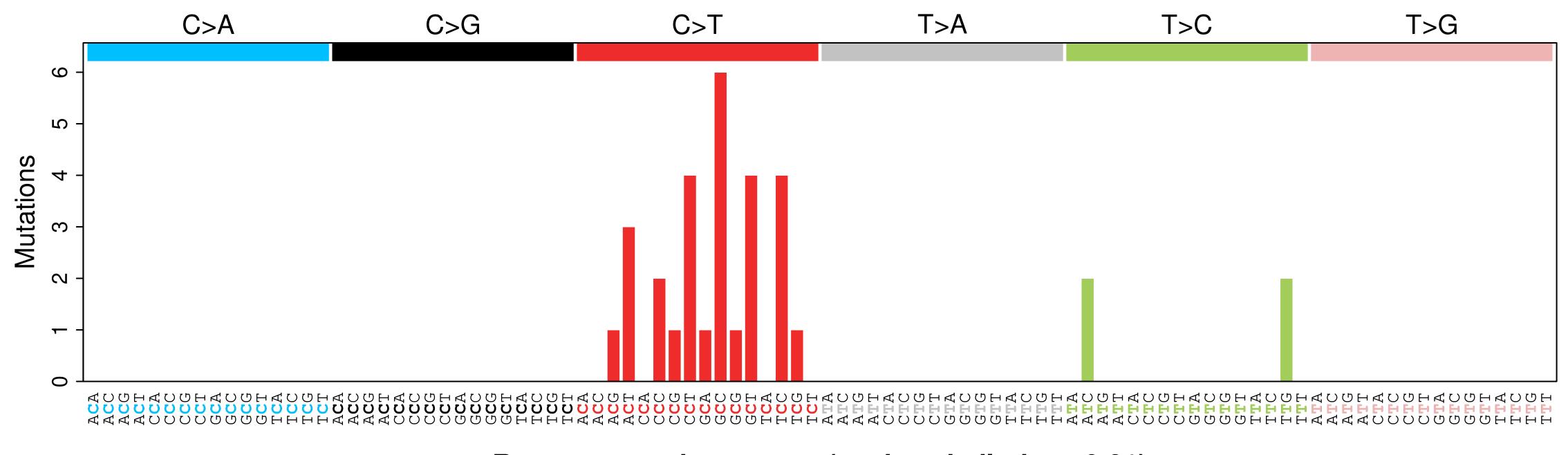
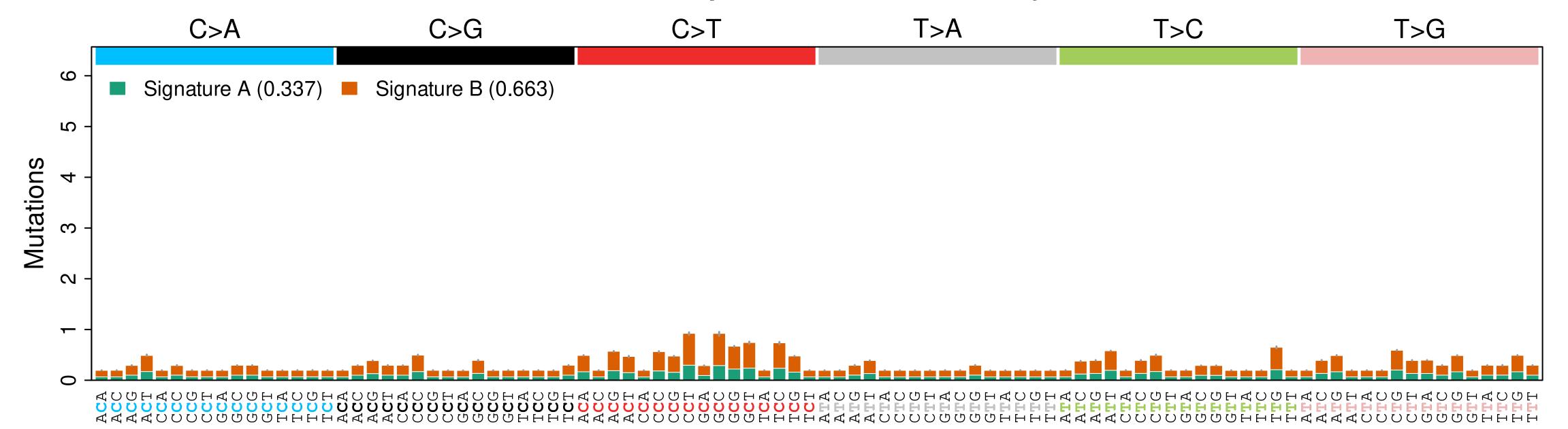
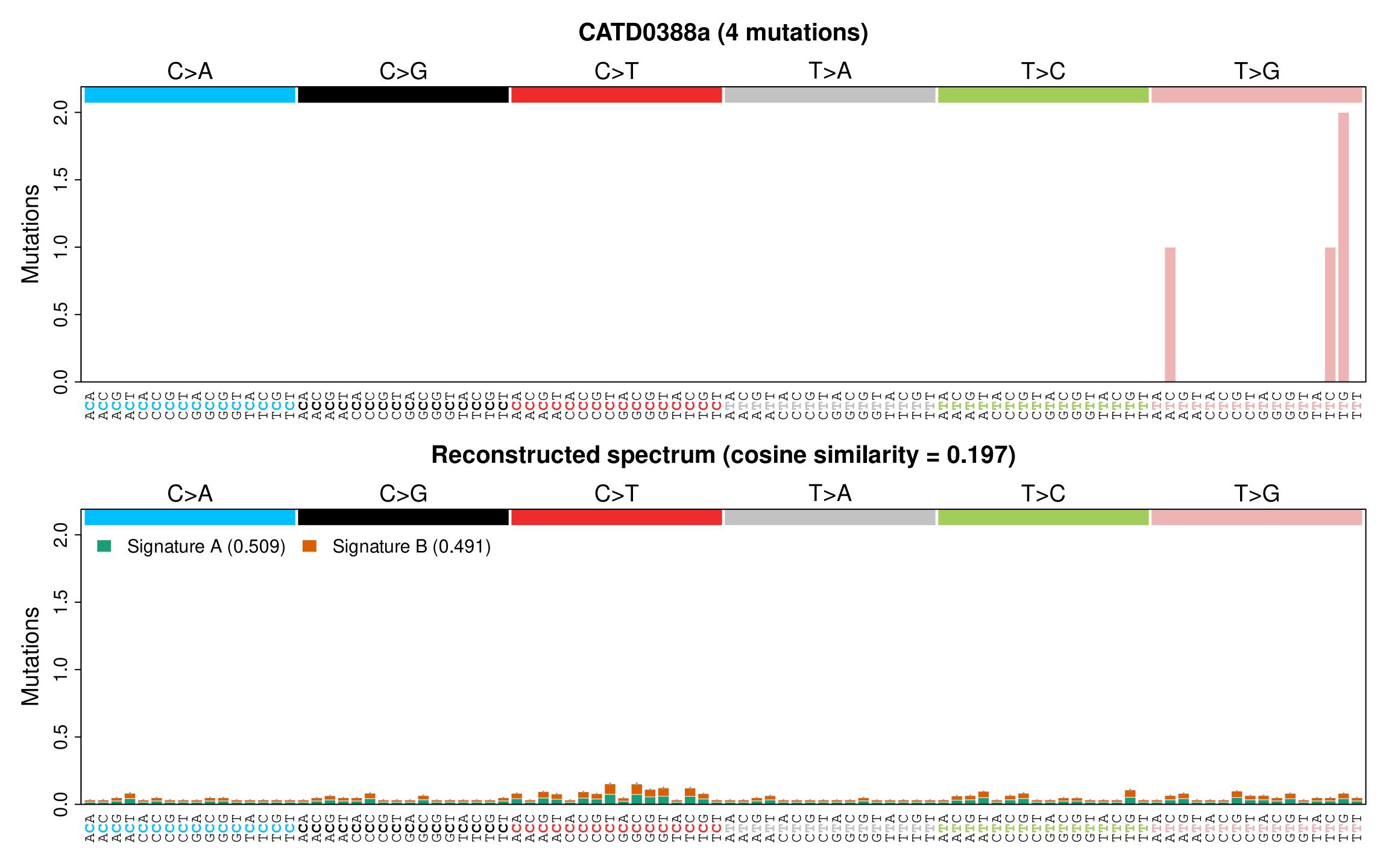
CATD0393a (32 mutations)

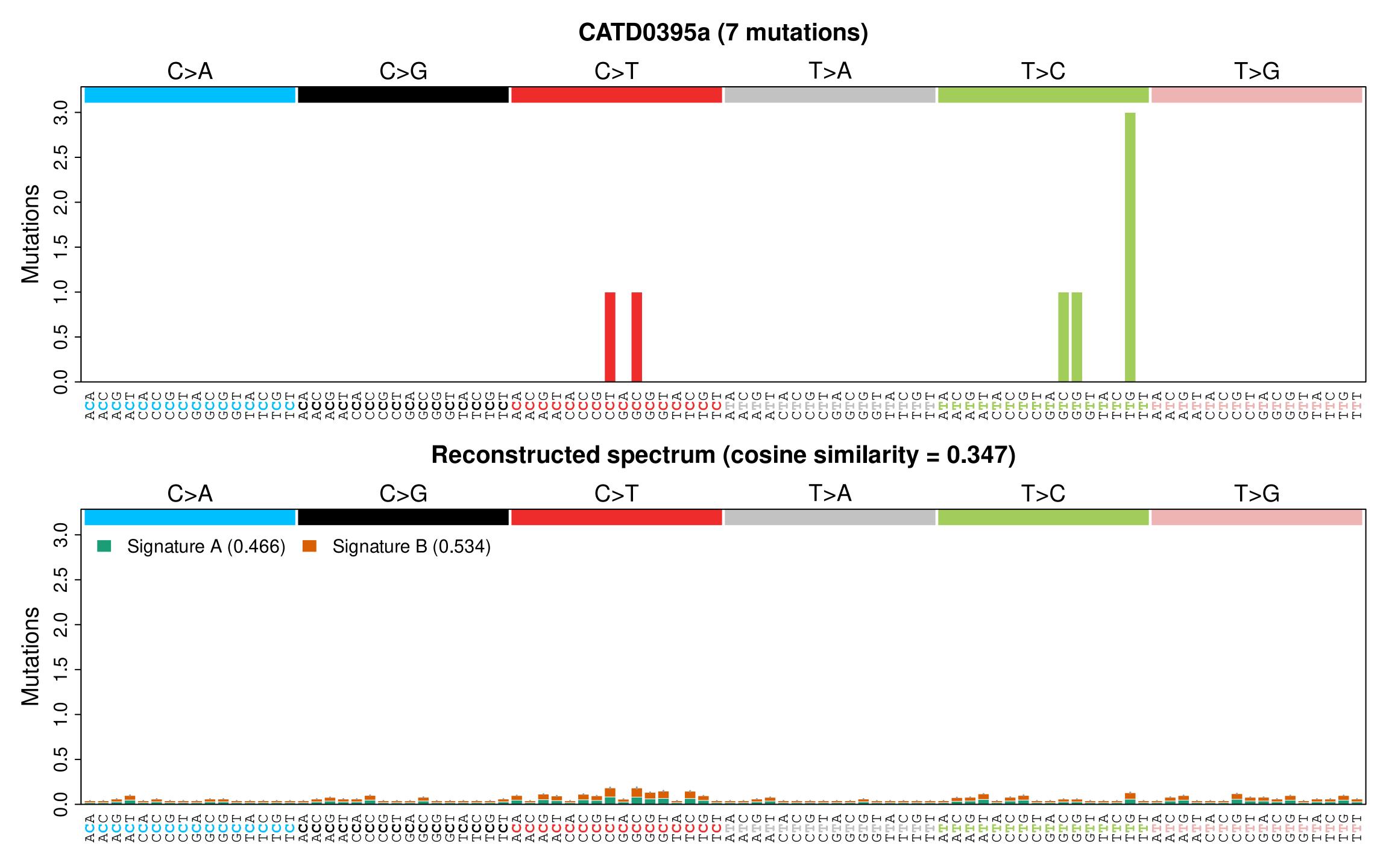


Reconstructed spectrum (cosine similarity = 0.61)

