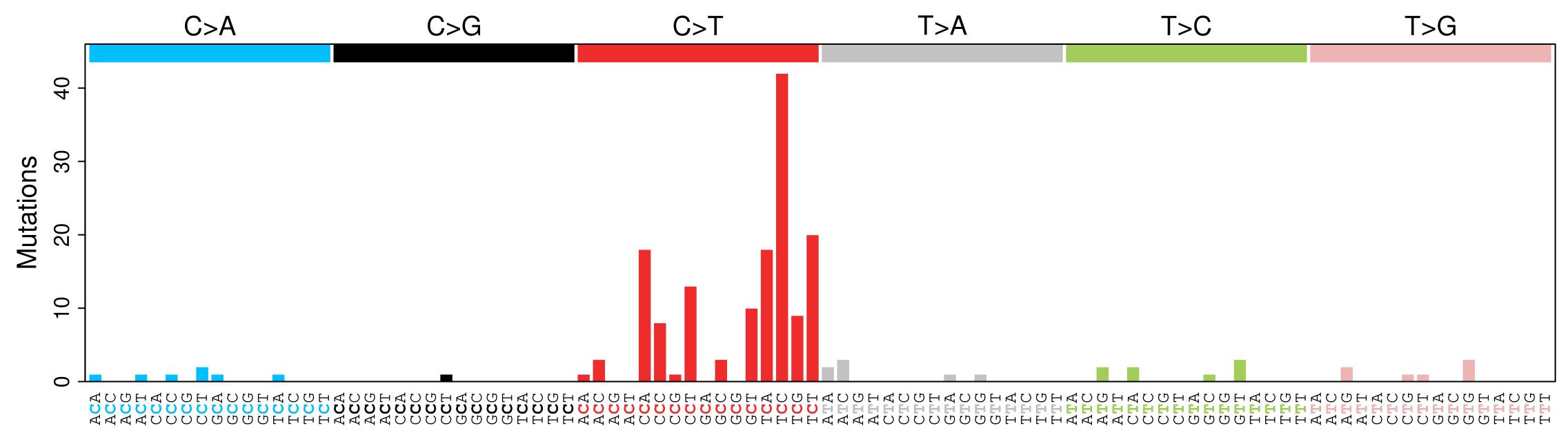
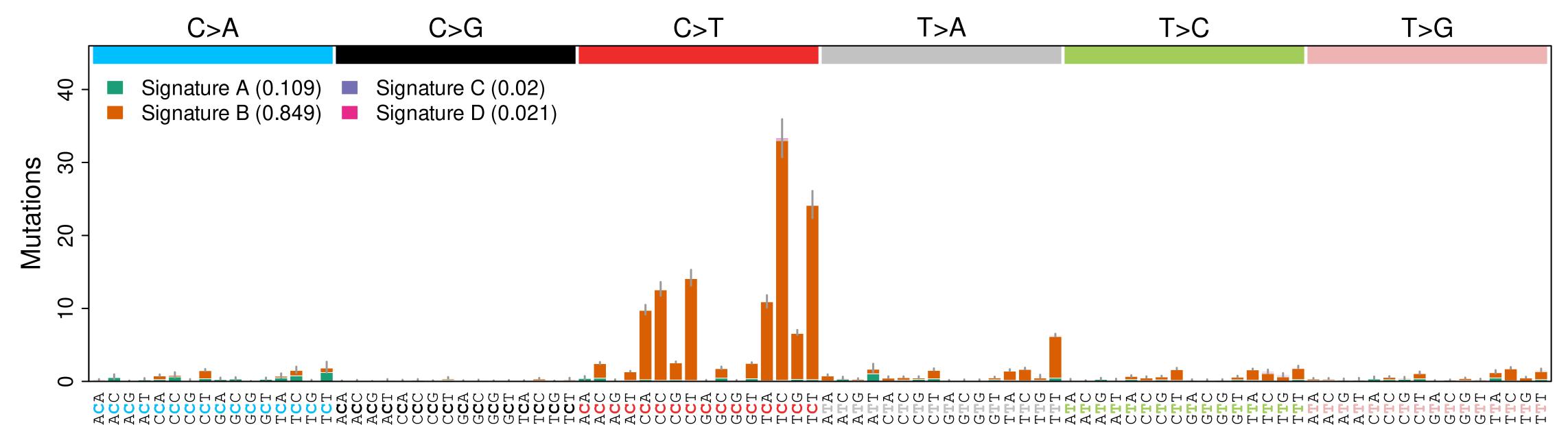
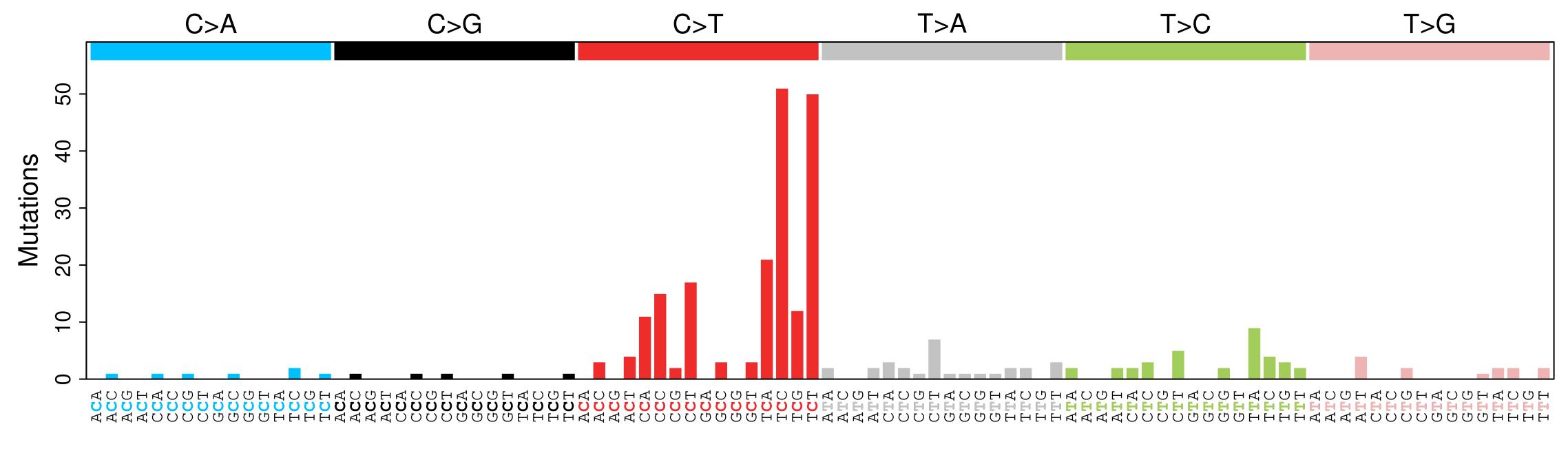
CATD269a (176 mutations)



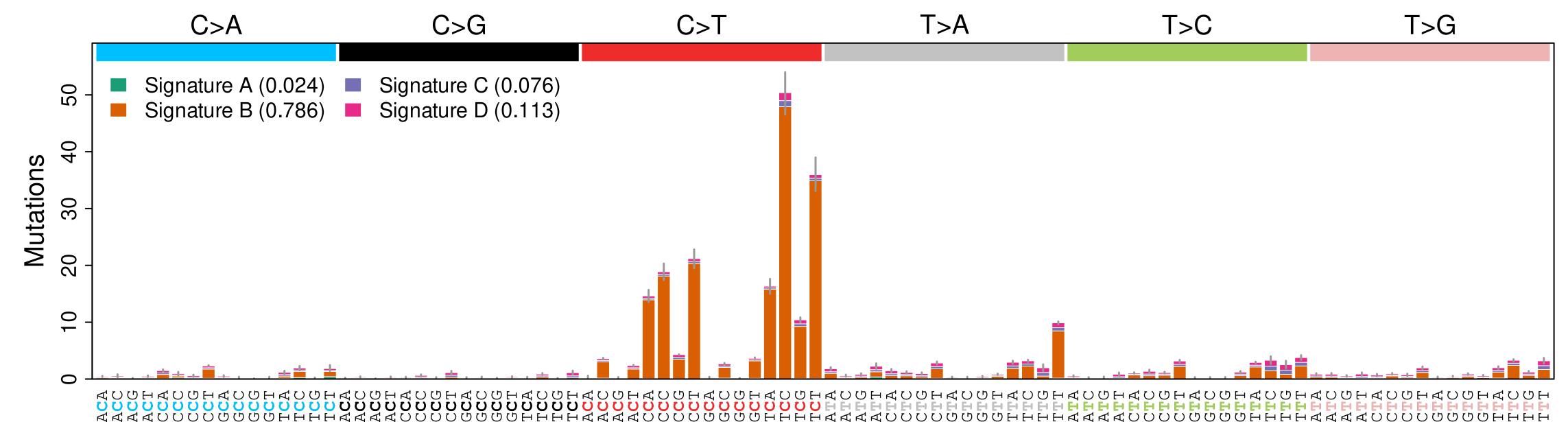
Reconstructed spectrum (cosine similarity = 0.938)



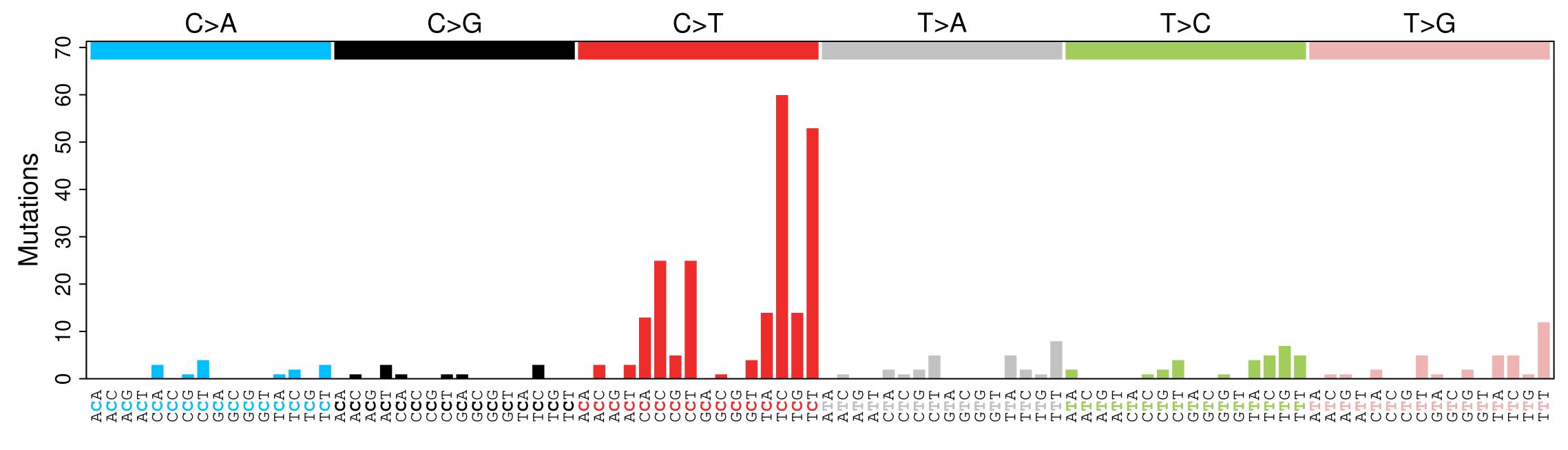
CATD256a (279 mutations)

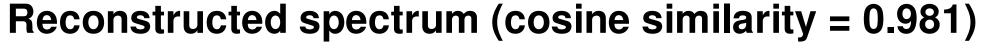


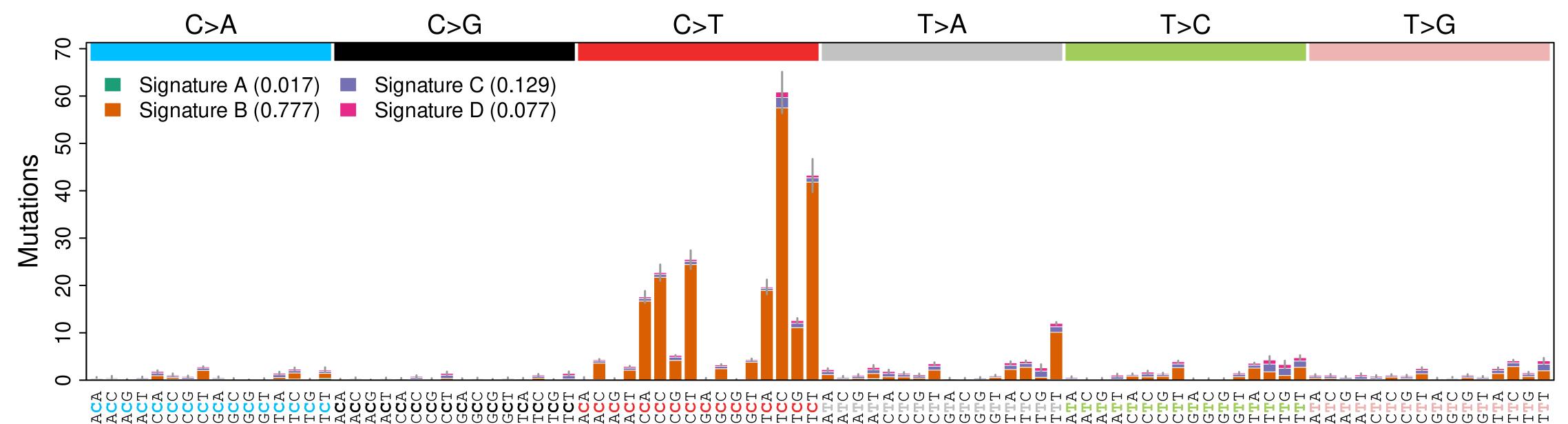
Reconstructed spectrum (cosine similarity = 0.967)



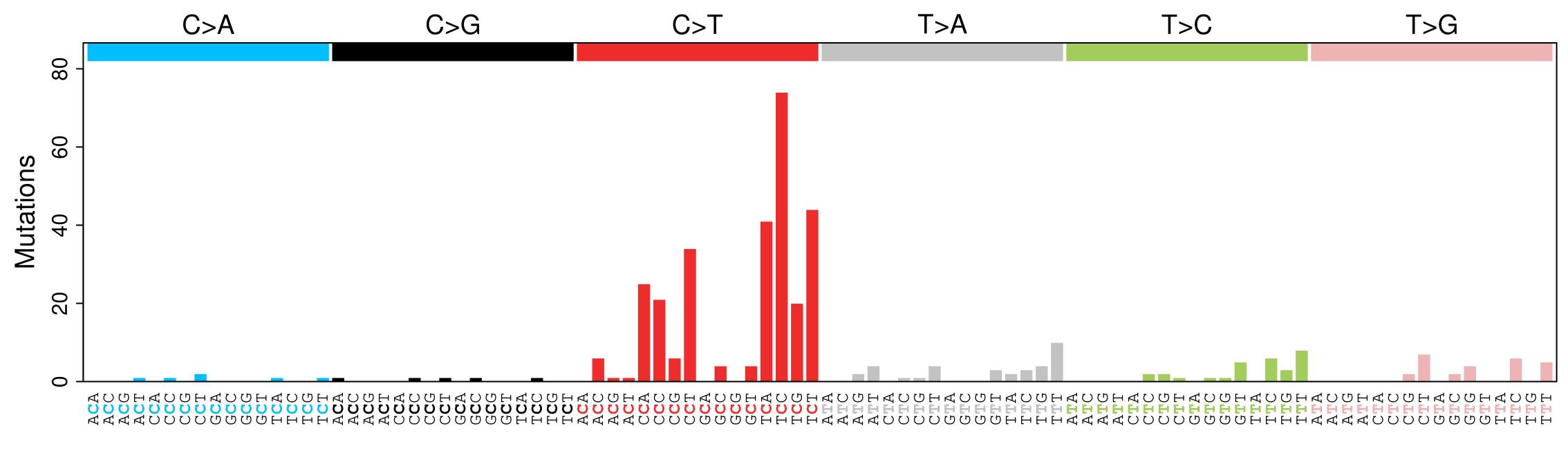
CATD251a (337 mutations)



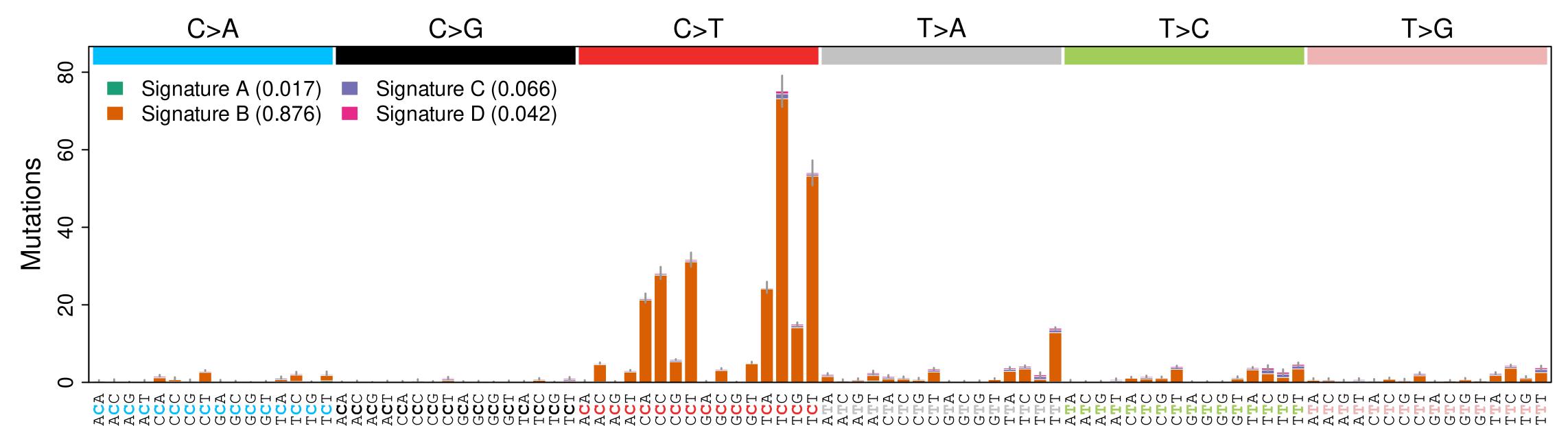




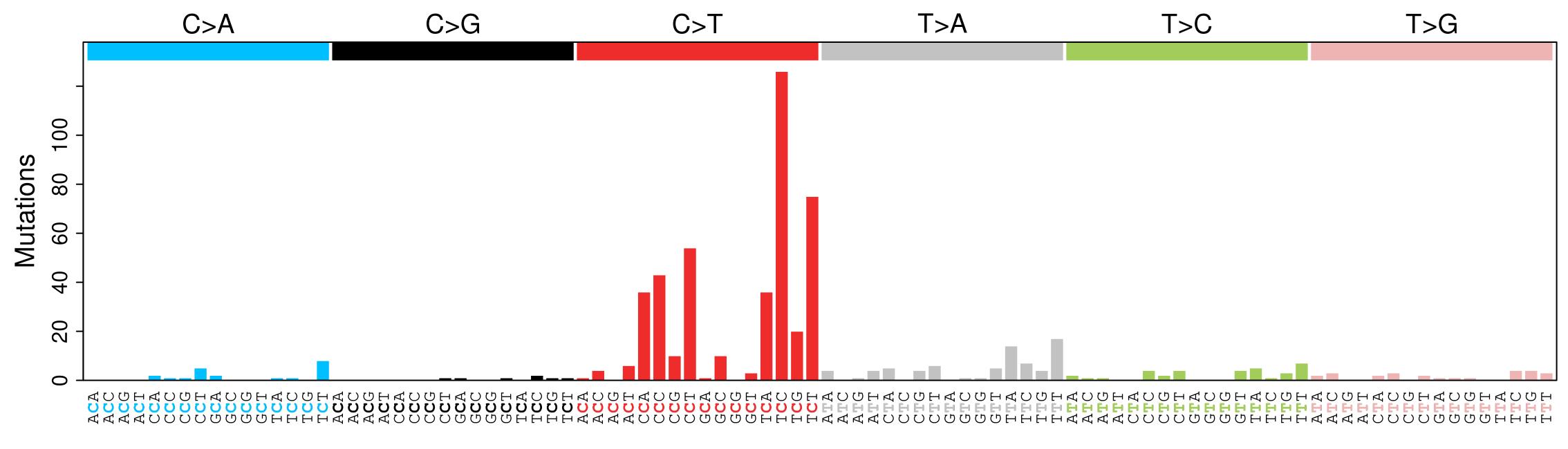
CATD0132a (381 mutations)



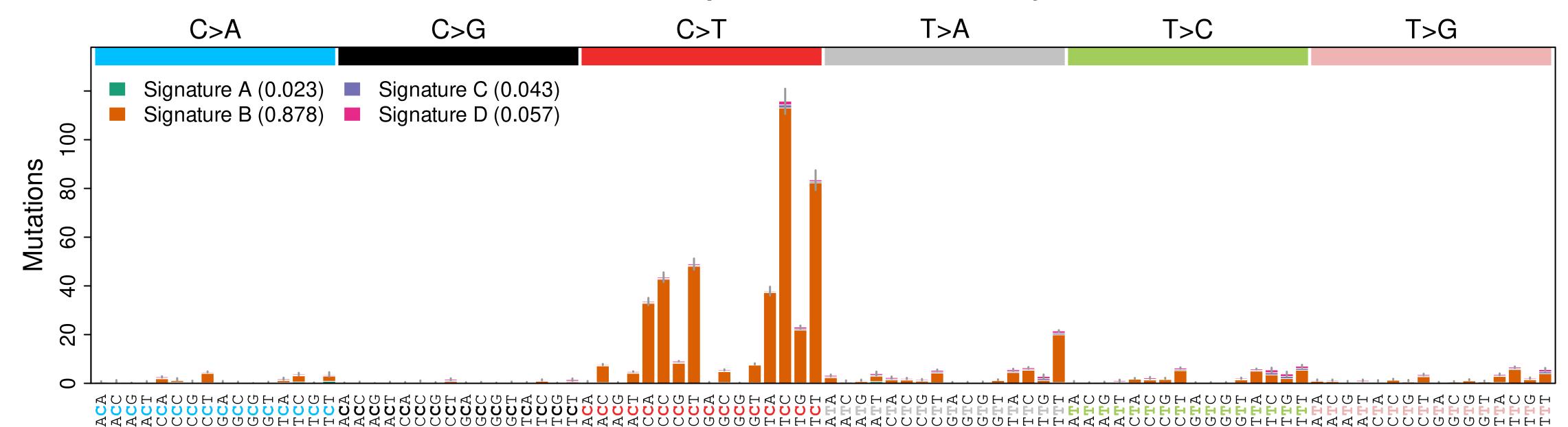
Reconstructed spectrum (cosine similarity = 0.974)



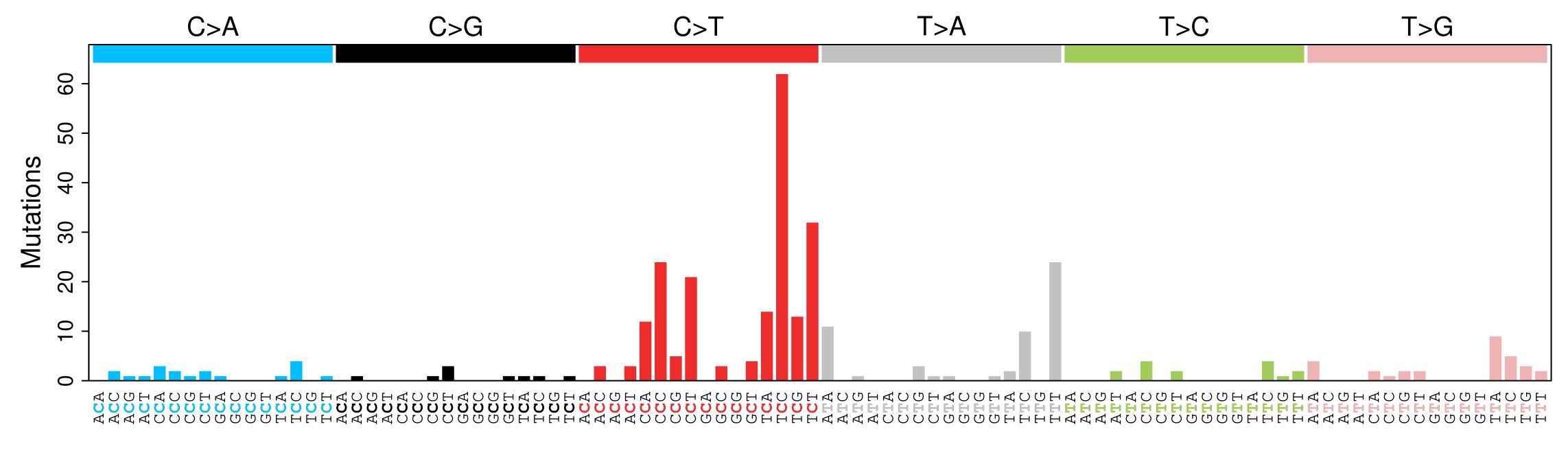
CATD0119a (586 mutations)



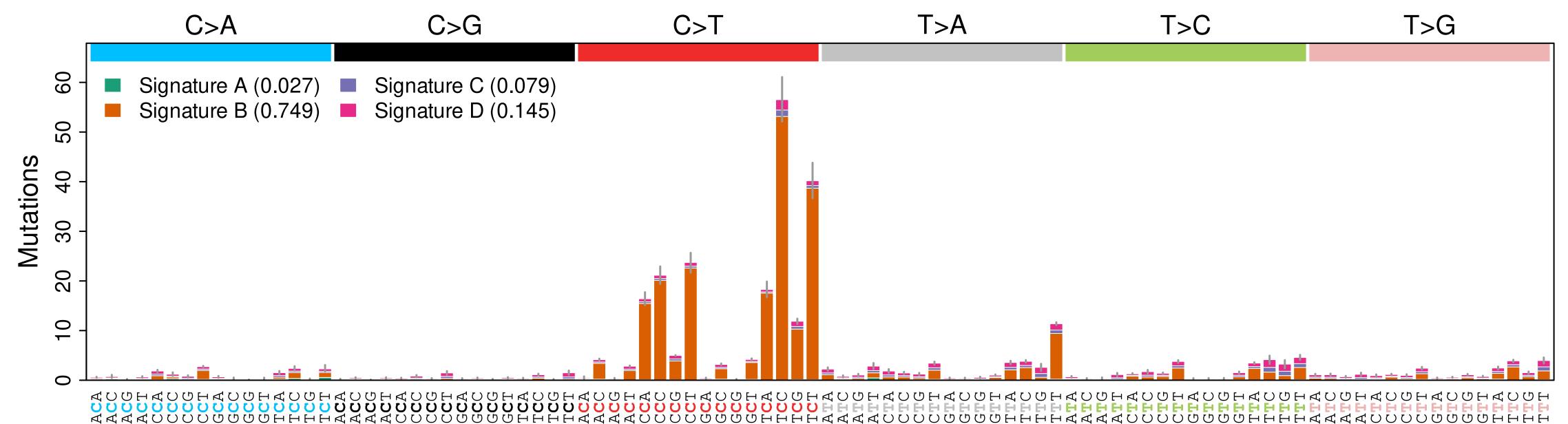
Reconstructed spectrum (cosine similarity = 0.991)



