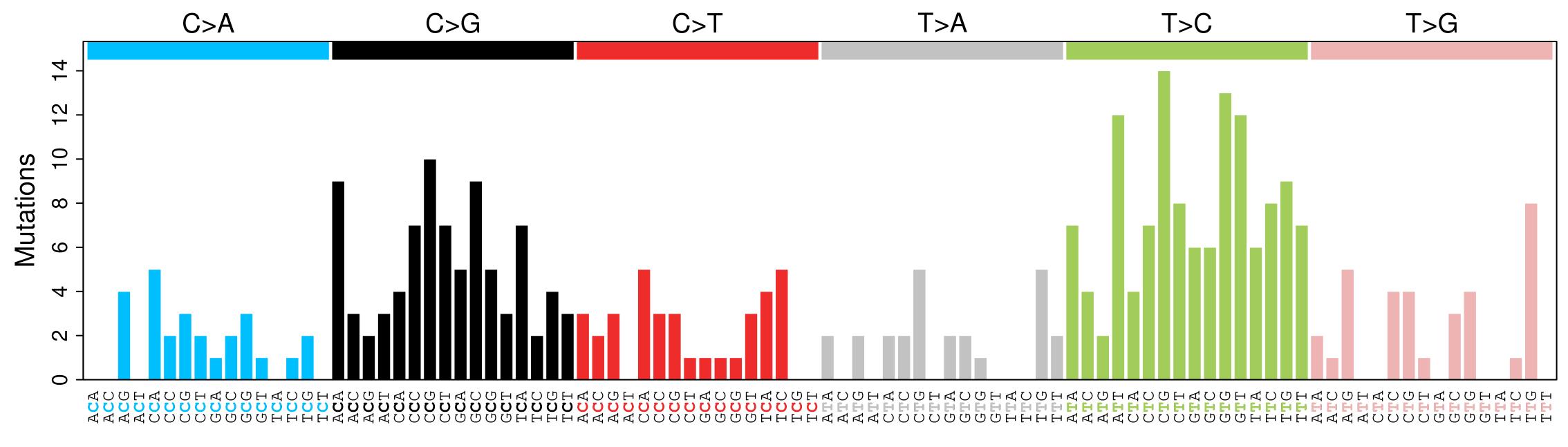
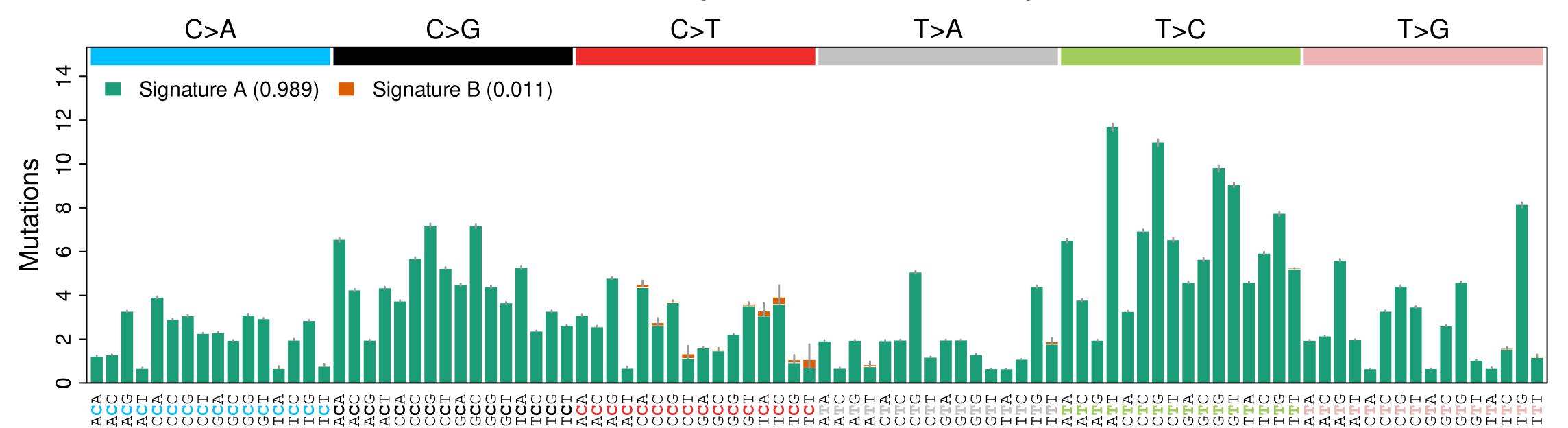
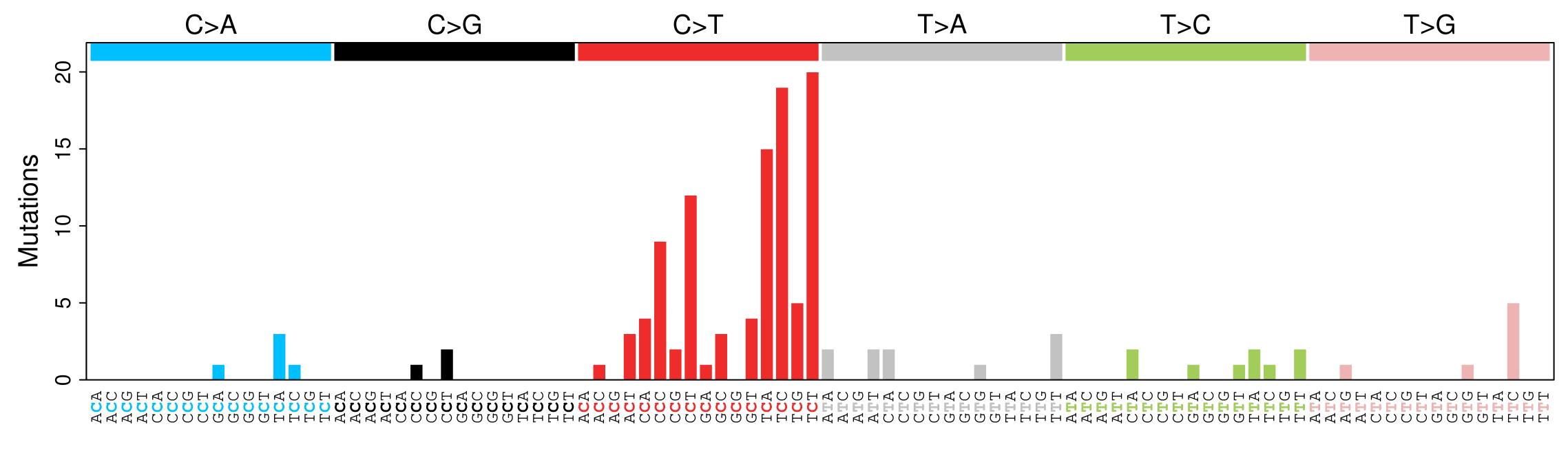
CATD292a (327 mutations)



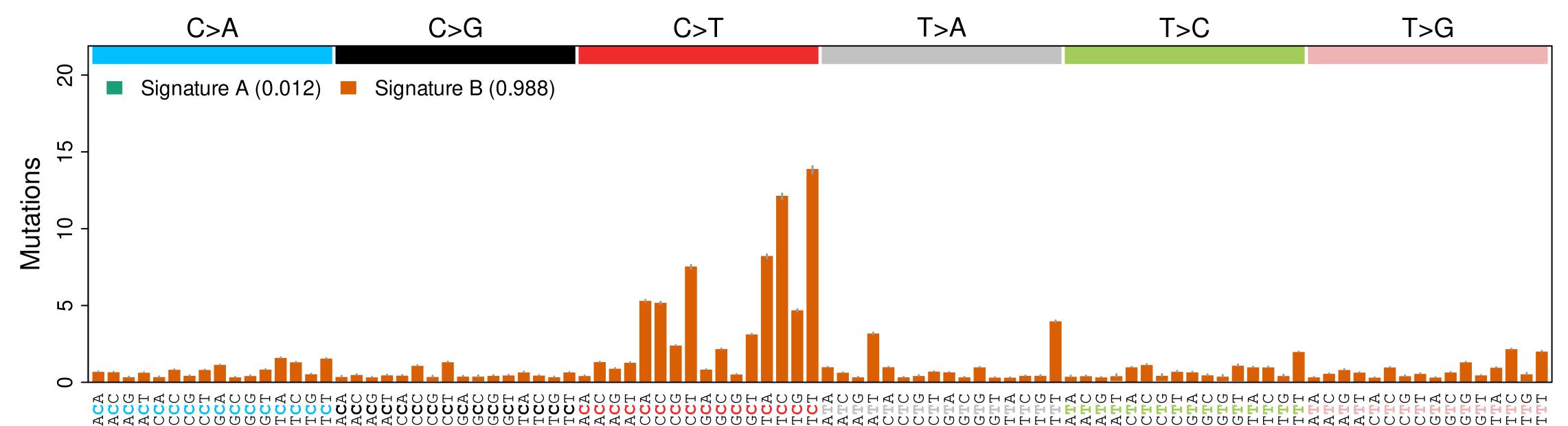
Reconstructed spectrum (cosine similarity = 0.975)



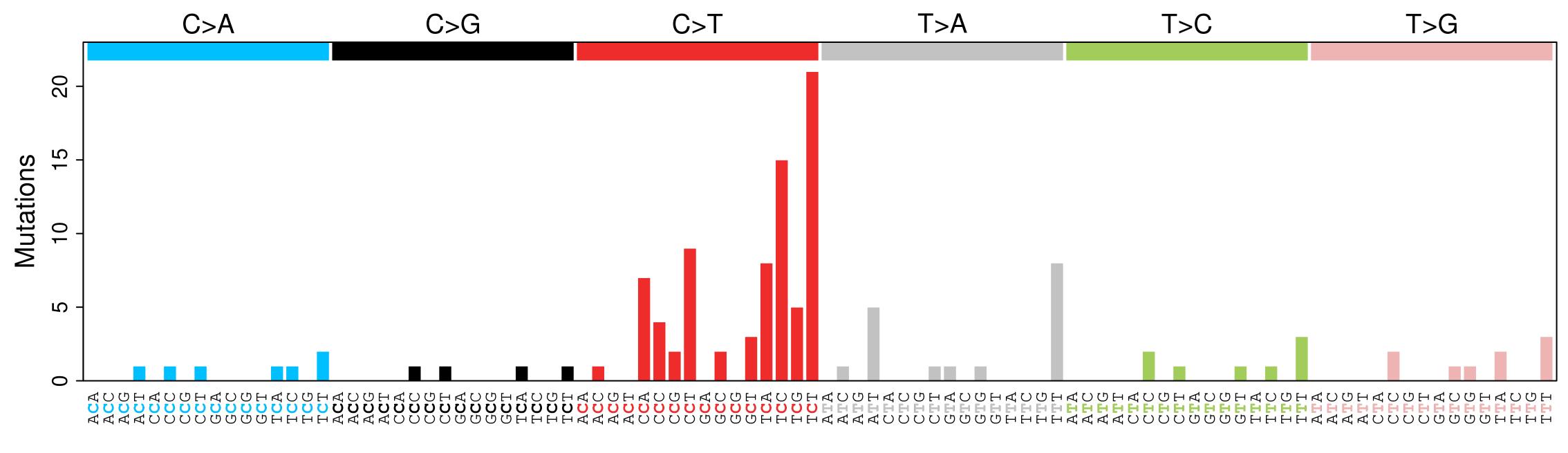
CATD0653a (132 mutations)



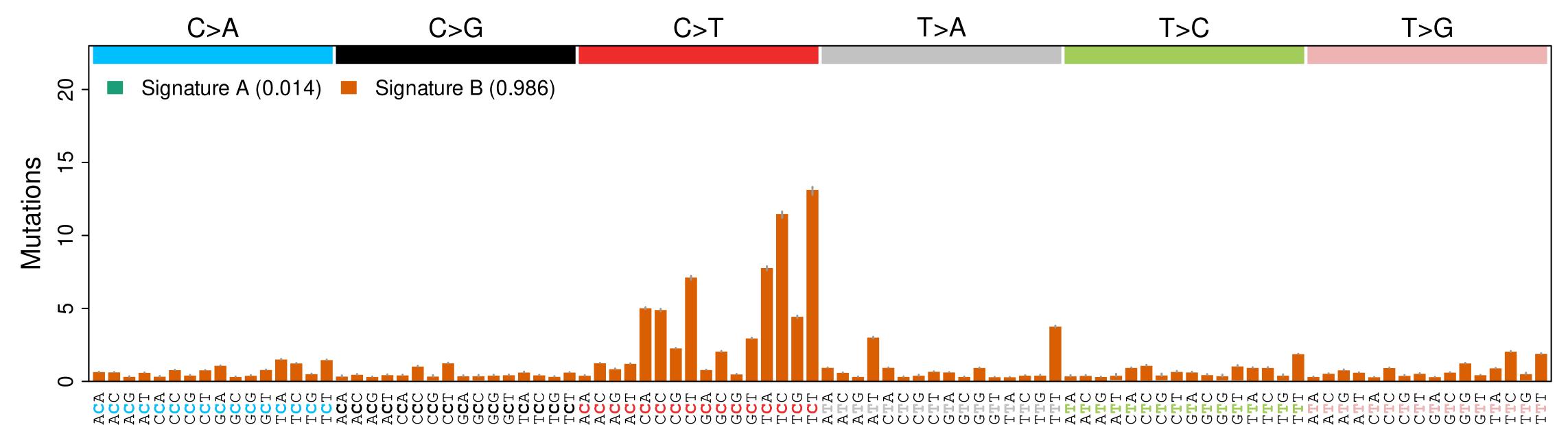
Reconstructed spectrum (cosine similarity = 0.958)



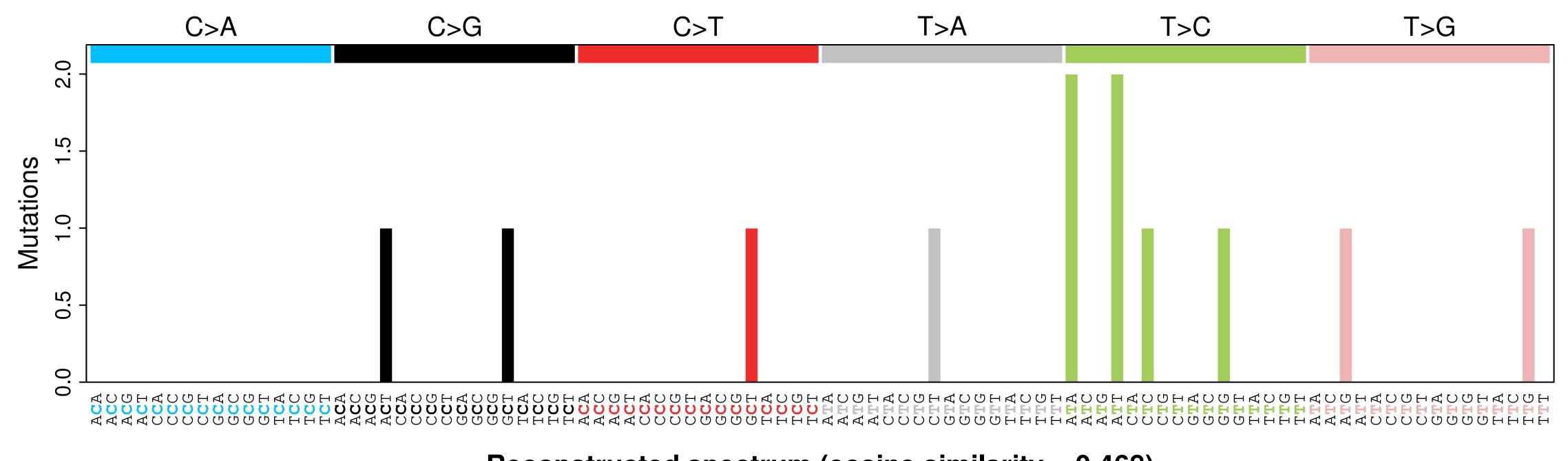
CATD294a (122 mutations)



