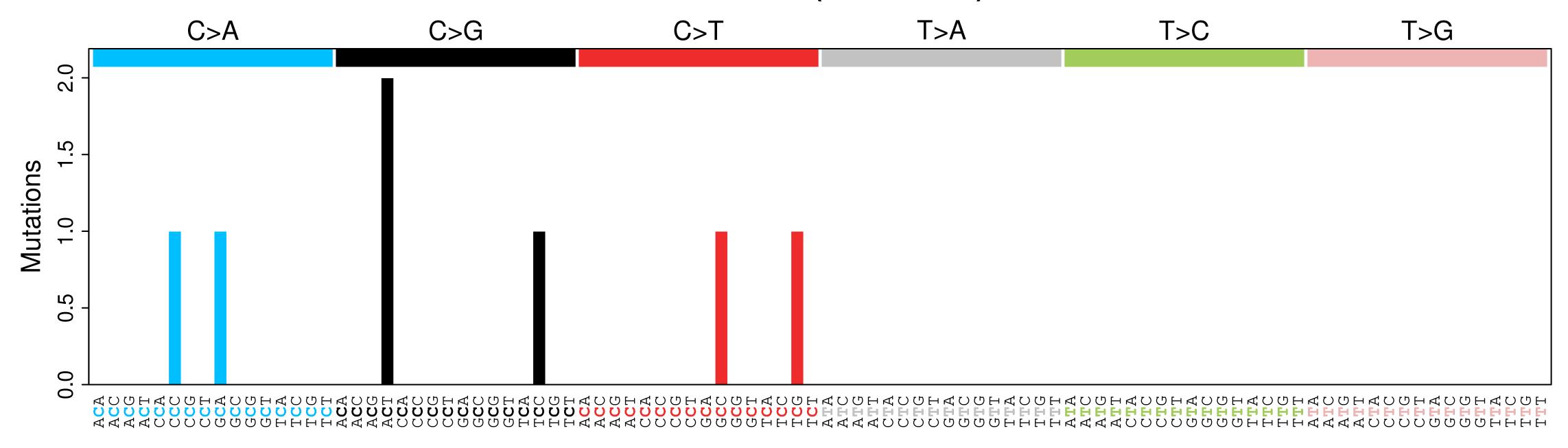
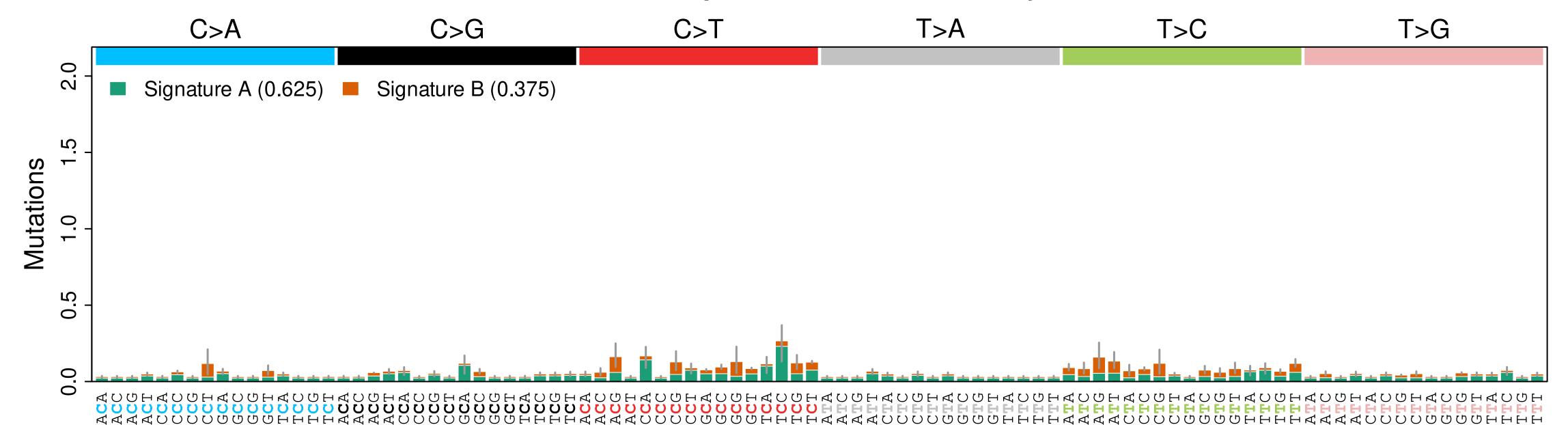
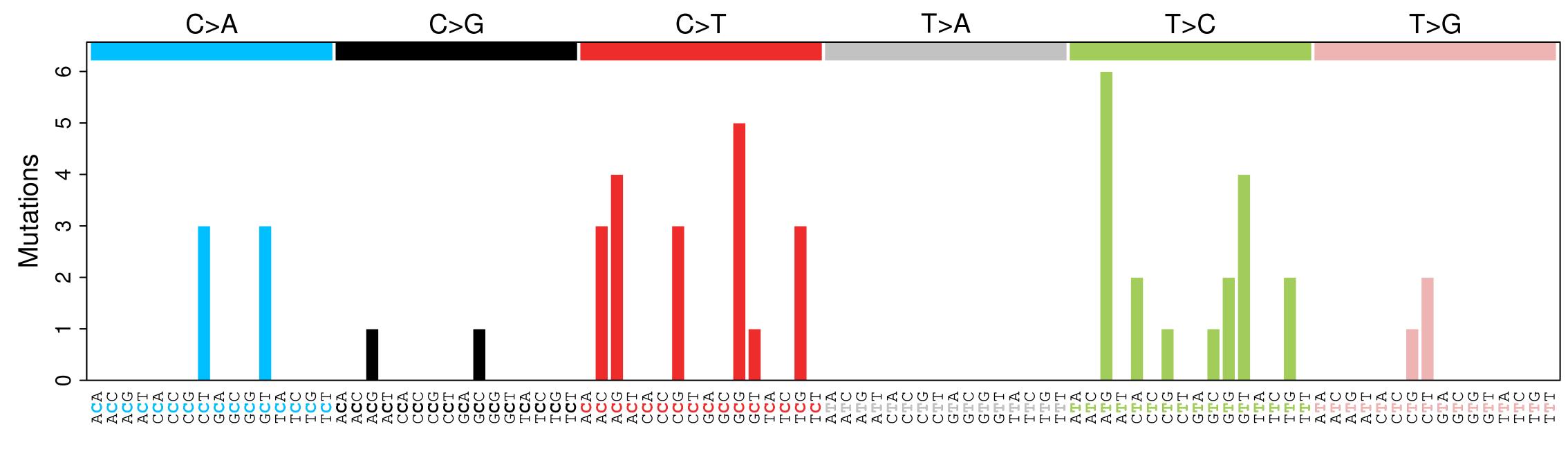
CATD0621a (7 mutations)



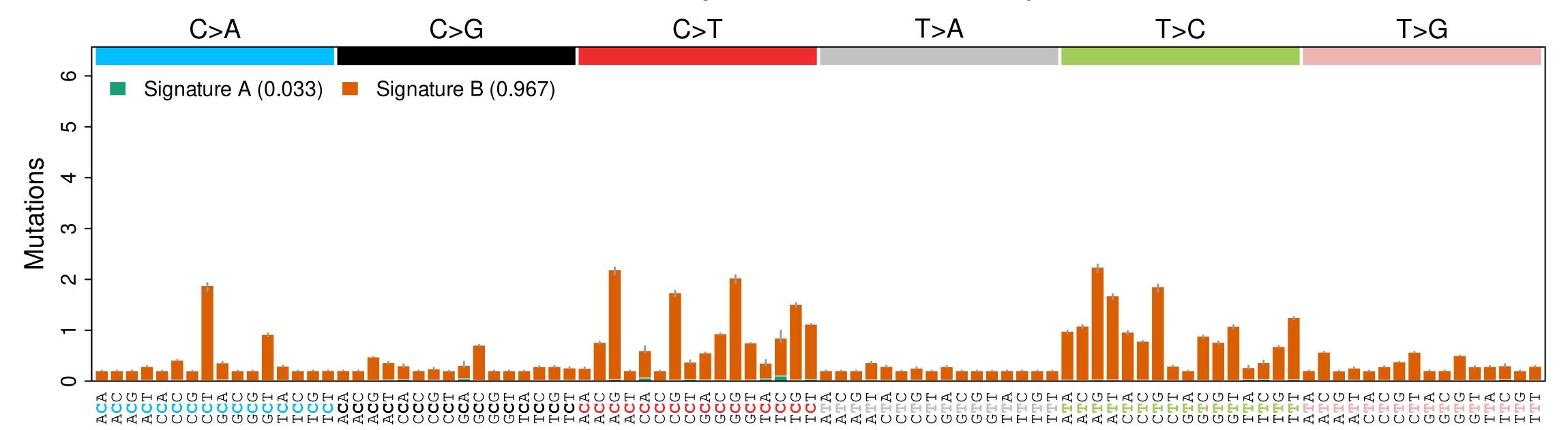
Reconstructed spectrum (cosine similarity = 0.244)



CATD0463a (48 mutations)

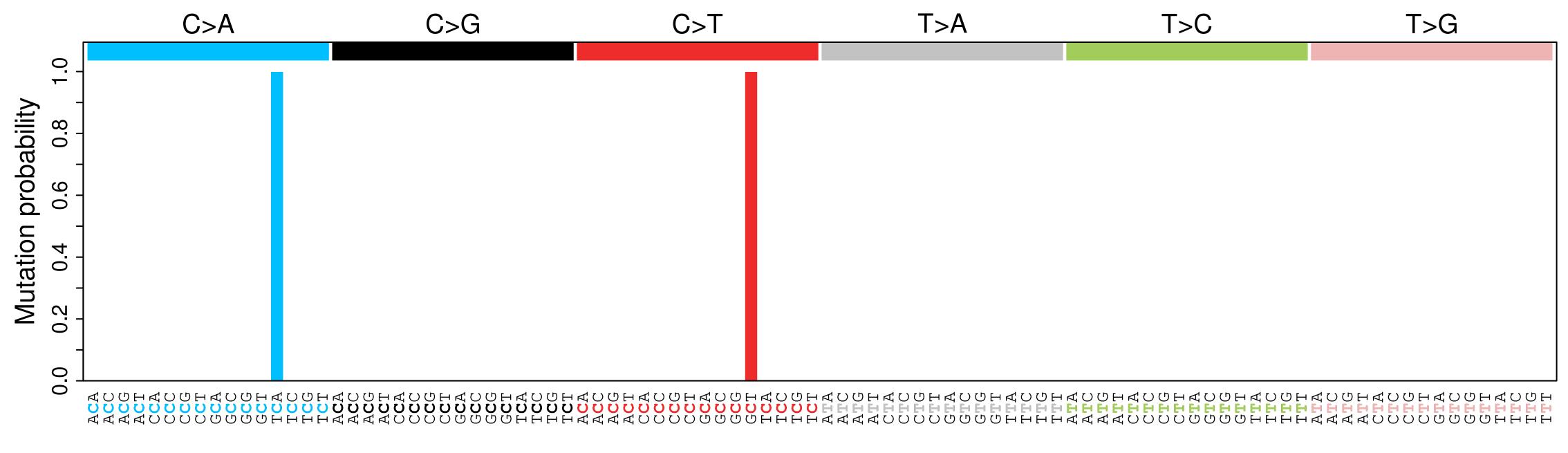


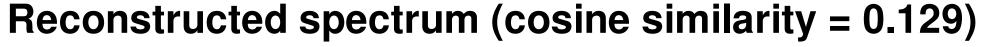
Reconstructed spectrum (cosine similarity = 0.772)

