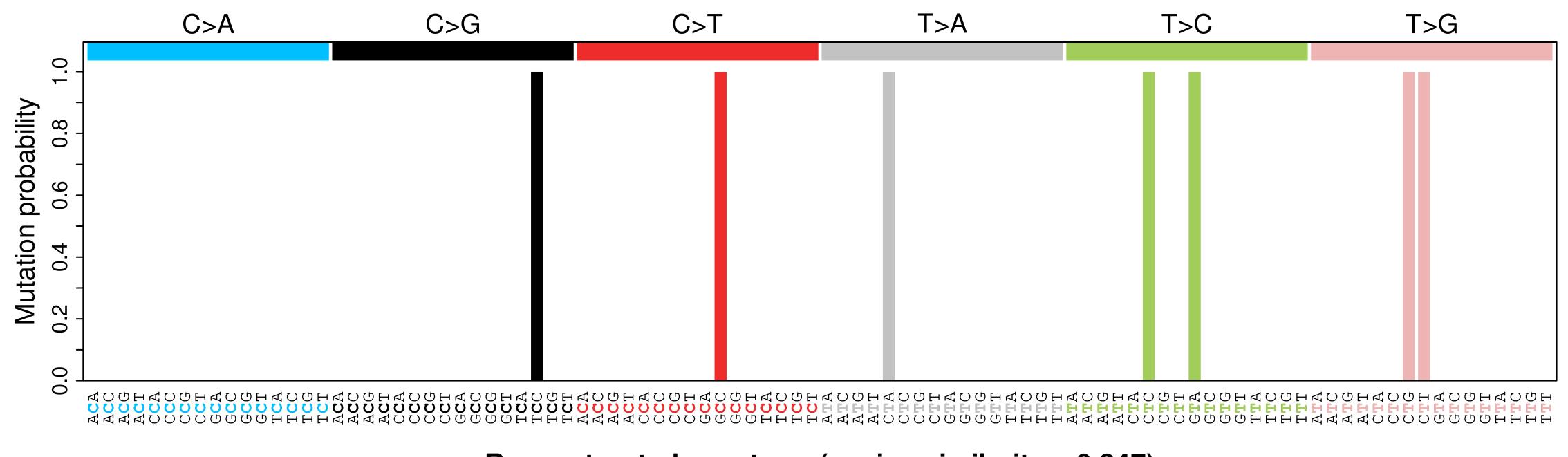
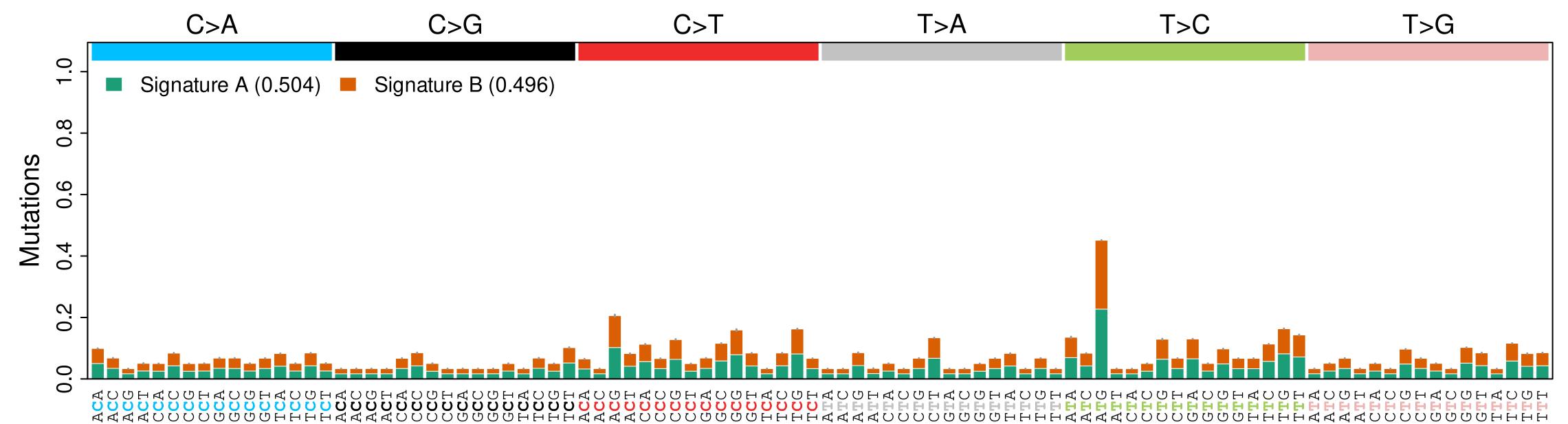
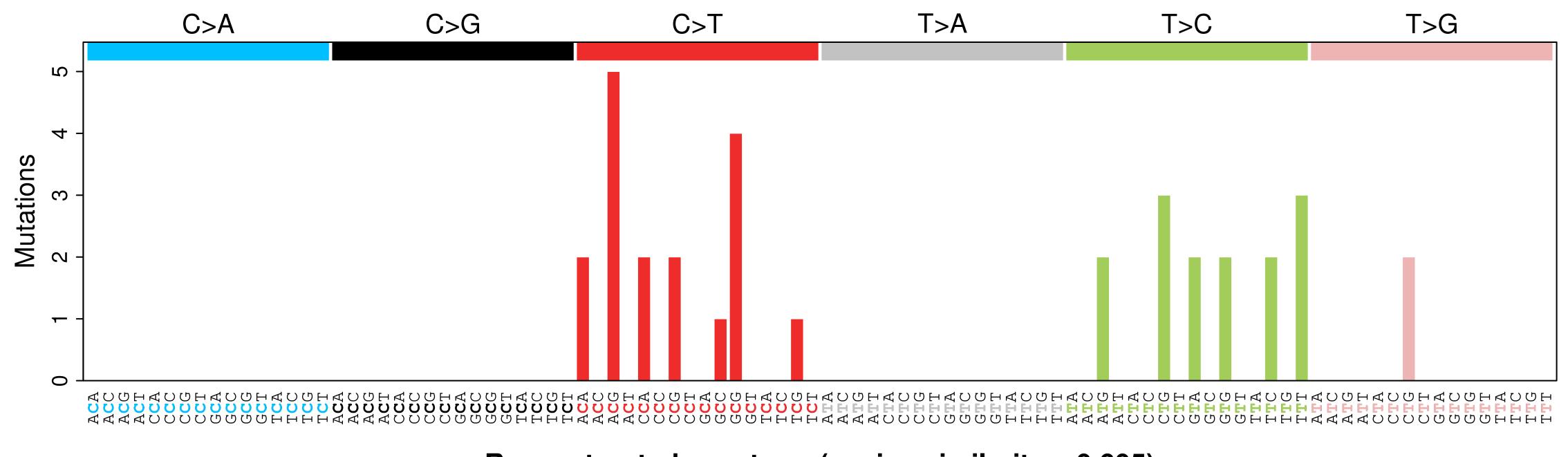
CATD0507a



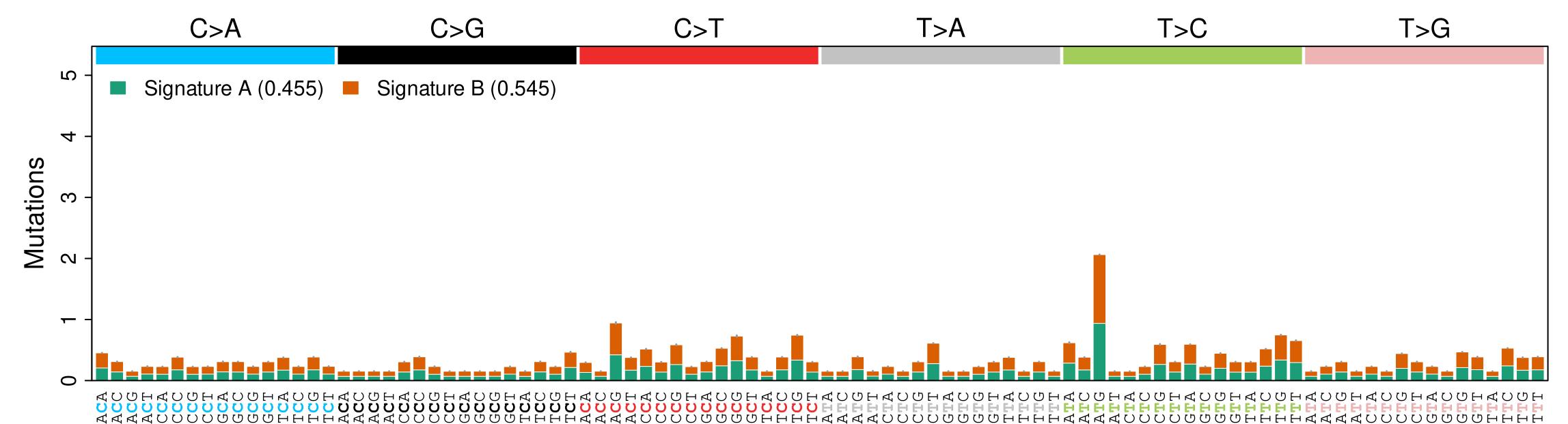
Reconstructed spectrum (cosine similarity = 0.247)



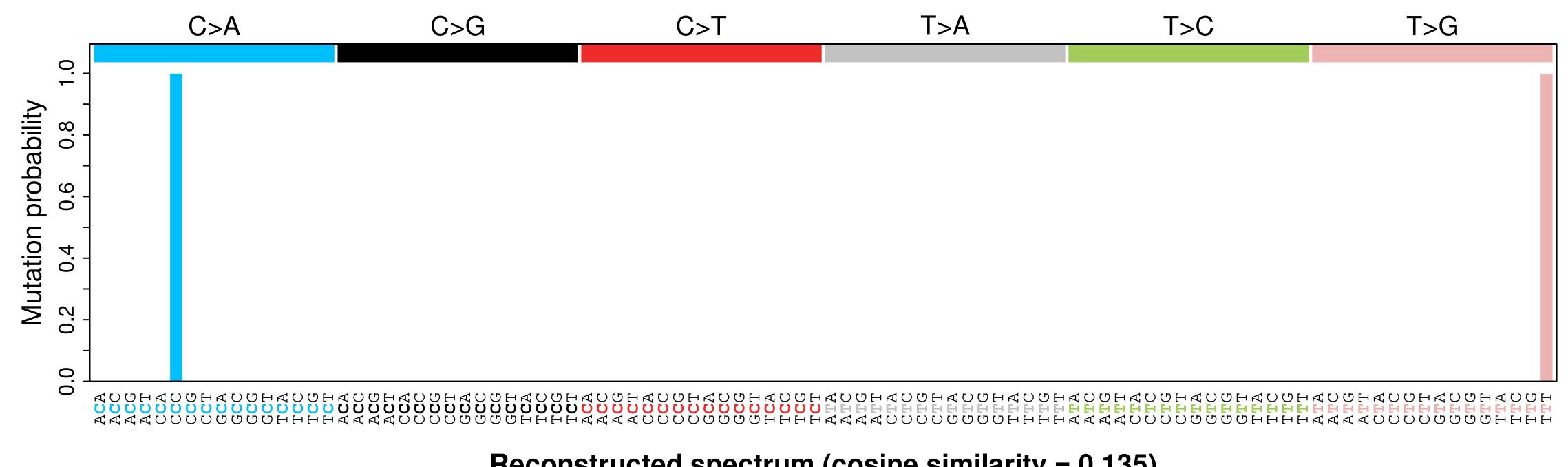
CATD0500a (33 mutations)



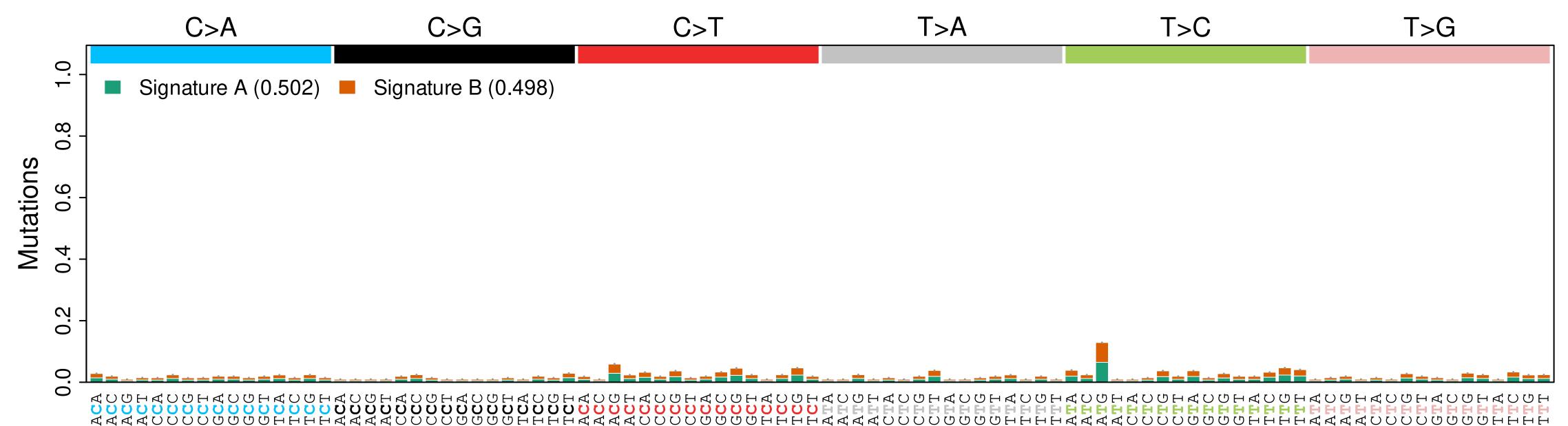
Reconstructed spectrum (cosine similarity = 0.605)



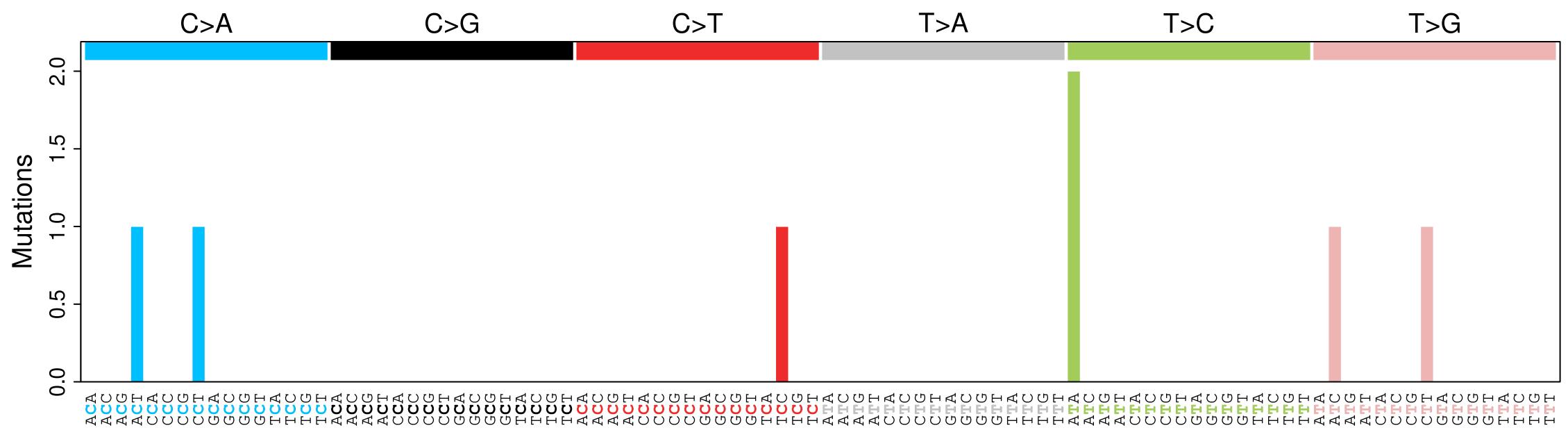




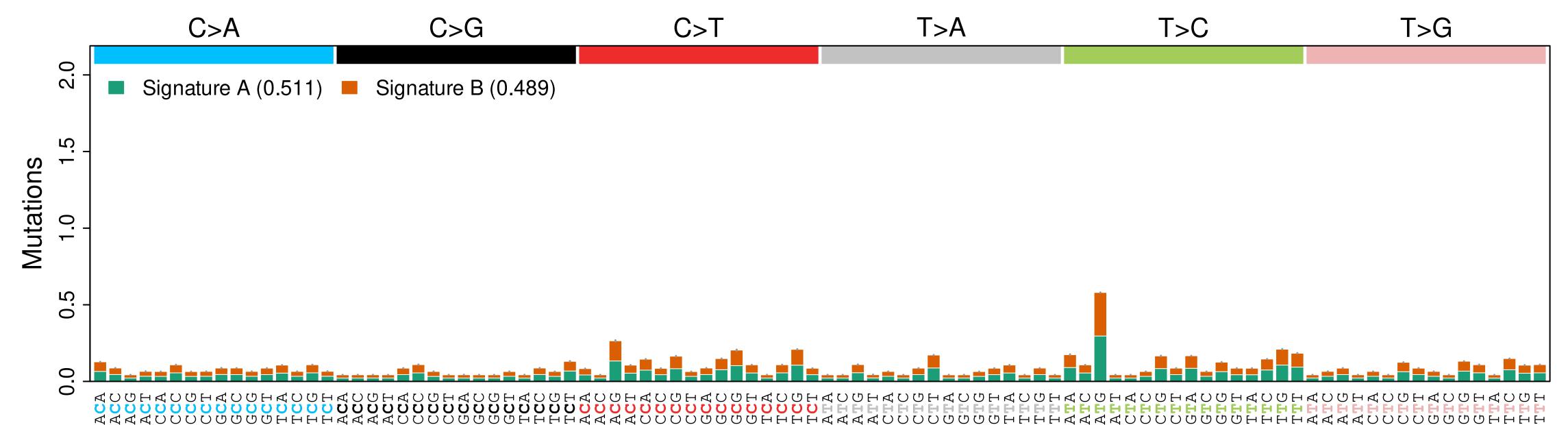
Reconstructed spectrum (cosine similarity = 0.135)