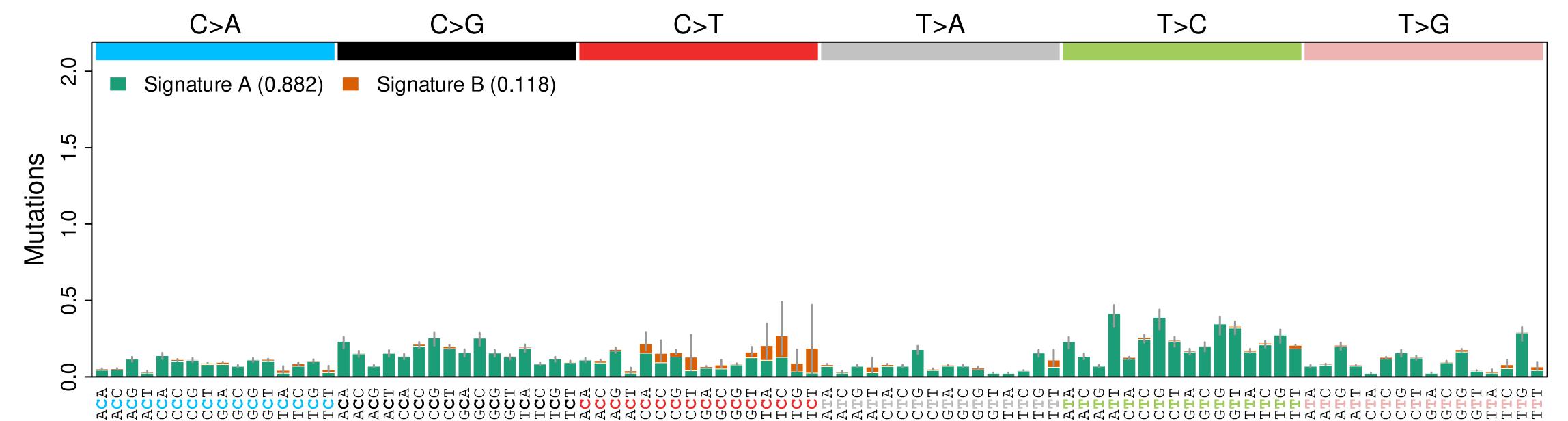
Reconstructed spectrum (cosine similarity = 0.961)



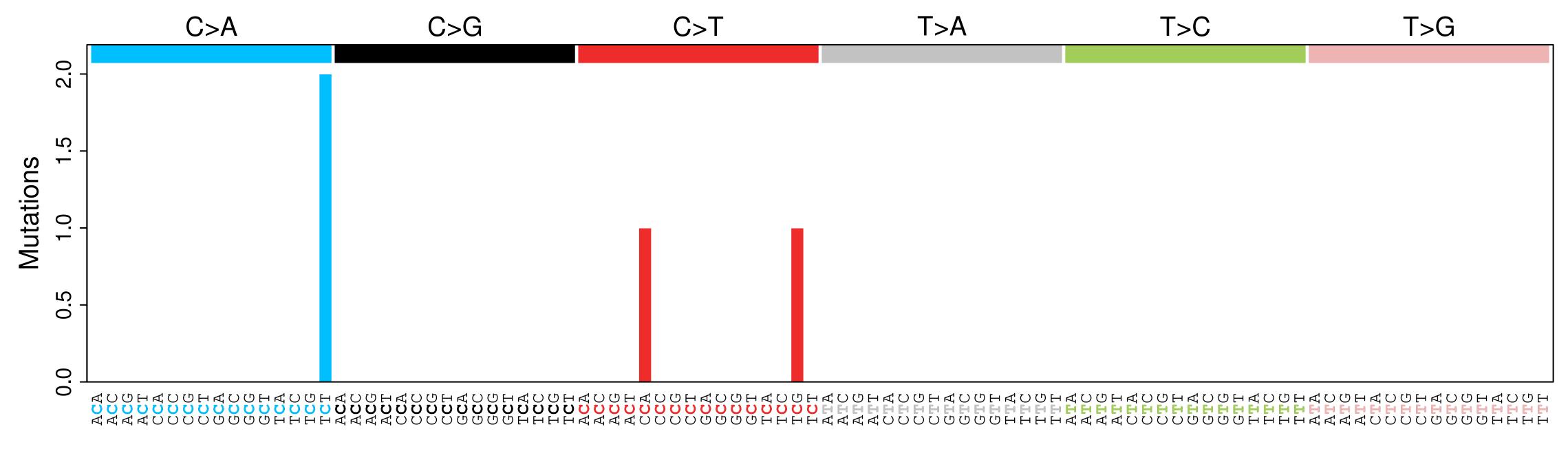
CATD283a (12 mutations)



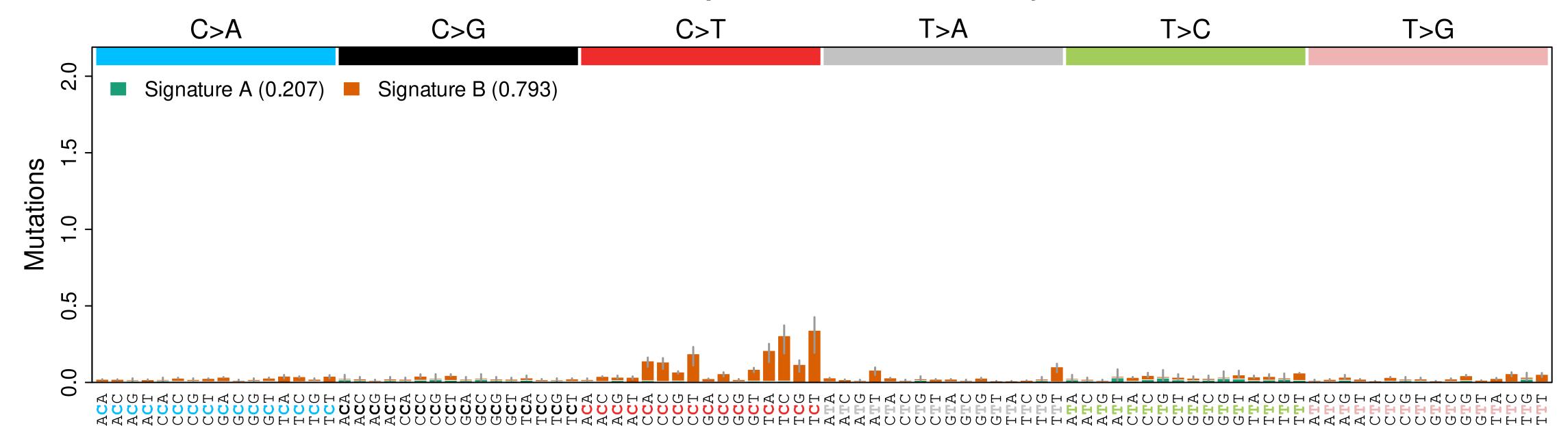
Reconstructed spectrum (cosine similarity = 0.468)



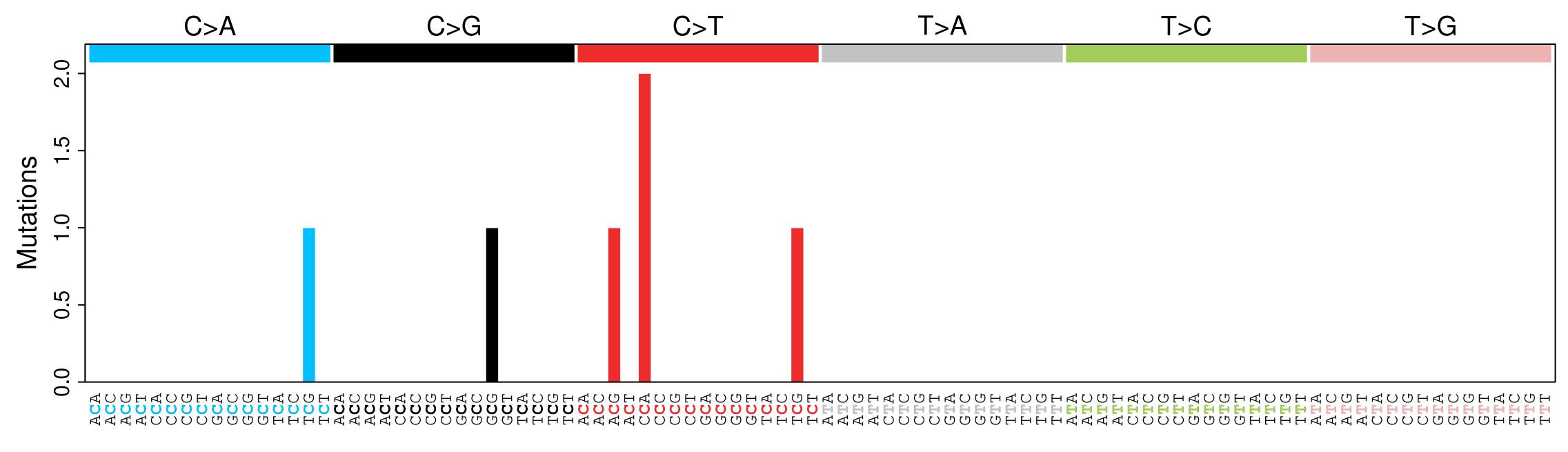
CATD0645a (4 mutations)



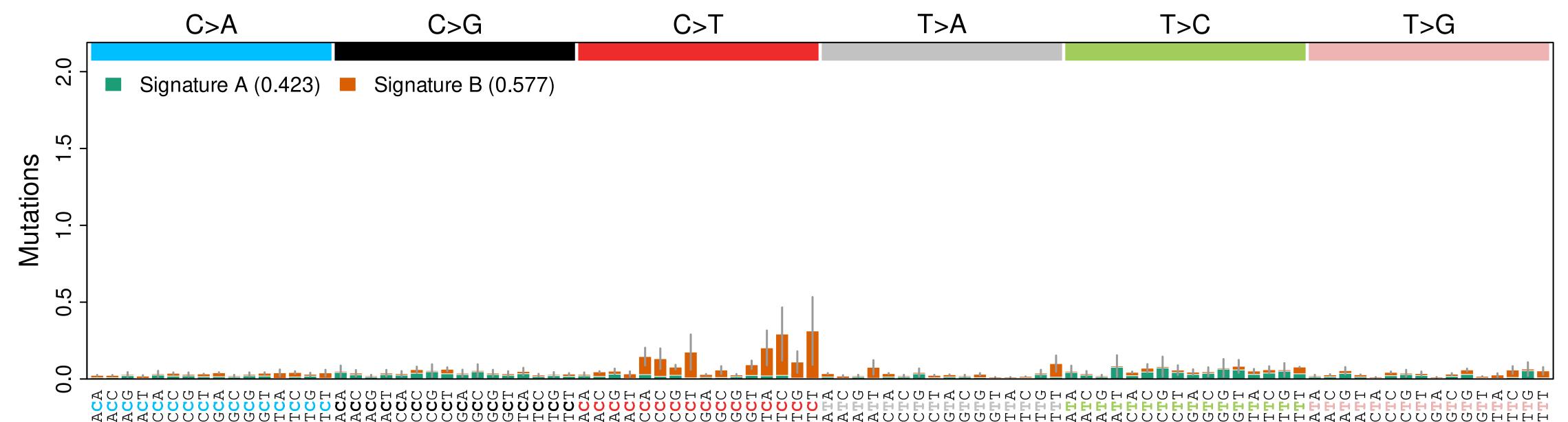
Reconstructed spectrum (cosine similarity = 0.208)

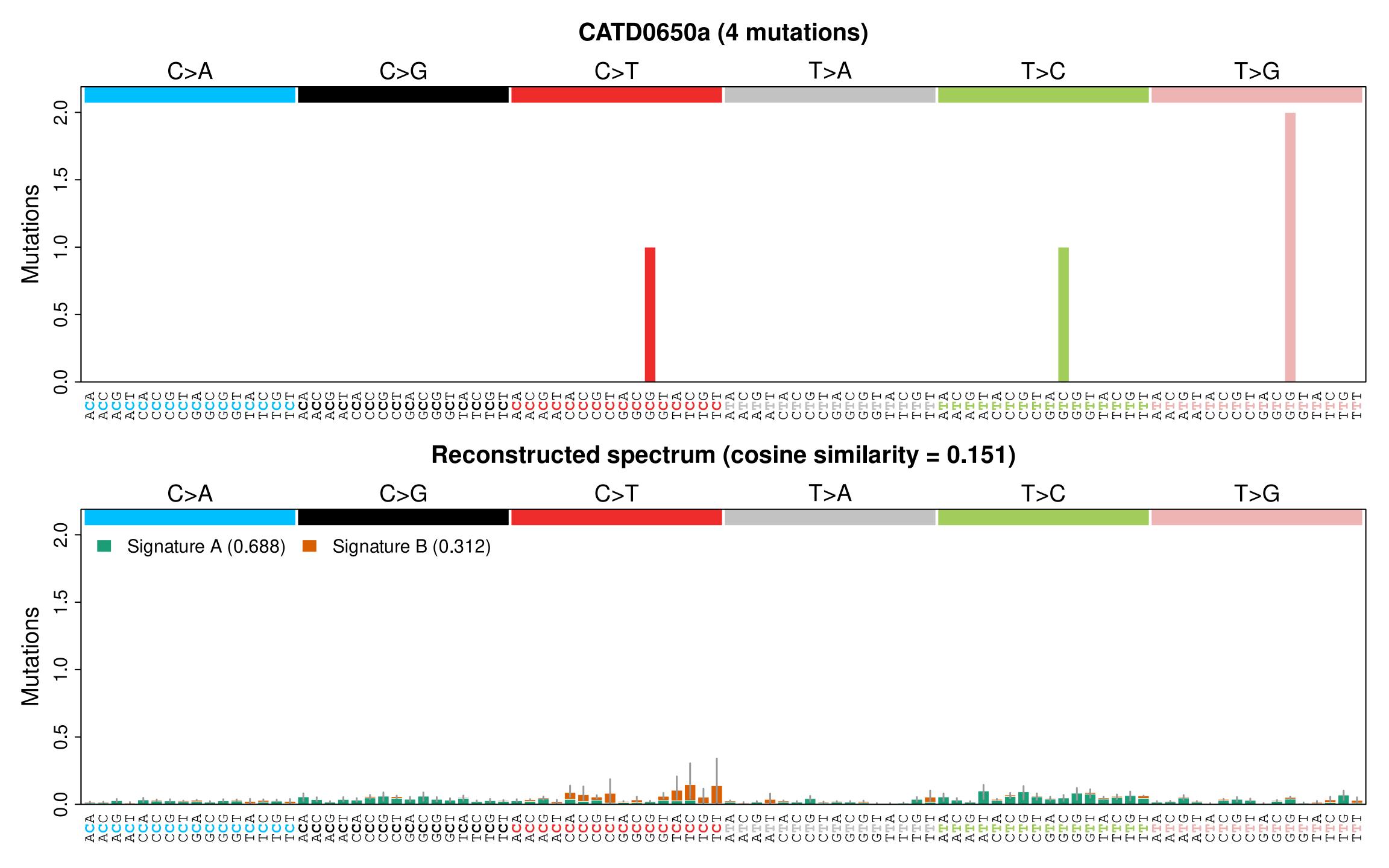


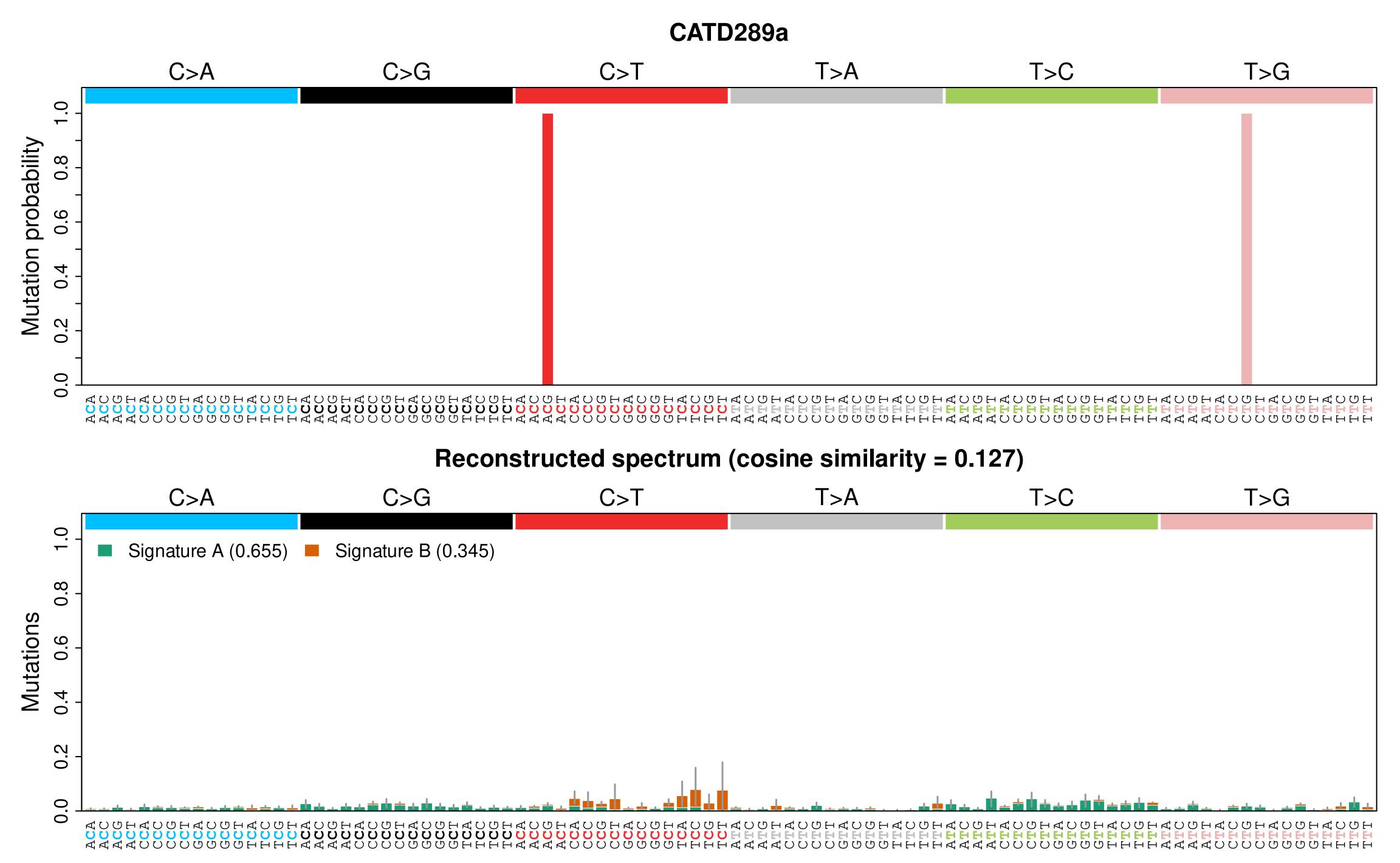
CATD0670a (6 mutations)



