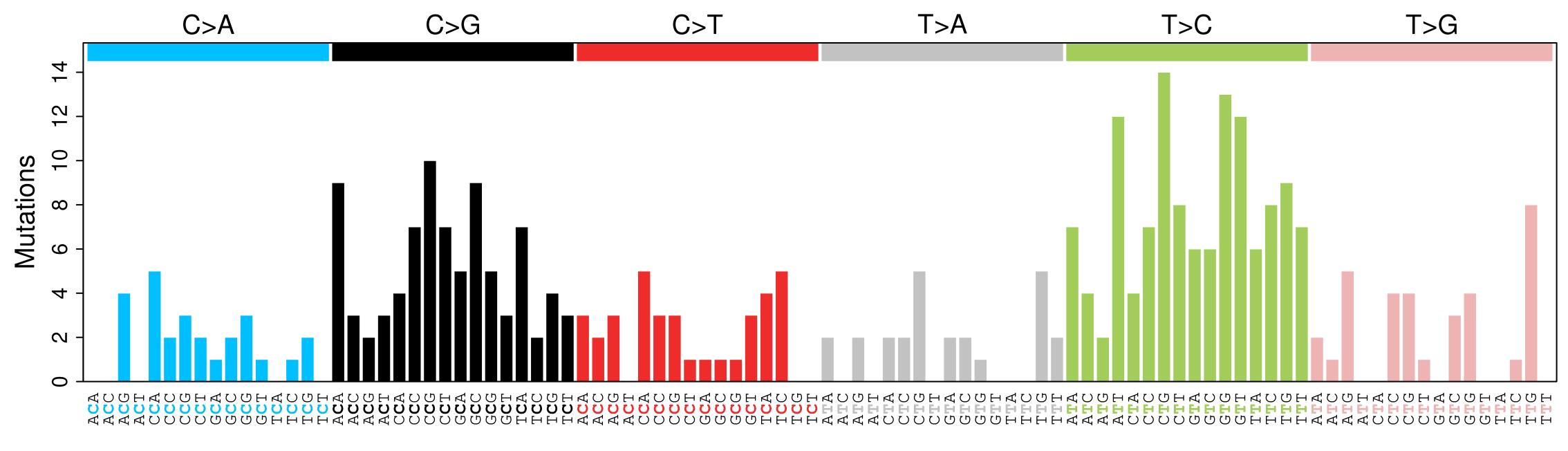
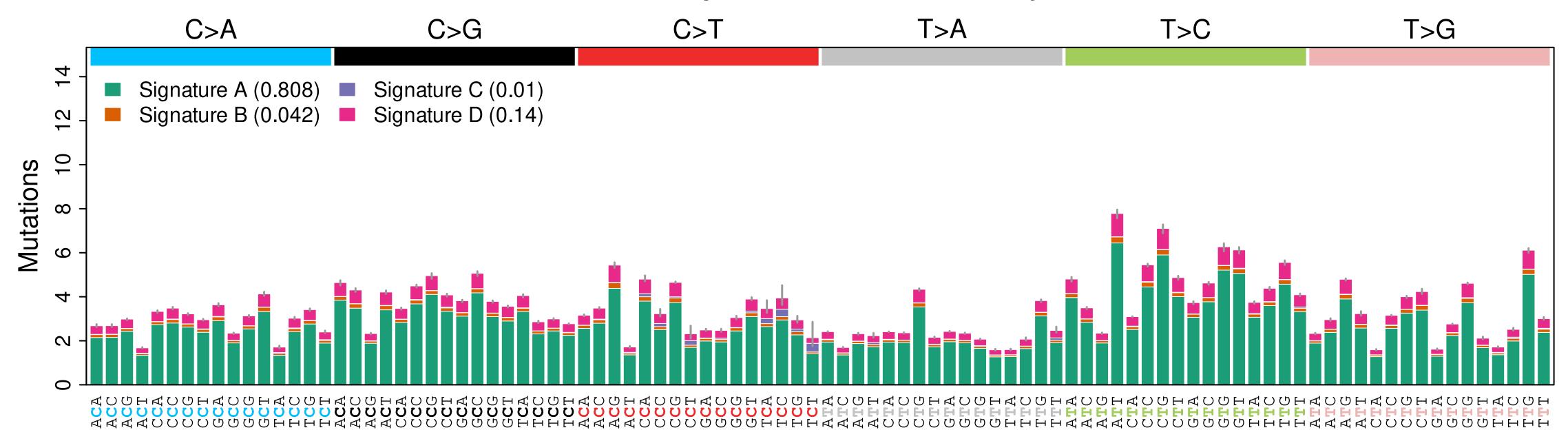
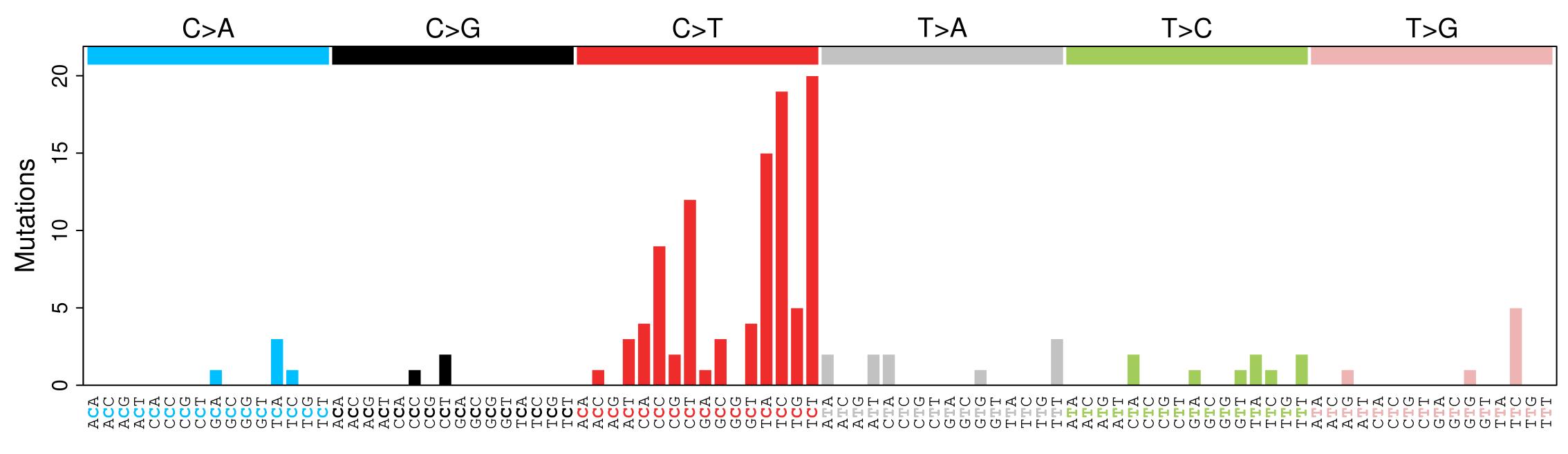
CATD292a (327 mutations)



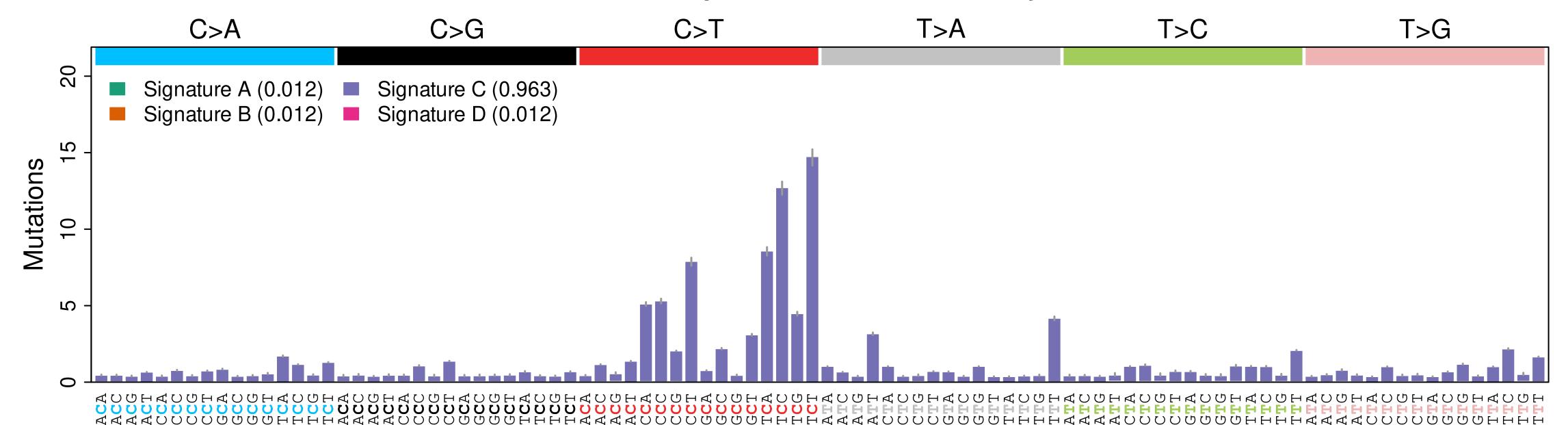
Reconstructed spectrum (cosine similarity = 0.888)



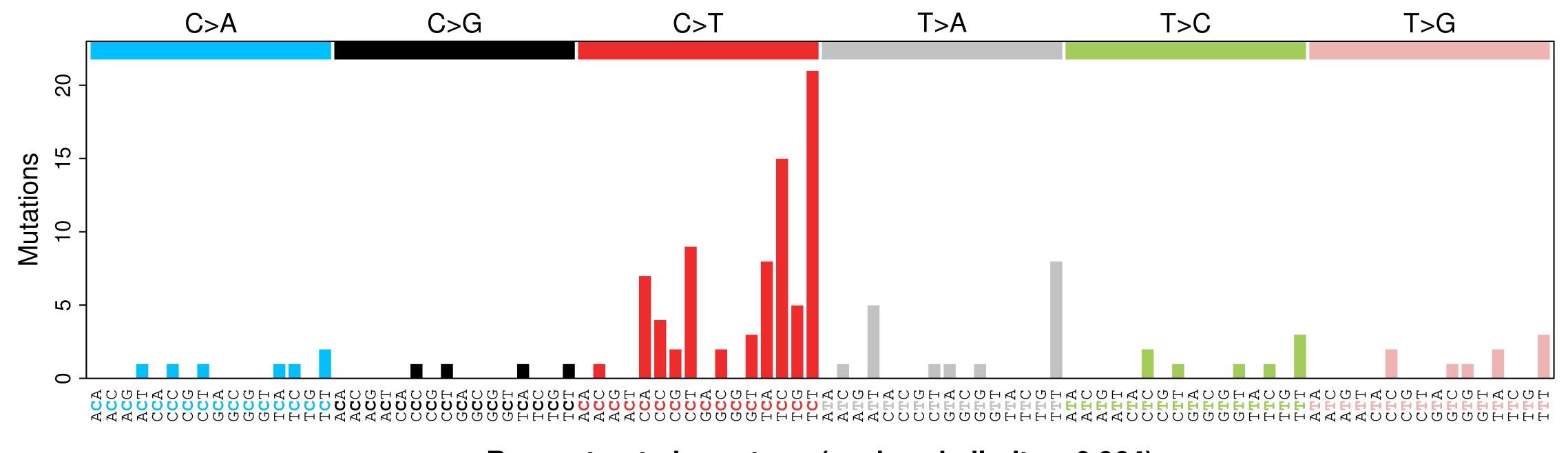
CATD0653a (132 mutations)



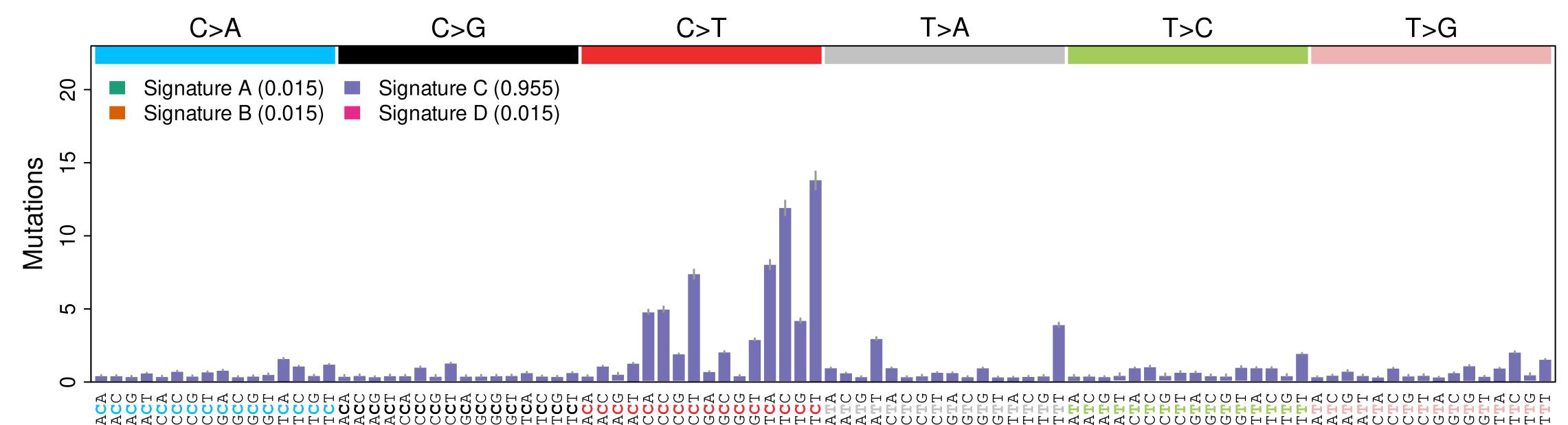
Reconstructed spectrum (cosine similarity = 0.966)



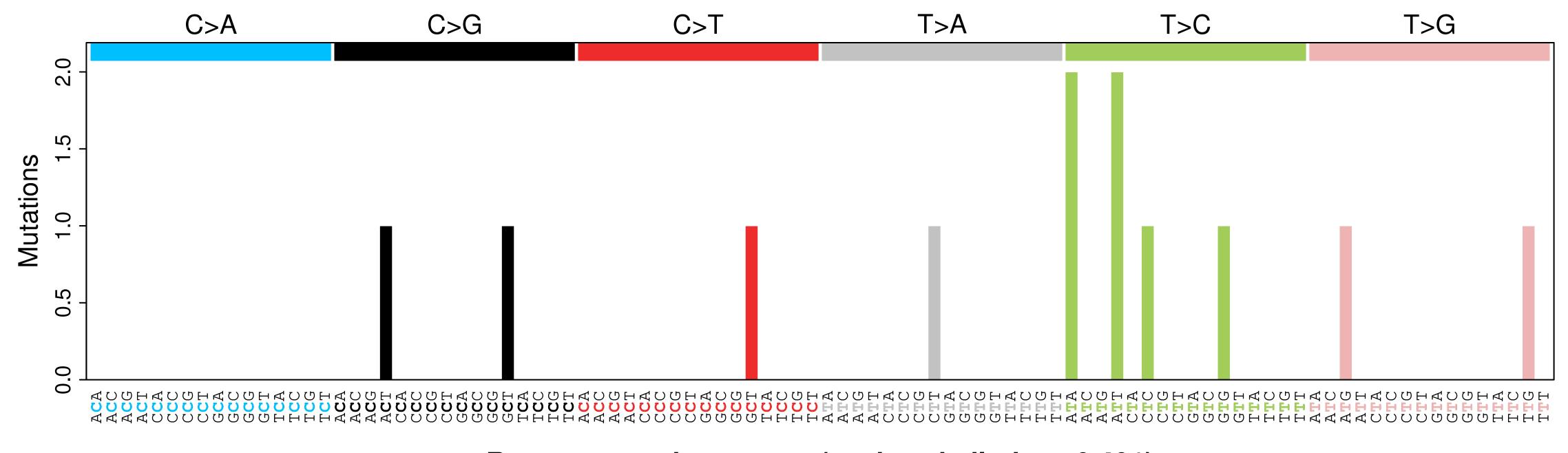
CATD294a (122 mutations)