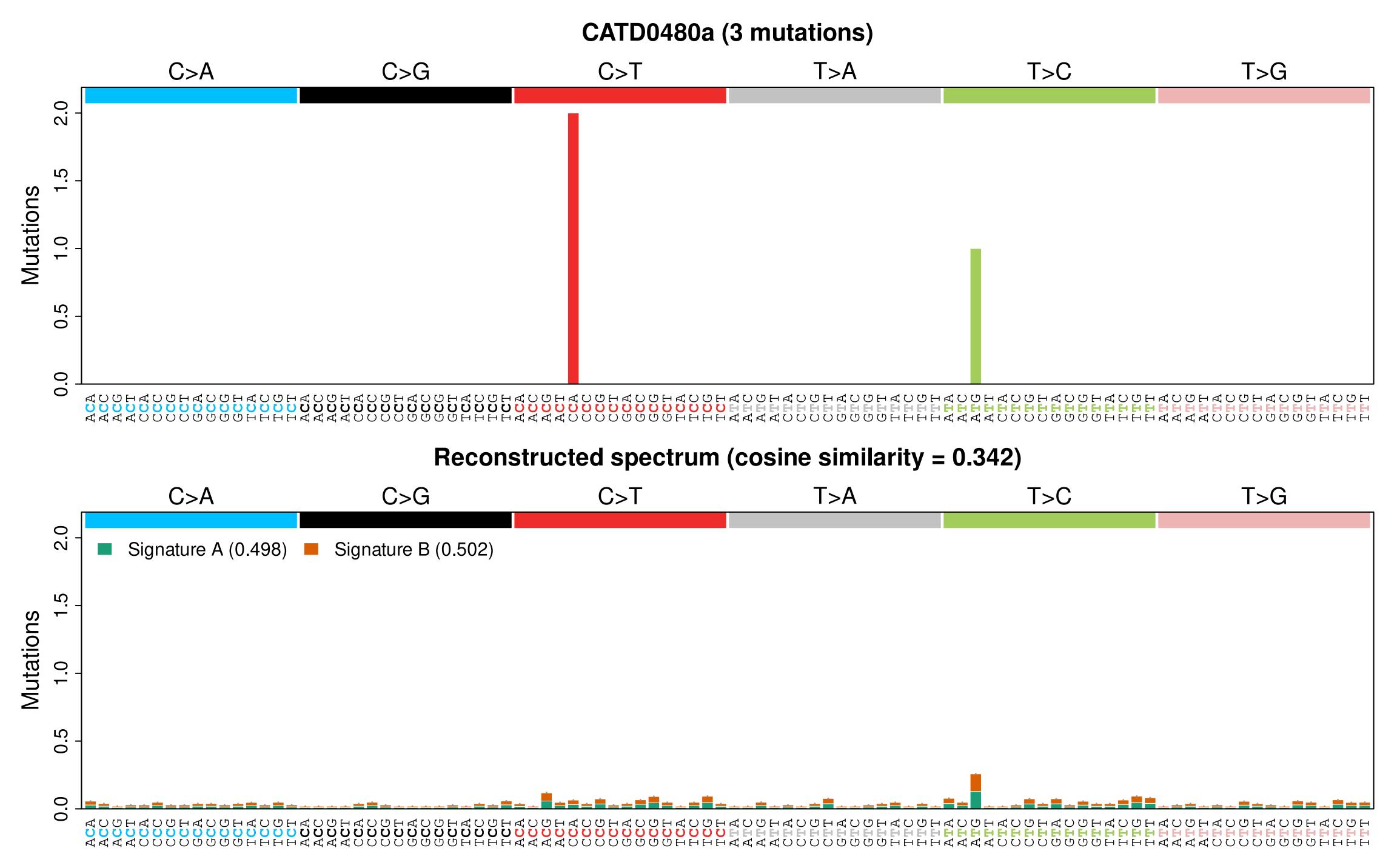


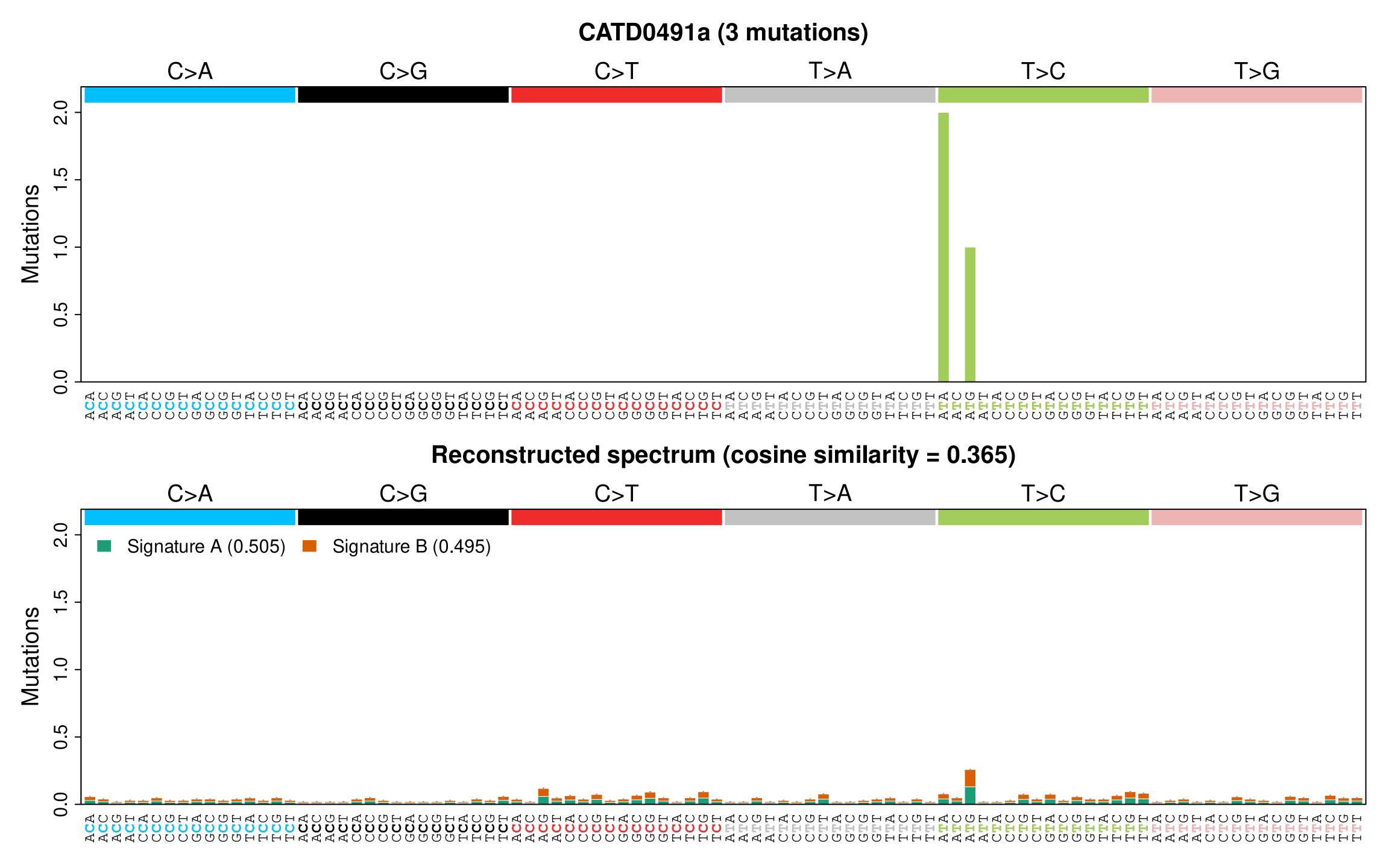
C>A C>G C>T T>A



Reconstructed spectrum (cosine similarity = 0.217)

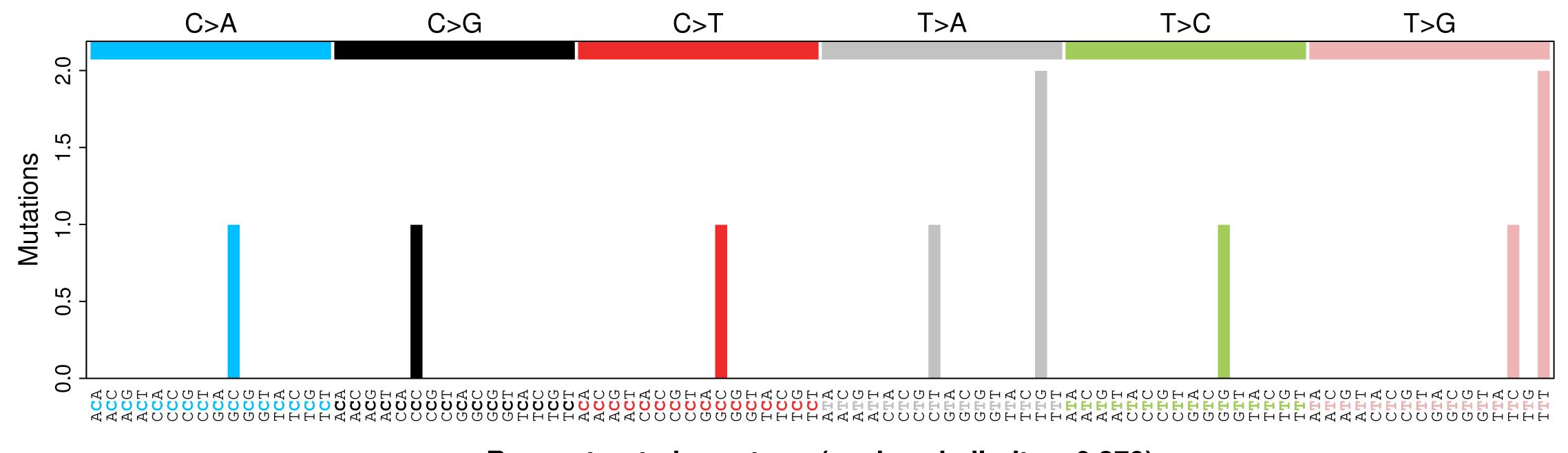




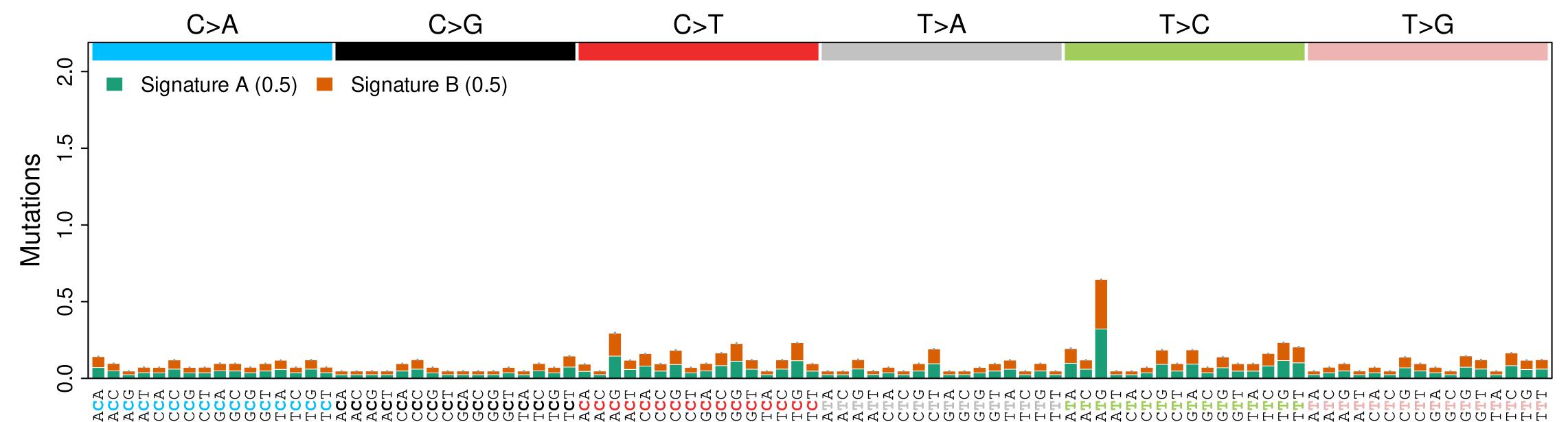


CATD0689a (7 mutations) T>G C>A C>G C>T T>A T>C 2.0 1.5 Mutations 0.5 0.0 Reconstructed spectrum (cosine similarity = 0.486) C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.499) Signature B (0.501) 5 Mutations 2 0

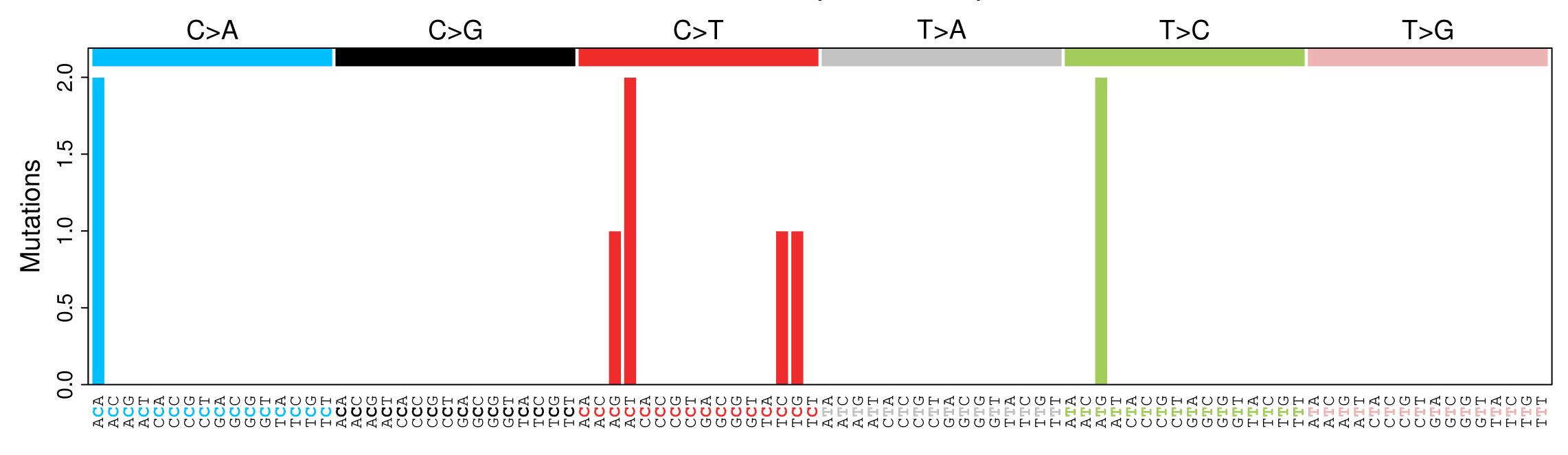
CATD0740a (10 mutations)

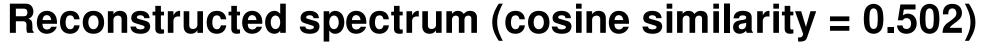


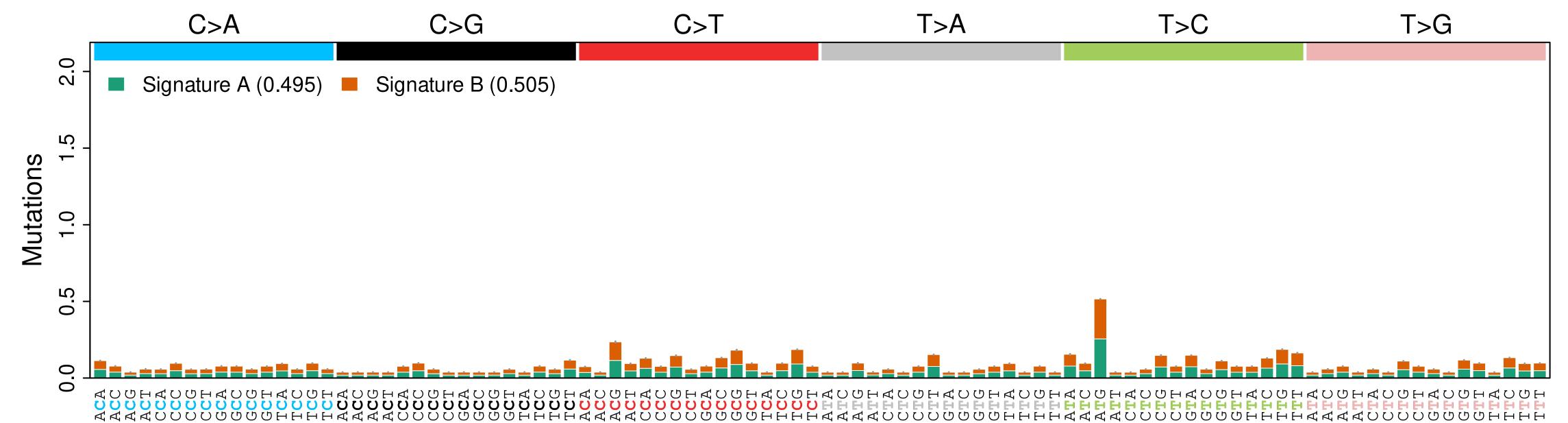
Reconstructed spectrum (cosine similarity = 0.279)



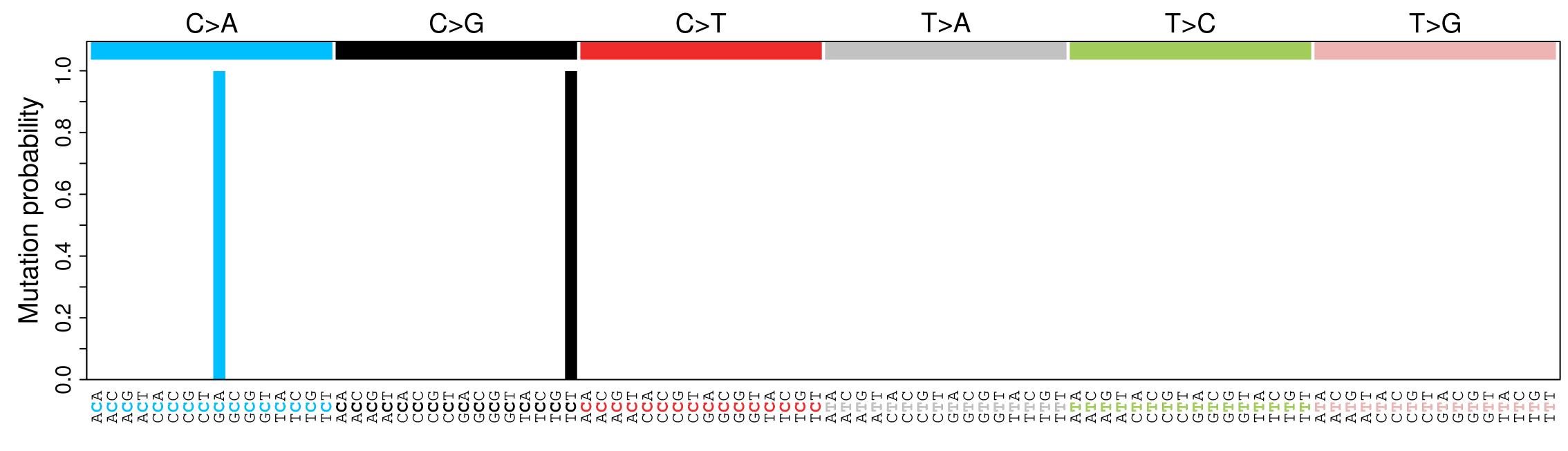
CATD0701a (9 mutations)



