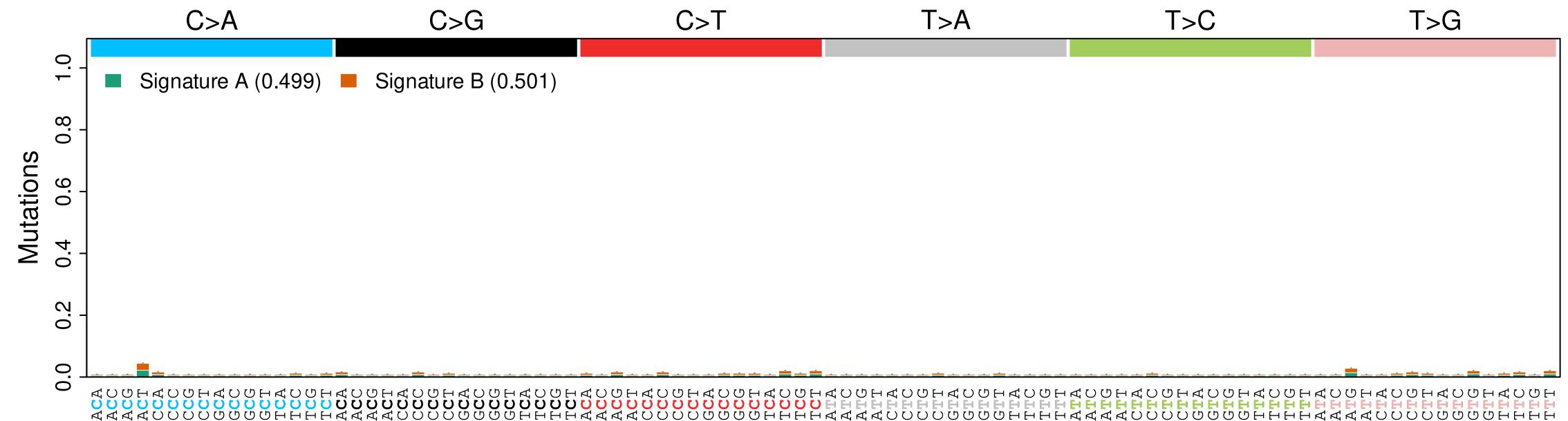




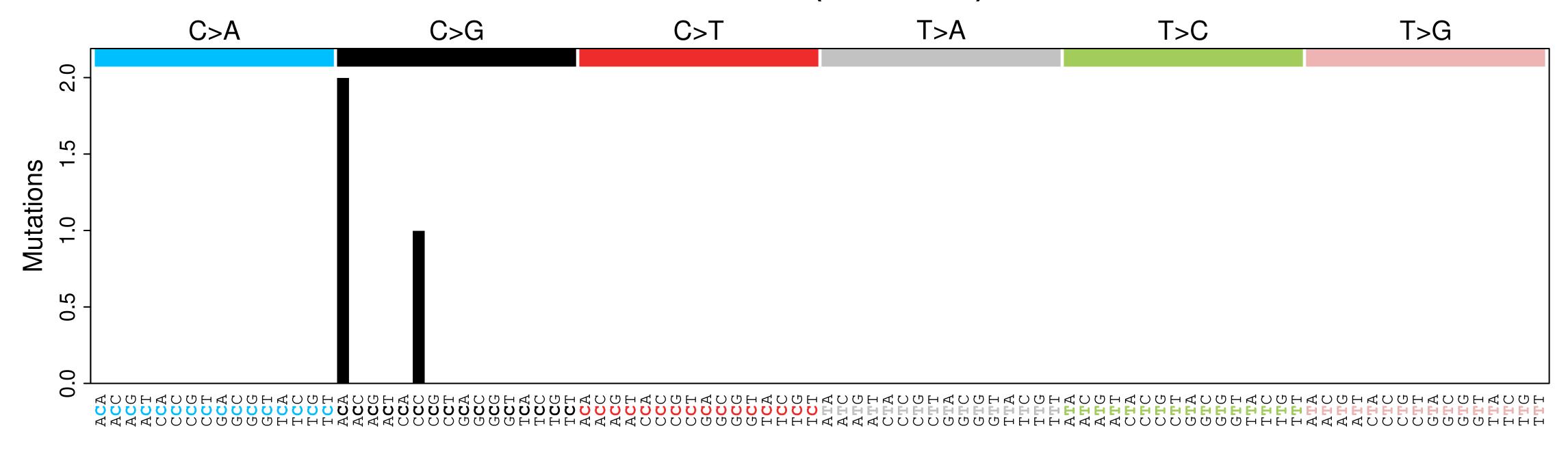


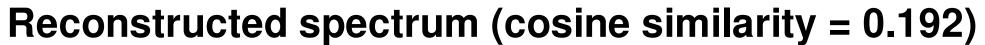


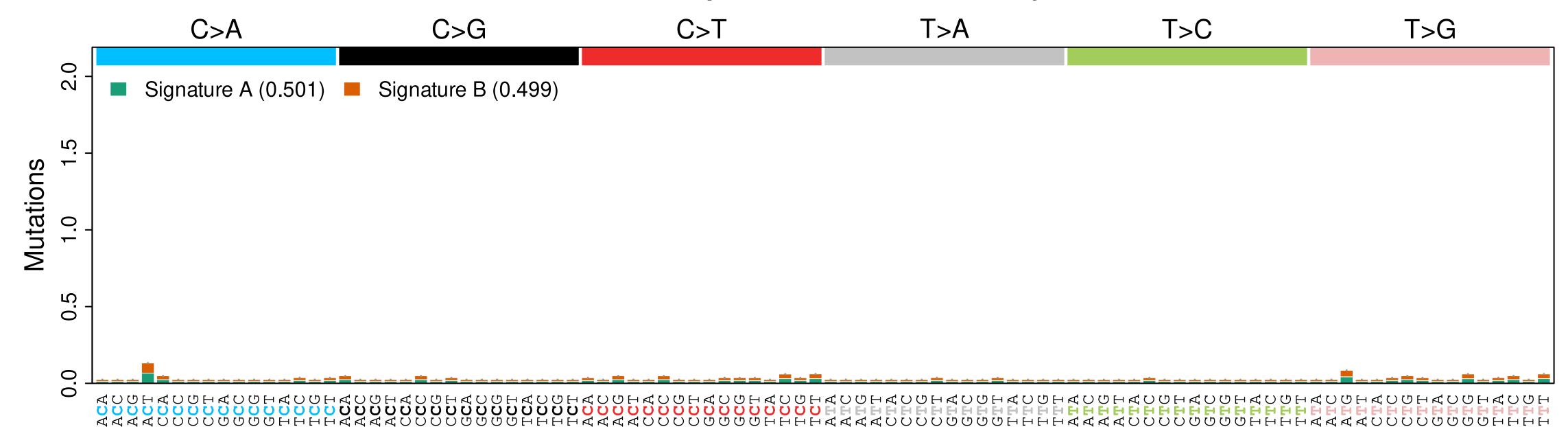


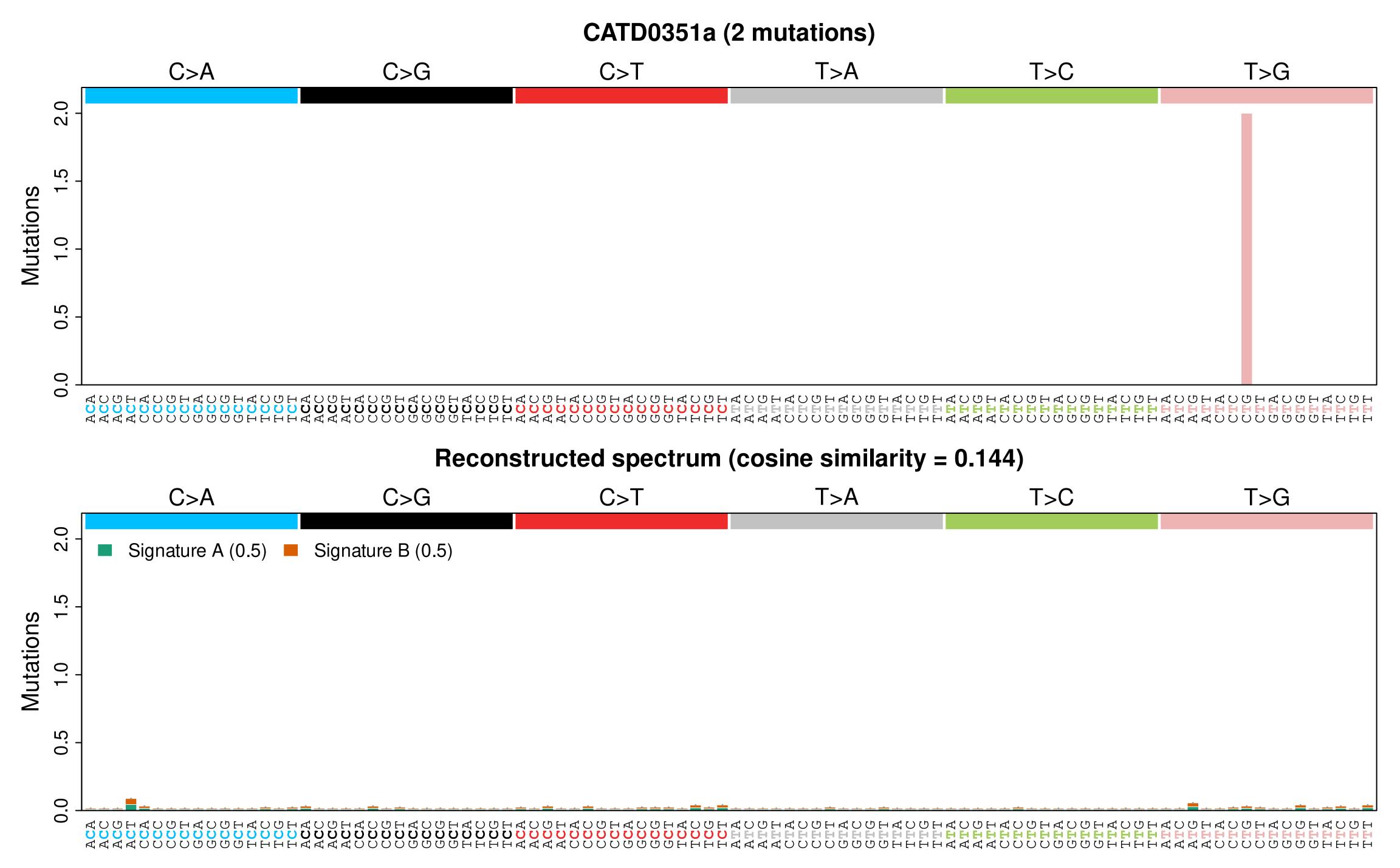


CATD0375a (3 mutations)