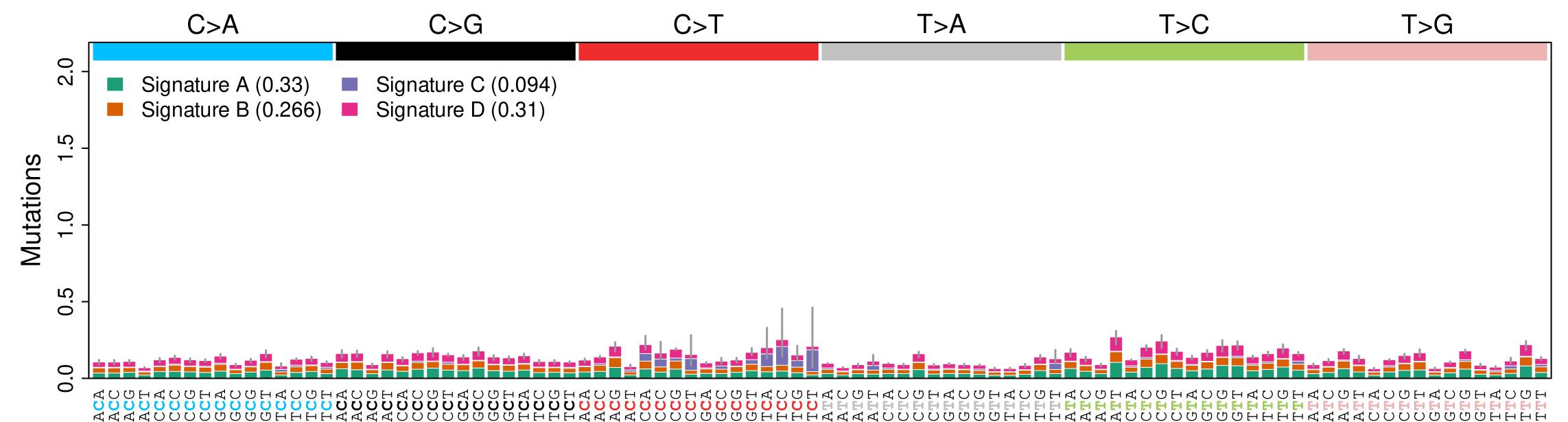
Reconstructed spectrum (cosine similarity = 0.964)



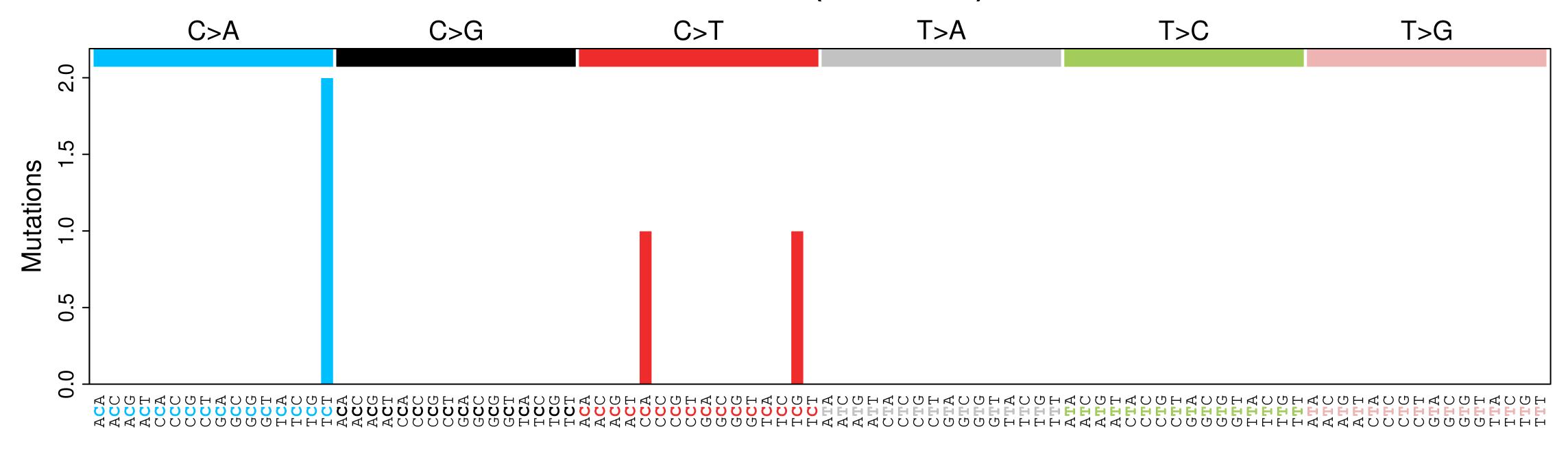
CATD283a (12 mutations)



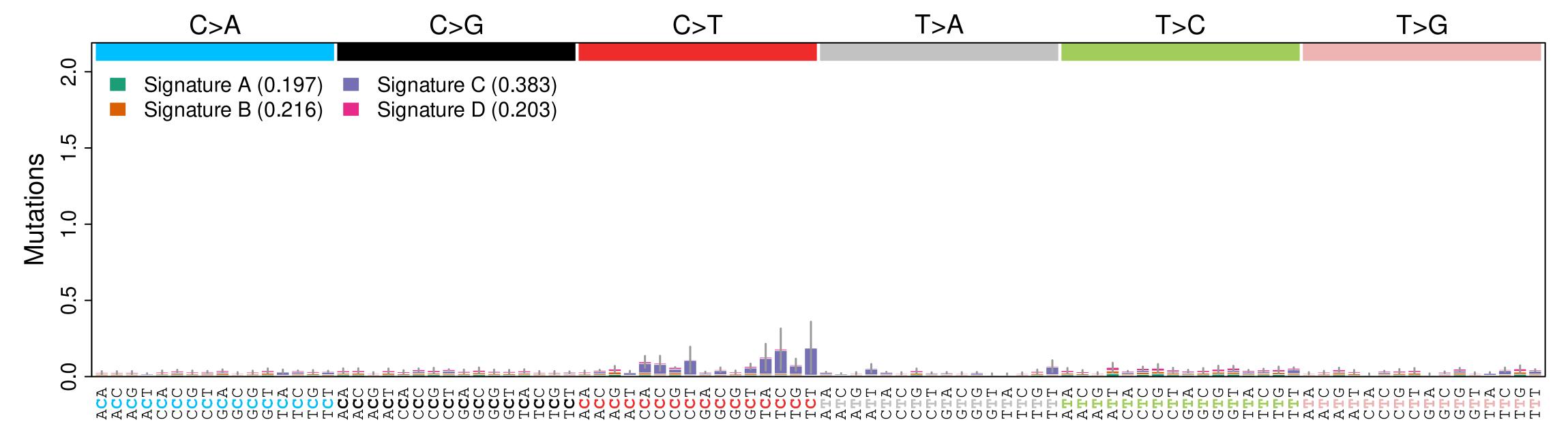
Reconstructed spectrum (cosine similarity = 0.401)



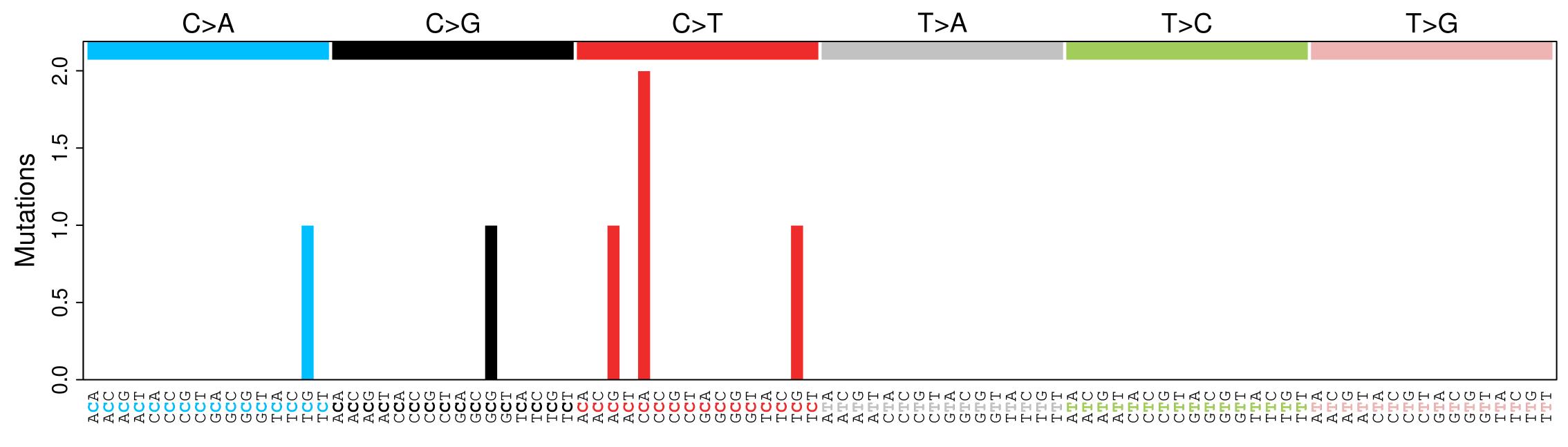
CATD0645a (4 mutations)



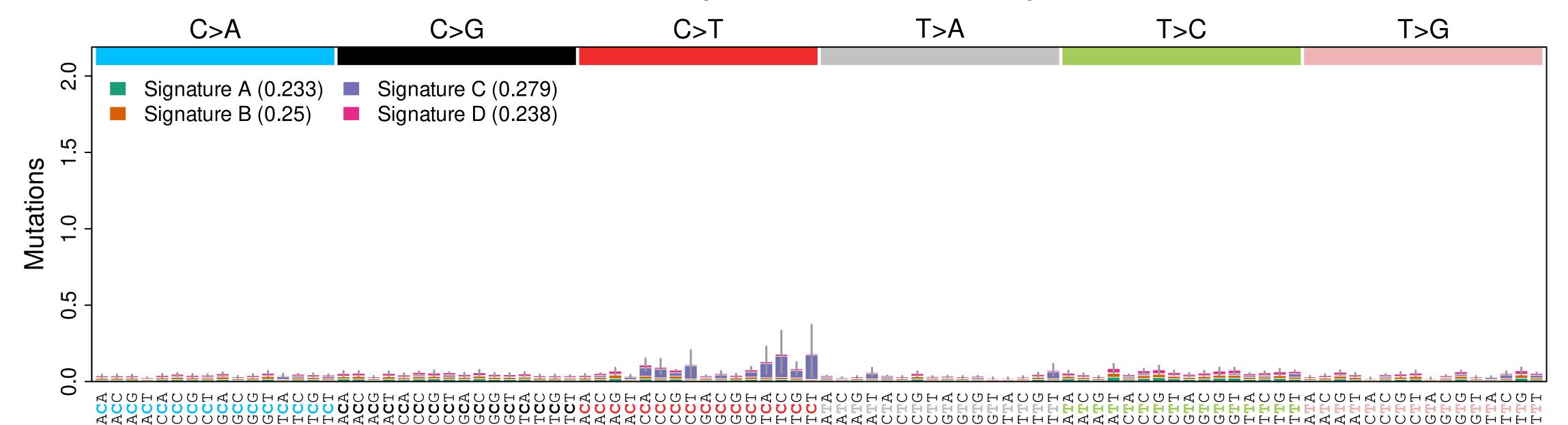
Reconstructed spectrum (cosine similarity = 0.201)



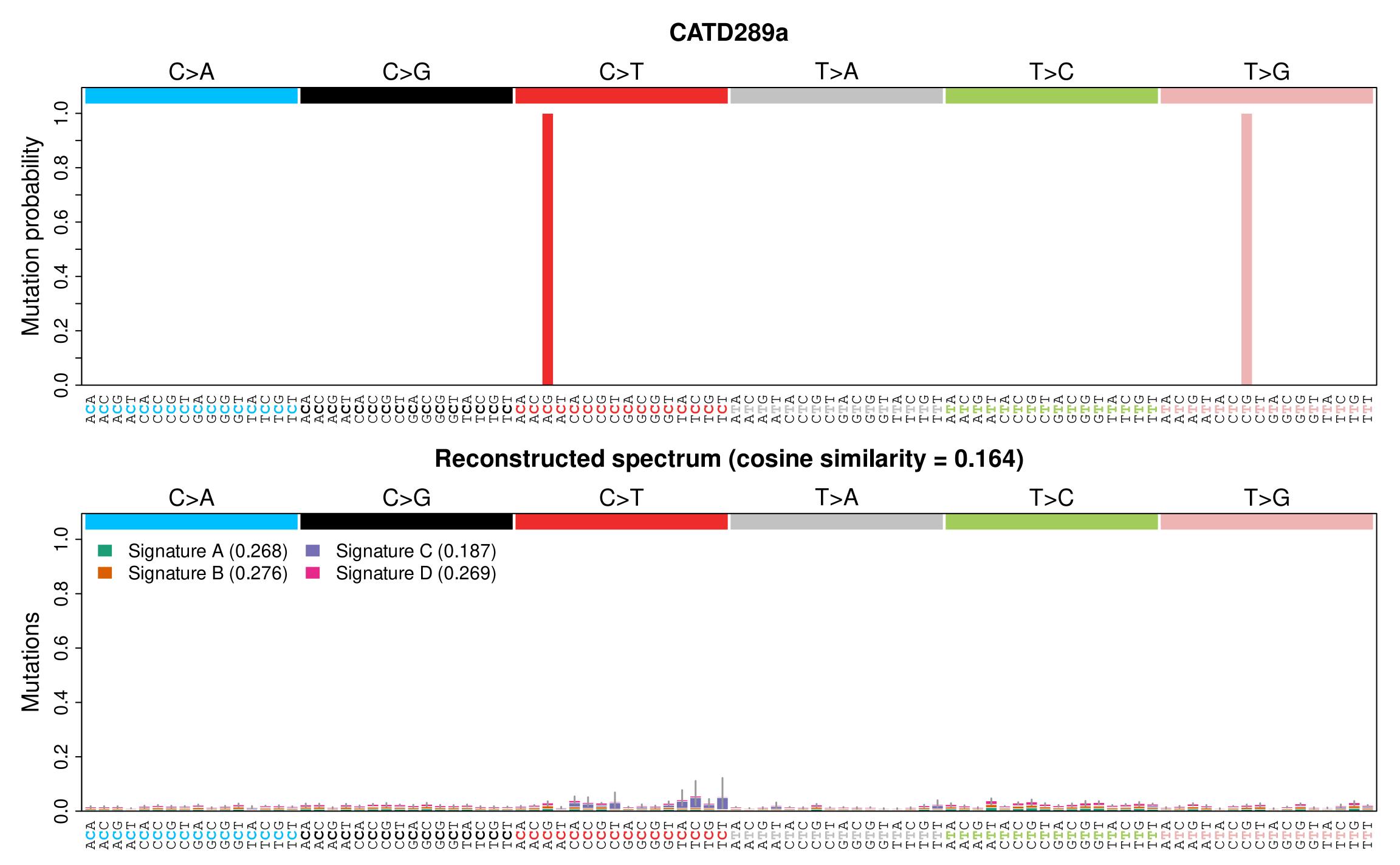
CATD0670a (6 mutations)