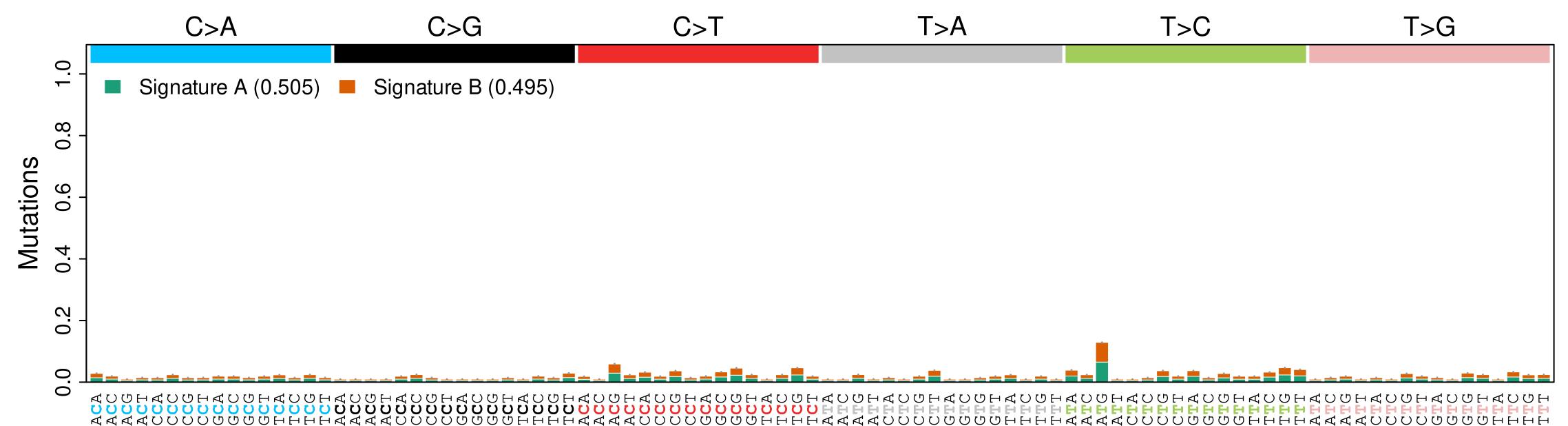




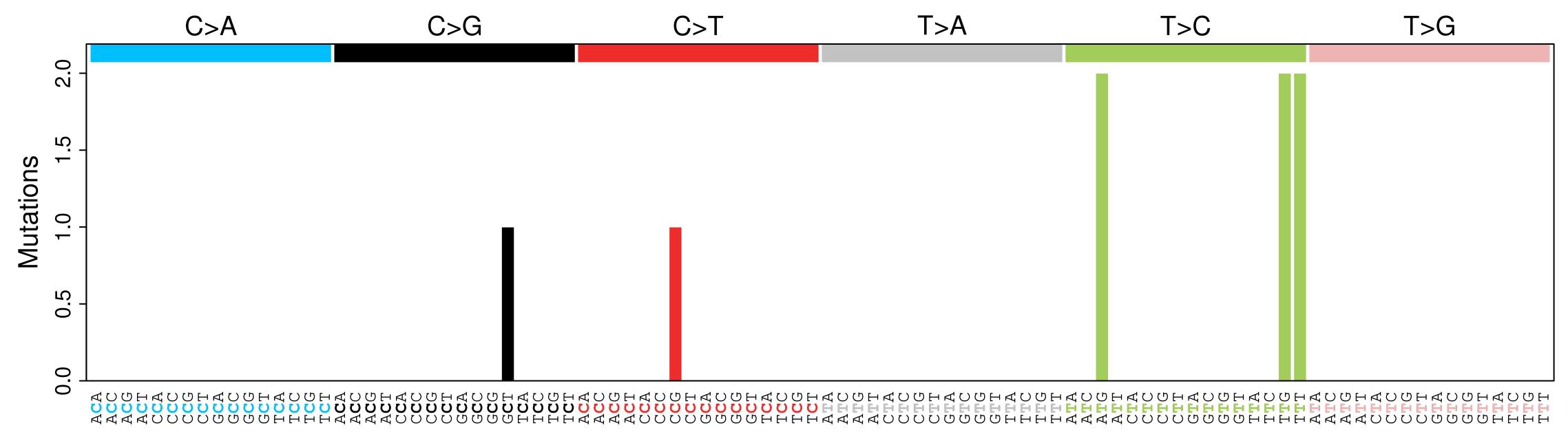


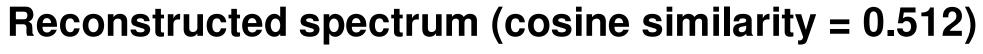


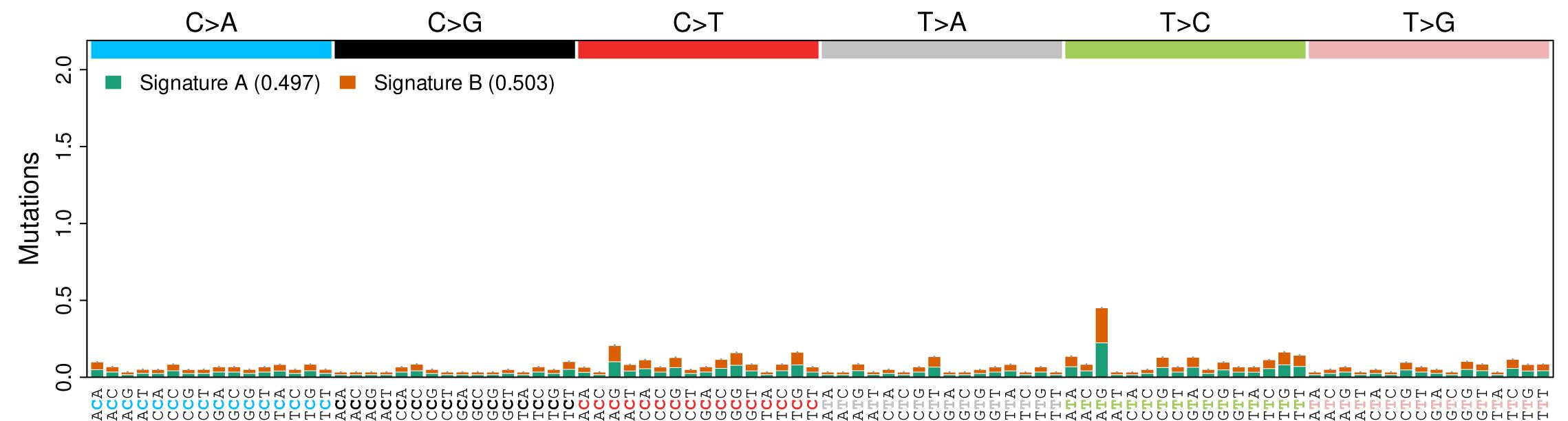




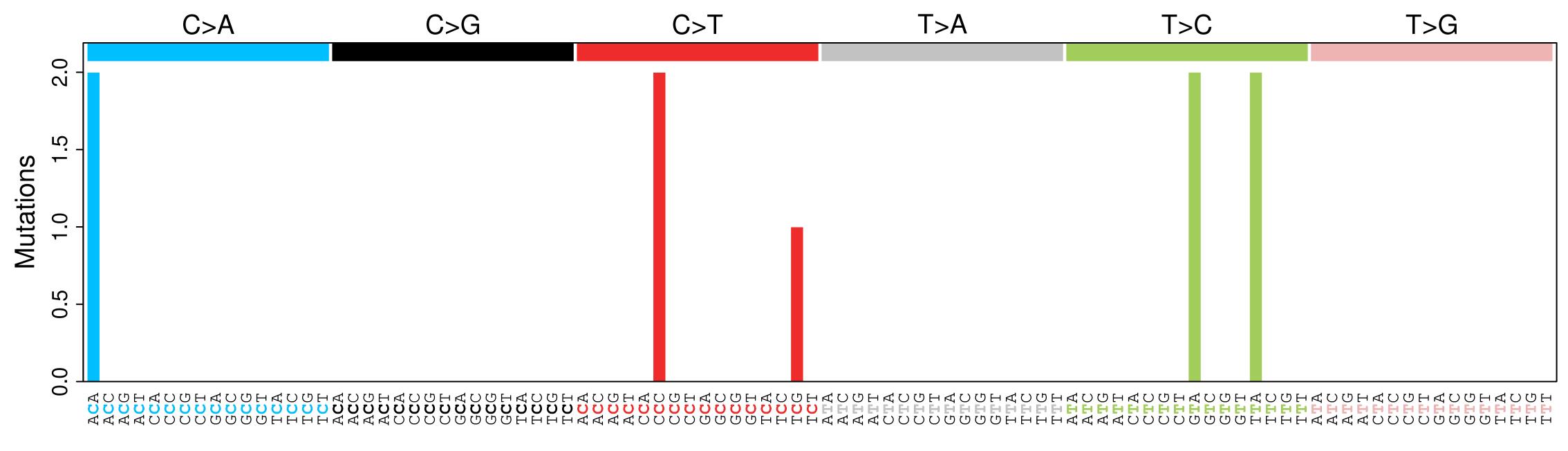
CATD0702a (8 mutations)

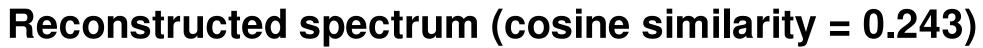


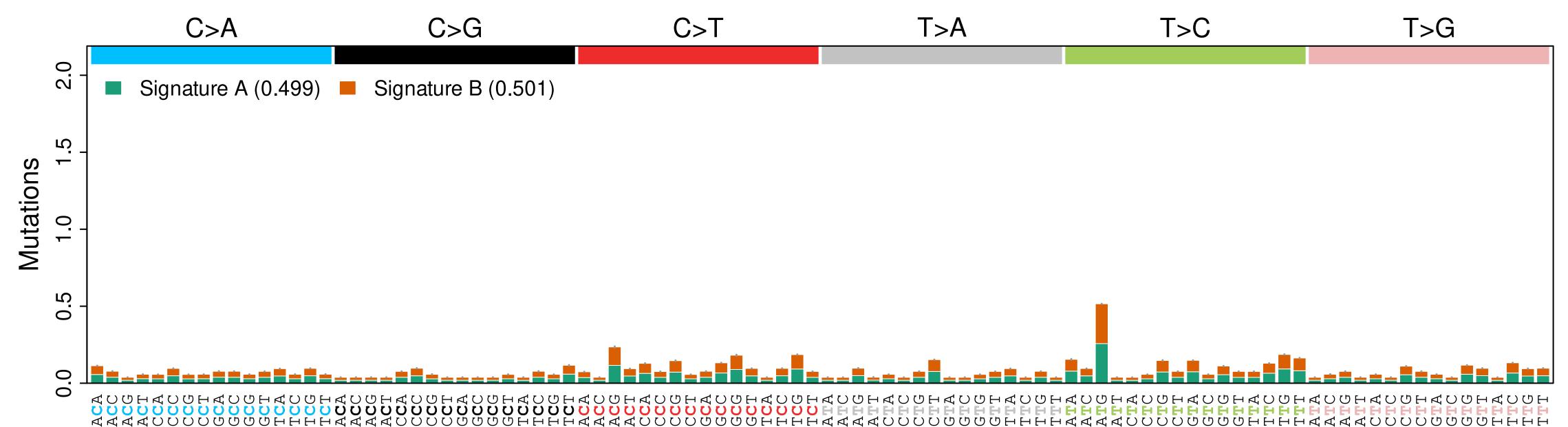




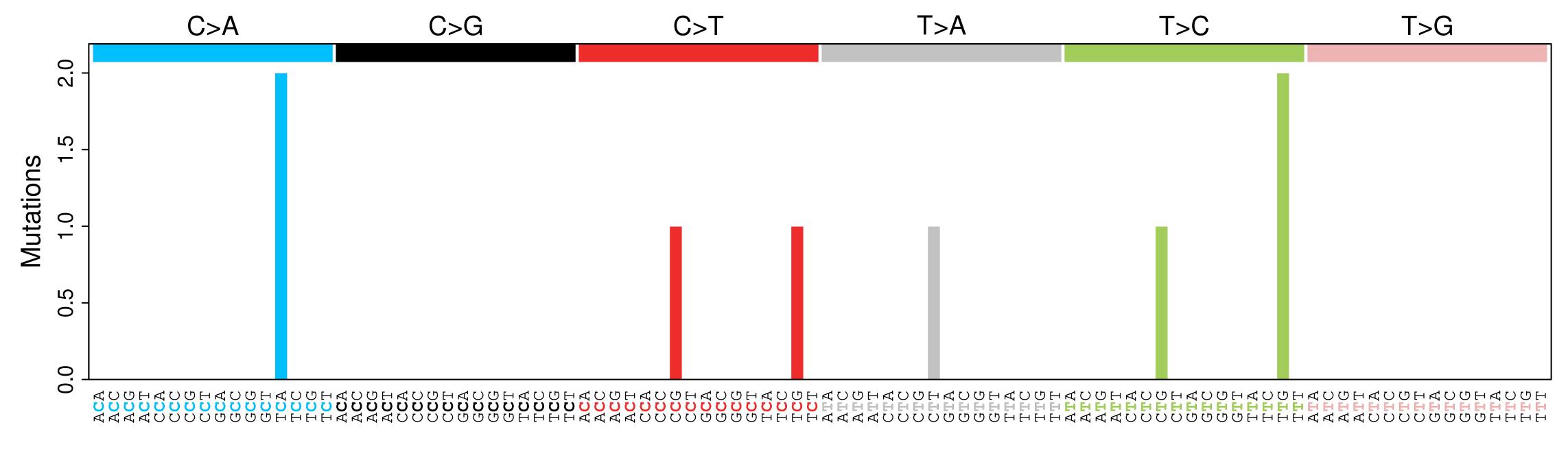
CATD0505a (9 mutations)



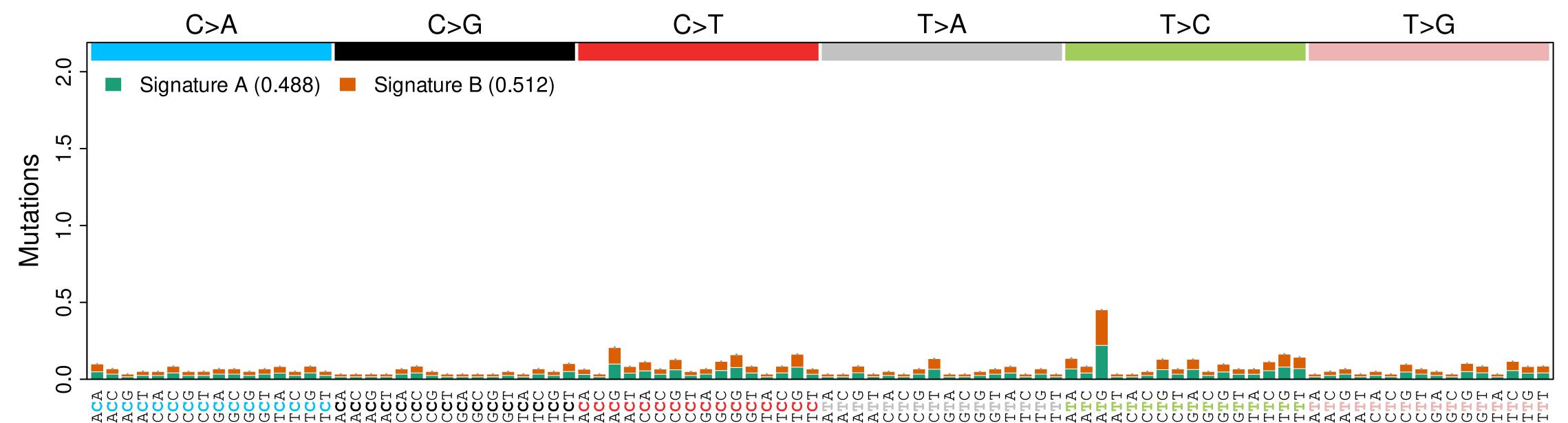


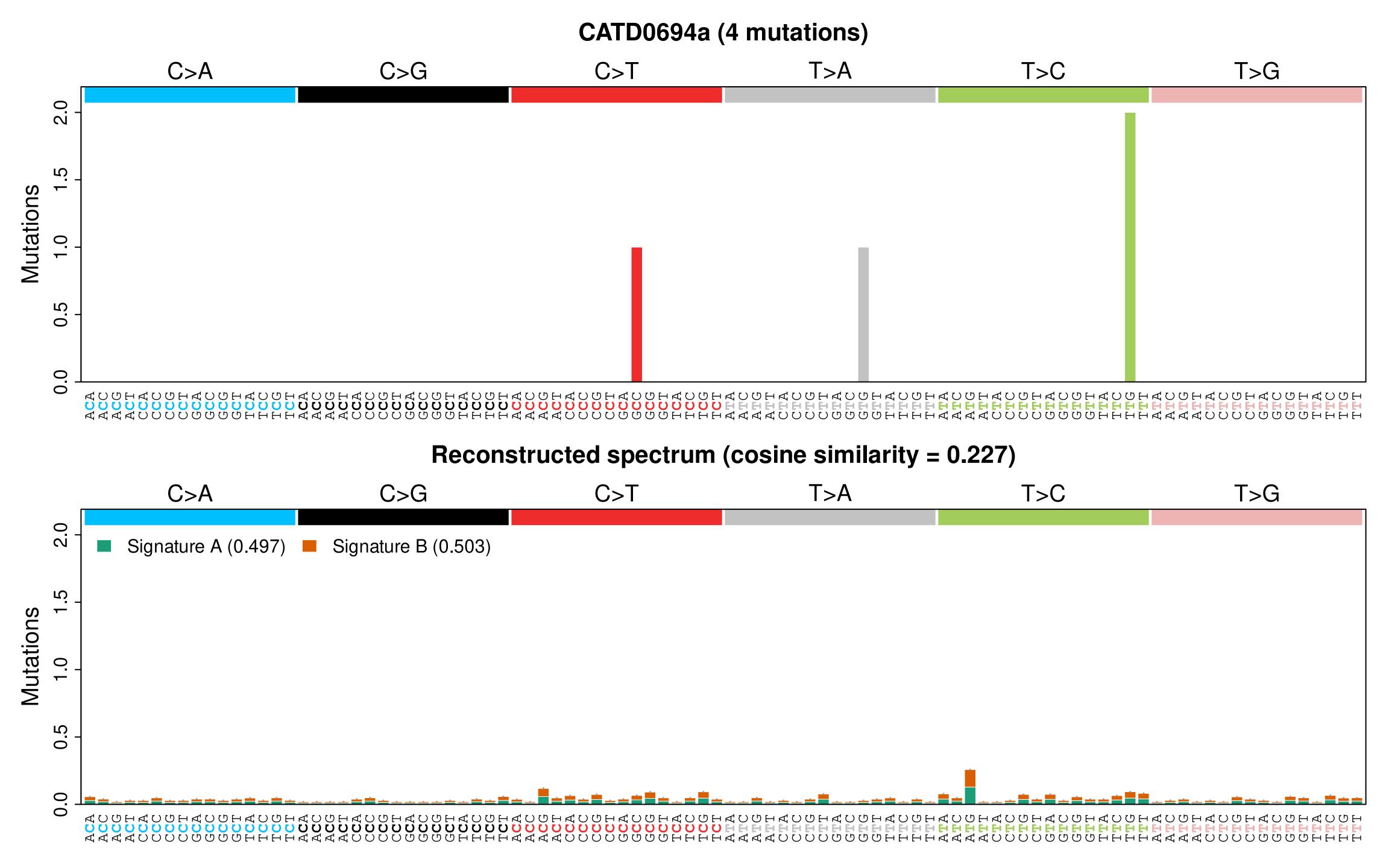


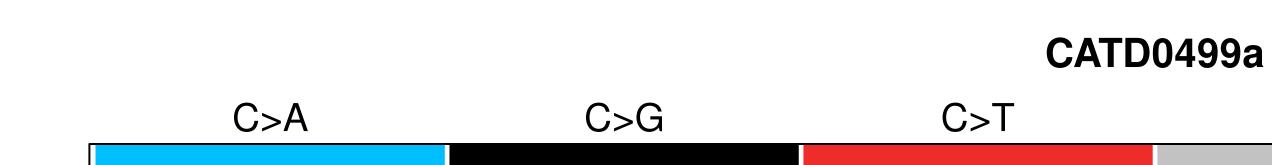
CATD0482a (8 mutations)