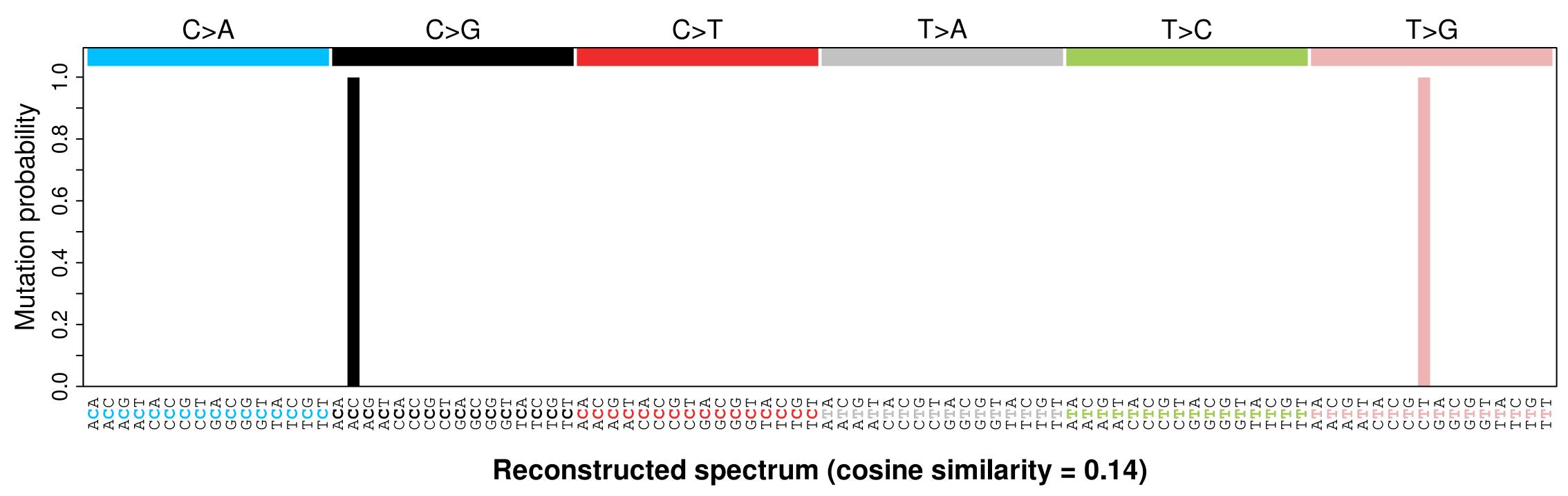


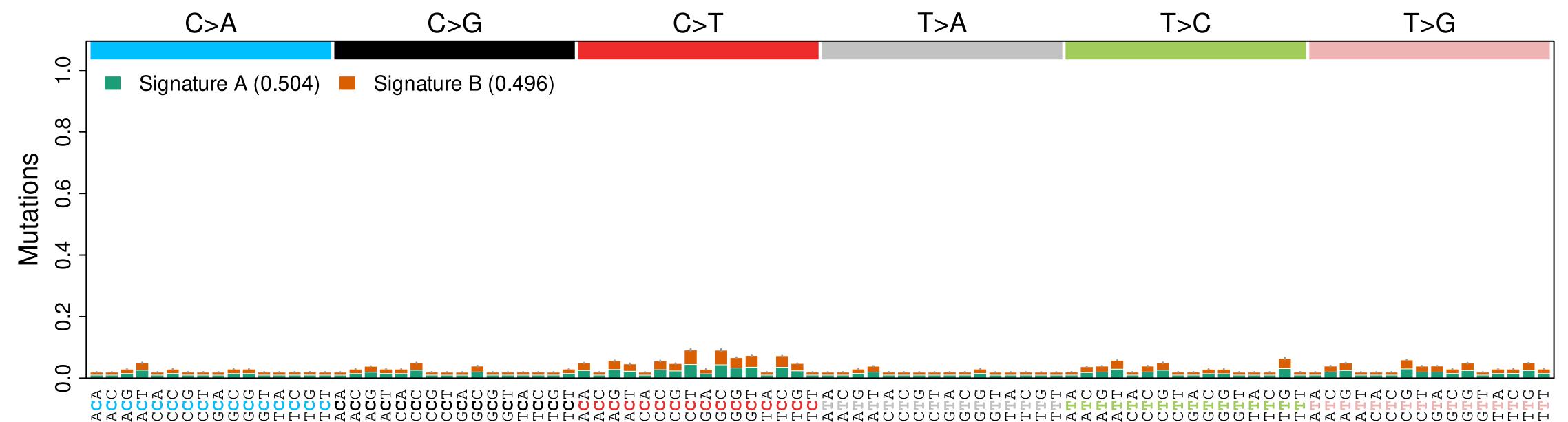
CATD0657a (7 mutations) T>G C>A C>G C>T T>A T>C 3.0 2.5 Mutations 2.0 1.5 0.5 0 **Reconstructed spectrum (cosine similarity = 0.335)** T>G C>G T>A T>C C>A C>T 3.0 Signature A (0.49) Signature B (0.51) 5 S Mutations 2.0 1.5 5 0