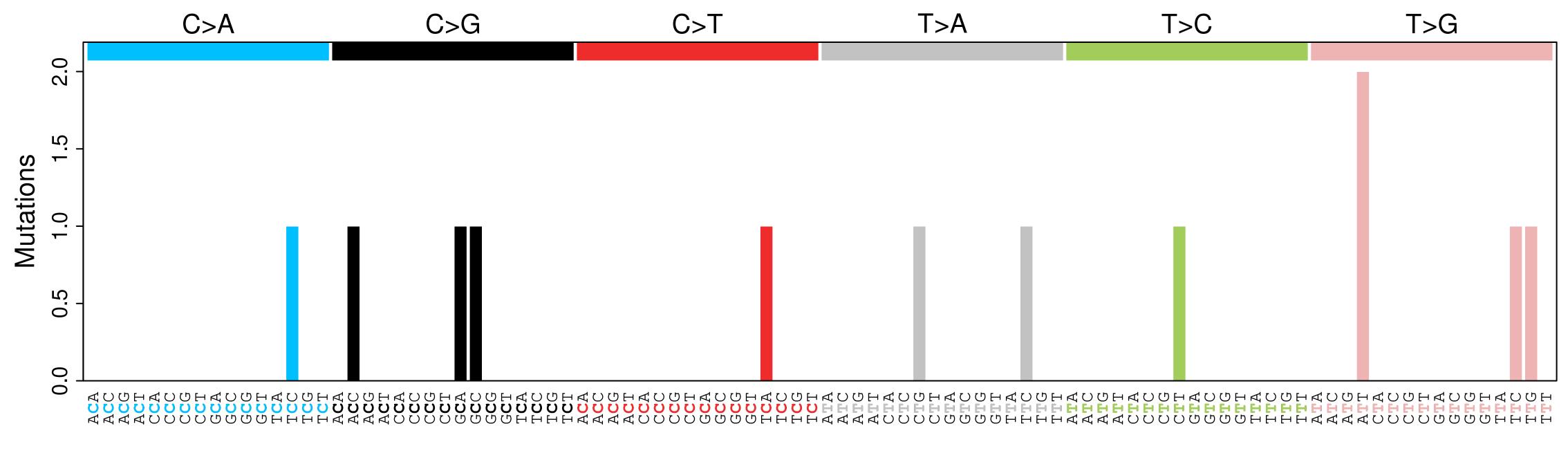
Reconstructed spectrum (cosine similarity = 0.281)

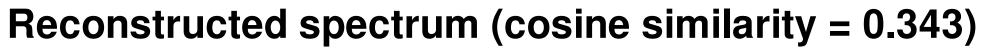


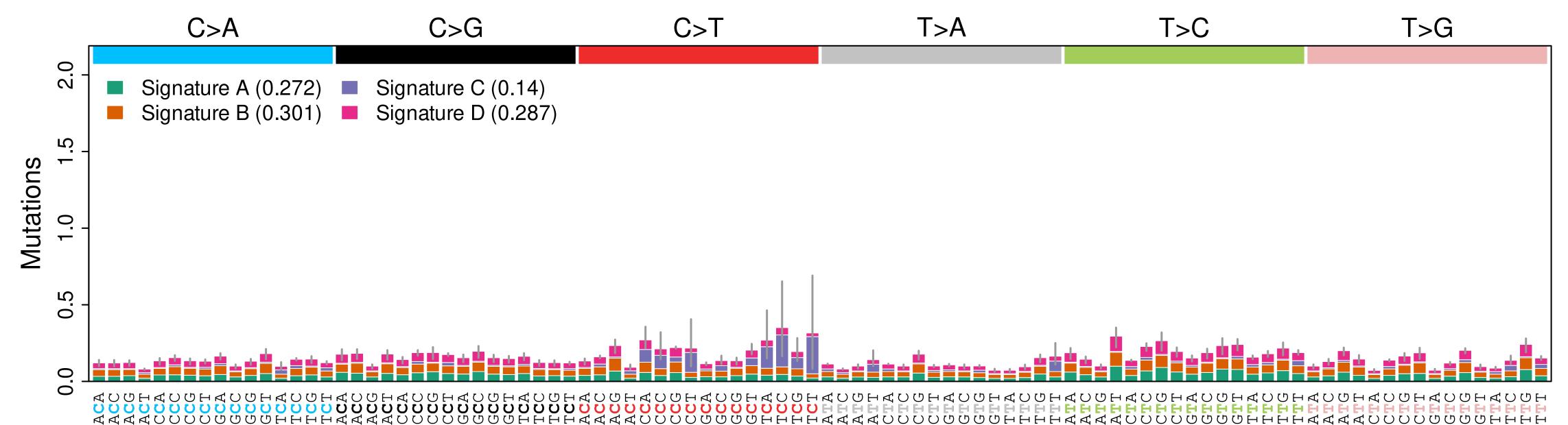
CATD0650a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 Reconstructed spectrum (cosine similarity = 0.178) T>C T>G C>A C>G T>A C>T 2.0 Signature A (0.272) Signature C (0.17) Signature B (0.281) Signature D (0.277) 5 Mutations 2 0 0



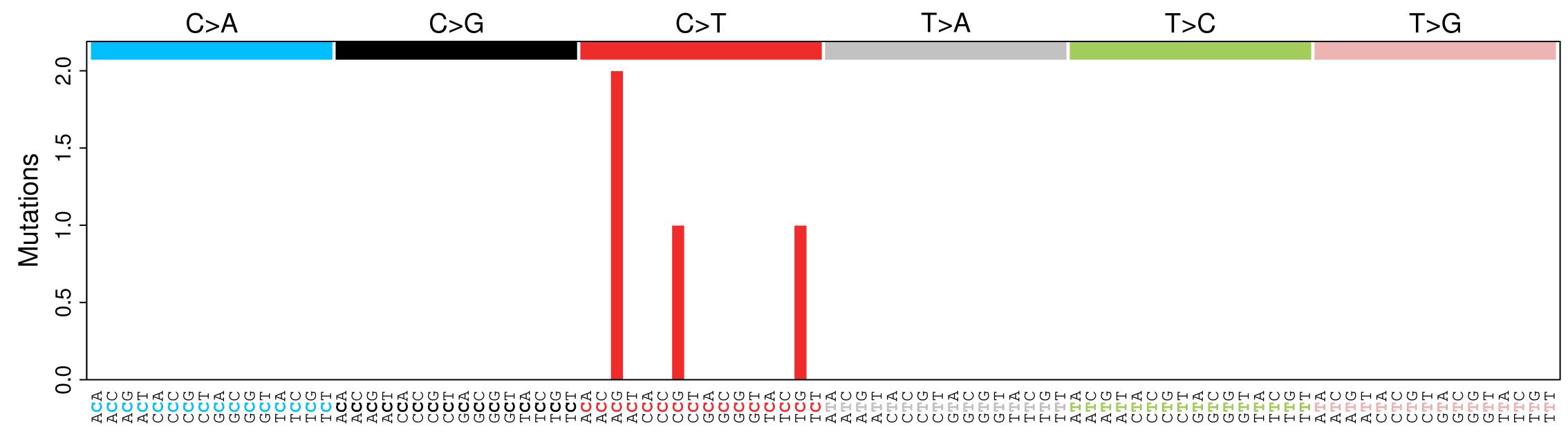
CATD0144a (12 mutations)



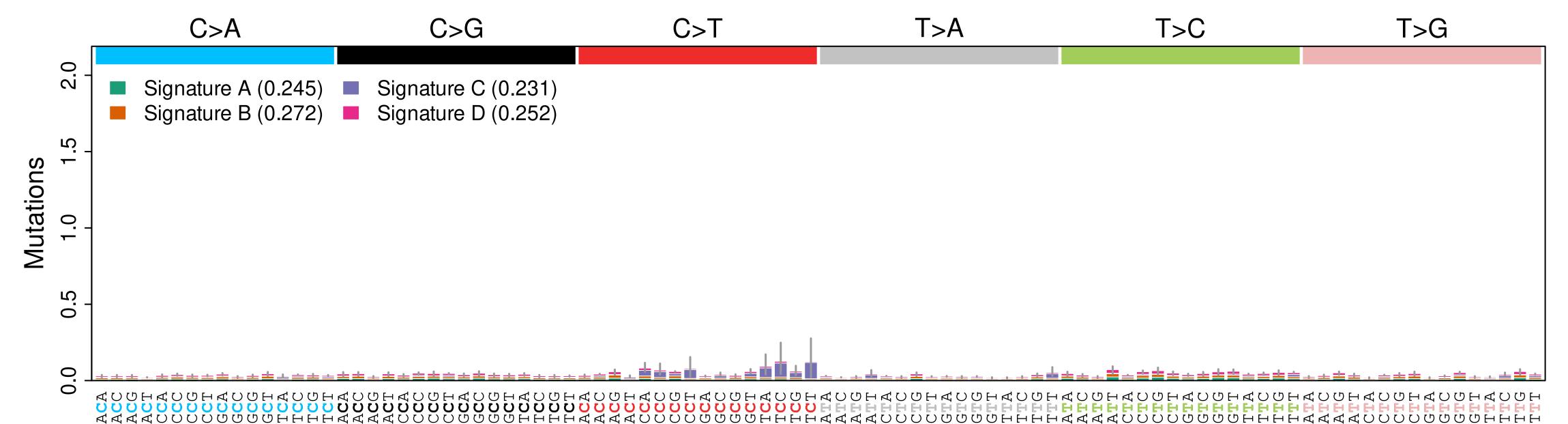




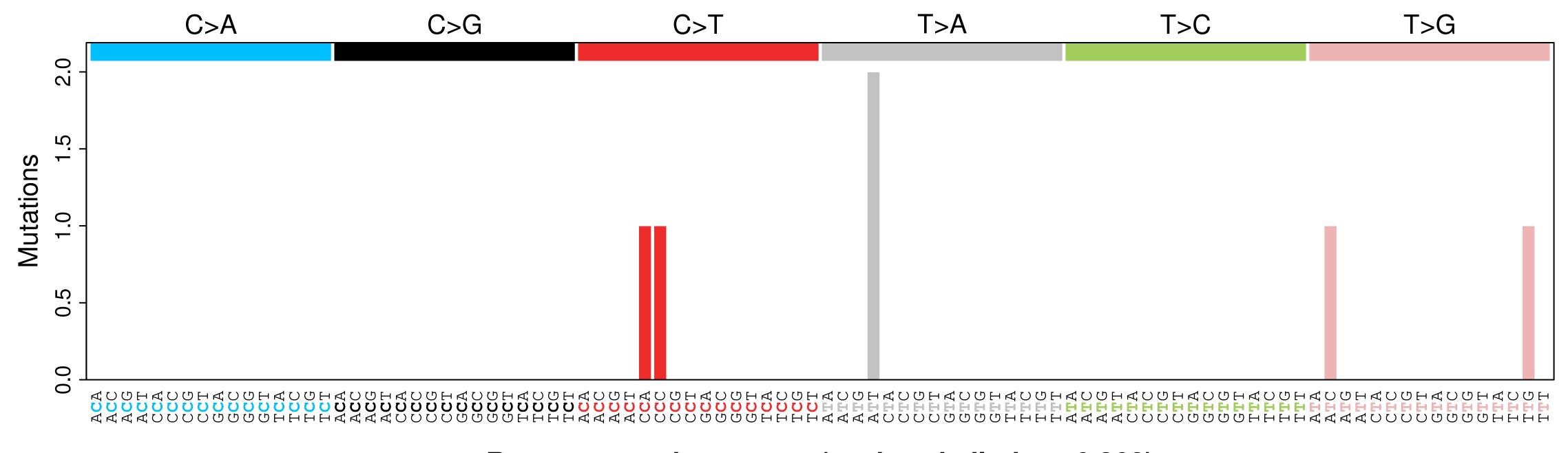
CATD293a (4 mutations)



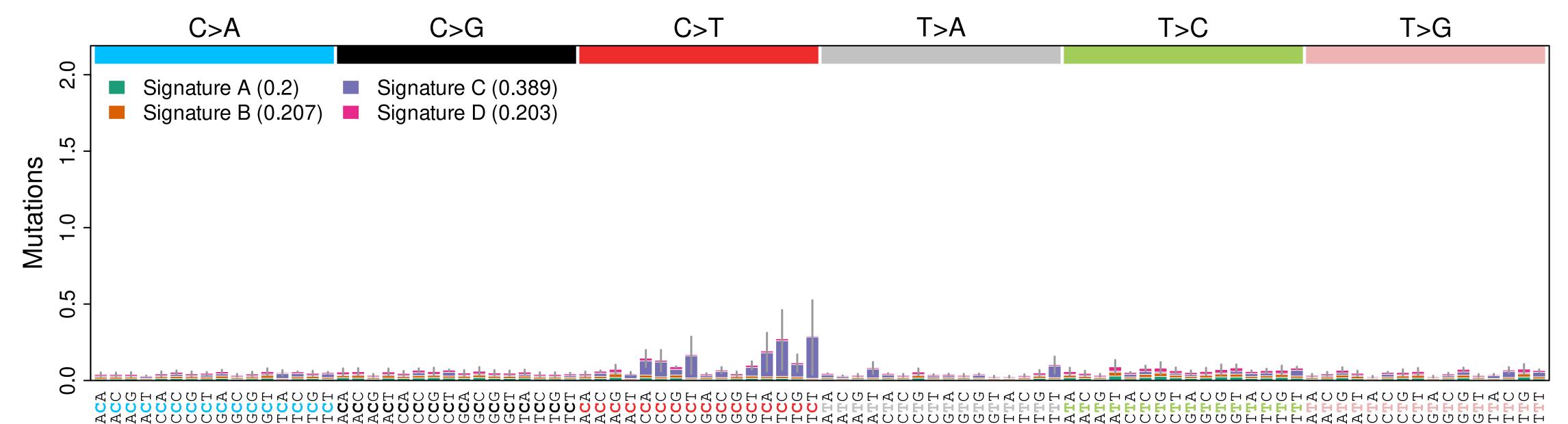
Reconstructed spectrum (cosine similarity = 0.214)