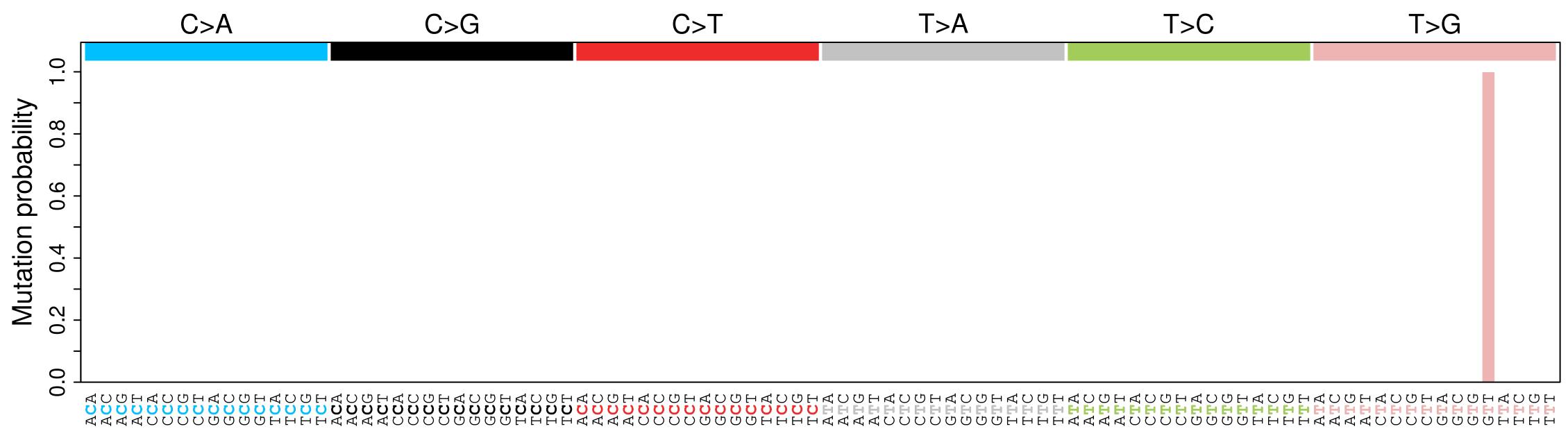


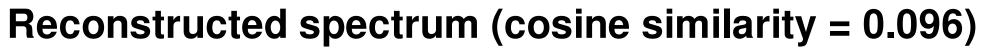
Reconstructed spectrum (cosine similarity = 0.341)

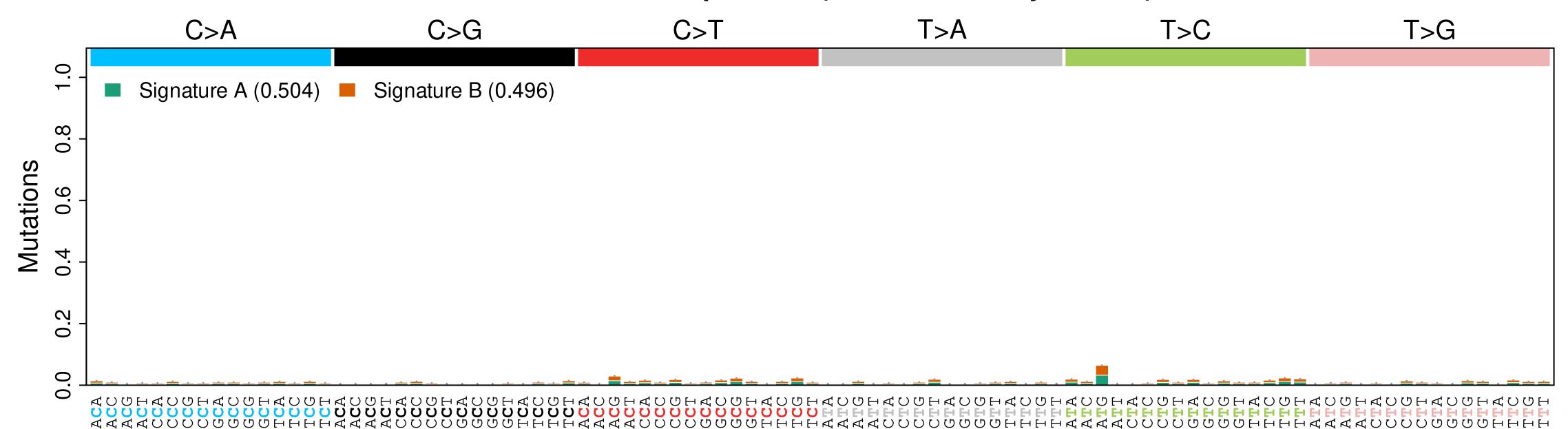




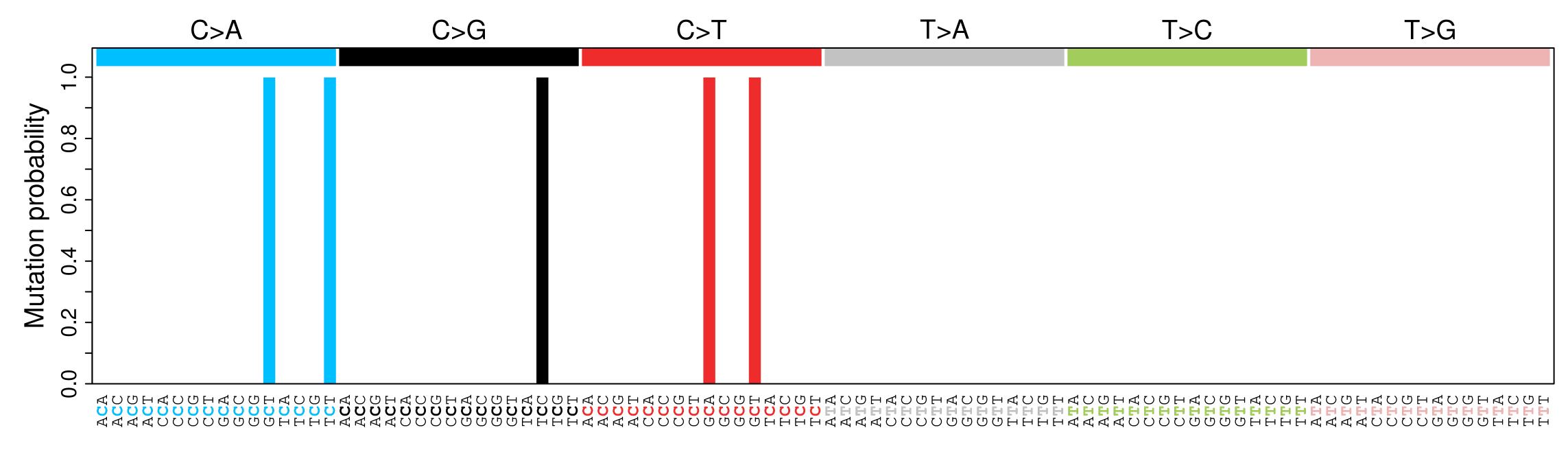


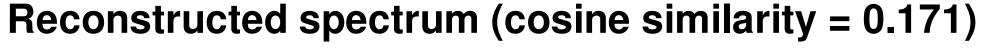


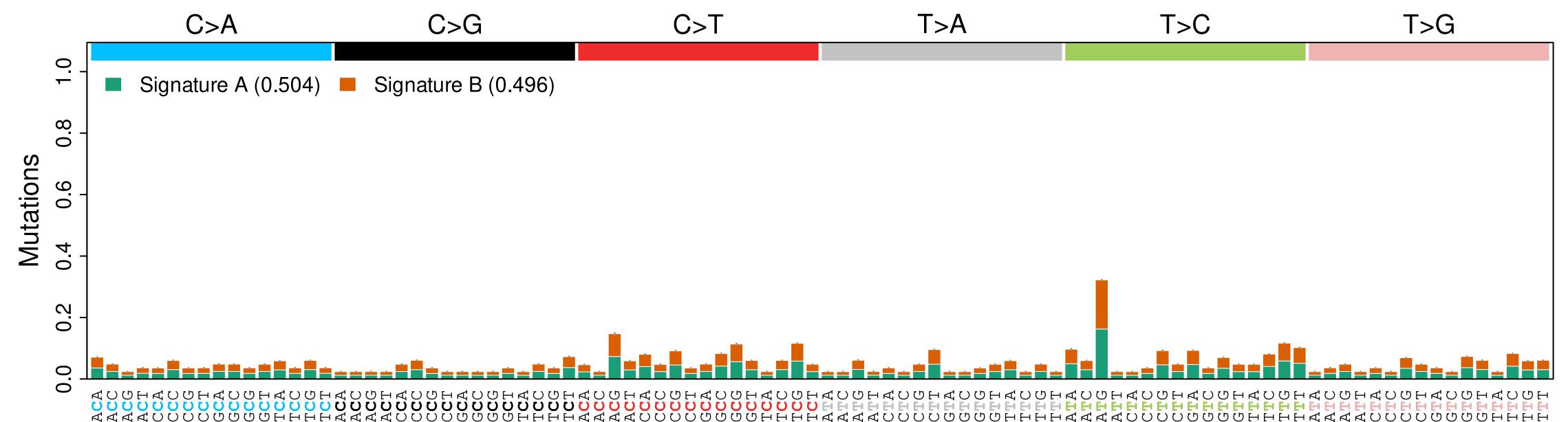




CATD0504a



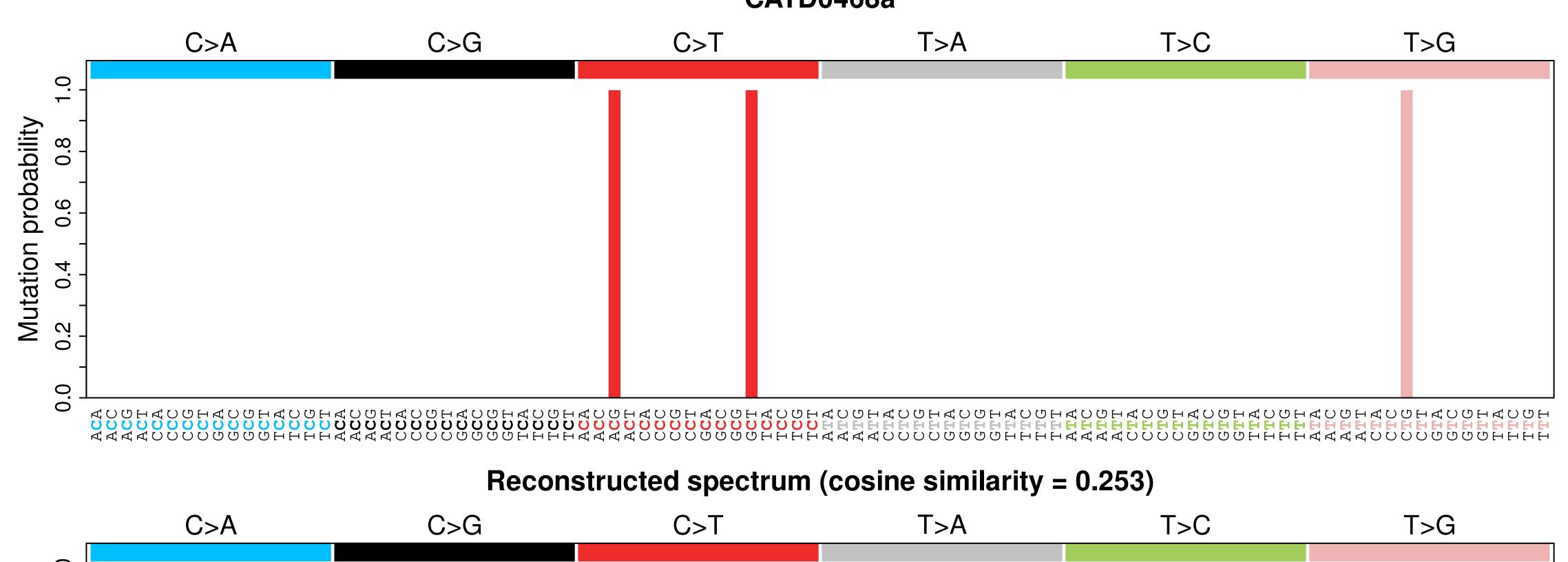


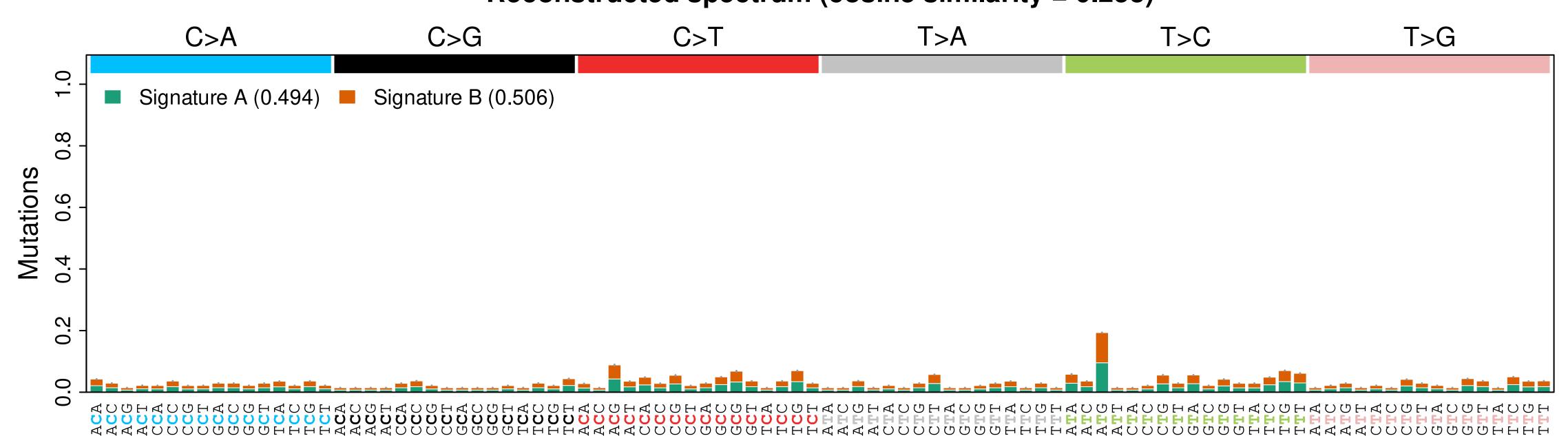


CATD0700a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0 **Reconstructed spectrum (cosine similarity = 0.214)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.506) Signature B (0.494) 5 Mutations 2 0

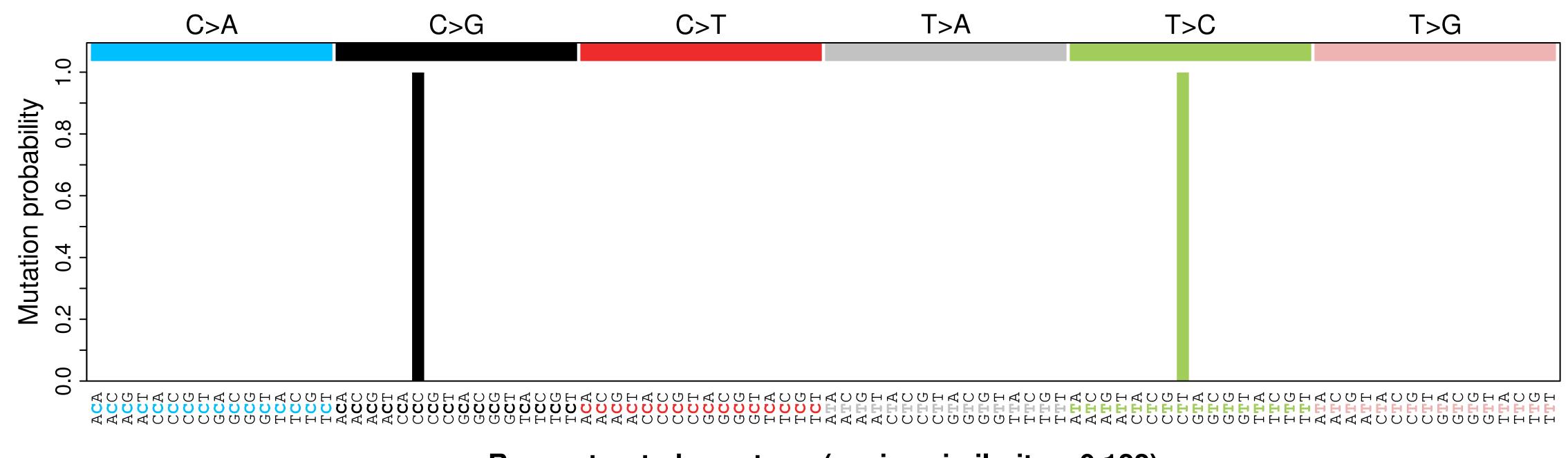
CATD0469a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.446)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.499) Signature B (0.501) 5 Mutations 2 0