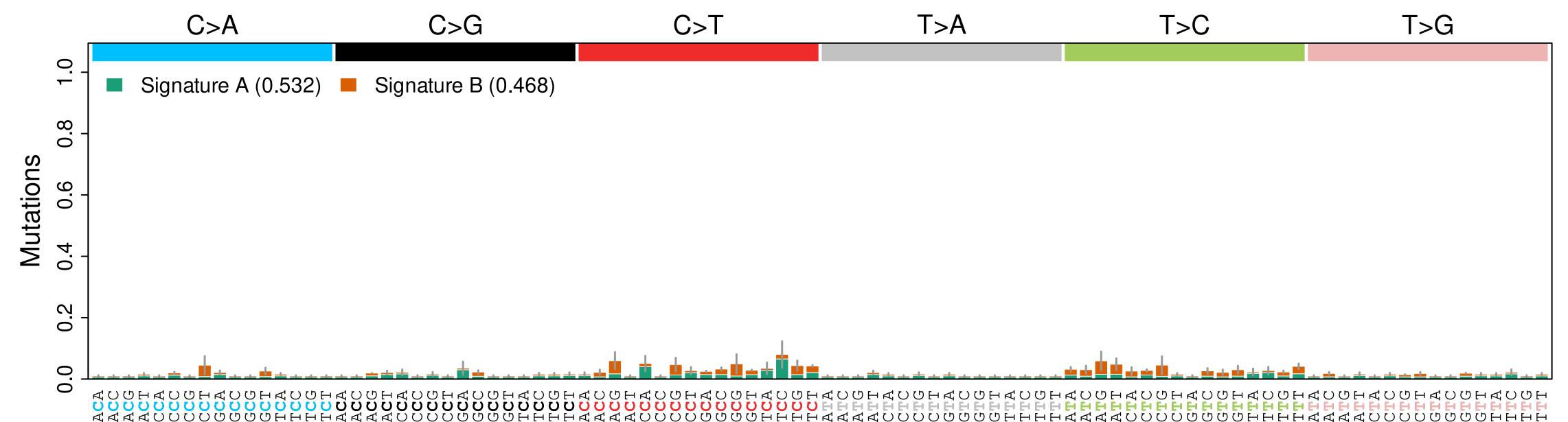


CATD0453a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.347)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.655) Signature B (0.345) 5 Mutations 2 0 0

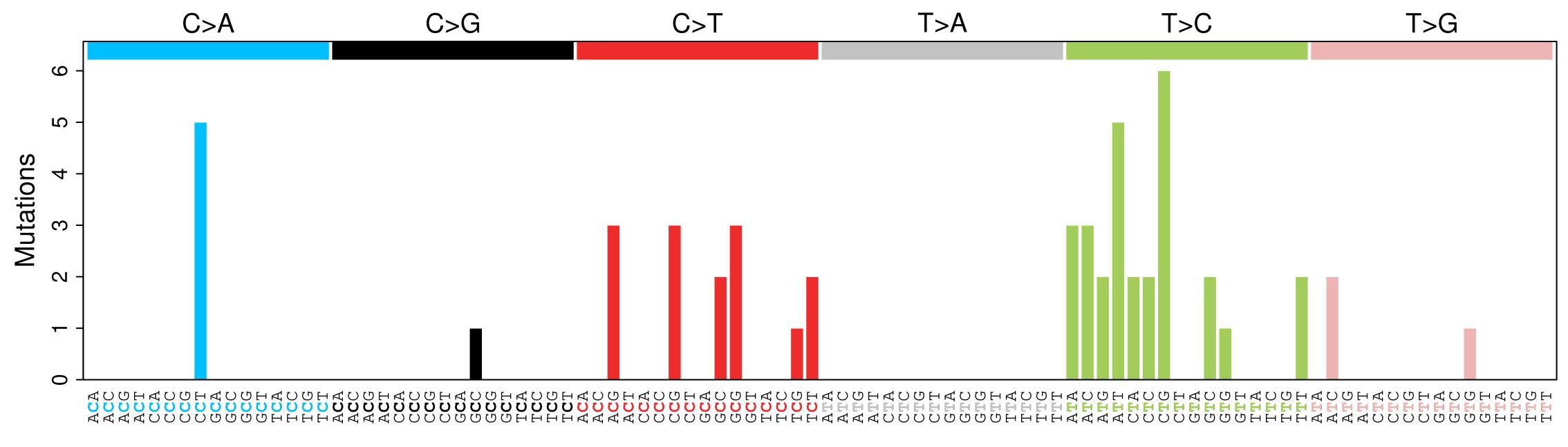




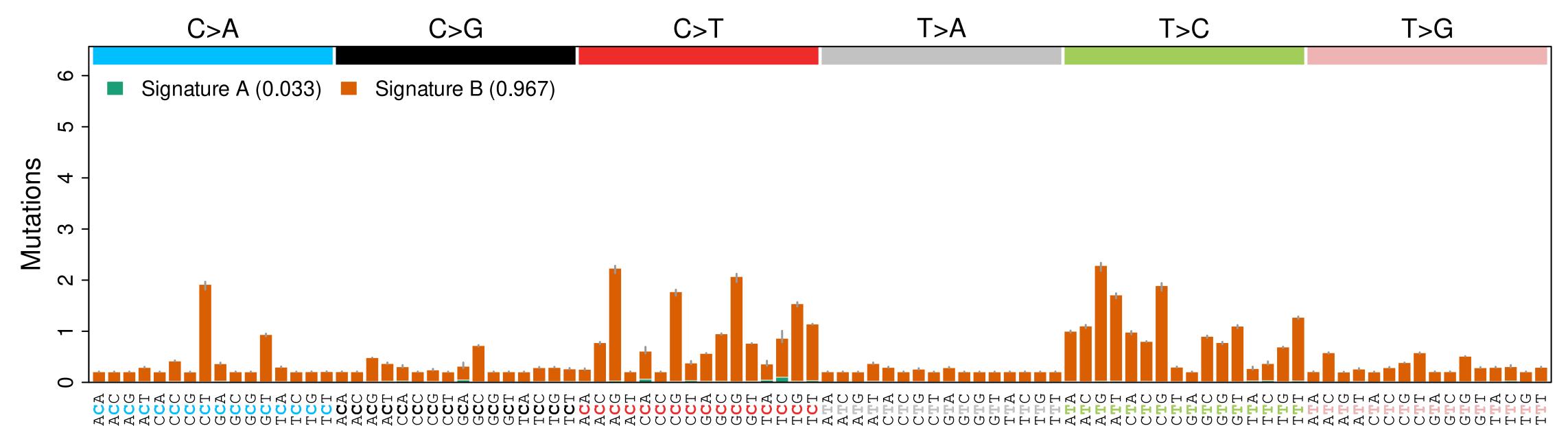




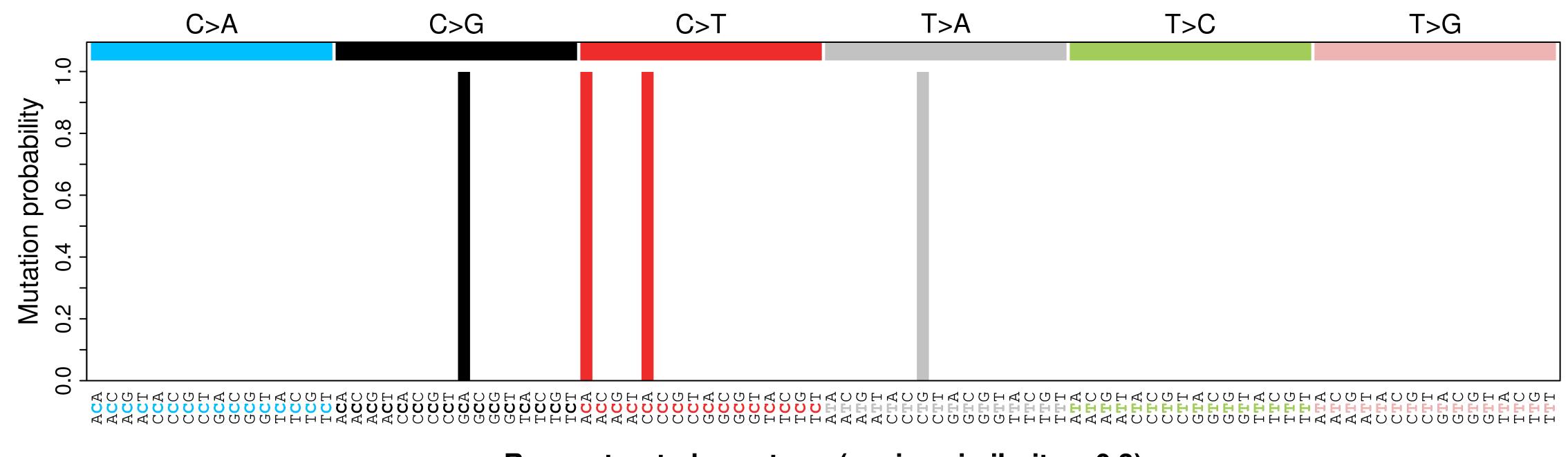
CATD0465a (51 mutations)



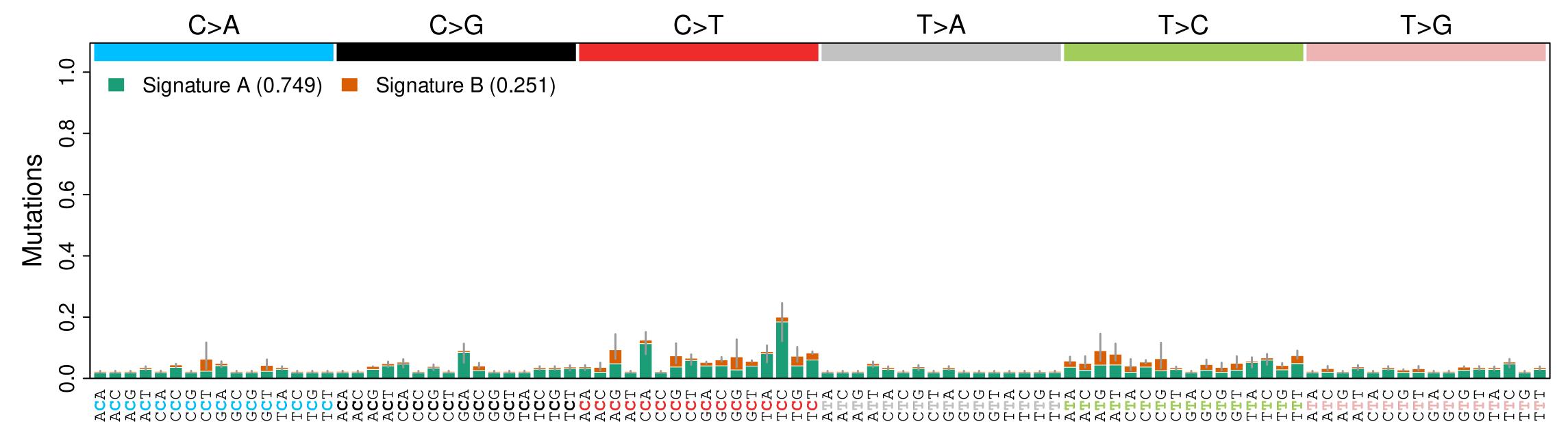
Reconstructed spectrum (cosine similarity = 0.821)



CATD0458a



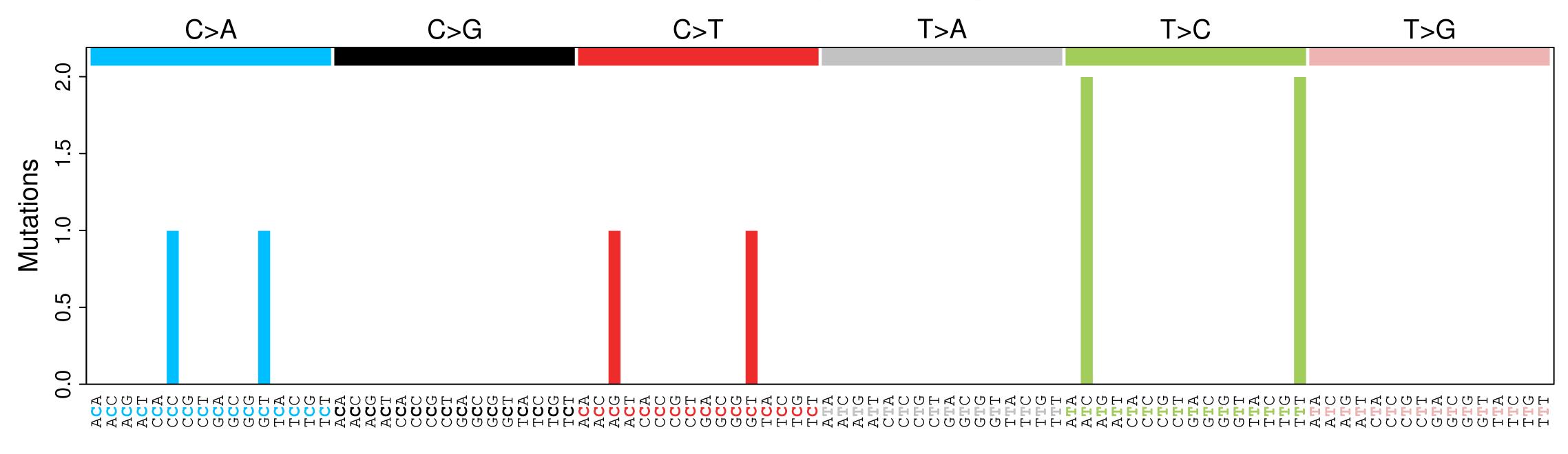
Reconstructed spectrum (cosine similarity = 0.3)