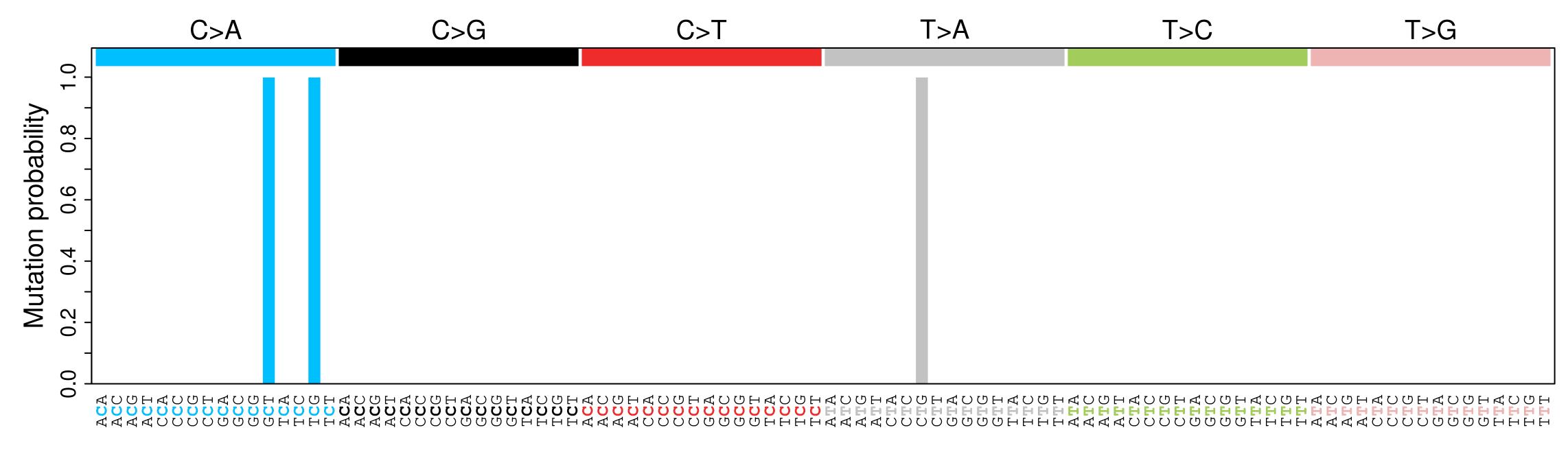
CATD0668a (6 mutations)

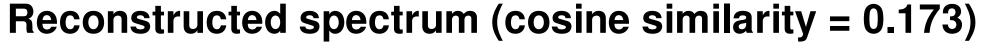


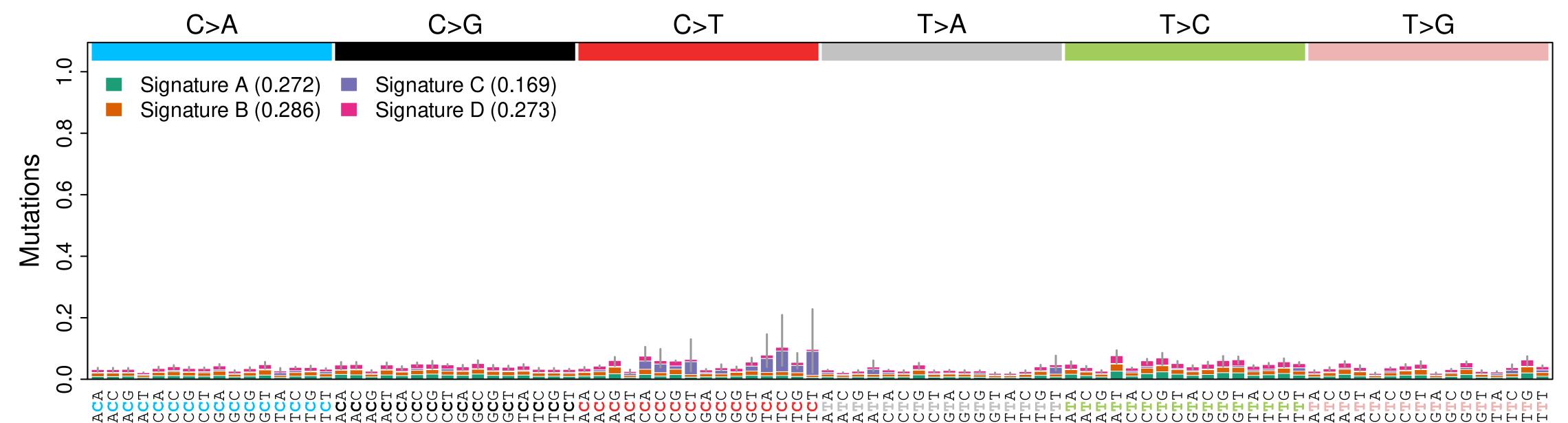
Reconstructed spectrum (cosine similarity = 0.268)



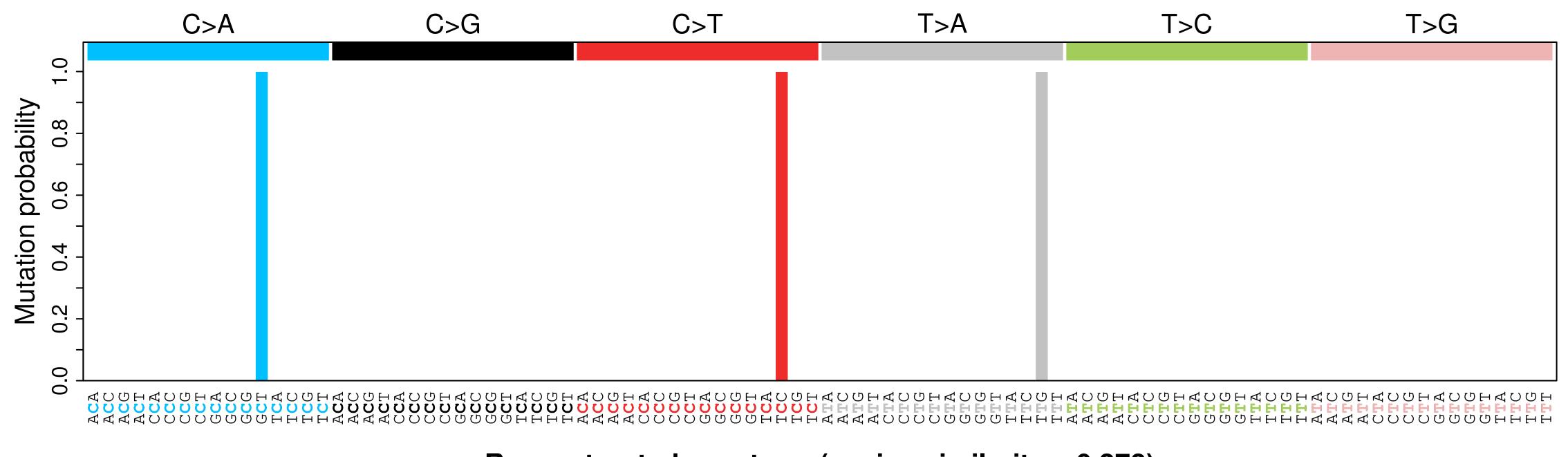




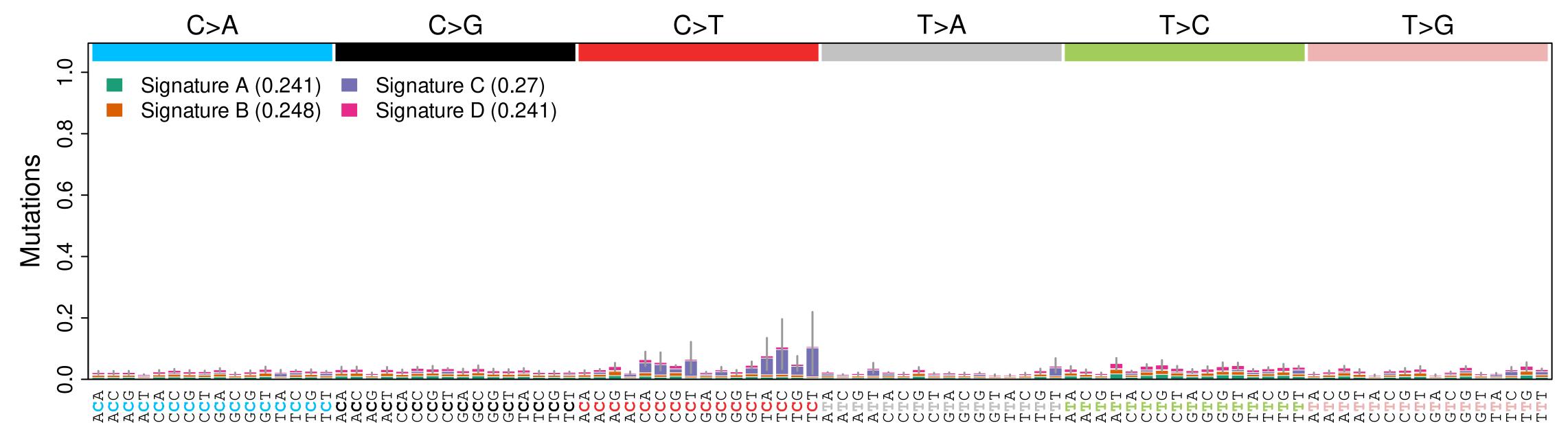




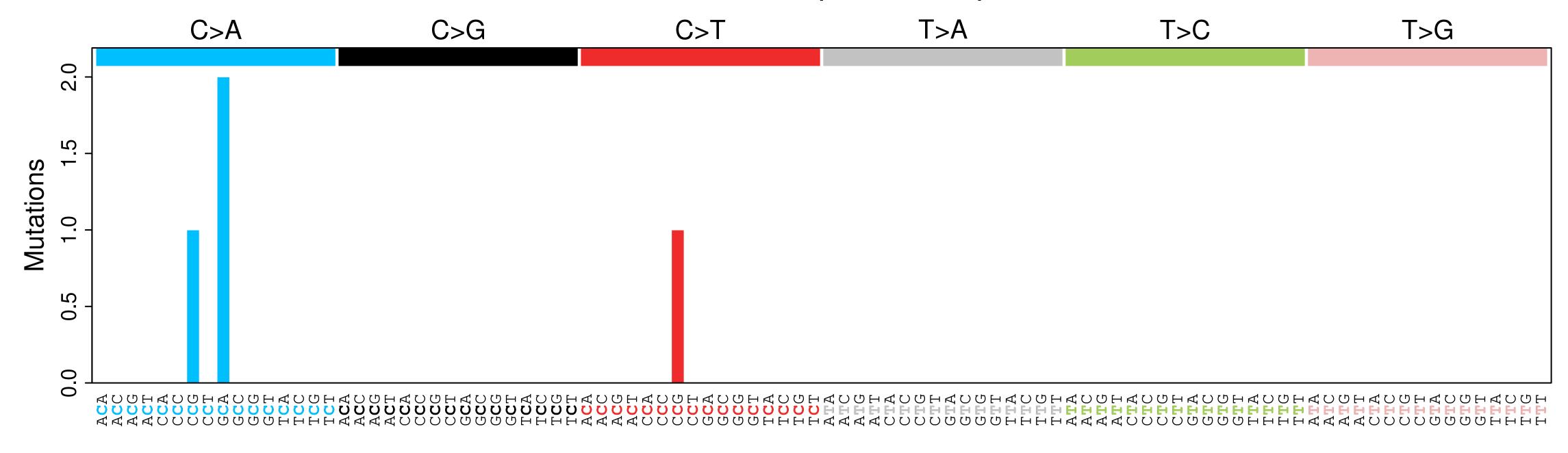


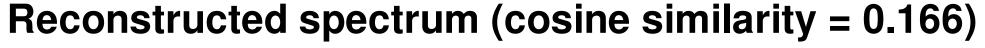


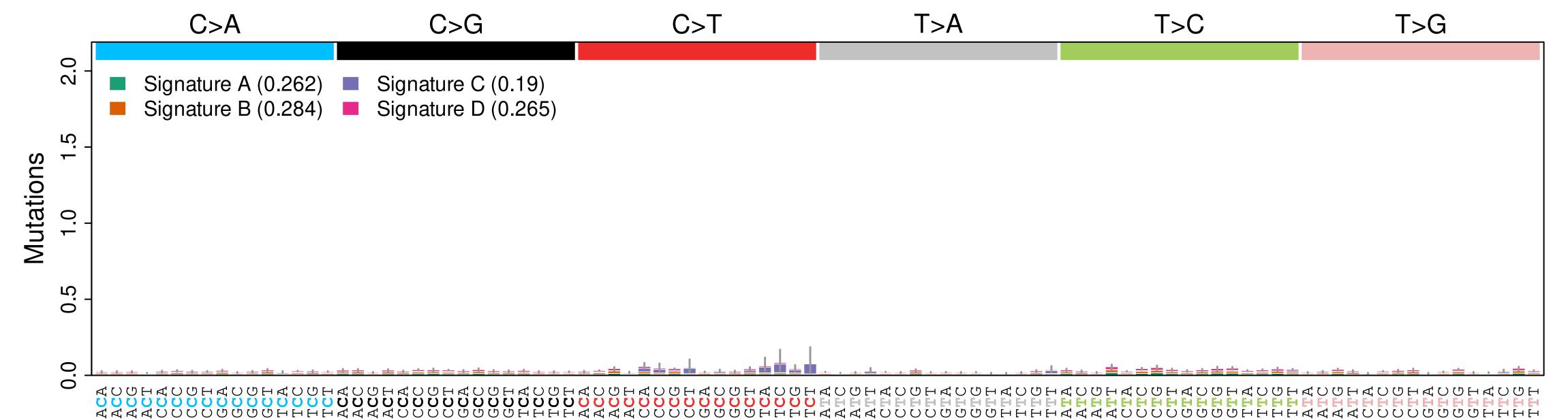
Reconstructed spectrum (cosine similarity = 0.278)



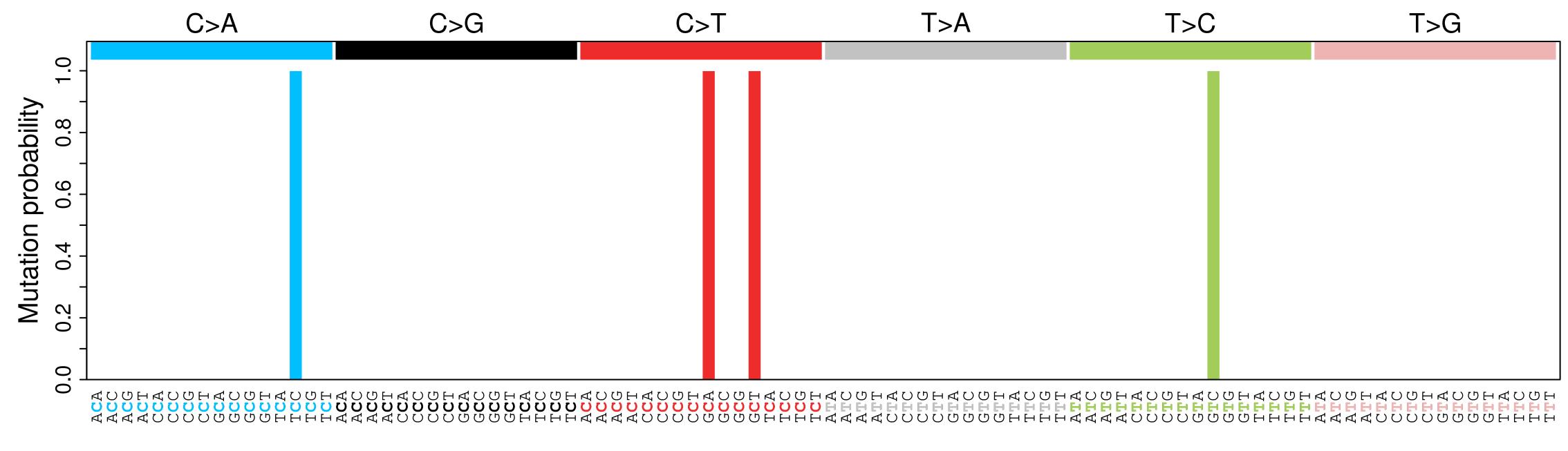
CATD0143a (4 mutations)