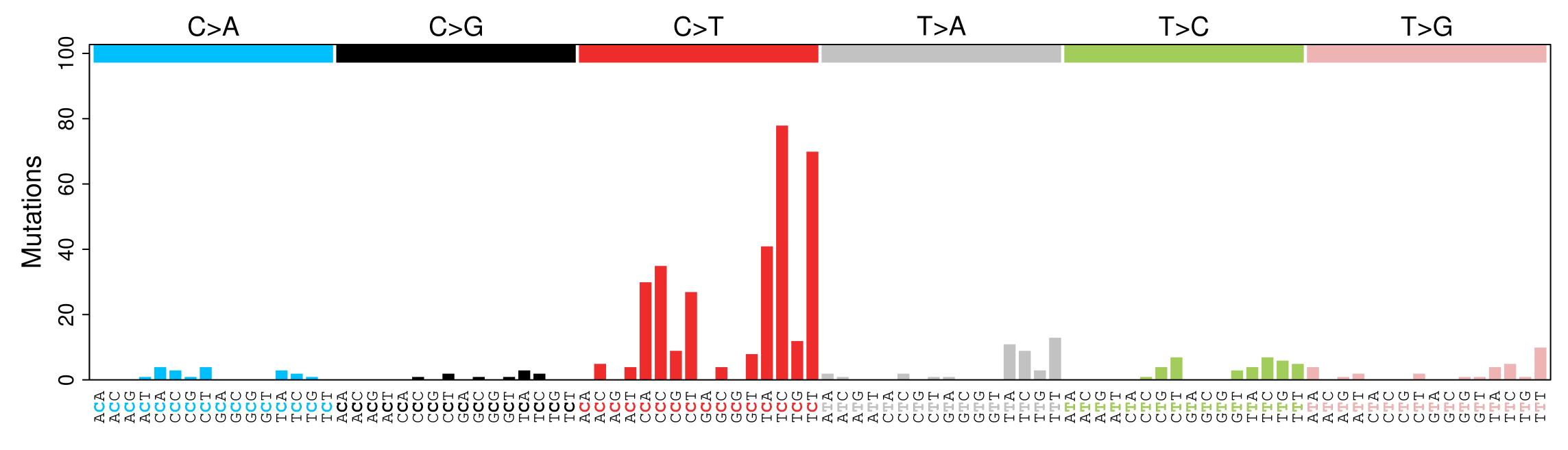
CATD262a (323 mutations)



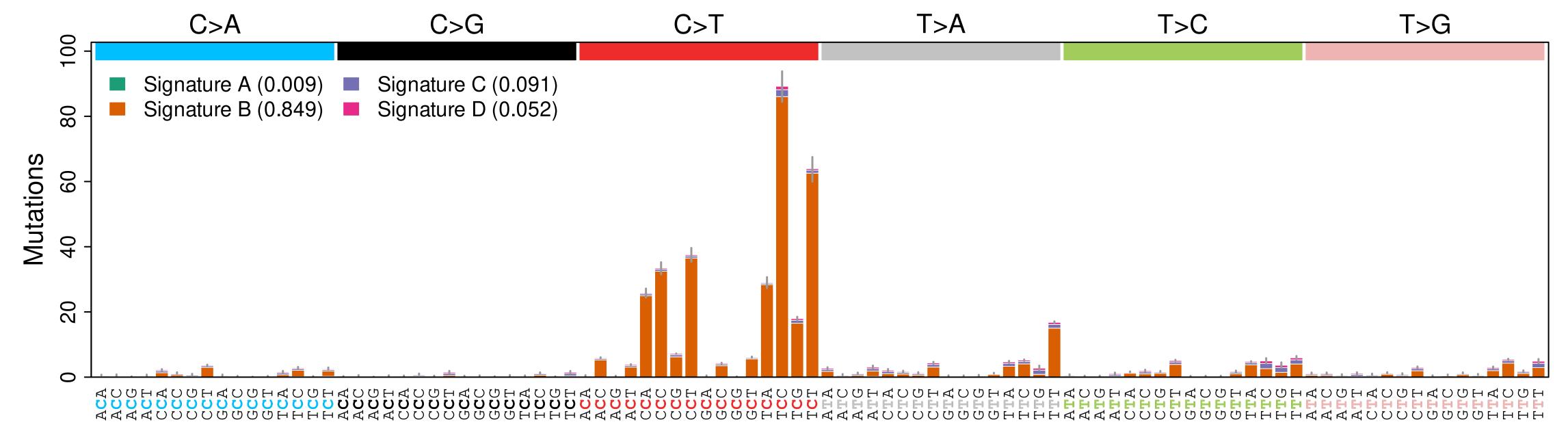
Reconstructed spectrum (cosine similarity = 0.961)



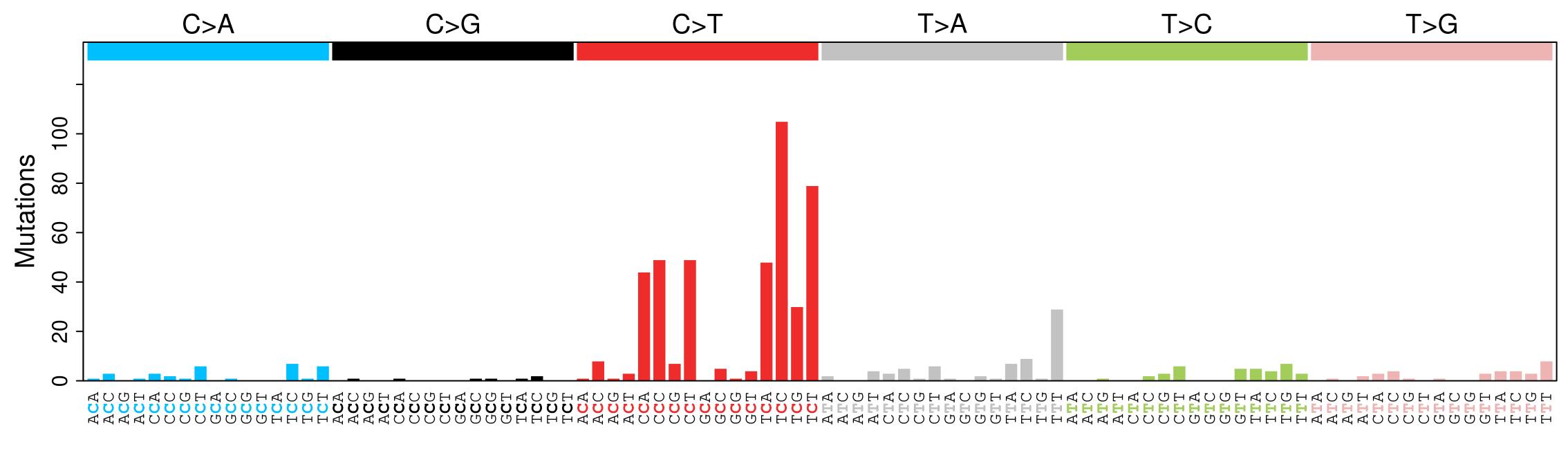
CATD248a (463 mutations)



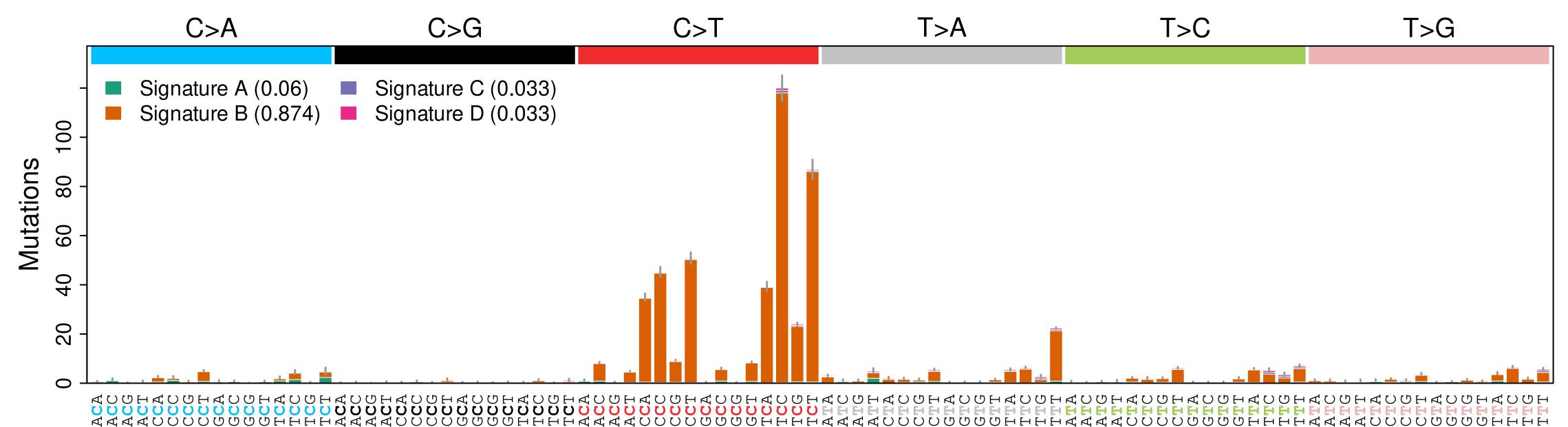
Reconstructed spectrum (cosine similarity = 0.98)



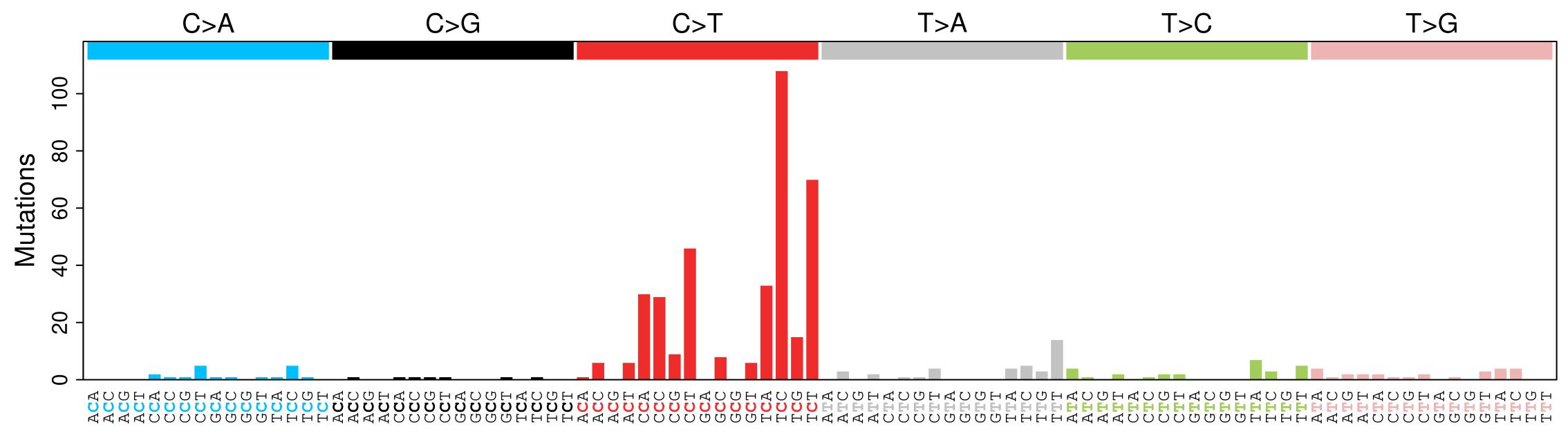
CATD0122a (614 mutations)



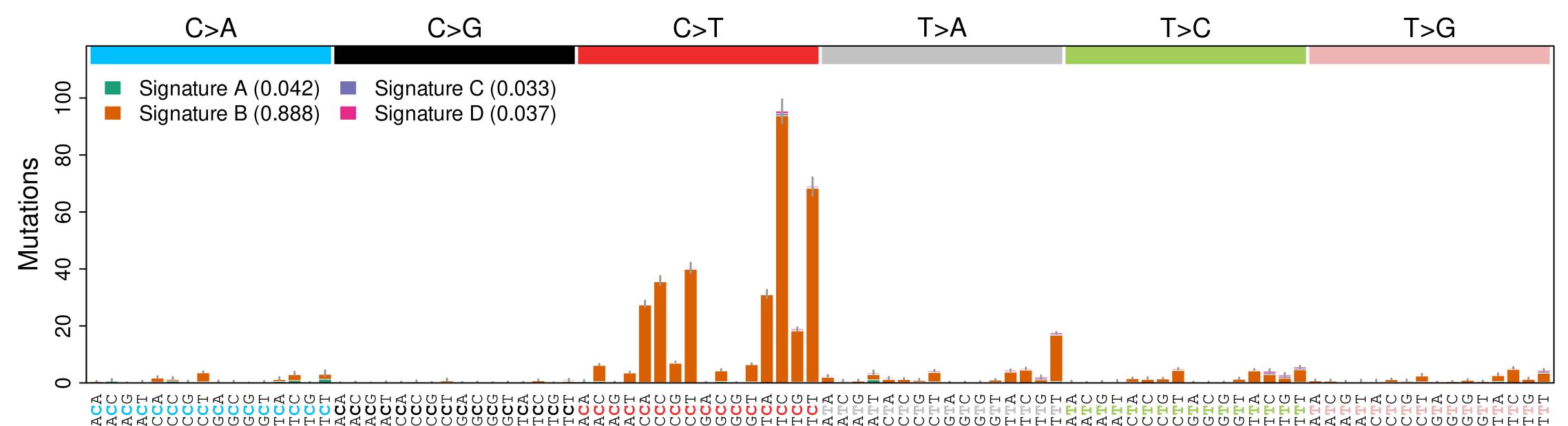
Reconstructed spectrum (cosine similarity = 0.989)



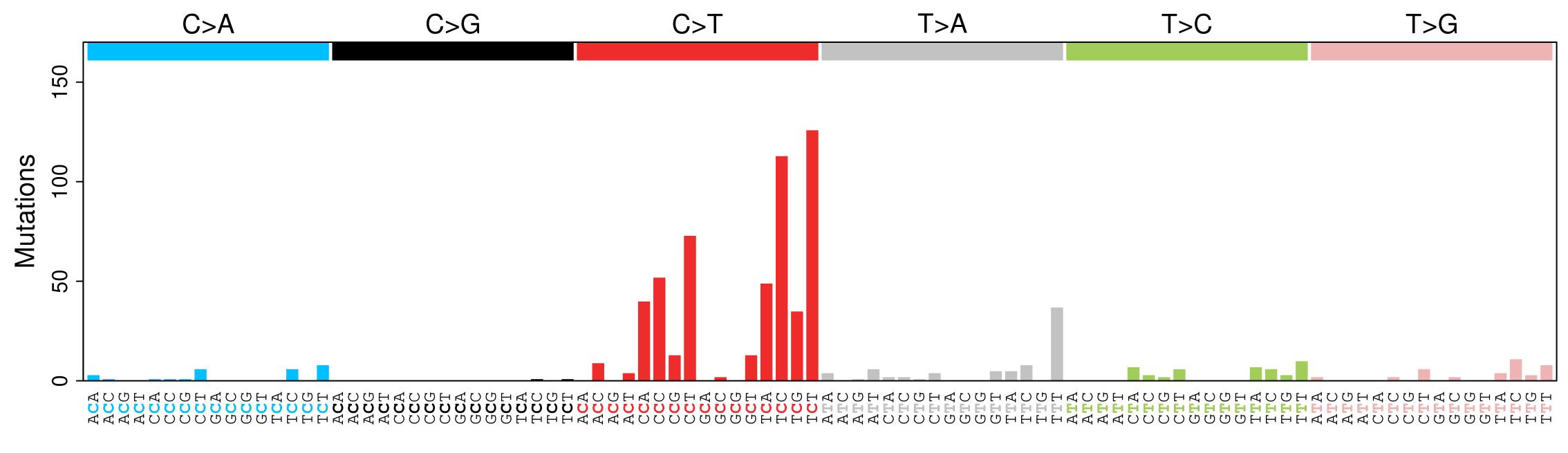
CATD252a (484 mutations)

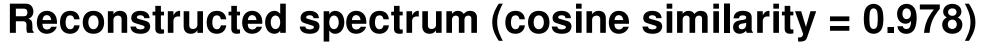


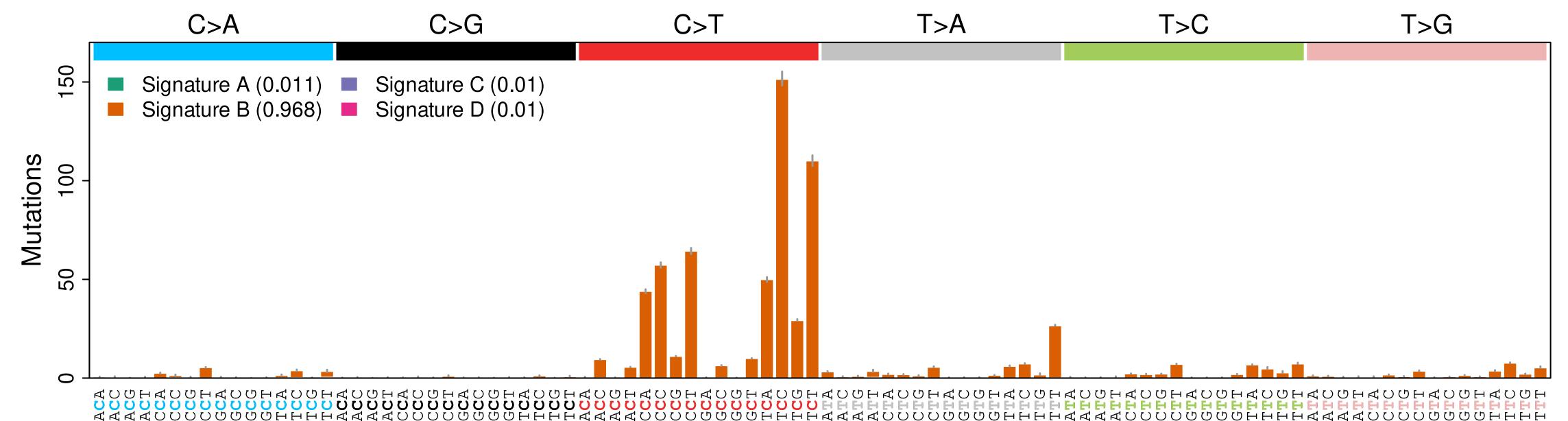
Reconstructed spectrum (cosine similarity = 0.992)



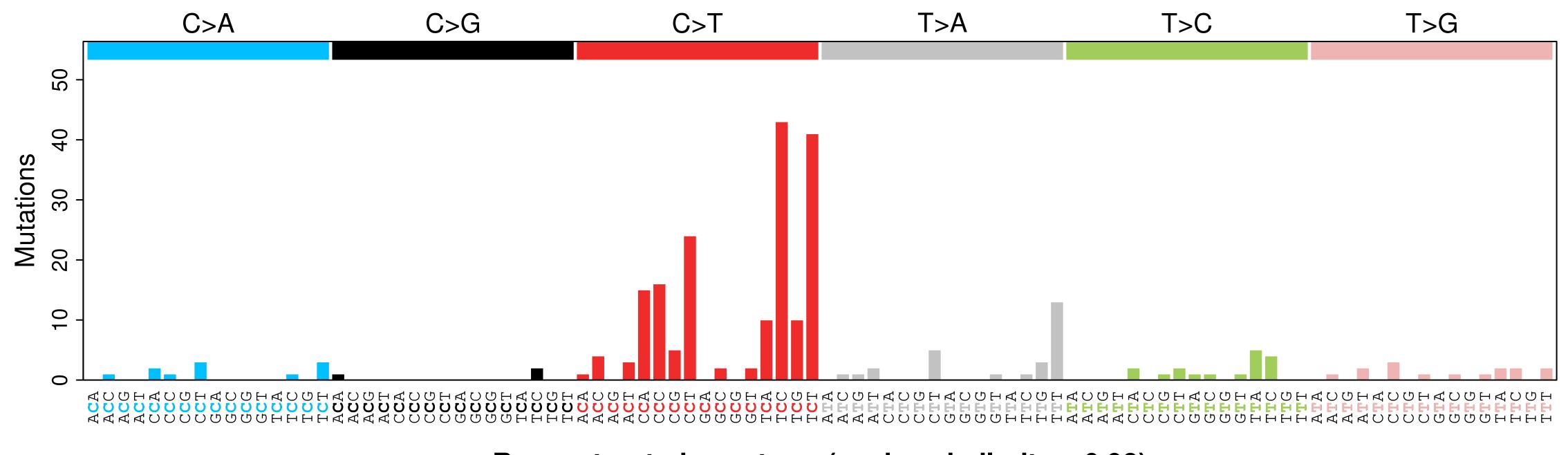
CATD268a (715 mutations)



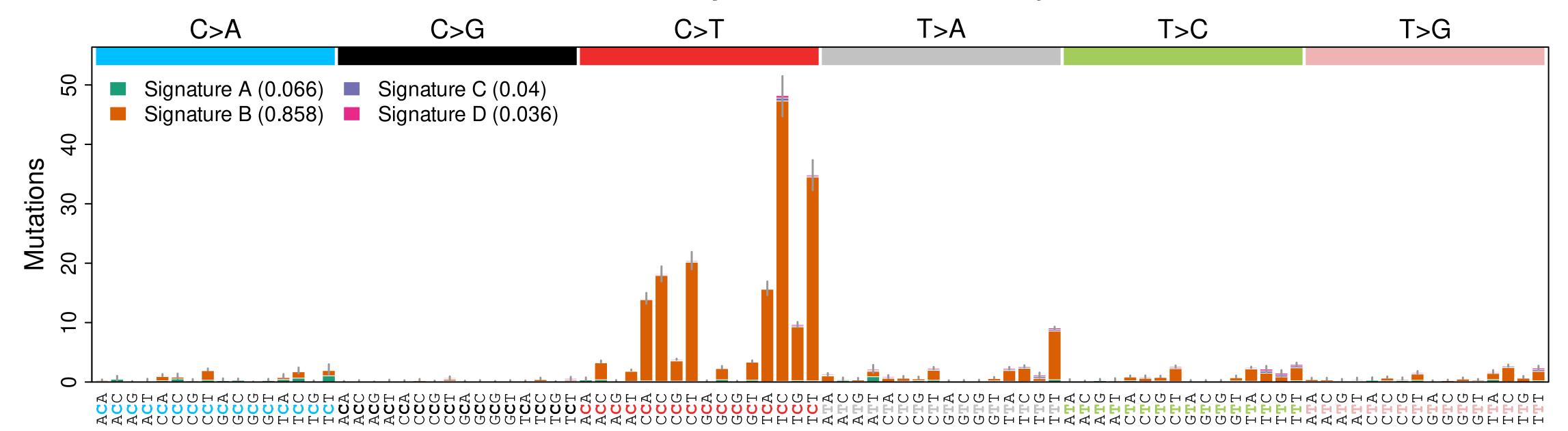




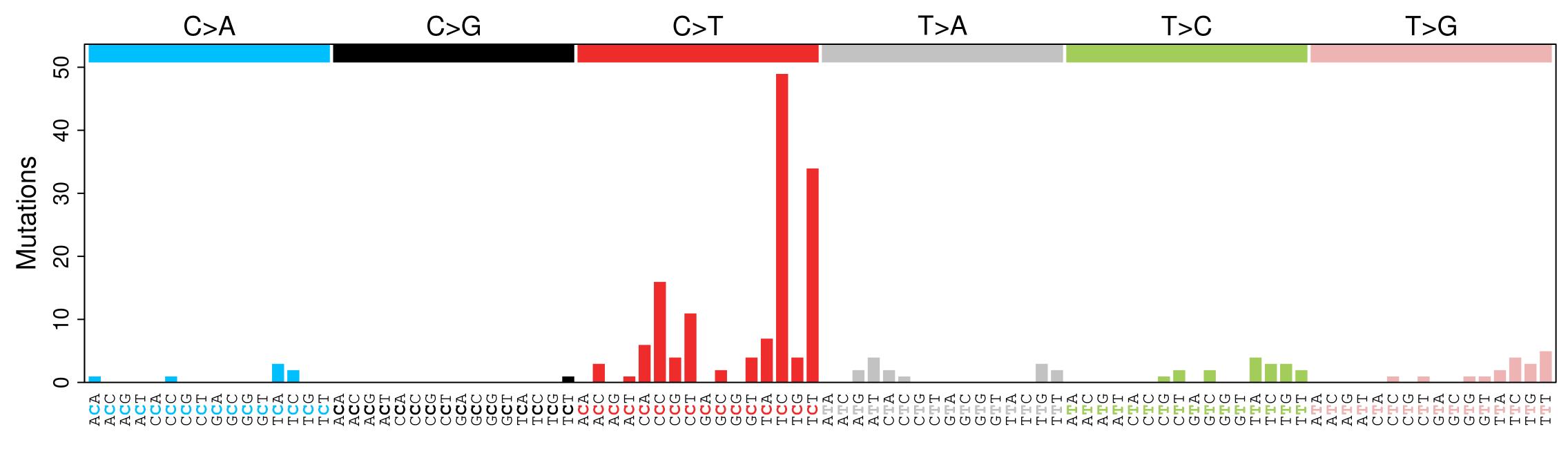
CATD187a (249 mutations)

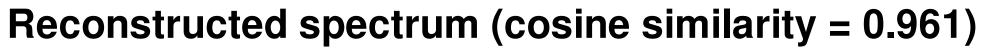


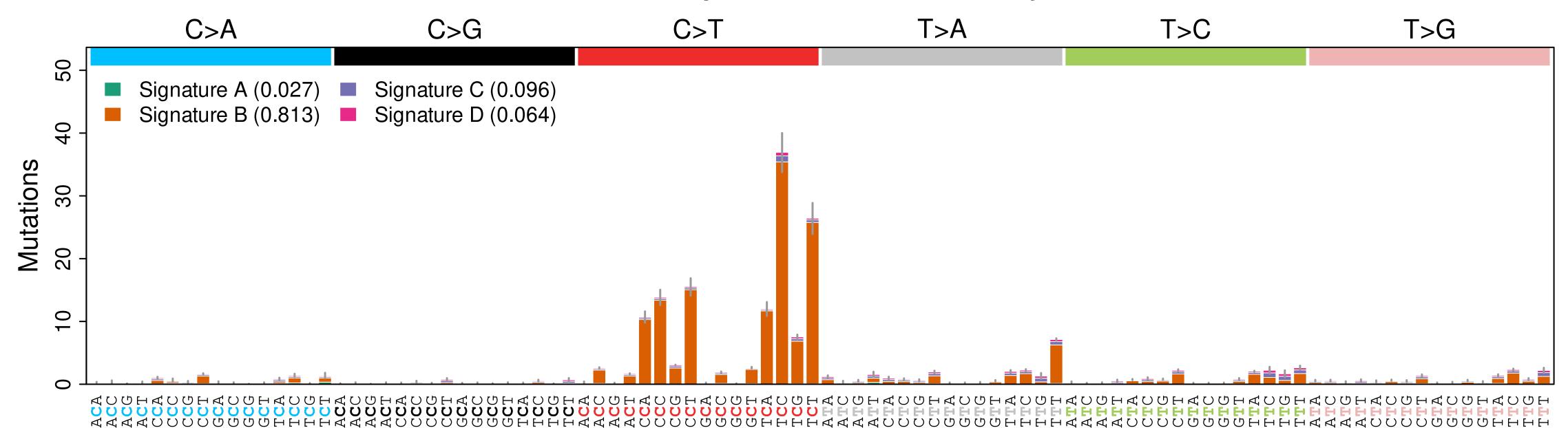
Reconstructed spectrum (cosine similarity = 0.98)