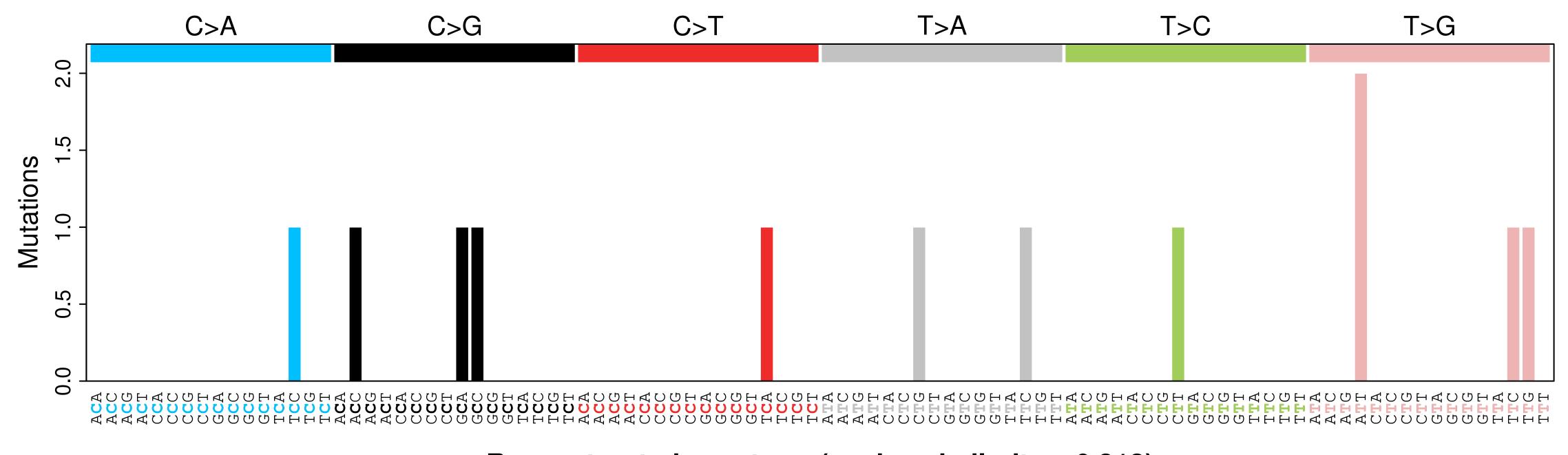
Reconstructed spectrum (cosine similarity = 0.264)

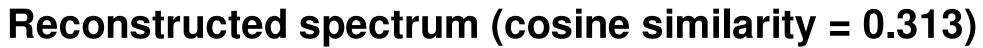


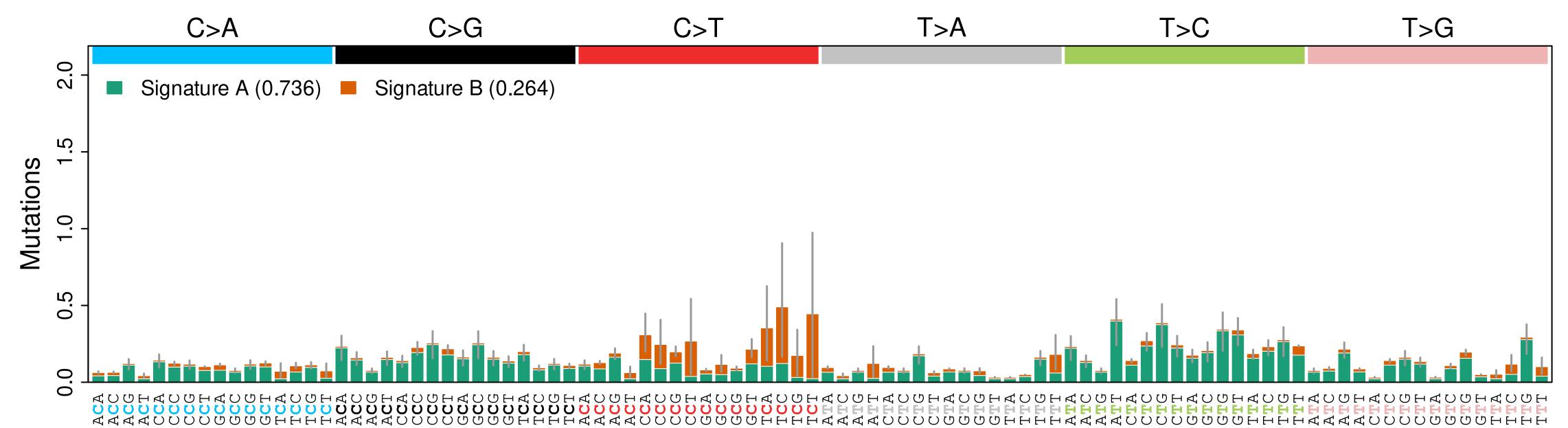




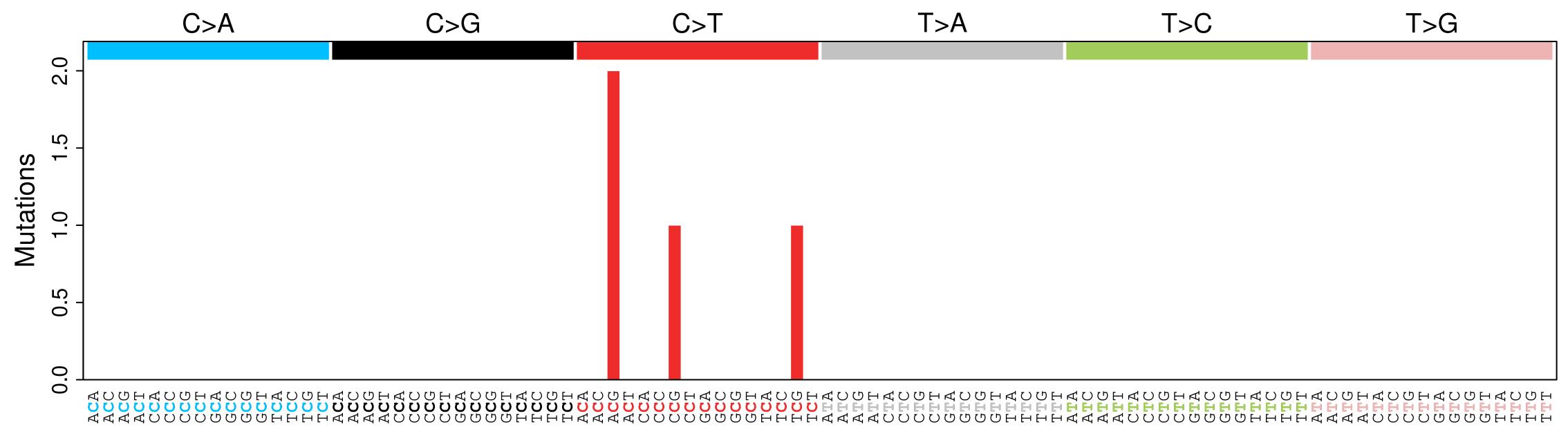
CATD0144a (12 mutations)



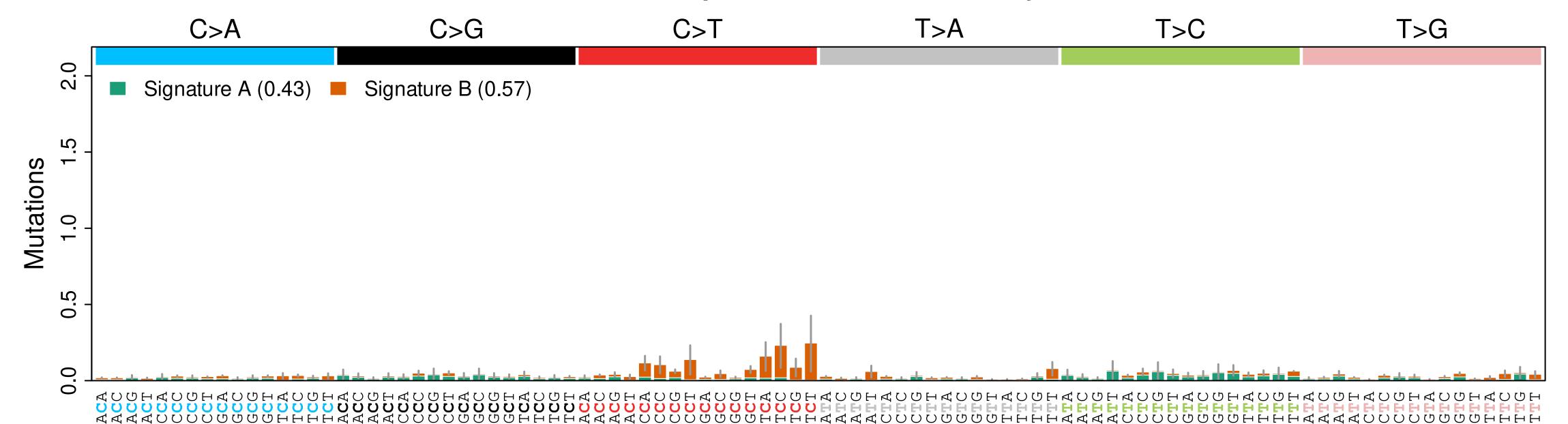




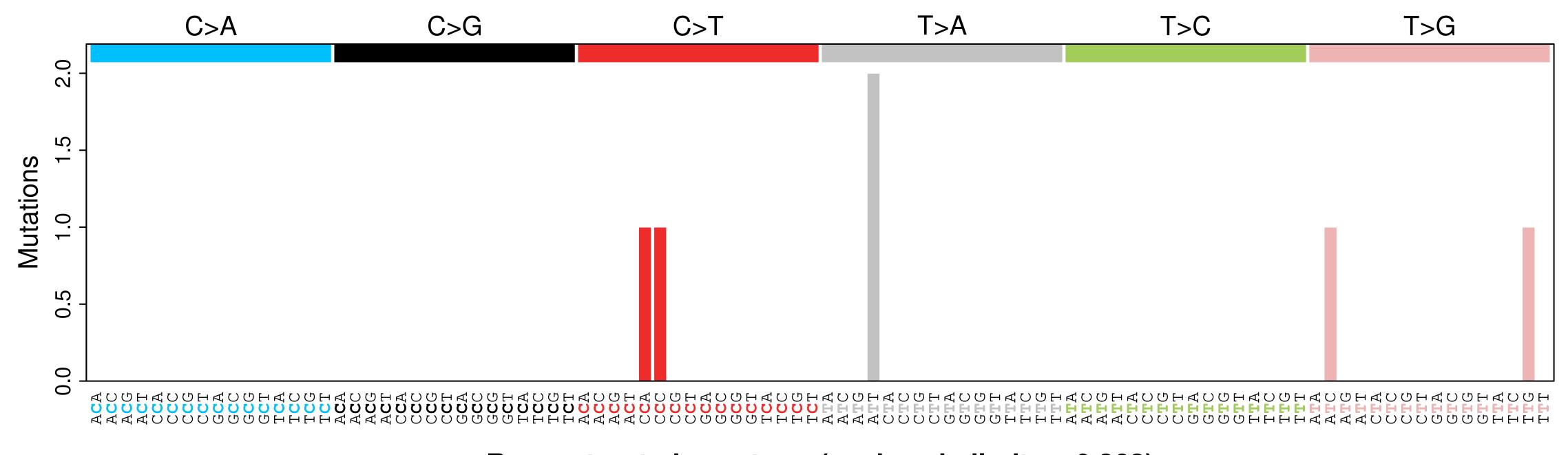
CATD293a (4 mutations)

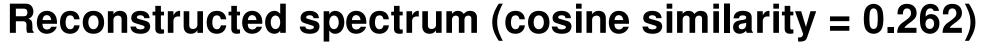


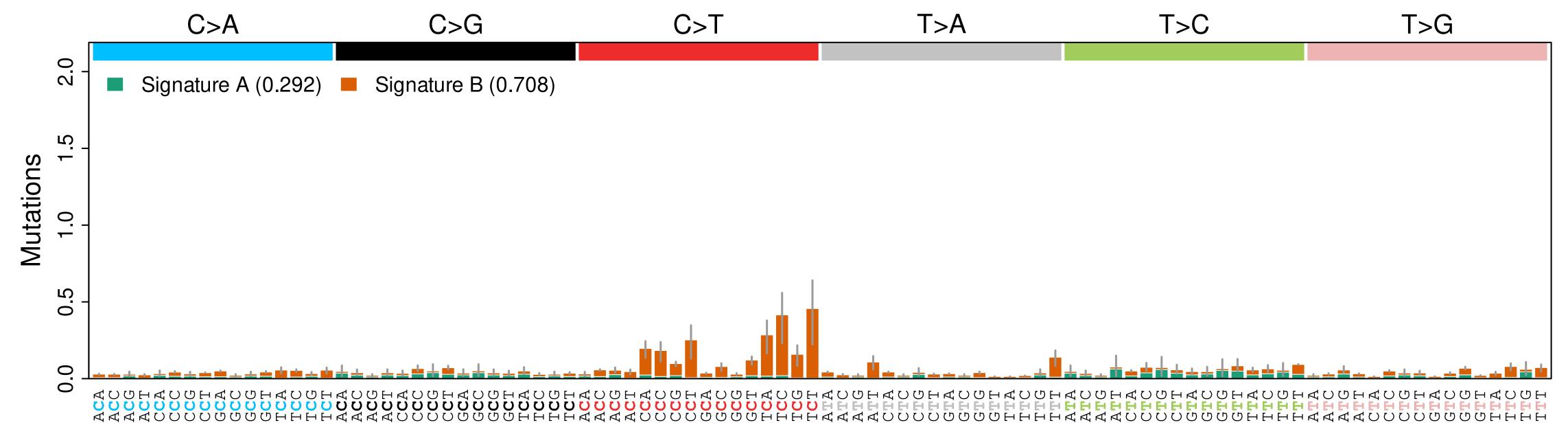
Reconstructed spectrum (cosine similarity = 0.169)



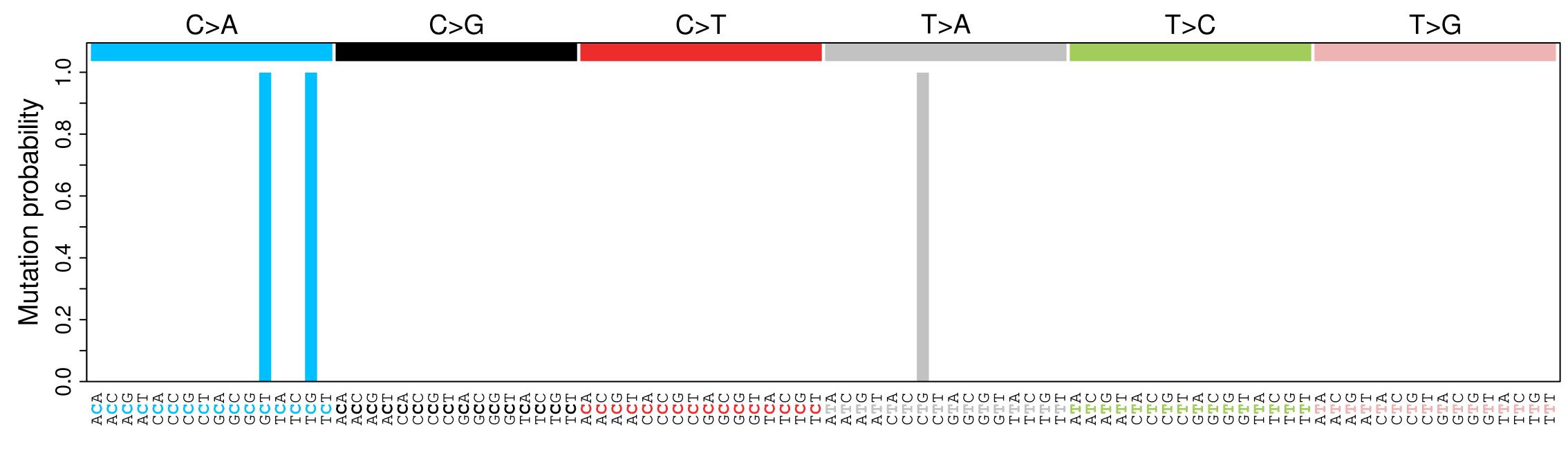
CATD0668a (6 mutations)