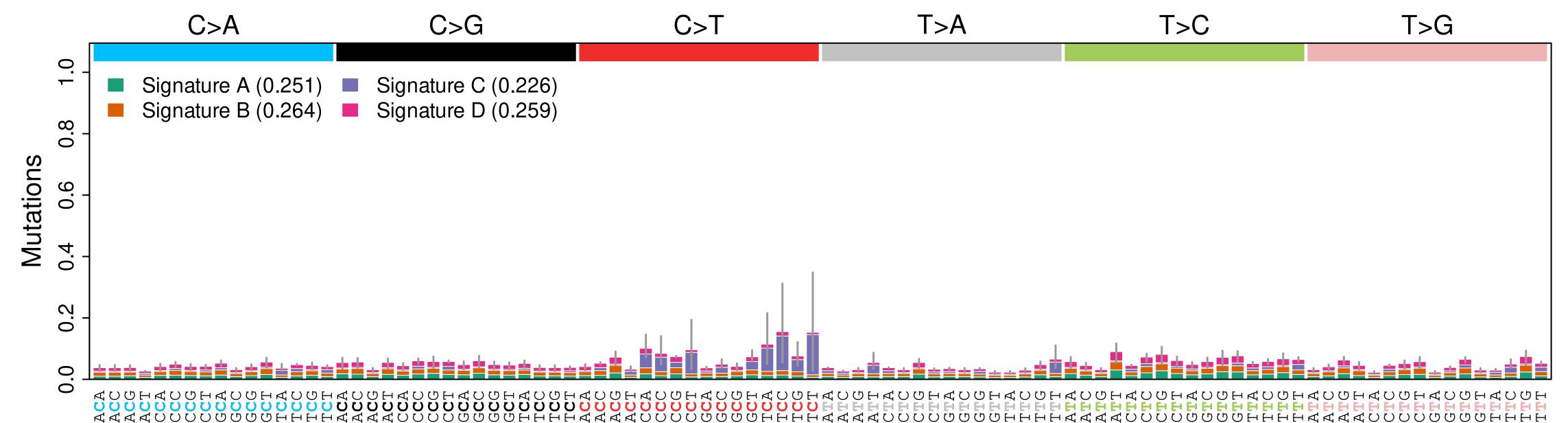




CATD0632a

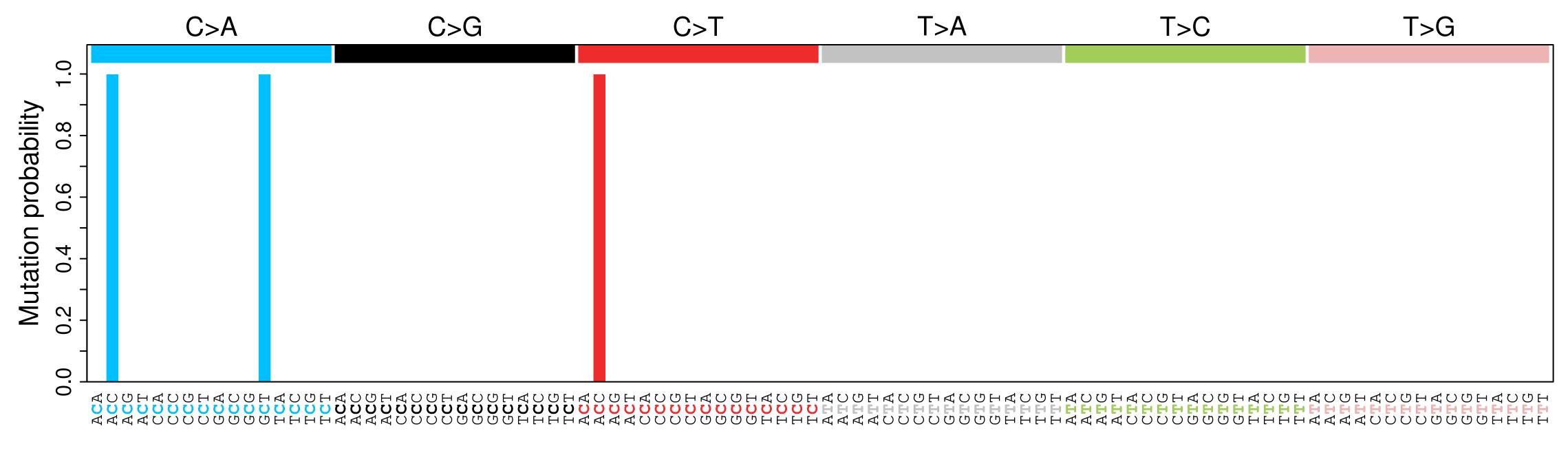




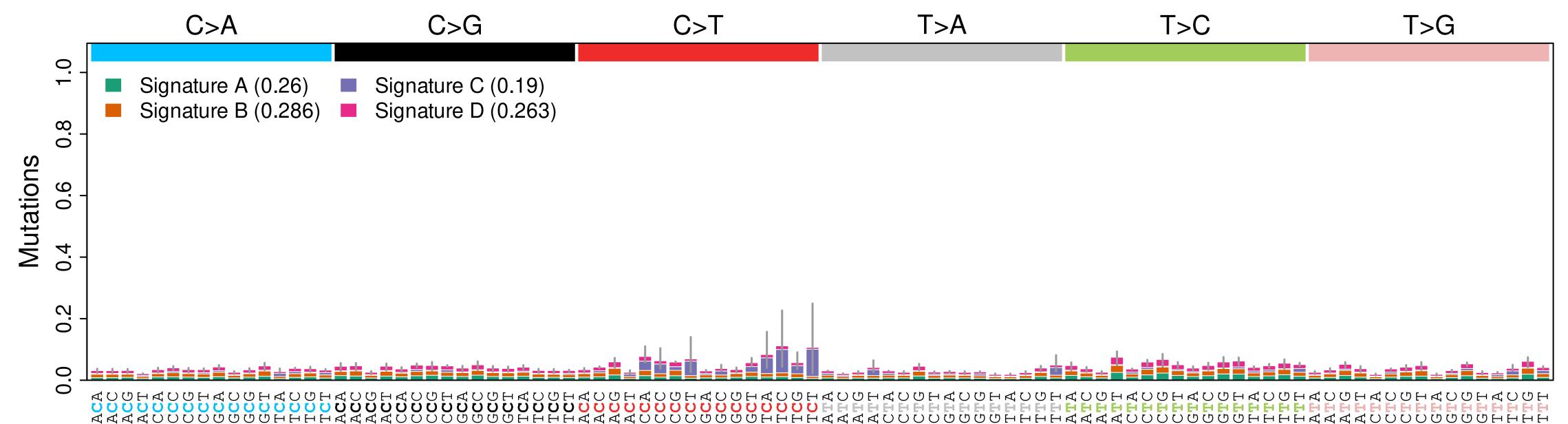


CATD0633a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 1.5 Mutations 0.0 Reconstructed spectrum (cosine similarity = 0.098) T>A T>C T>G C>A C>G C>T 2.0 Signature A (0.259) Signature C (0.189) Signature B (0.288) Signature D (0.265) 5 Mutations 5 0