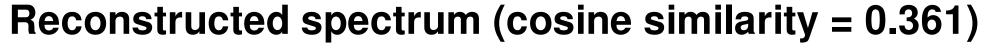


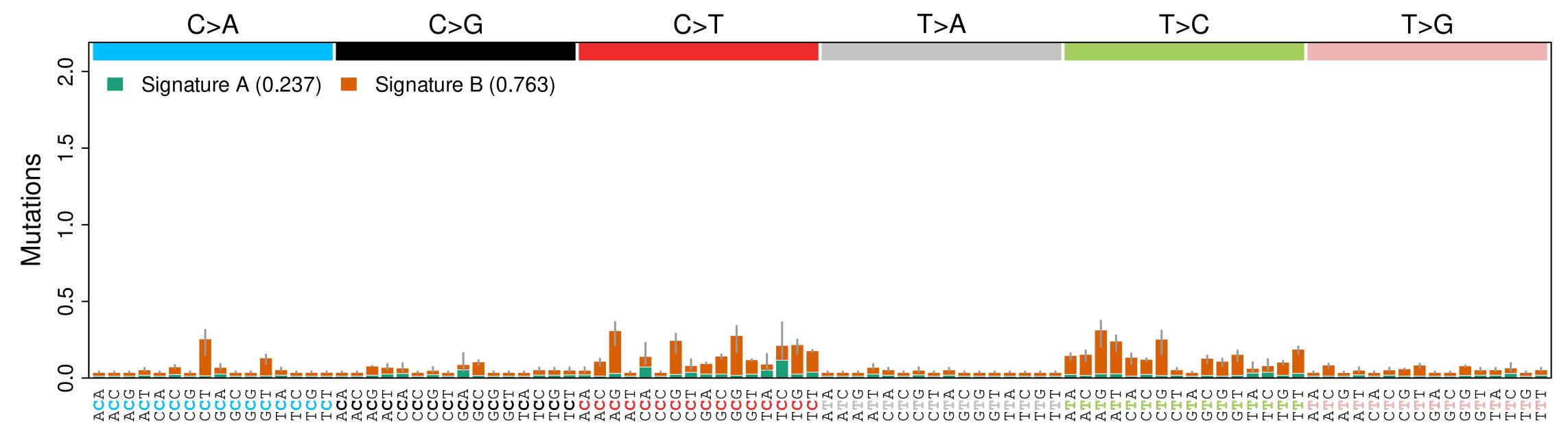
CATD0466a C>G T>C T>G C>A C>T T>A 1.0 Mutation probability 0.8 9.0 0.4 0.2 0.0 **Reconstructed spectrum (cosine similarity = 0.065)** C>A C>G T>A T>C T>G C>T 1.0 Signature A (0.545) Signature B (0.455) 0.8 Mutations 9.0 \mathcal{O} 0

0.0

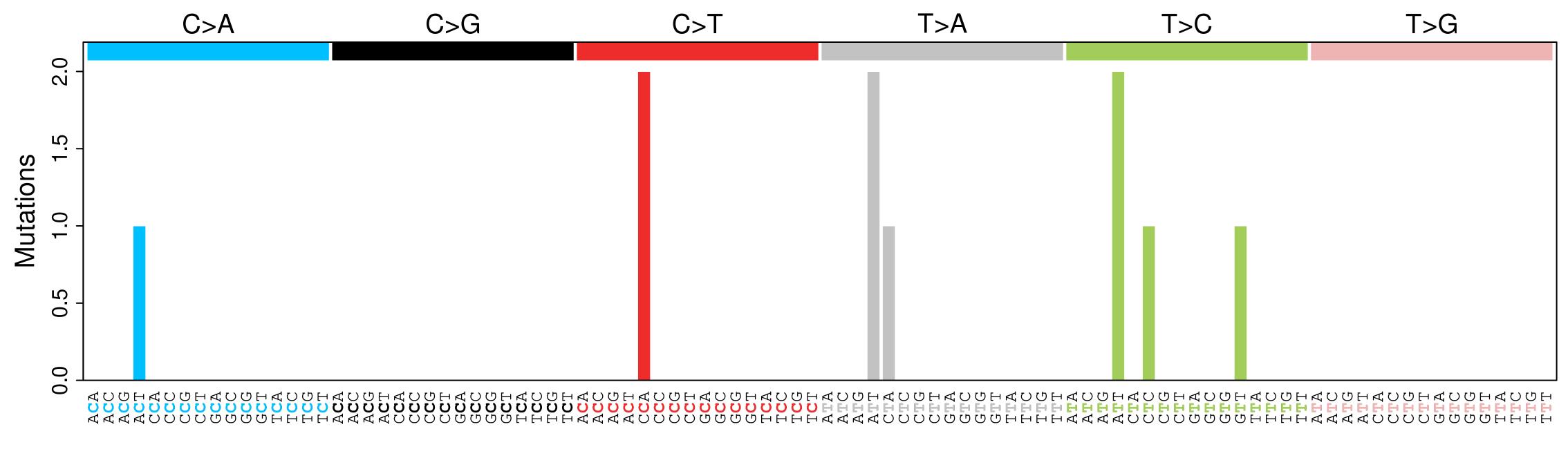
CATD0454a (8 mutations)



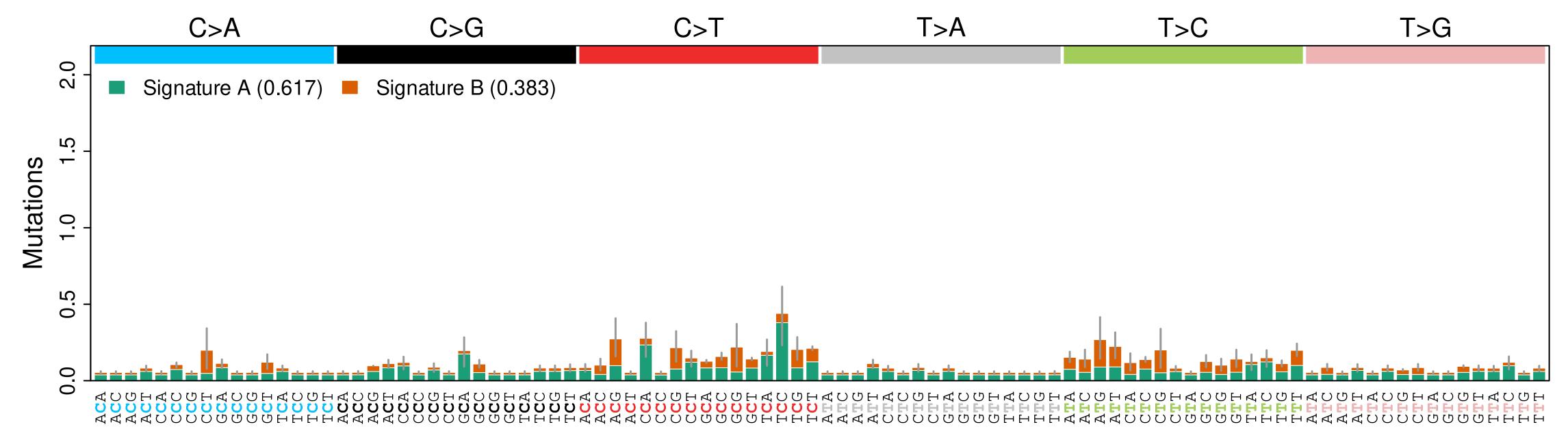




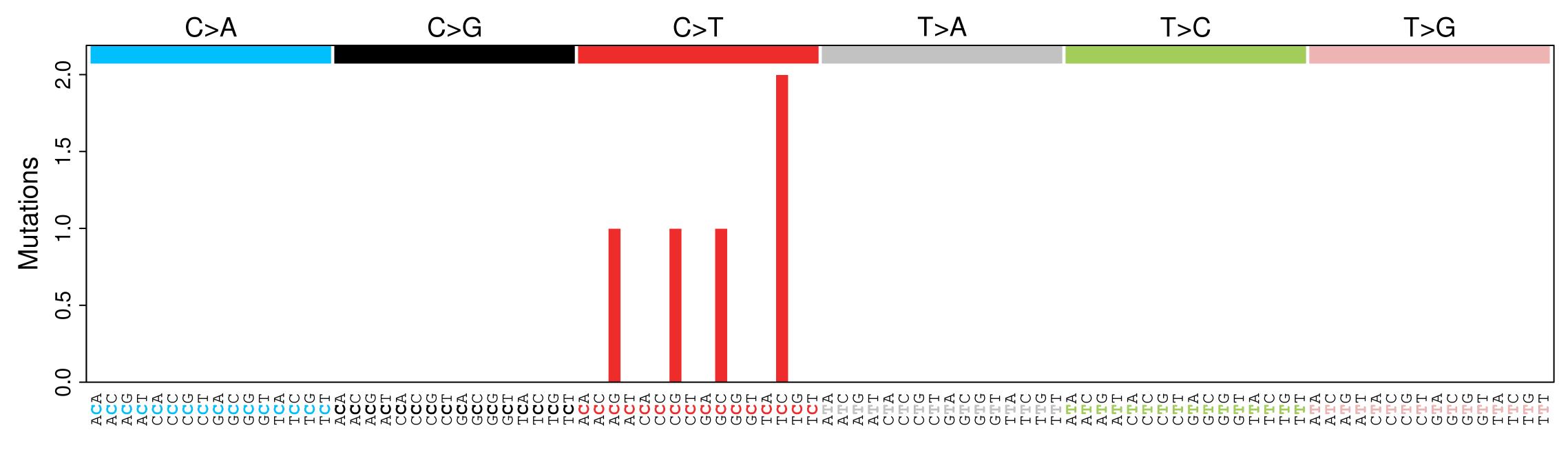
CATD0446a (10 mutations)



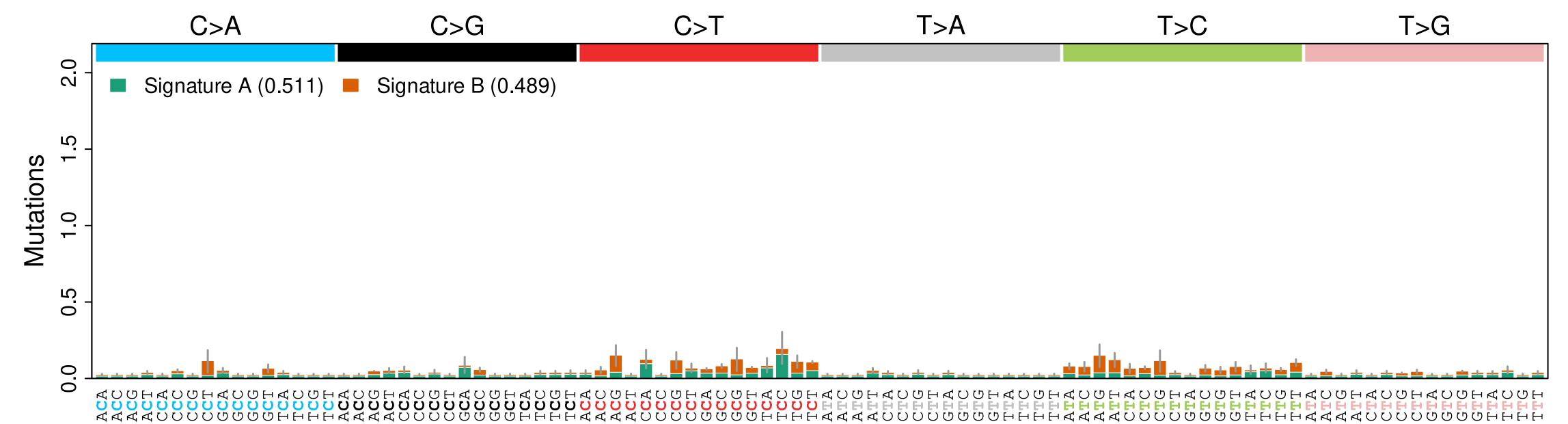
Reconstructed spectrum (cosine similarity = 0.344)