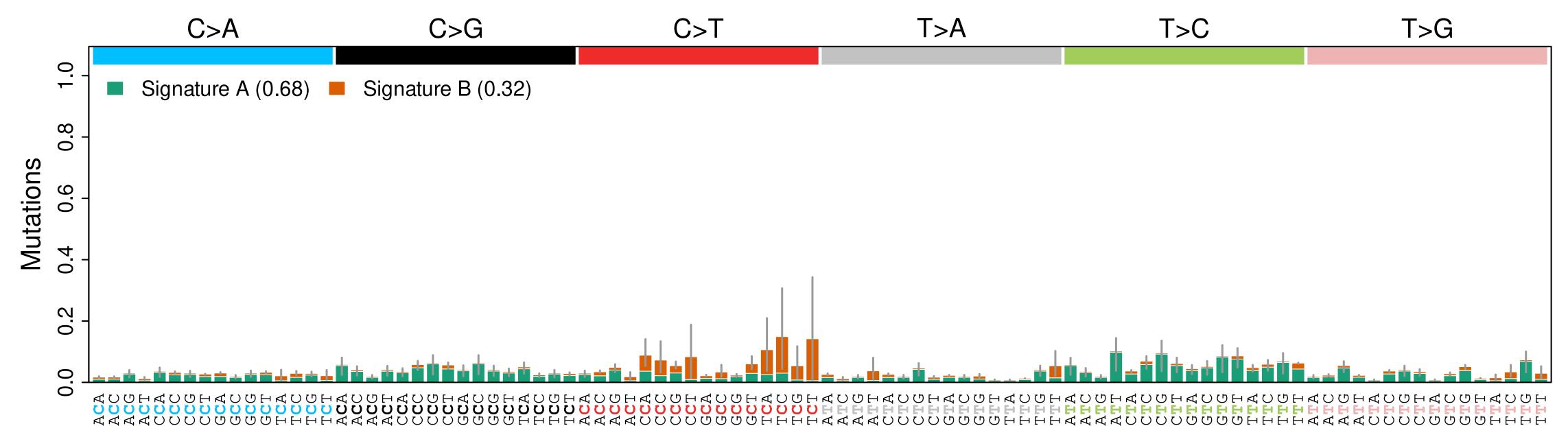




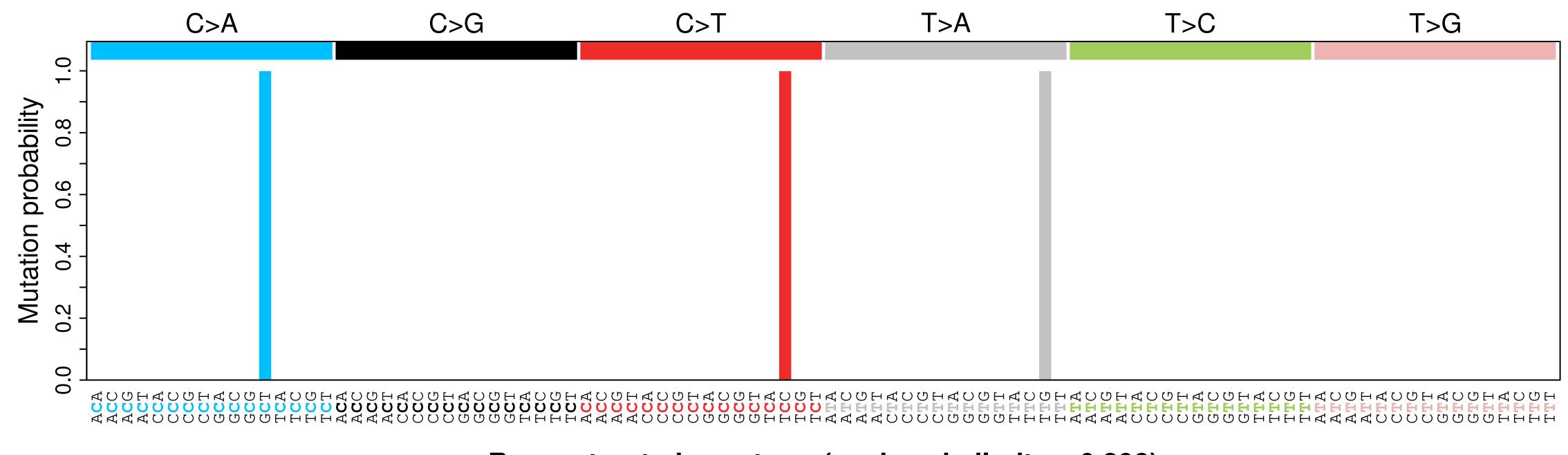
CATD0146a

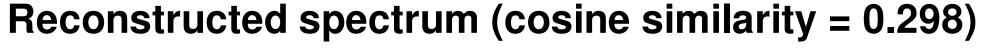


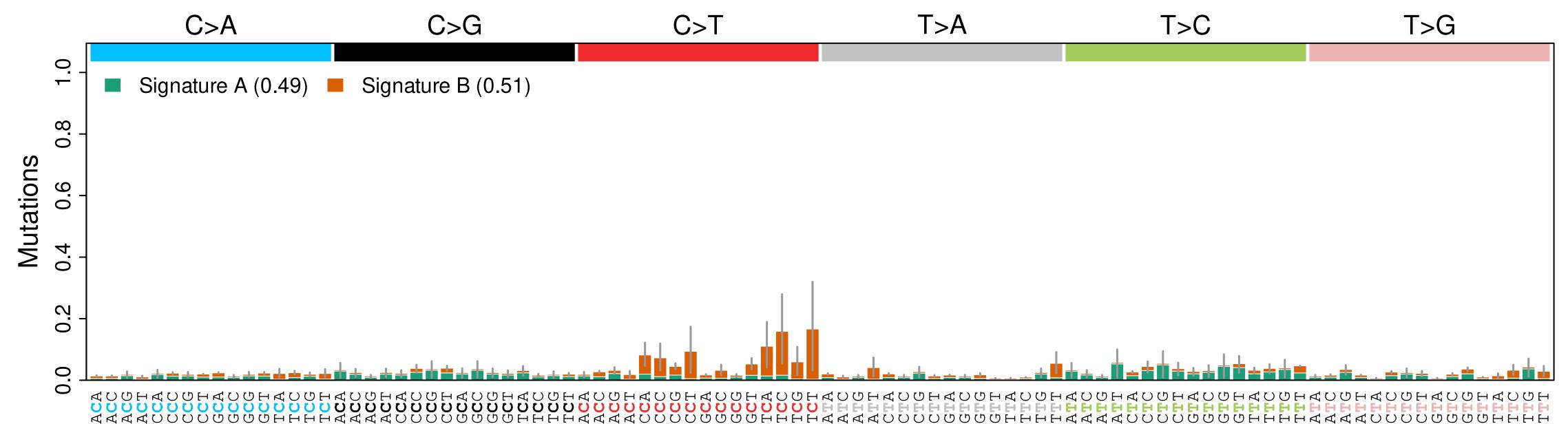




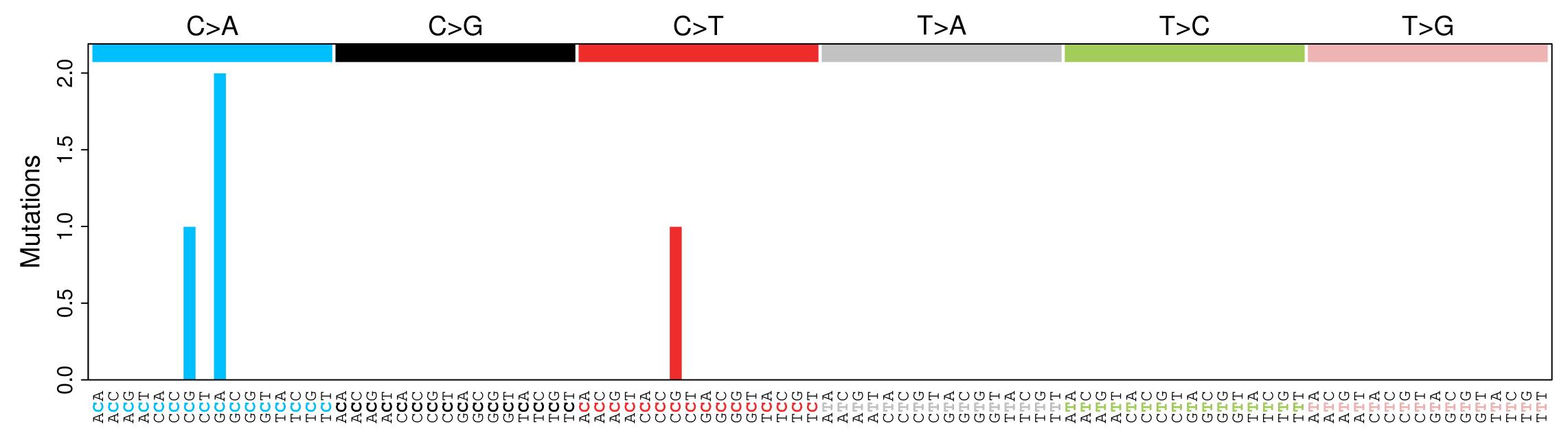
CATD0641a



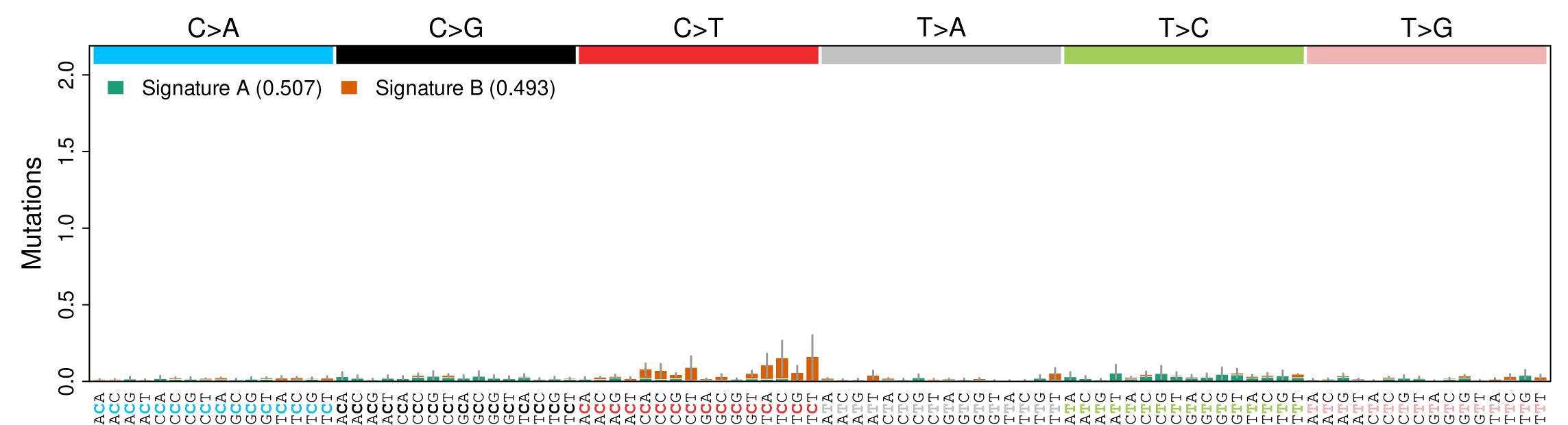




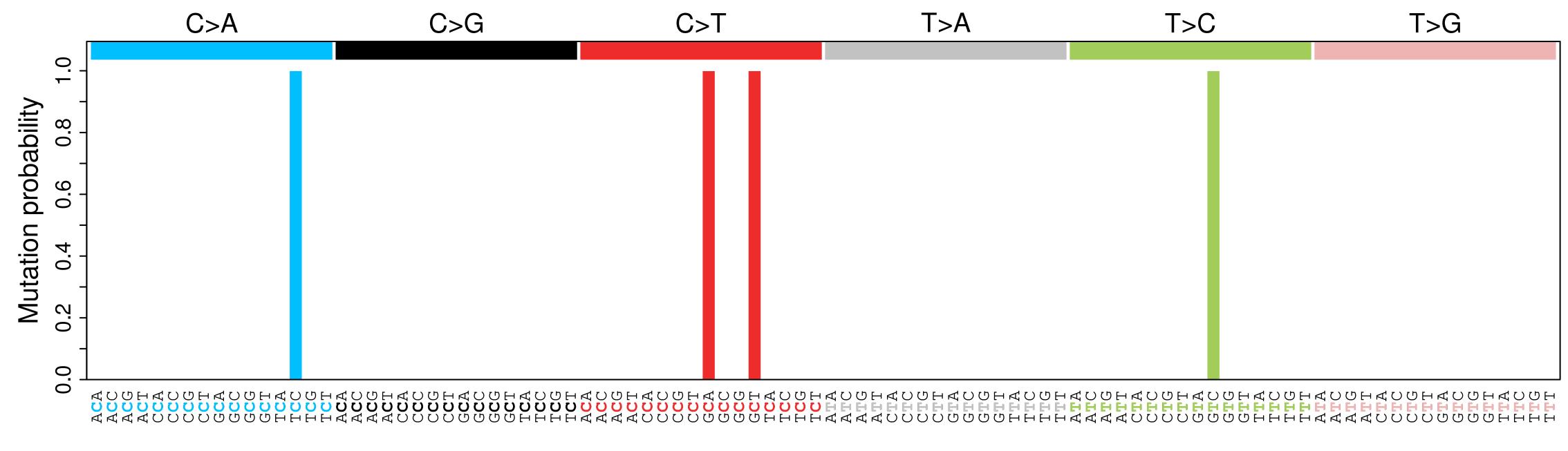
CATD0143a (4 mutations)



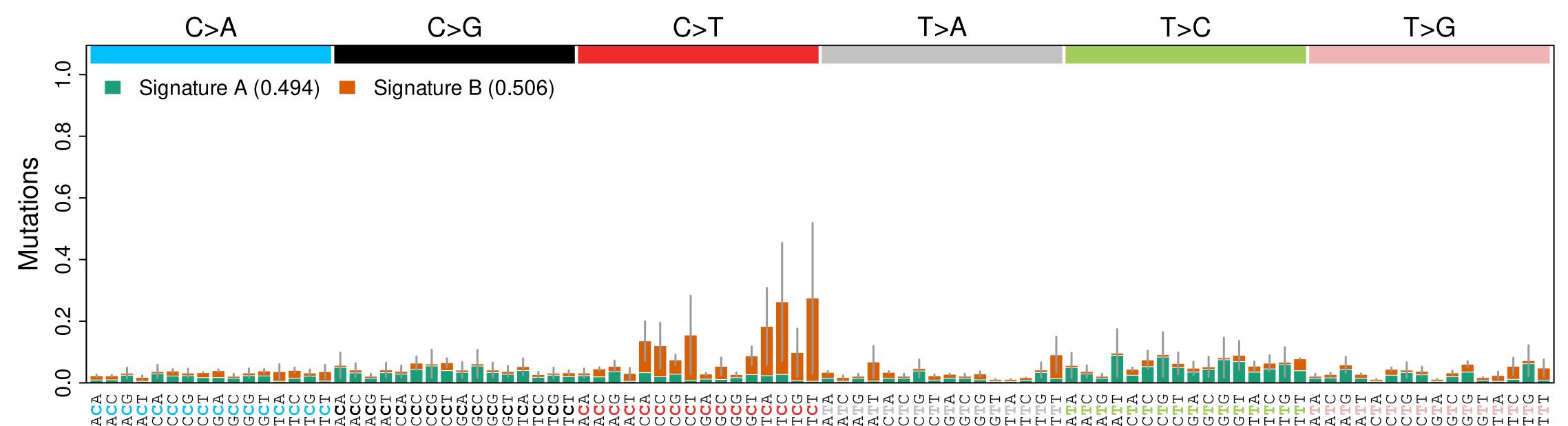
Reconstructed spectrum (cosine similarity = 0.115)