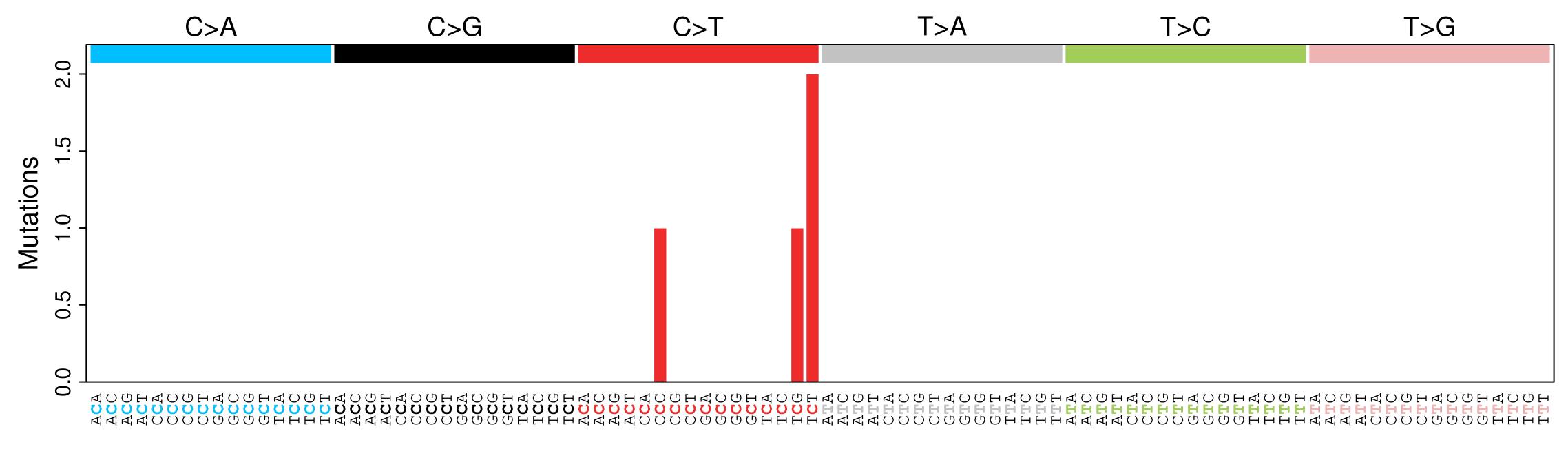




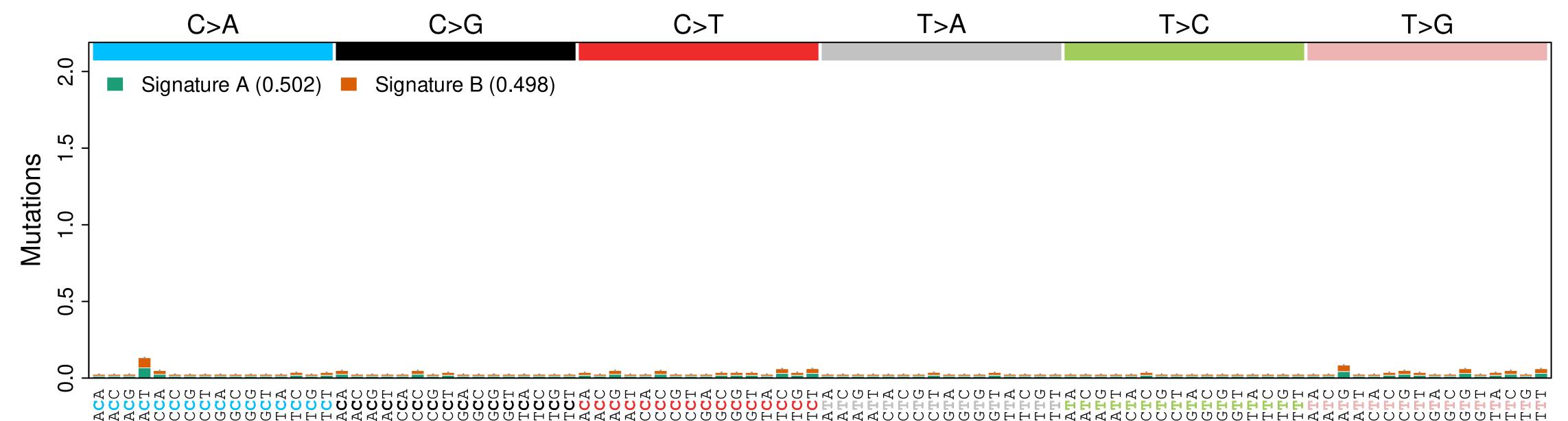


CATD0182a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.207)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.497) Signature B (0.503) 5 Mutations 5 0 0

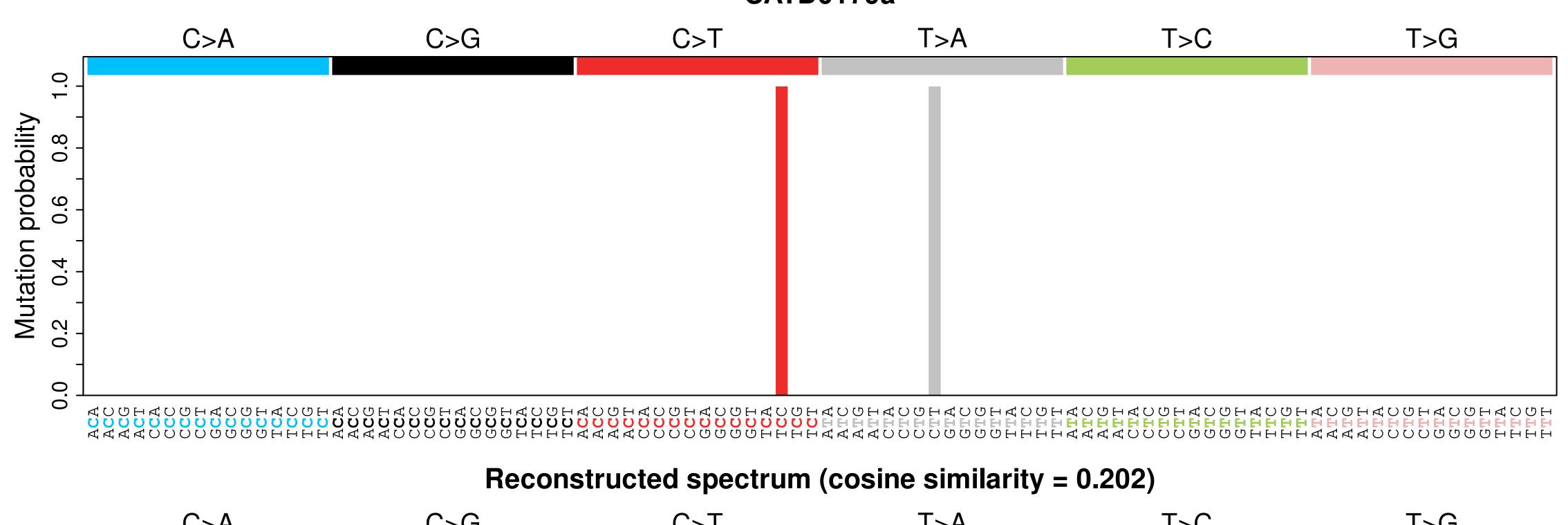
CATD0184a (4 mutations)

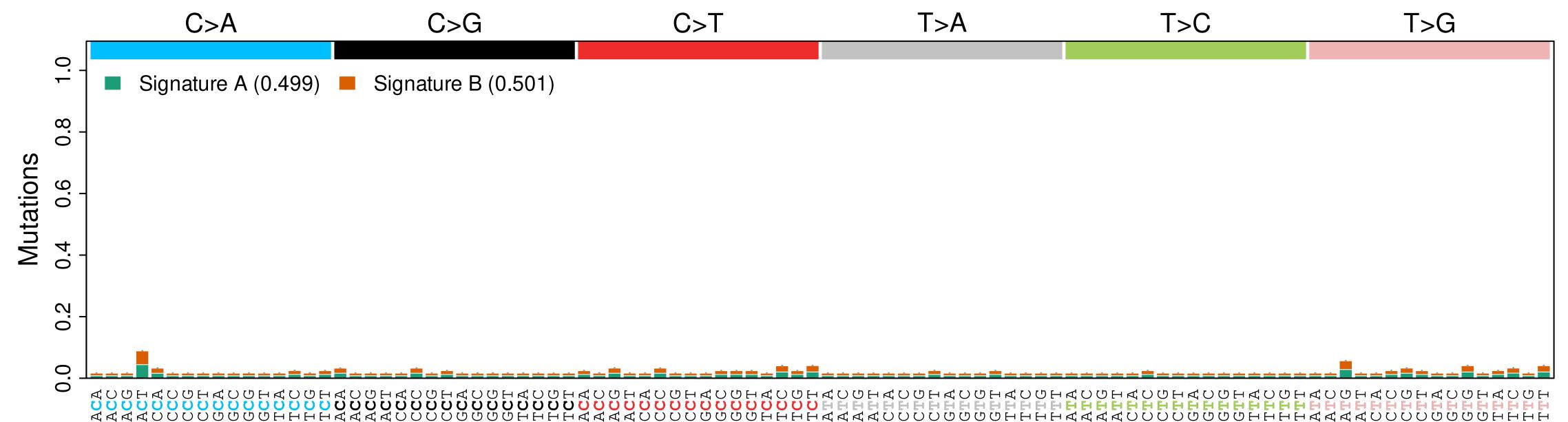


Reconstructed spectrum (cosine similarity = 0.249)