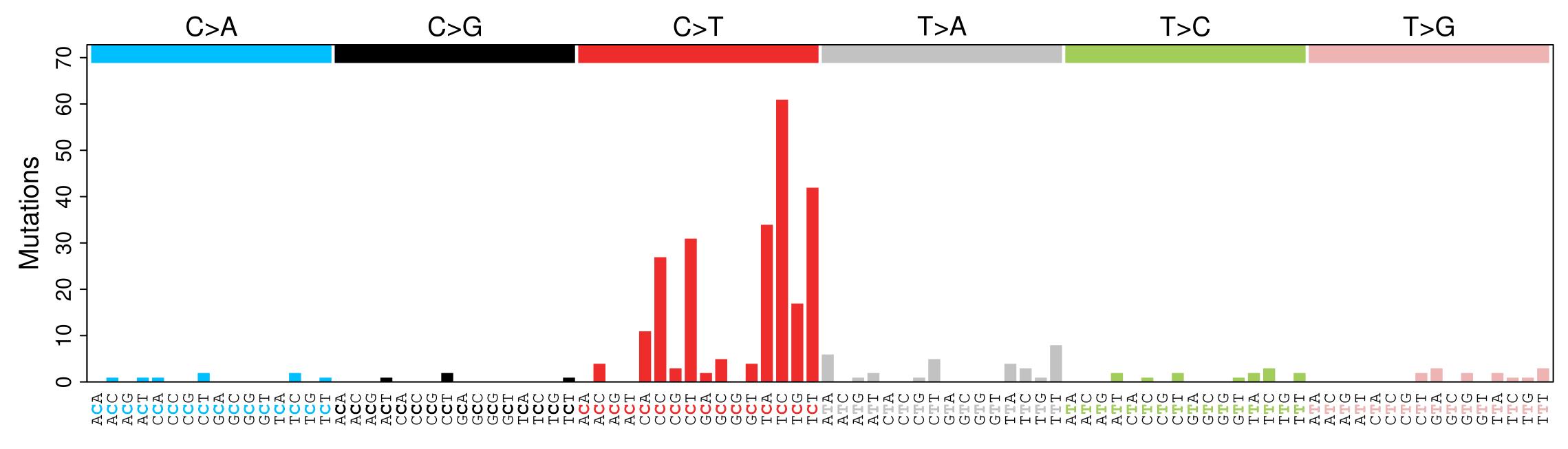
CATD245a (198 mutations)



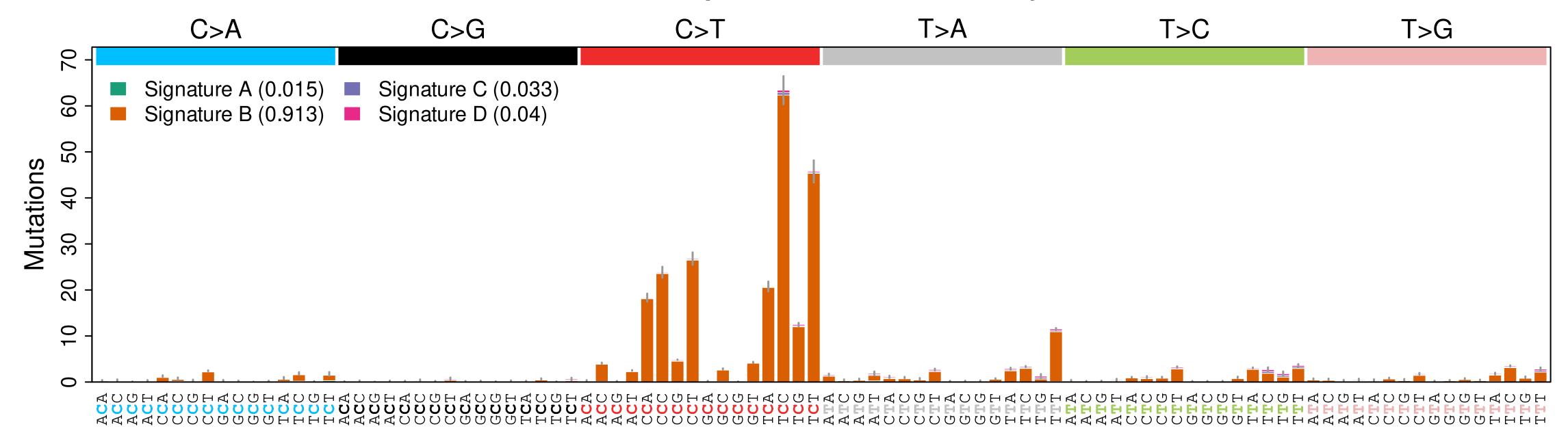




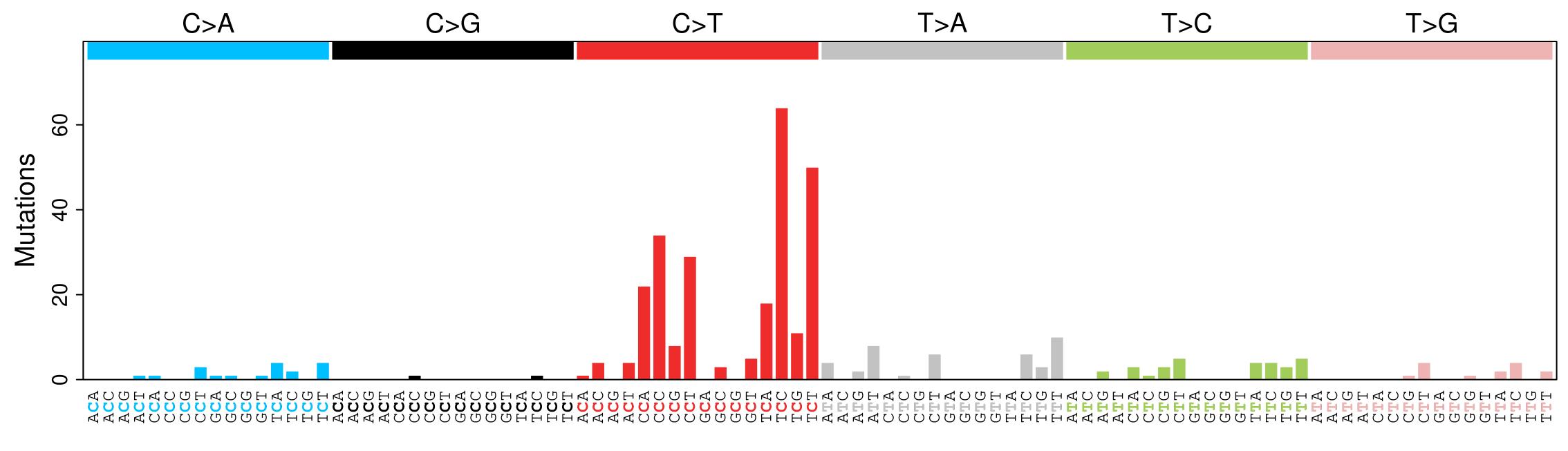
CATD0123a (311 mutations)



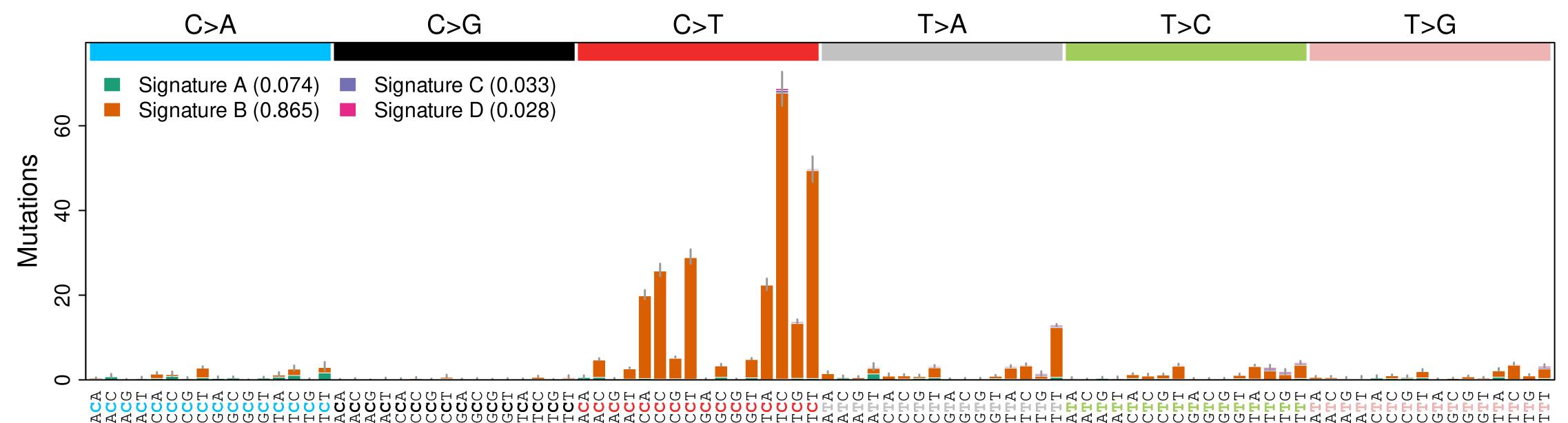
Reconstructed spectrum (cosine similarity = 0.978)



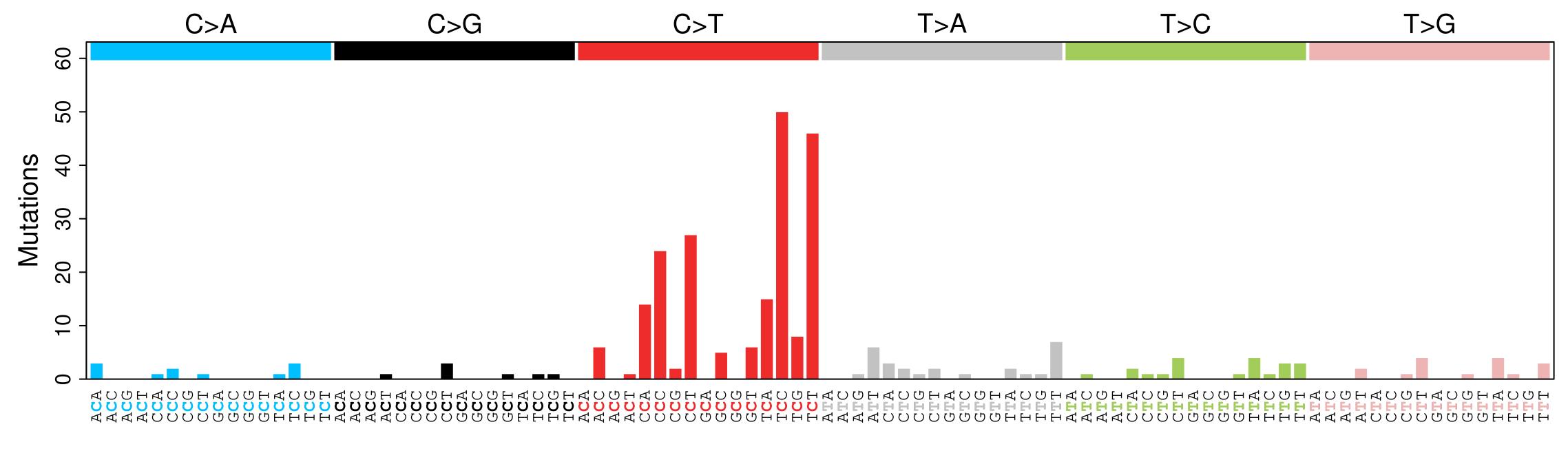
CATD255a (357 mutations)



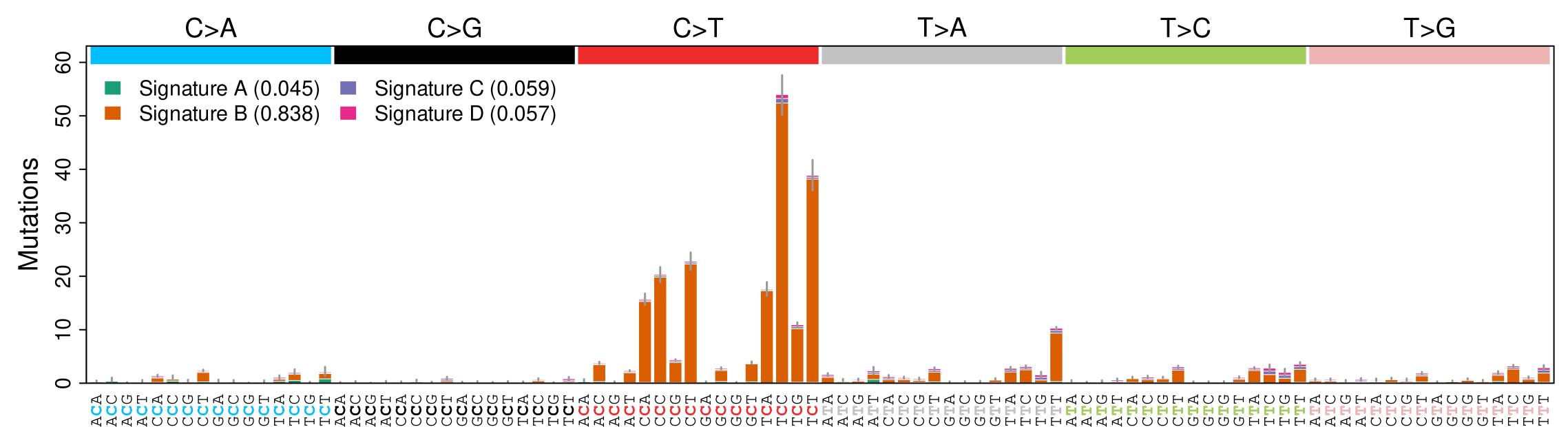
Reconstructed spectrum (cosine similarity = 0.988)



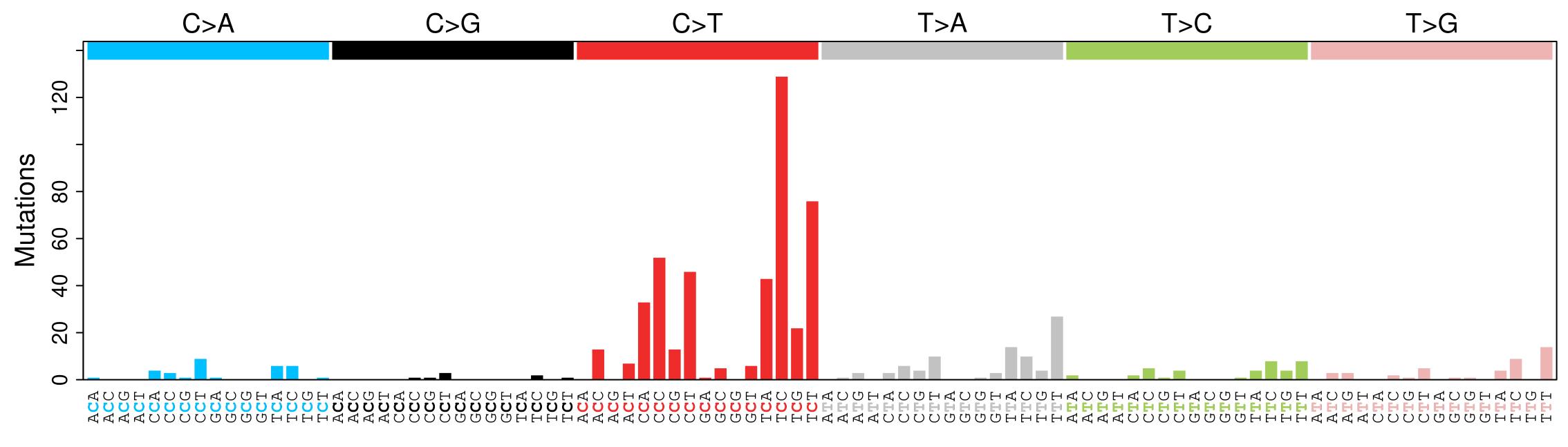
CATD244a (286 mutations)



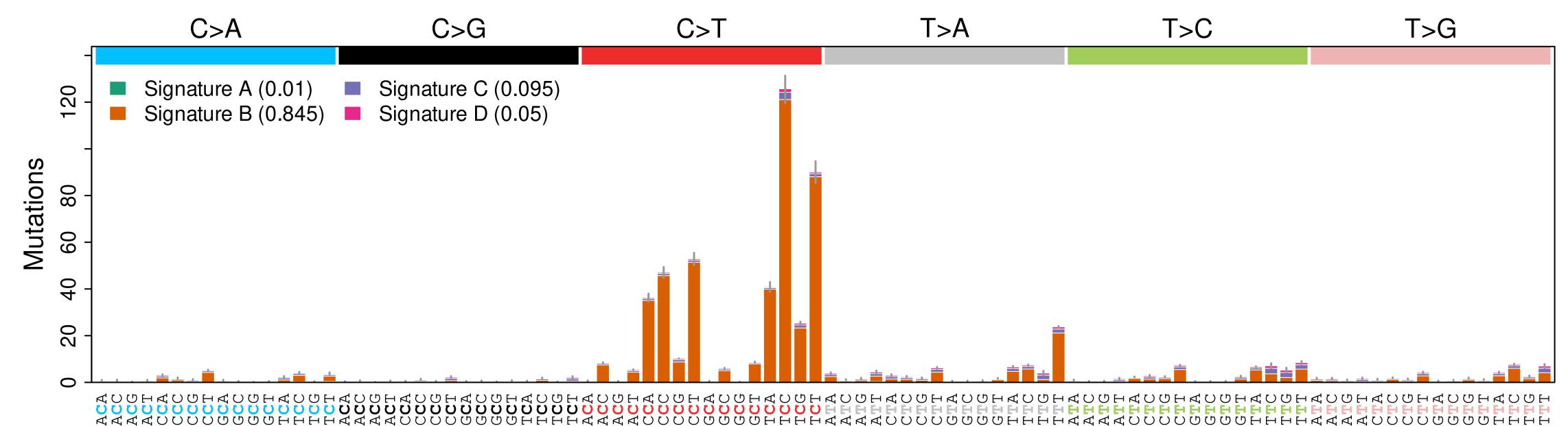
Reconstructed spectrum (cosine similarity = 0.983)



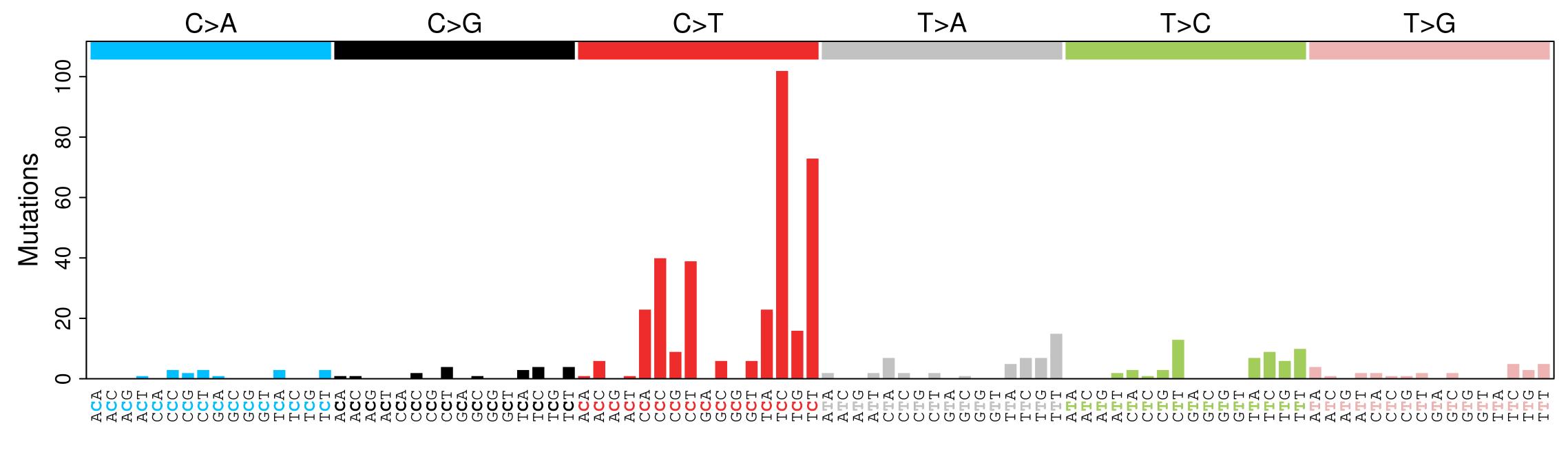
CATD0120a (654 mutations)



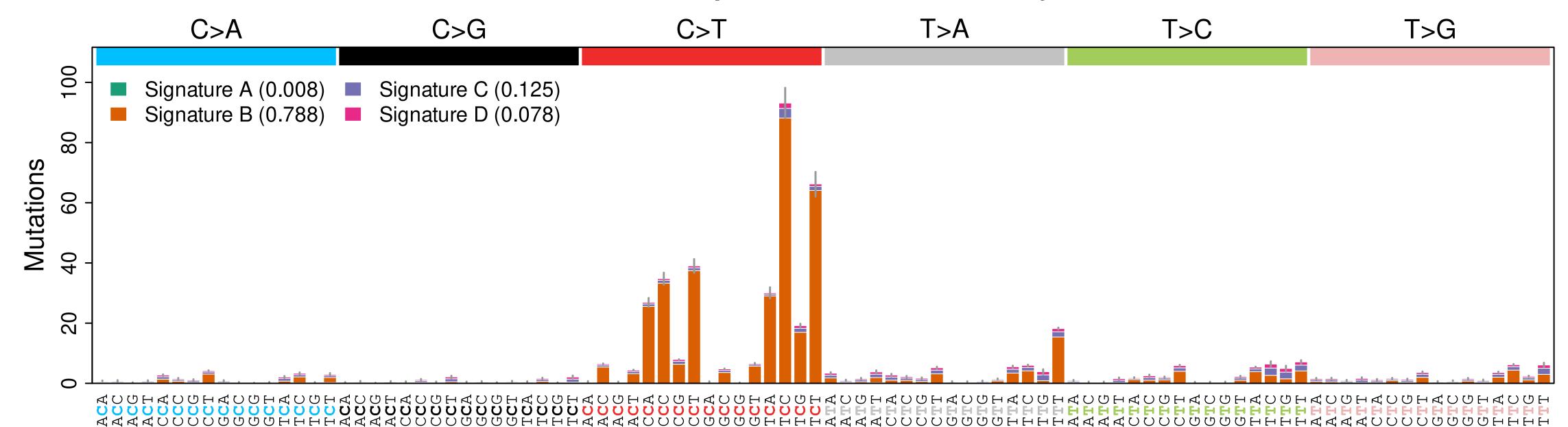
Reconstructed spectrum (cosine similarity = 0.991)



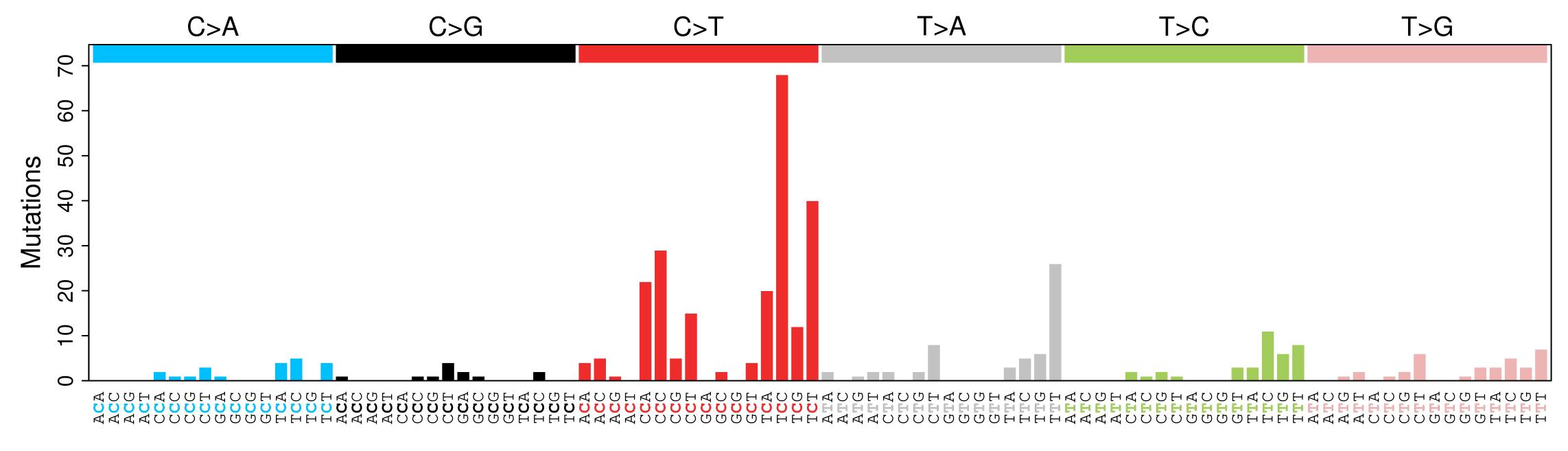
CATD247a (513 mutations)



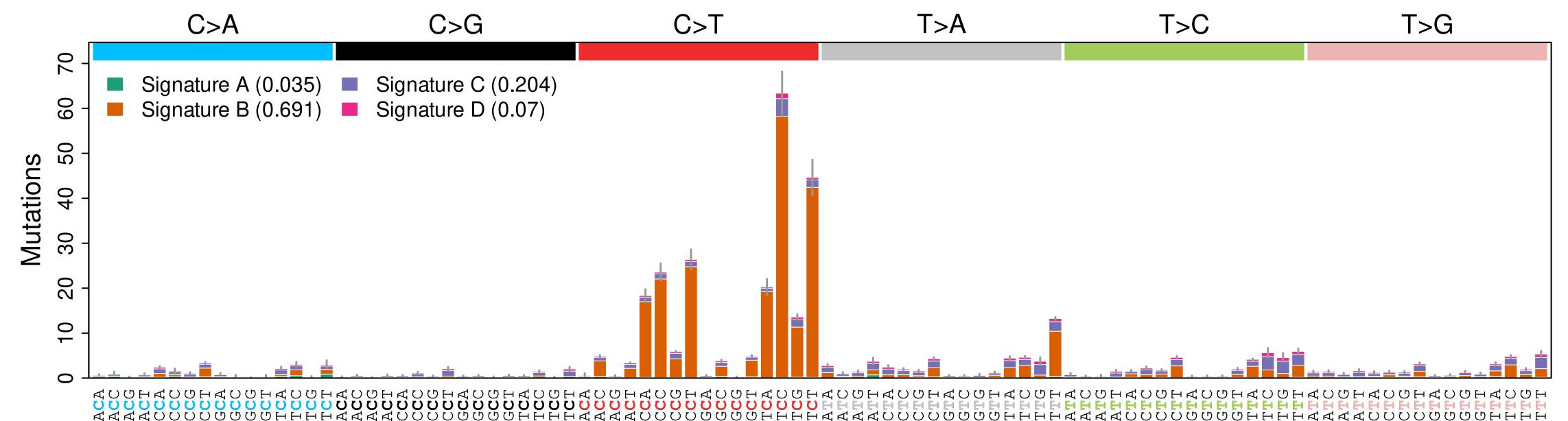
Reconstructed spectrum (cosine similarity = 0.99)



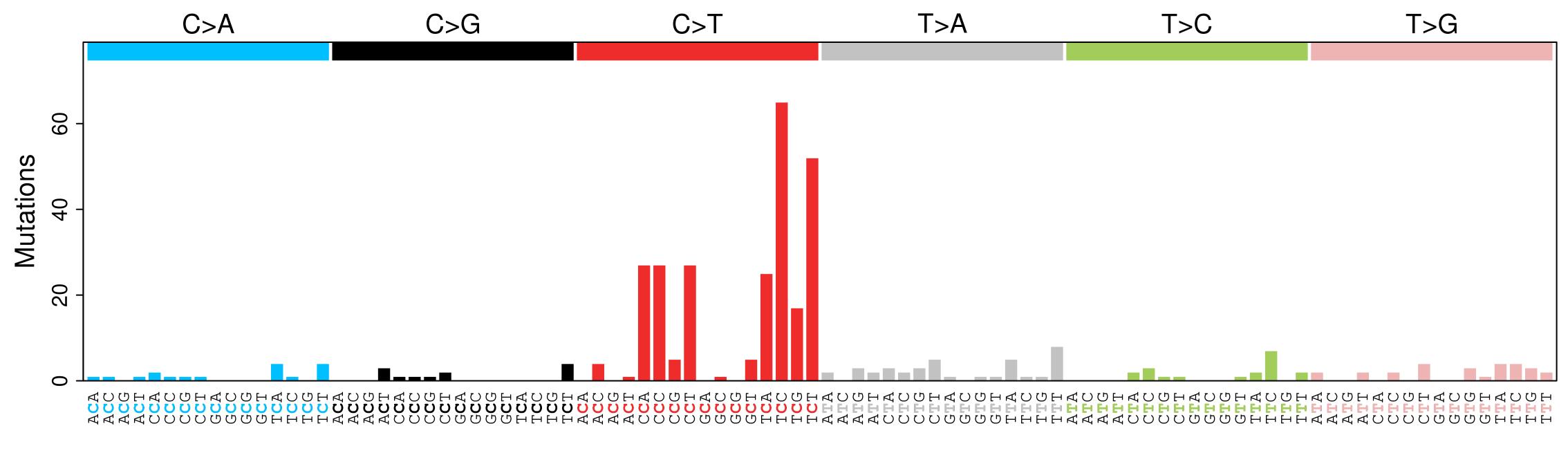
CATD260a (388 mutations)