CATD0632a

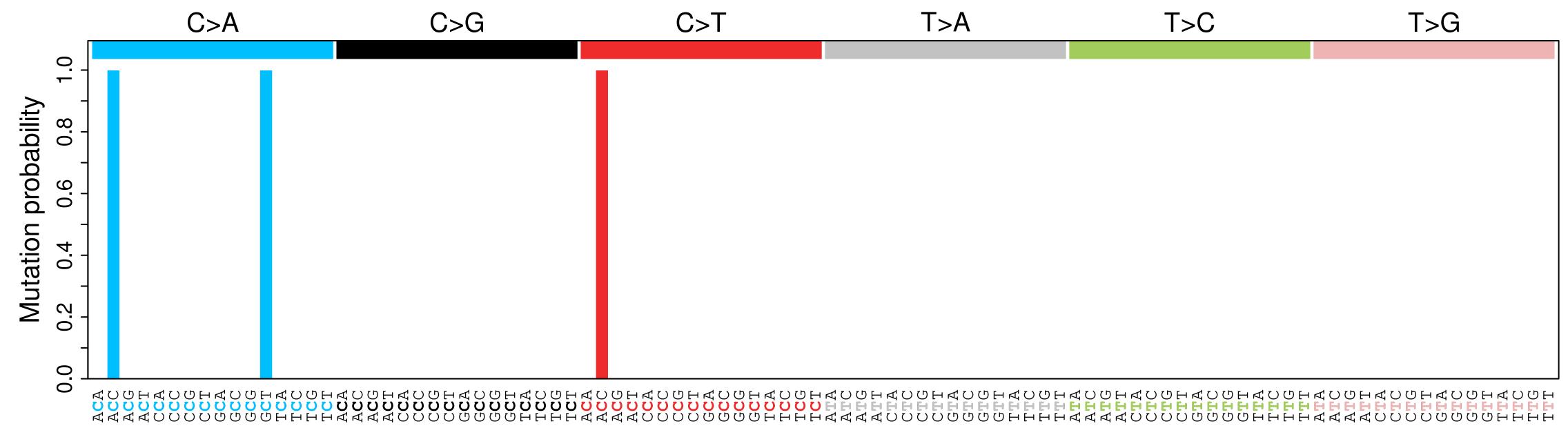




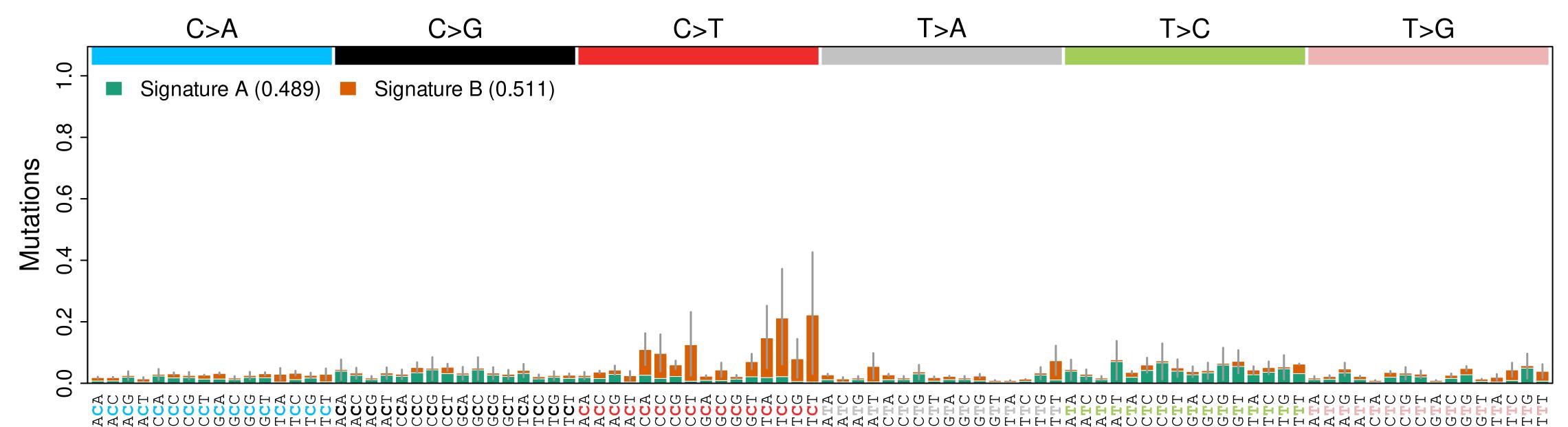


CATD0633a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 Mutations 0.0 **Reconstructed spectrum (cosine similarity = 0.052)** C>A T>G C>G T>A T>C C>T 2.0 Signature A (0.453) Signature B (0.547) 5 Mutations 5 0 0

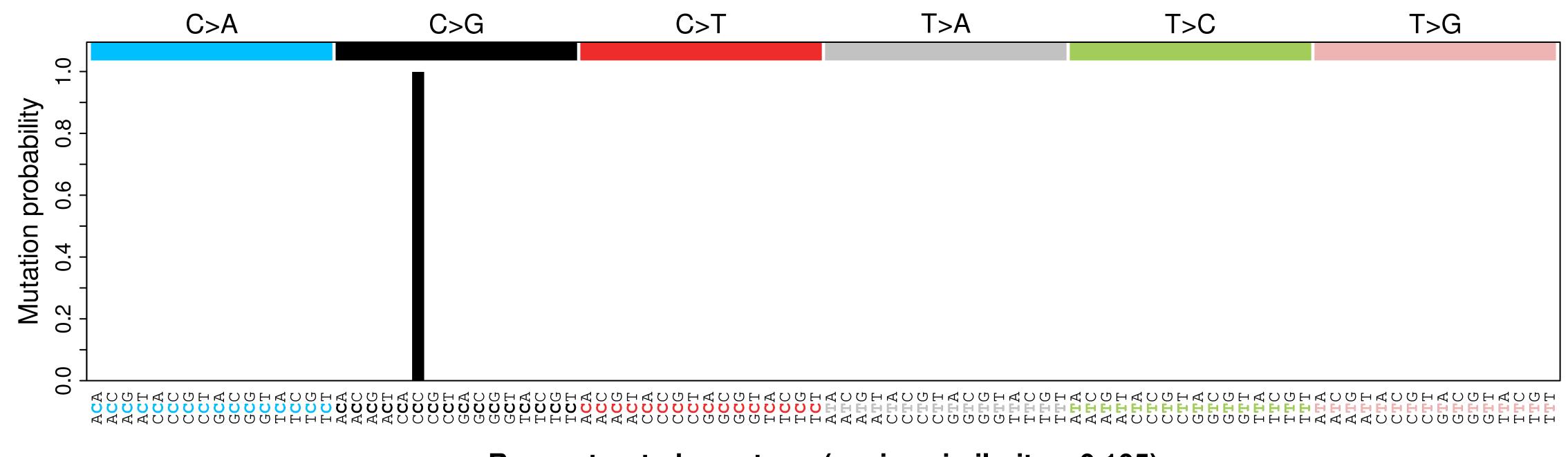
CATD0157a

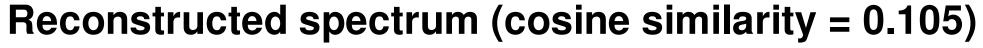


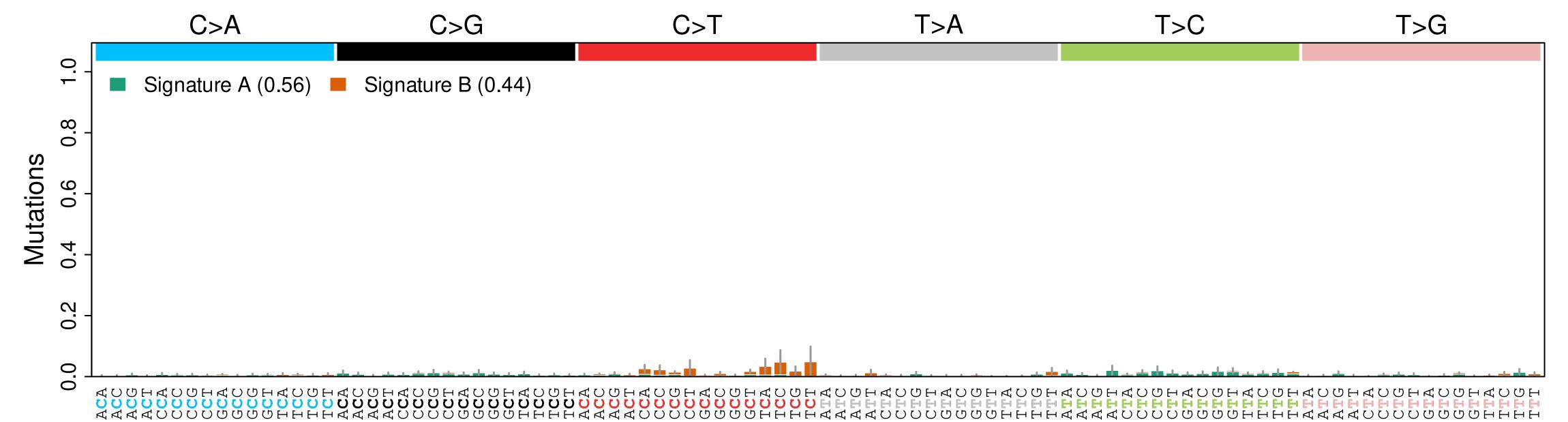
Reconstructed spectrum (cosine similarity = 0.092)



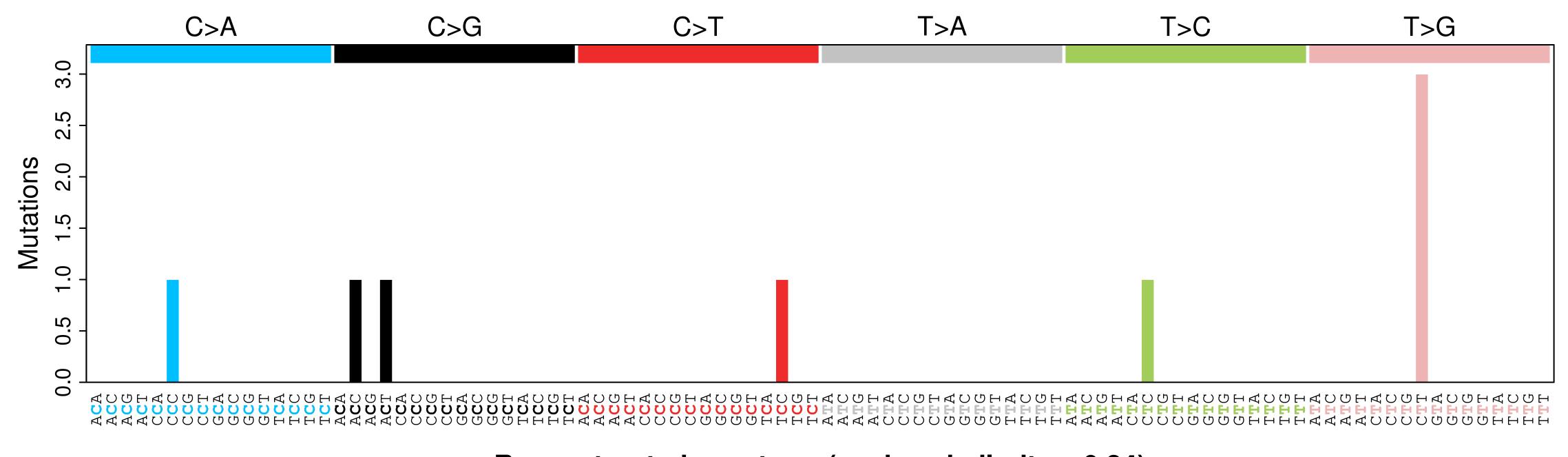




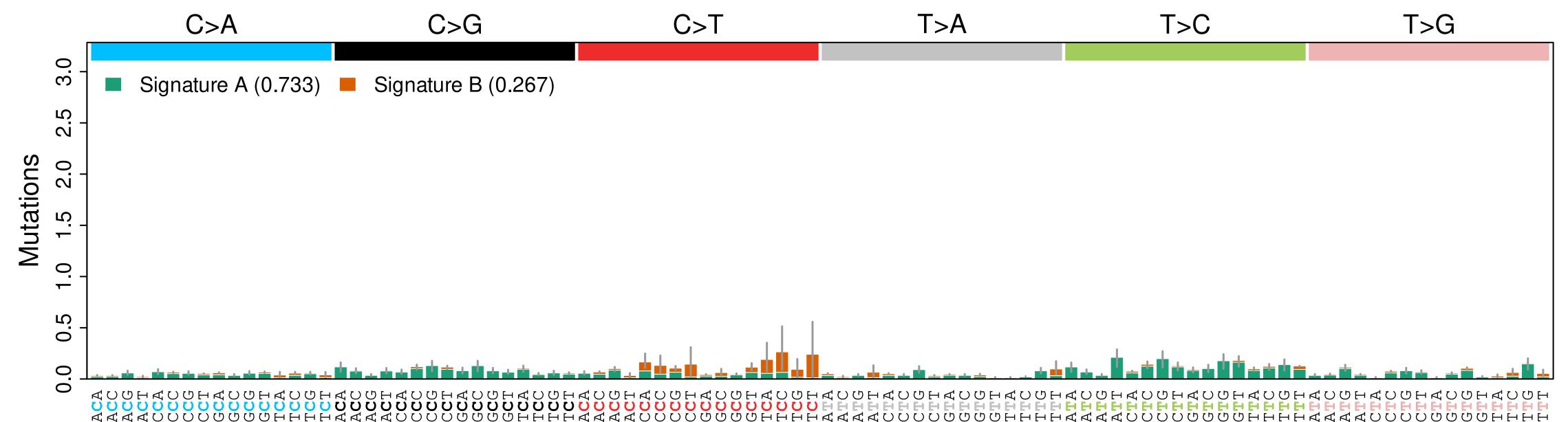


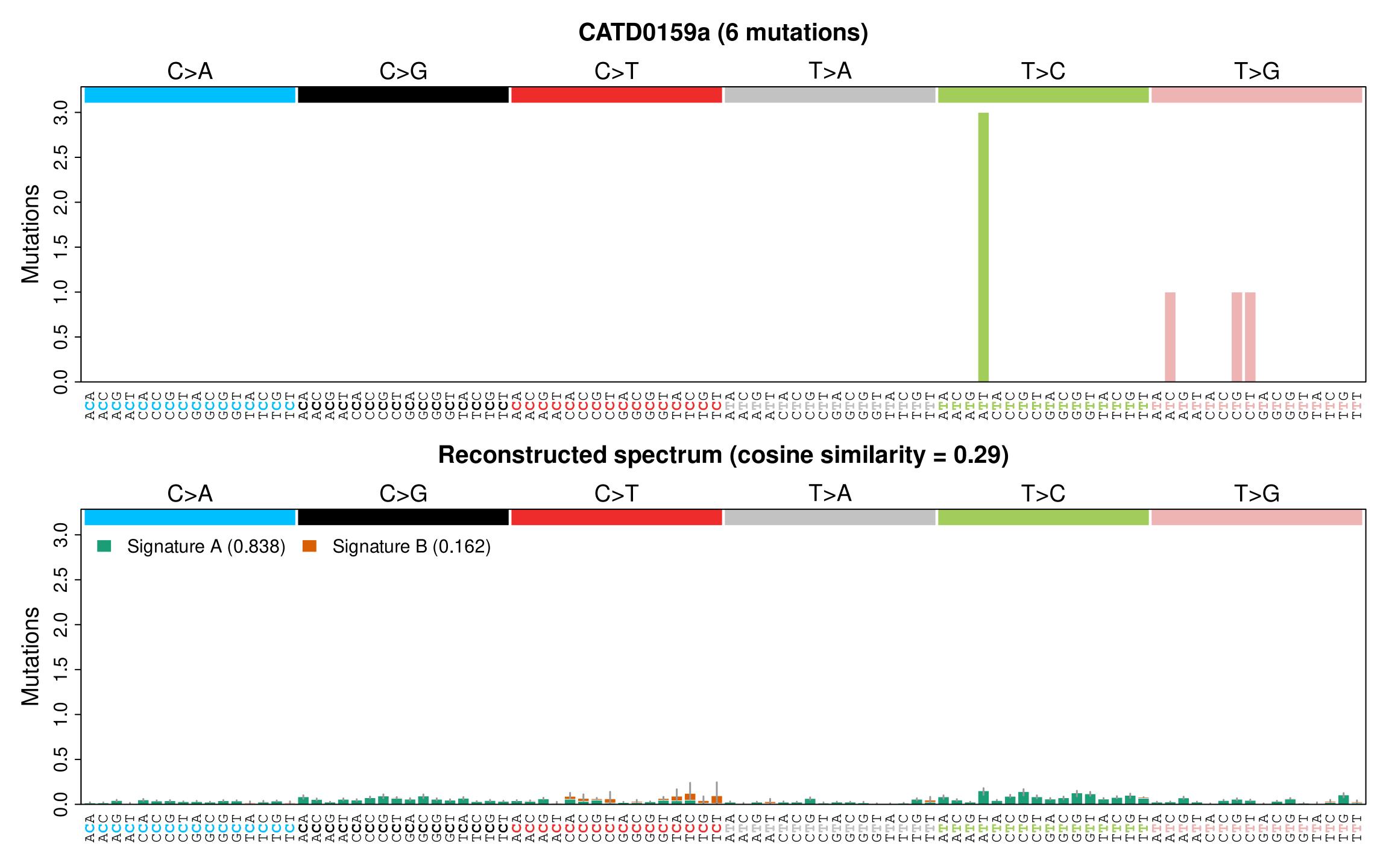


CATD0145a (8 mutations)