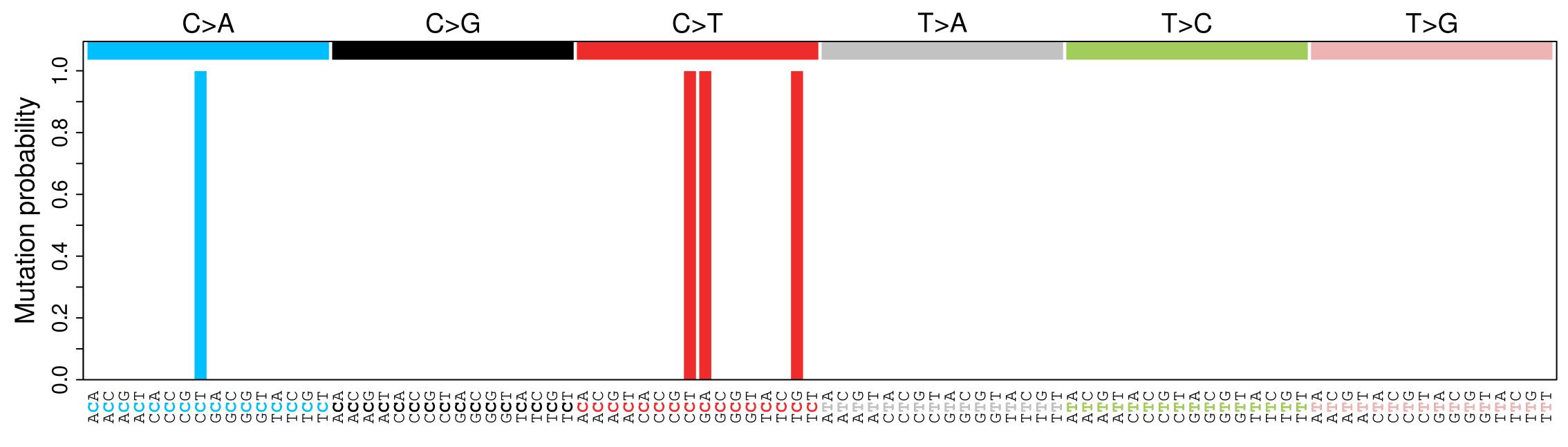
CATD0451a (5 mutations)

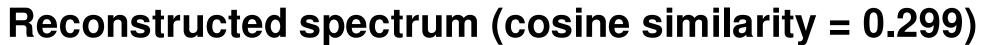


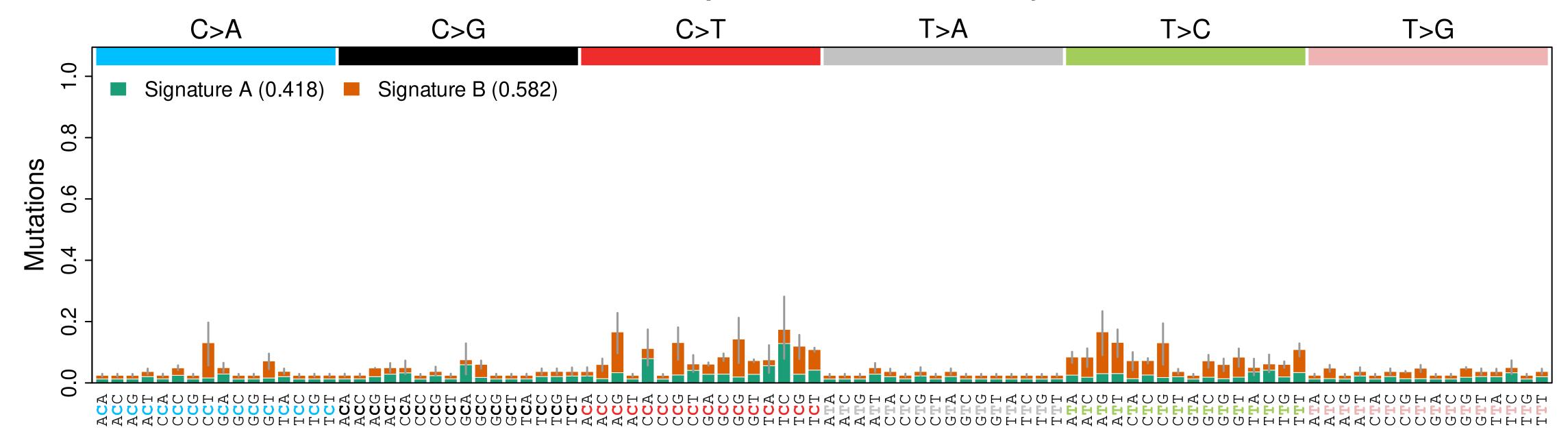
Reconstructed spectrum (cosine similarity = 0.46)



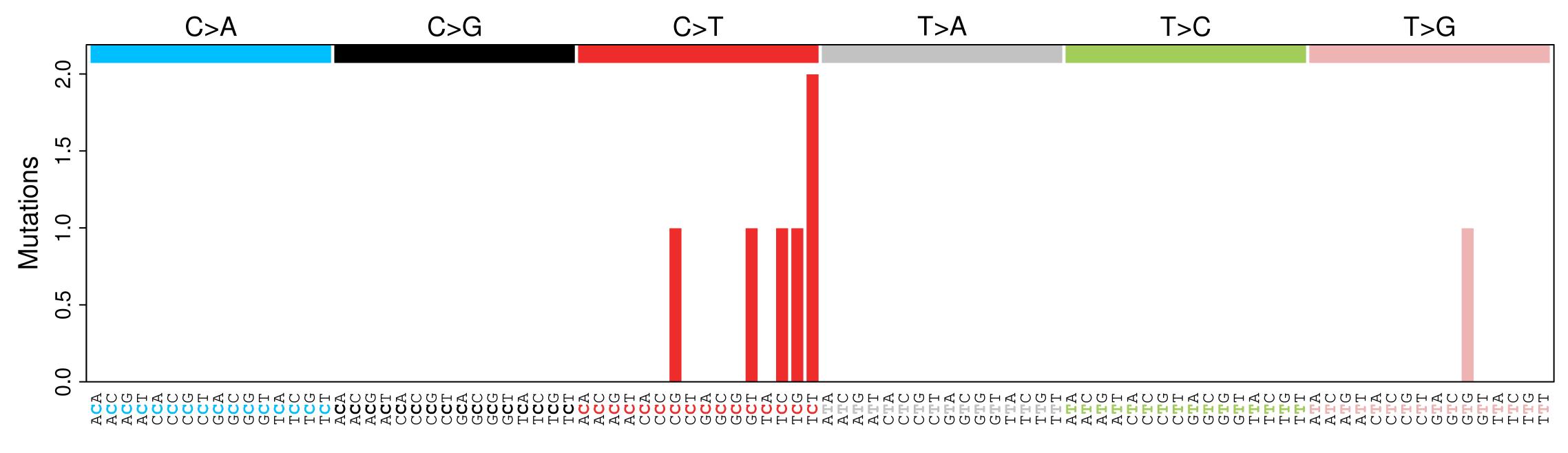
CATD0455a



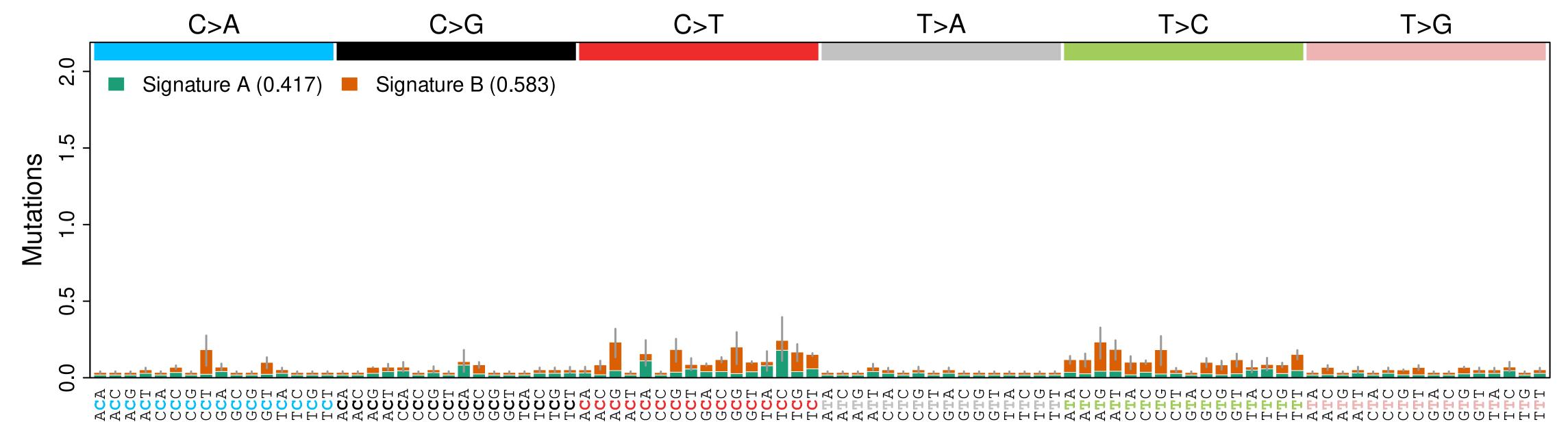




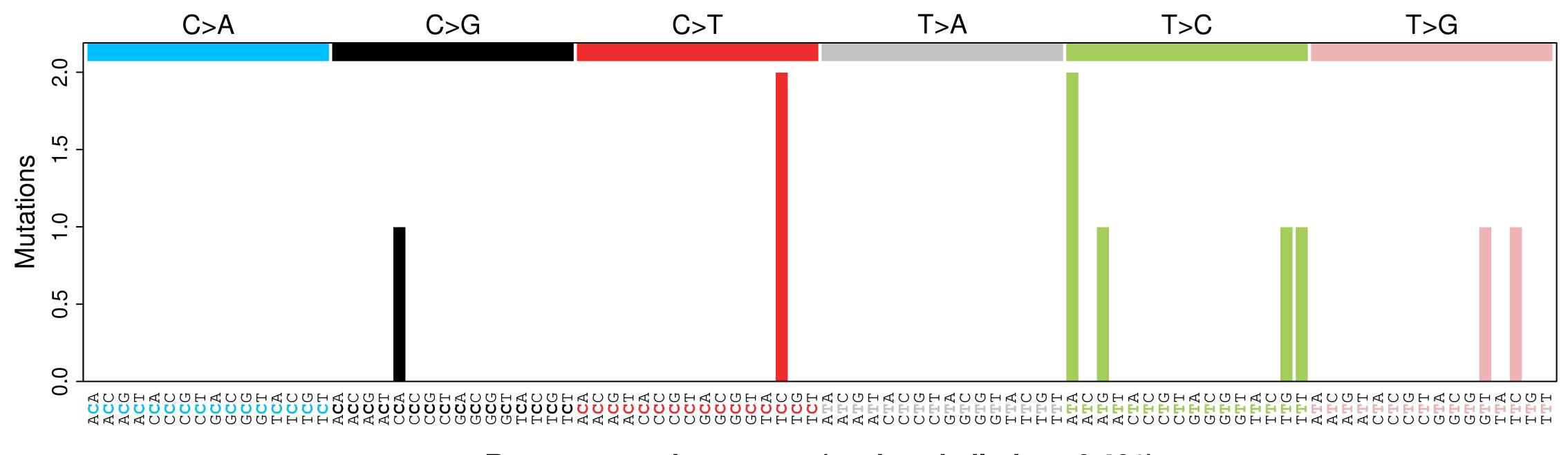
CATD0457a (7 mutations)