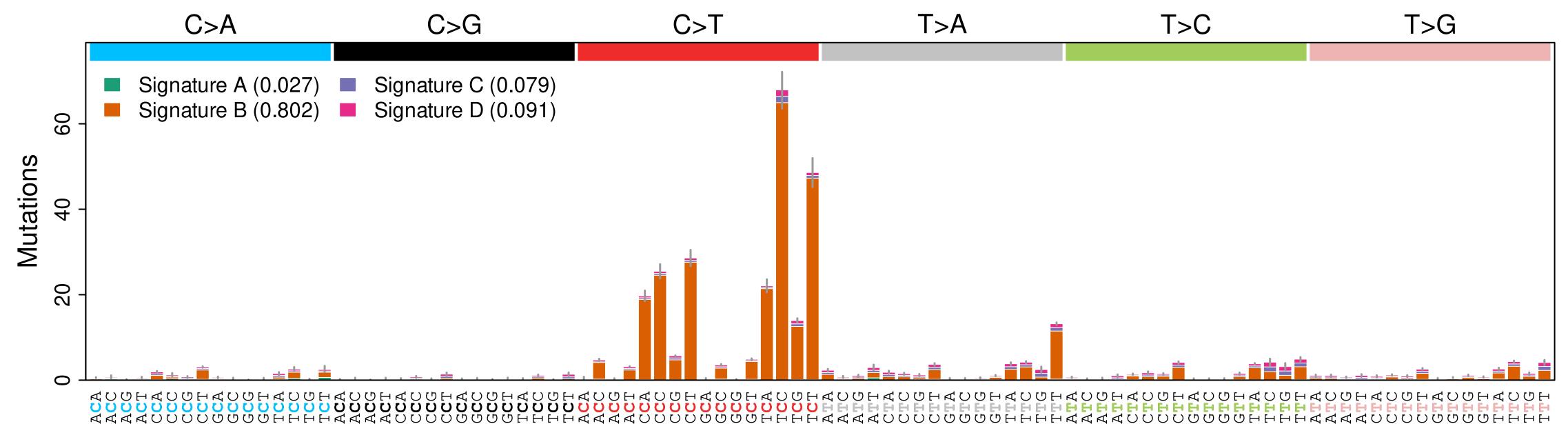
Reconstructed spectrum (cosine similarity = 0.972)



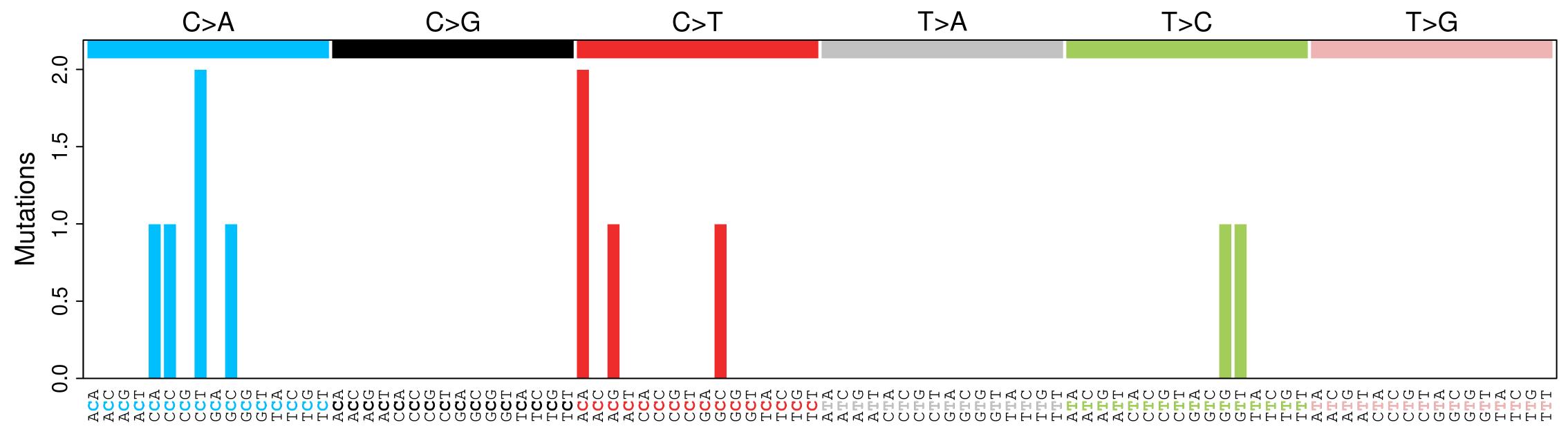
CATD246a (369 mutations)



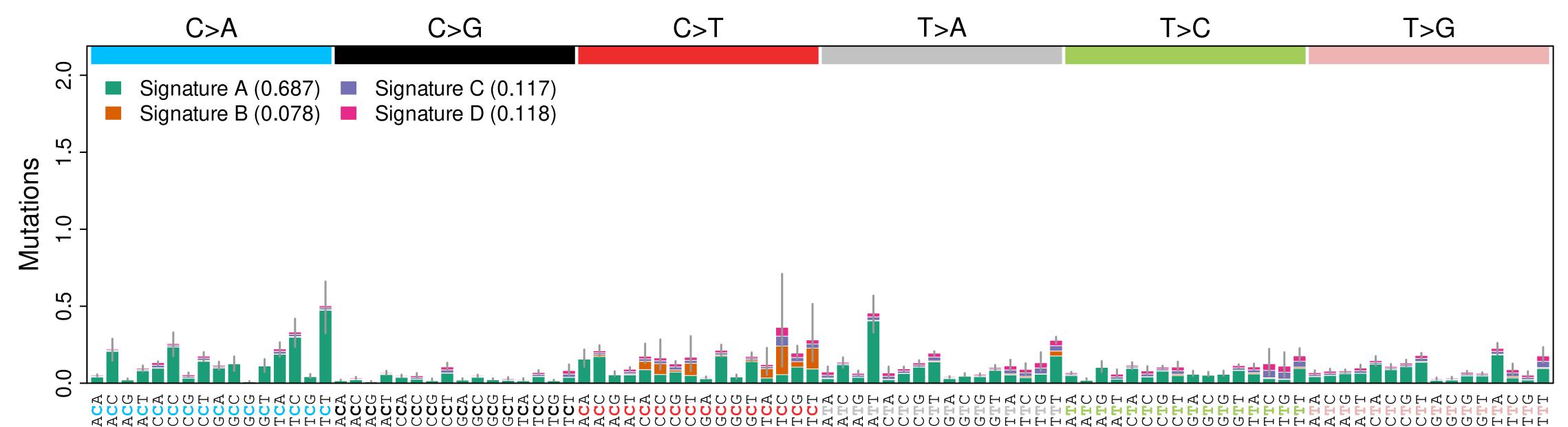
Reconstructed spectrum (cosine similarity = 0.988)



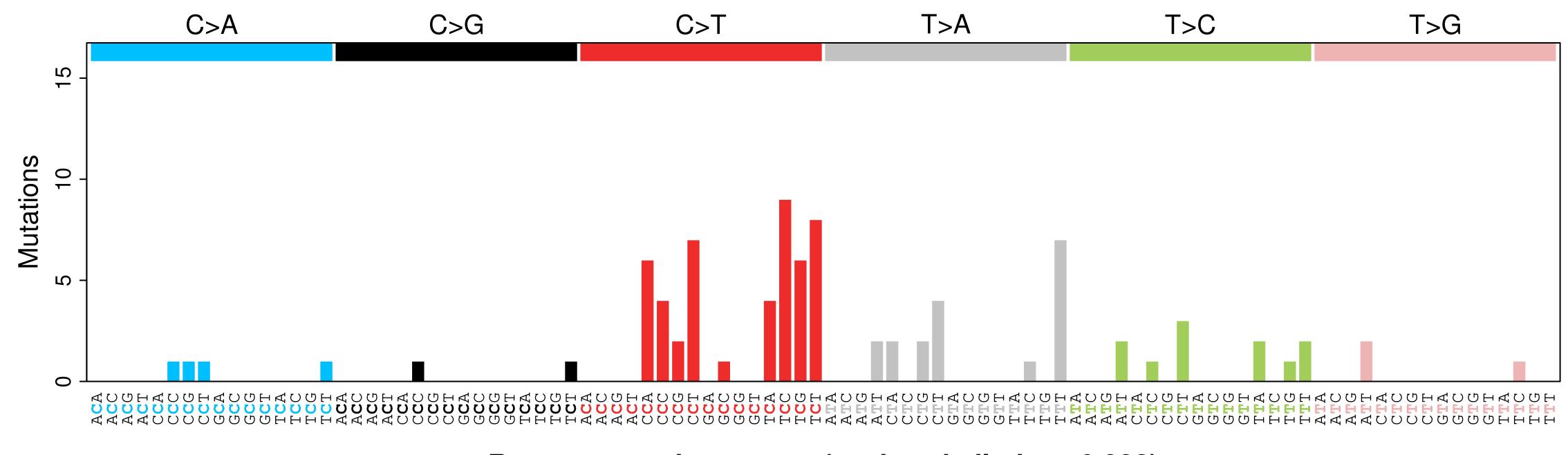
CATD279a (11 mutations)



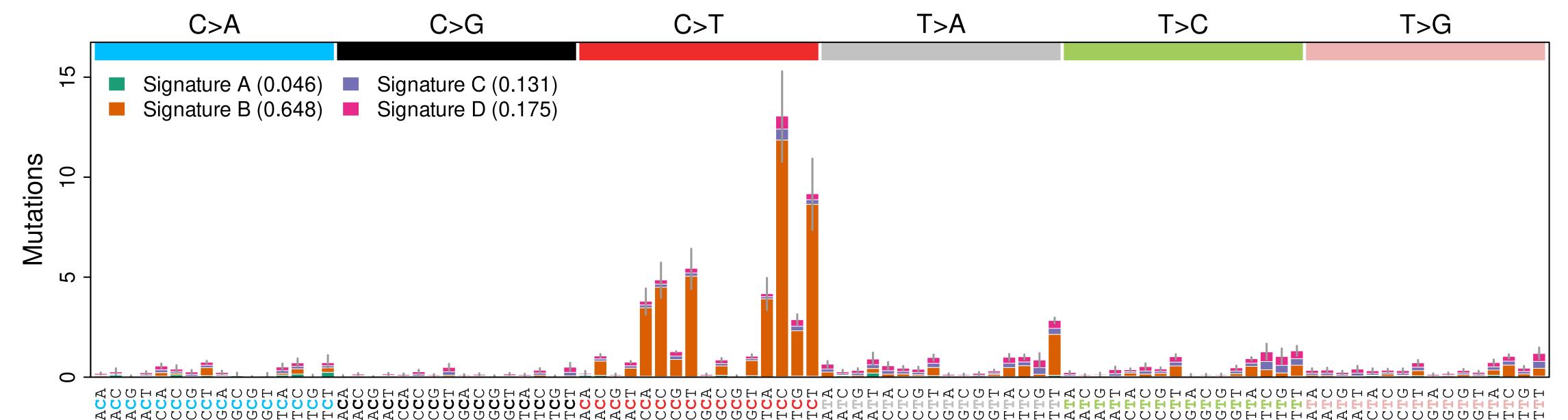
Reconstructed spectrum (cosine similarity = 0.302)



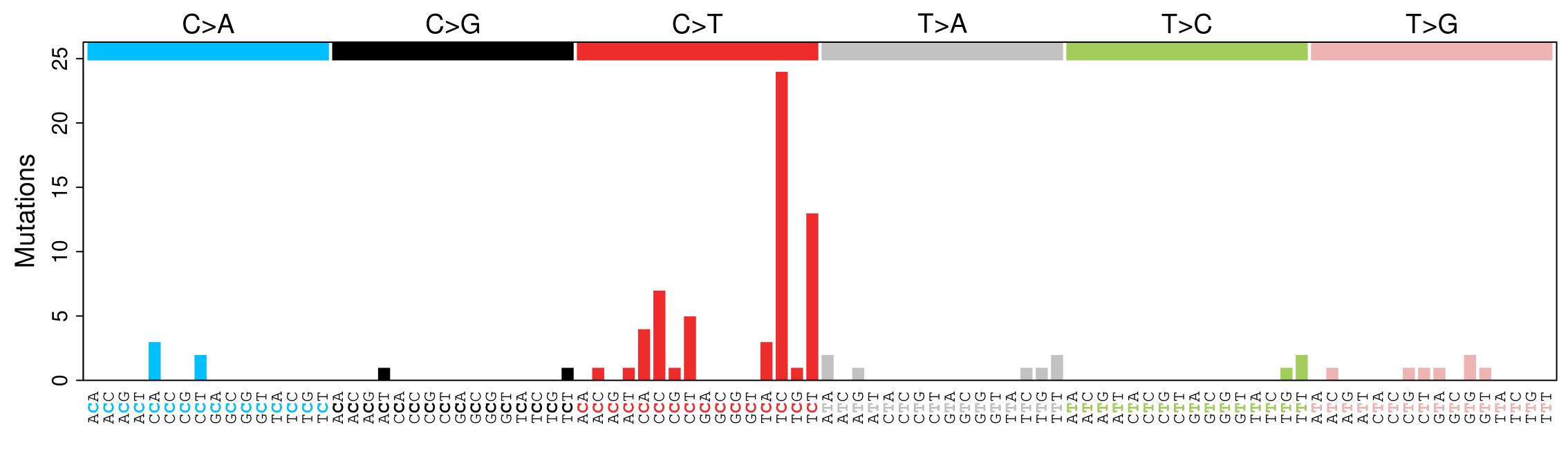
CATD261a (85 mutations)



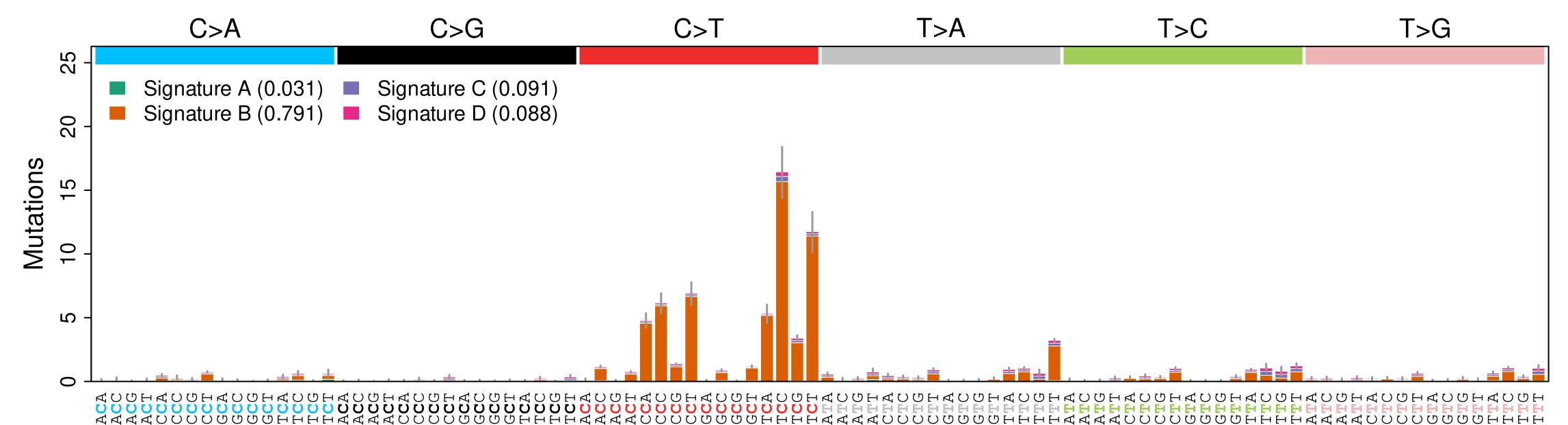
Reconstructed spectrum (cosine similarity = 0.882)



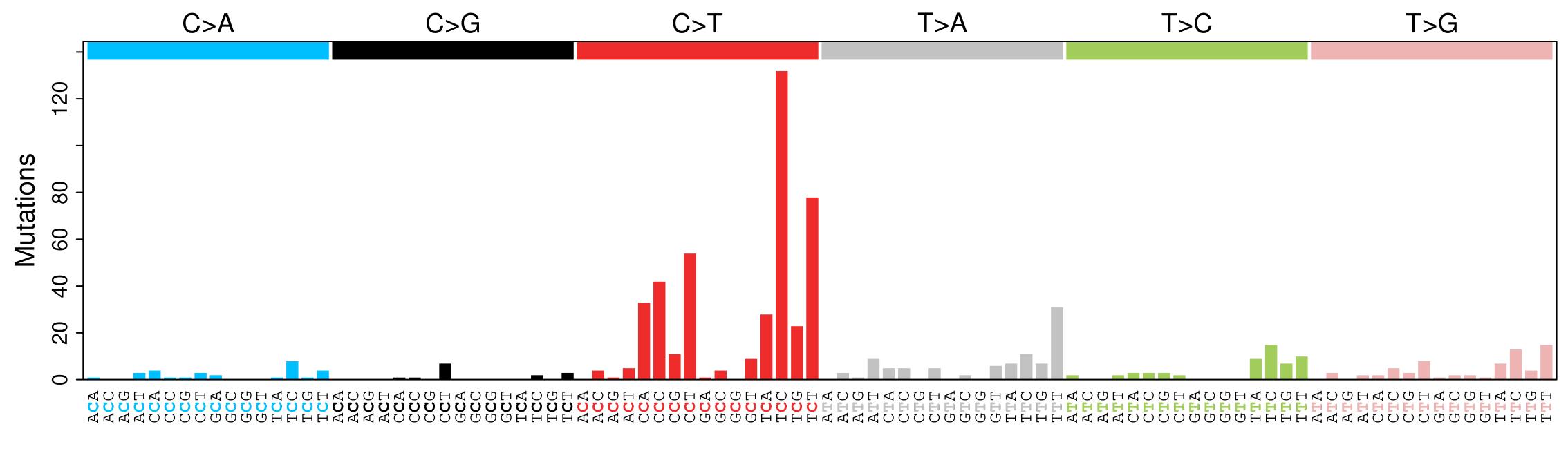
CATD280a (84 mutations)



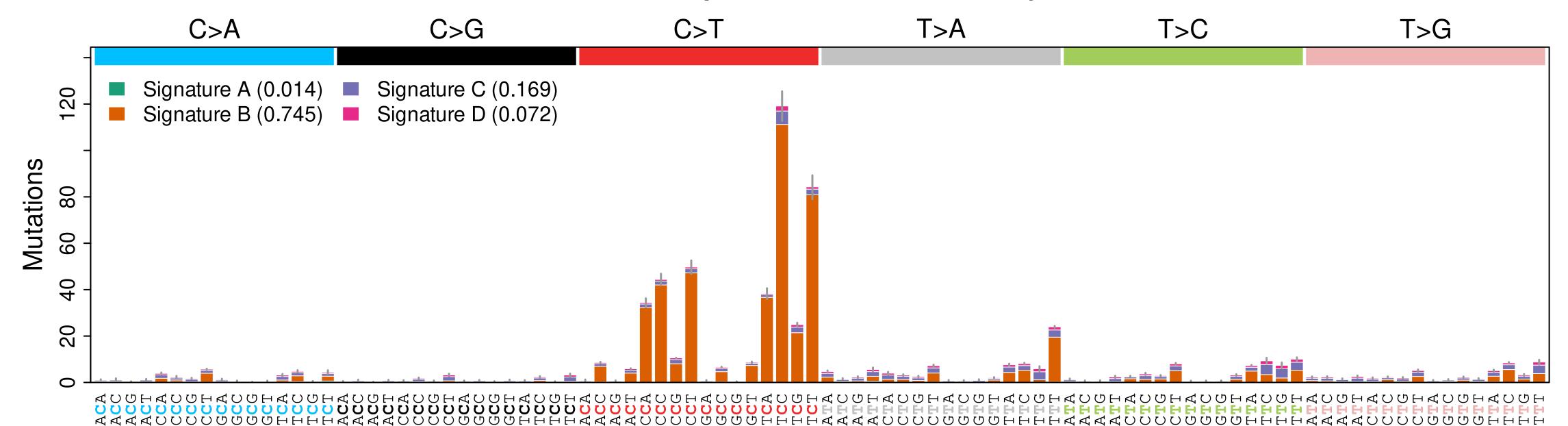
Reconstructed spectrum (cosine similarity = 0.946)



CATD272a (684 mutations)



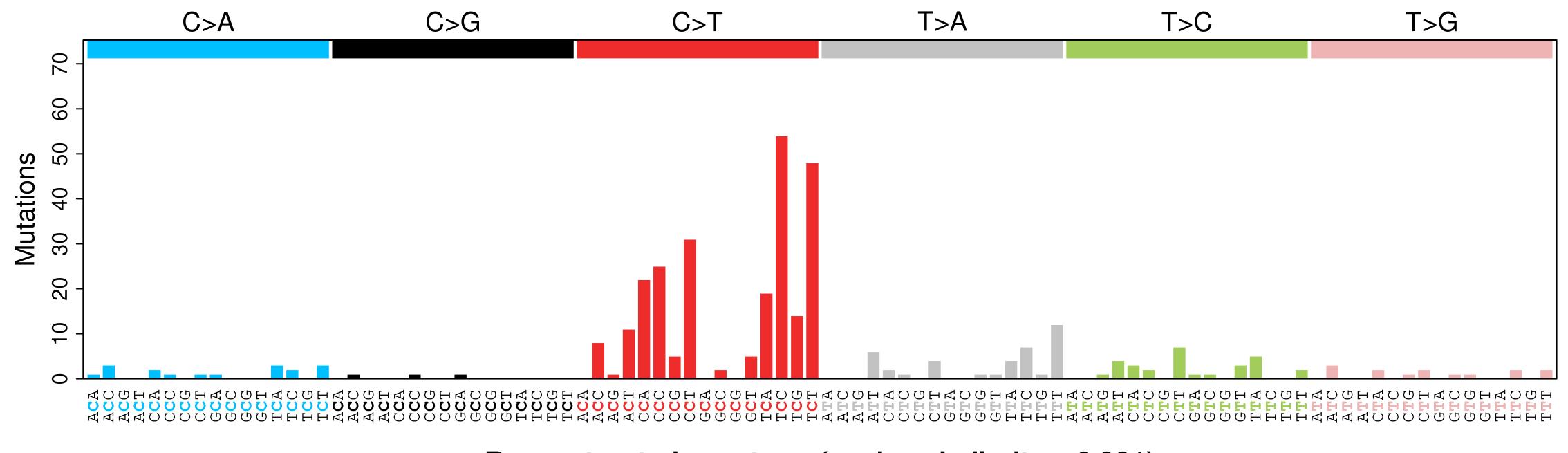




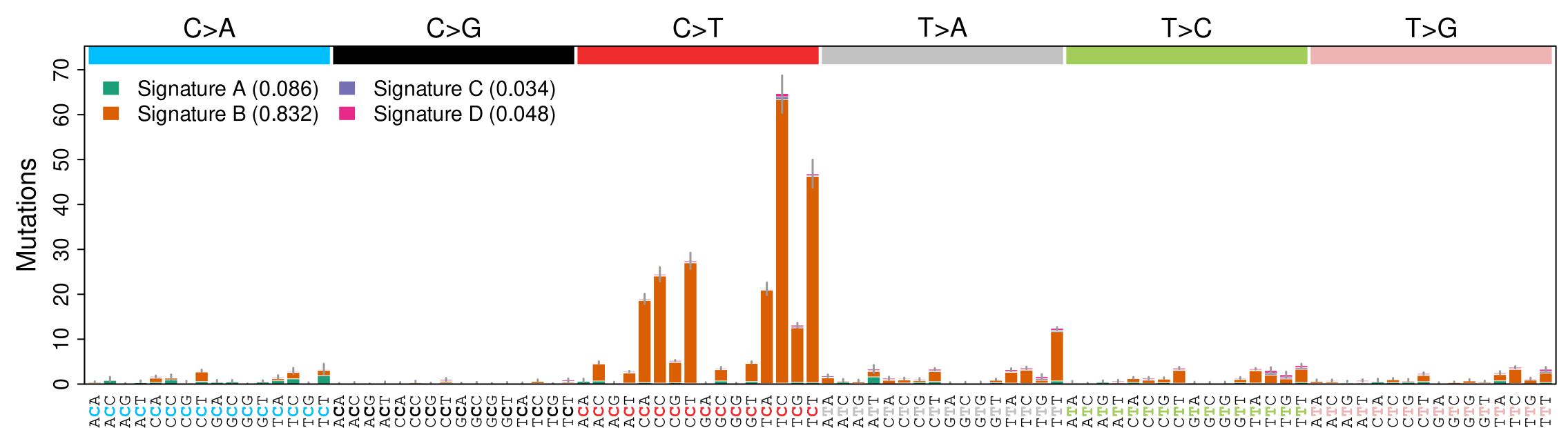
CATD275a T>C T>G C>A C>G C>T T>A 1.0 Mutation probability 0.8 9.0 0.4 0.2 0.0 Reconstructed spectrum (cosine similarity = 0.094) C>A C>G T>A T>C T>G C>T 1.0 Signature A (0.235) Signature C (0.256) Signature B (0.255) Signature D (0.254) 0.8 Mutations 9.0 \mathcal{O} 0

0.0

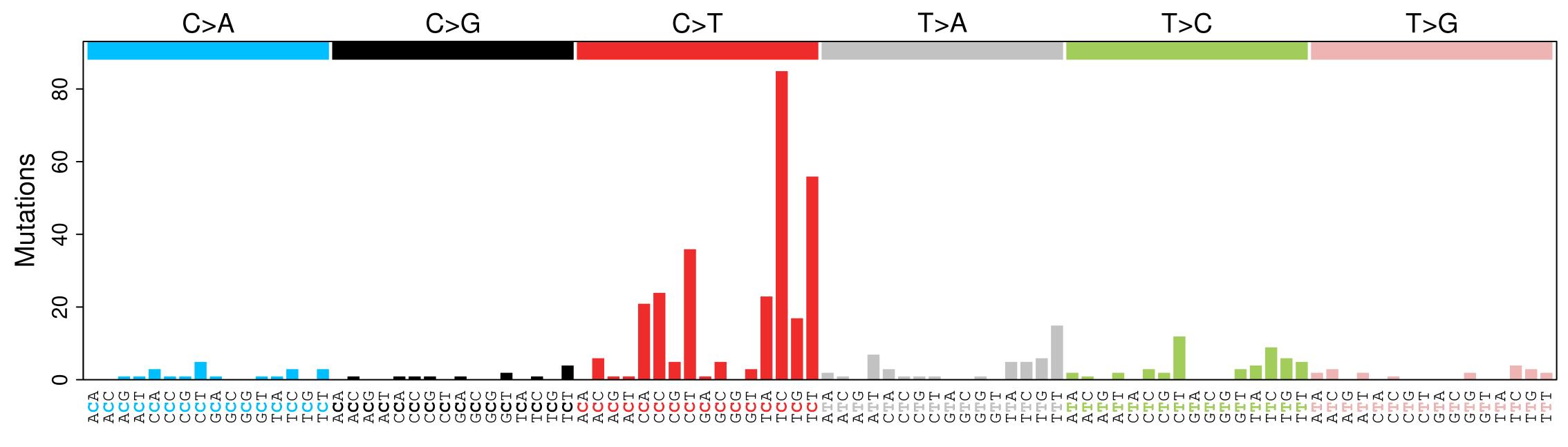
CATD276a (347 mutations)