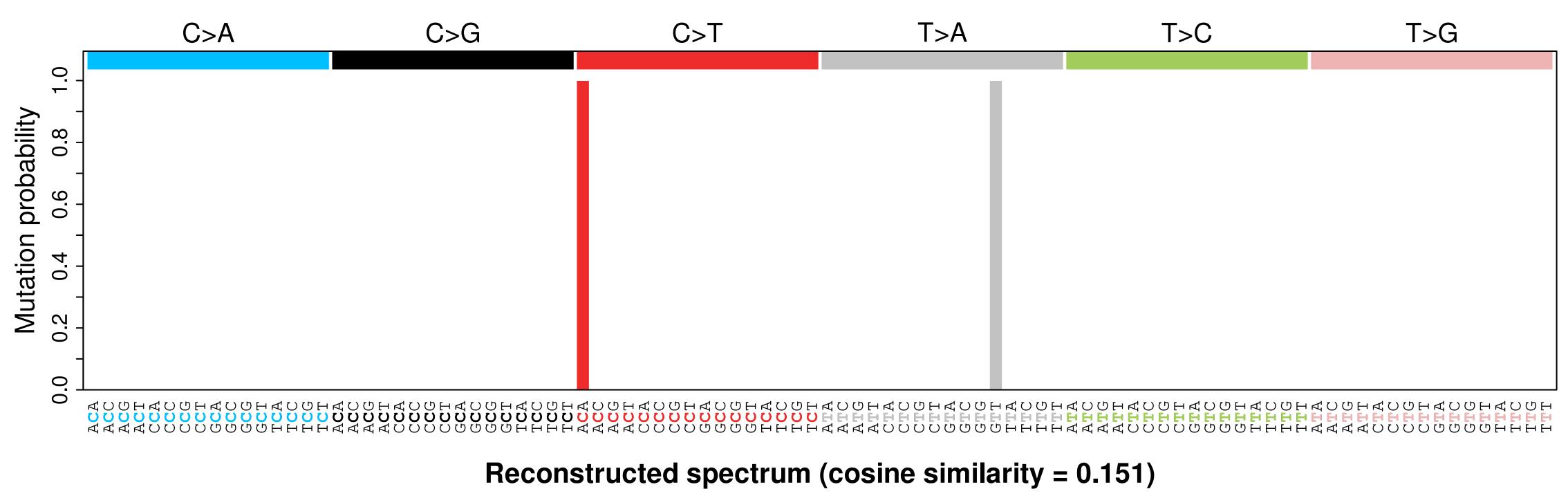


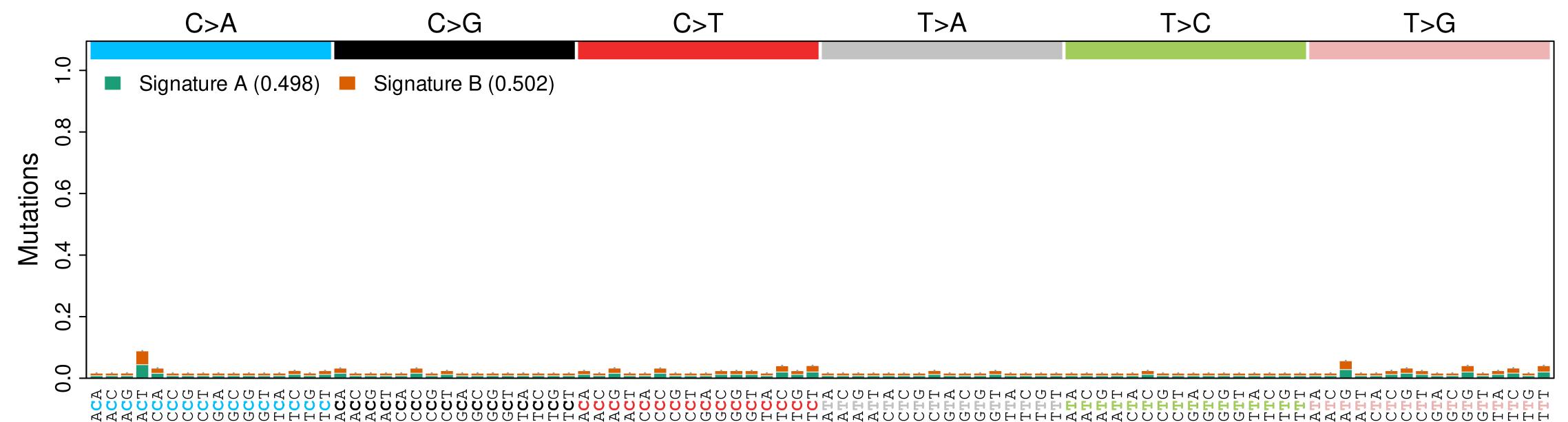




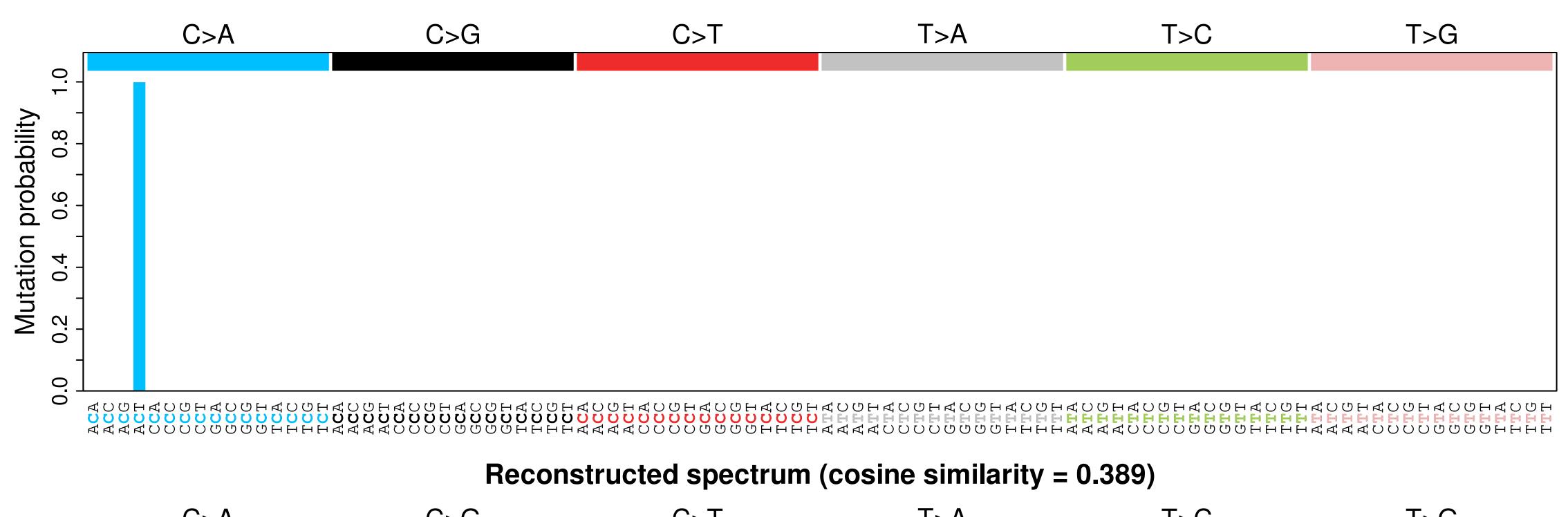


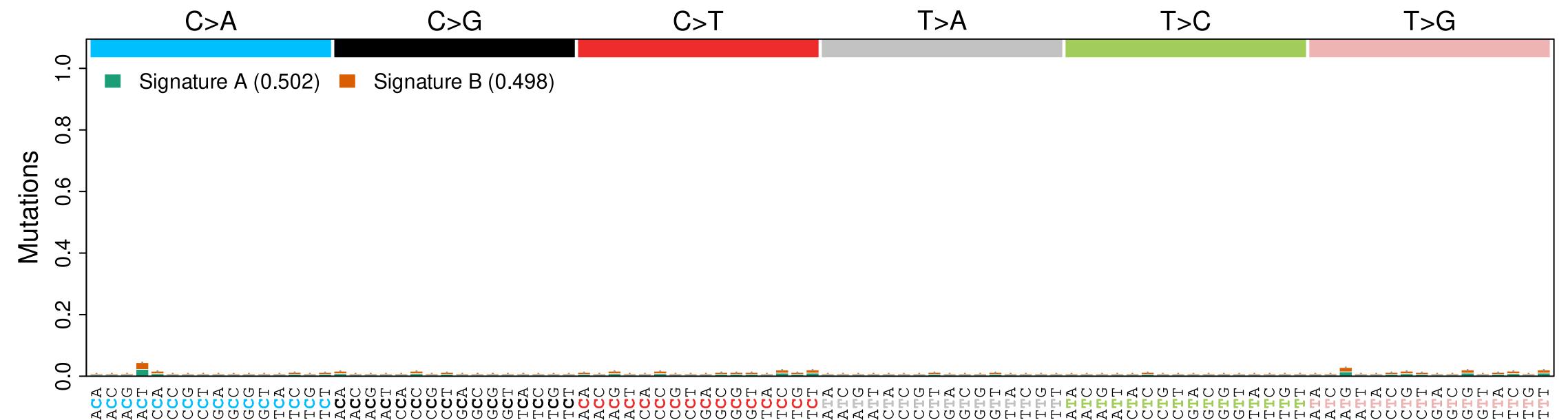




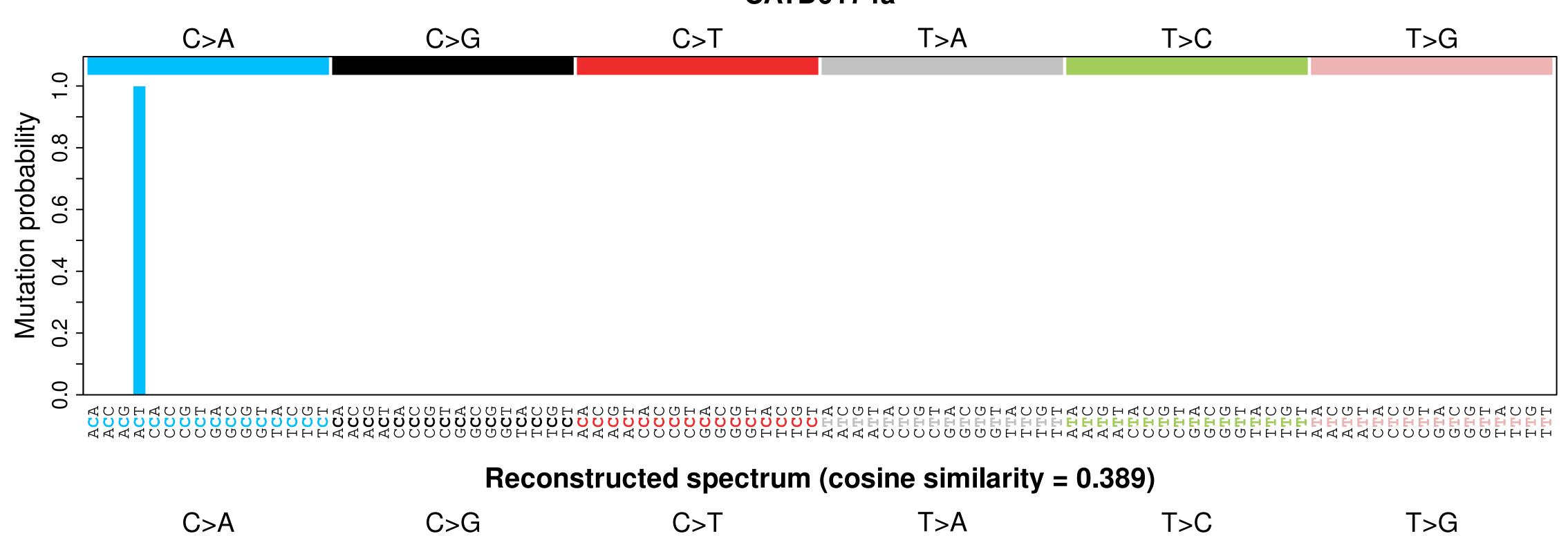


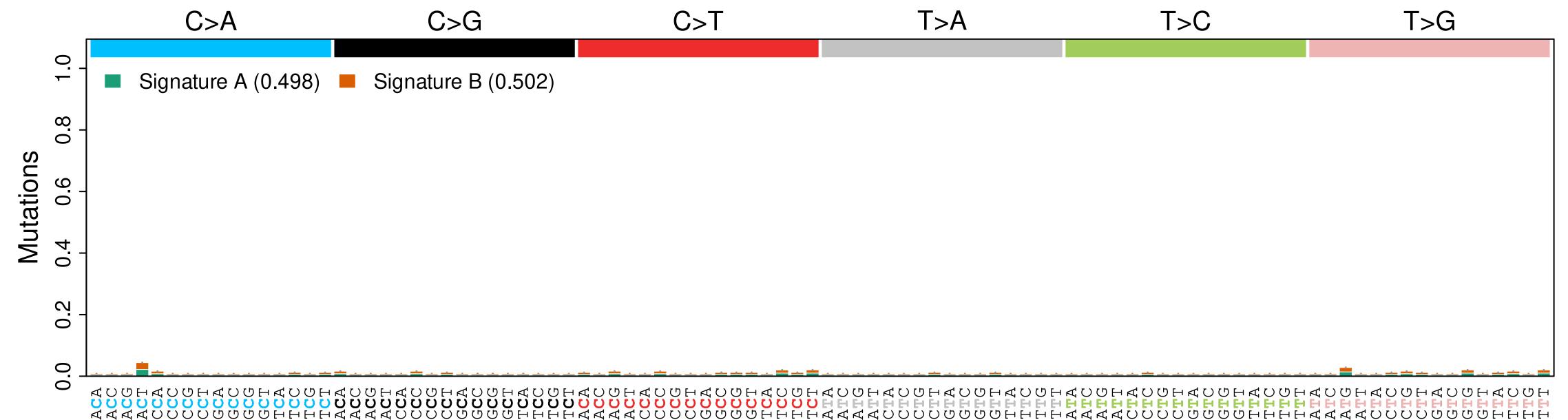