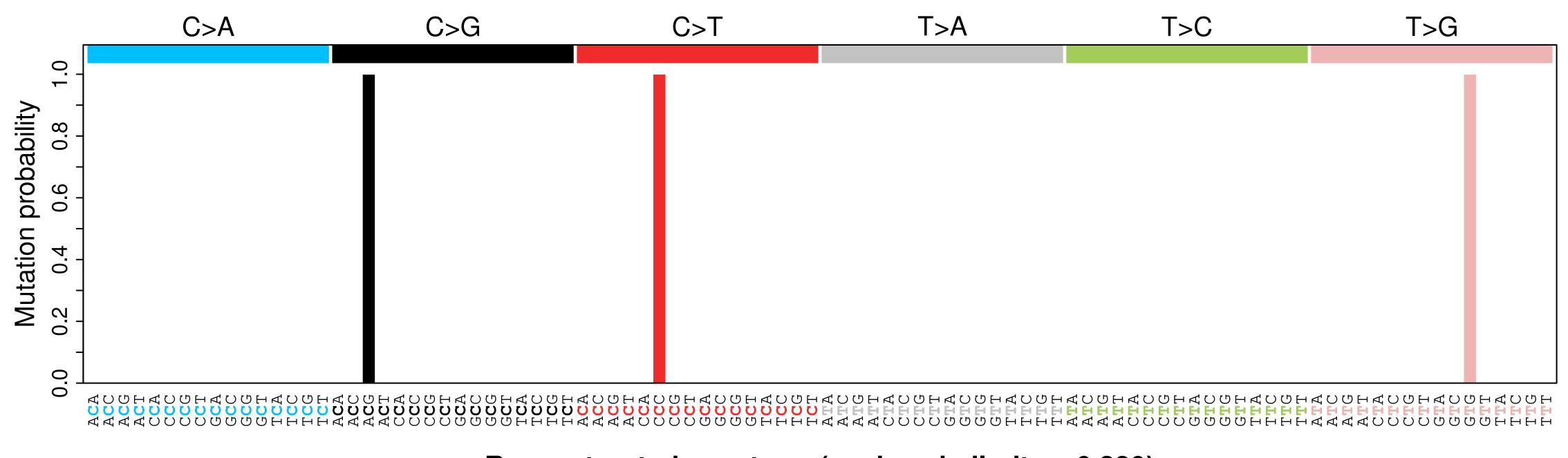


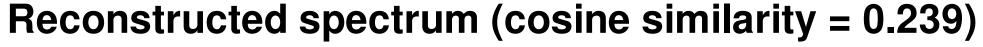


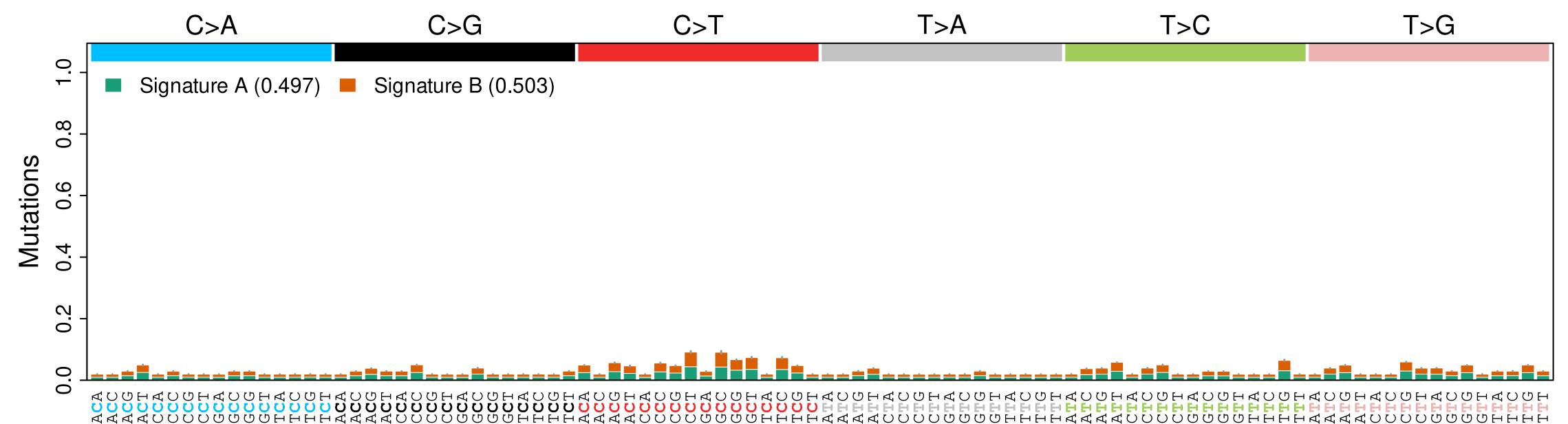






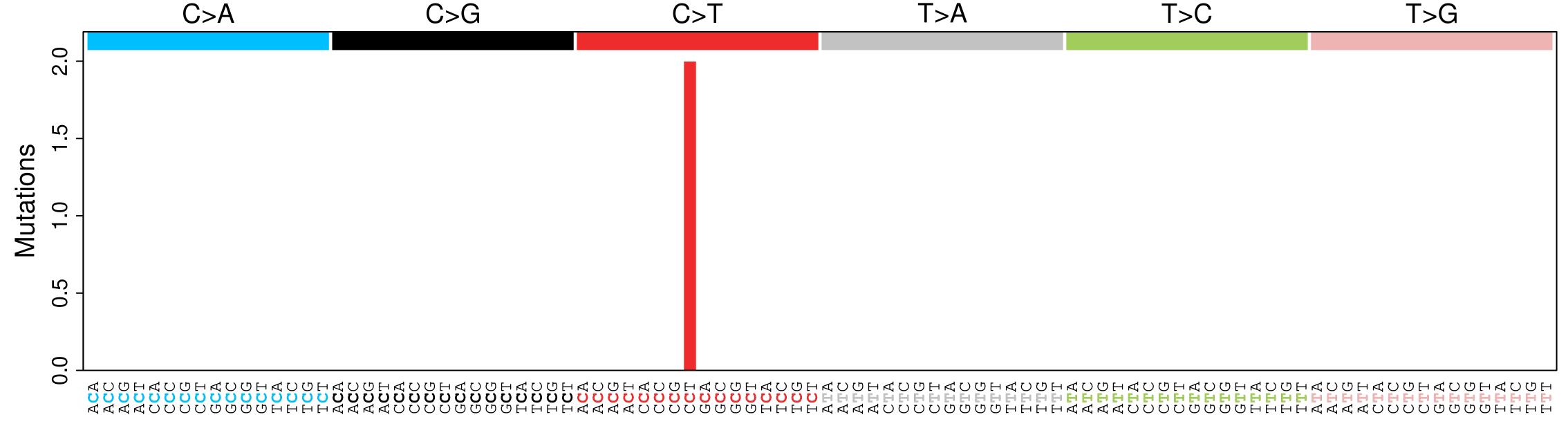




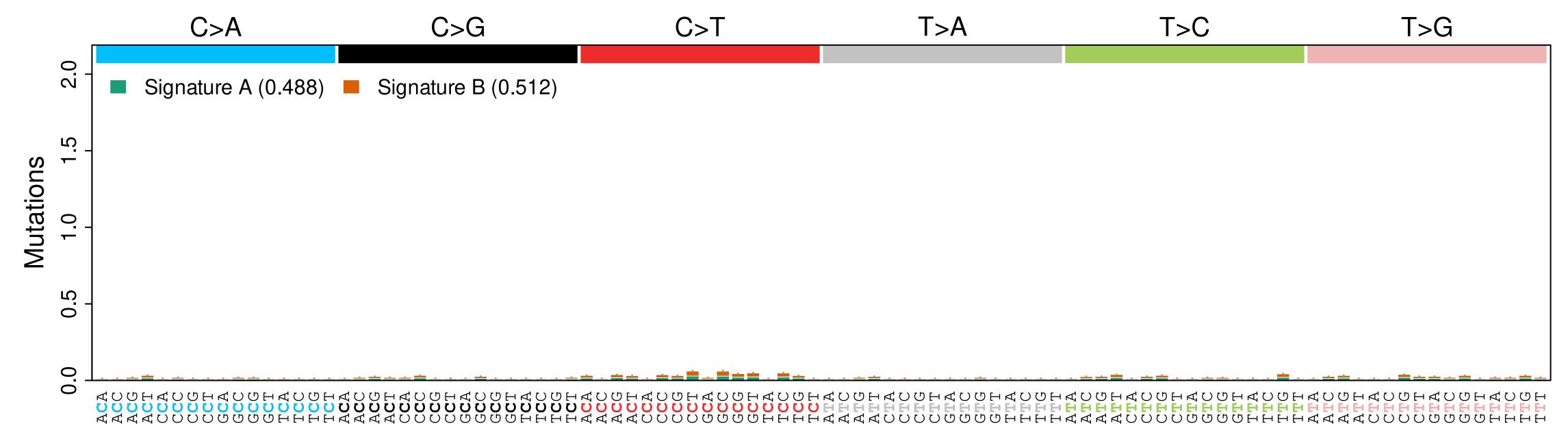


CATD0391a (2 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.171)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.503) Signature B (0.497) 5 Mutations 5 0 0