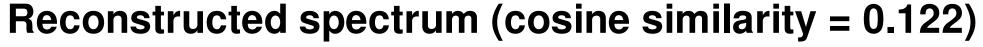


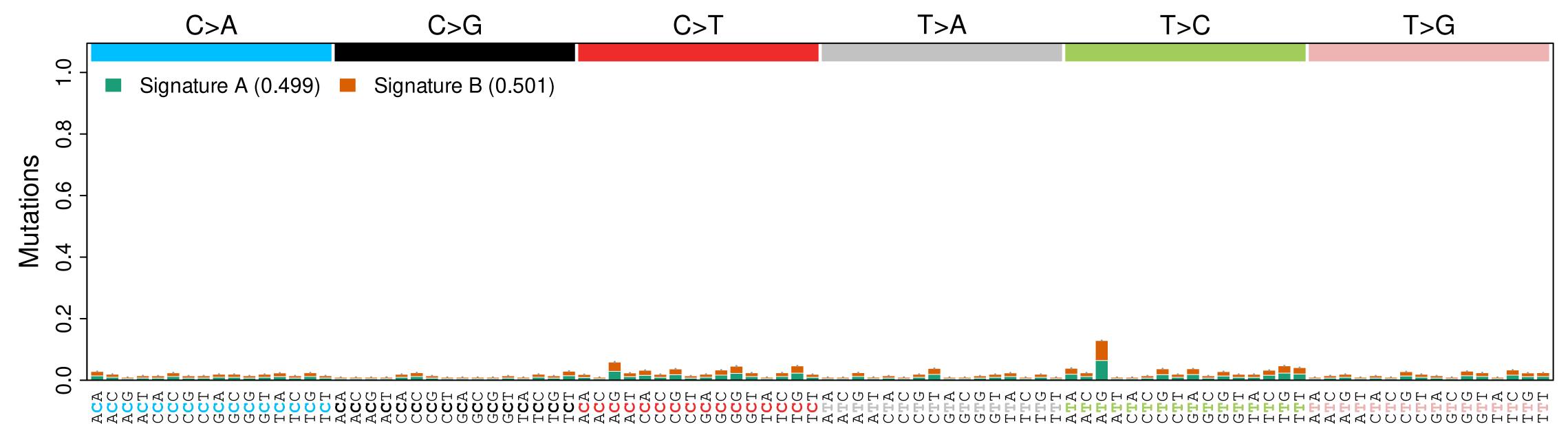




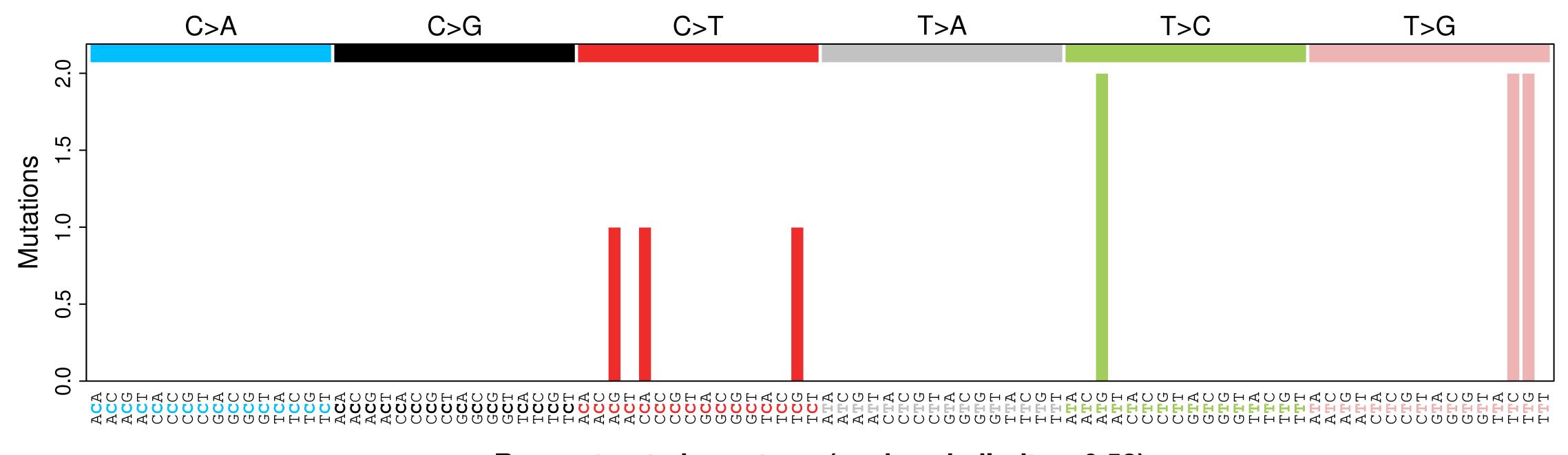


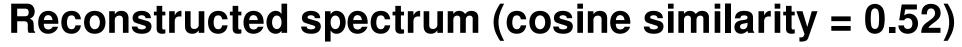


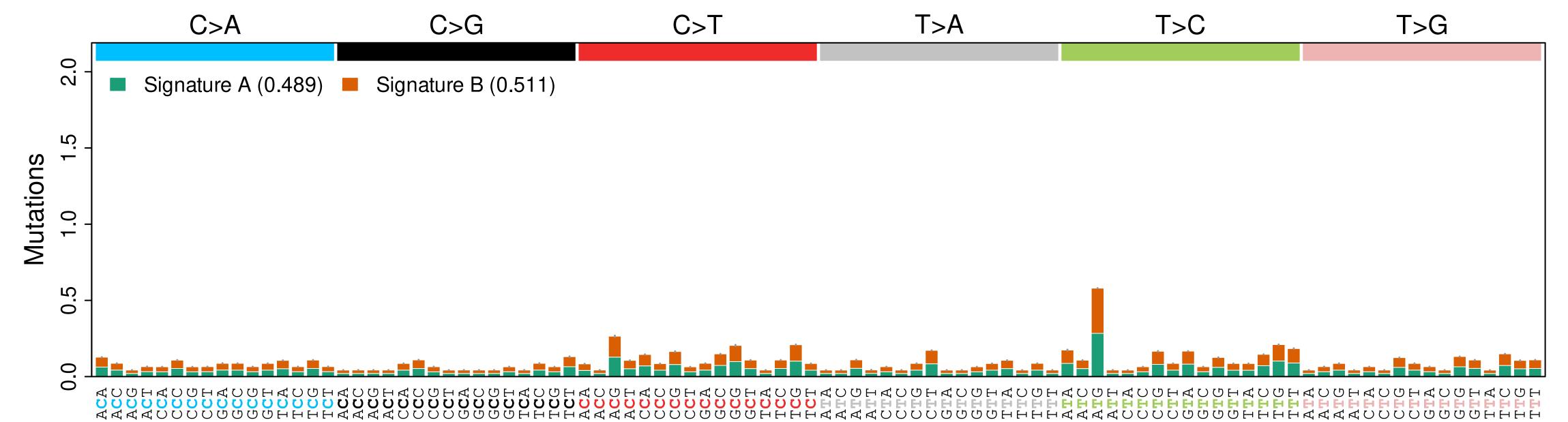




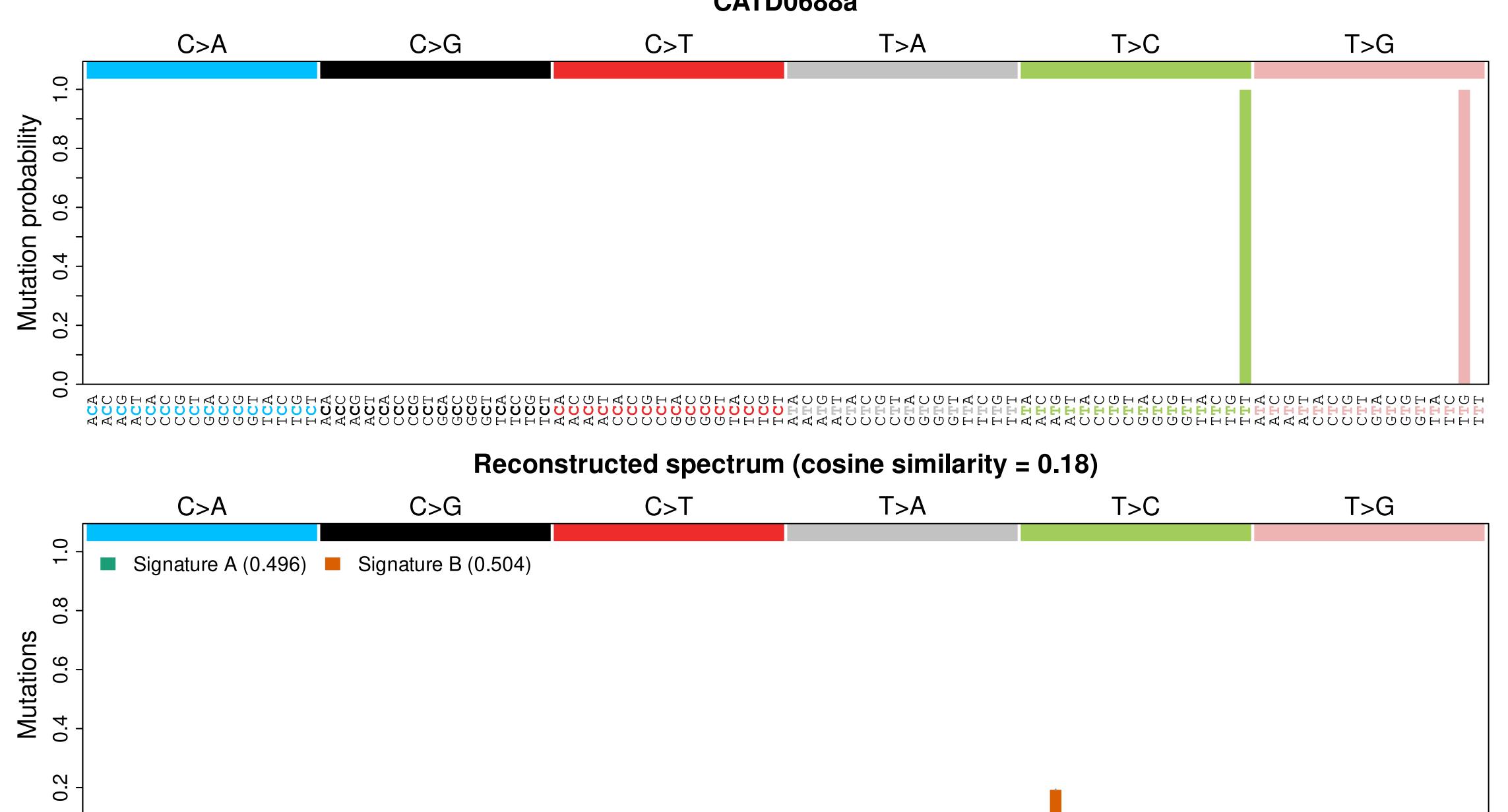
CATD0479a (9 mutations)