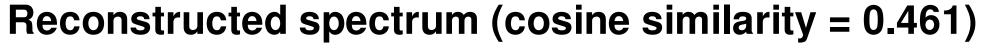


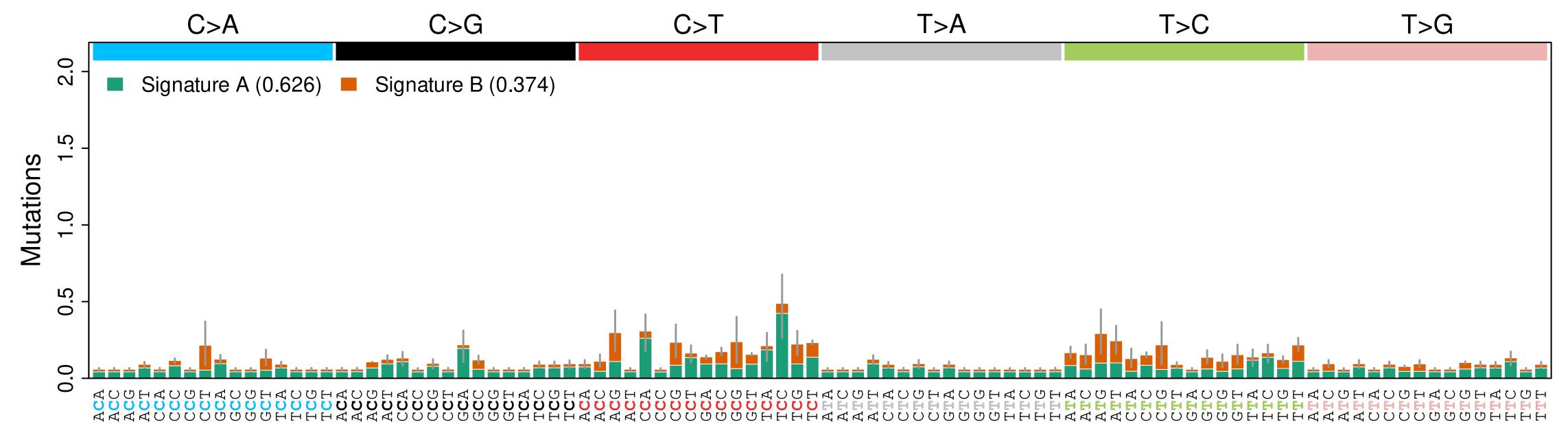
Reconstructed spectrum (cosine similarity = 0.408)



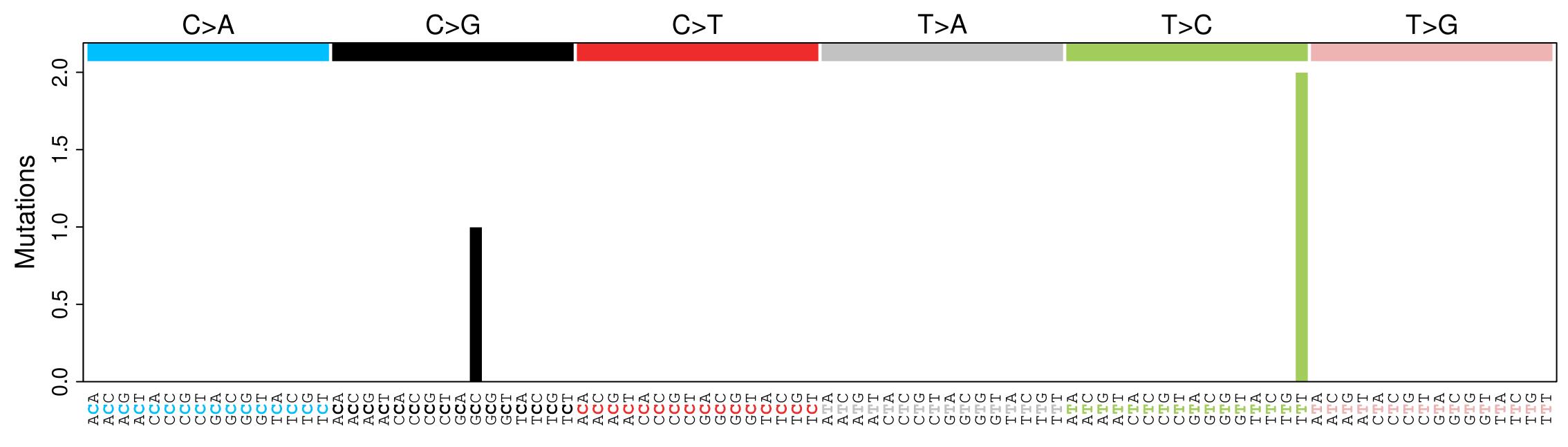
CATD0452a (10 mutations)



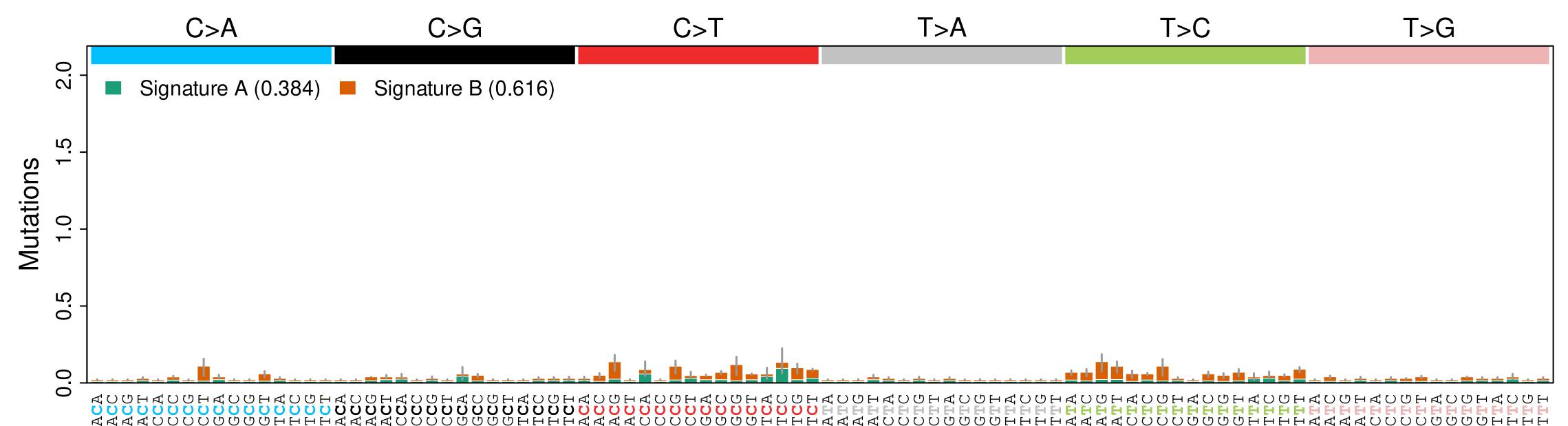




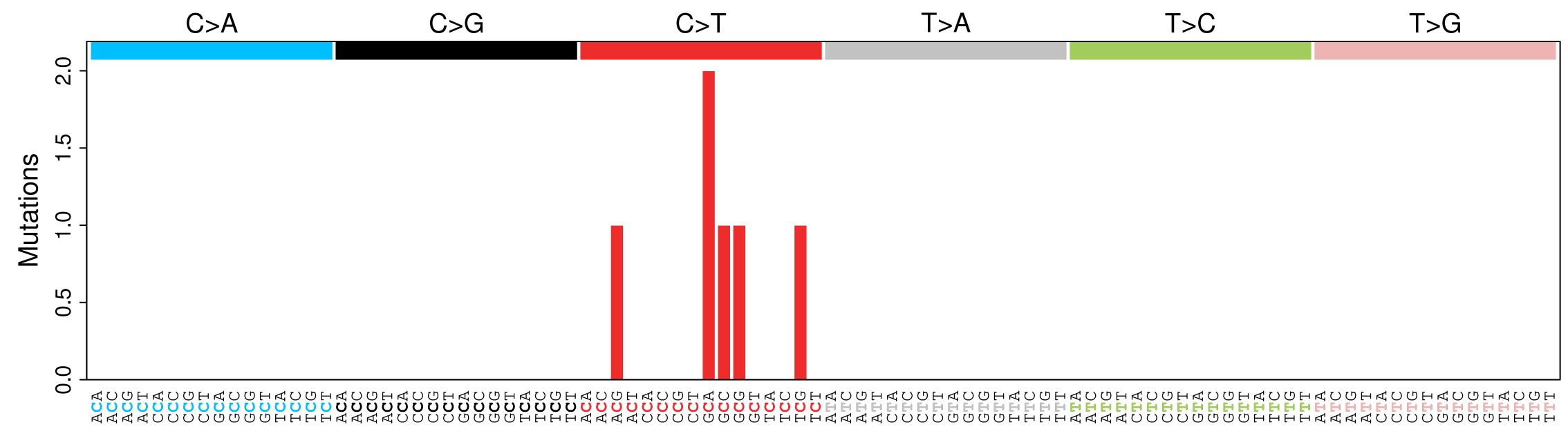
CATD0447a (3 mutations) C>A C>G C>T T>A



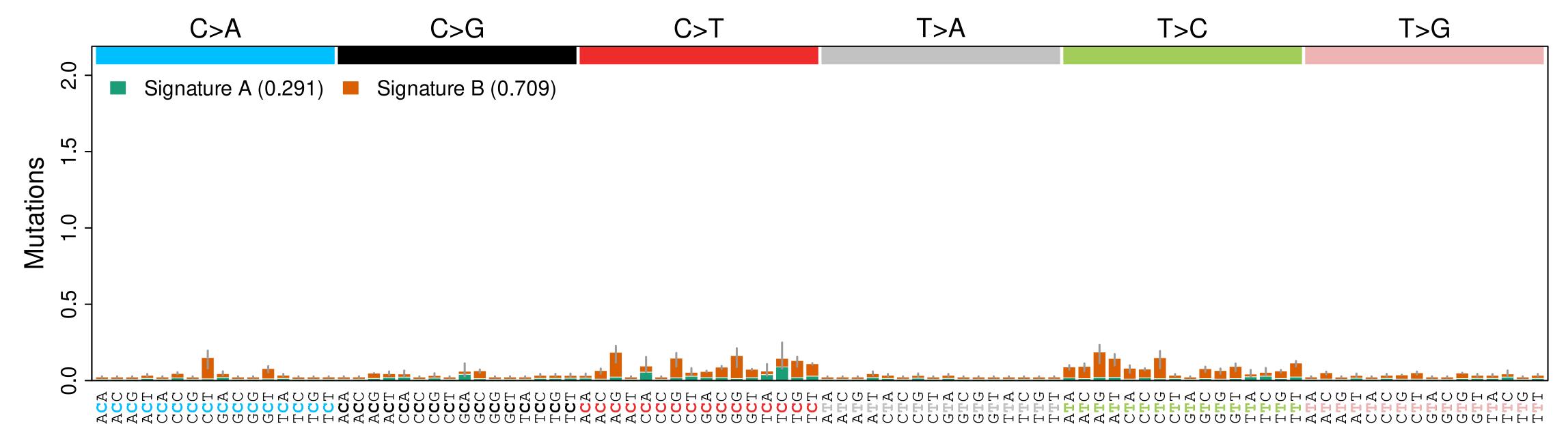
Reconstructed spectrum (cosine similarity = 0.2)