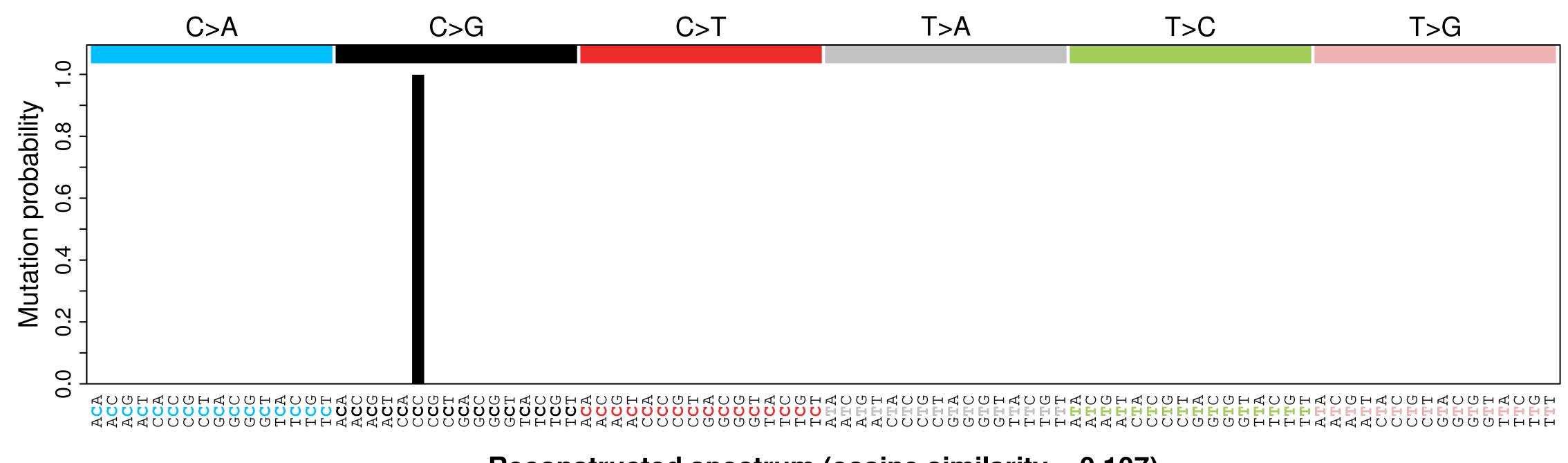


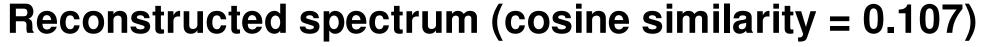


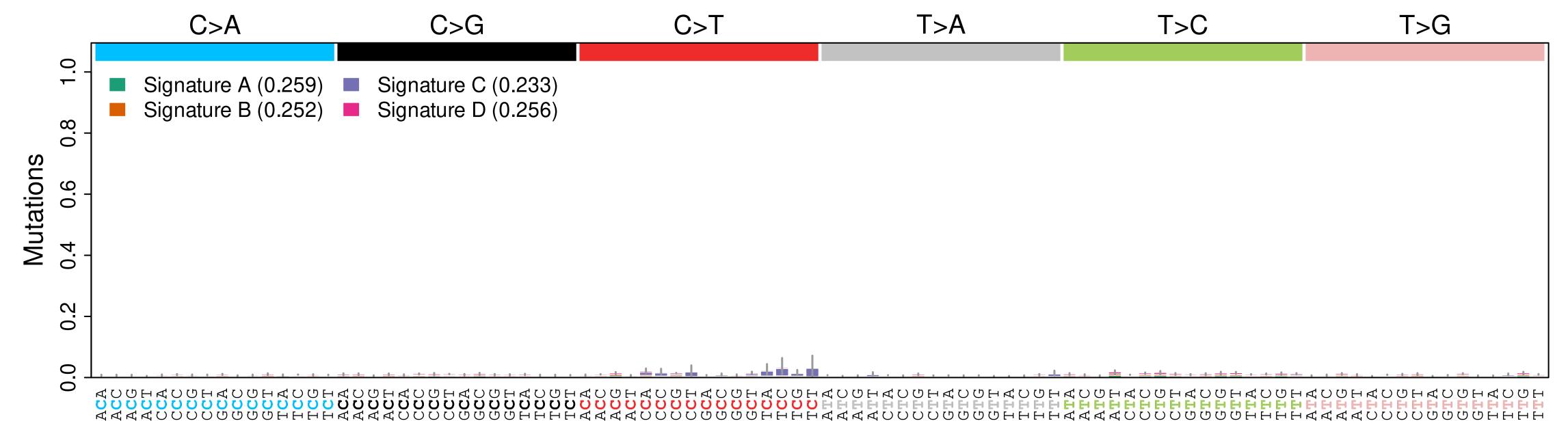






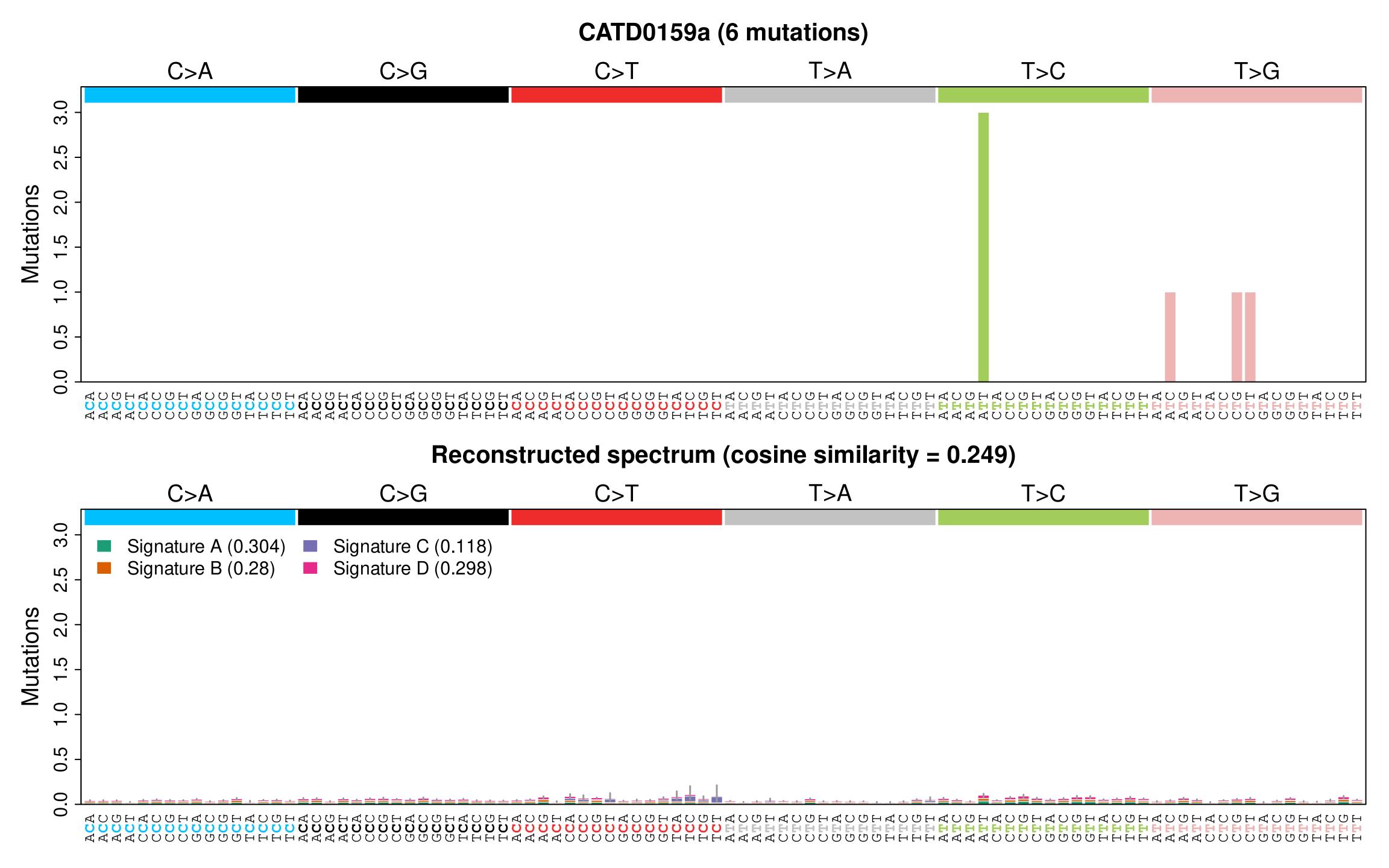




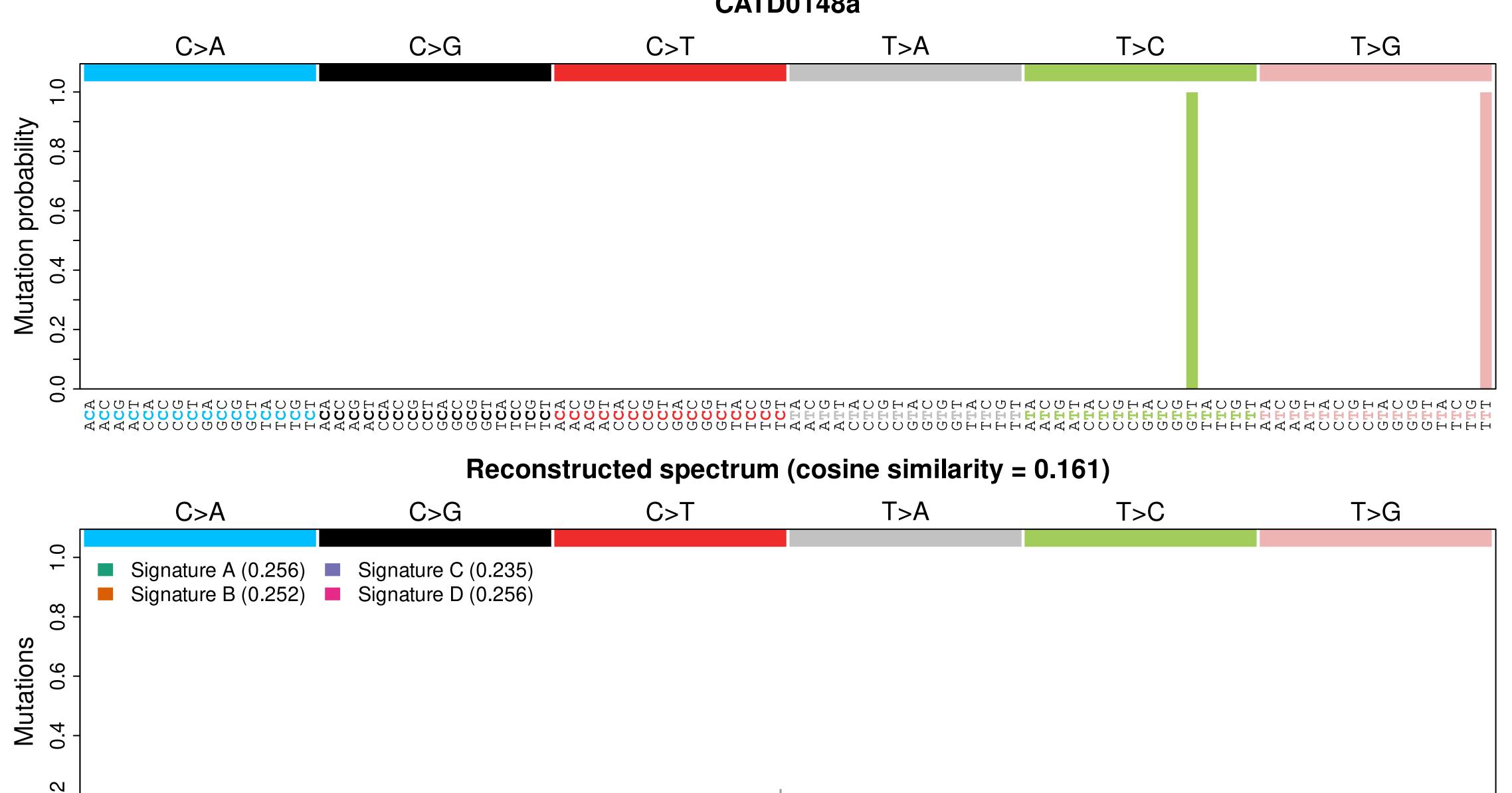


CATD0145a (8 mutations) T>G C>A C>G C>T T>A T>C 3.0 2.5 Mutations 2.0 1.5 0.5 0 **Reconstructed spectrum (cosine similarity = 0.272)** T>A T>C T>G C>A C>G C>T 3.0 Signature A (0.257) Signature C (0.168) Signature B (0.305) Signature D (0.27) 5 S Mutations 2.0 1.5