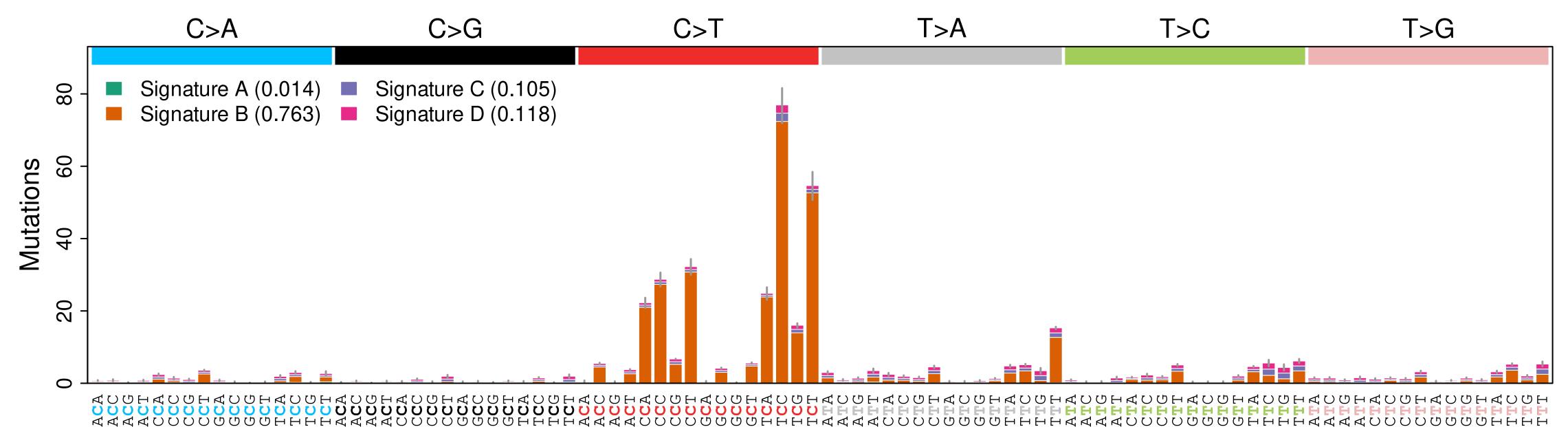
Reconstructed spectrum (cosine similarity = 0.981)



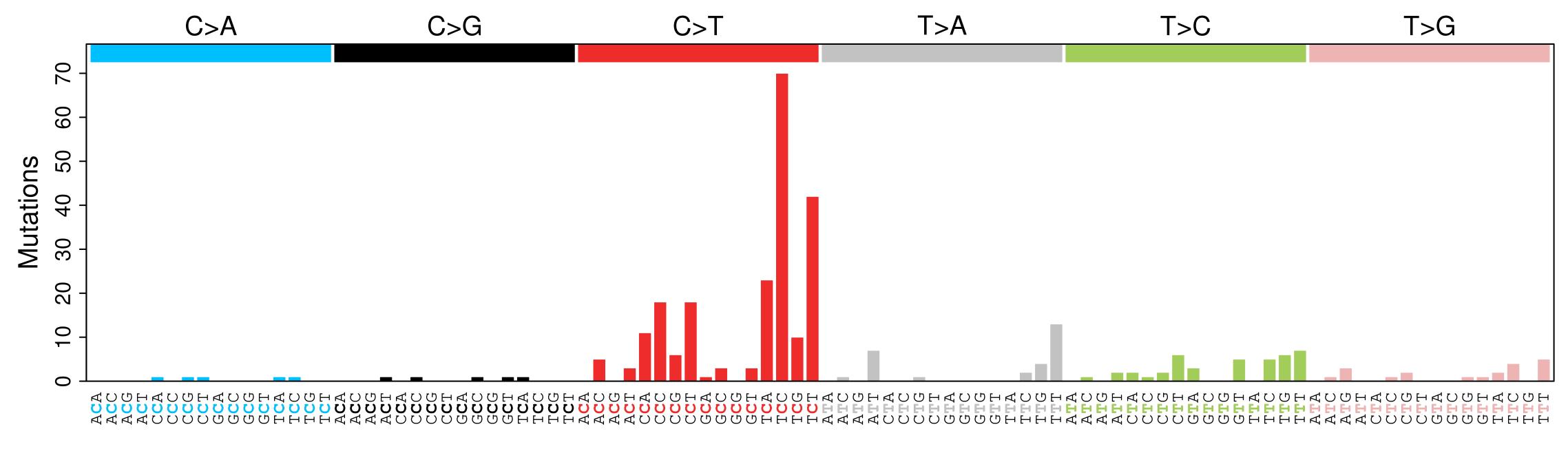
CATD0128a (433 mutations)



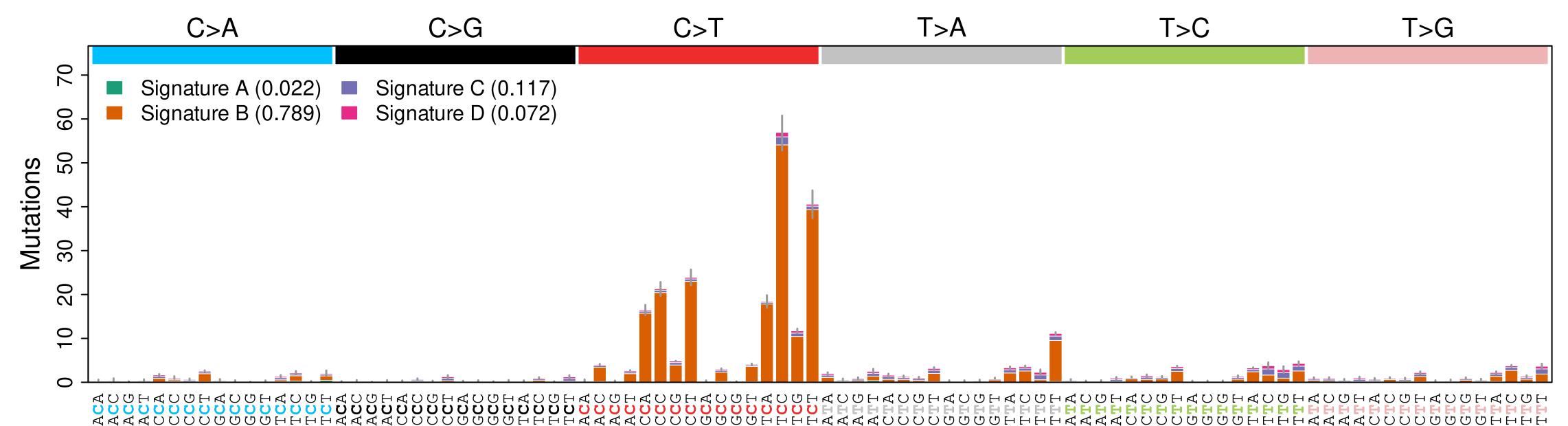
Reconstructed spectrum (cosine similarity = 0.991)



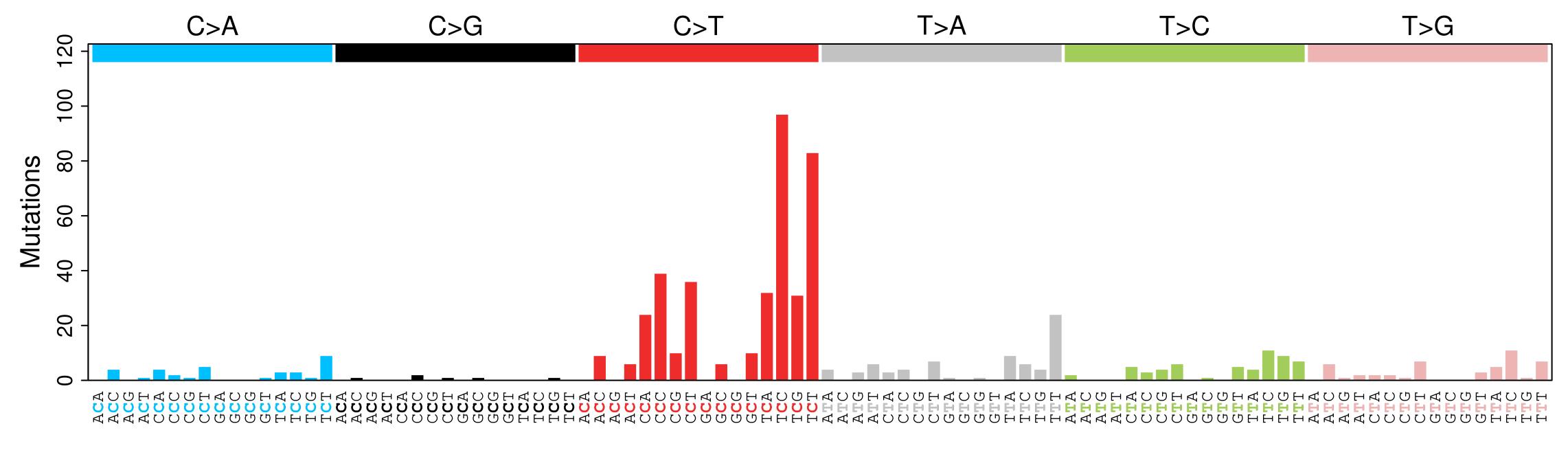
CATD273a (311 mutations)



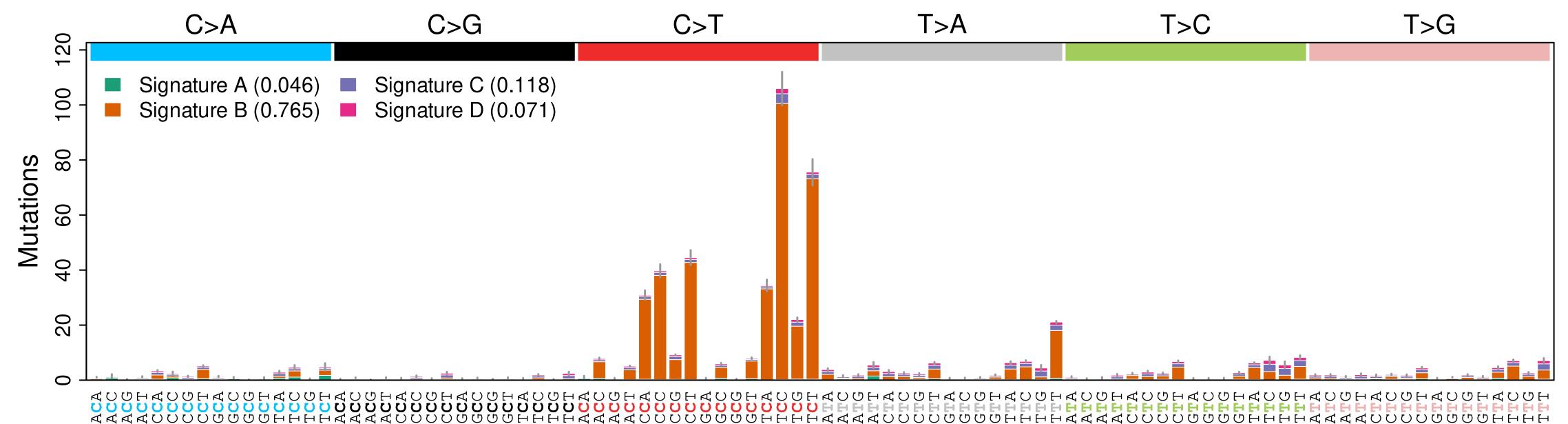
Reconstructed spectrum (cosine similarity = 0.977)



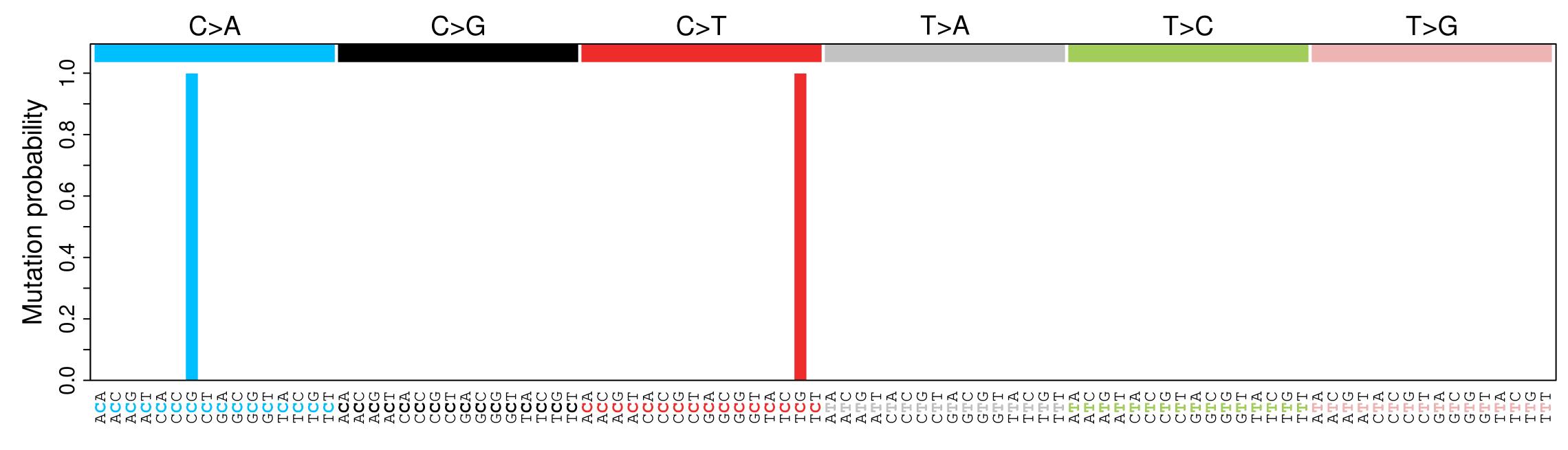
CATD253a (600 mutations)

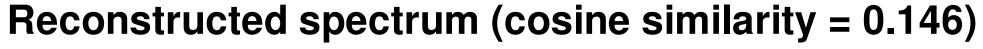


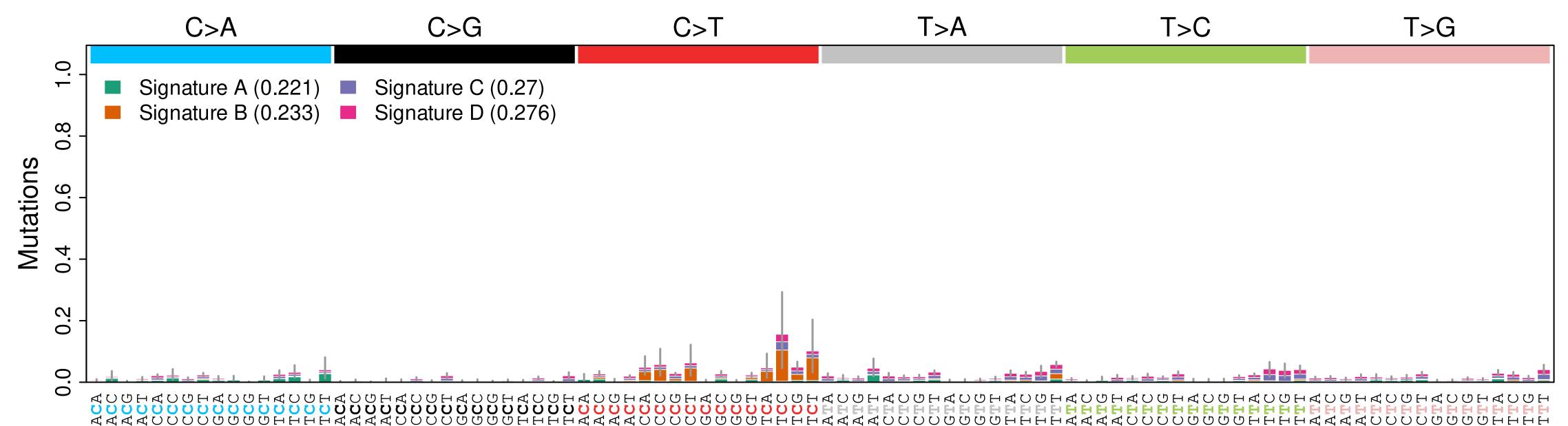
Reconstructed spectrum (cosine similarity = 0.989)



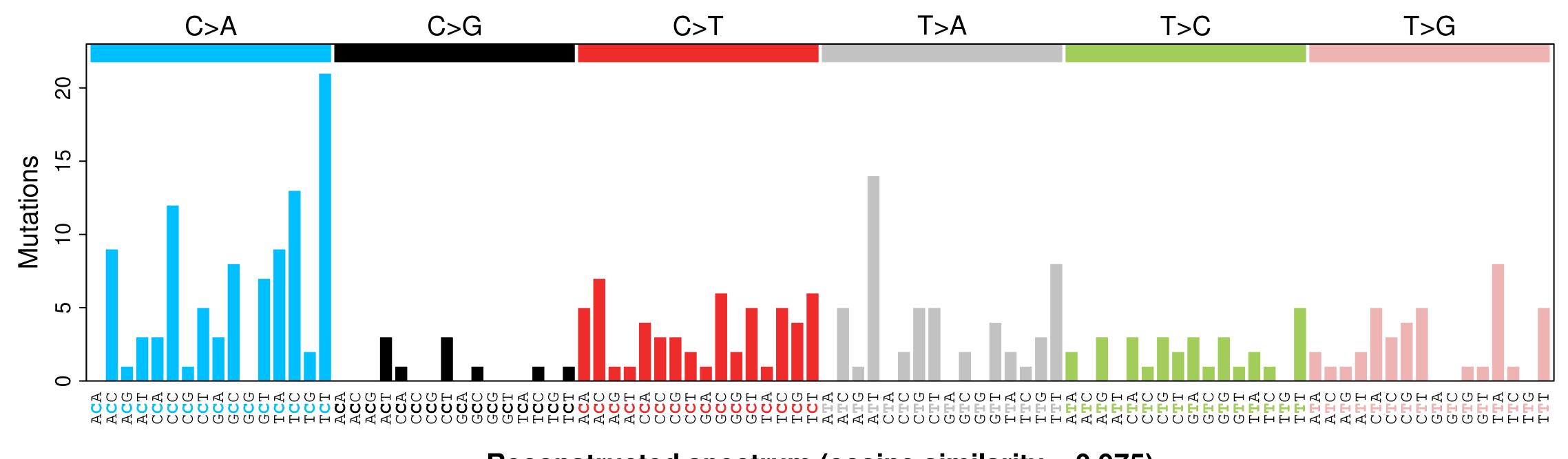




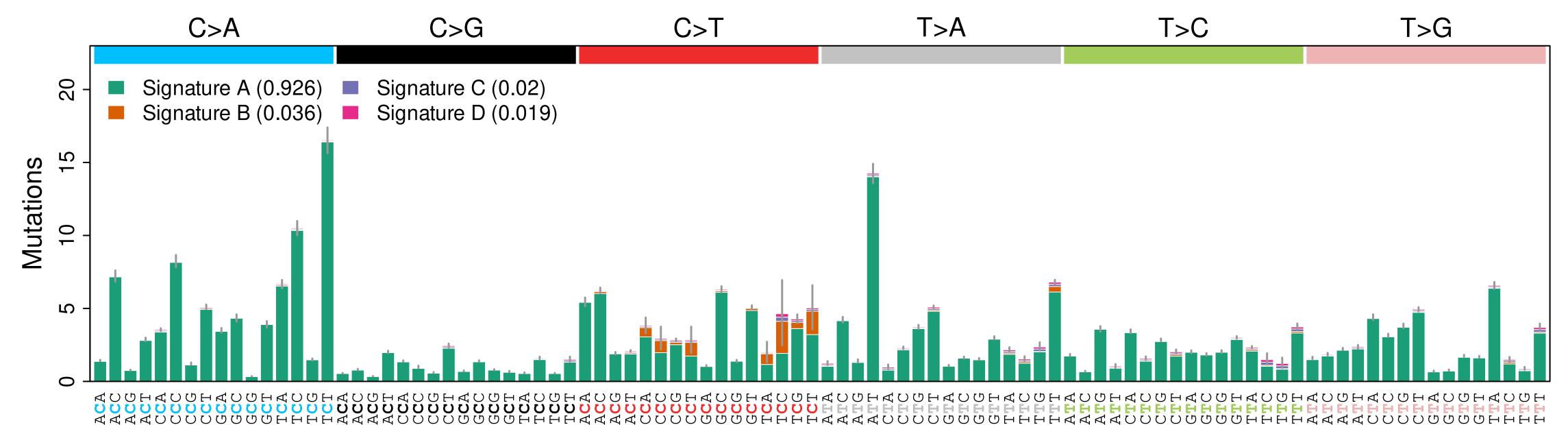




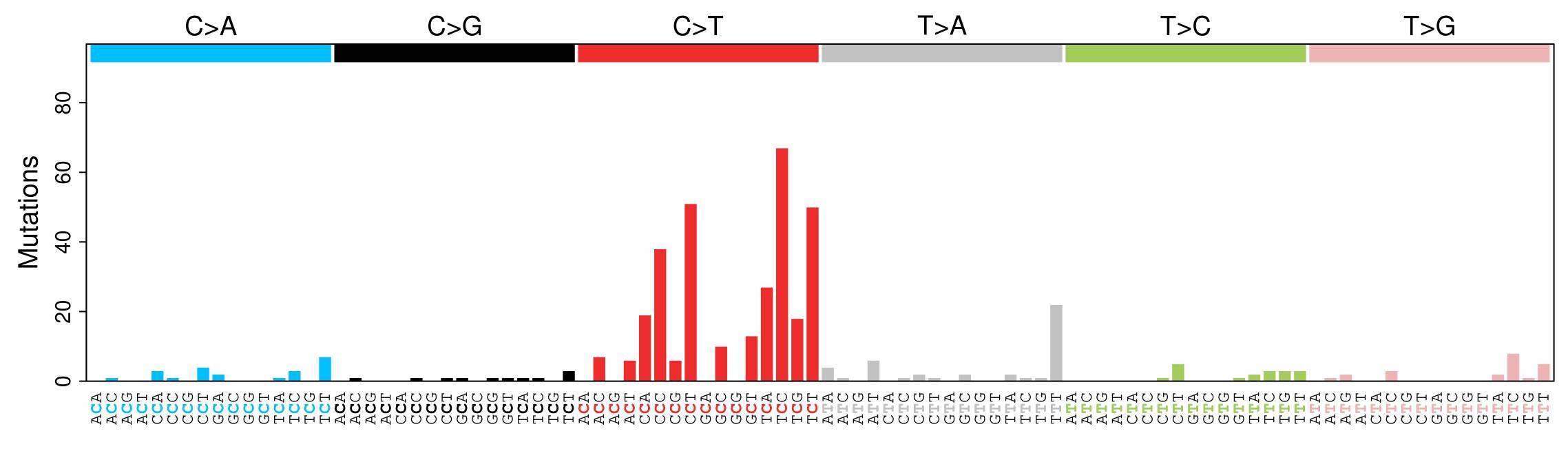
CATD186a (284 mutations)



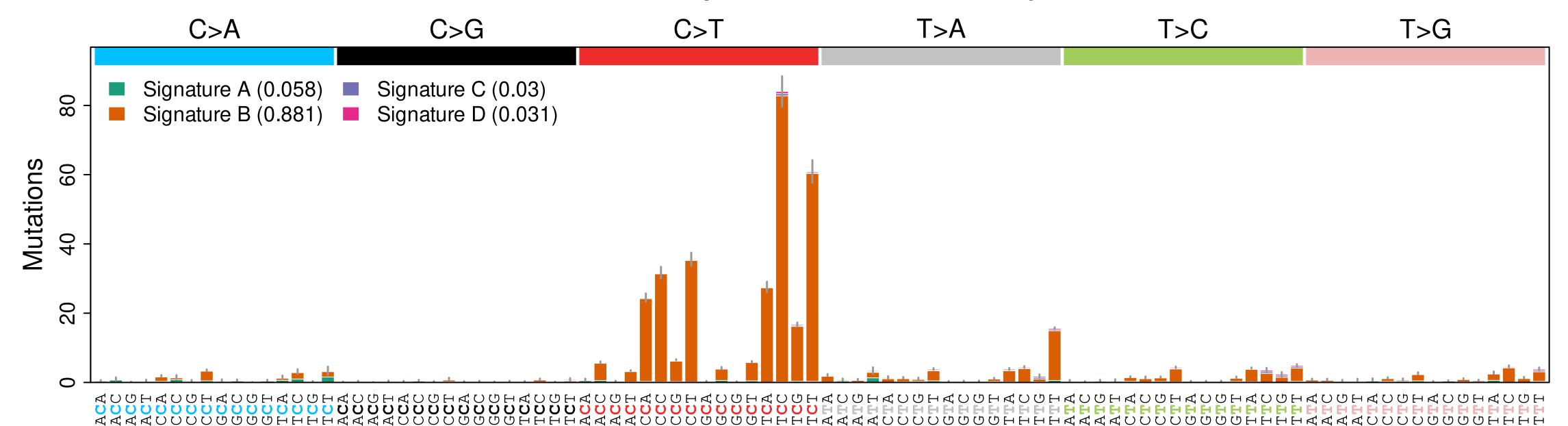
Reconstructed spectrum (cosine similarity = 0.975)



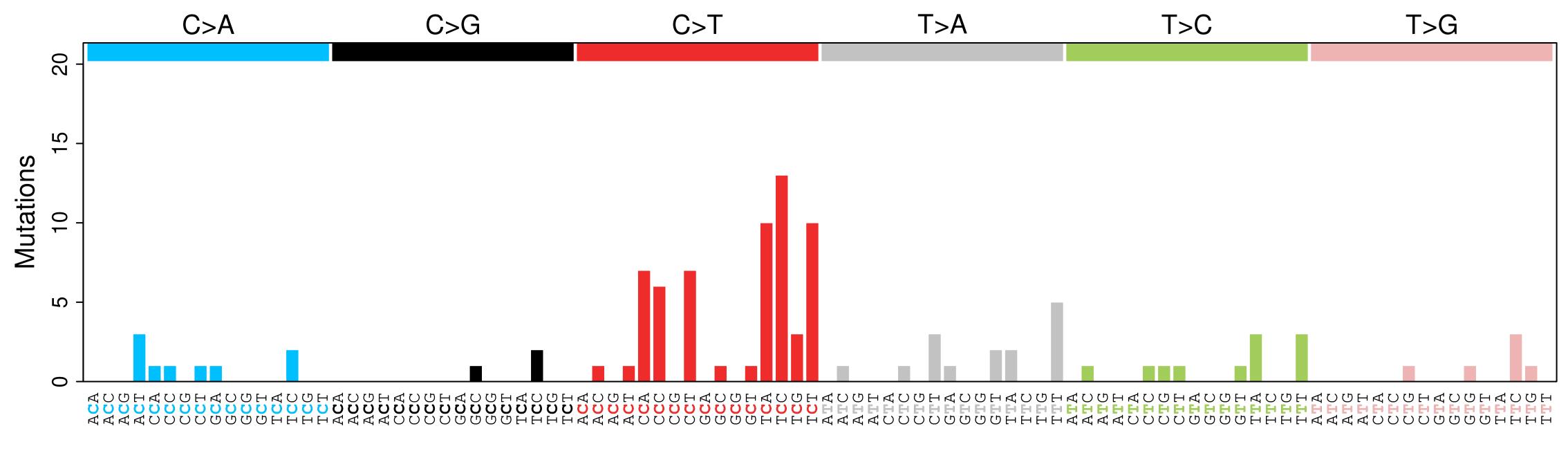
CATD0632c (428 mutations)