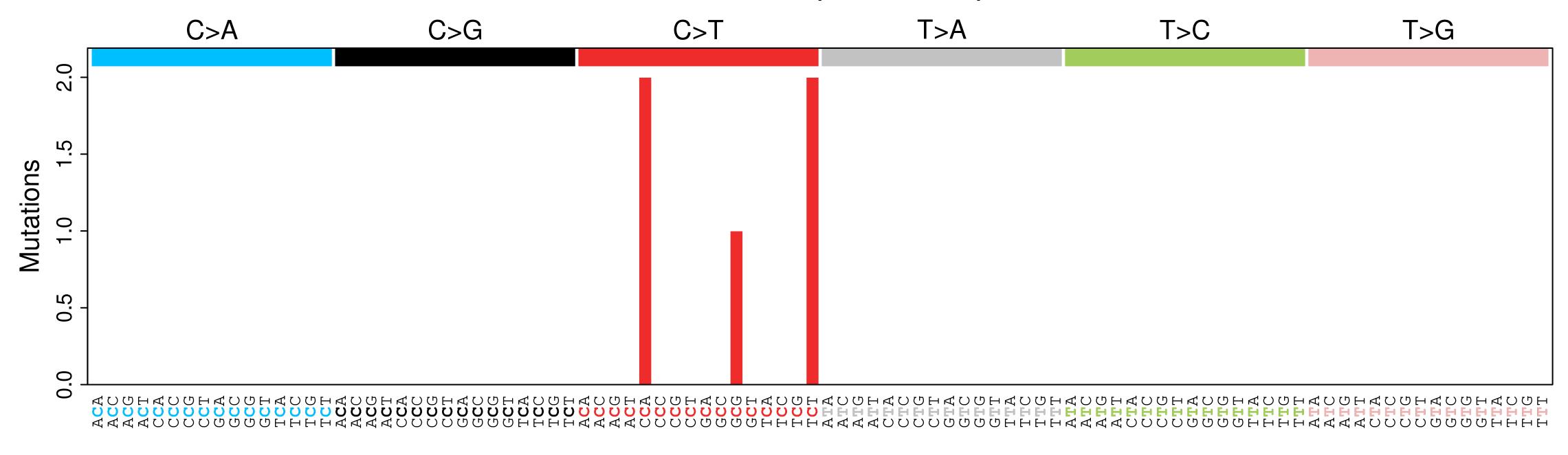
CATD0449a (6 mutations)



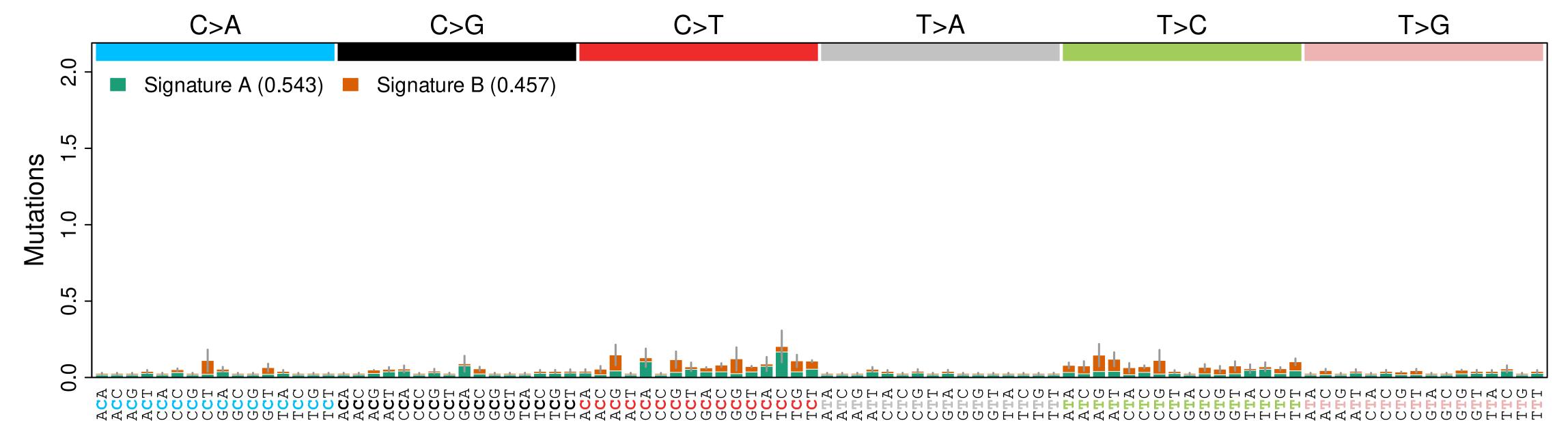
Reconstructed spectrum (cosine similarity = 0.376)



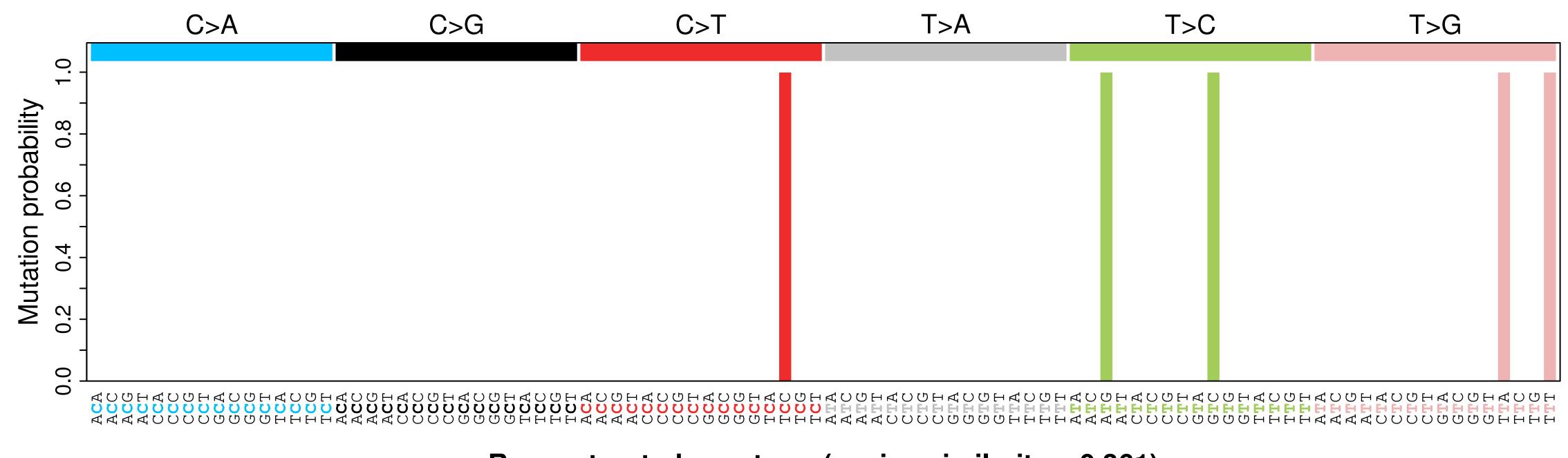
CATD0617a (5 mutations)

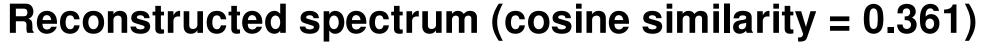


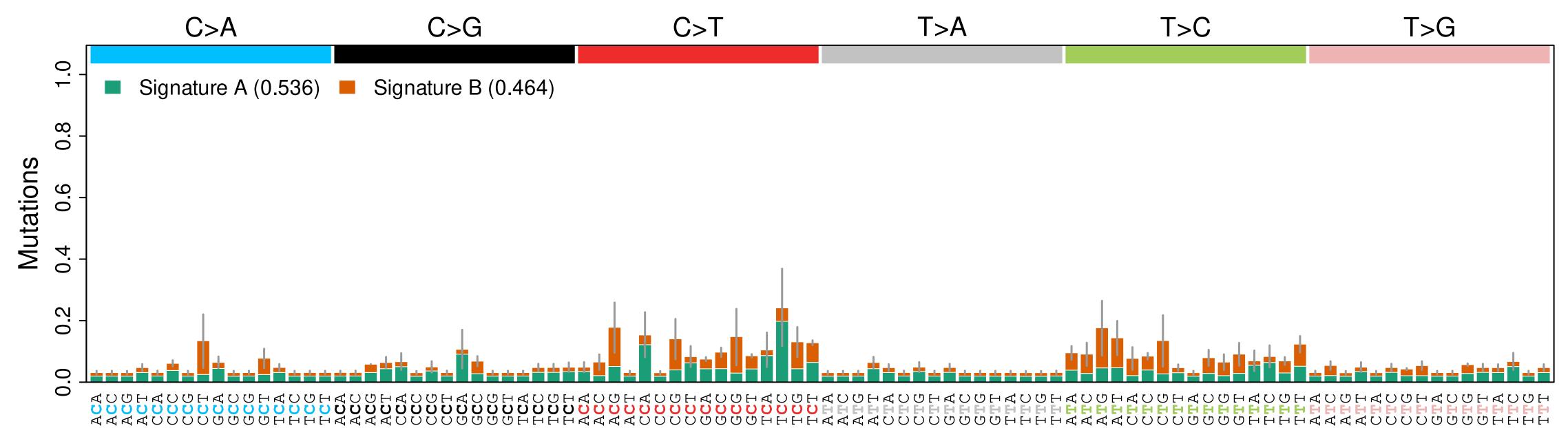
Reconstructed spectrum (cosine similarity = 0.324)



CATD0623a





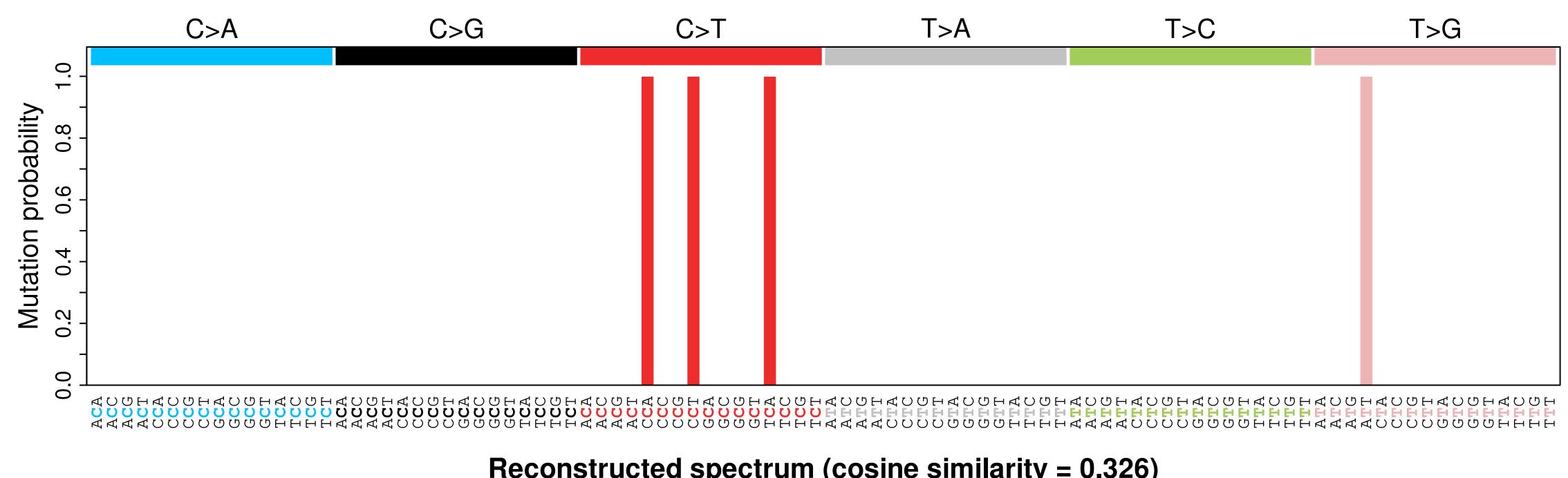


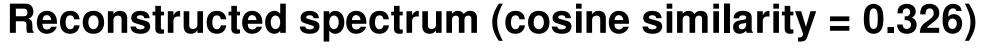
CATD0456a (2 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.229)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.312) Signature B (0.688) 5 Mutations 5 0 0 0