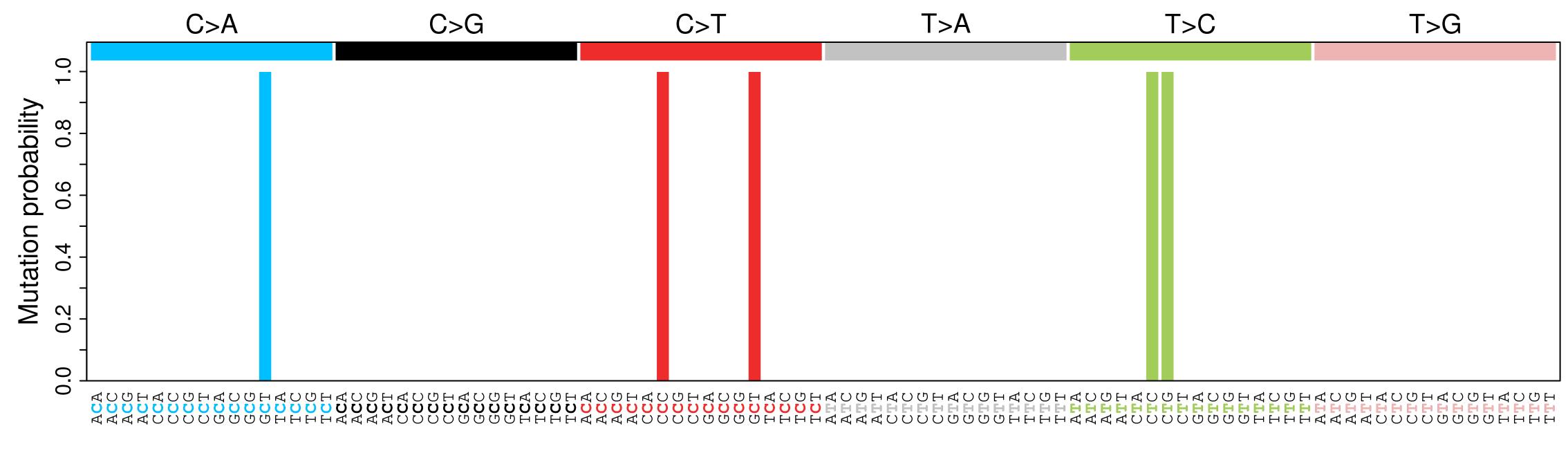
0.5

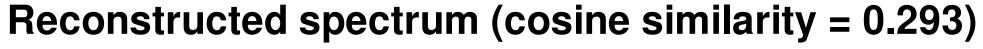


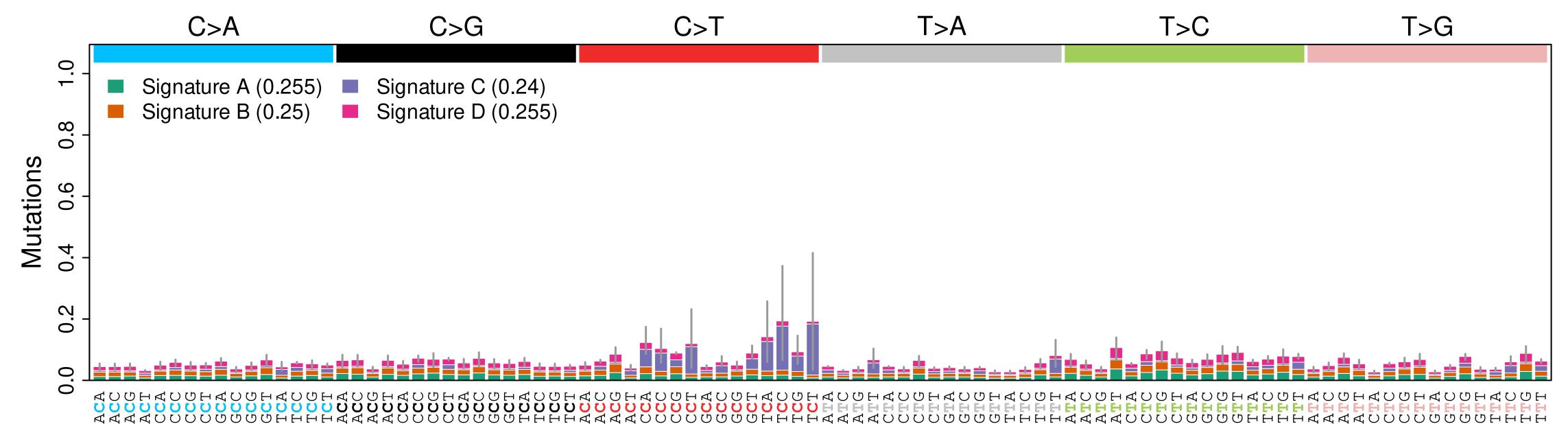




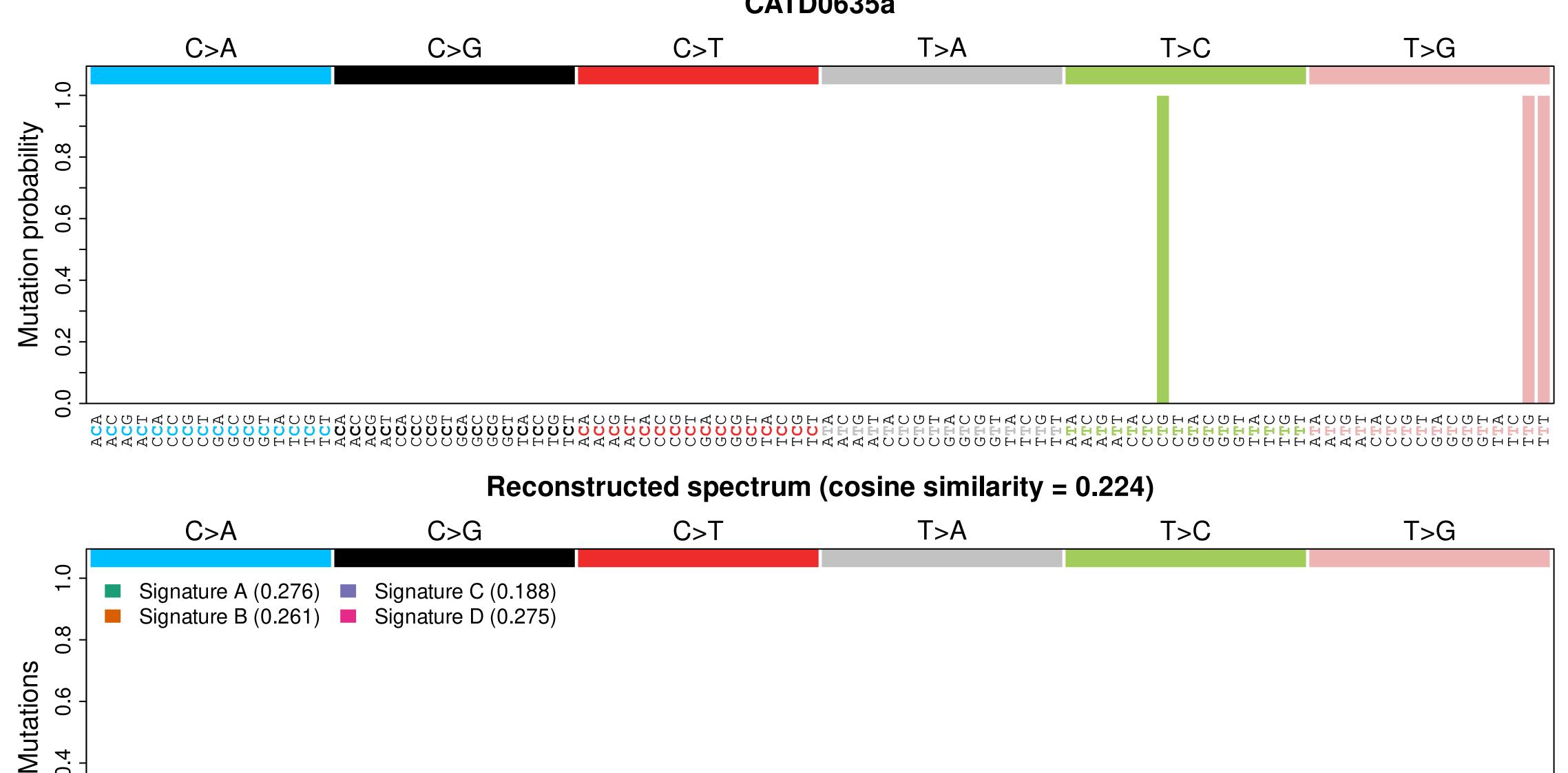
CATD0153a









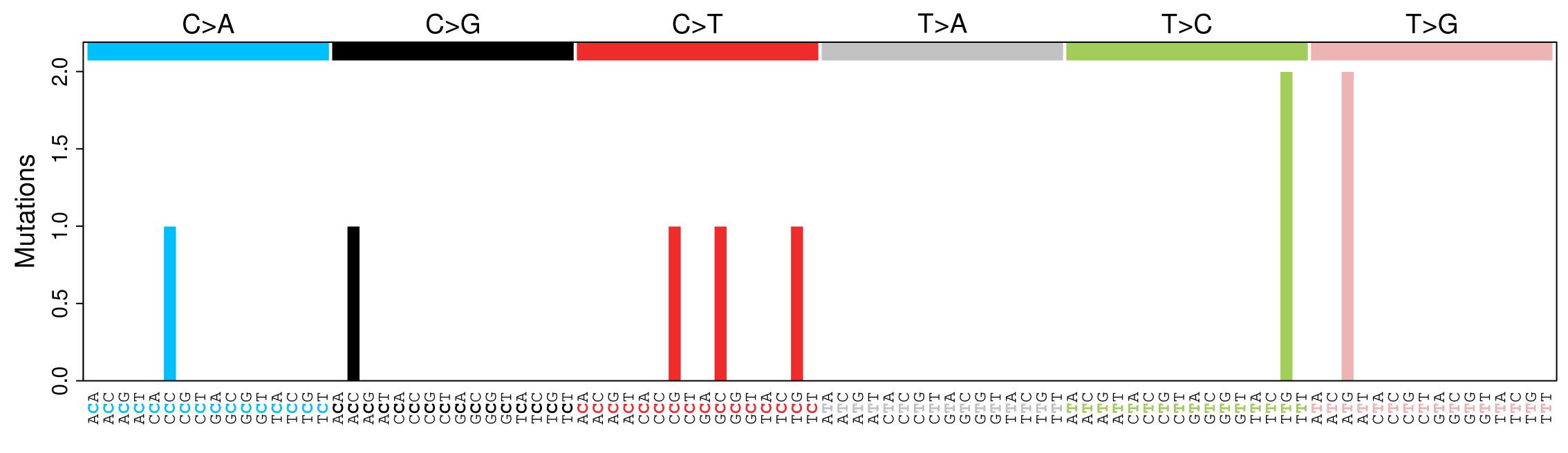


 \mathcal{O} 0

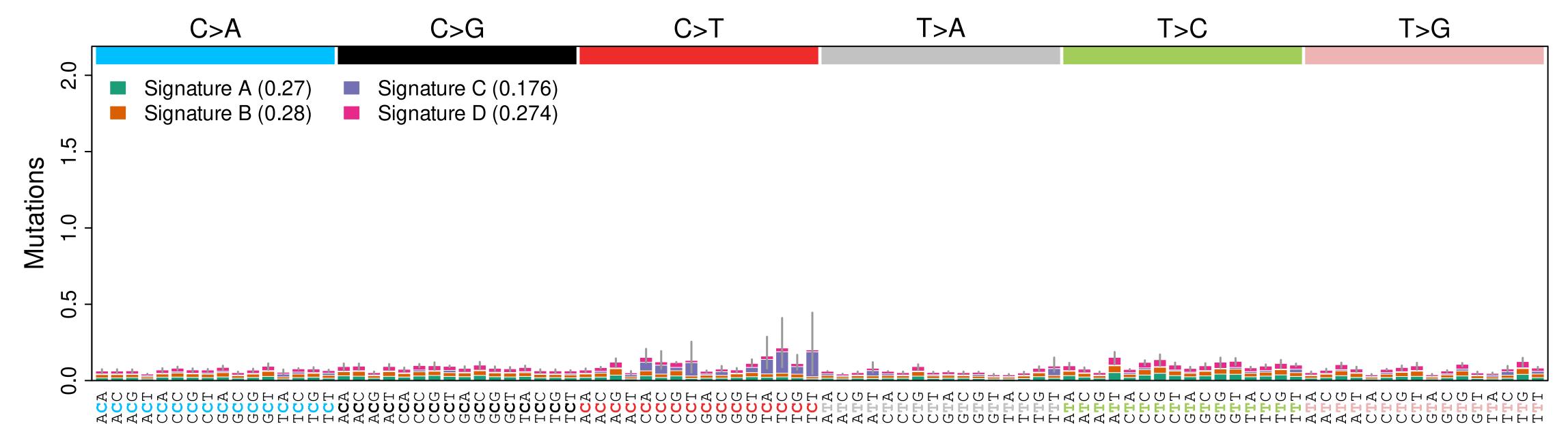
CATD0646a T>C T>G C>A C>G C>T T>A 1.0 Mutation probability 0.8 9.0 0.4 0.2 0.0 **Reconstructed spectrum (cosine similarity = 0.116)** C>A C>G T>A T>C T>G C>T 1.0 Signature A (0.254) Signature C (0.236) Signature B (0.255) Signature D (0.255) 0.8 Mutations 9.0 \mathcal{O} 0

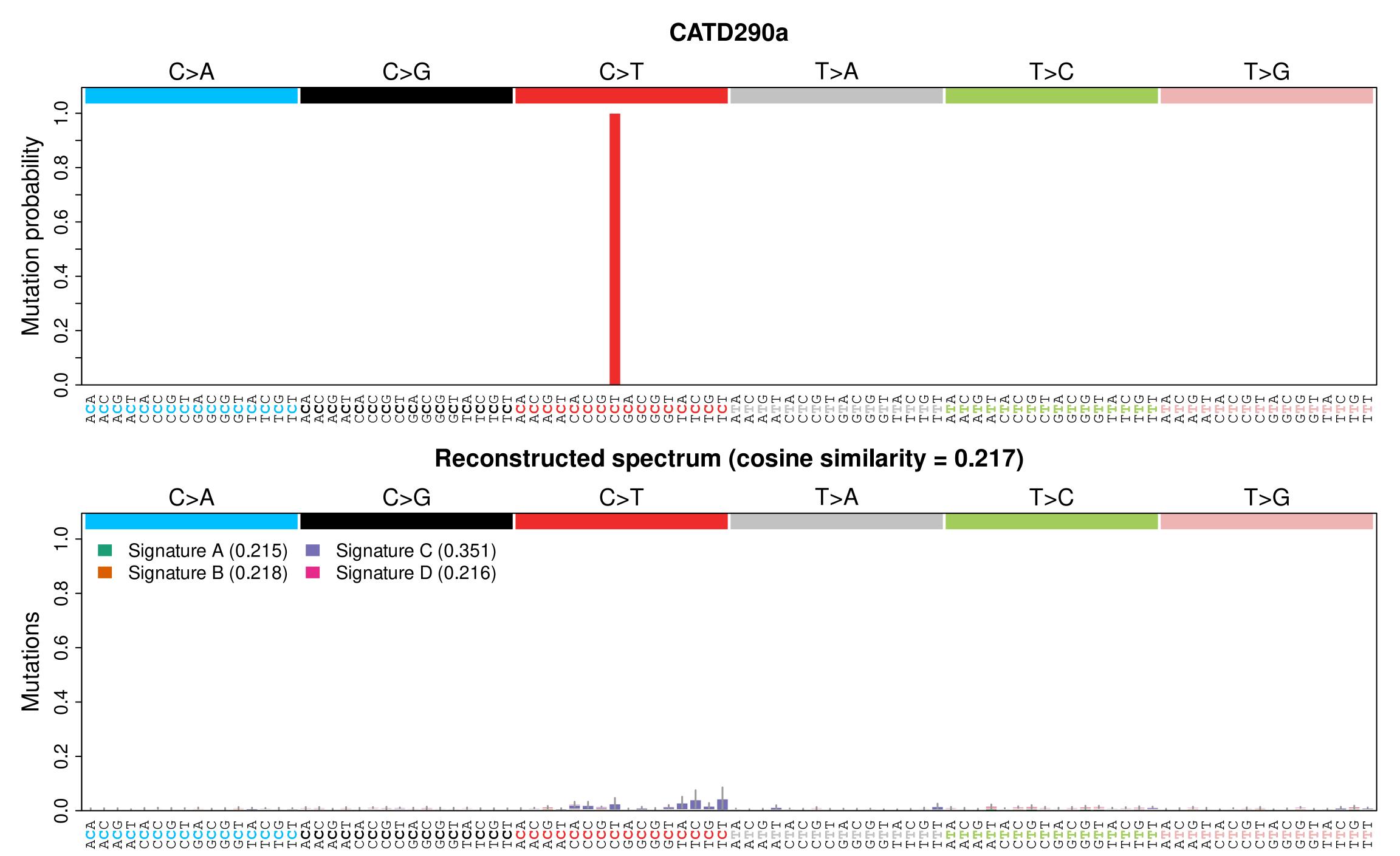
0.0

CATD295a (9 mutations)

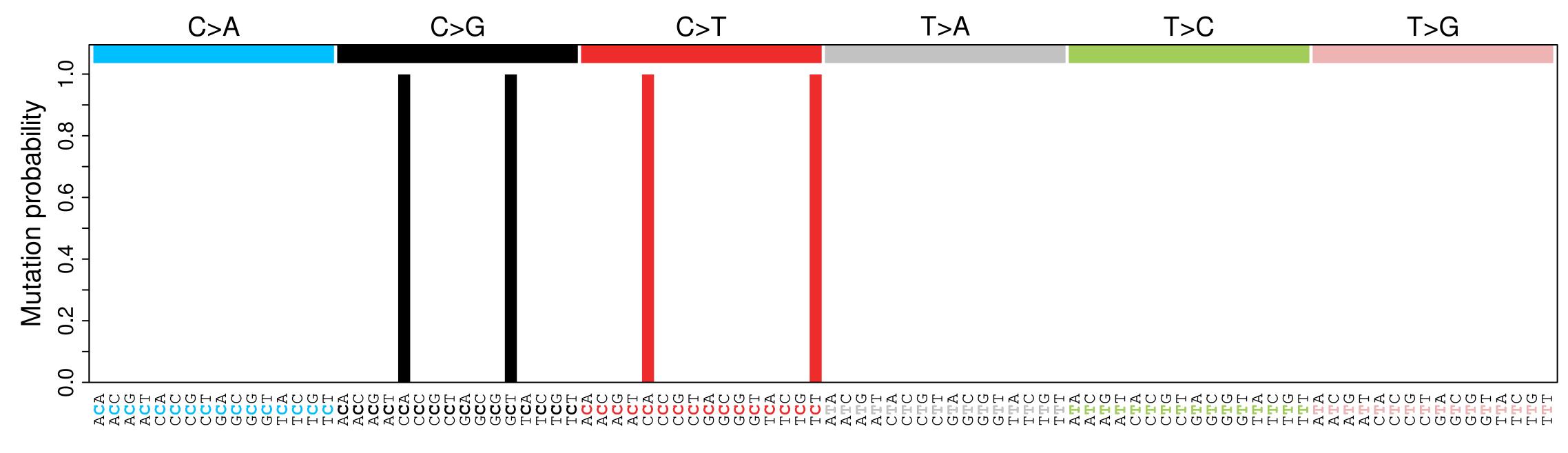


Reconstructed spectrum (cosine similarity = 0.288)

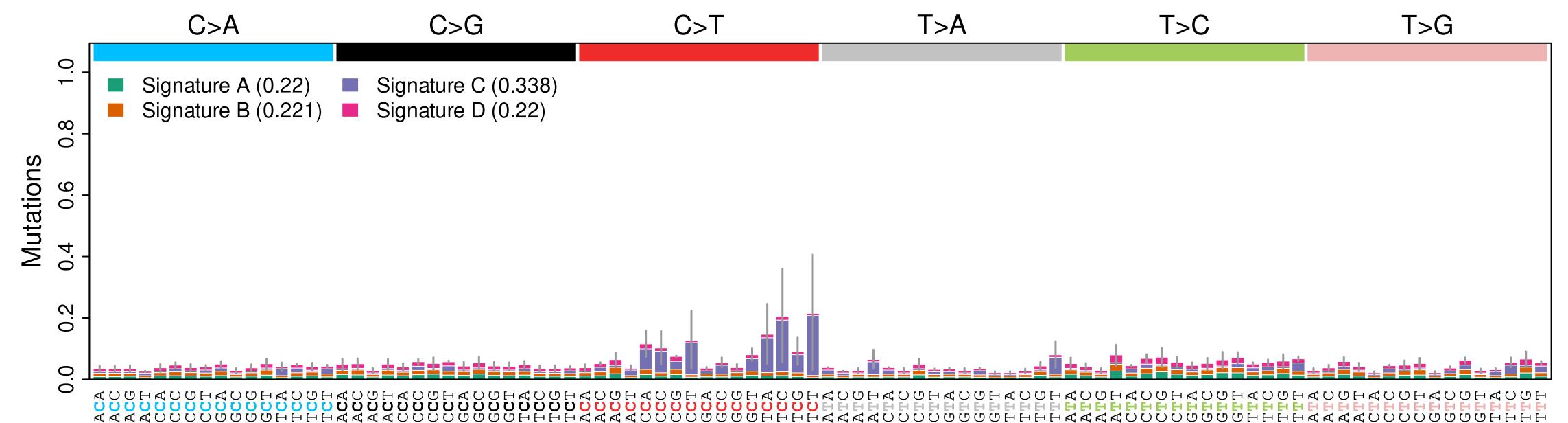




CATD0142a



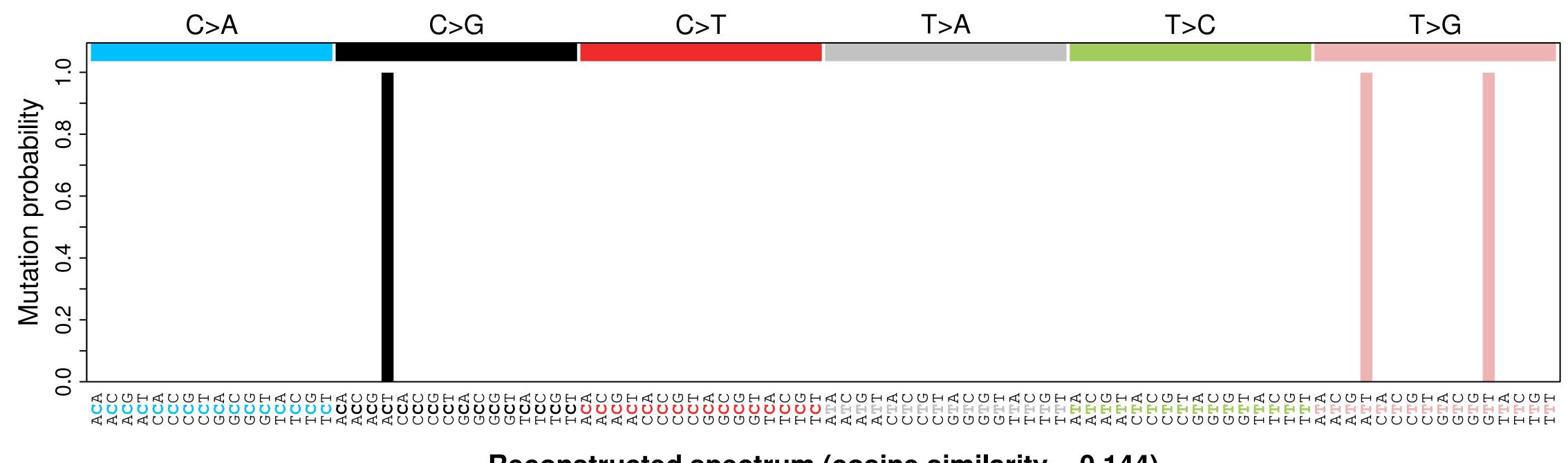
Reconstructed spectrum (cosine similarity = 0.346)

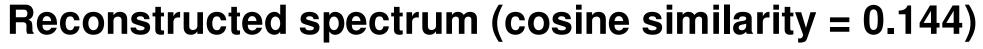


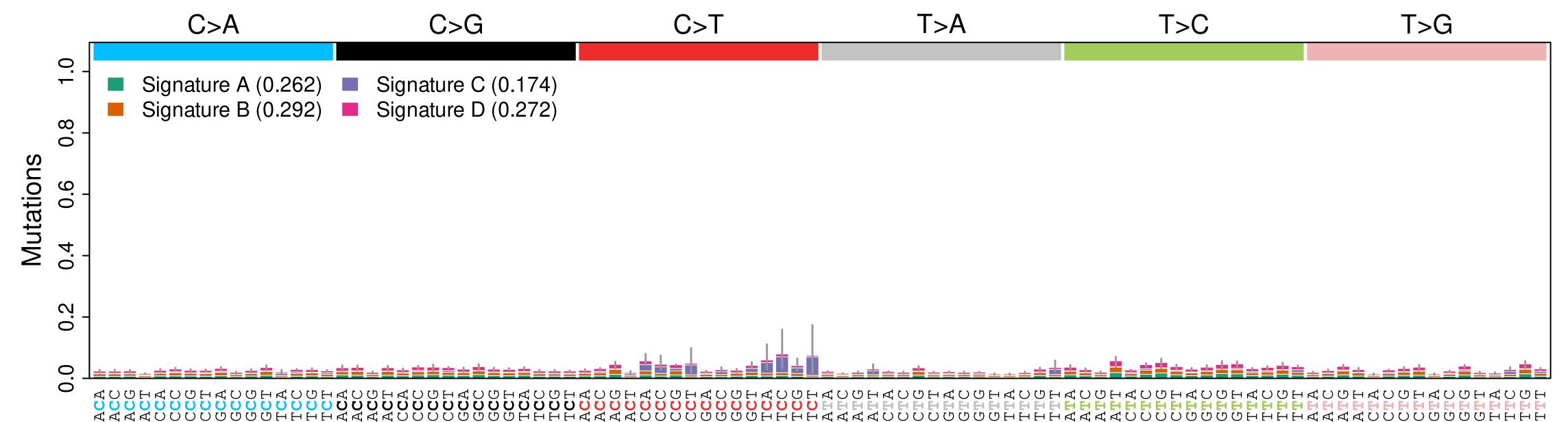
CATD291a C>A T>C T>G C>G C>T T>A 1.0 Mutation probability 0.8 9.0 0.4 0.2 0 **Reconstructed spectrum (cosine similarity = 0.127)** C>A C>G T>A T>C T>G C>T 1.0 Signature A (0.263) Signature C (0.201) Signature D (0.265) Signature B (0.27) 0.8 Mutations 9.0 \mathcal{O}