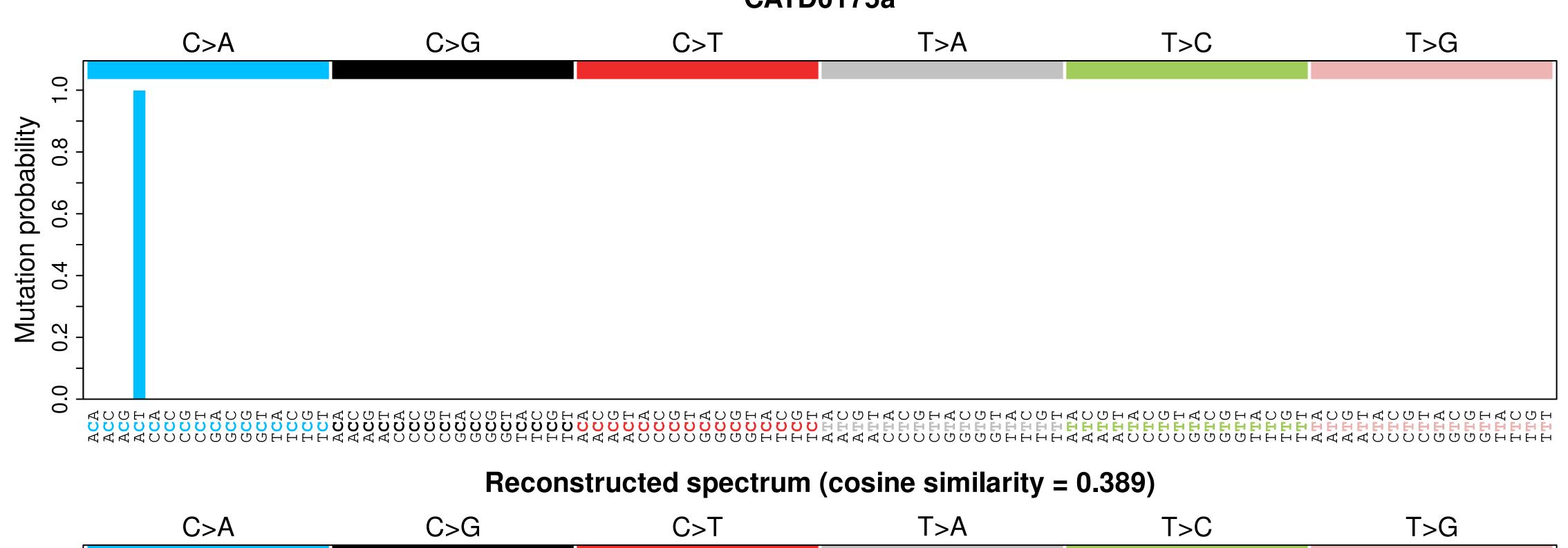


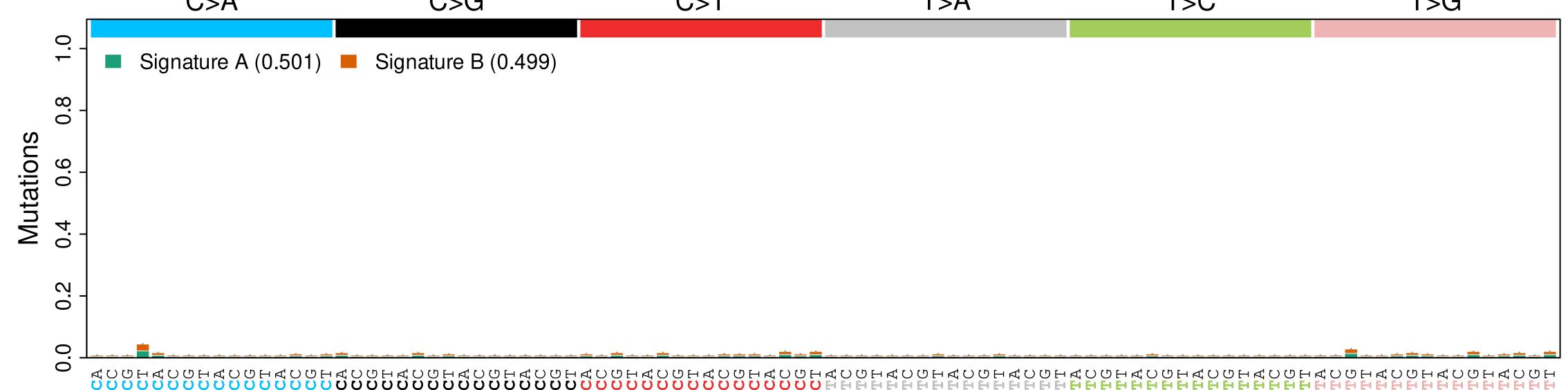




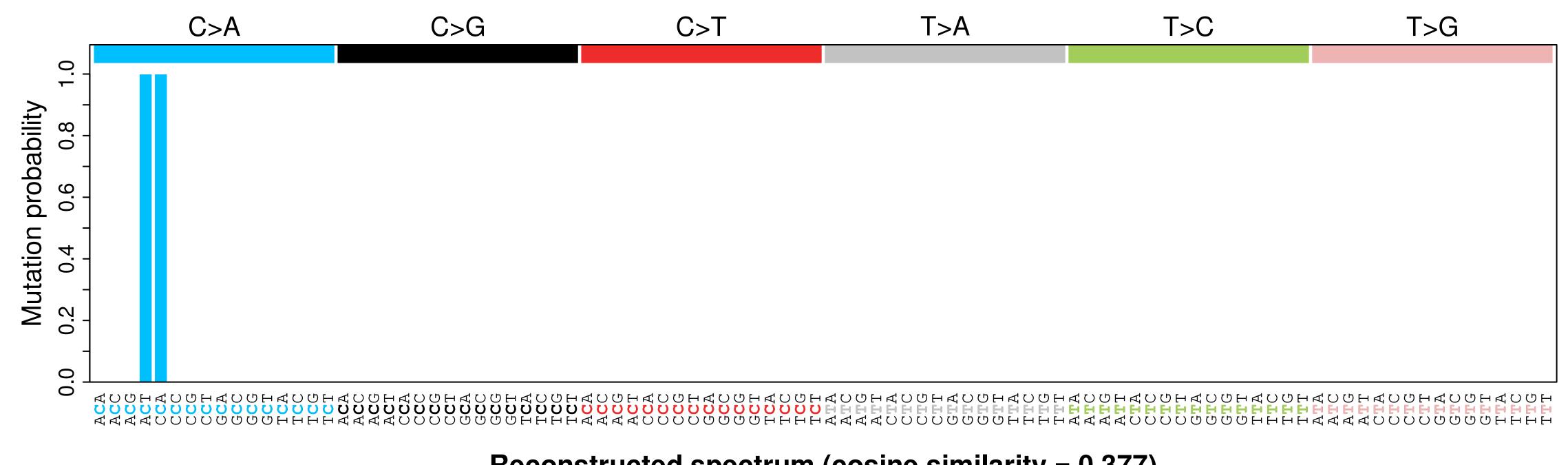


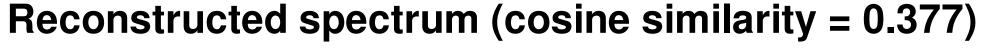


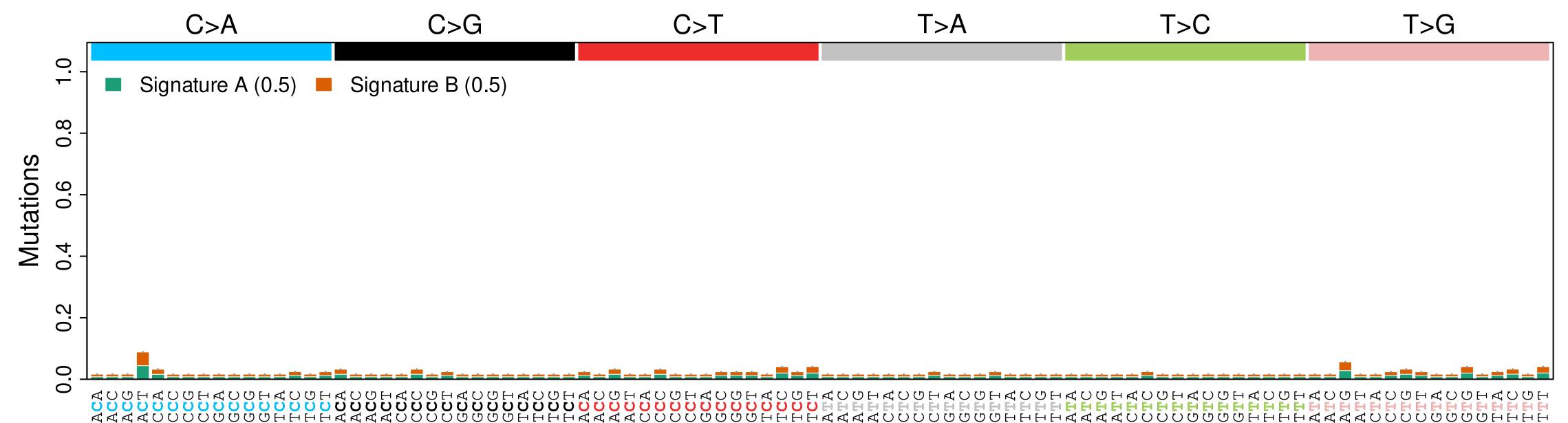




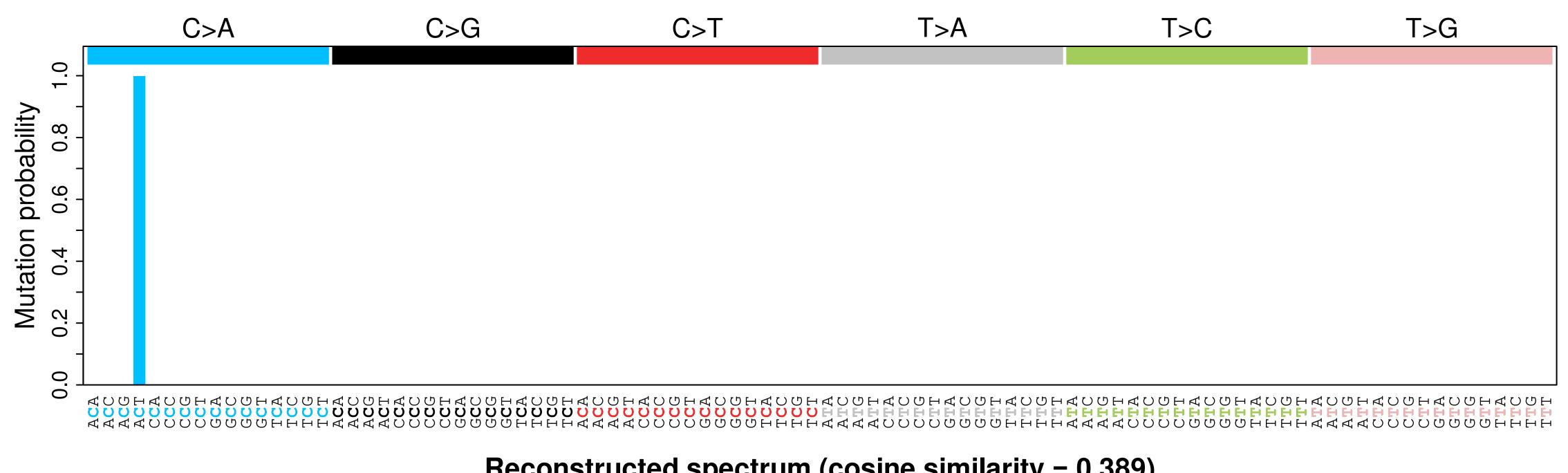


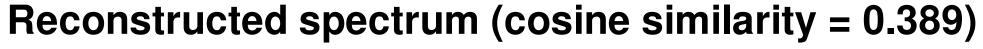