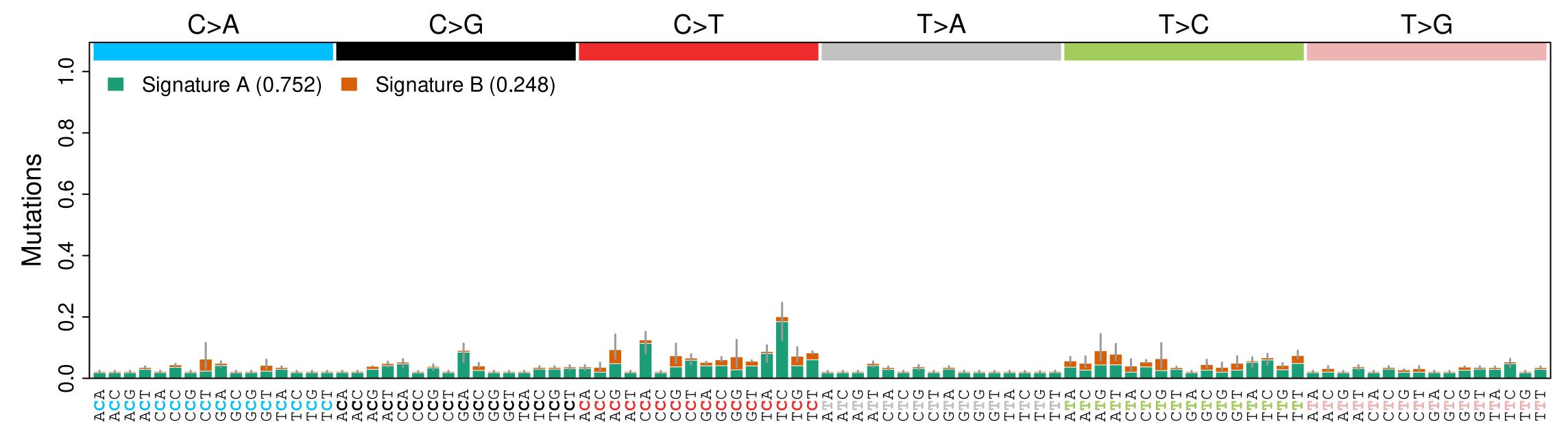
CATD0618a (8 mutations) C>G T>G C>A C>T T>A T>C 3.0 2.5 Mutations 2.0 1.5 0.5 0 **Reconstructed spectrum (cosine similarity = 0.298)** C>A T>G C>G T>A T>C C>T 3.0 Signature A (0.861) Signature B (0.139) 5 \circ Mutations 2.0 1.5 5

0



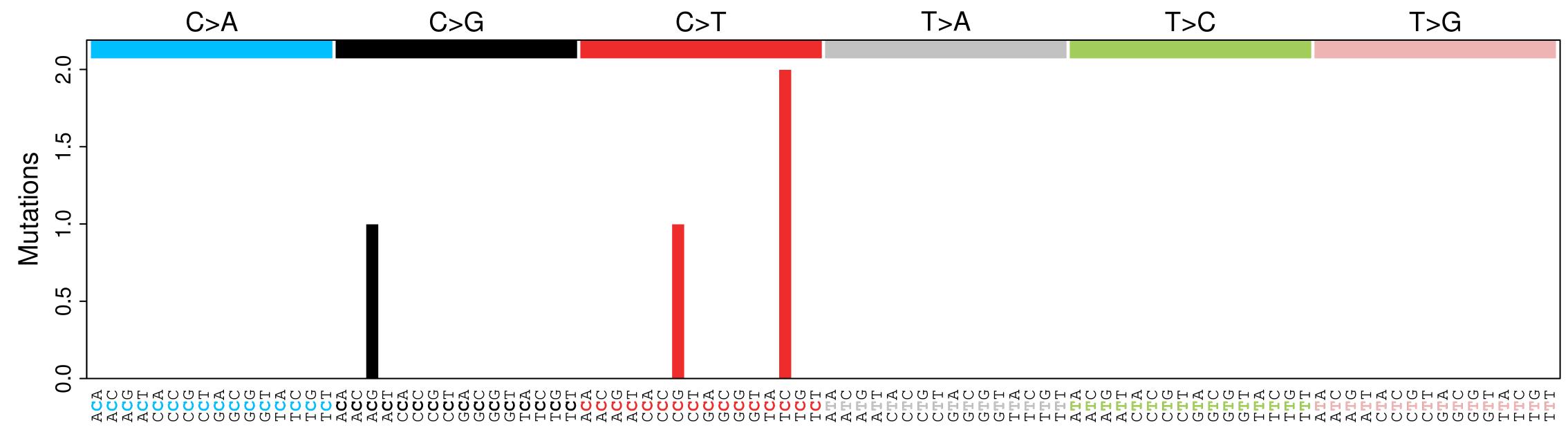




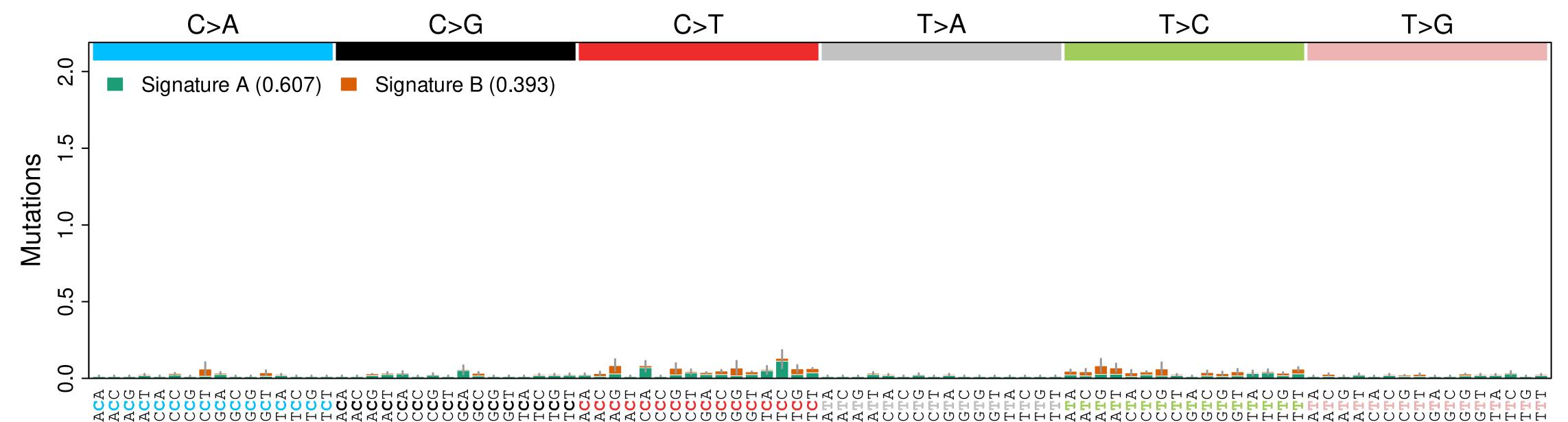


CATD0460a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.441)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.759) Signature B (0.241) 5 Mutations 2 0

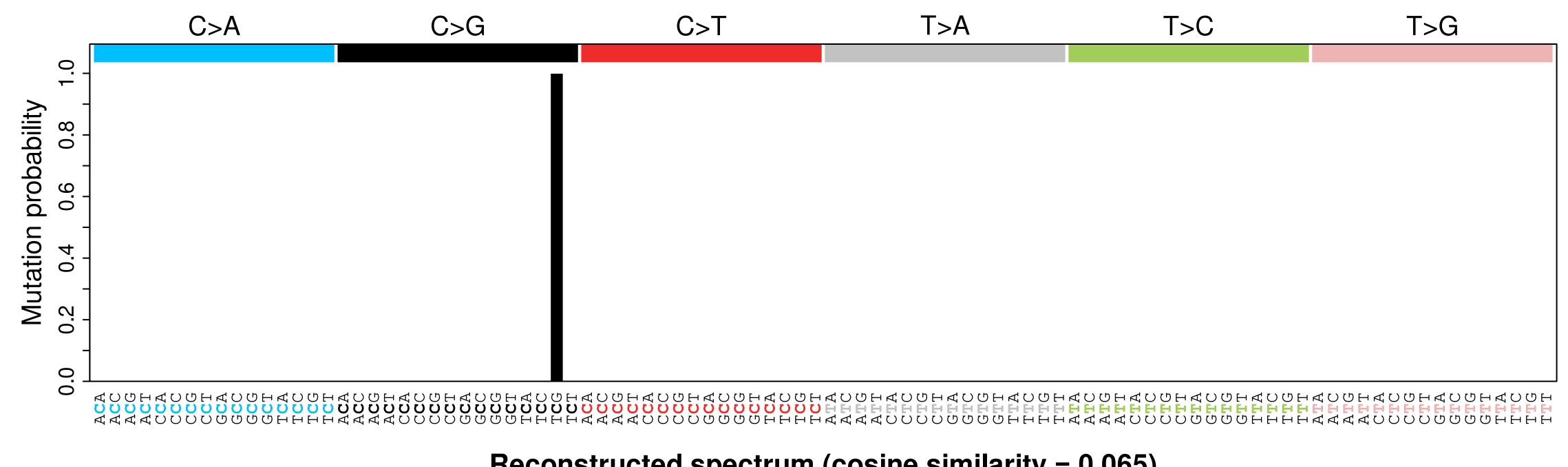
CATD0448a (4 mutations)



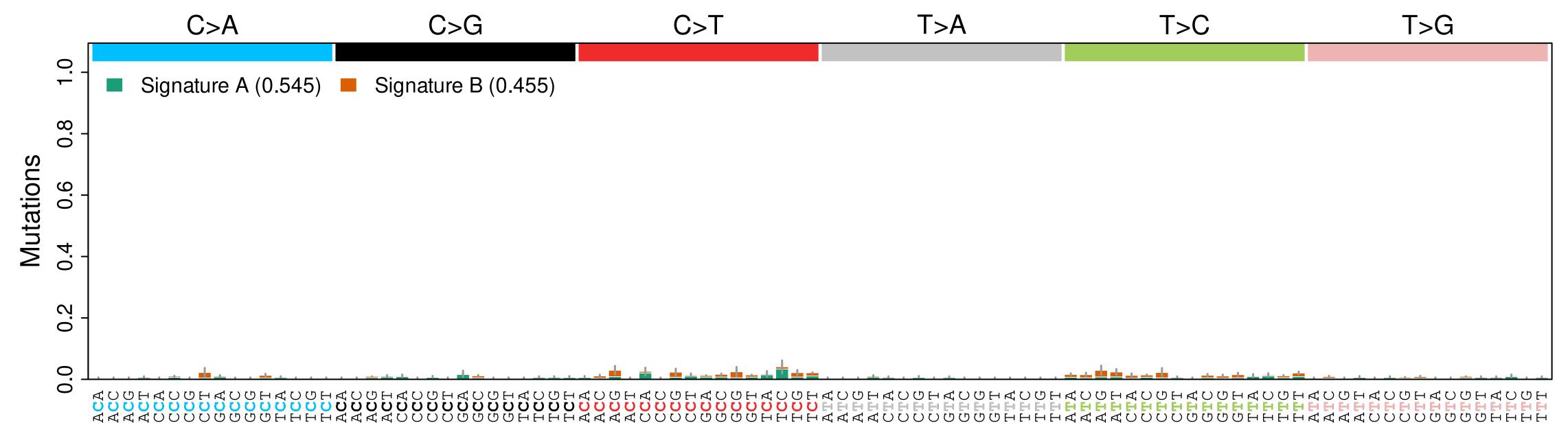
Reconstructed spectrum (cosine similarity = 0.399)