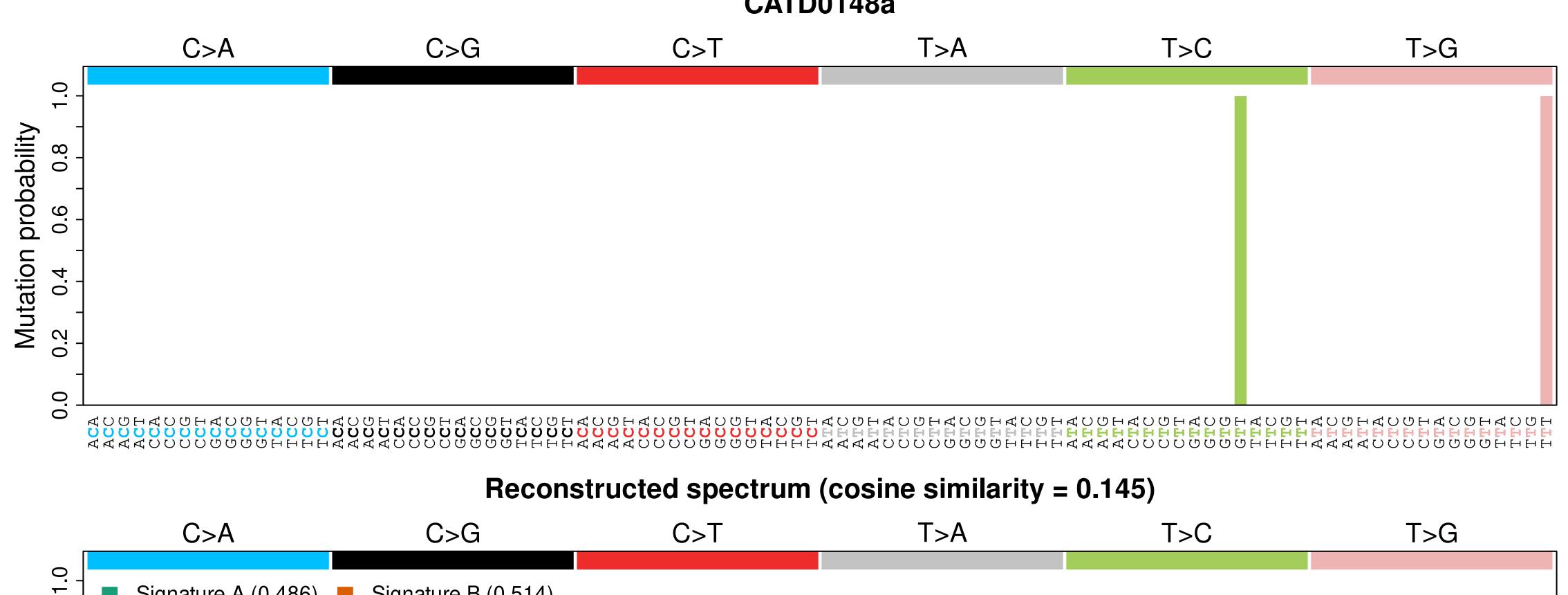


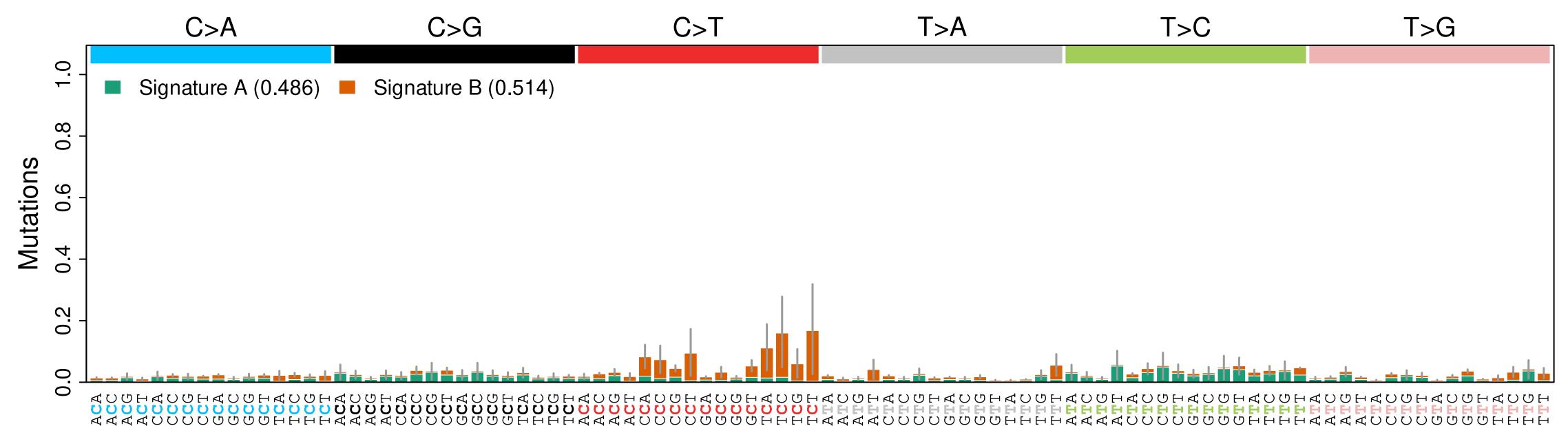
Reconstructed spectrum (cosine similarity = 0.24)