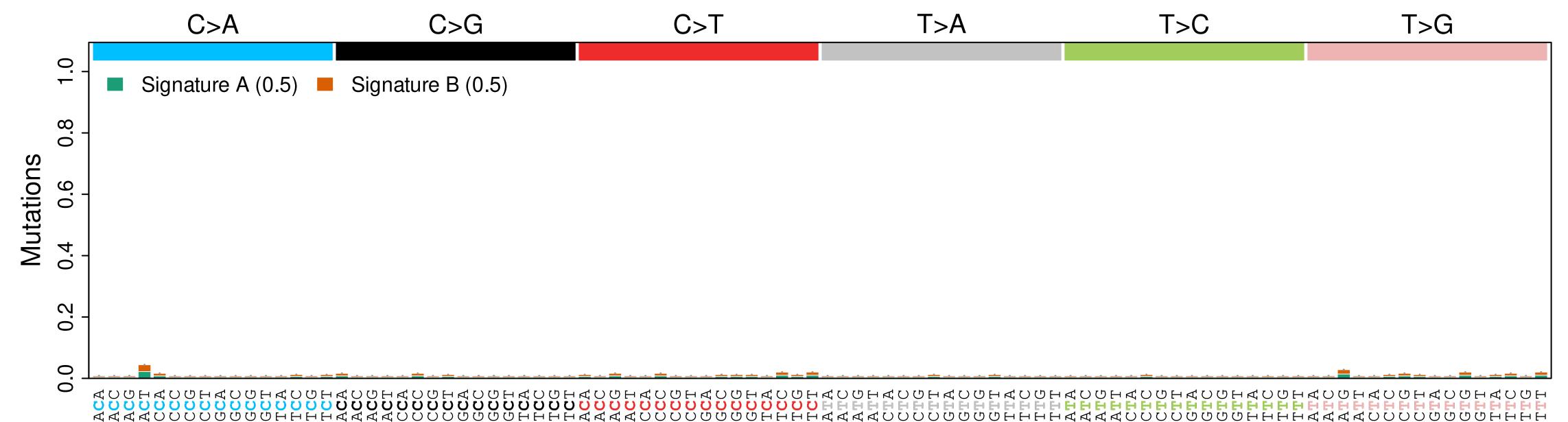




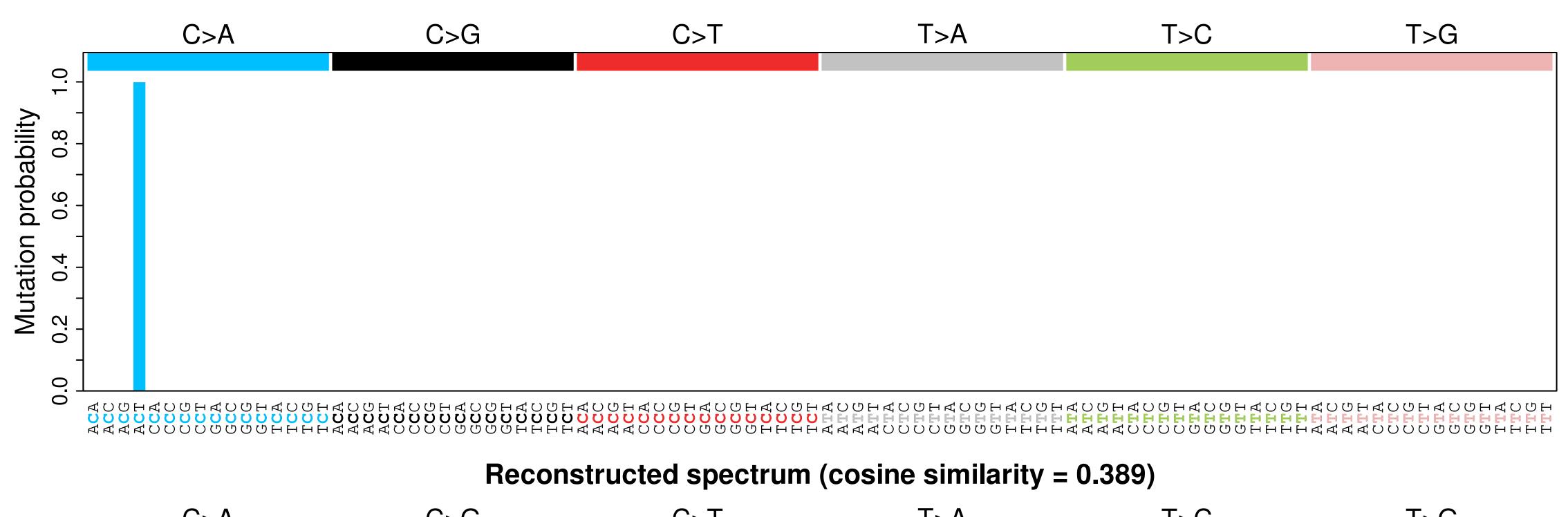


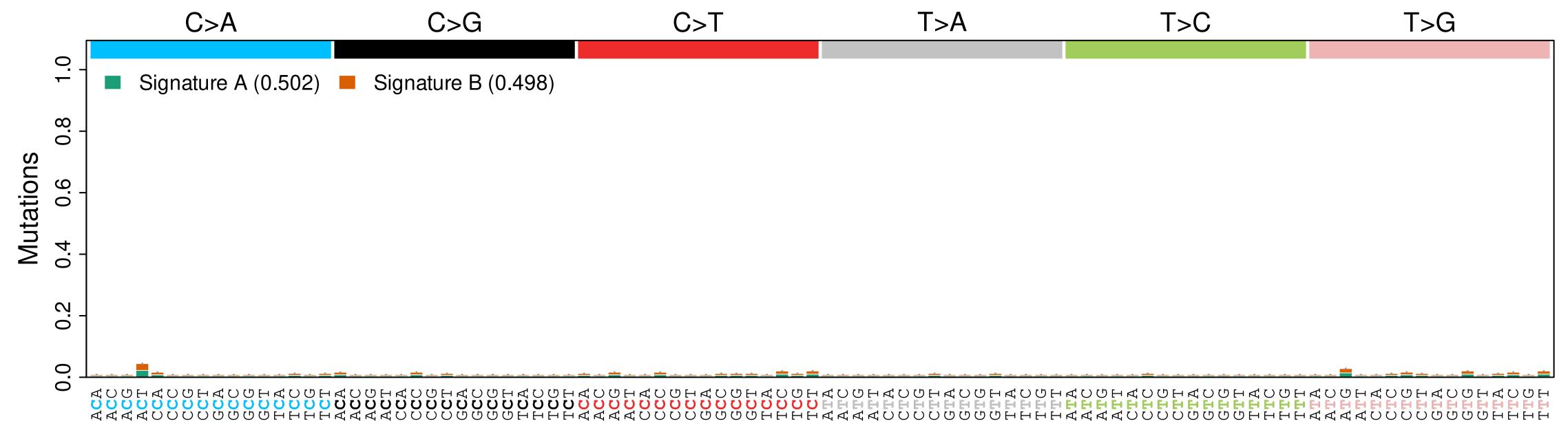




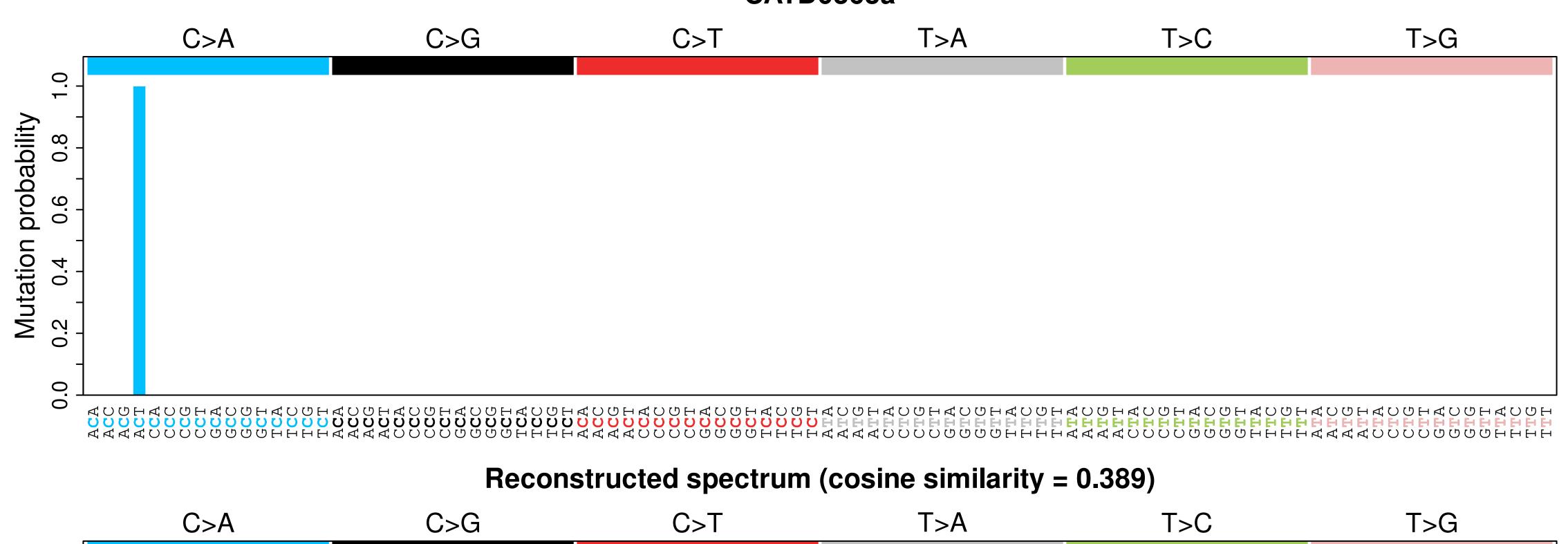


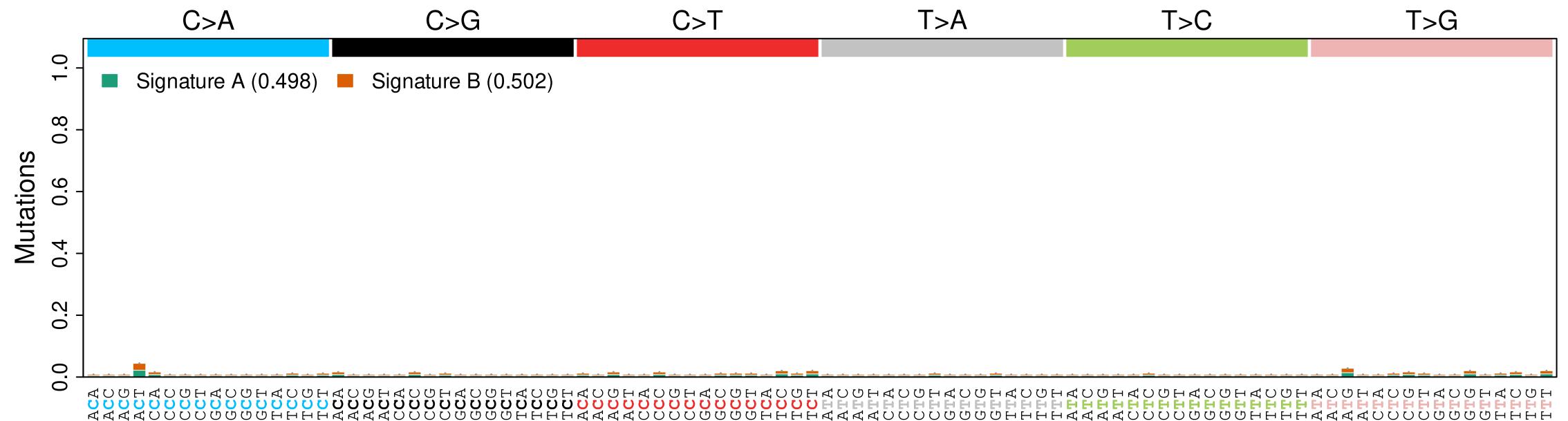




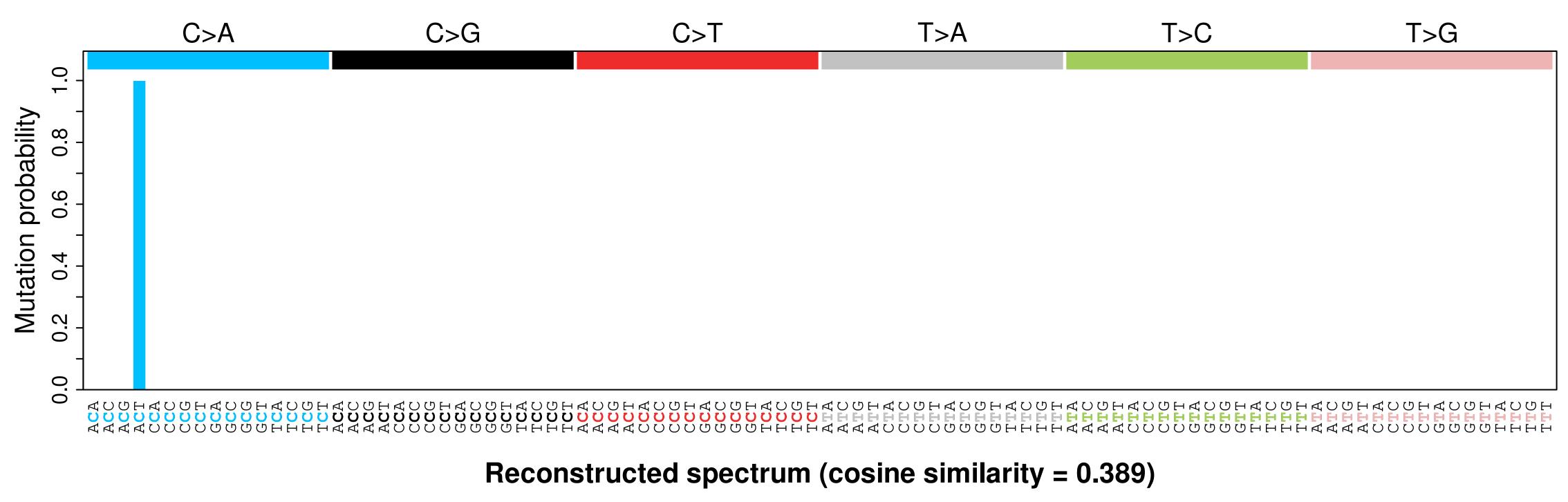