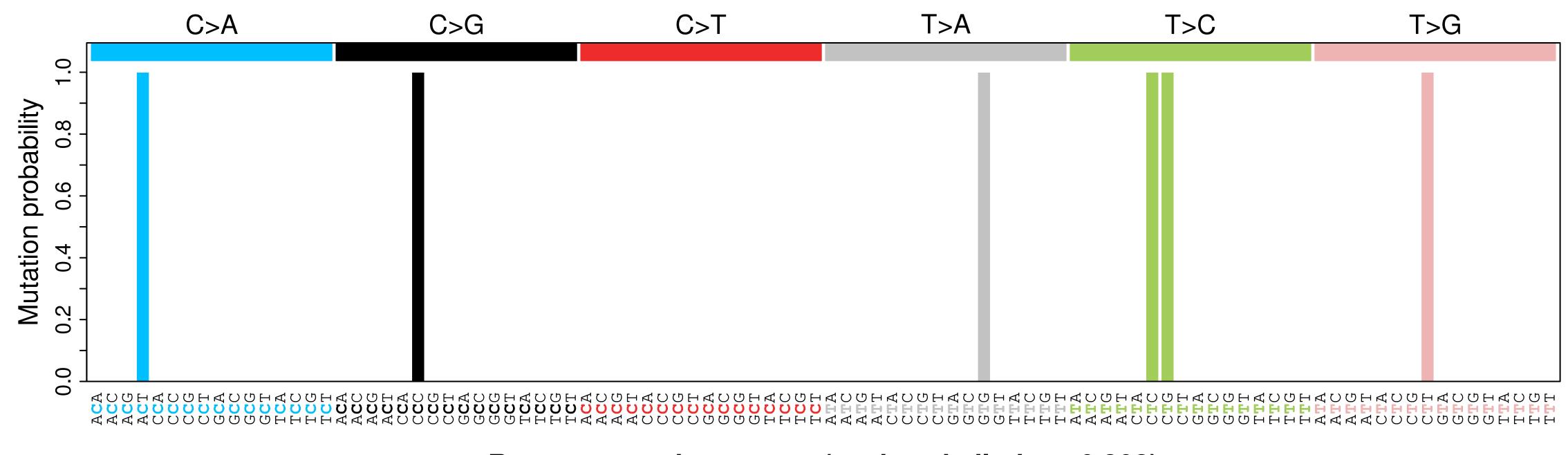
CATD0387a (2 mutations) C>A C>G C>T T>A

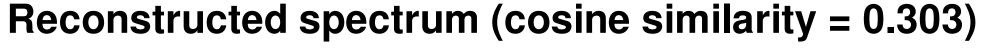


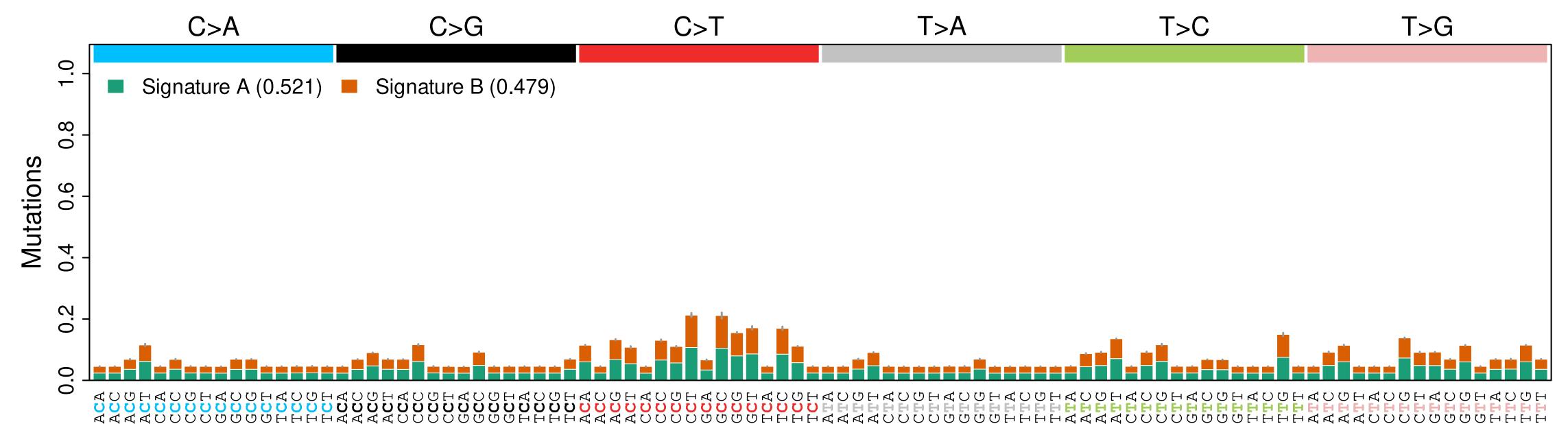




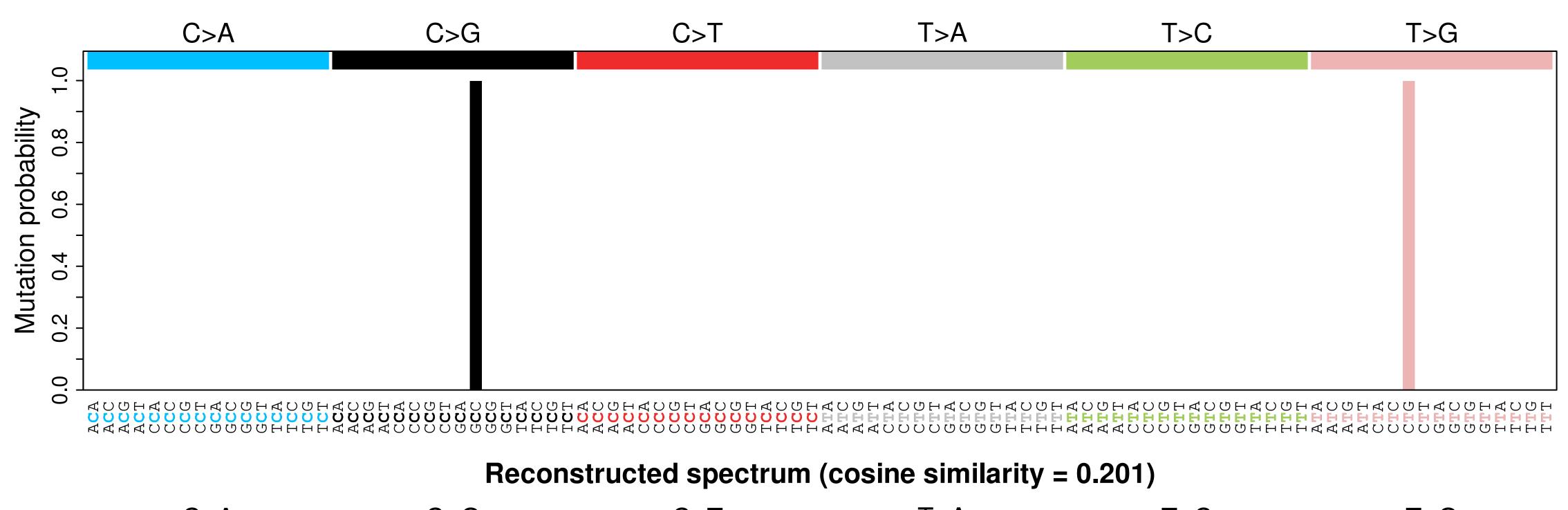
CATD0381a

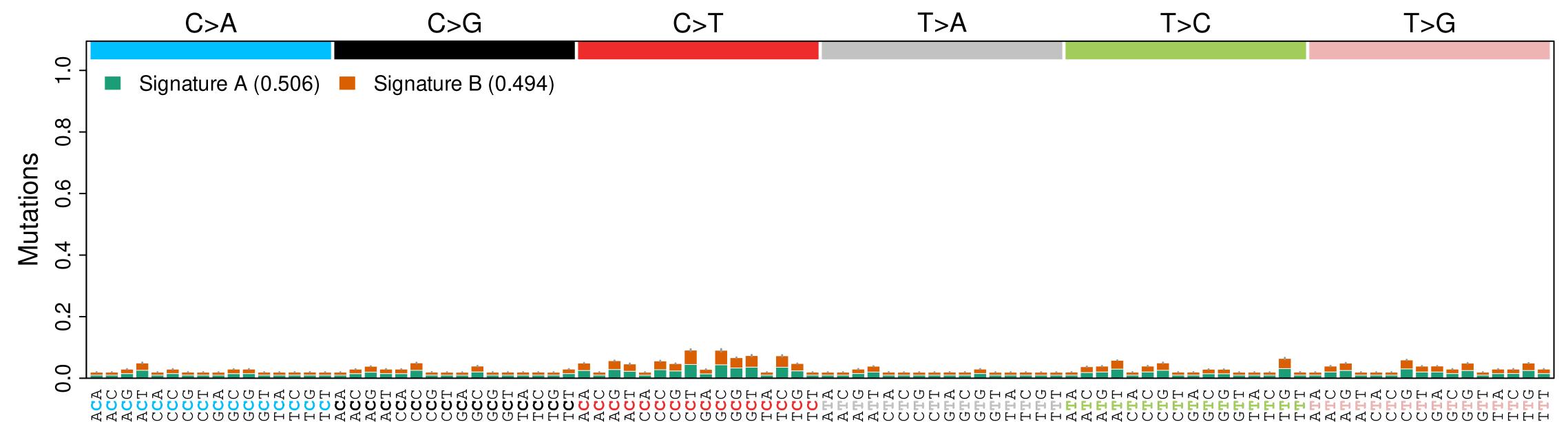




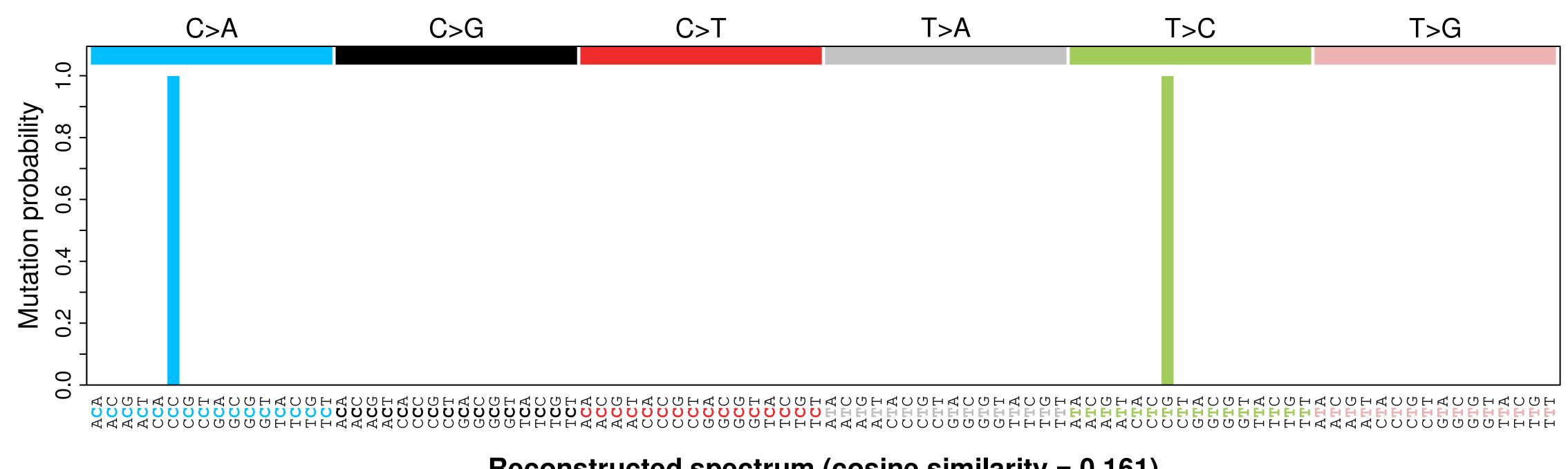




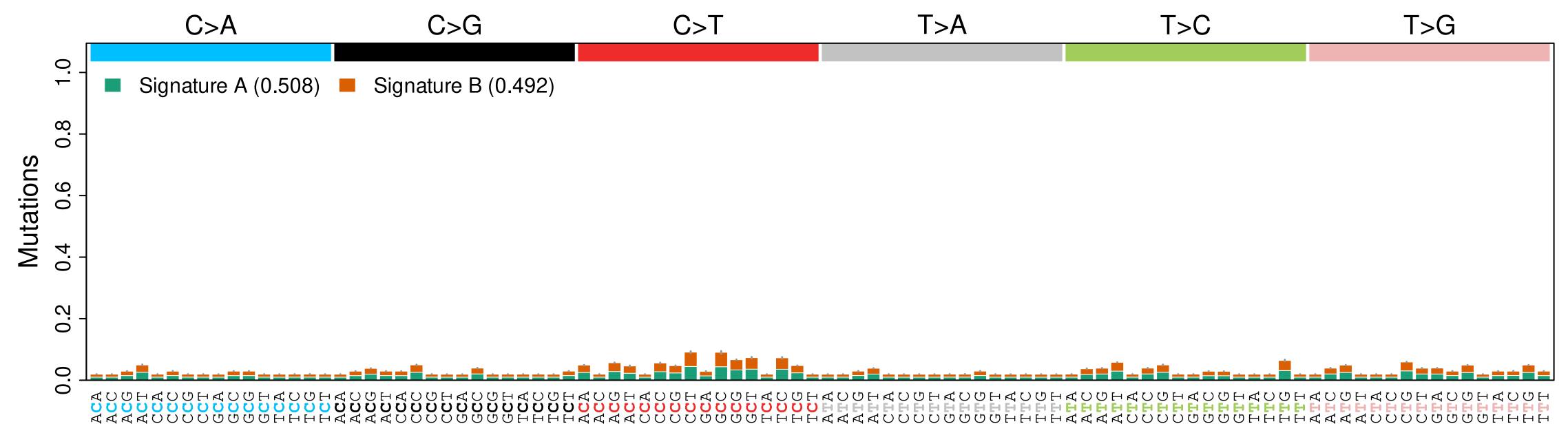




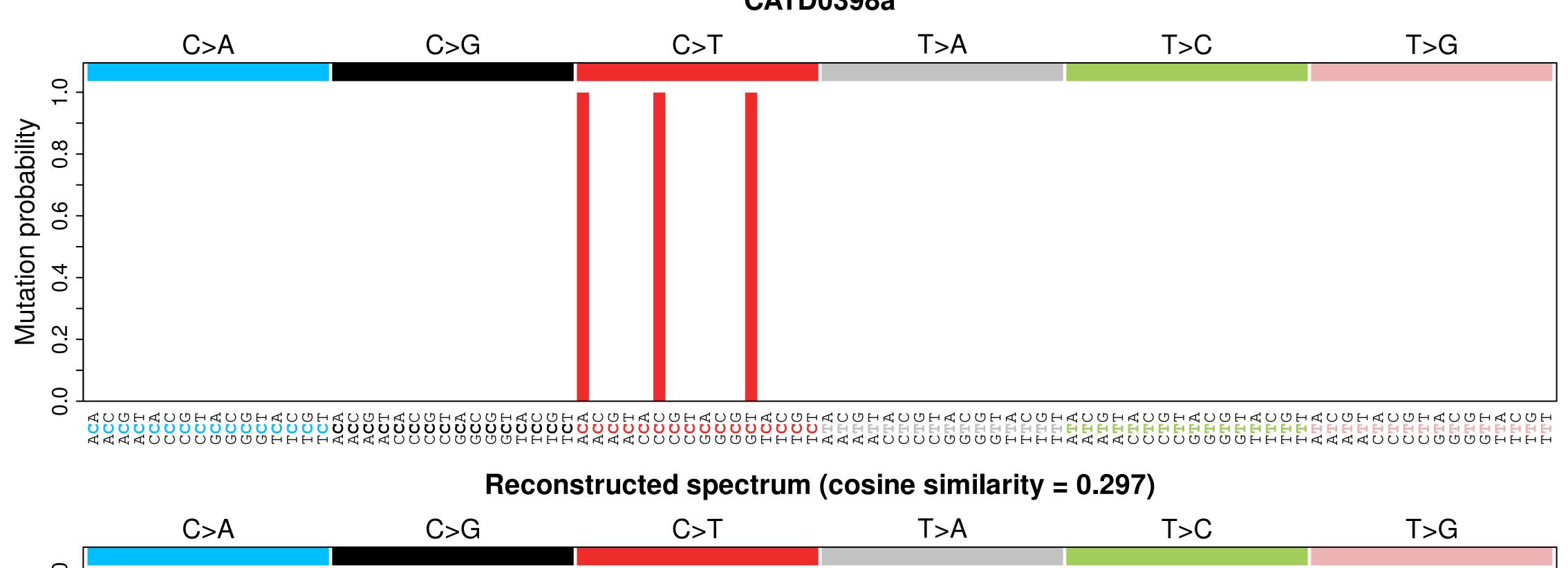