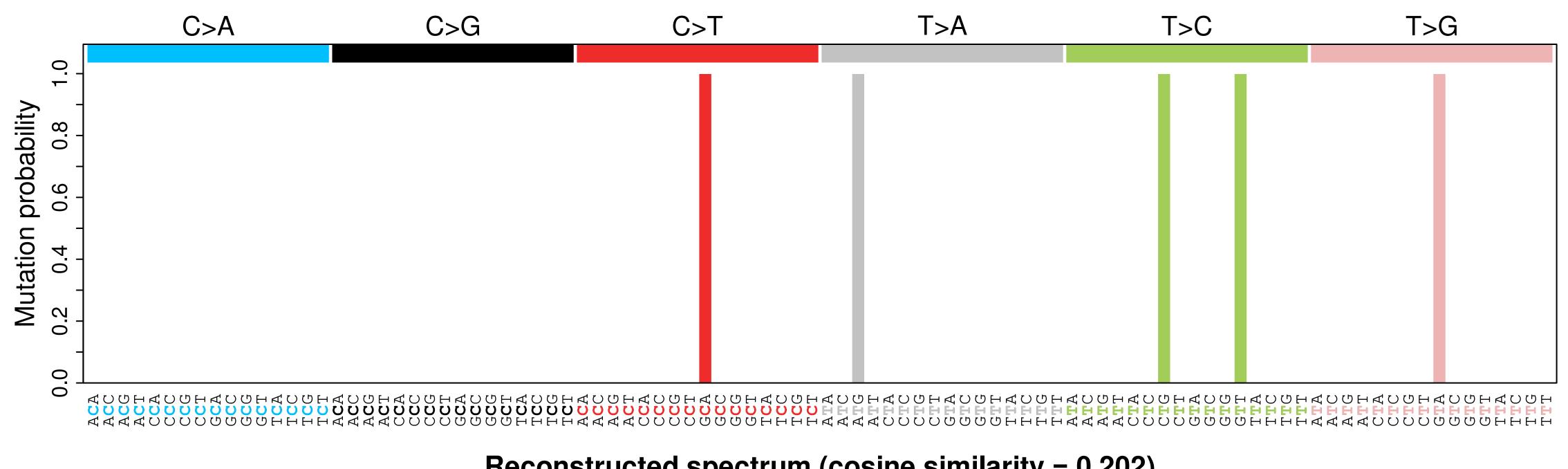




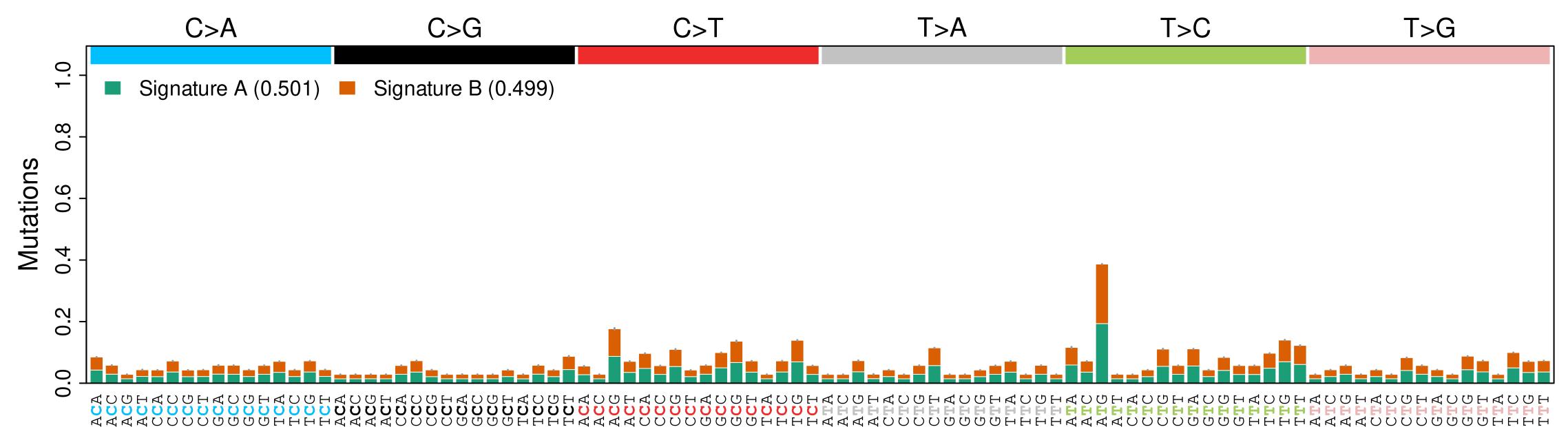




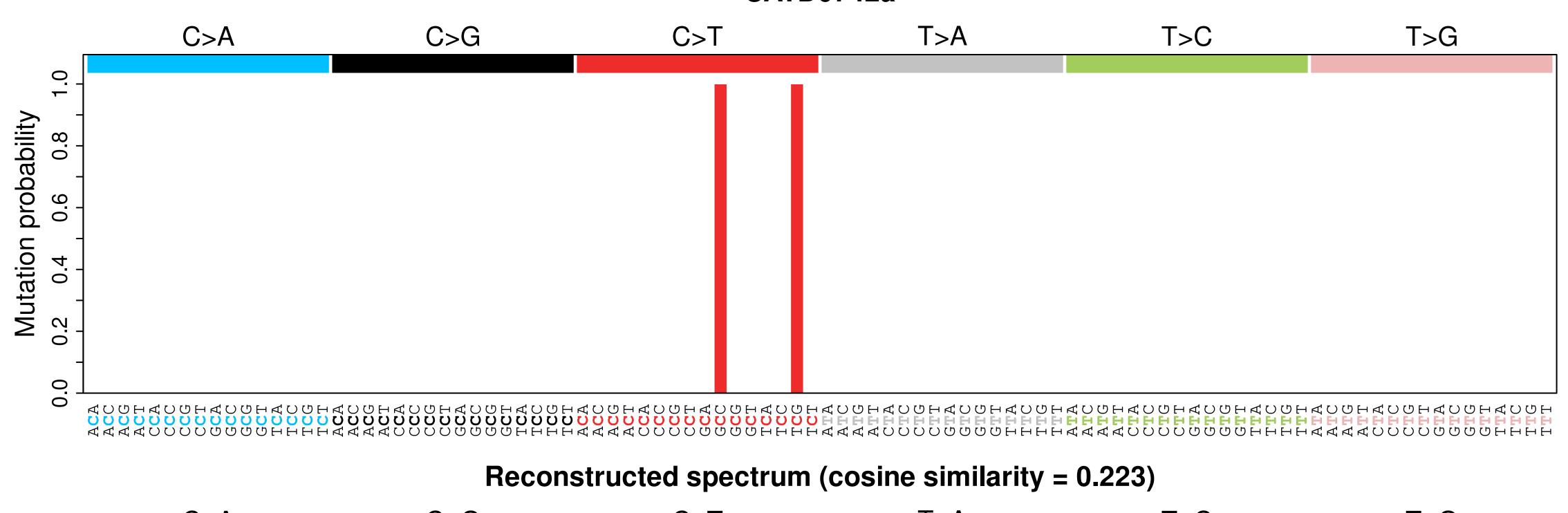
CATD0494a

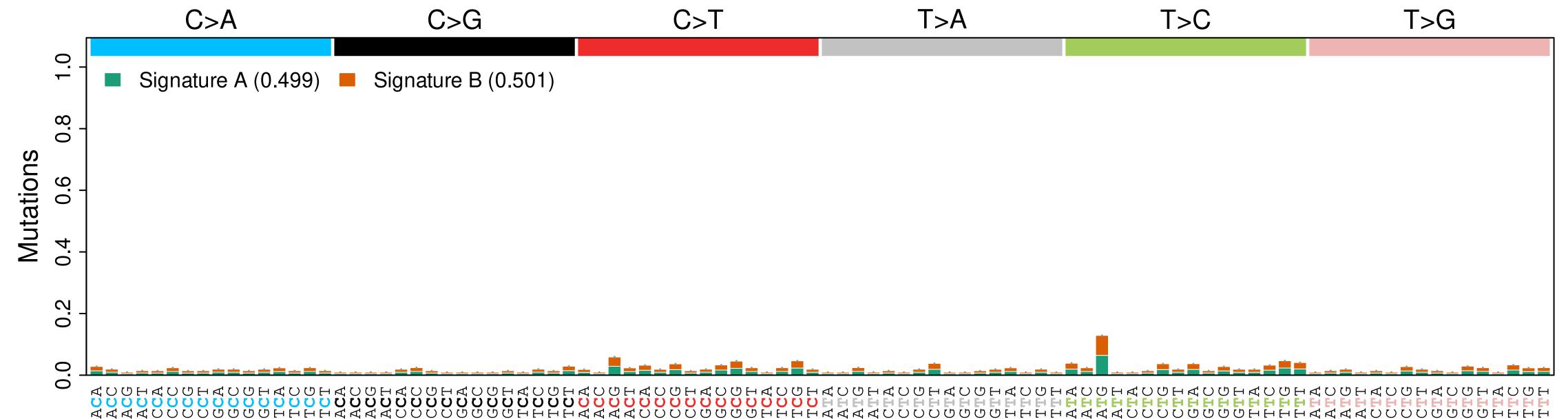




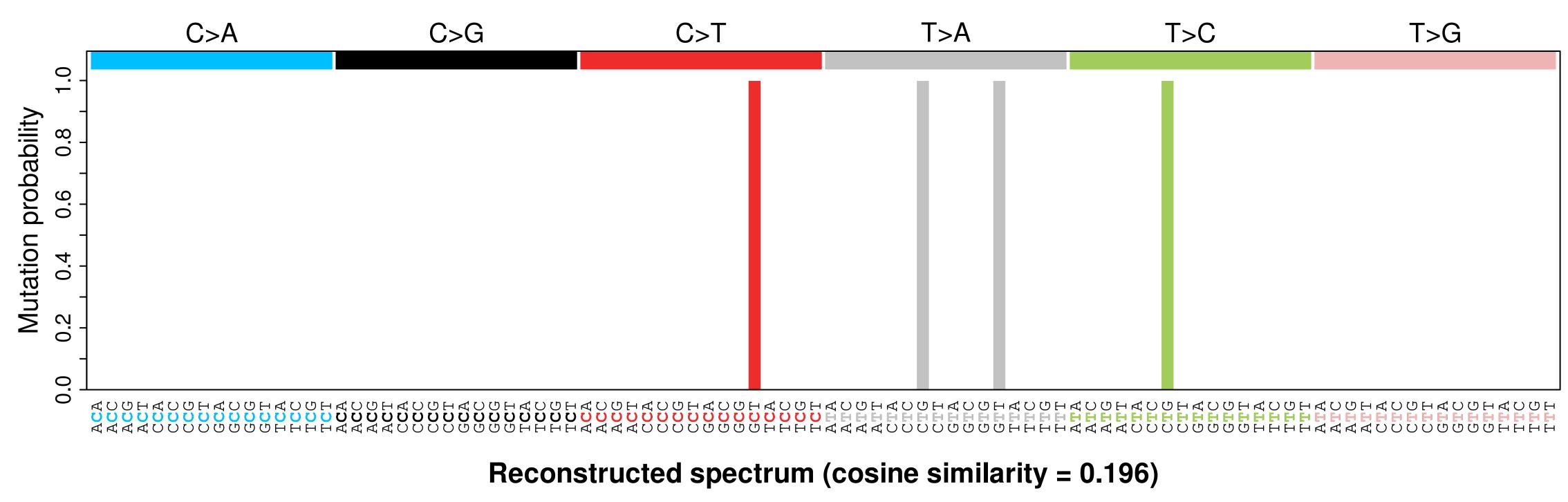


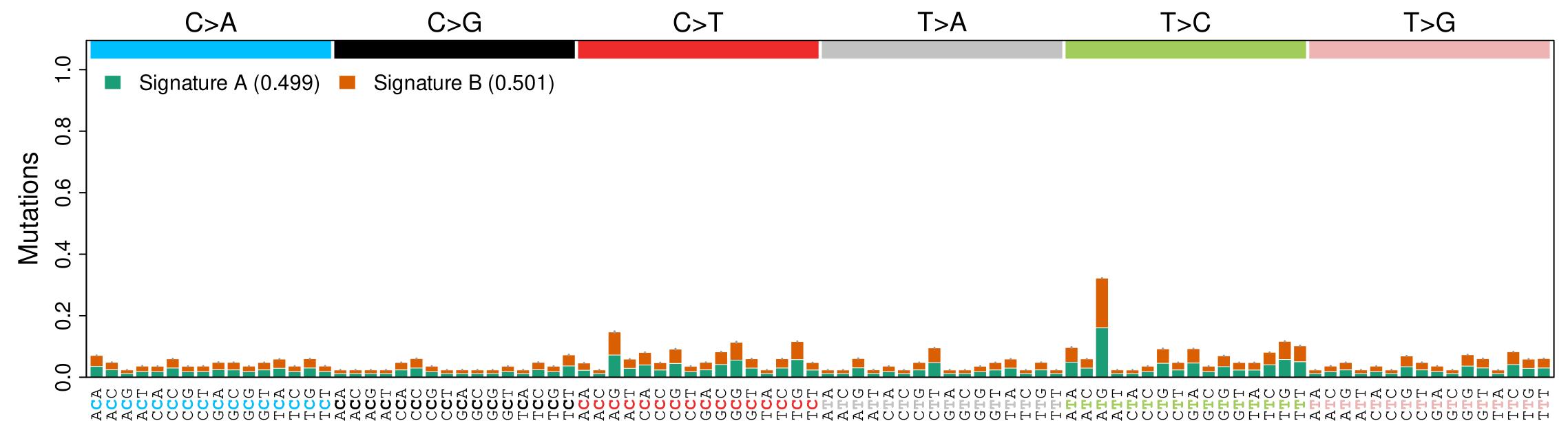




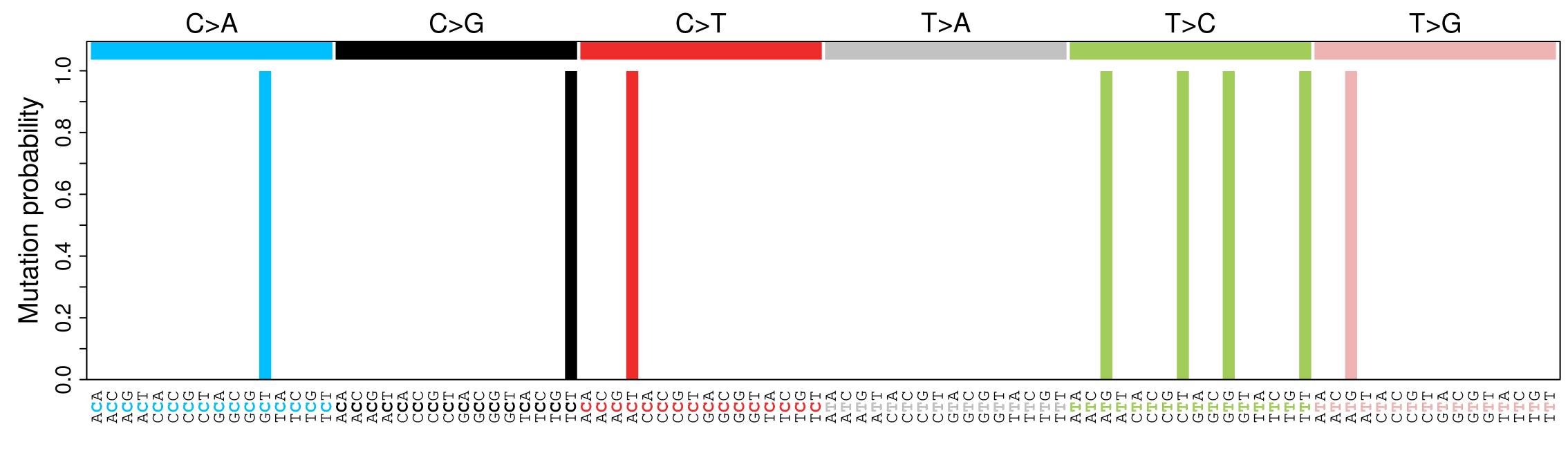


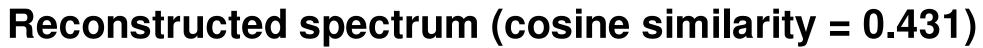


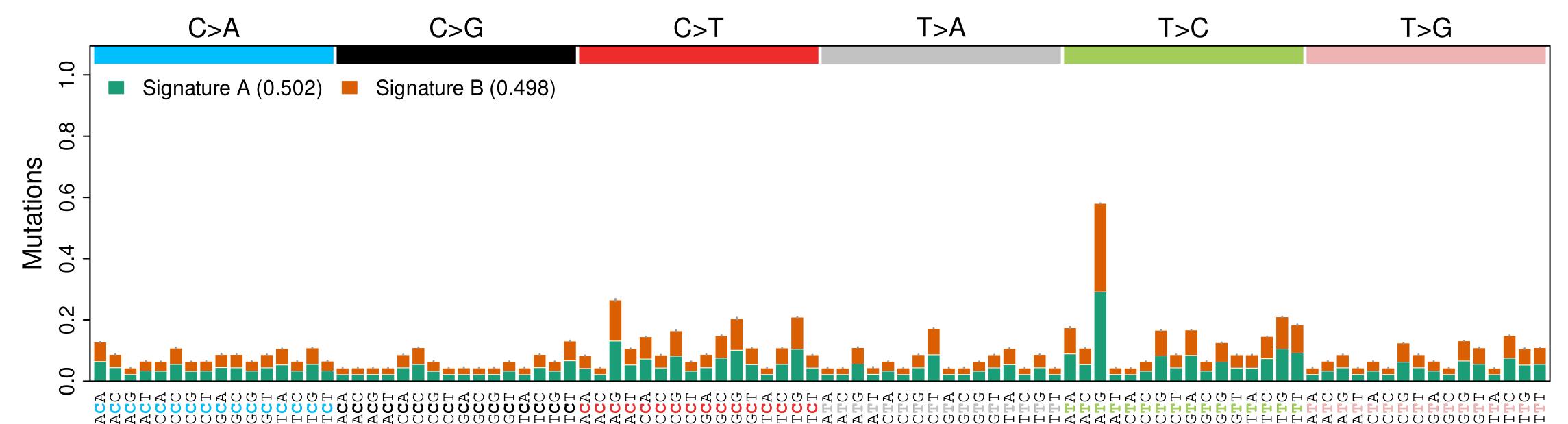




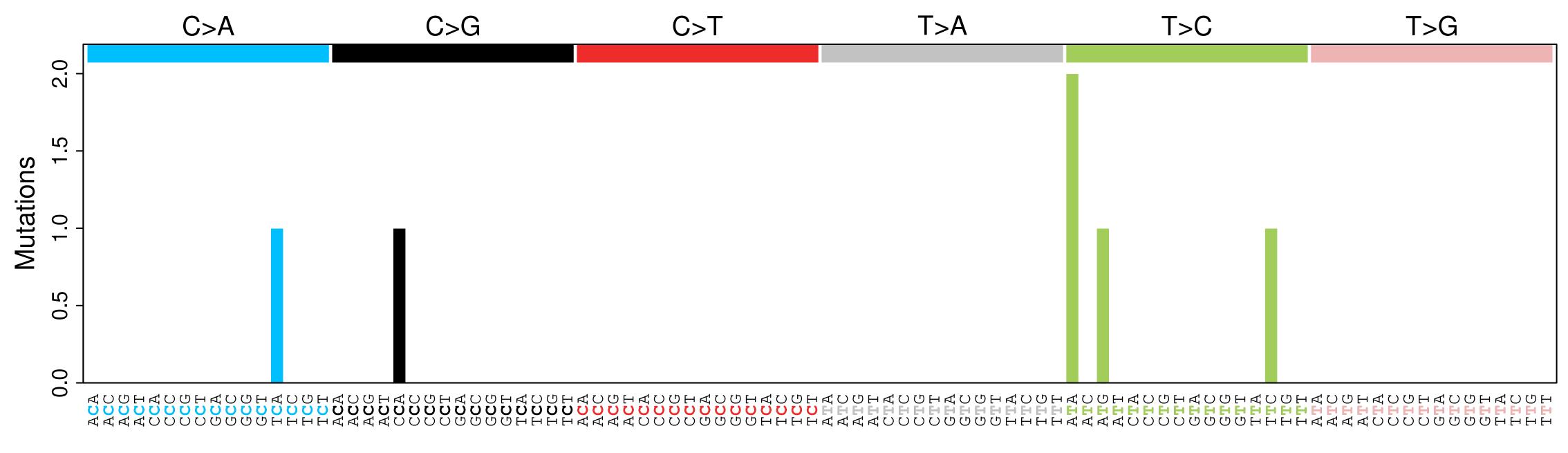
CATD0745a



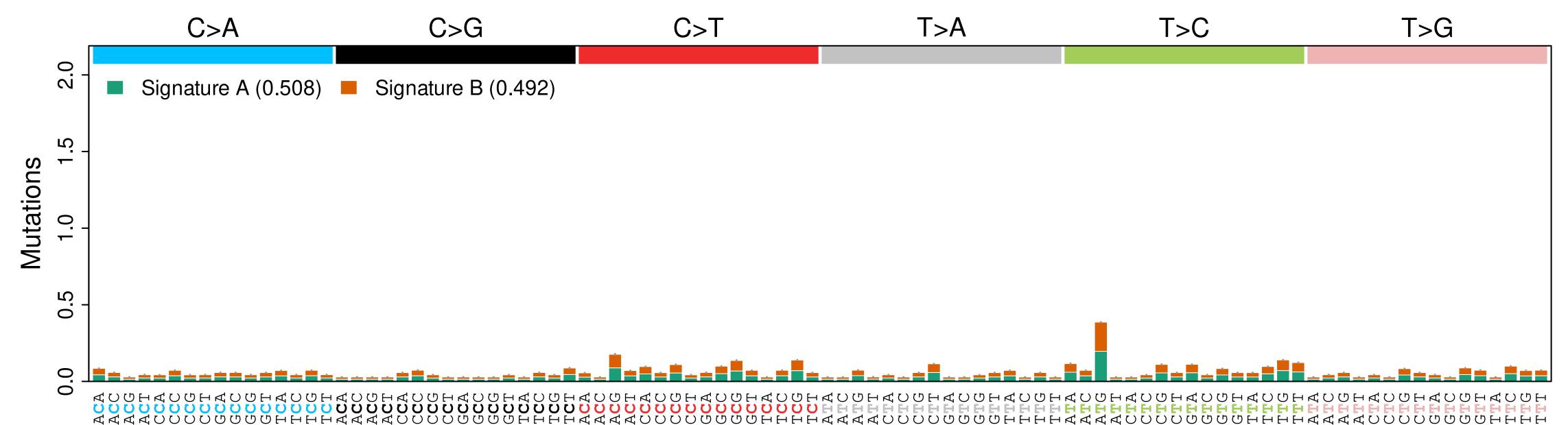


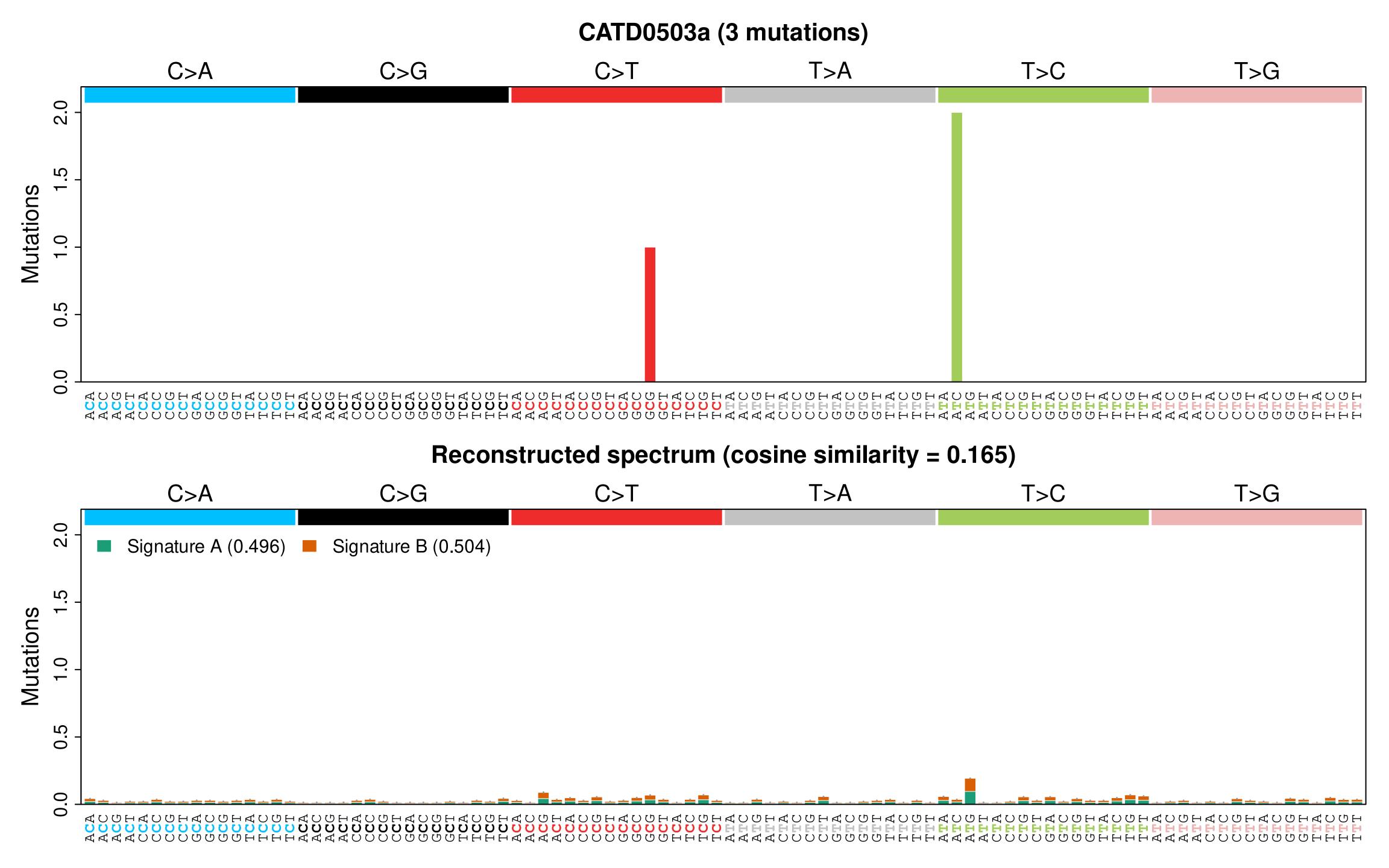


CATD0475a (6 mutations)