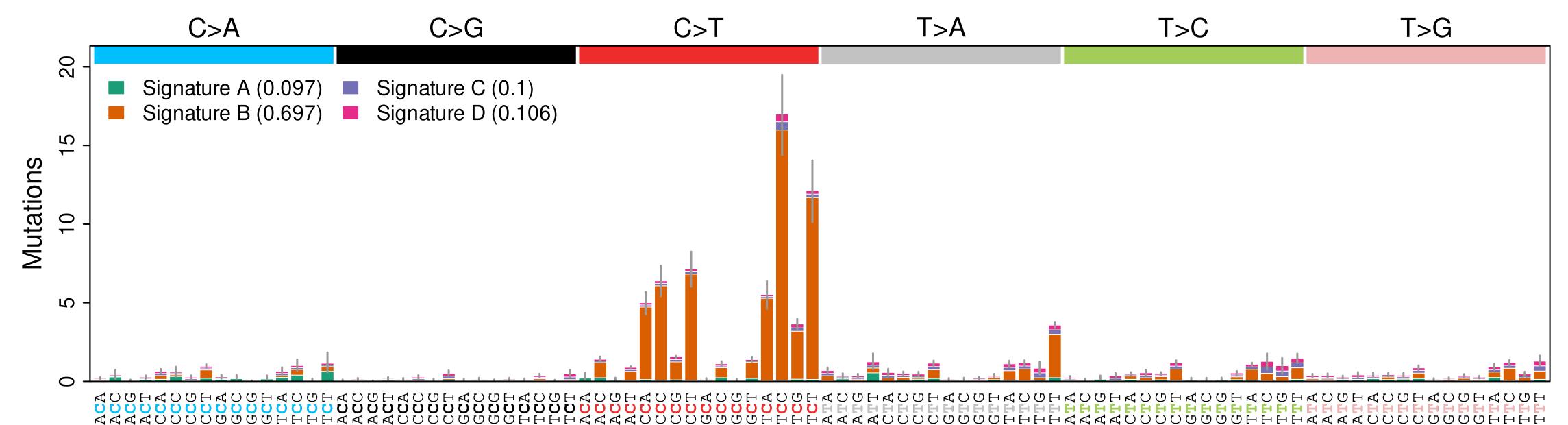
Reconstructed spectrum (cosine similarity = 0.968)



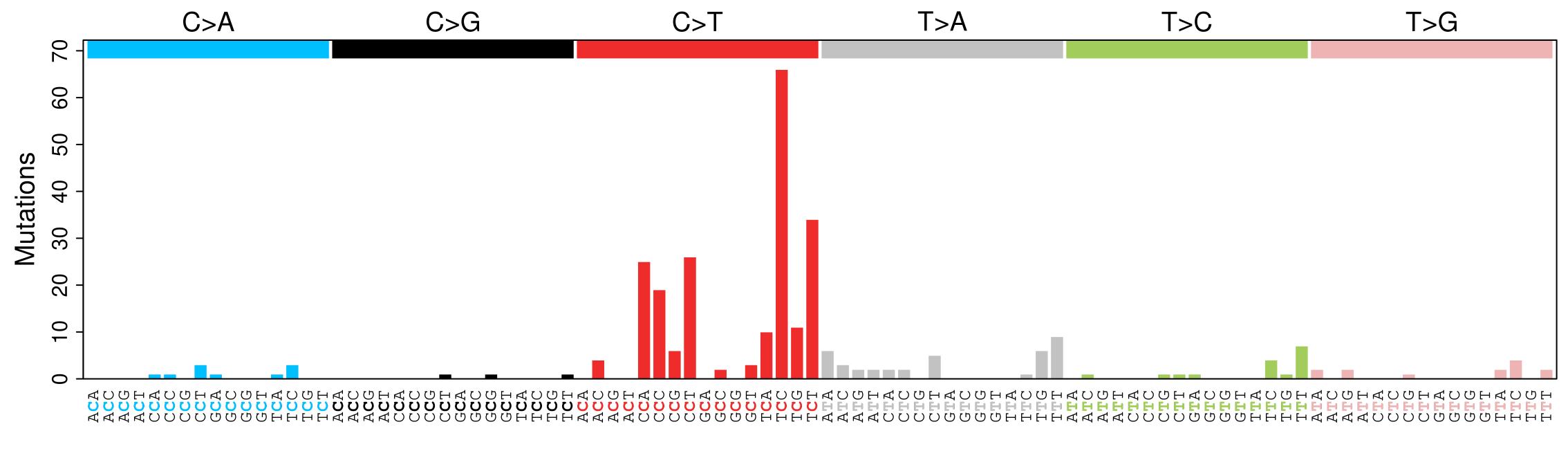
CATD0126a (104 mutations)



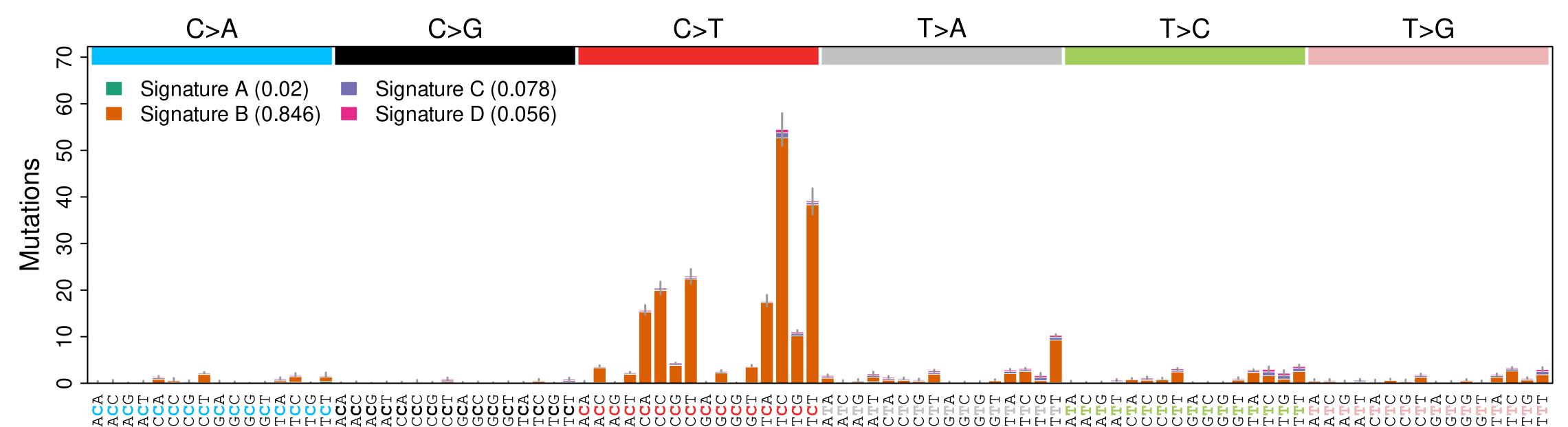
Reconstructed spectrum (cosine similarity = 0.923)



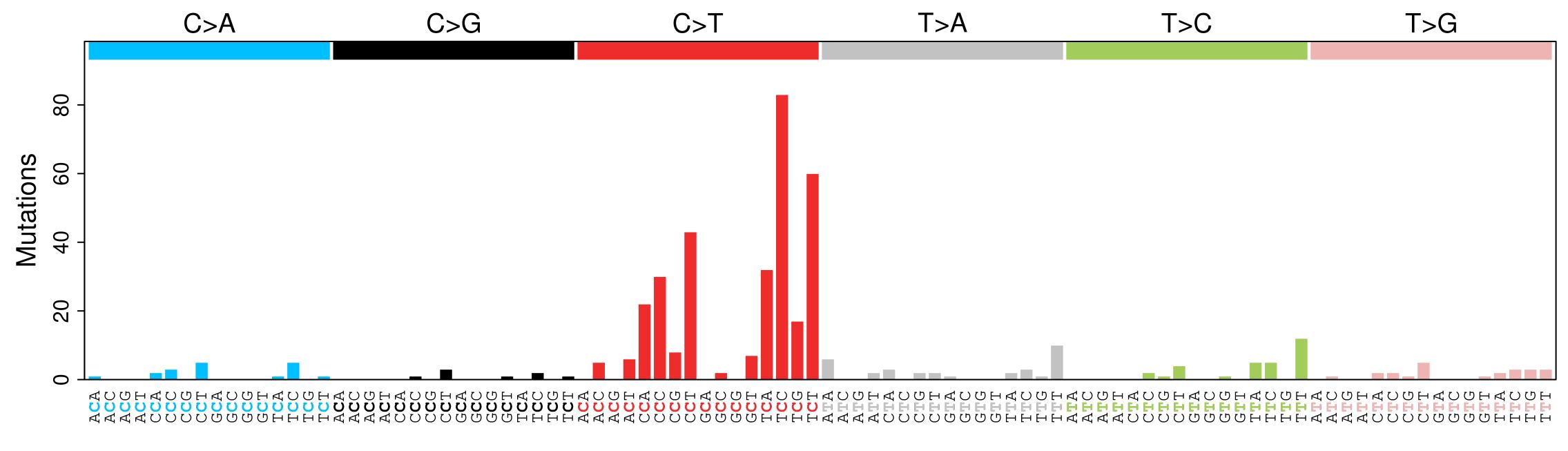
CATD274a (286 mutations)



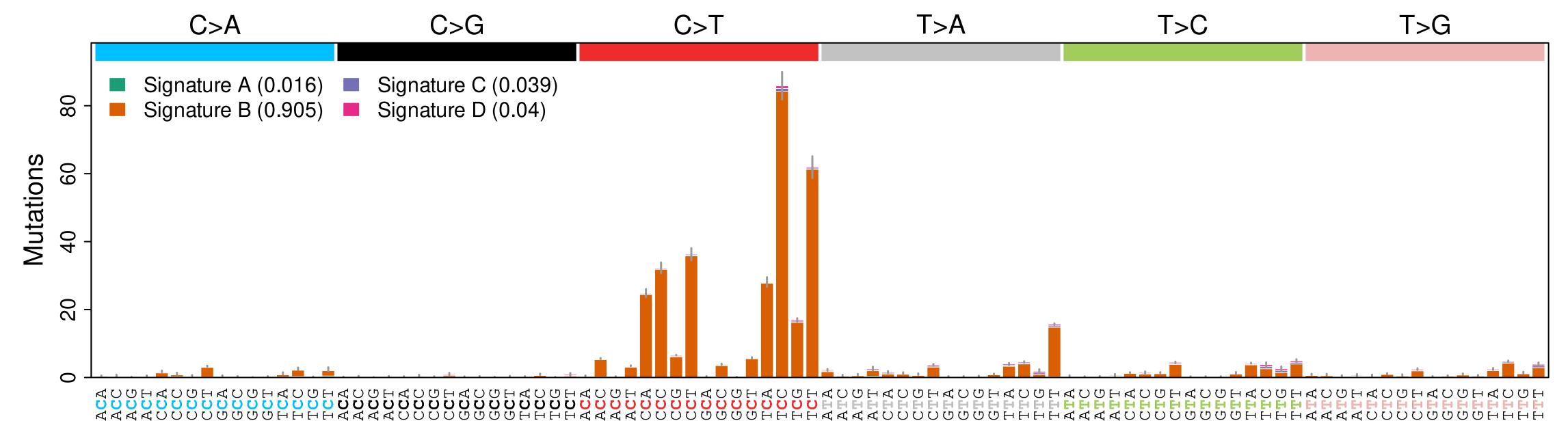




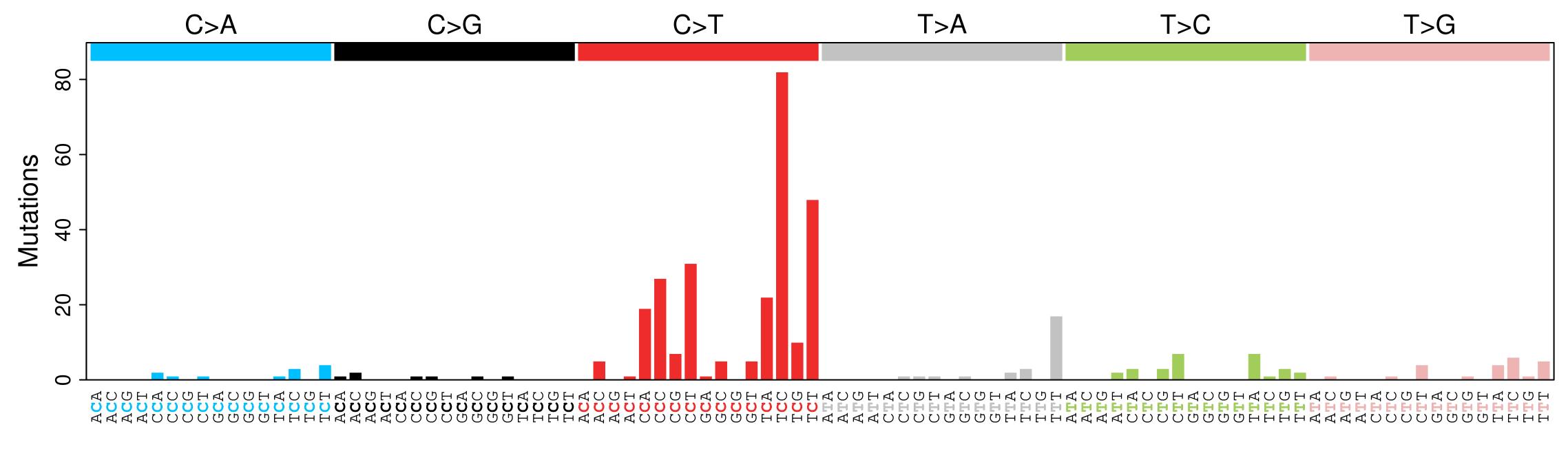
CATD278a (426 mutations)



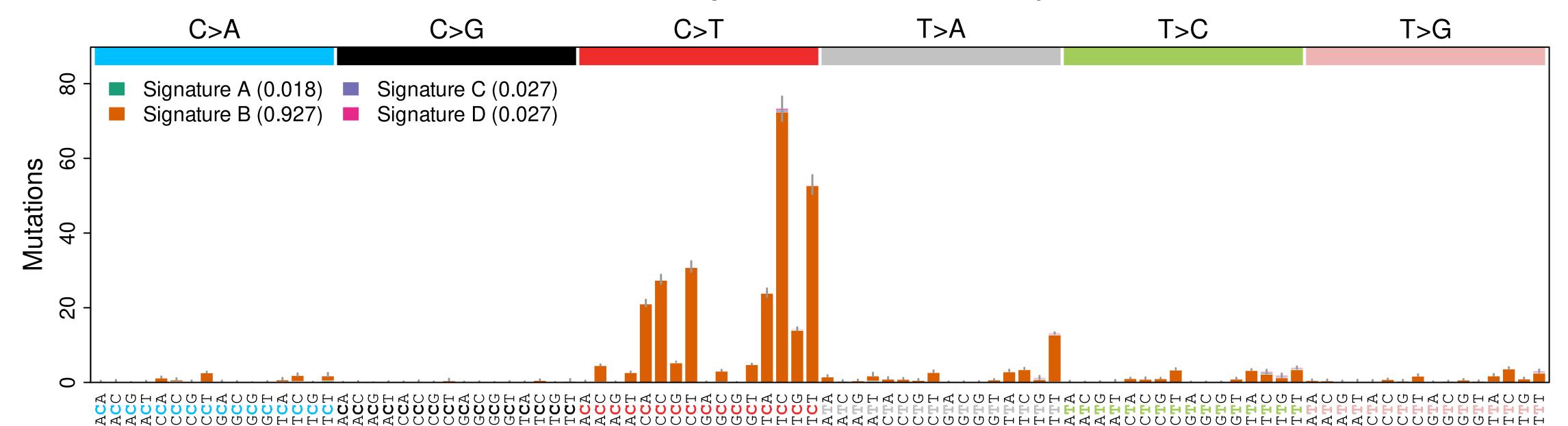
Reconstructed spectrum (cosine similarity = 0.991)



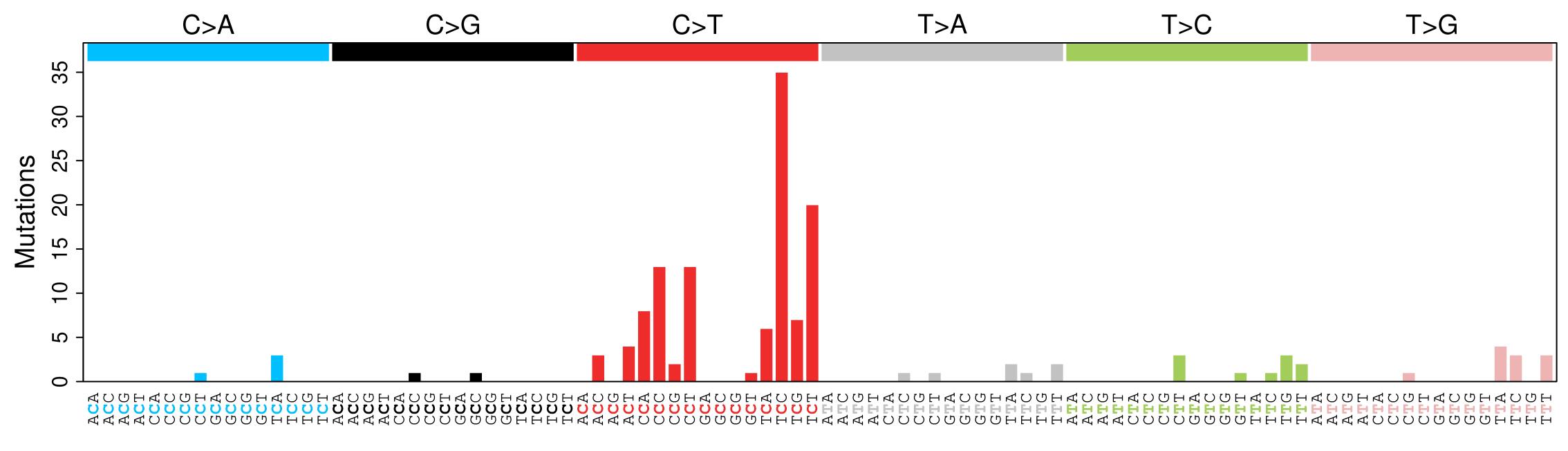
CATD243a (359 mutations)

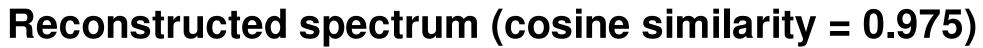


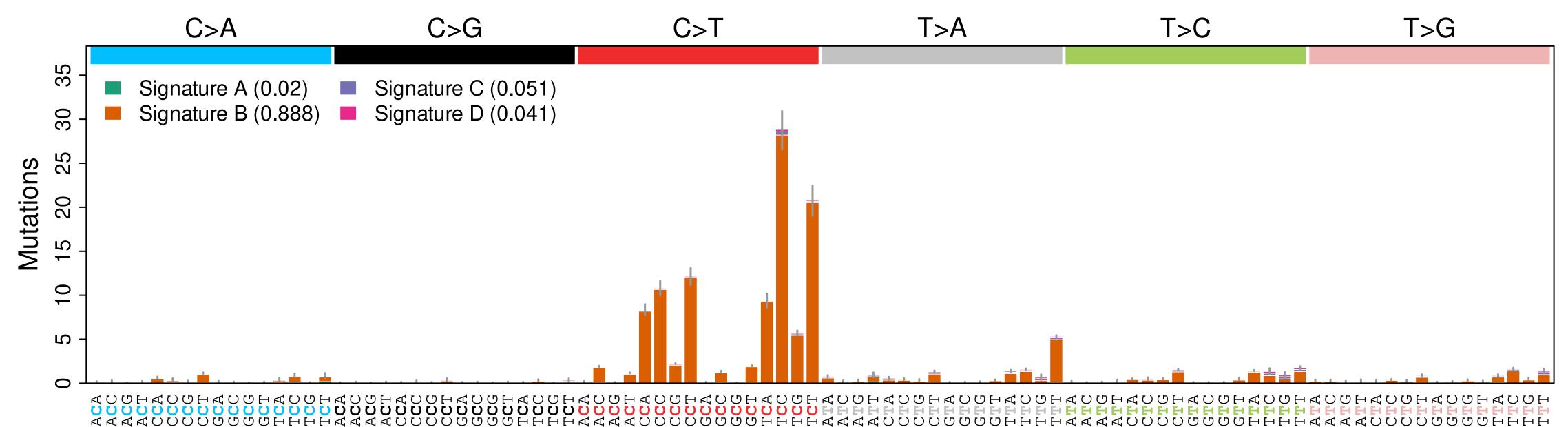
Reconstructed spectrum (cosine similarity = 0.99)



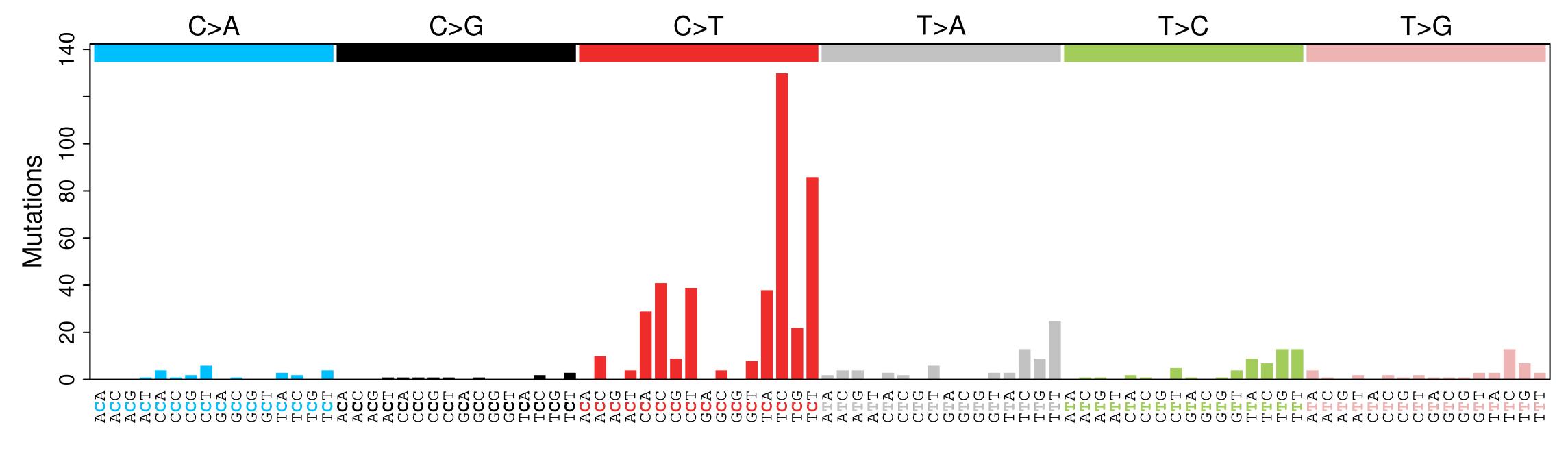
CATD265a (146 mutations)

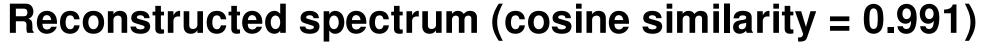


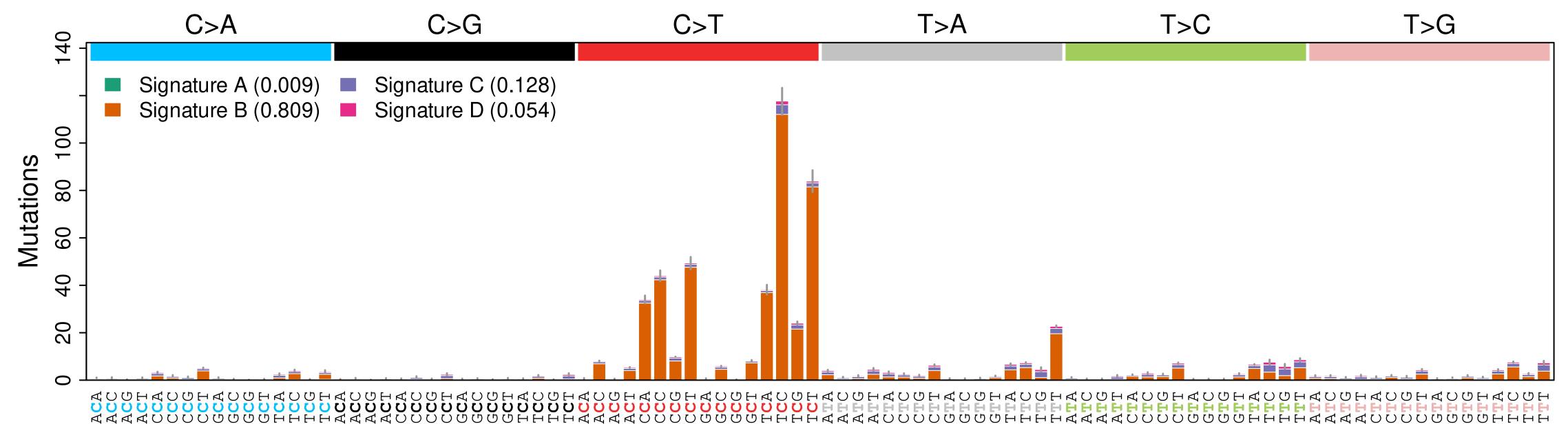




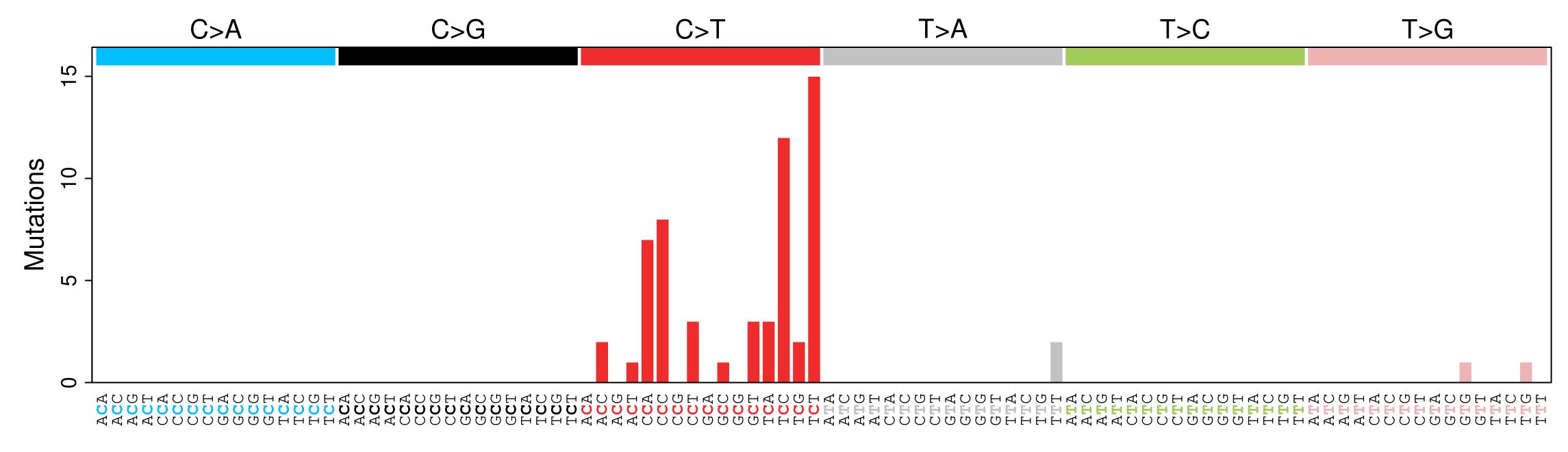
CATD264a (631 mutations)