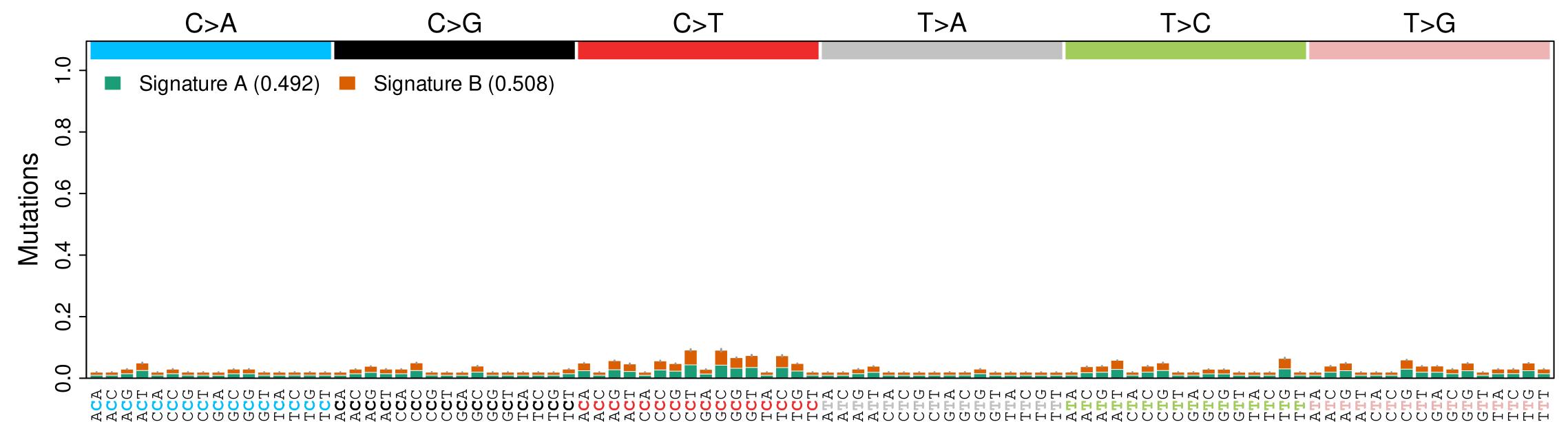


Reconstructed spectrum (cosine similarity = 0.161)



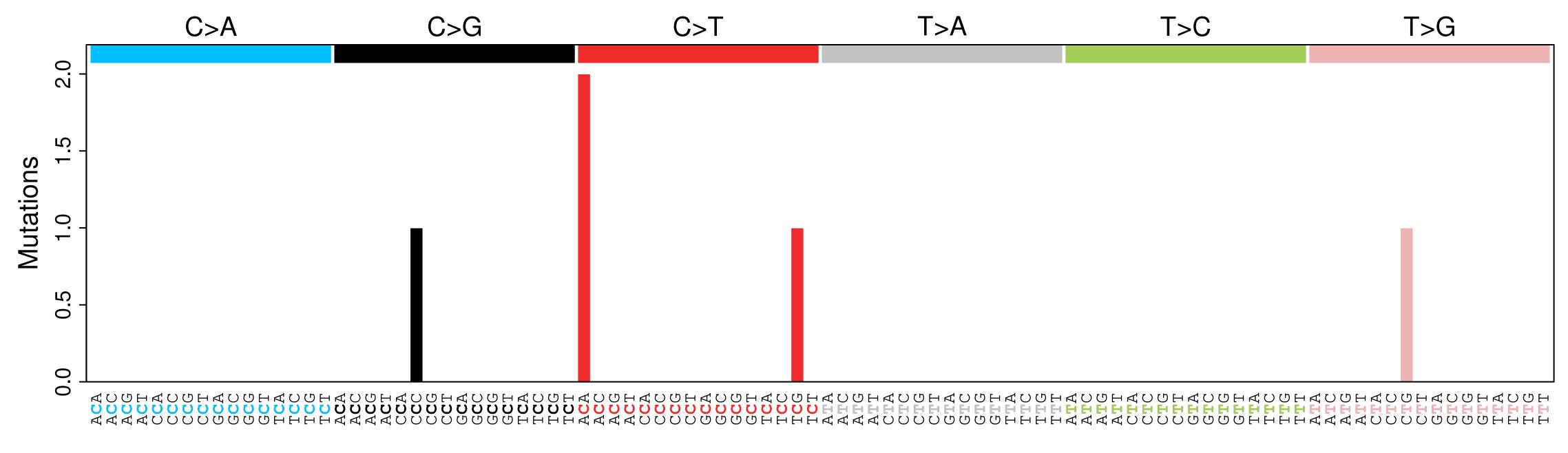




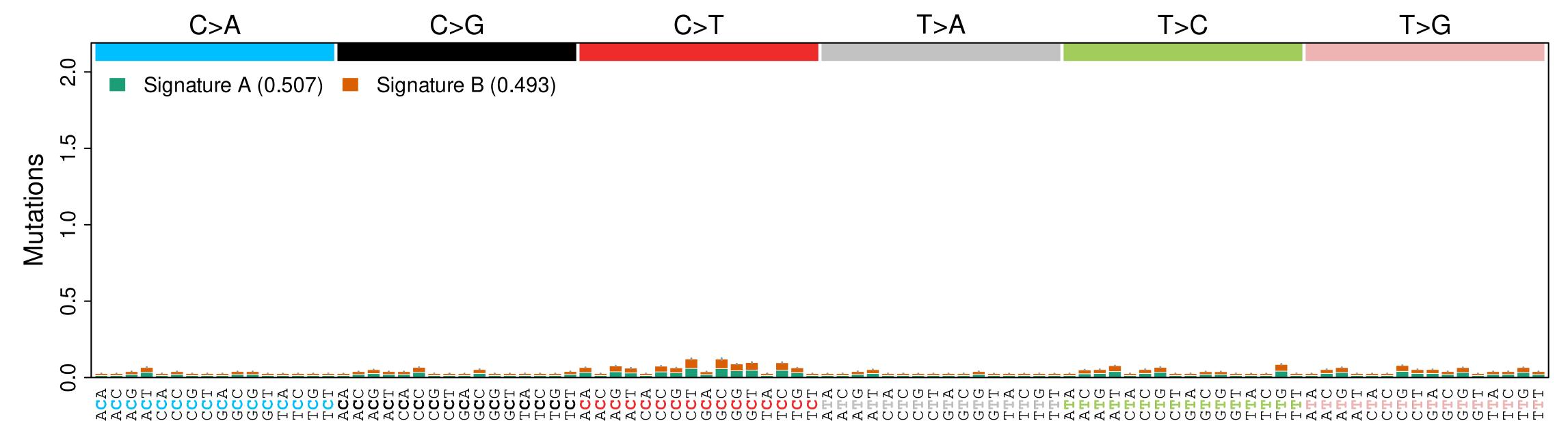


CATD0428a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.236)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.502) Signature B (0.498) 5 Mutations 2 0

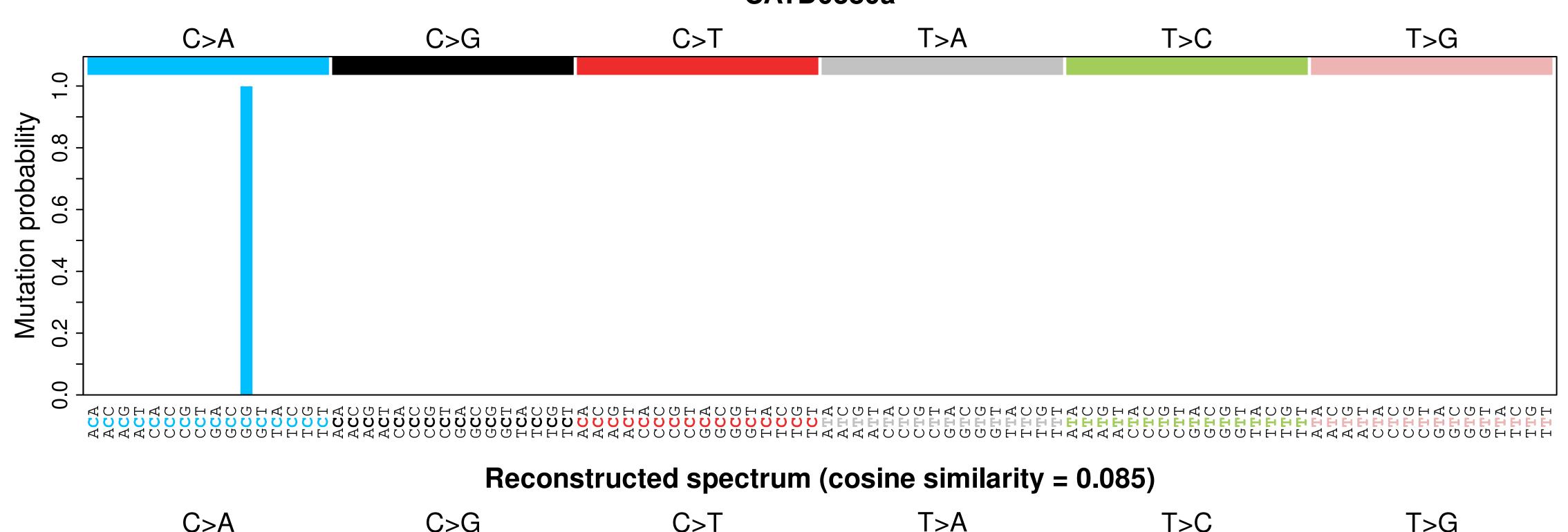
CATD0378a (5 mutations)