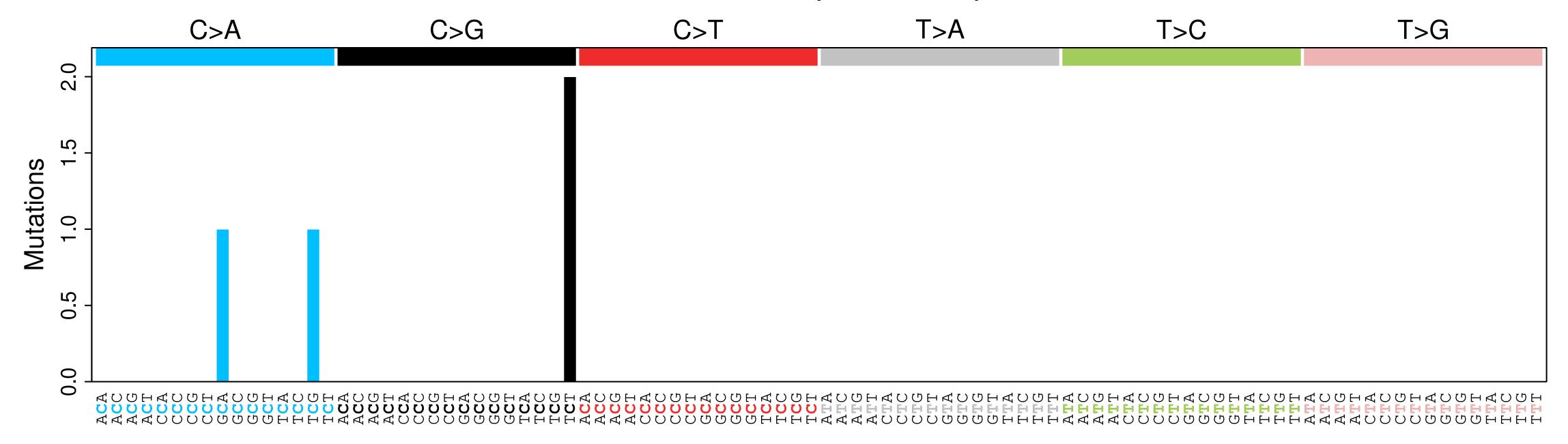
Reconstructed spectrum (cosine similarity = 0.394)



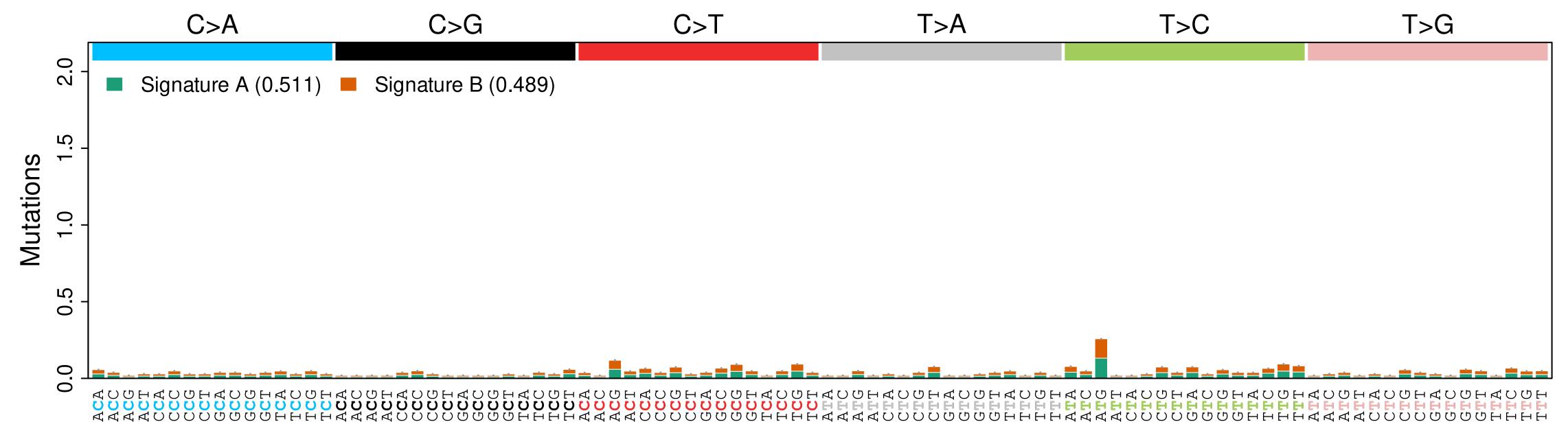


CATD0743a (5 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.198)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.503) Signature B (0.497) 5 Mutations 2 0

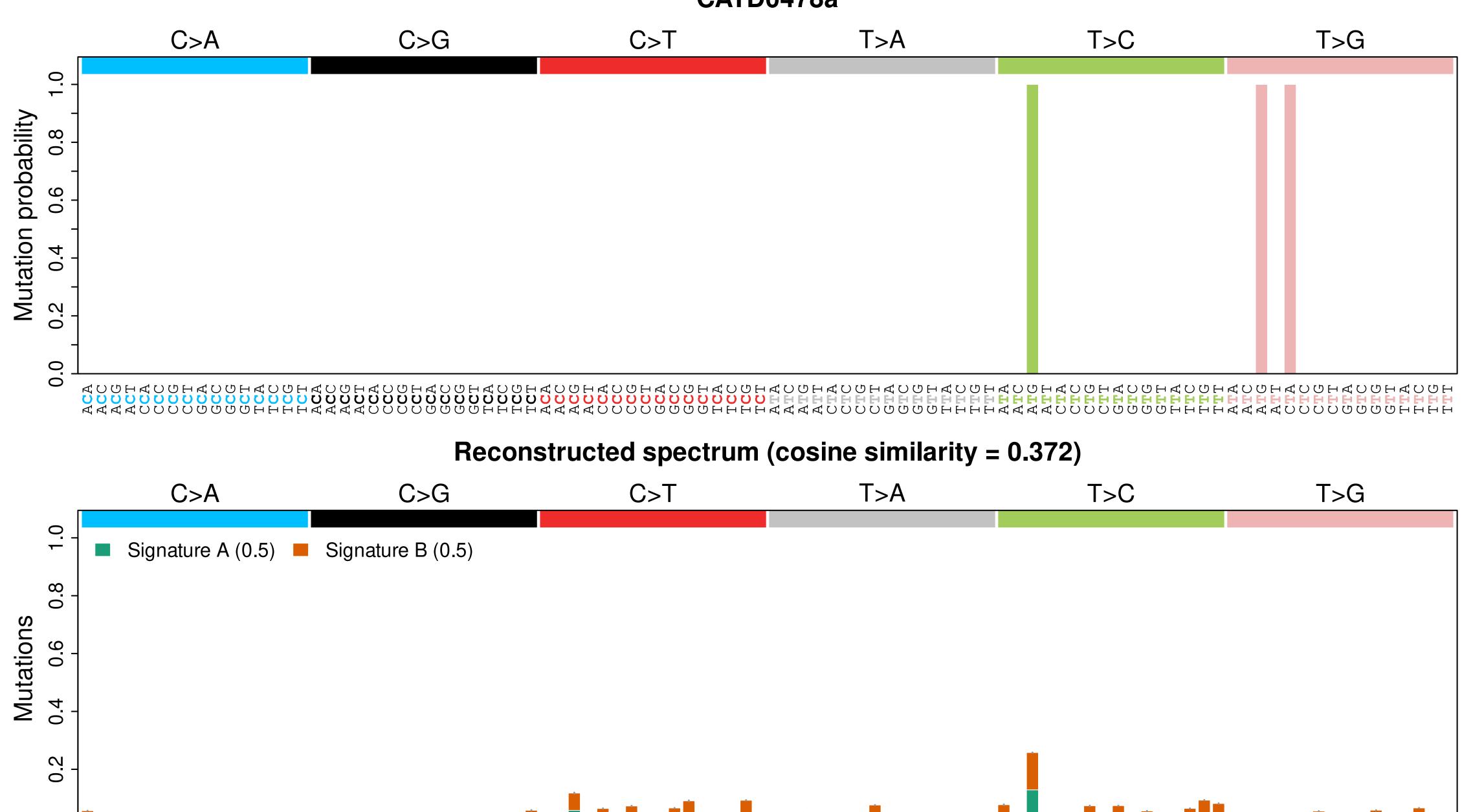
CATD0737a (4 mutations)

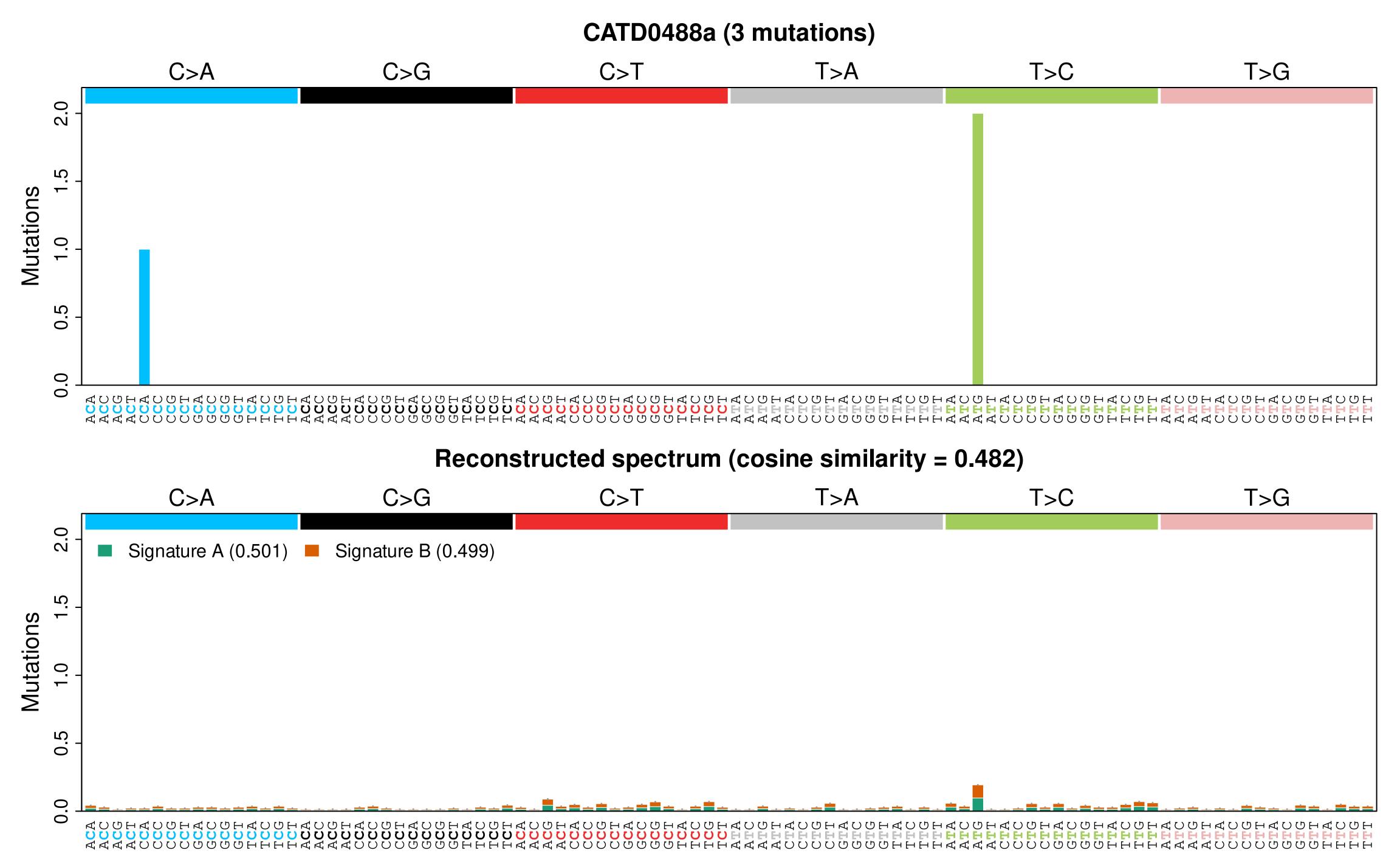


Reconstructed spectrum (cosine similarity = 0.164)





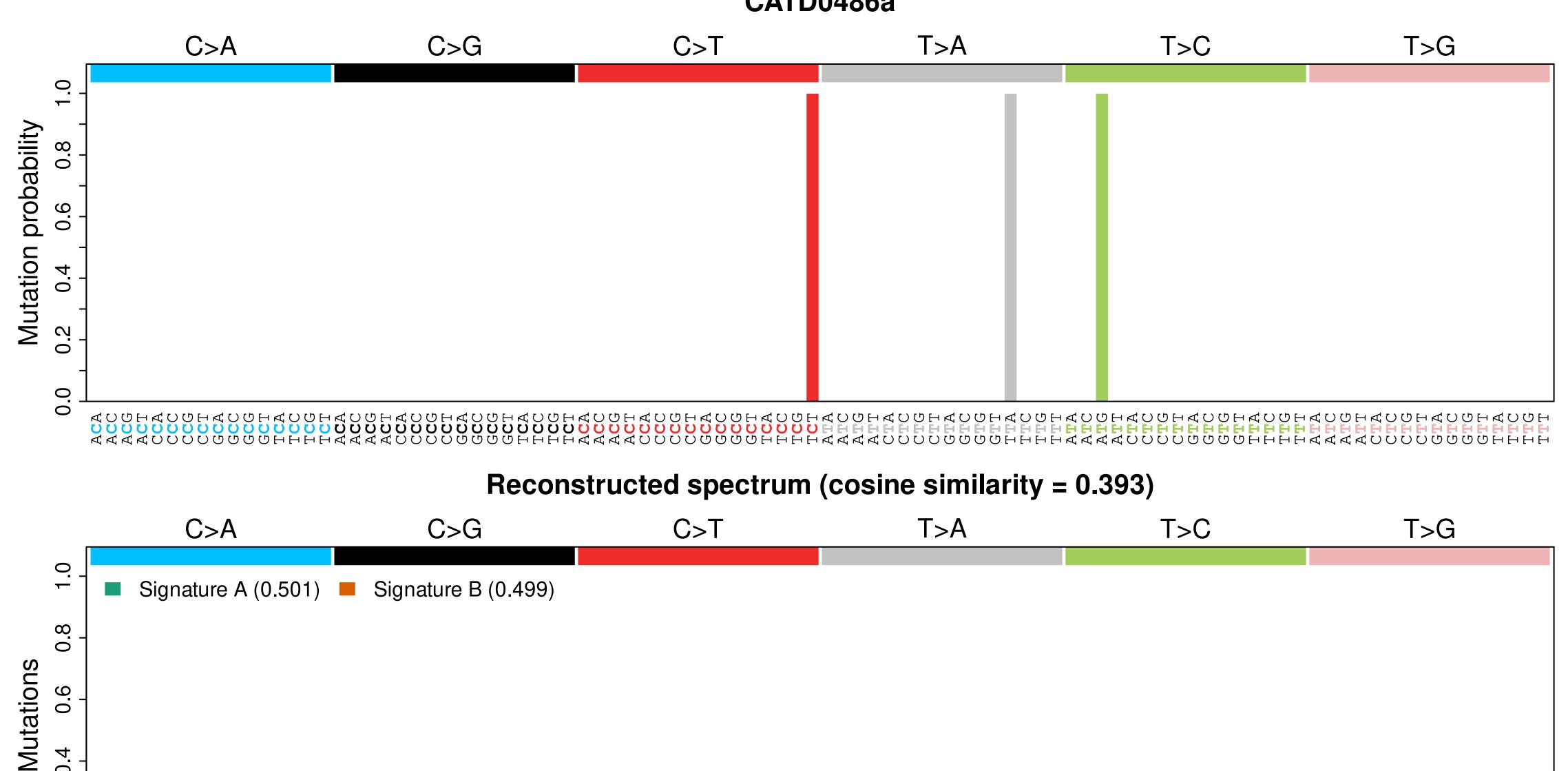




CATD0697a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 1.5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.147)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.5) Signature B (0.5) 5 Mutations 5 0 0

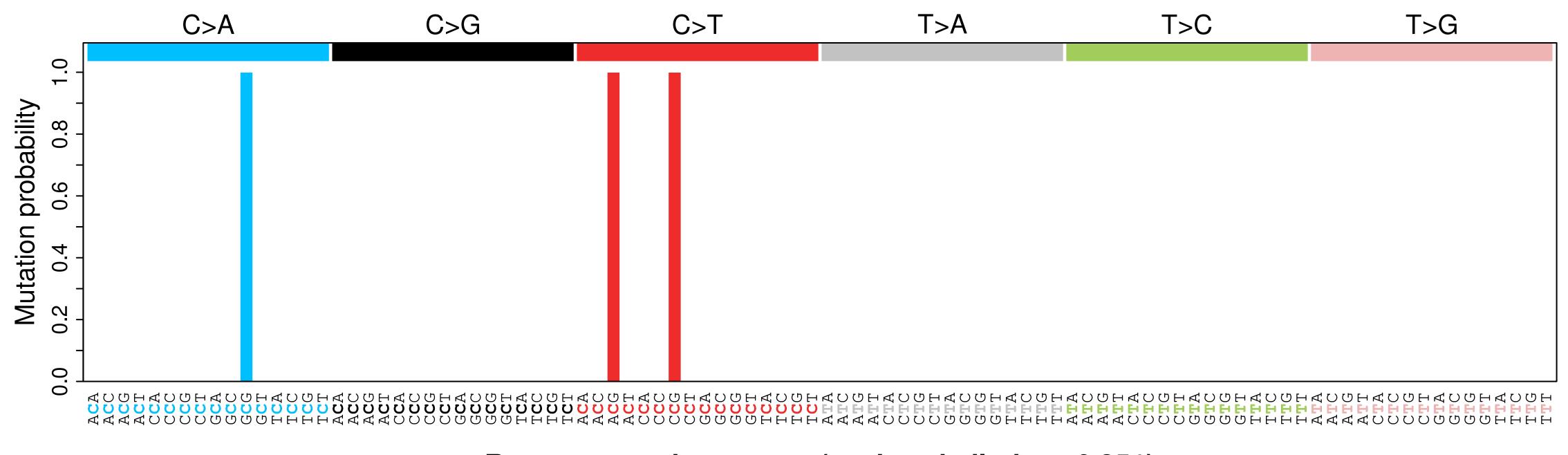
CATD0485a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0 **Reconstructed spectrum (cosine similarity = 0.551)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.495) Signature B (0.505) 5 Mutations 2 0 0