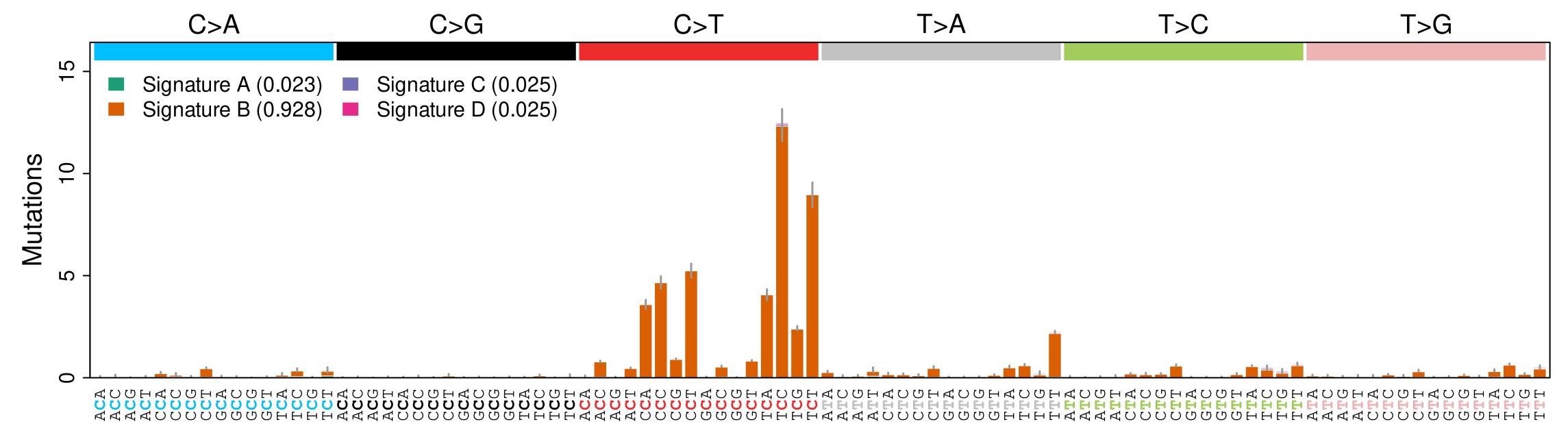




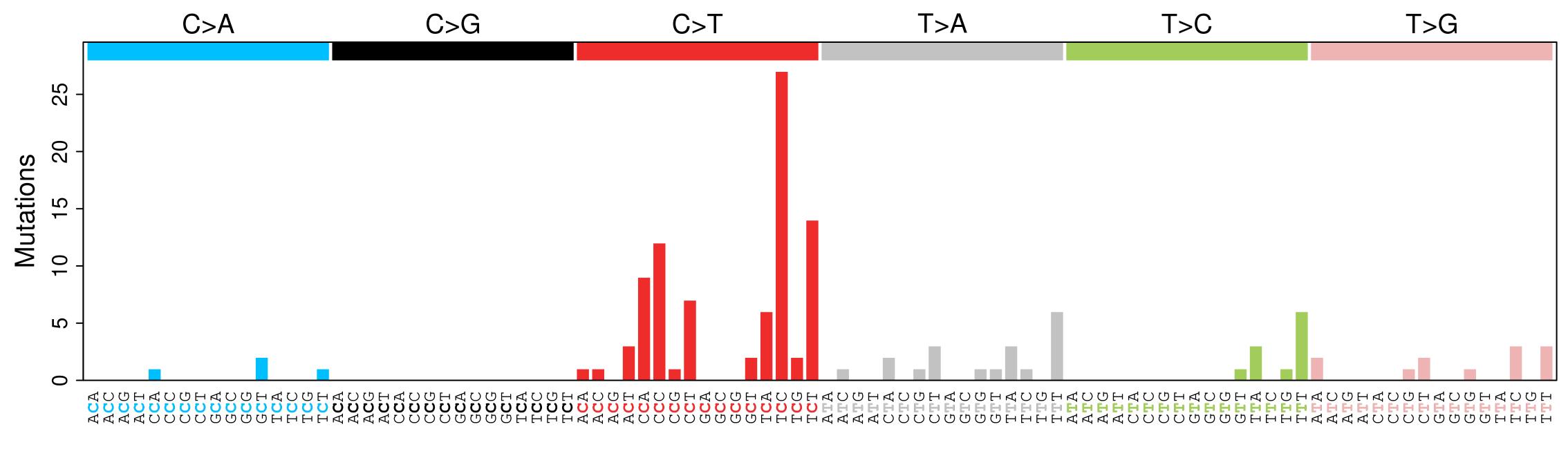
CATD0135a (61 mutations)



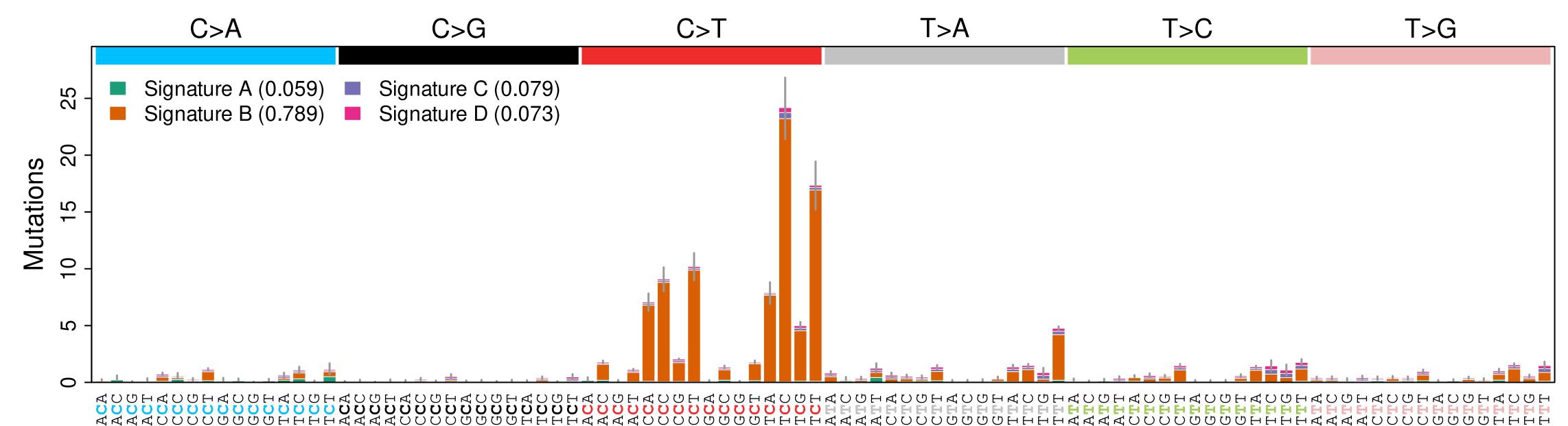
Reconstructed spectrum (cosine similarity = 0.932)



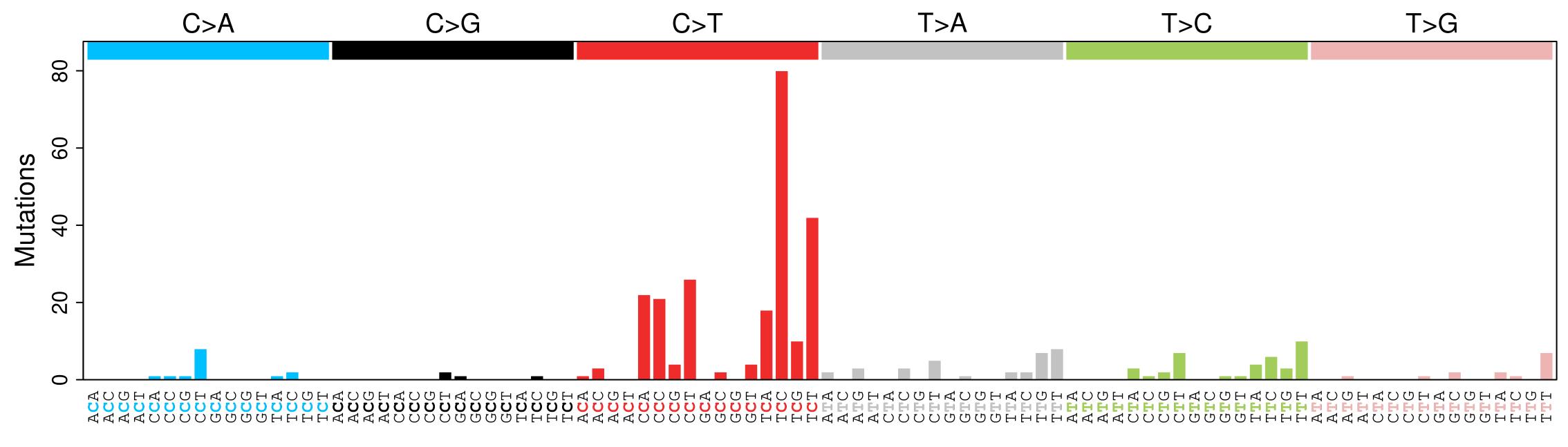
CATD282a (131 mutations)



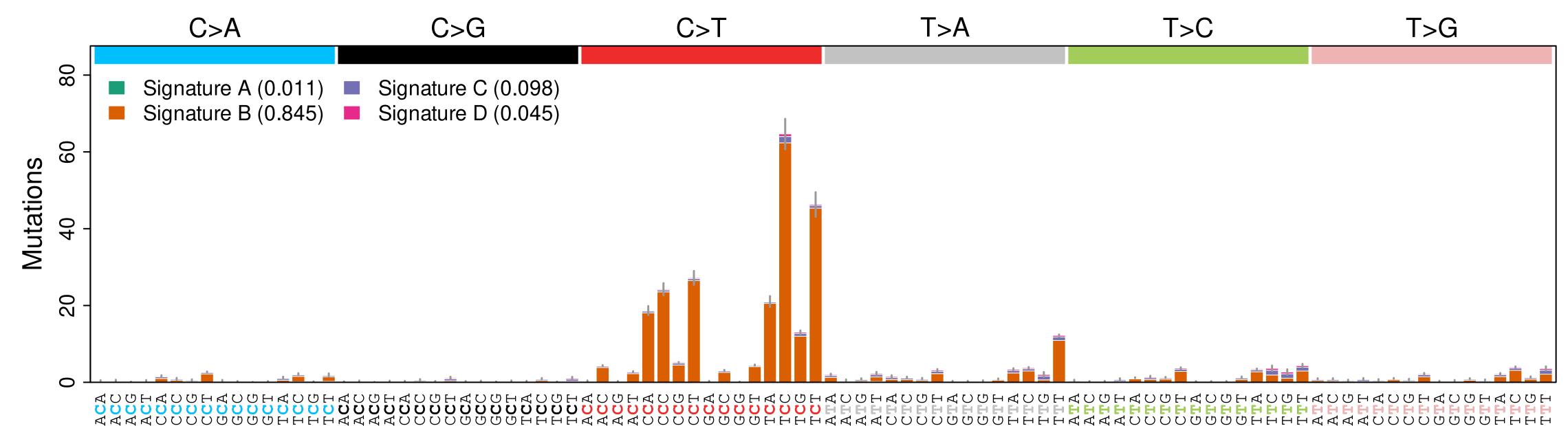
Reconstructed spectrum (cosine similarity = 0.956)



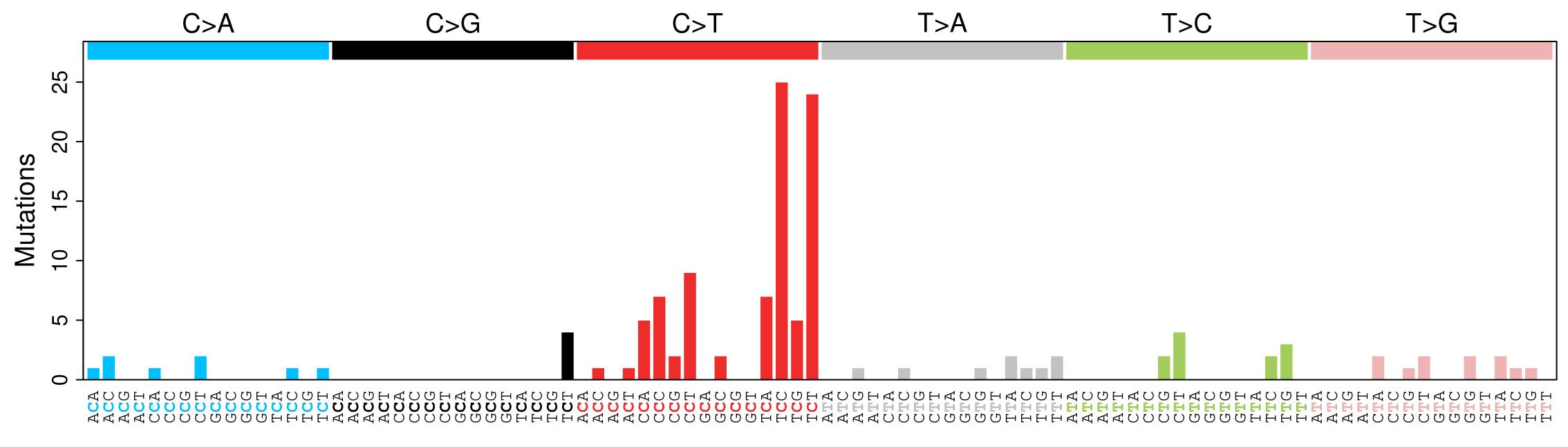
CATD250a (336 mutations)



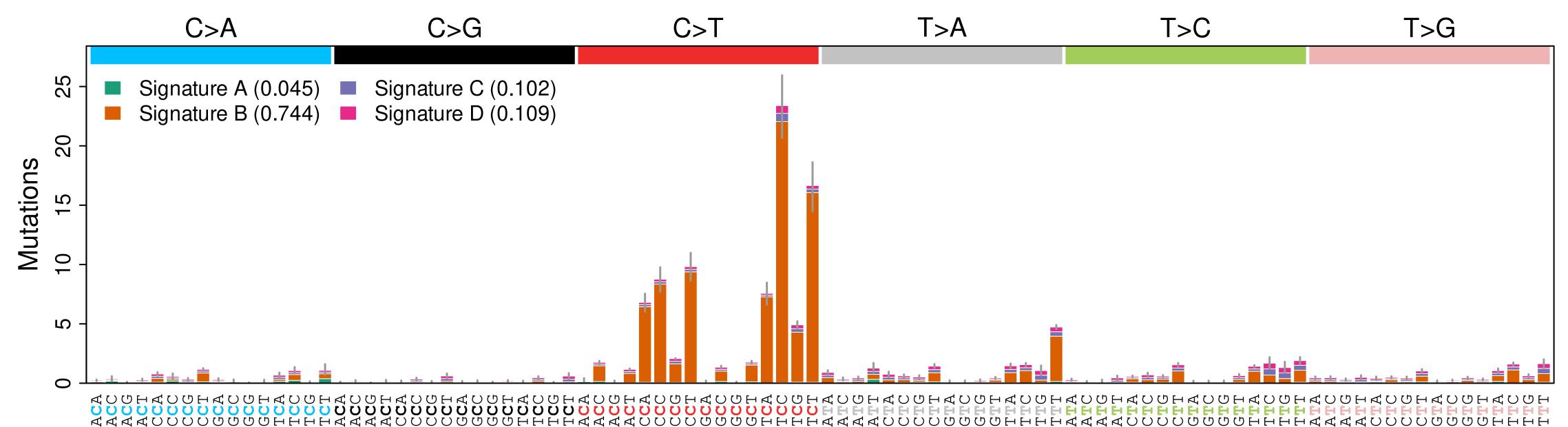
Reconstructed spectrum (cosine similarity = 0.978)



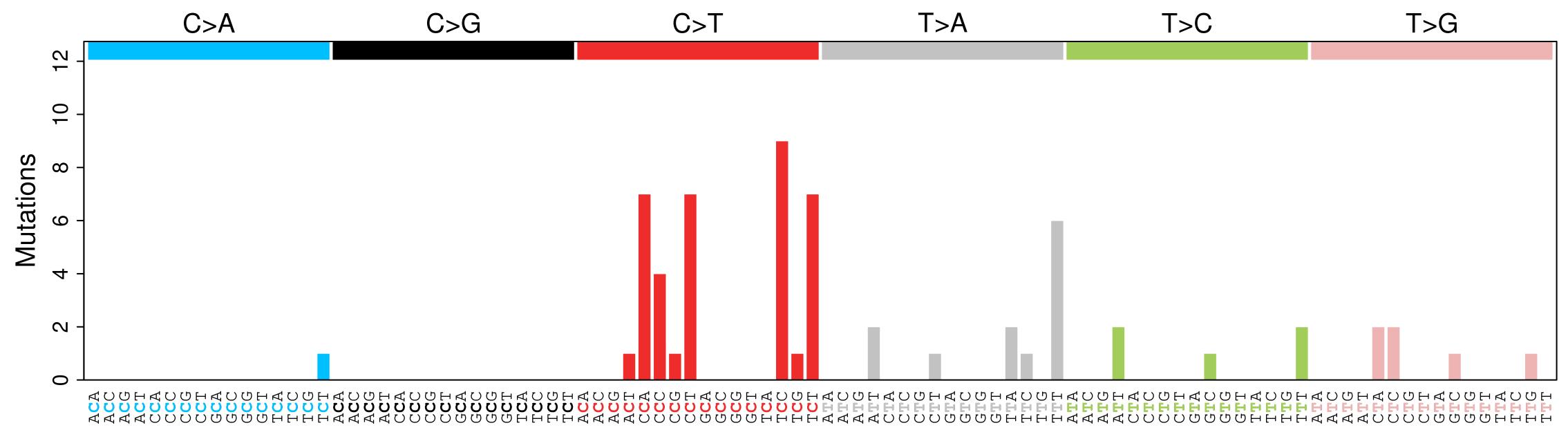
CATD263a (131 mutations)



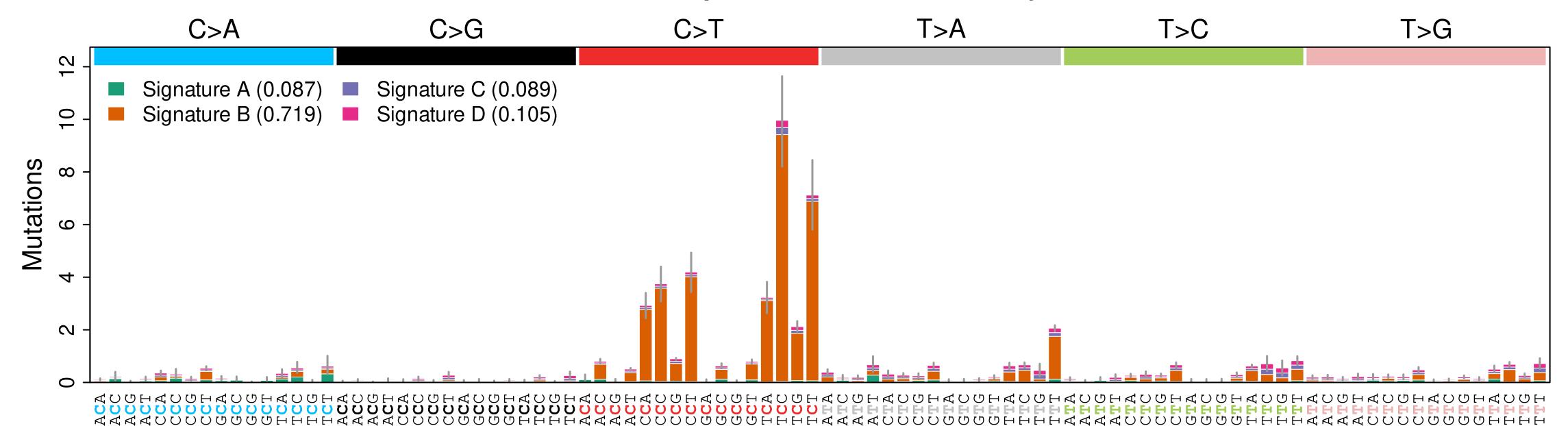
Reconstructed spectrum (cosine similarity = 0.959)



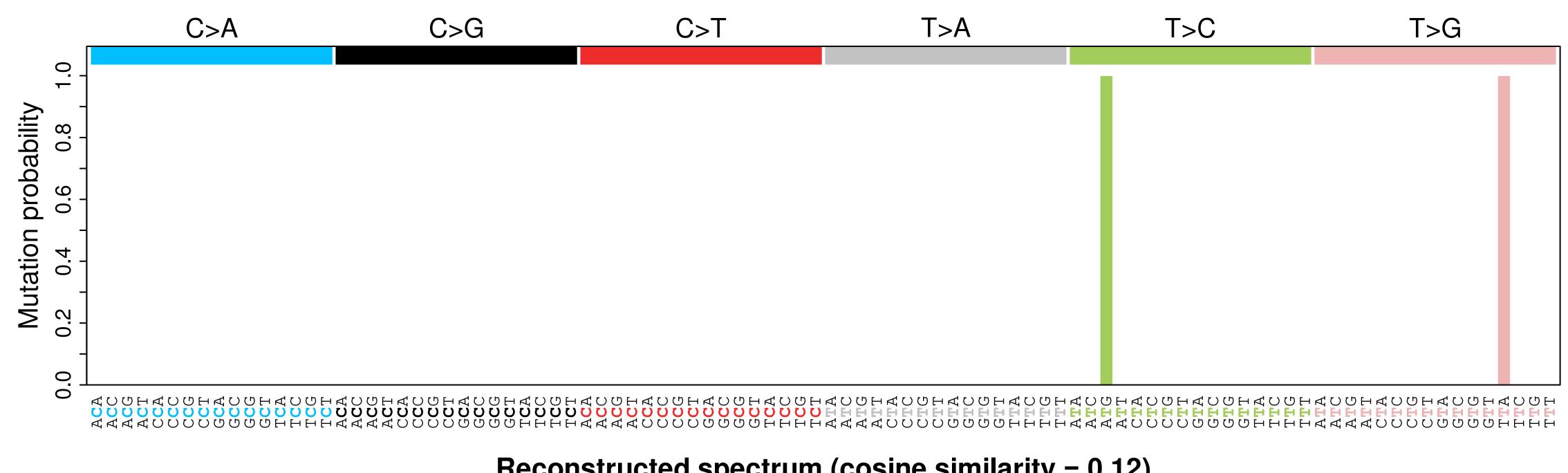
CATD254a (61 mutations)