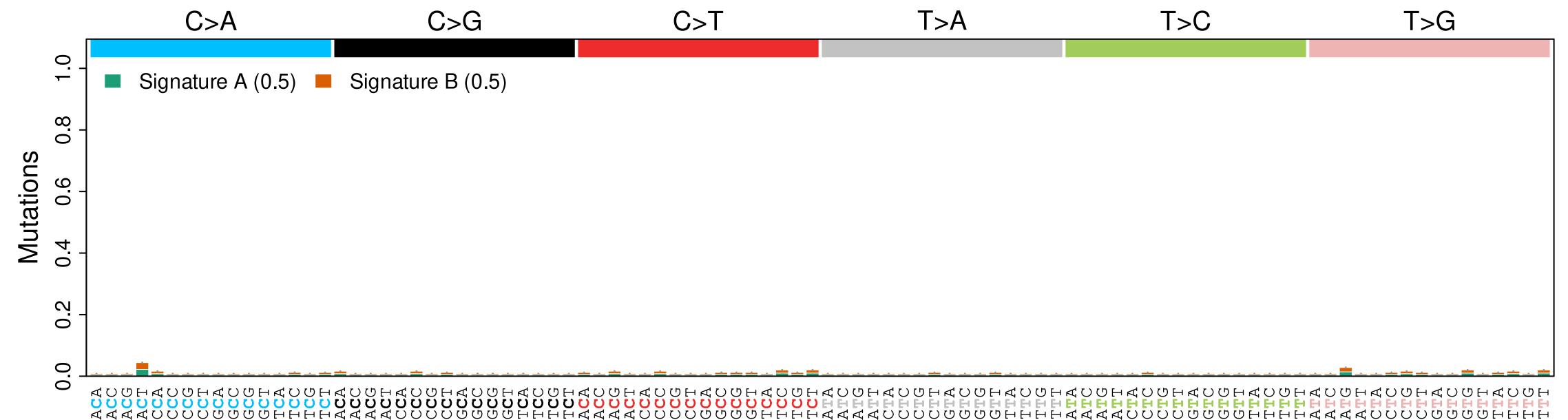




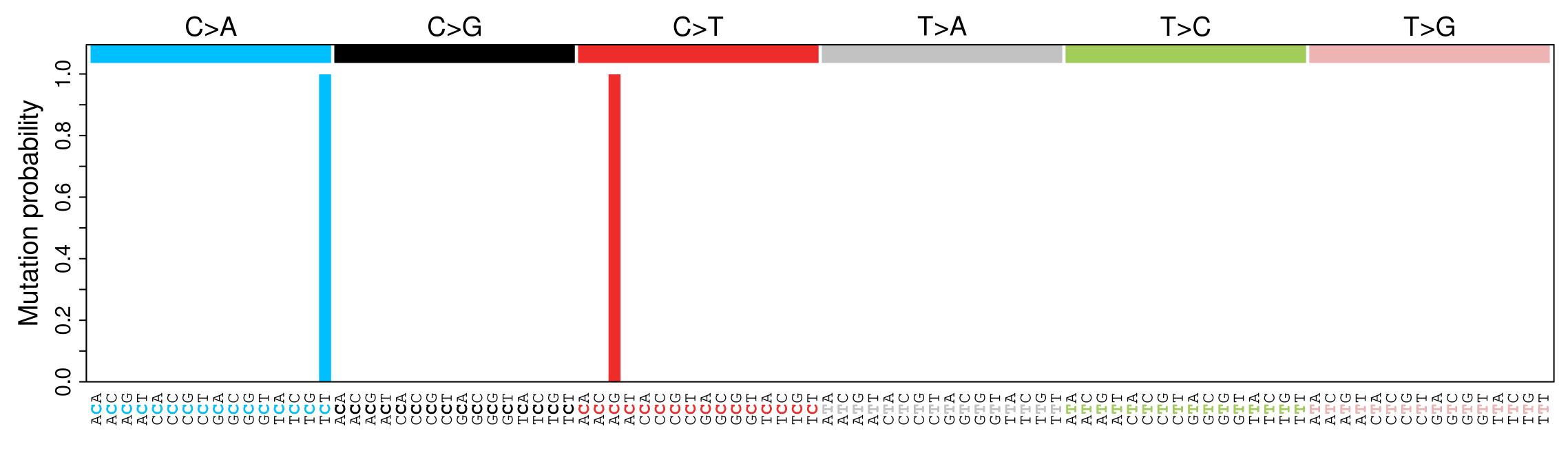




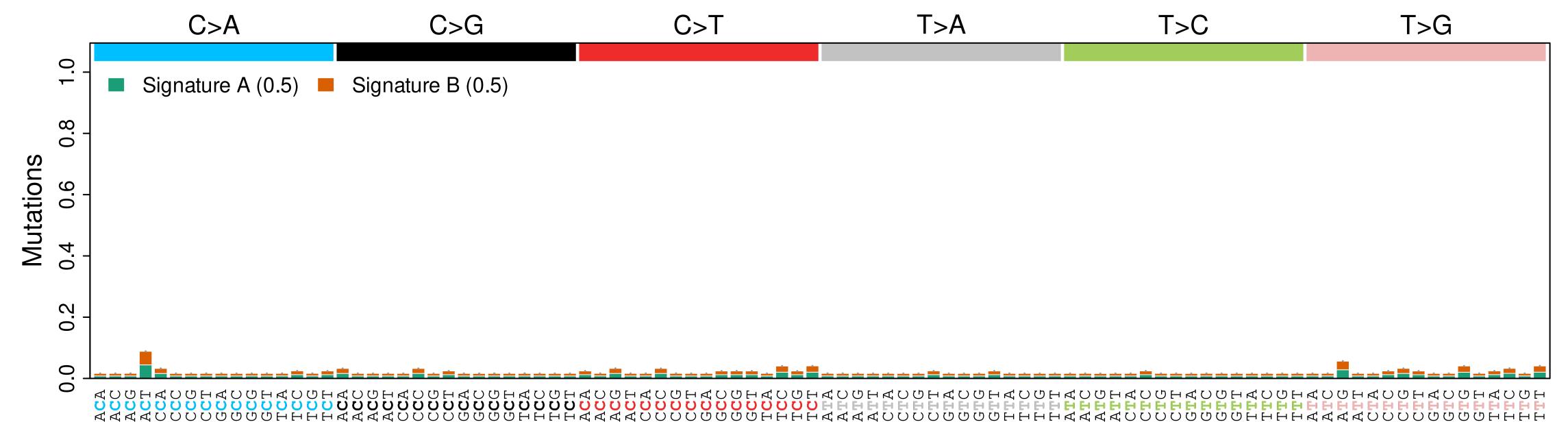






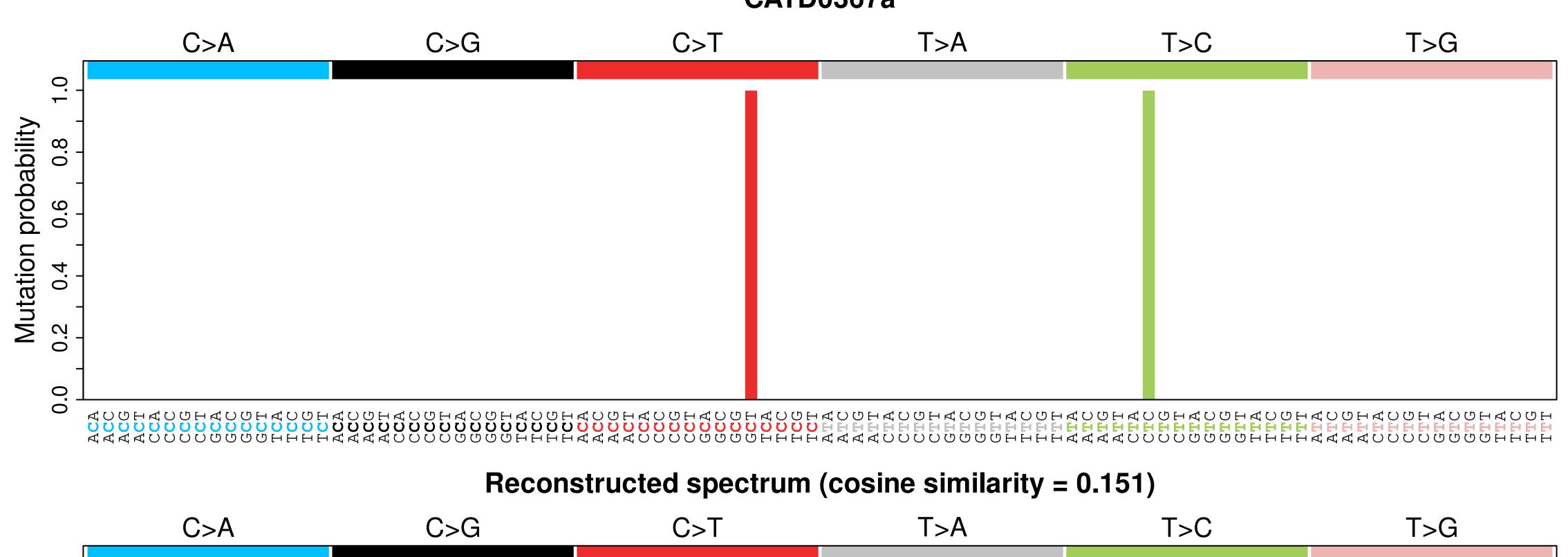


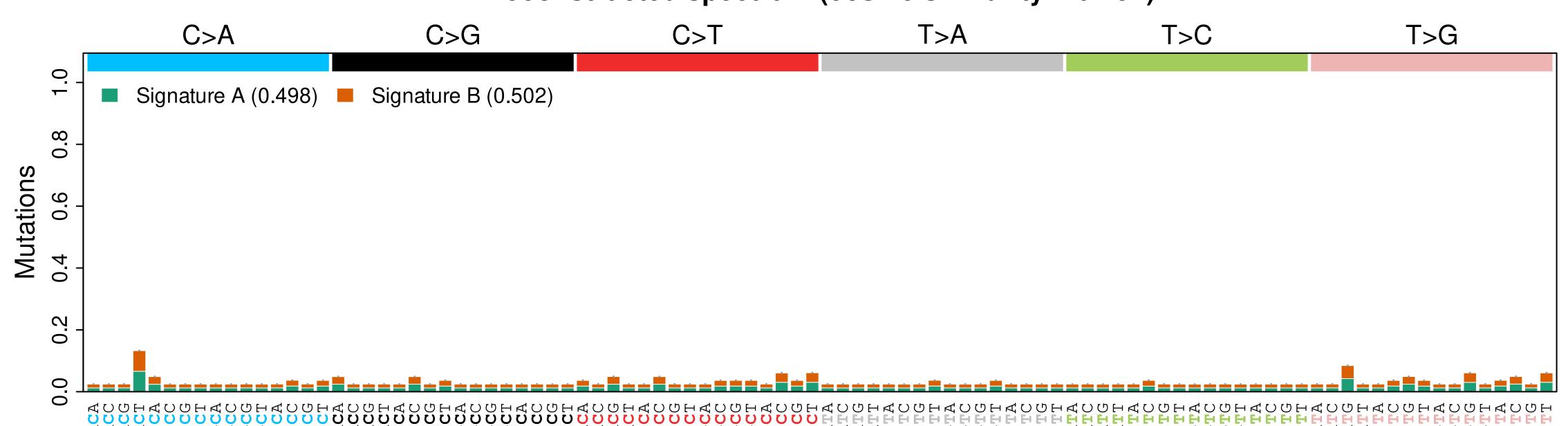
Reconstructed spectrum (cosine similarity = 0.177)