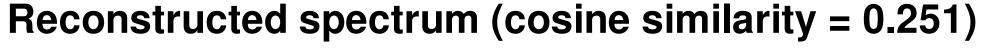


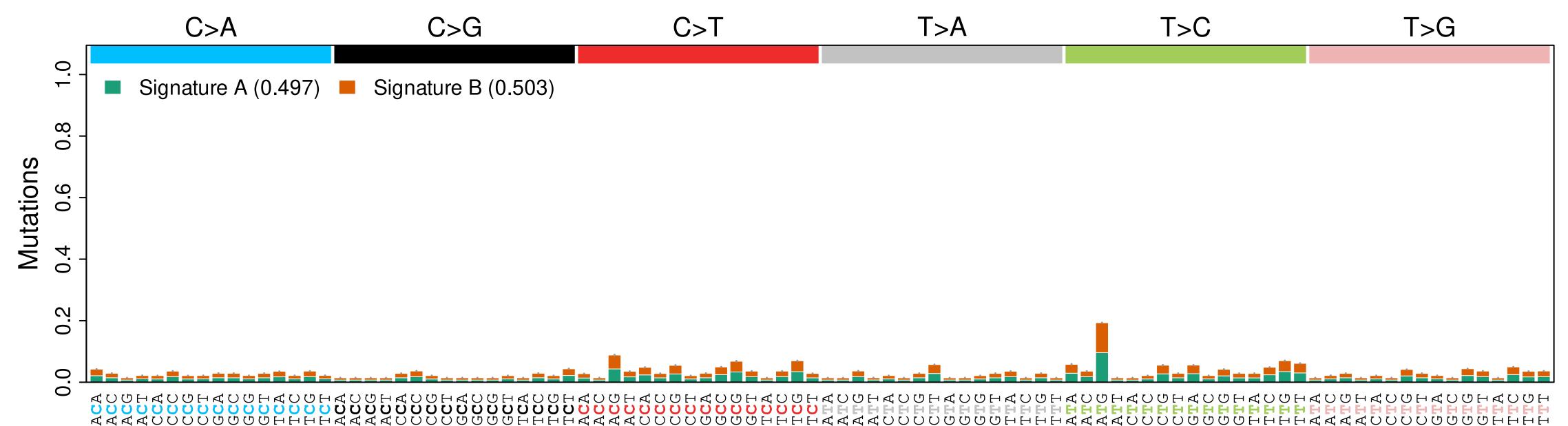


 \mathcal{O} 0





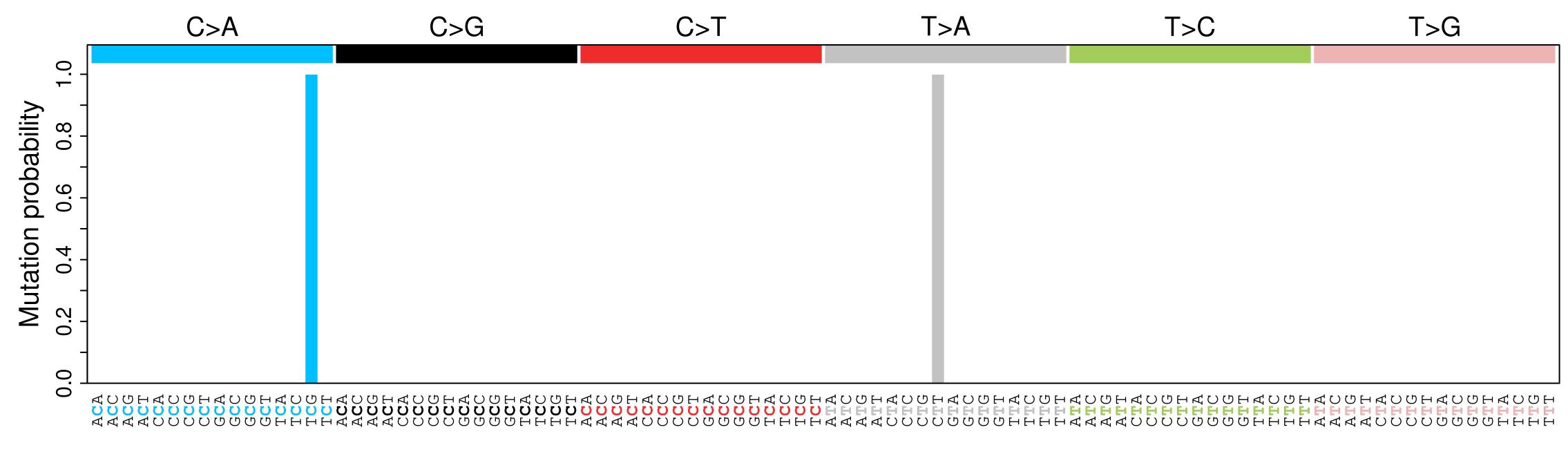


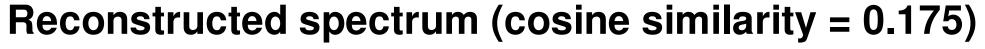


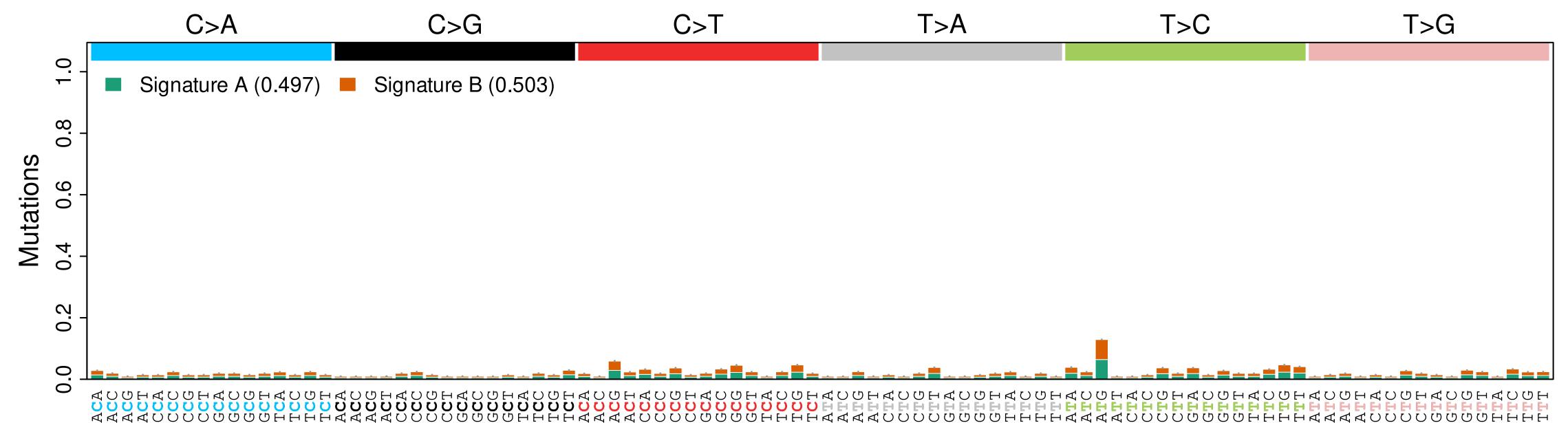
CATD0744a (5 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.482)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.499) Signature B (0.501) 5 Mutations 2 0

CATD0471a (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 = 0.501)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.502) Signature B (0.498) 5 Mutations 2 0



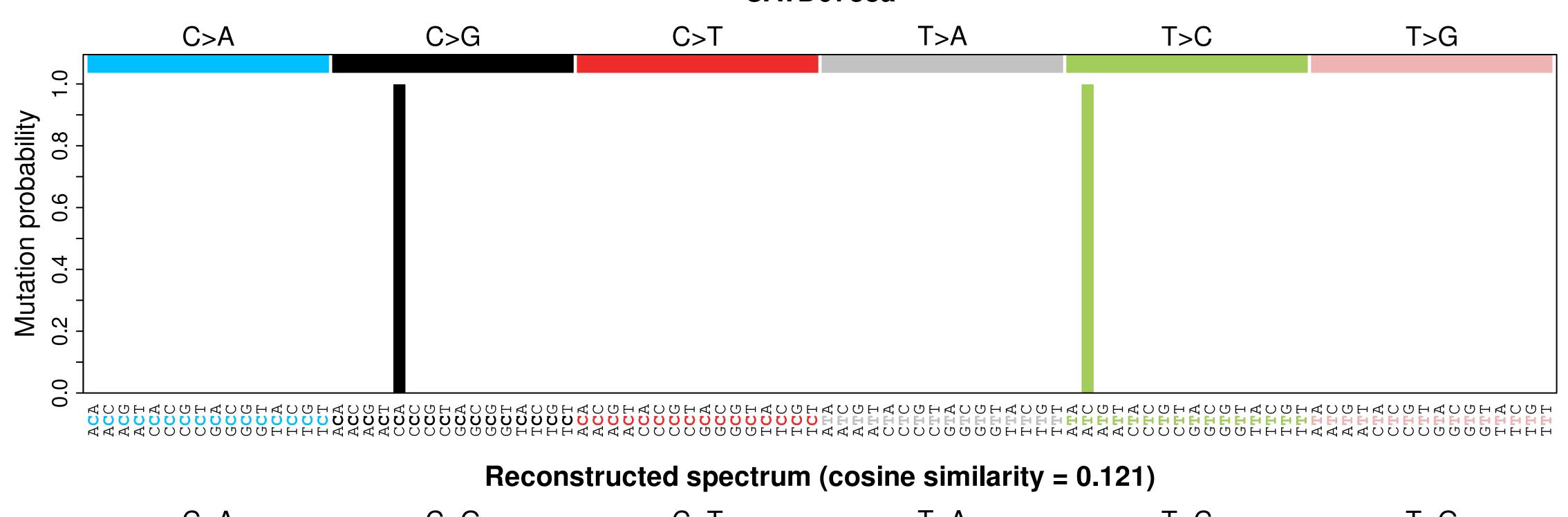


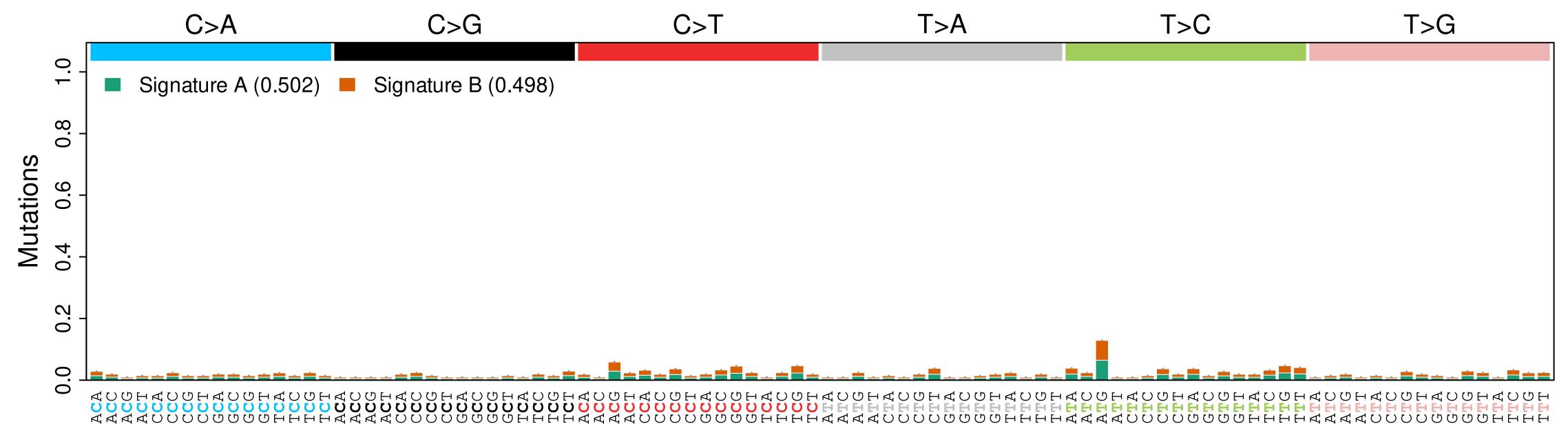




CATD0739a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.243)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.491) Signature B (0.509) 5 Mutations 5 0 0

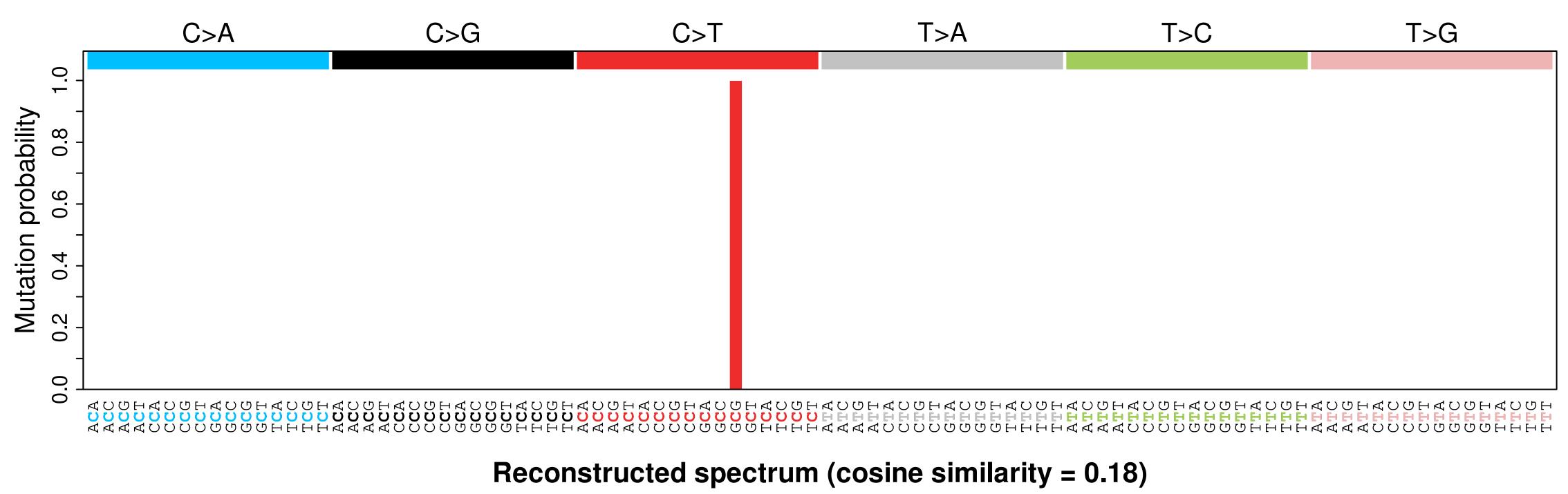


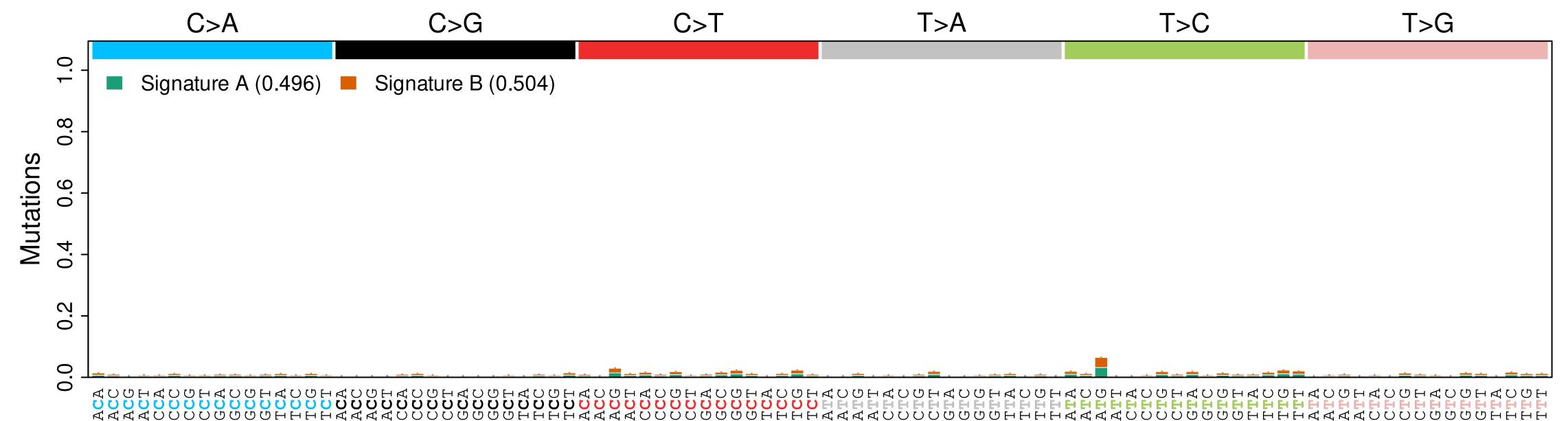




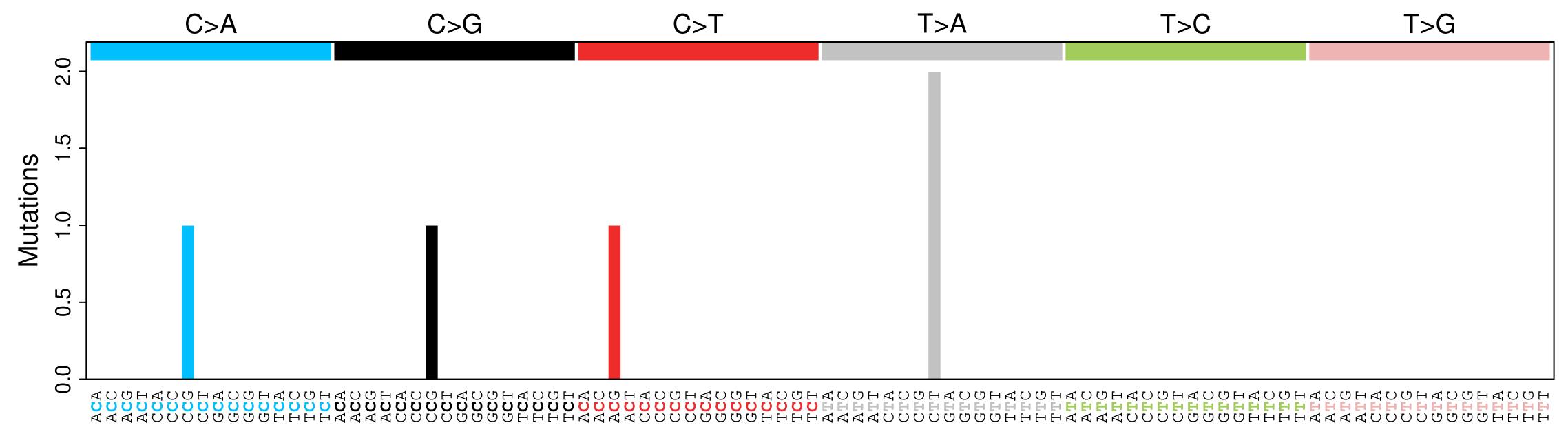
CATD0692a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.138)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.504) Signature B (0.496) 5 Mutations 5 0







CATD0498a (5 mutations)



Reconstructed spectrum (cosine similarity = 0.245)