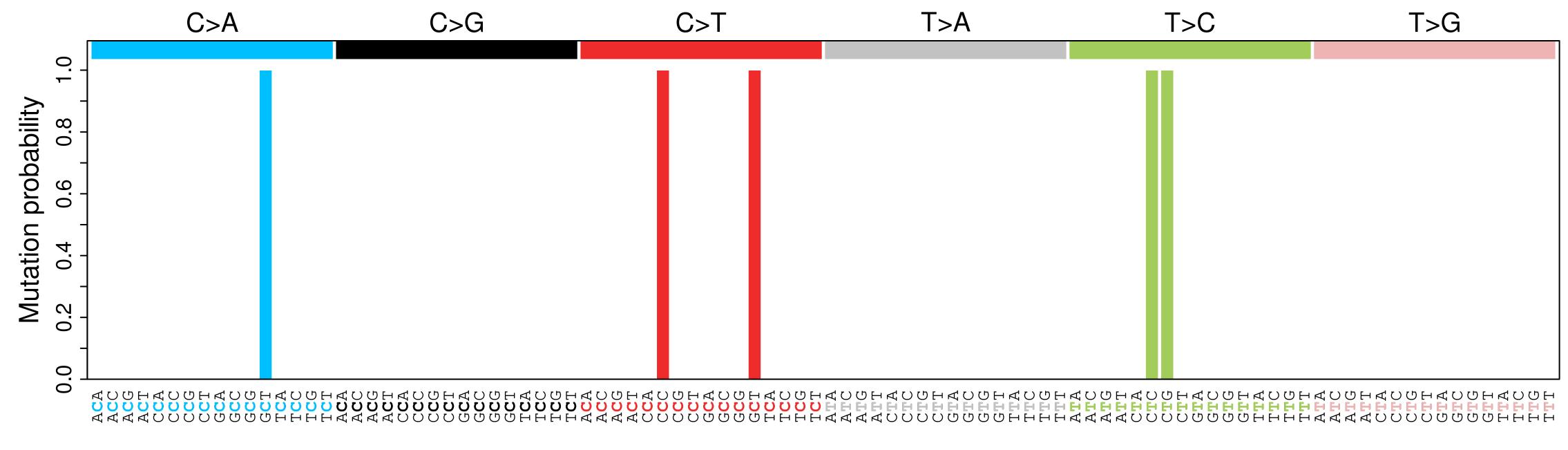


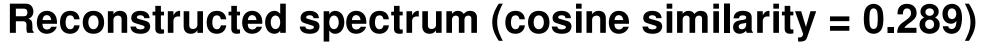


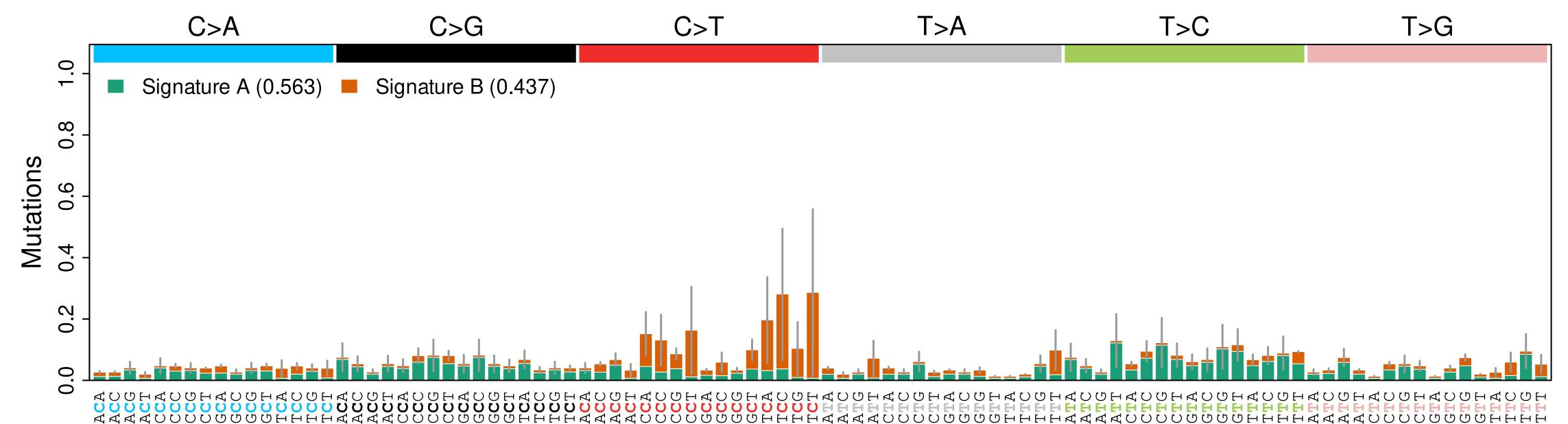




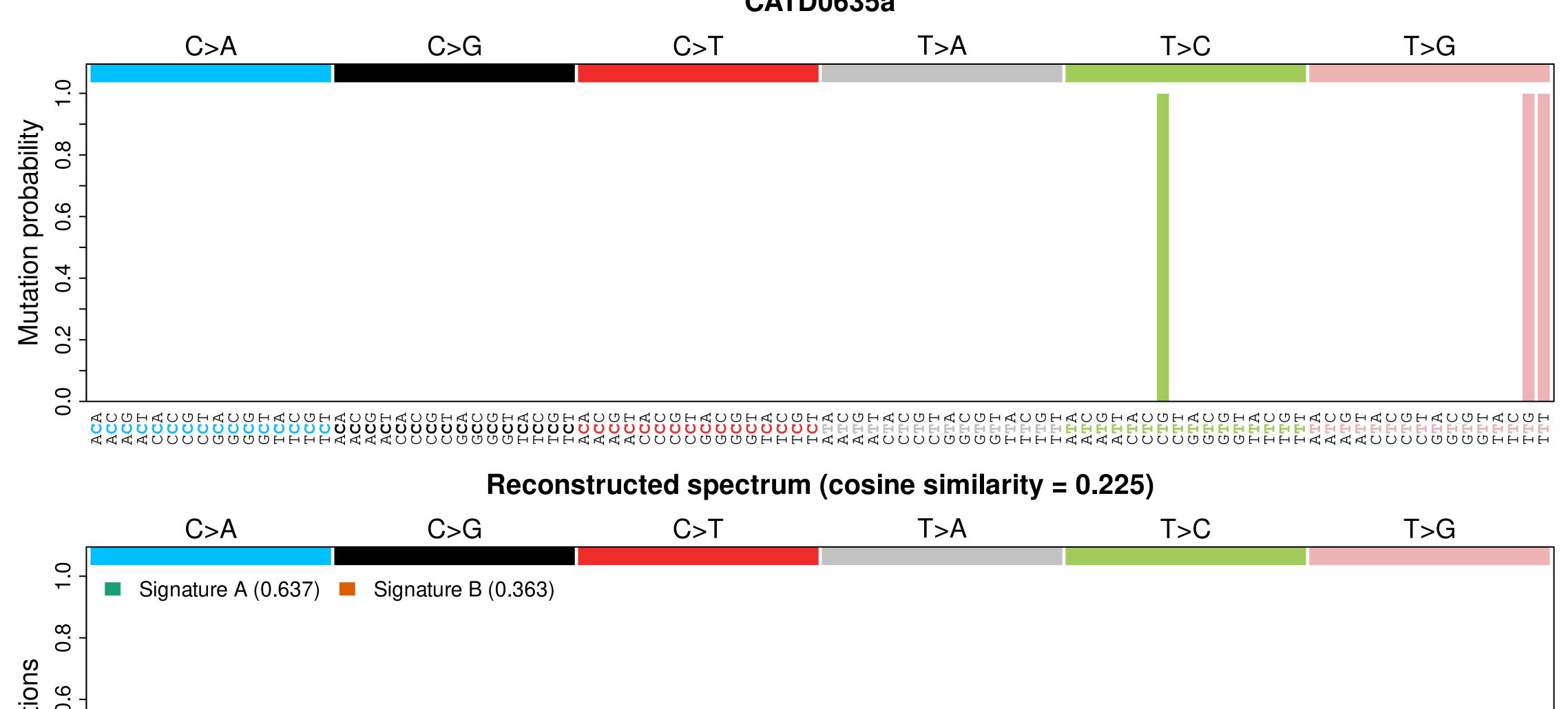
CATD0153a

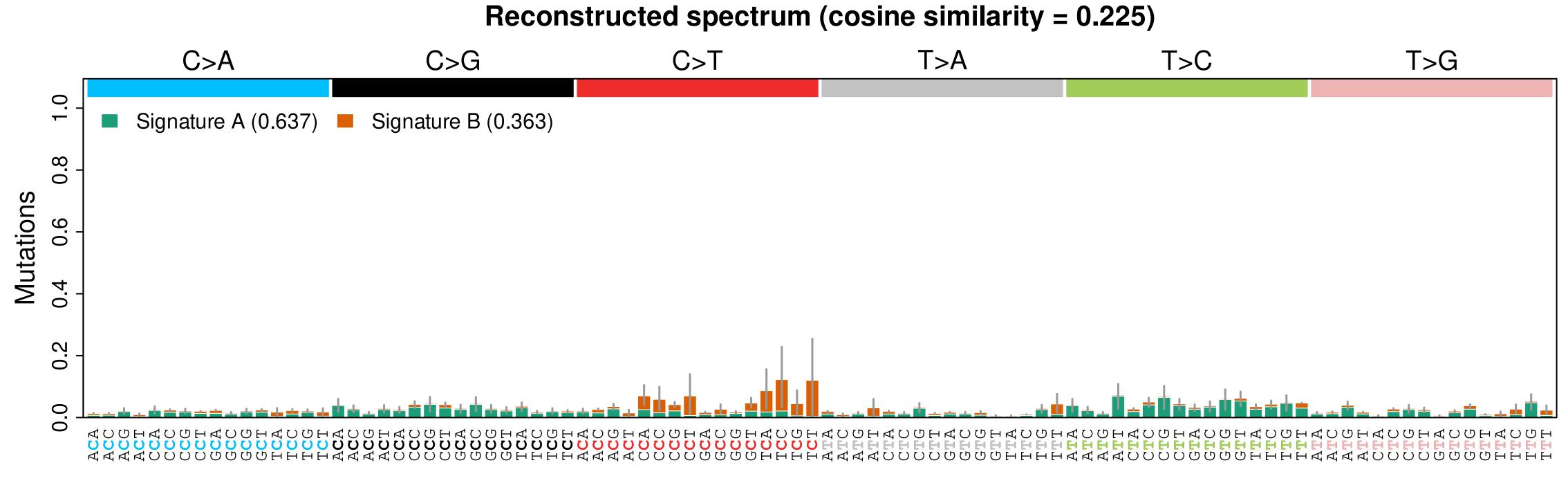








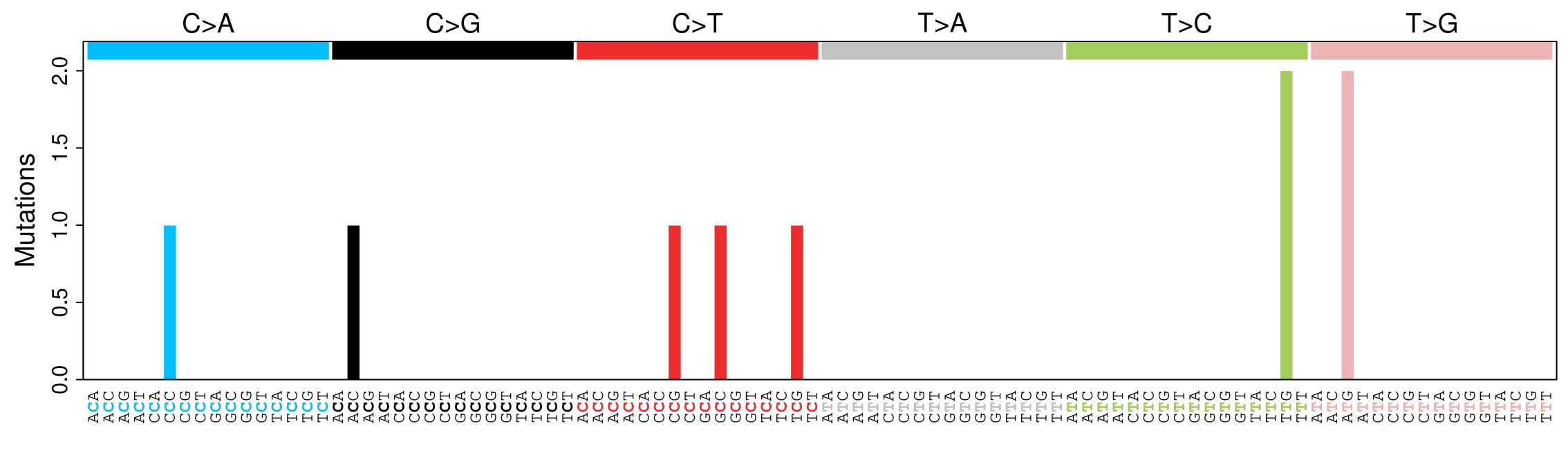


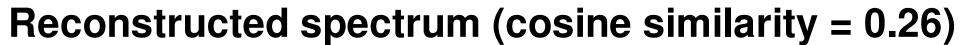


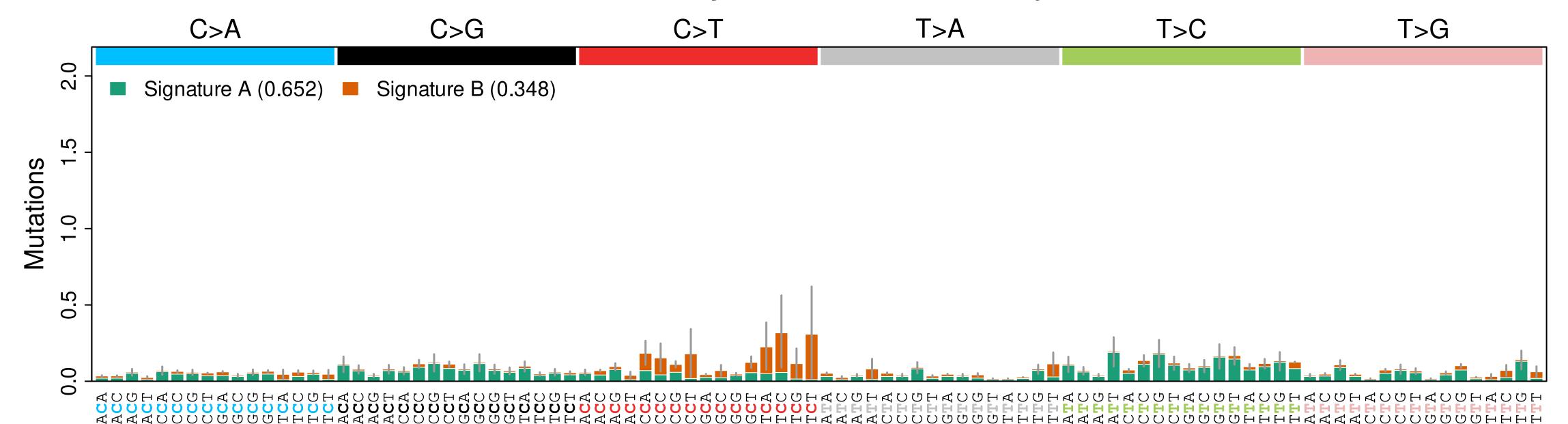
CATD0646a C>G T>C T>G C>A C>T T>A 1.0 Mutation probability 0.8 9.0 0.4 0.2 0.0 Reconstructed spectrum (cosine similarity = 0.094) C>A T>G C>G T>A T>C C>T 1.0 Signature A (0.53) Signature B (0.47) 0.8 Mutations 9.0 \mathcal{O} 0

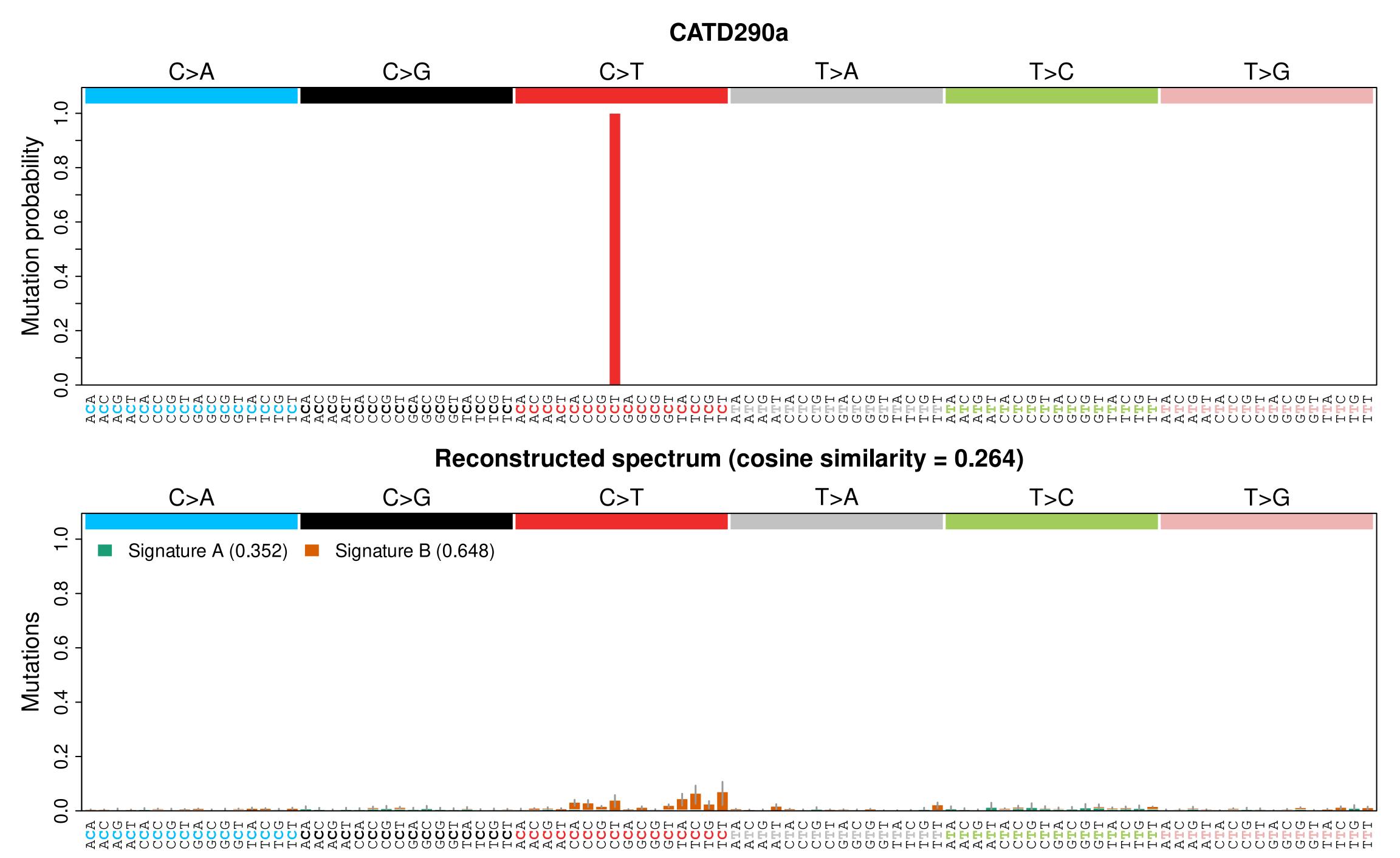
0.0

CATD295a (9 mutations)

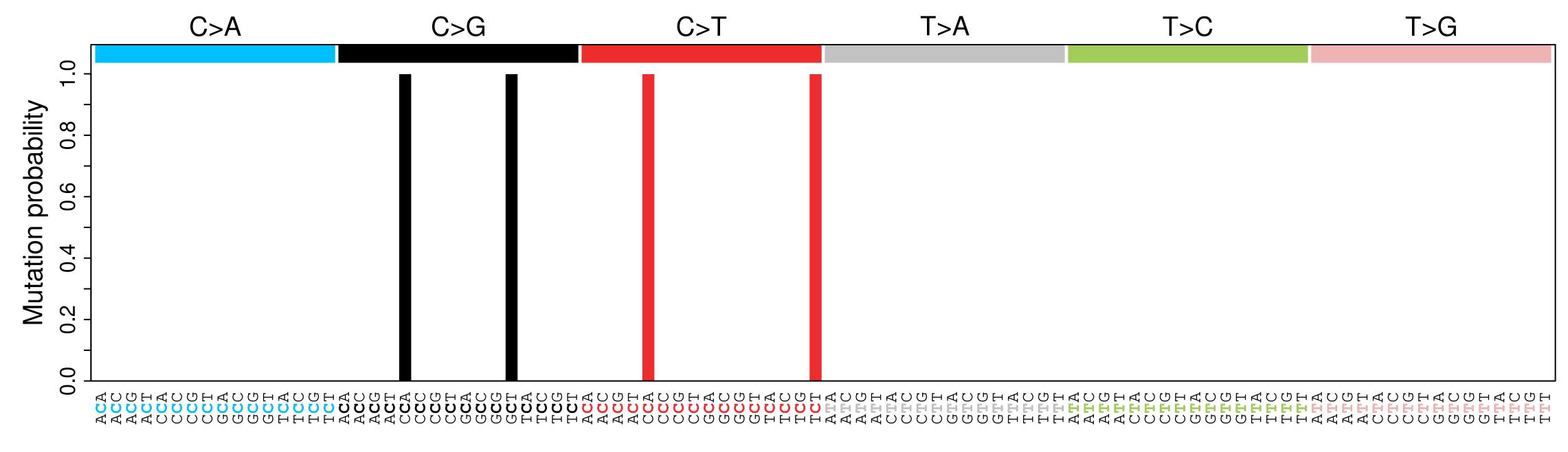


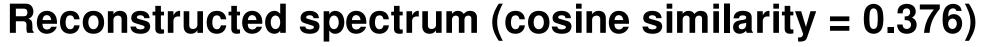


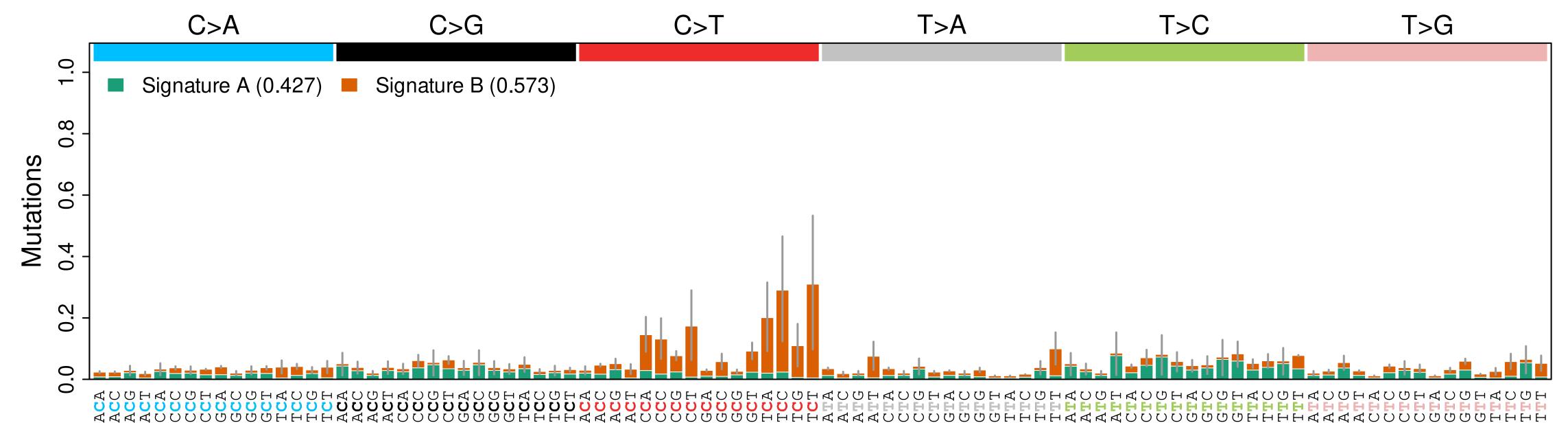




CATD0142a





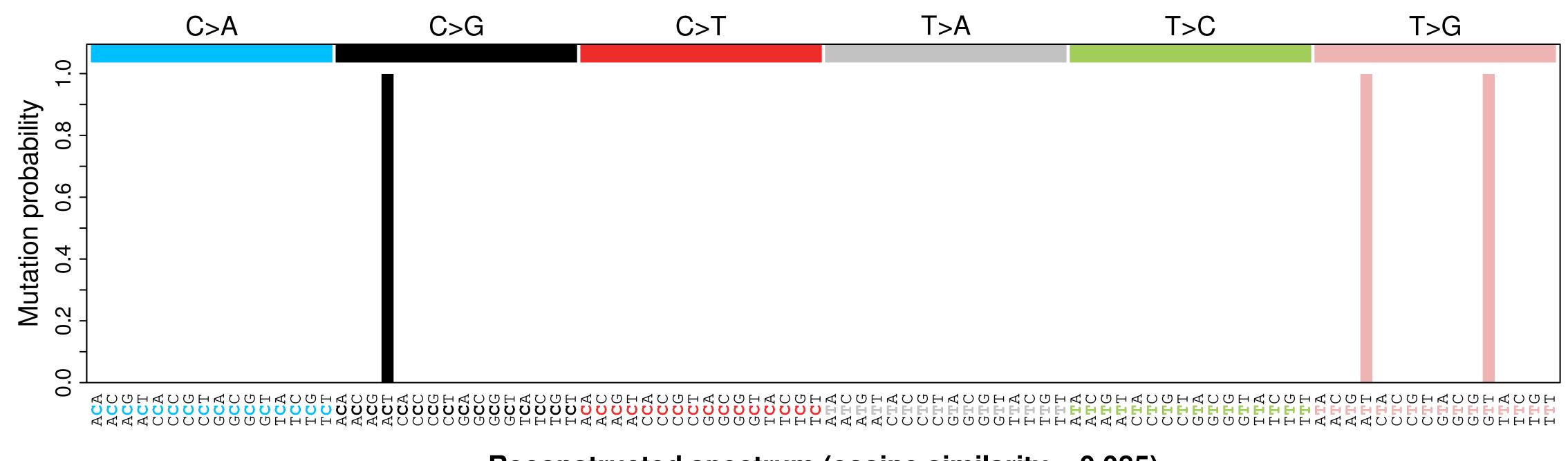


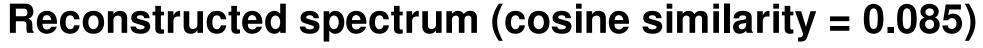
CATD291a C>A C>G T>C T>G C>T T>A 1.0 Mutation probability 0.8 9.0 0.4 0.2 0 Reconstructed spectrum (cosine similarity = 0.089) C>A T>G C>G T>A T>C C>T 1.0 Signature A (0.582) Signature B (0.418) 0.8 Mutations 9.0 \mathcal{O}