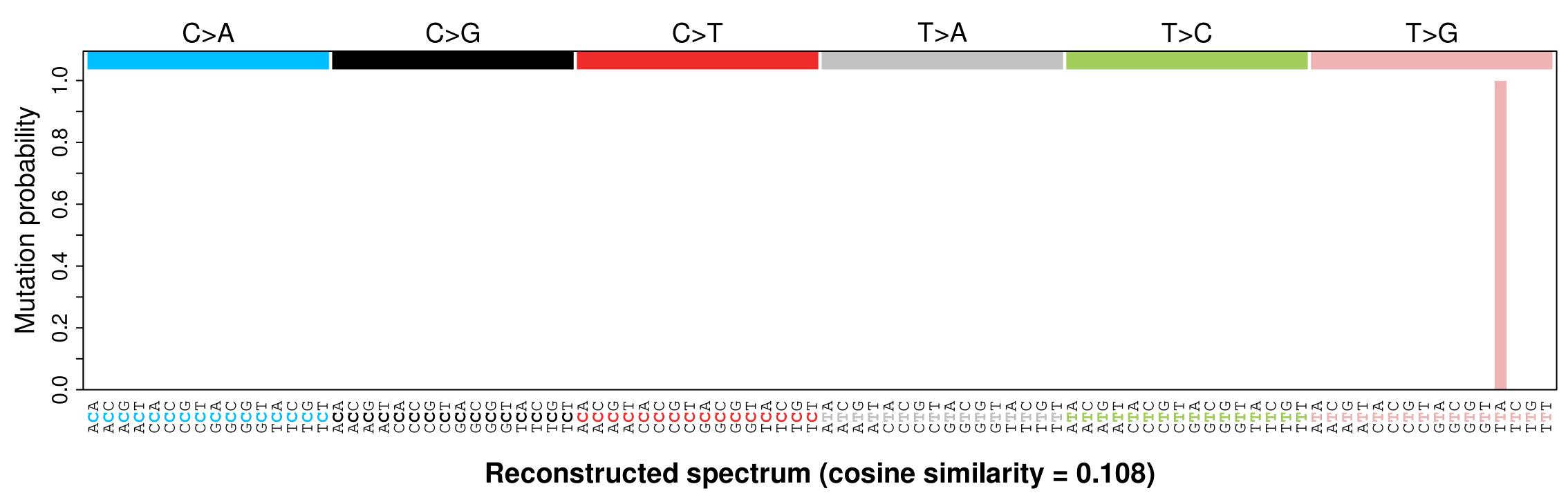
CATD0376a C>G T>C T>G C>A C>T T>A 1.0 Mutation probability 0.8 9.0 0.4 0.2 0.0 **Reconstructed spectrum (cosine similarity = 0.251)** C>A C>G T>A T>C T>G C>T 1.0 Signature A (0.502) Signature B (0.498) 0.8 Mutations 9.0 \mathcal{O} 0