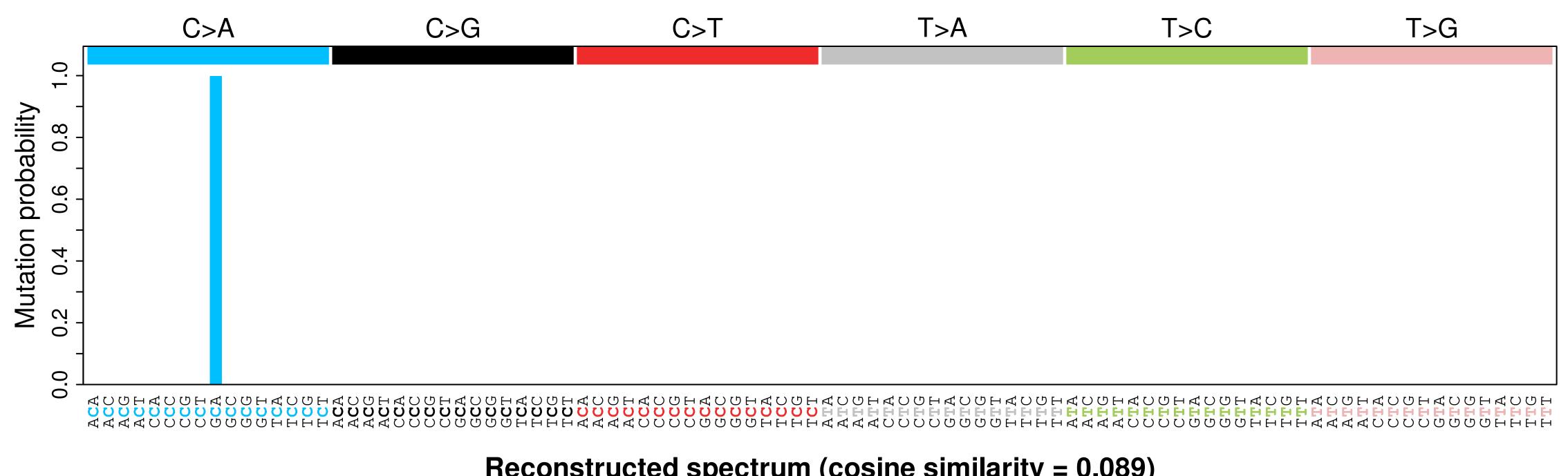




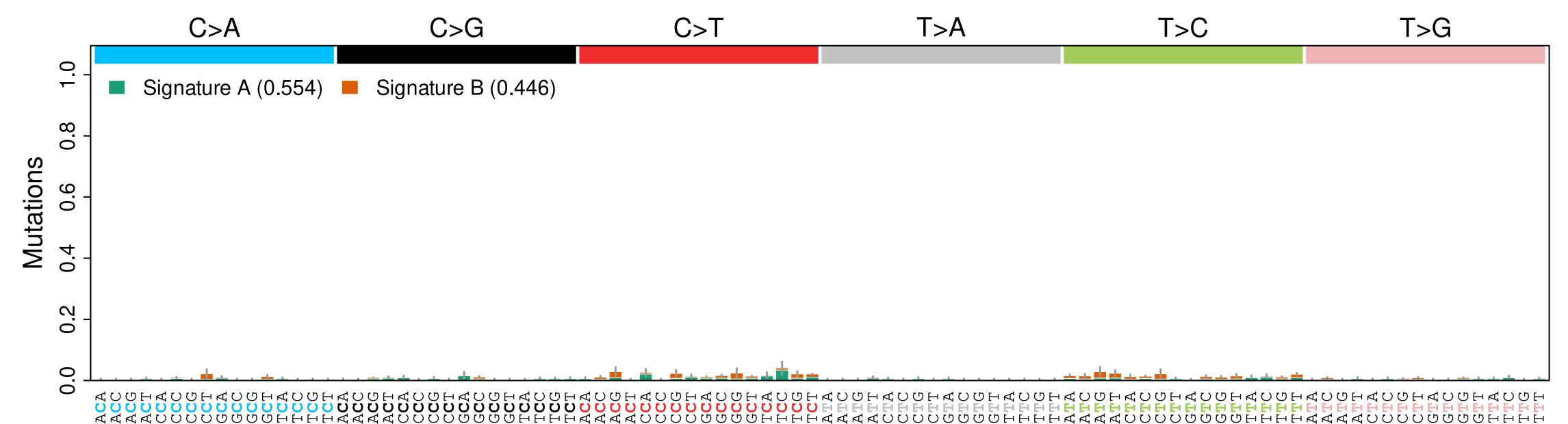
Reconstructed spectrum (cosine similarity = 0.065)



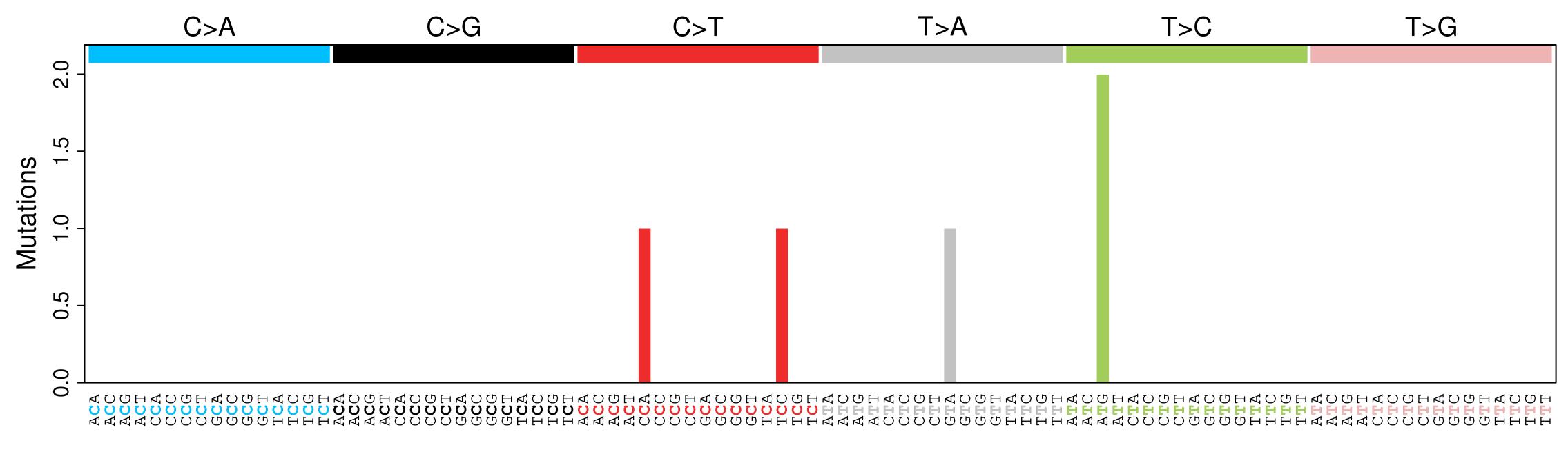




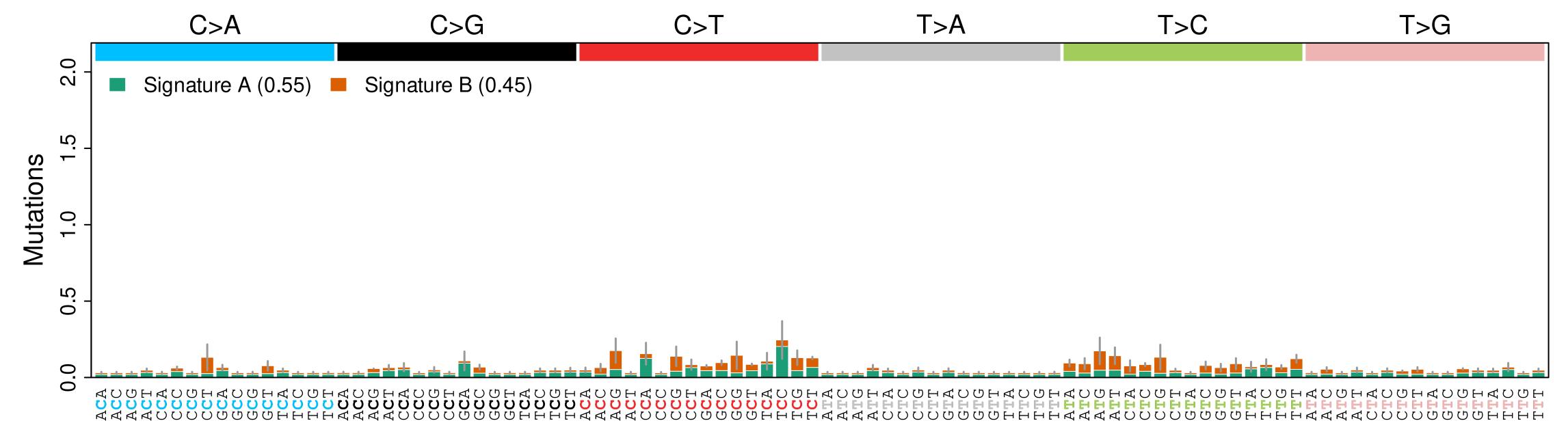




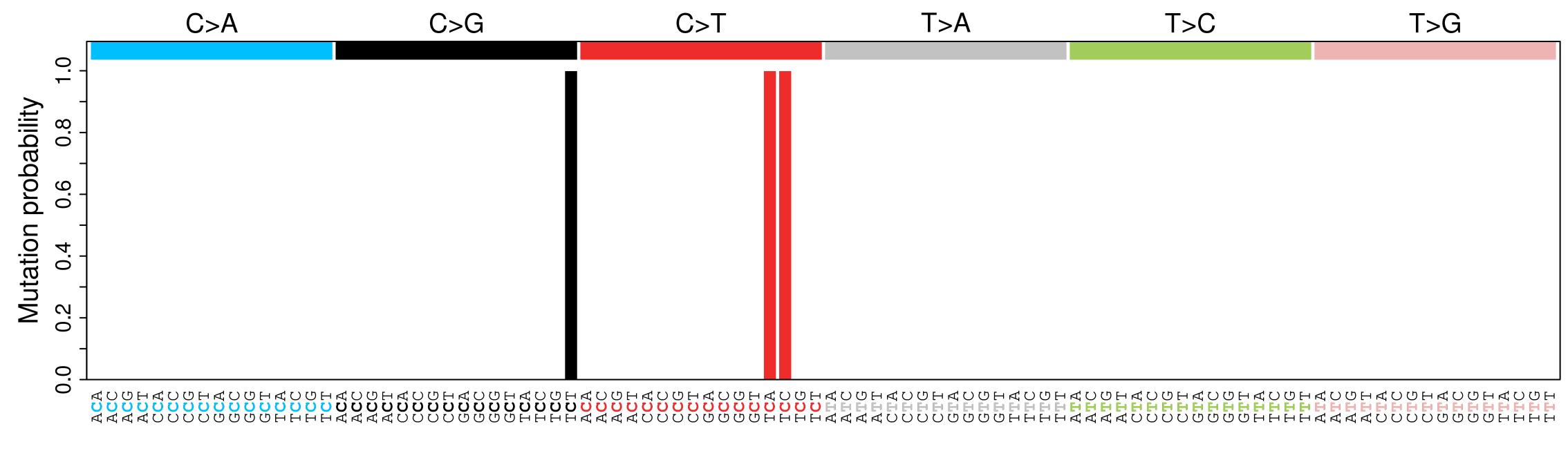
CATD0625a (5 mutations)

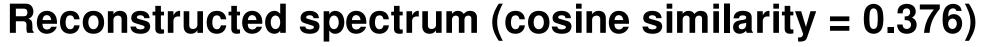


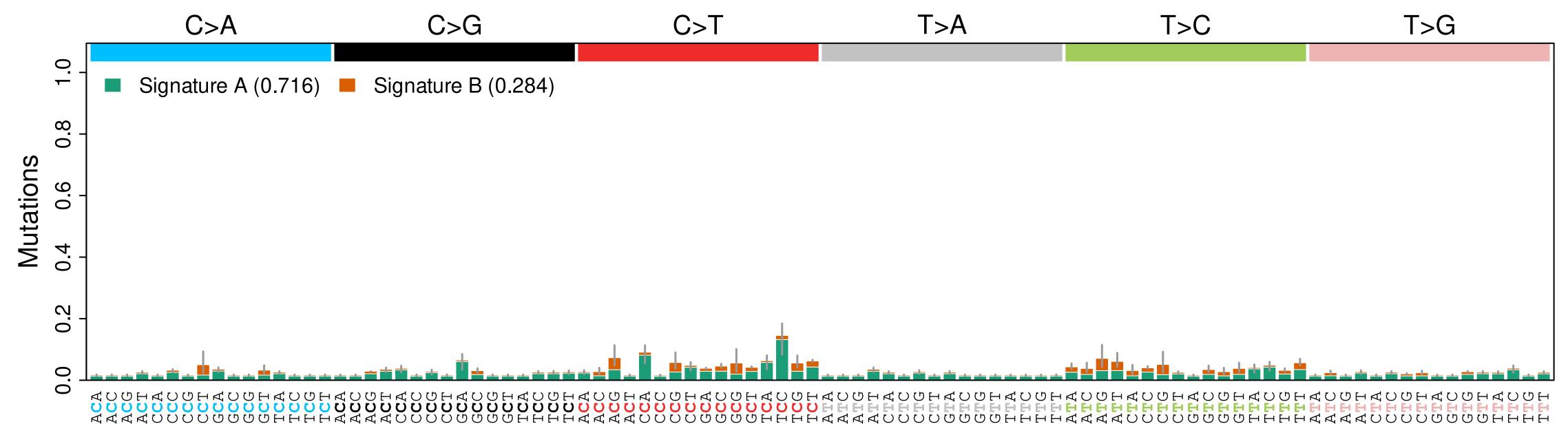
Reconstructed spectrum (cosine similarity = 0.412)











CATD0613a (2 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 = 0.216)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.372) Signature B (0.628) 5 Mutations 5 0