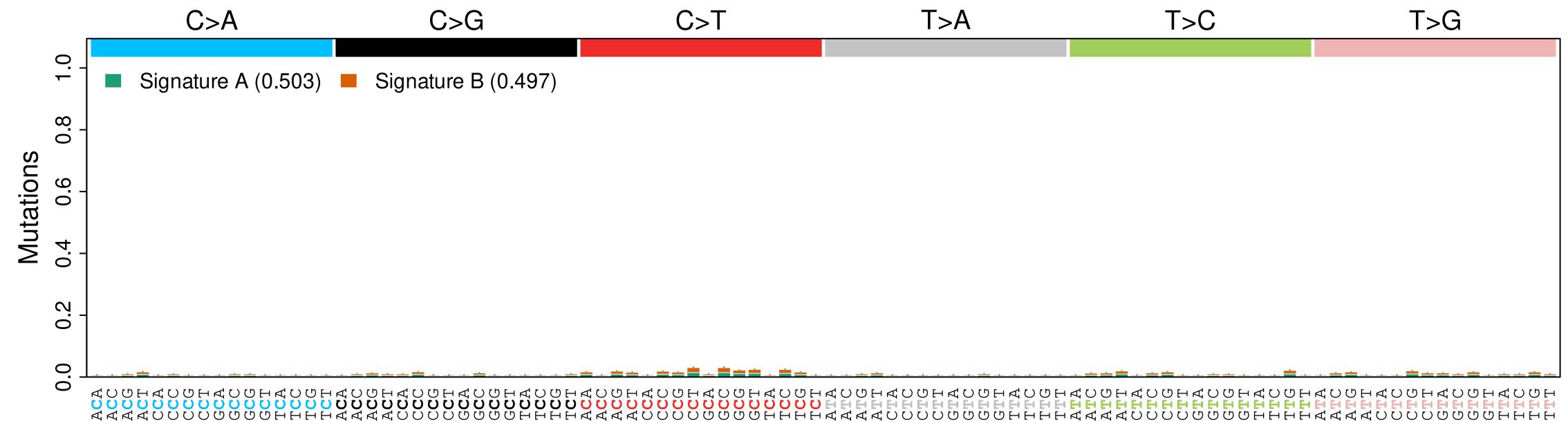




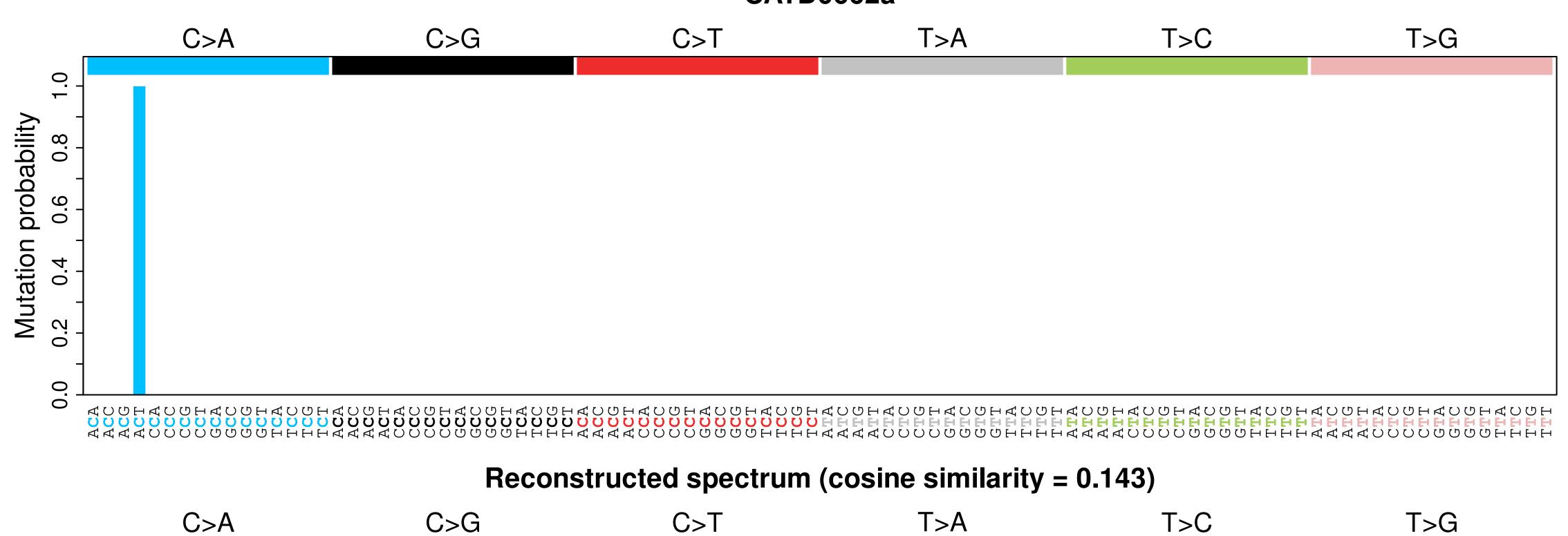


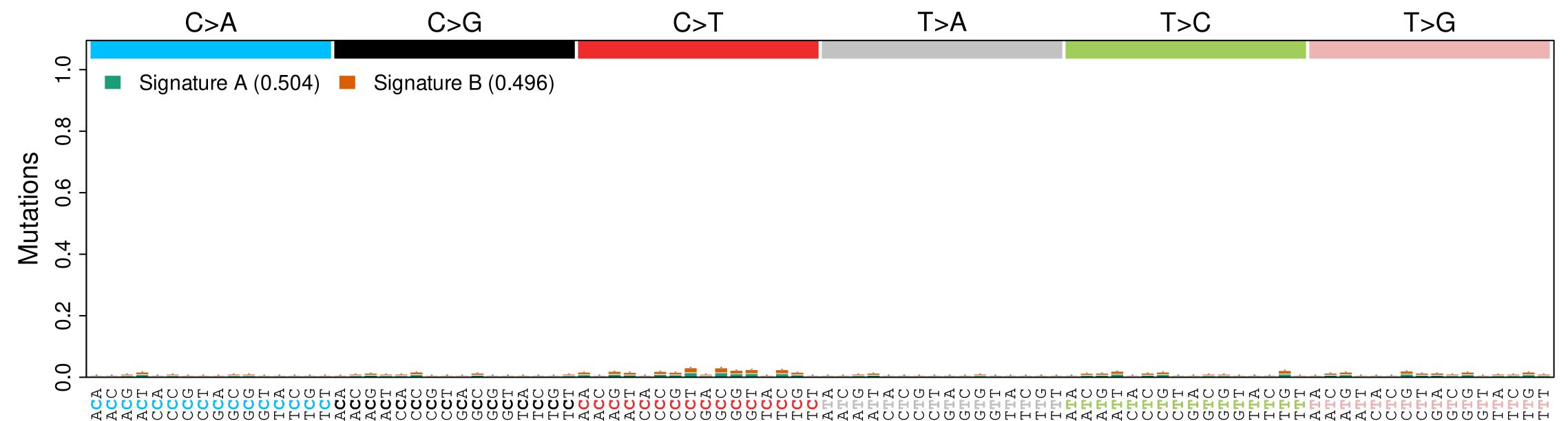




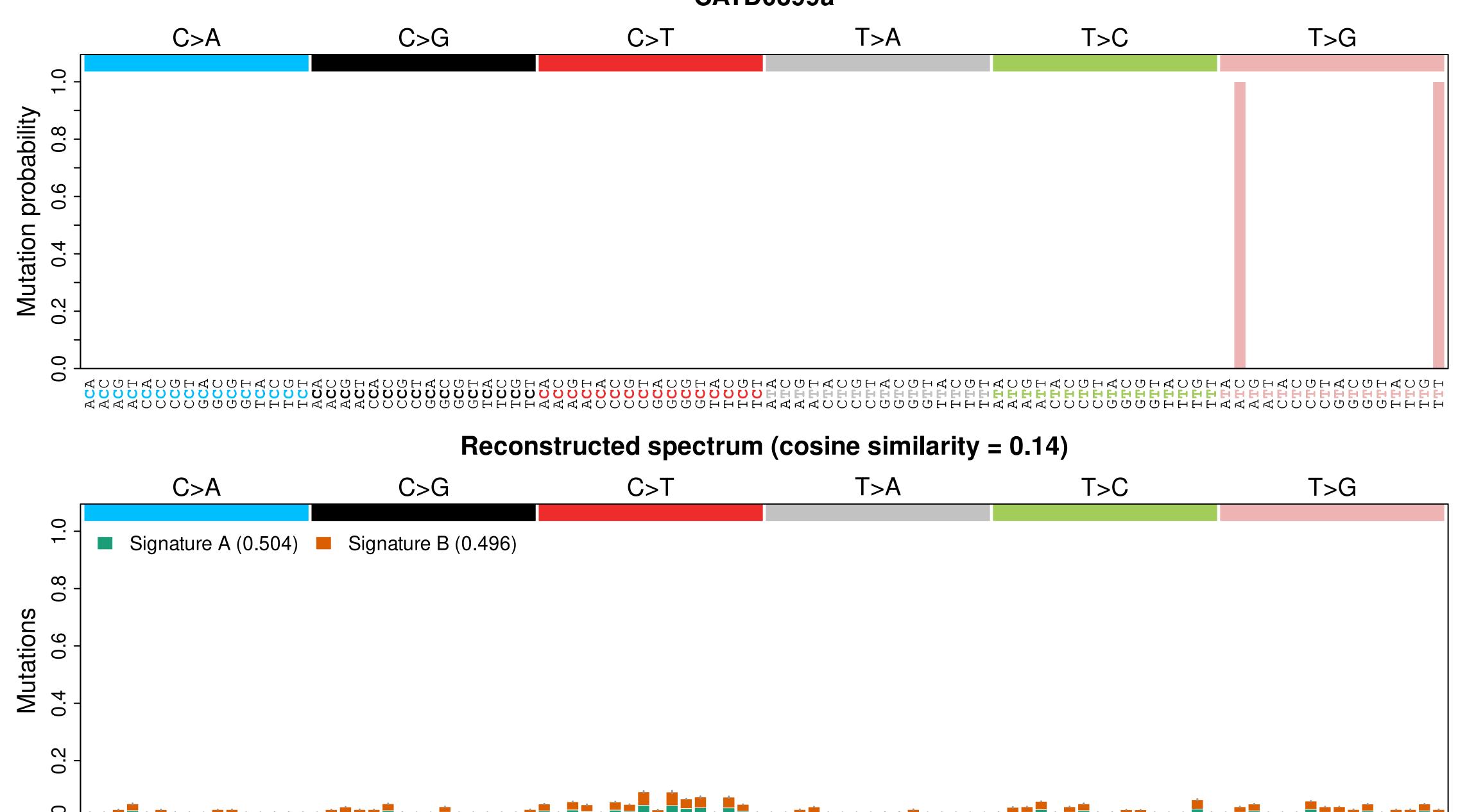




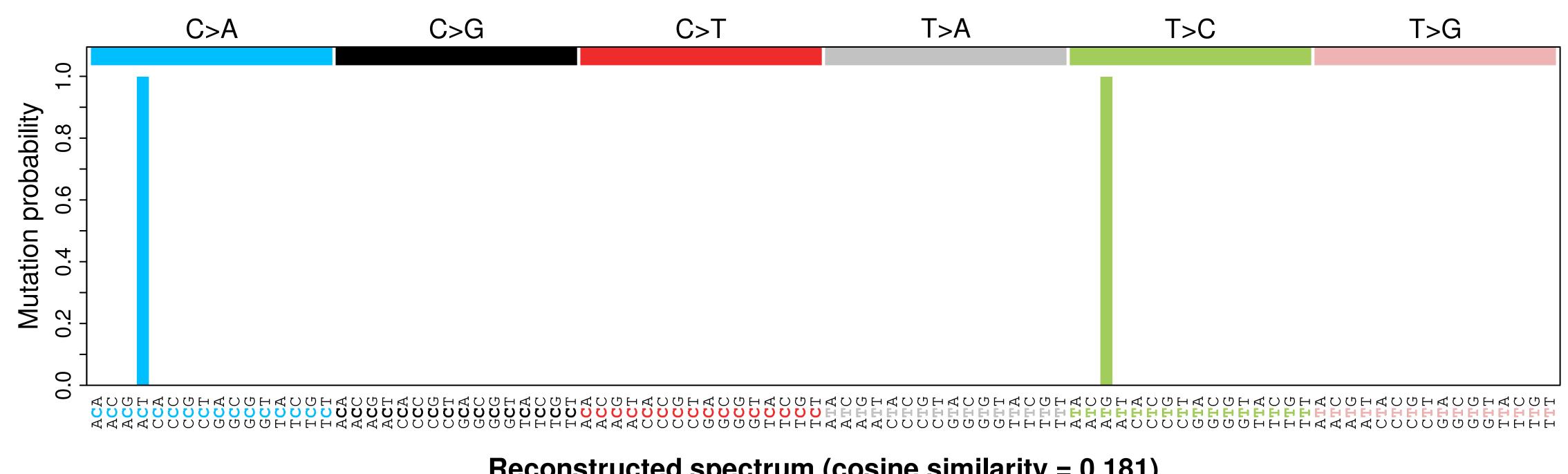


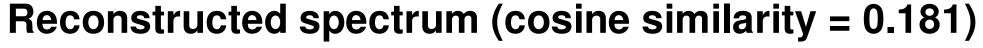


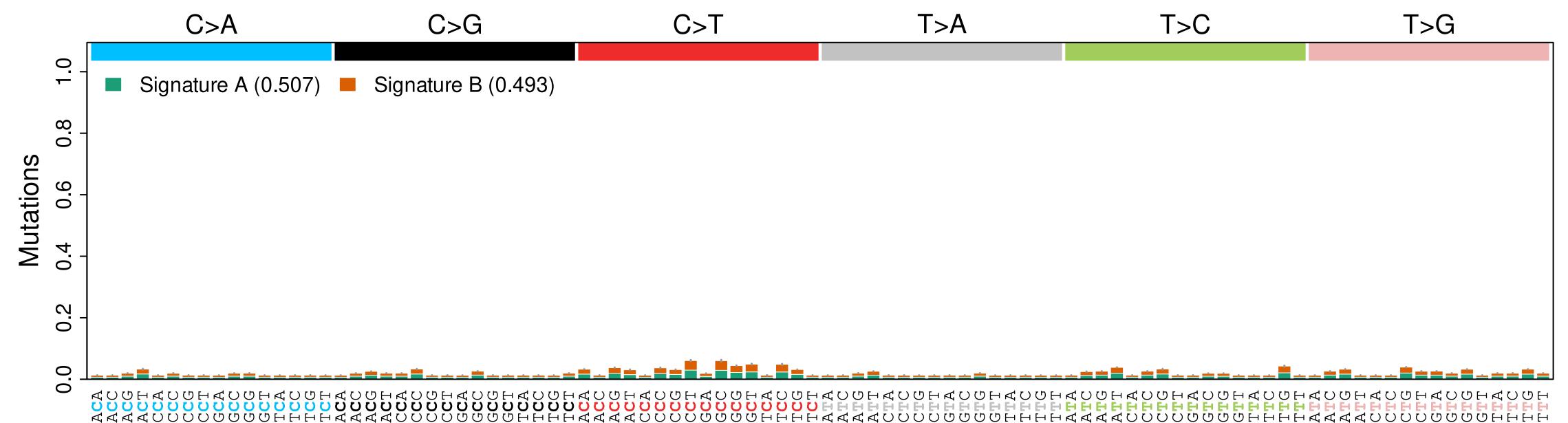