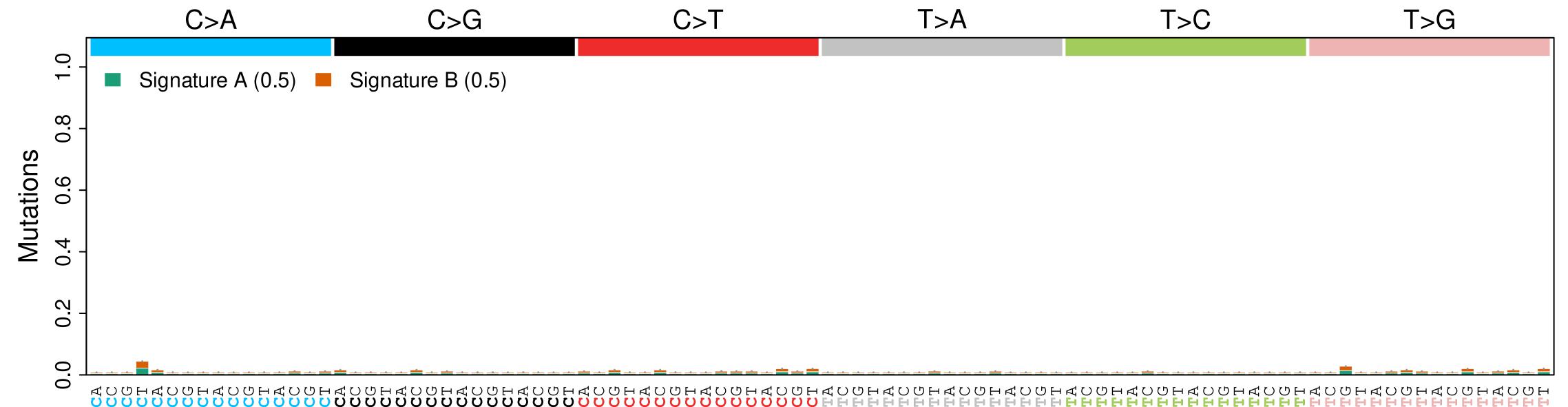




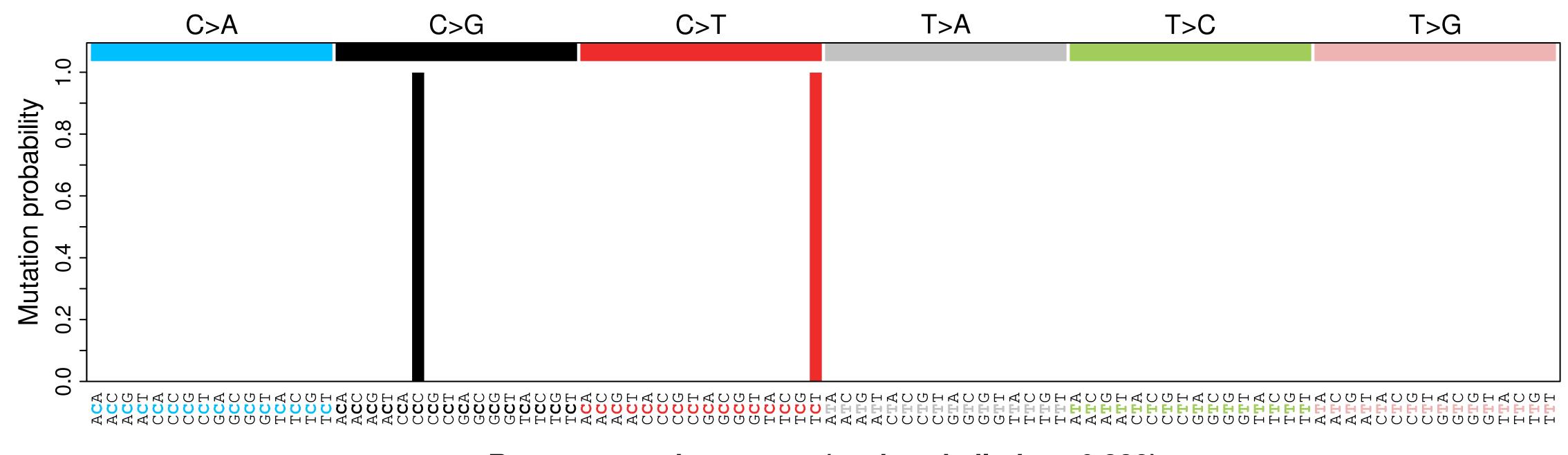


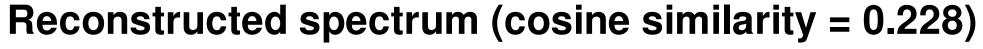


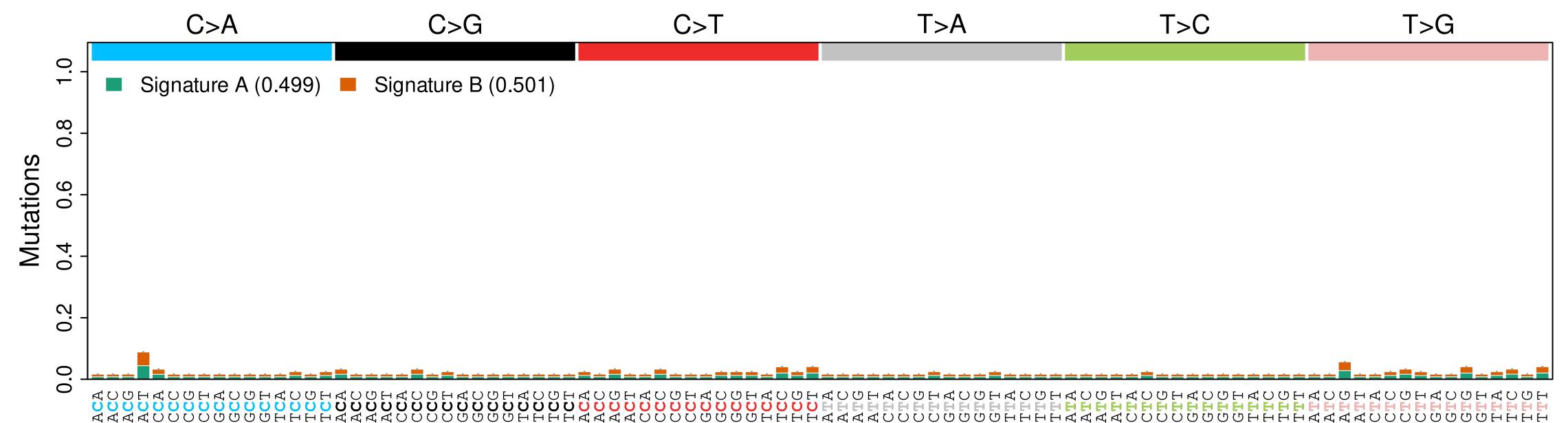




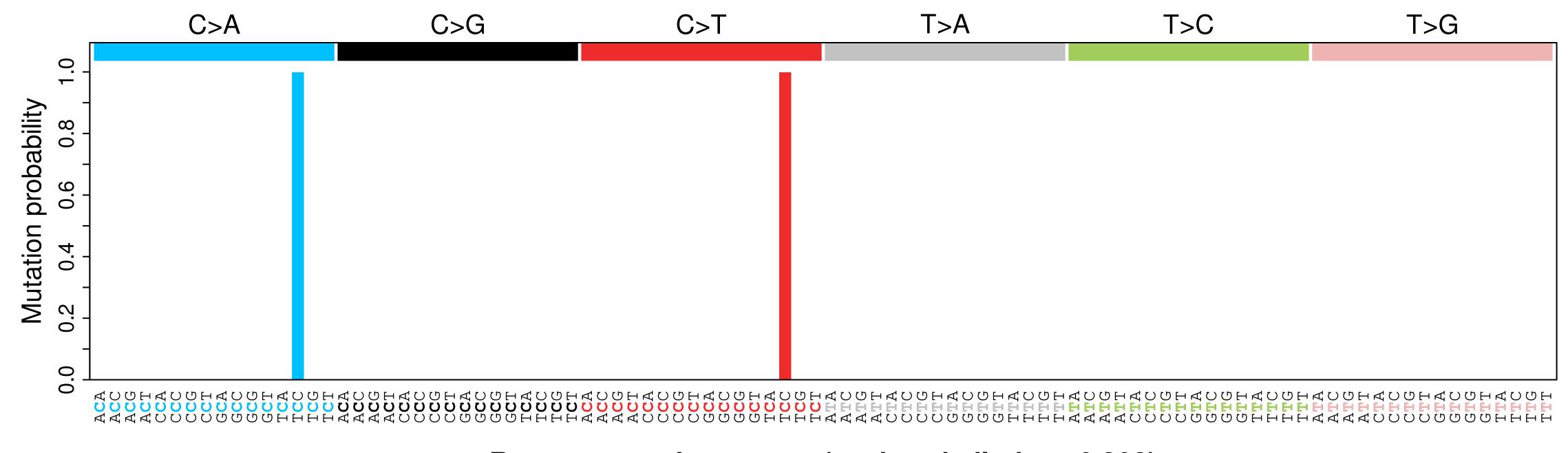




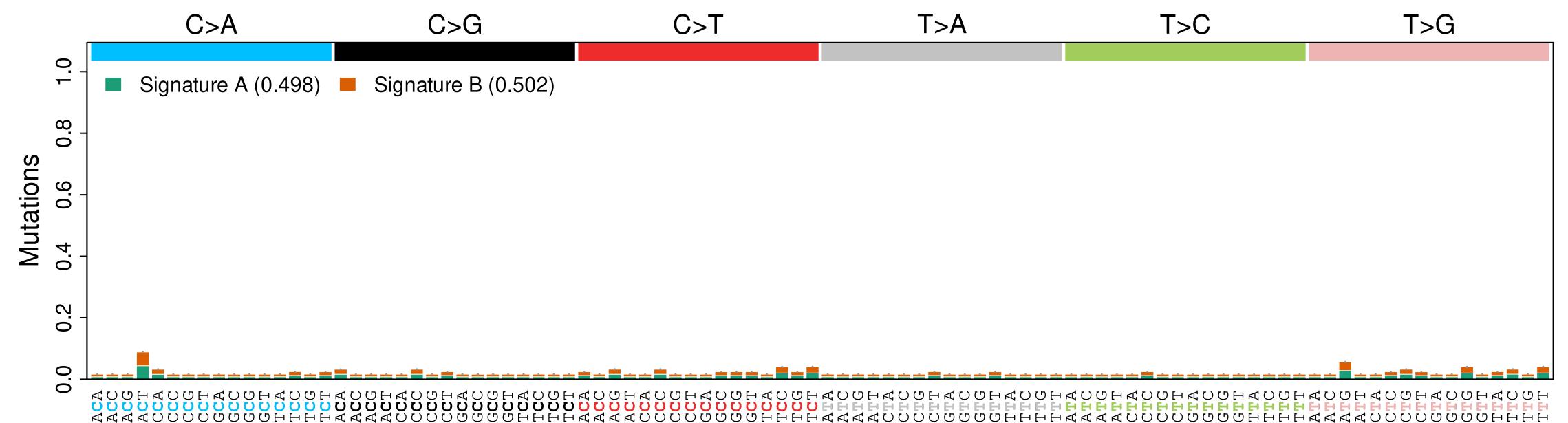








Reconstructed spectrum (cosine similarity = 0.202)



CATD0368a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0 **Reconstructed spectrum (cosine similarity = 0.286)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.501) Signature B (0.499) 5 Mutations 5 0 0