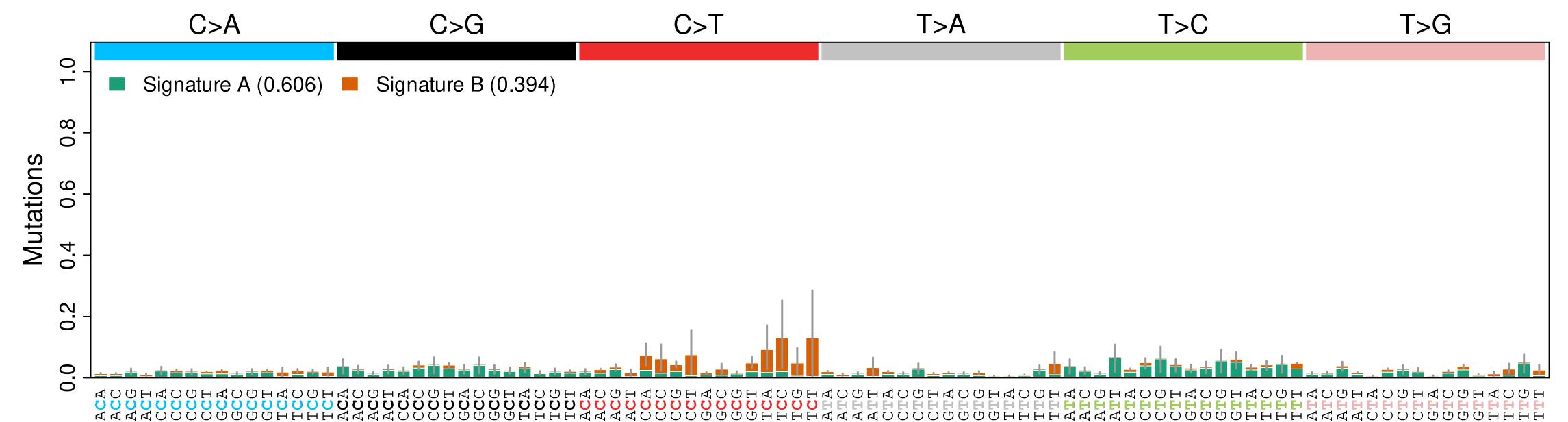
0

0

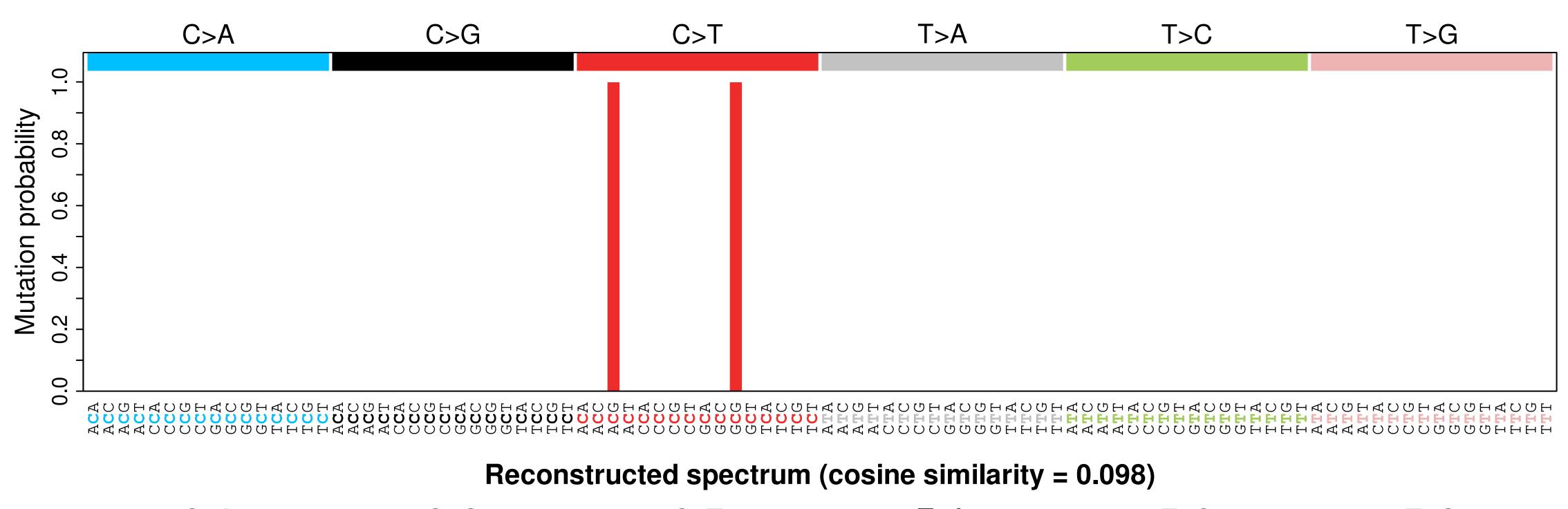


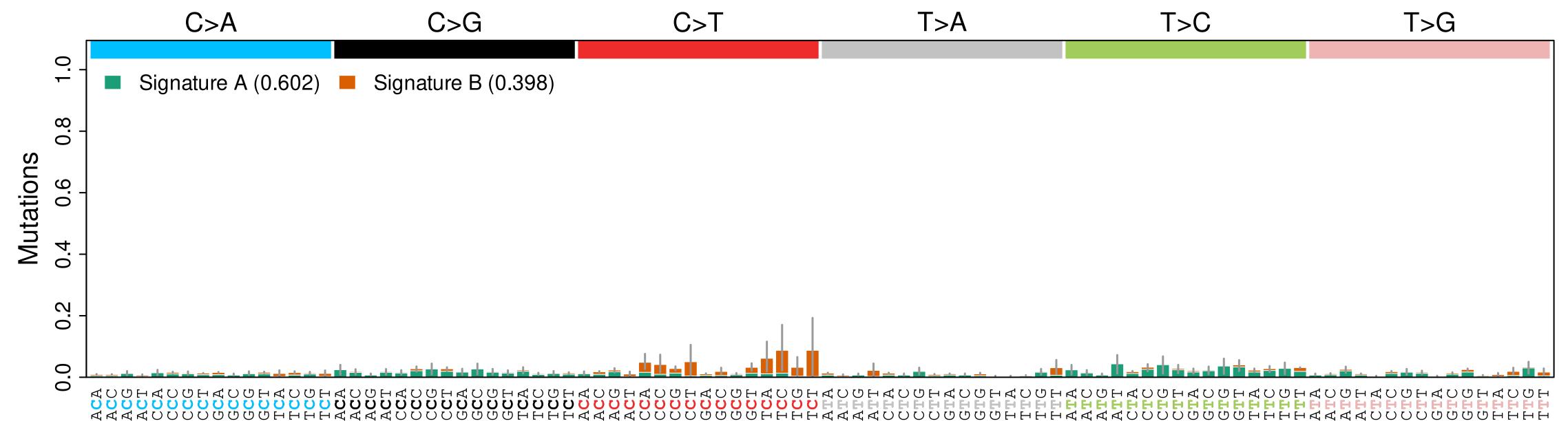




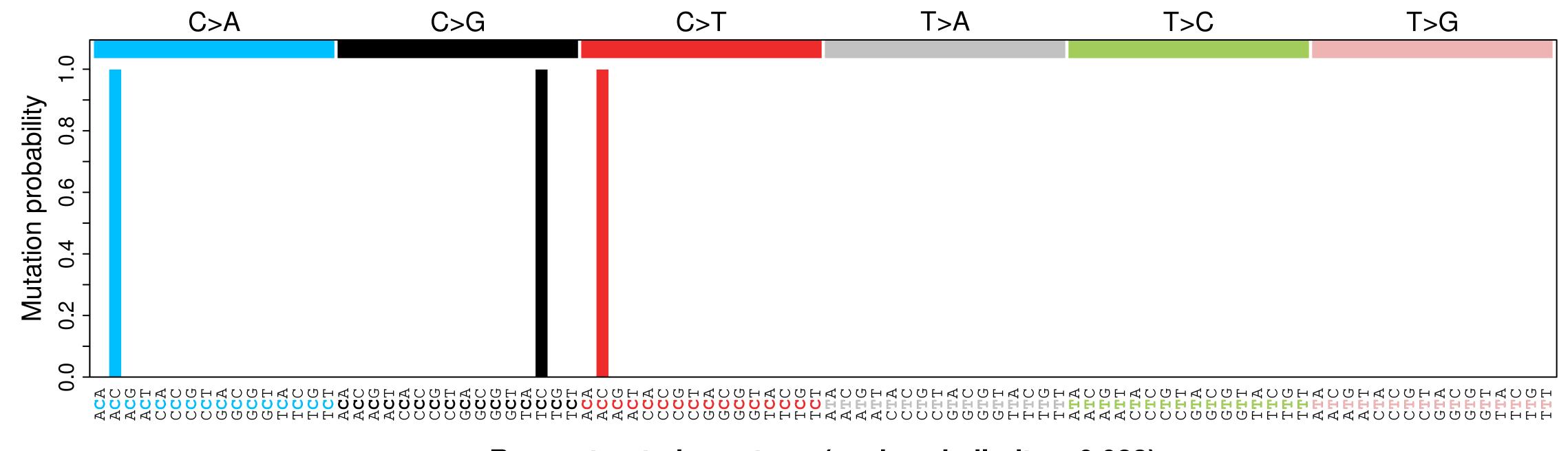




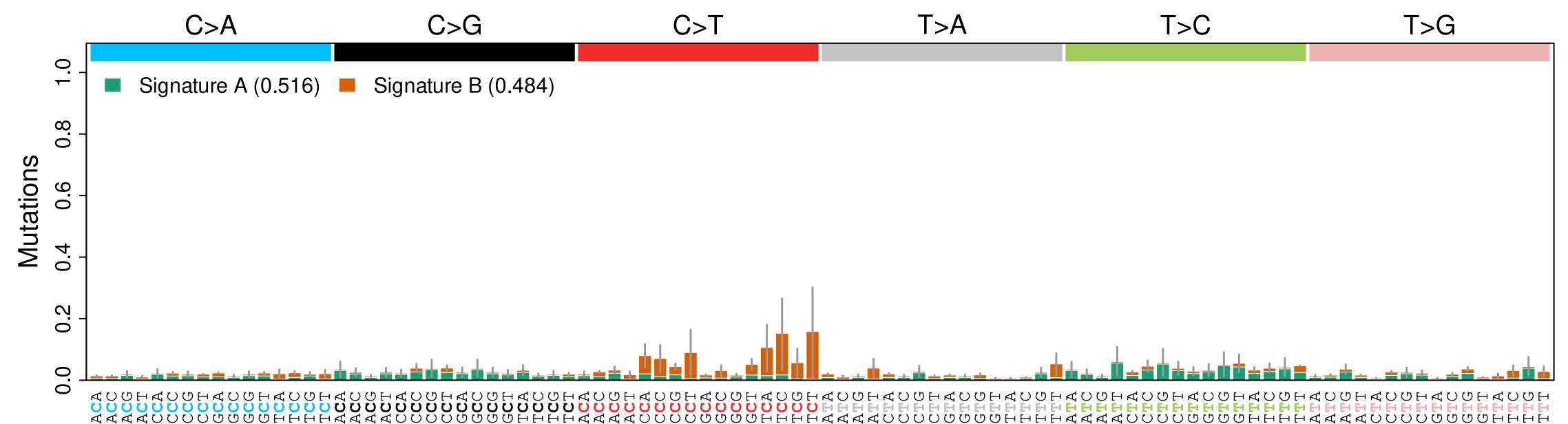




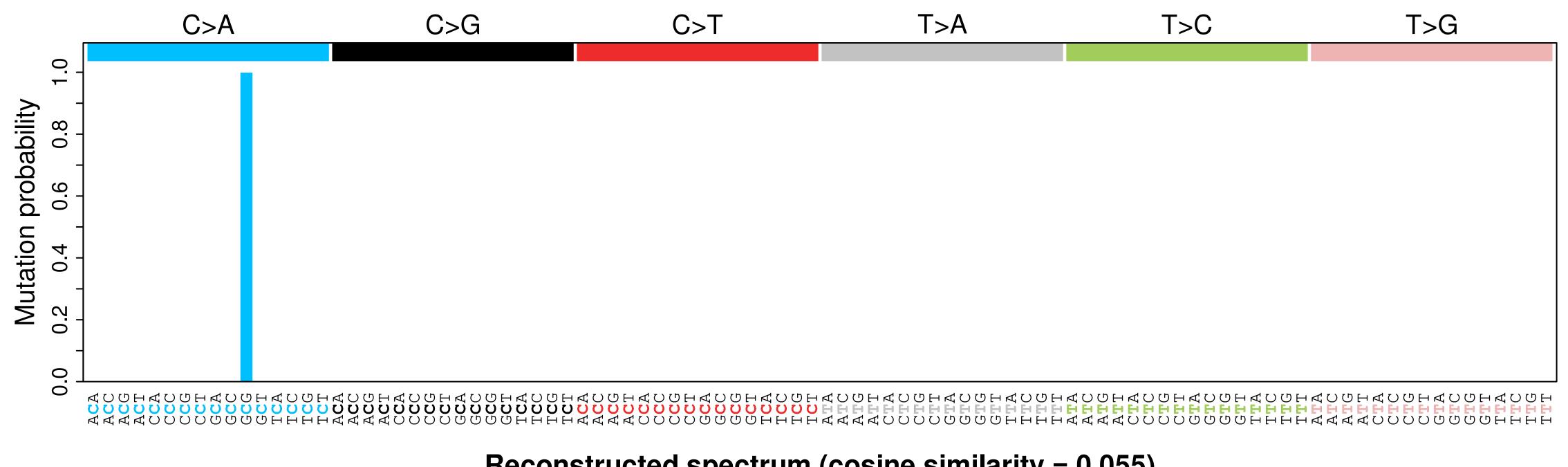
CATD0156a

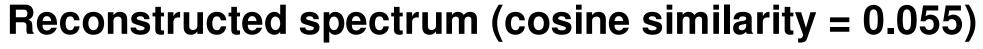


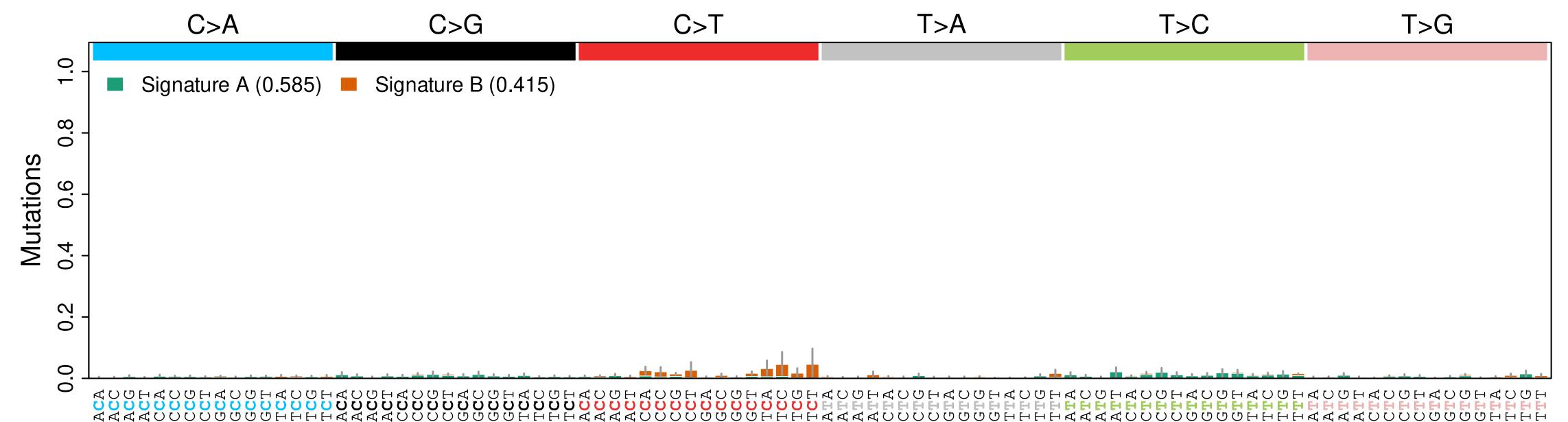
Reconstructed spectrum (cosine similarity = 0.083)











CATD0651a C>G T>C T>G C>A C>T T>A 1.0 Mutation probability 0.8

9.0

0.4

0.2