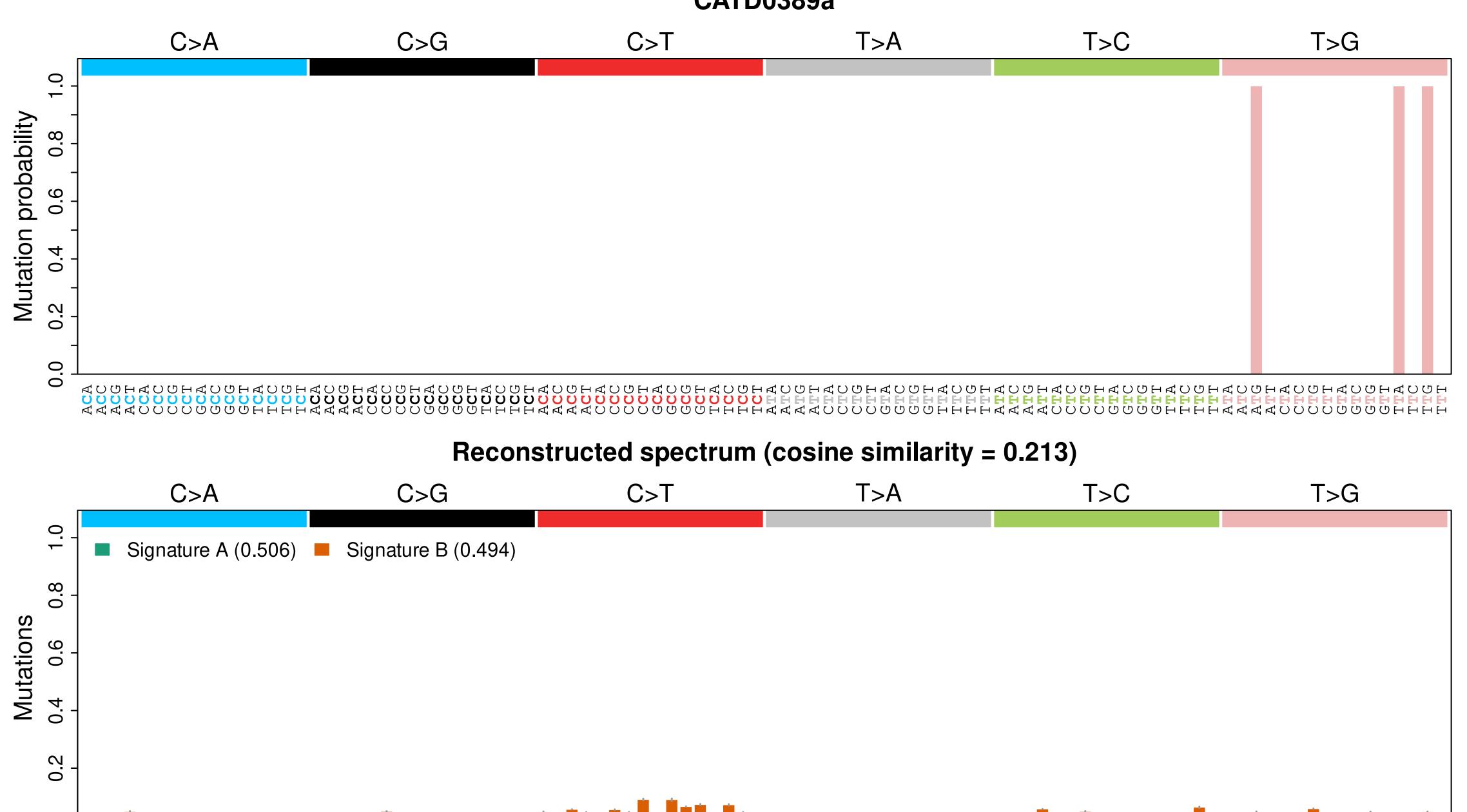




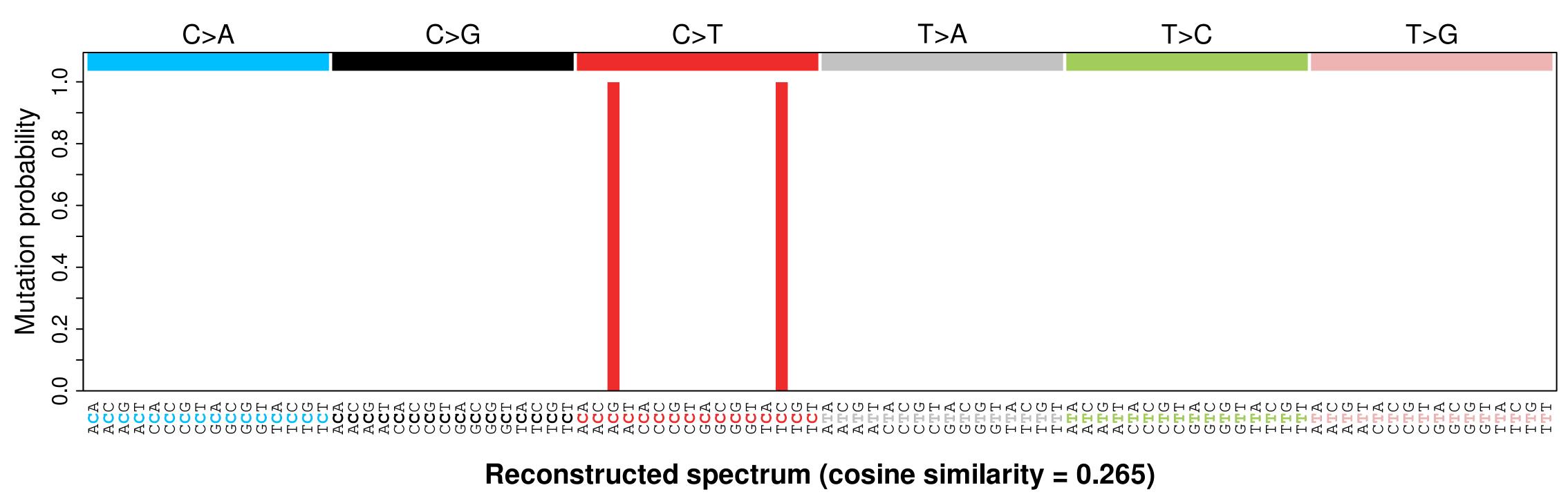


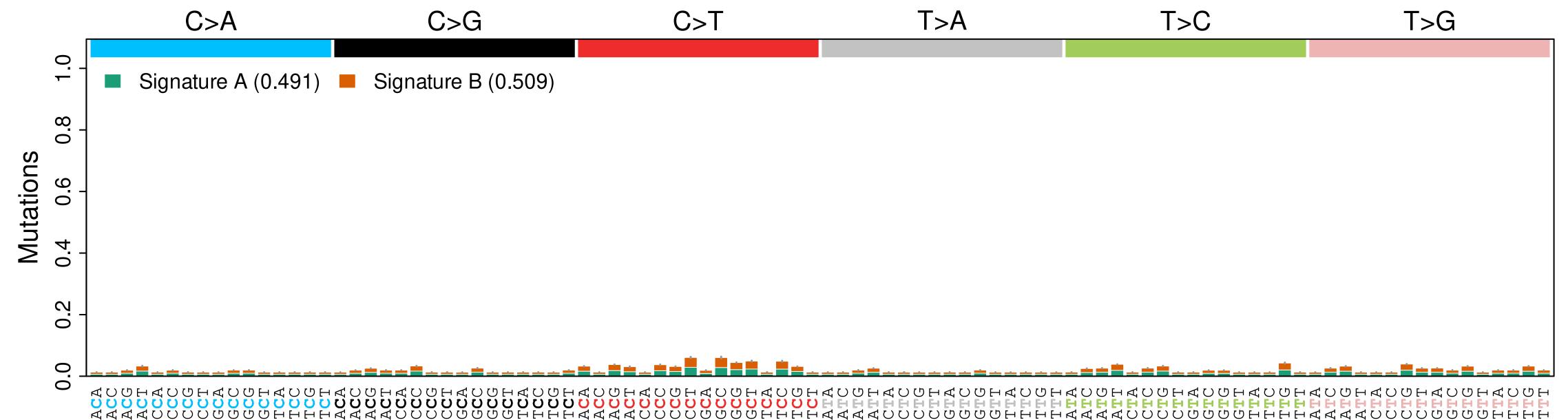






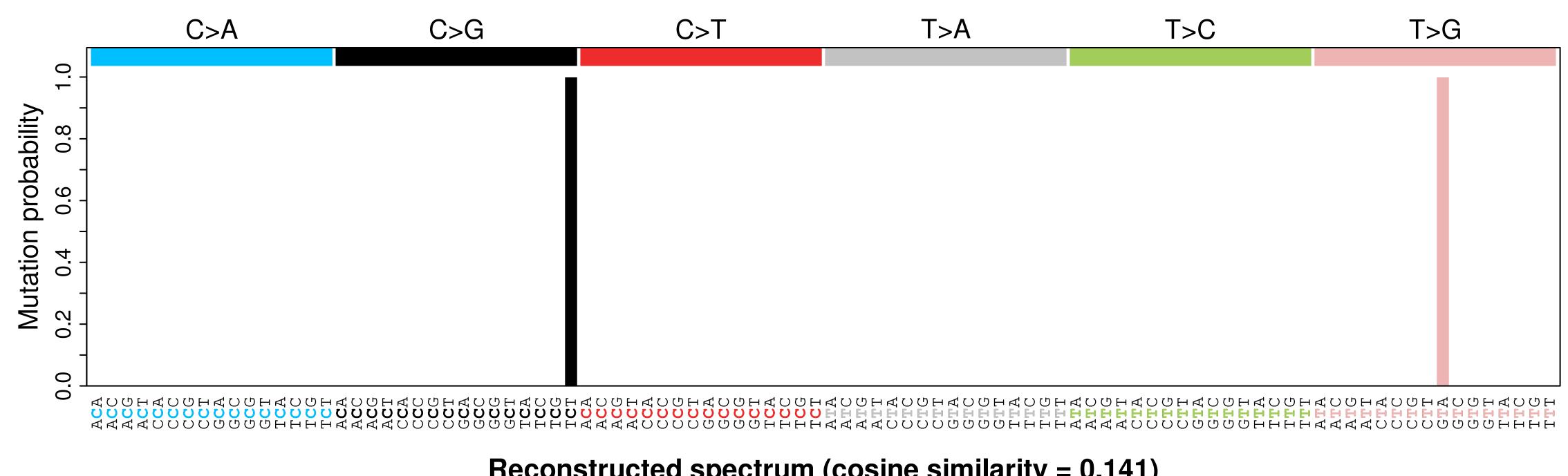


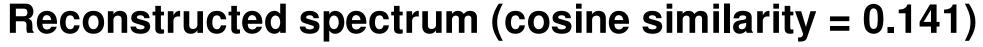


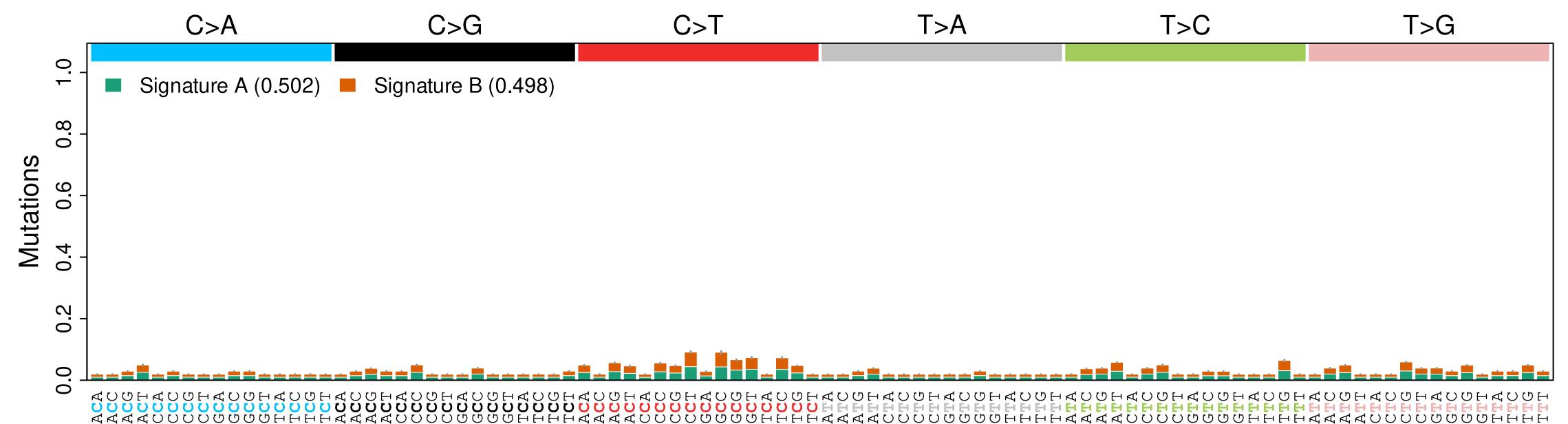