0

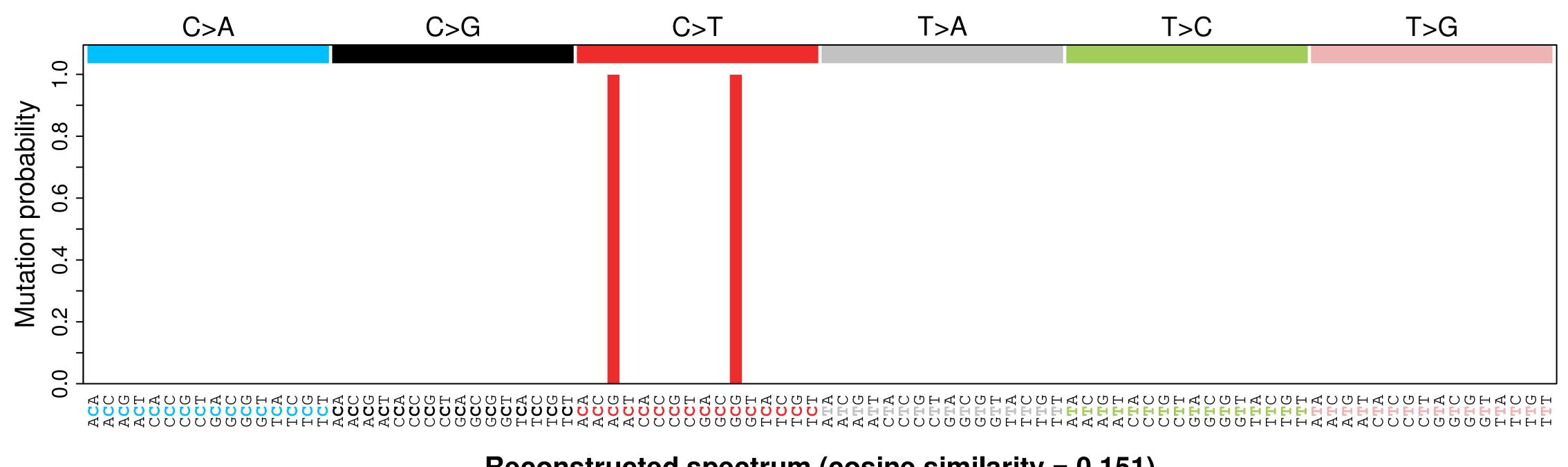


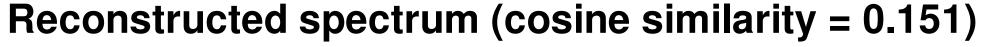


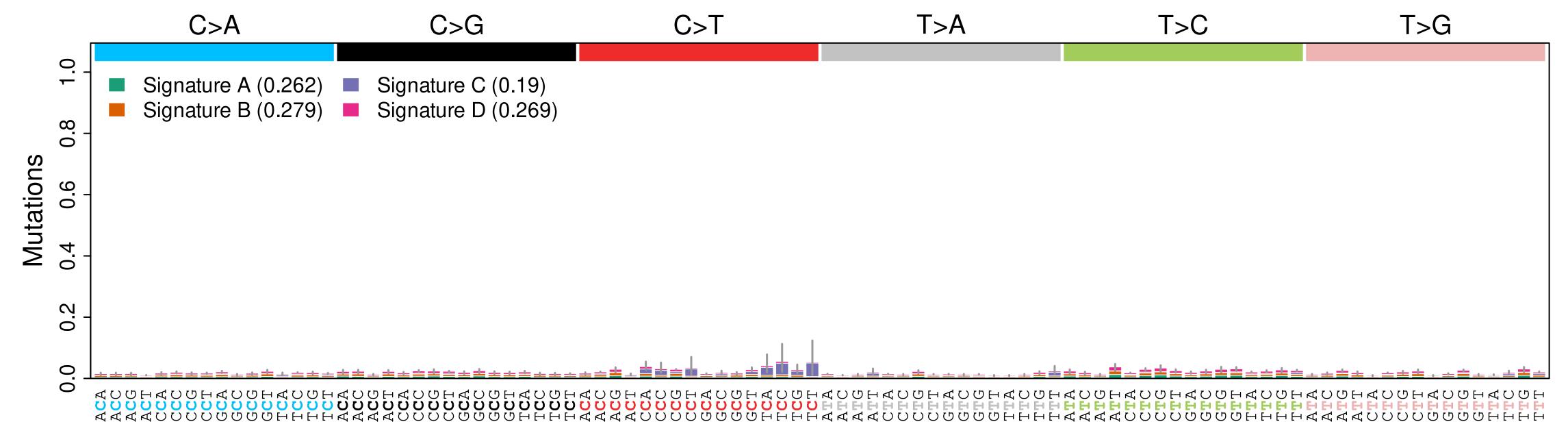




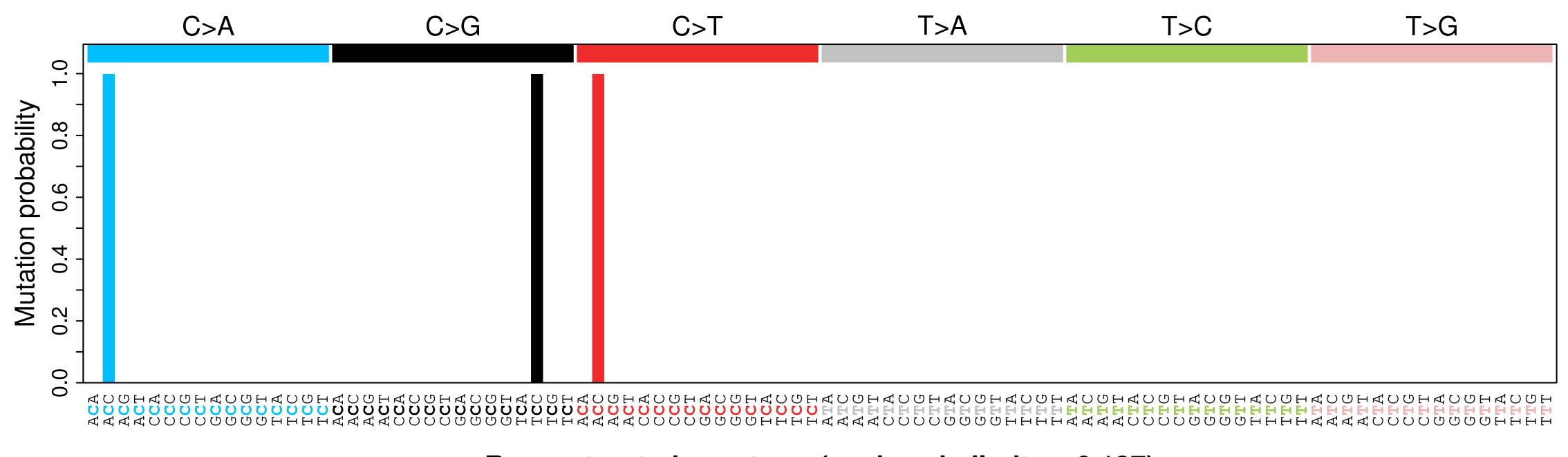




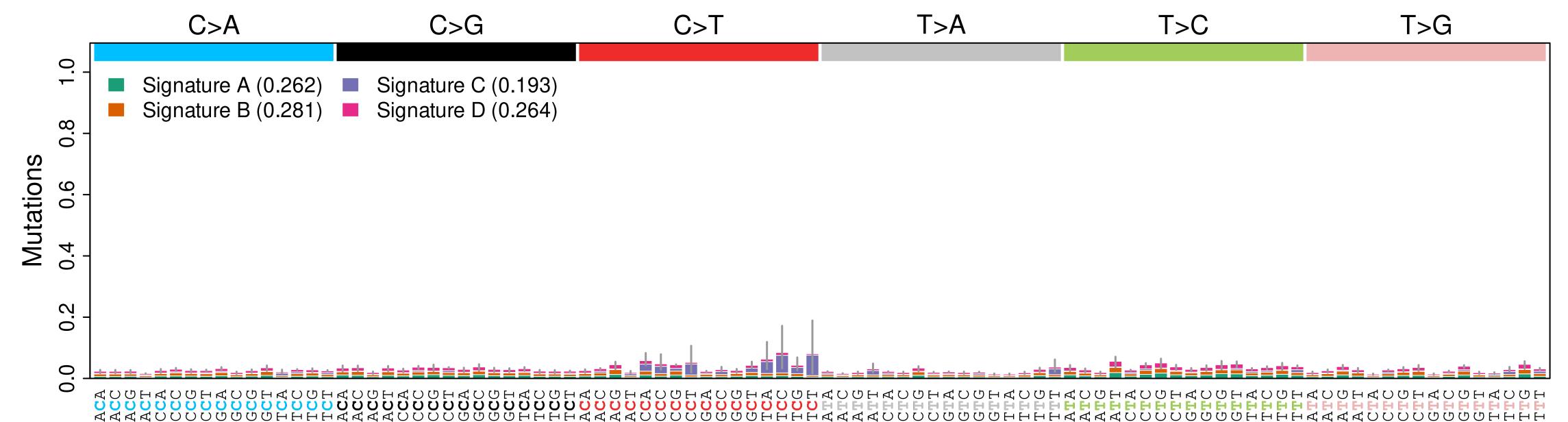




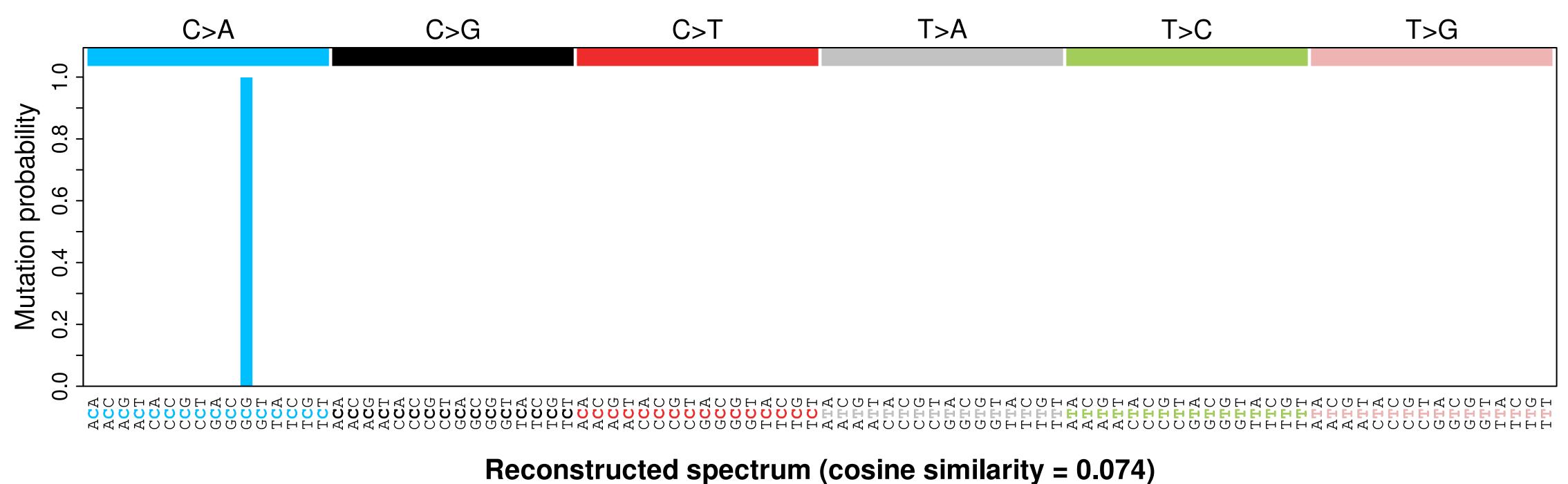




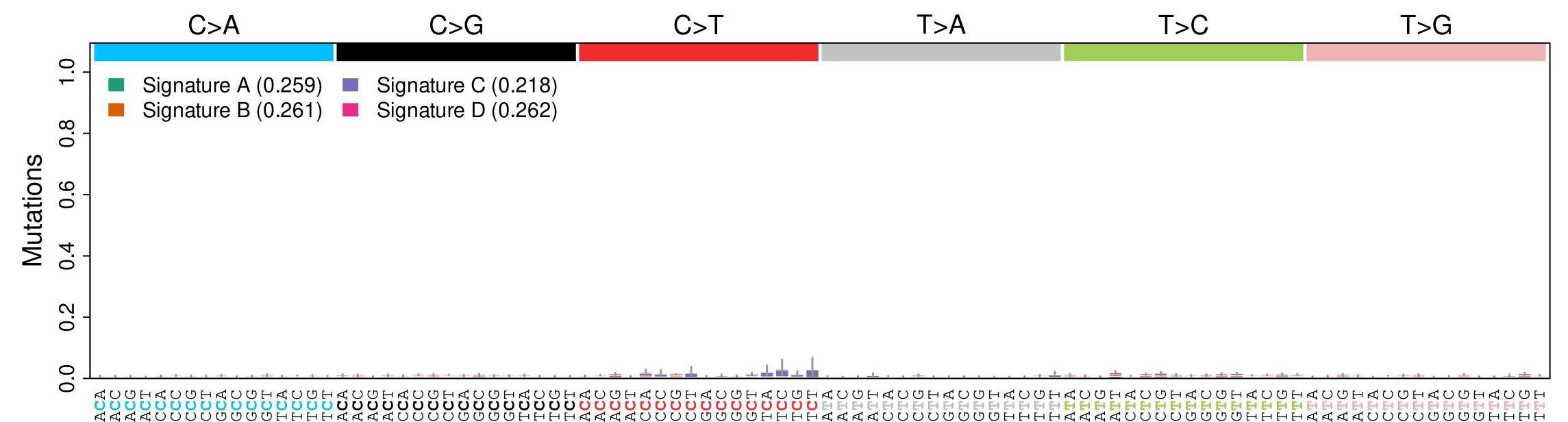












CATD0651a T>C T>G C>A C>G C>T T>A 1.0 Mutation probability 0.8 9.0 0.4 0.2 0.0 **Reconstructed spectrum (cosine similarity = 0.092)** C>A C>G T>A T>C T>G C>T 1.0 Signature A (0.243) Signature C (0.26) Signature D (0.246) Signature B (0.25) 0.8 Mutations 9.0 \mathcal{O} 0

0.0