CATD0665a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 Reconstructed spectrum (cosine similarity = 0.249) C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.498) Signature B (0.502) 5 Mutations 5 0 0

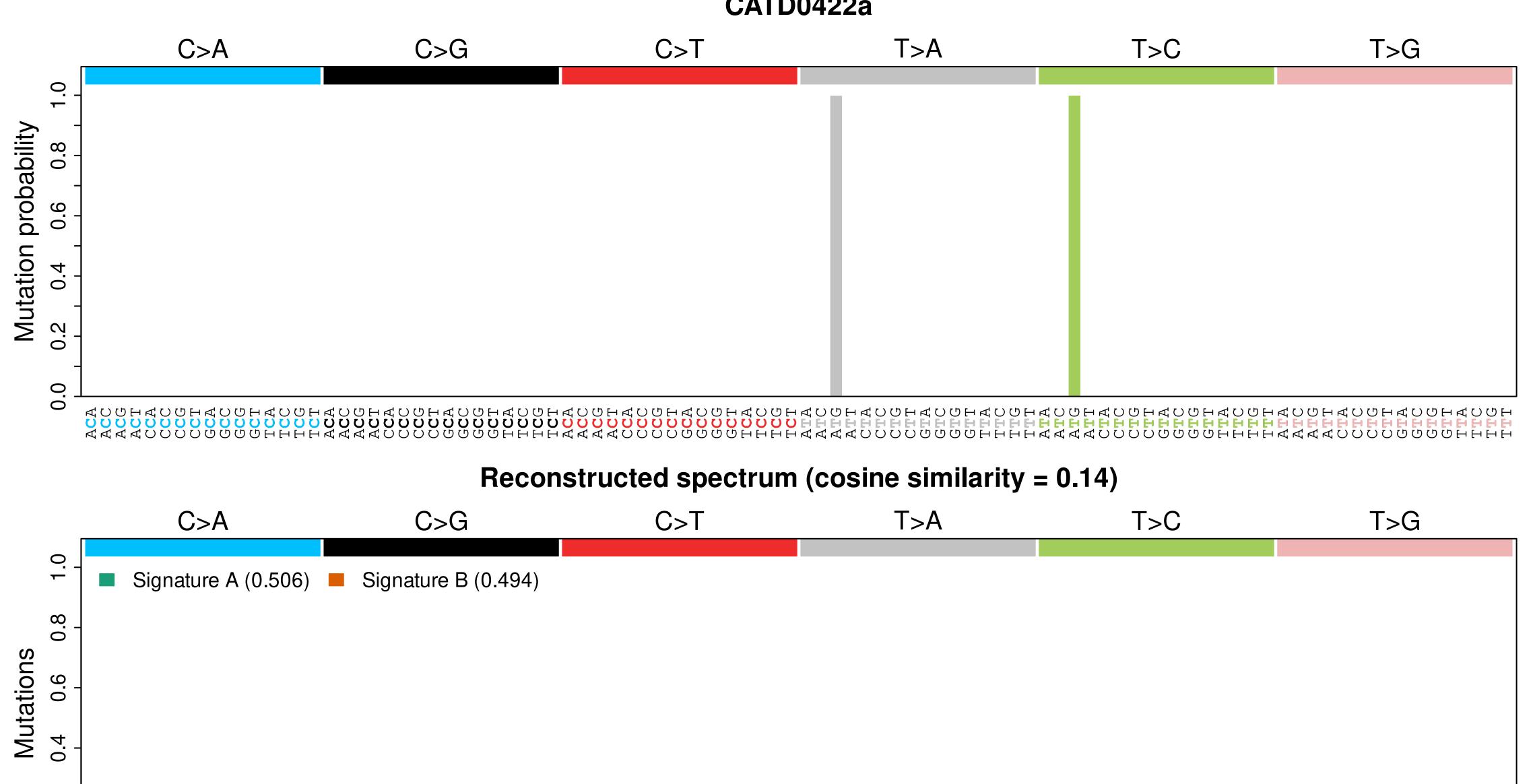












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