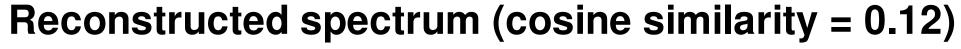


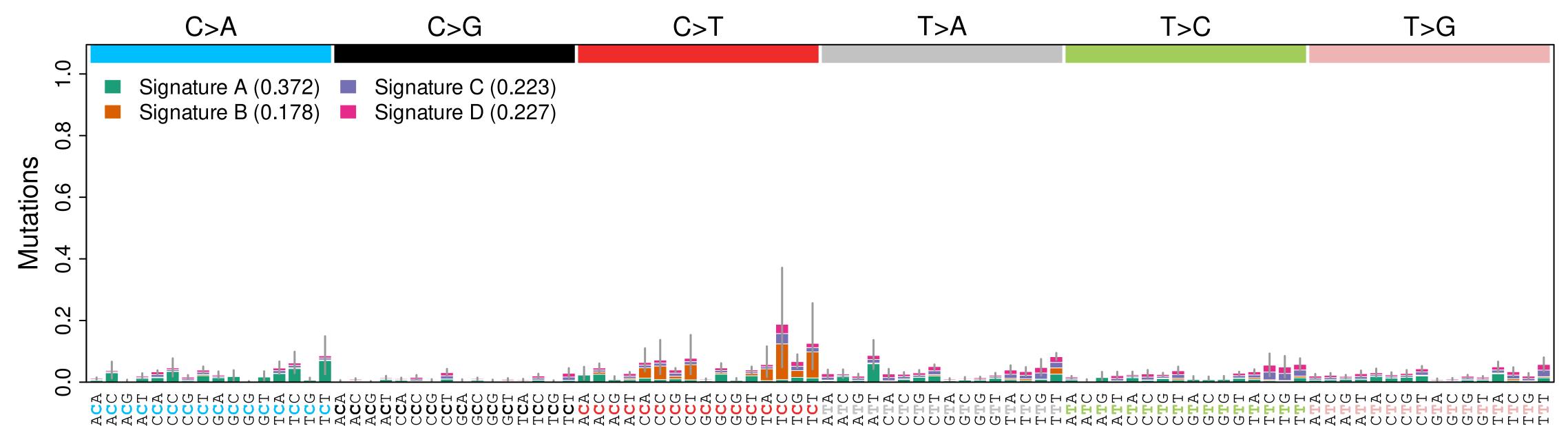




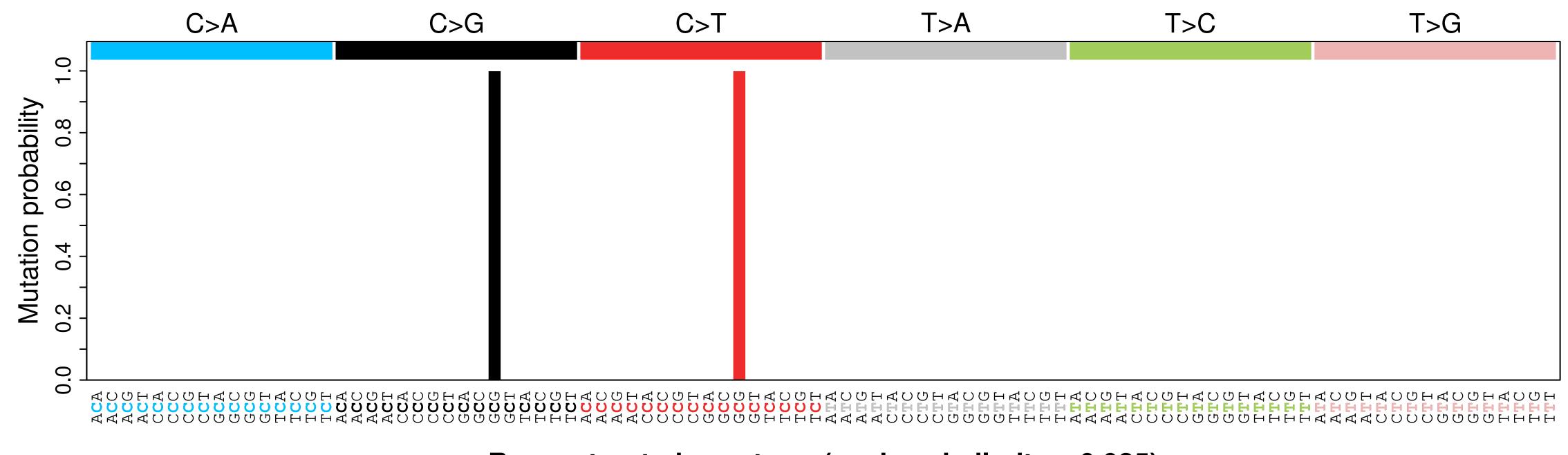
CATD0124a

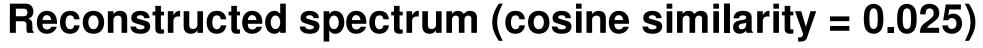


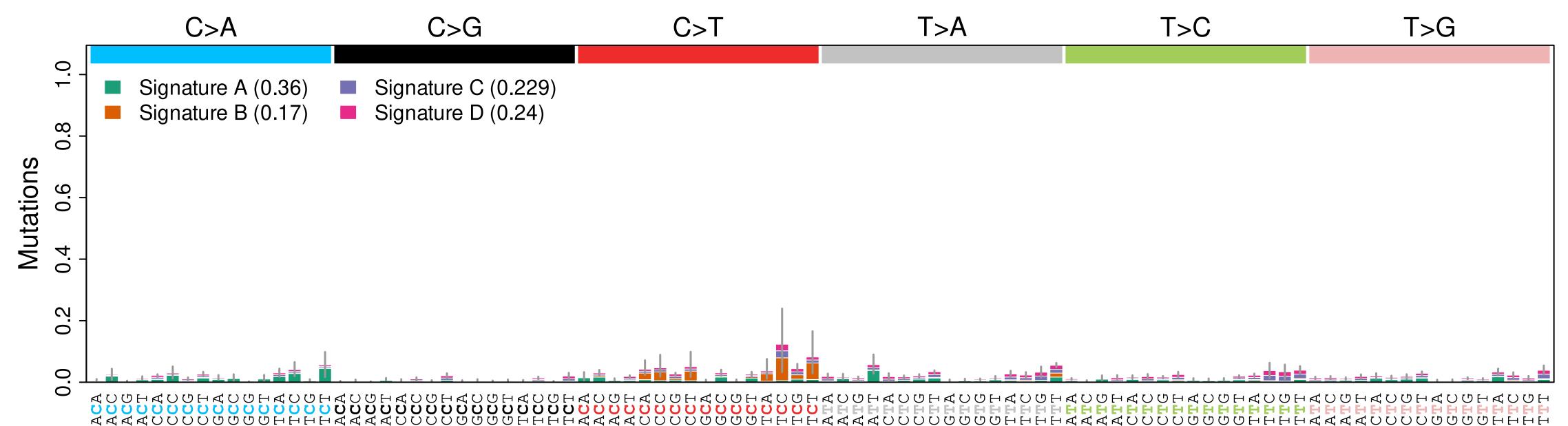




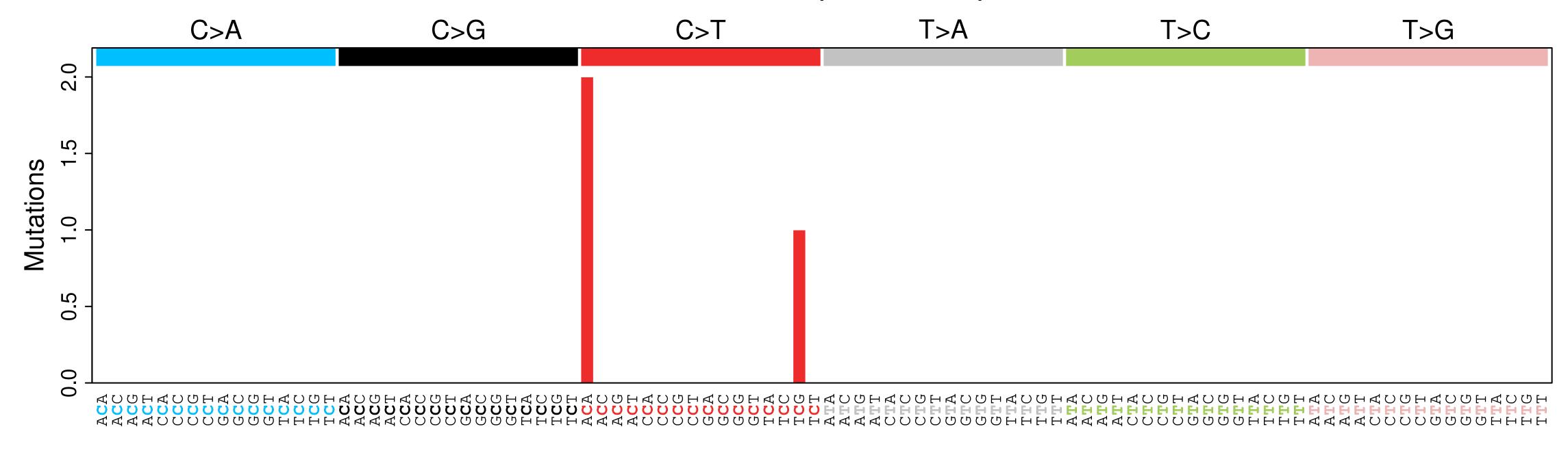
CATD0129a



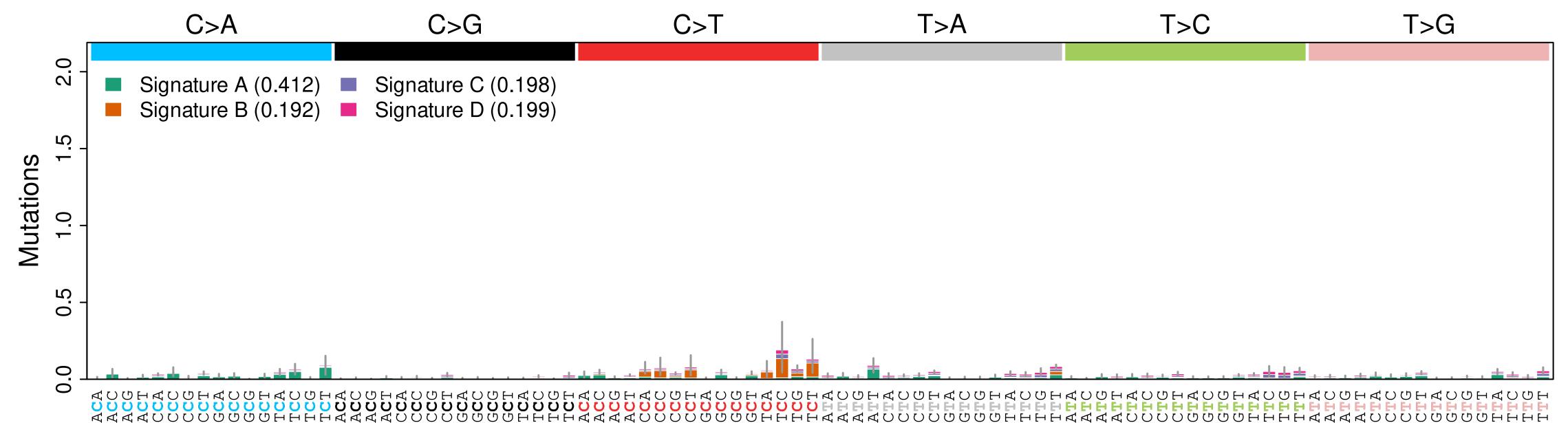




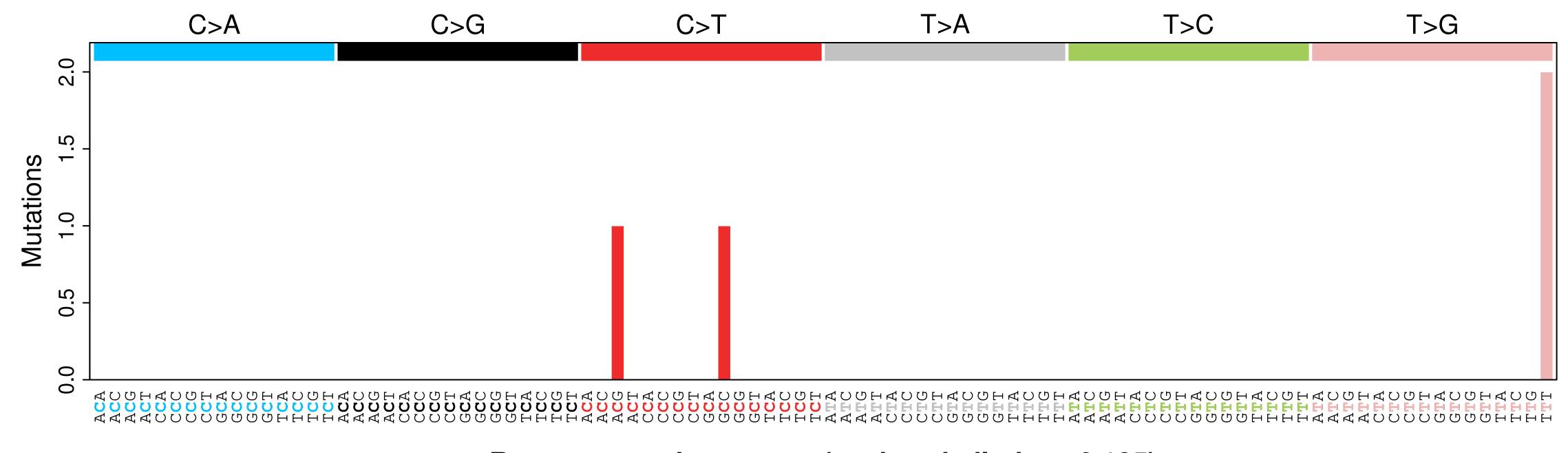
CATD0130a (3 mutations)



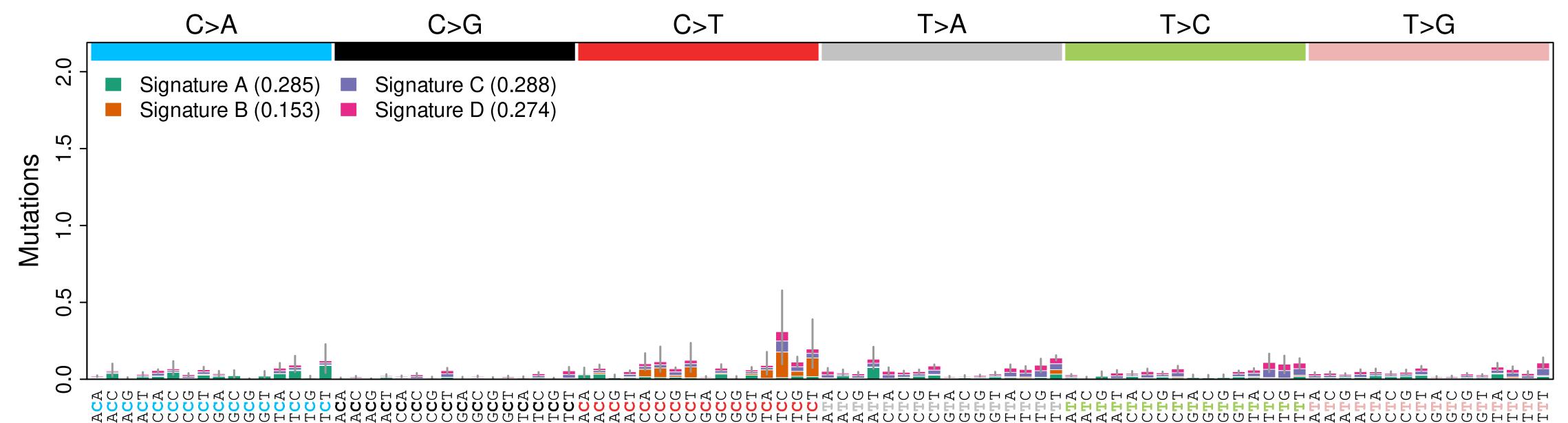
Reconstructed spectrum (cosine similarity = 0.138)



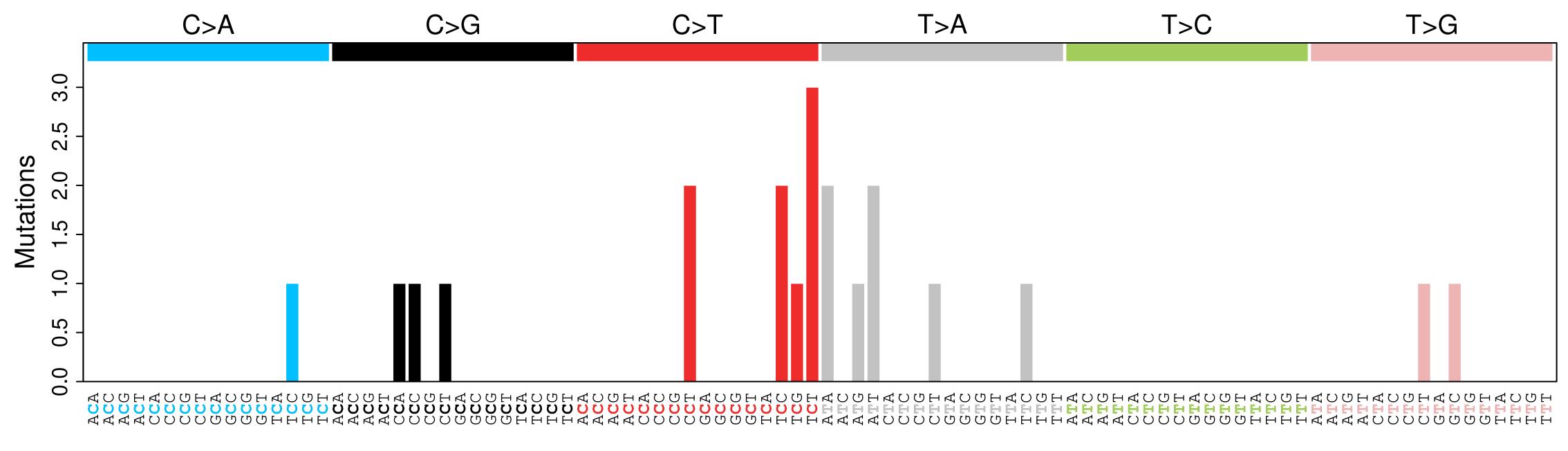
CATD0140a (4 mutations)



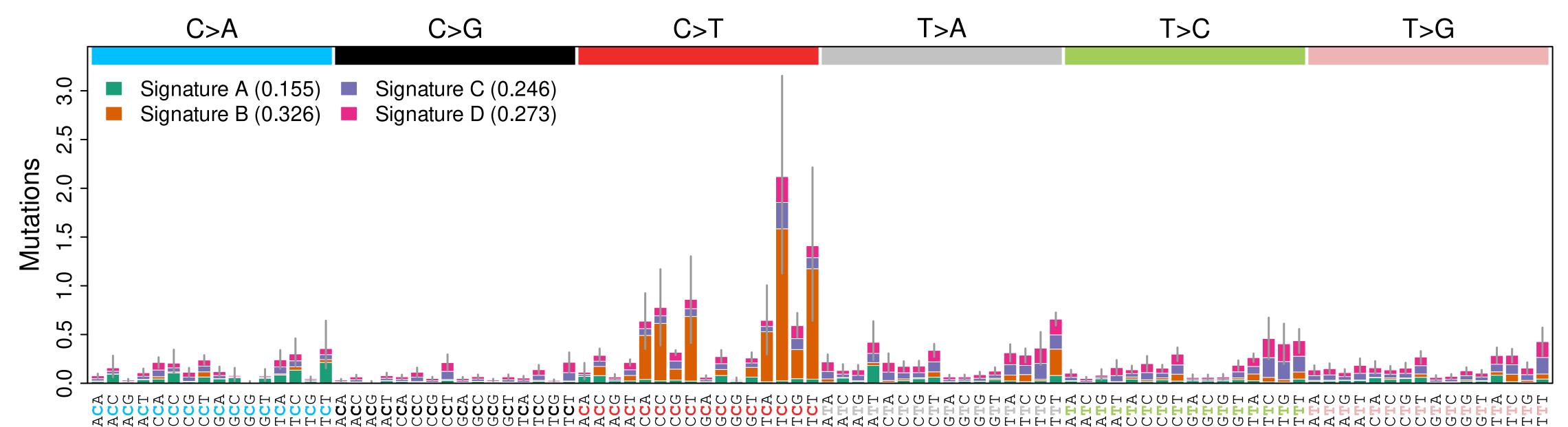
Reconstructed spectrum (cosine similarity = 0.185)



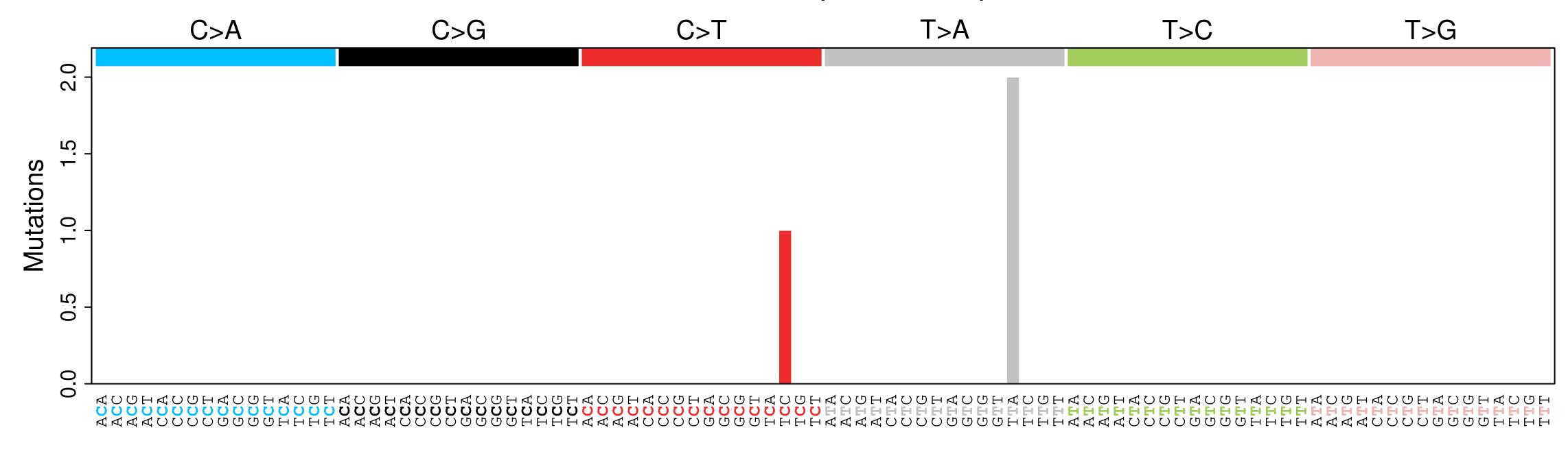
CATD0131a (21 mutations)

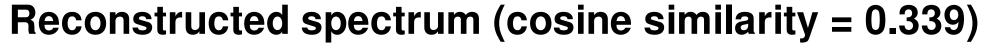


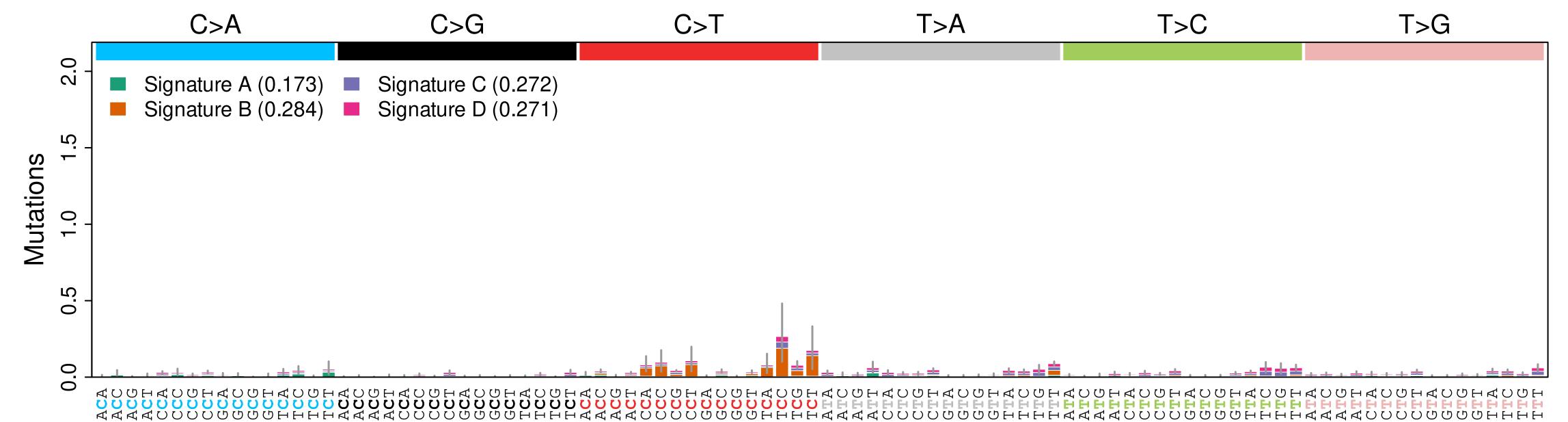
Reconstructed spectrum (cosine similarity = 0.654)



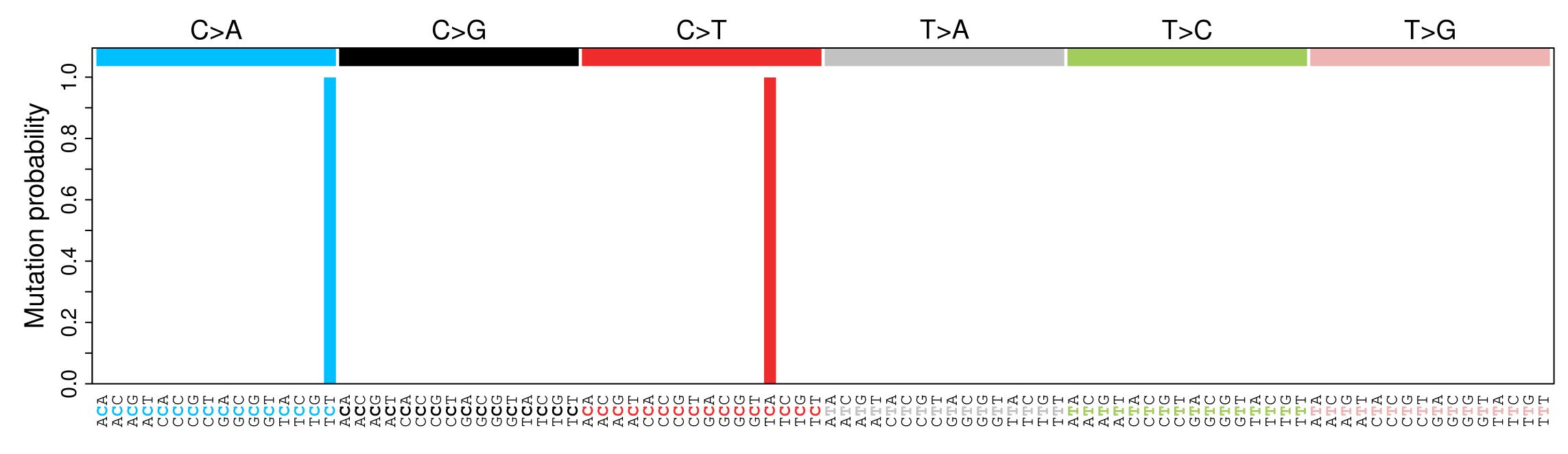
CATD0125a (3 mutations)

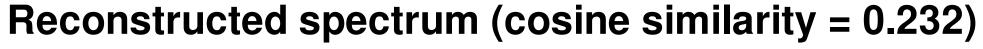


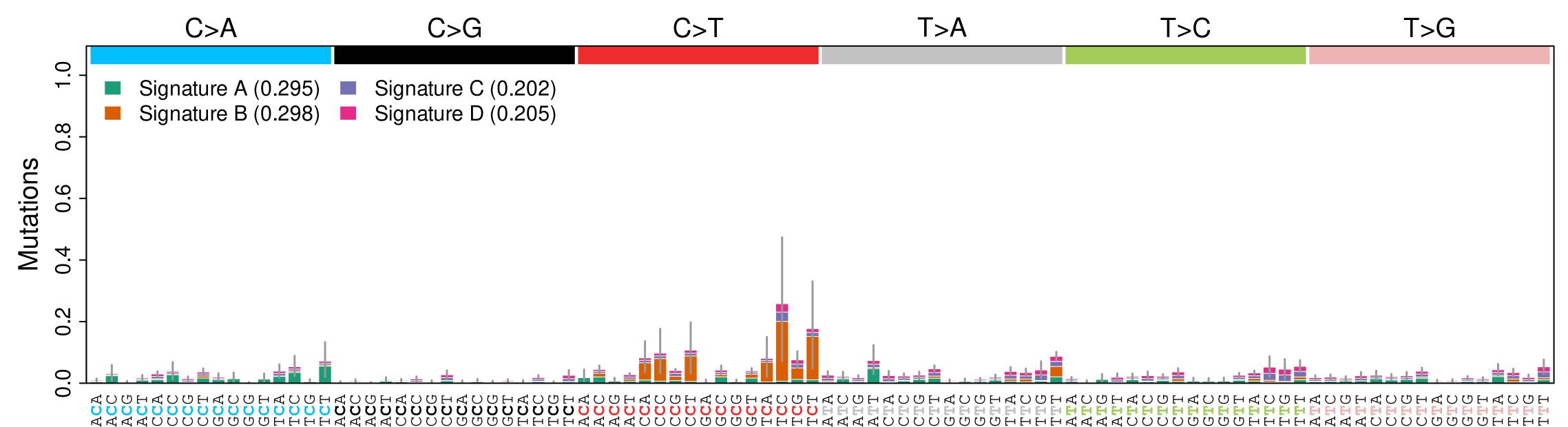




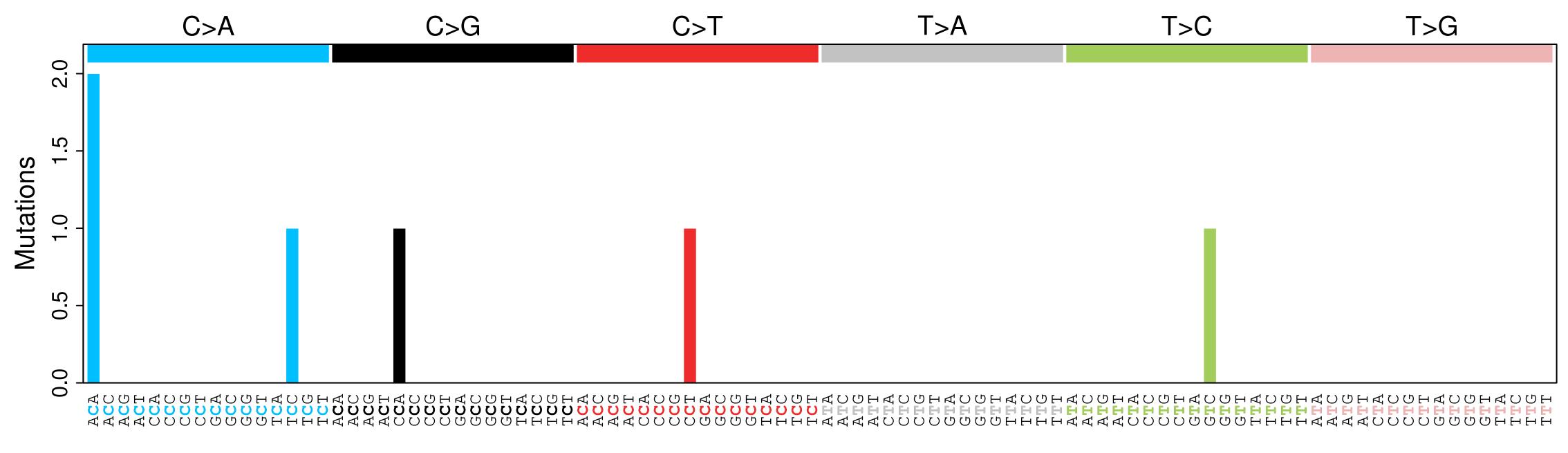
CATD0134a



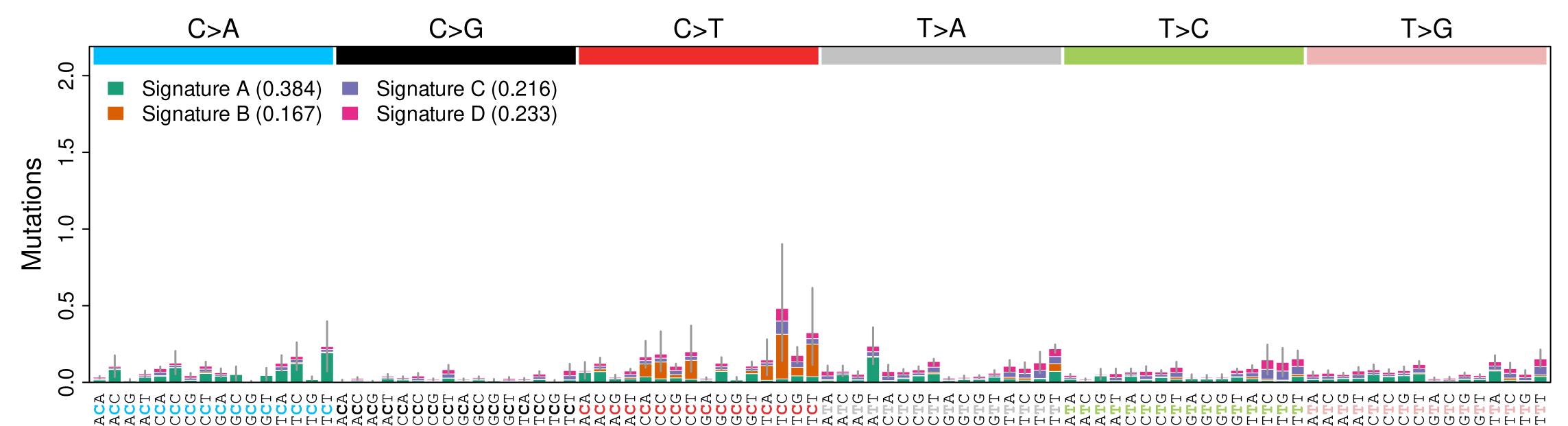




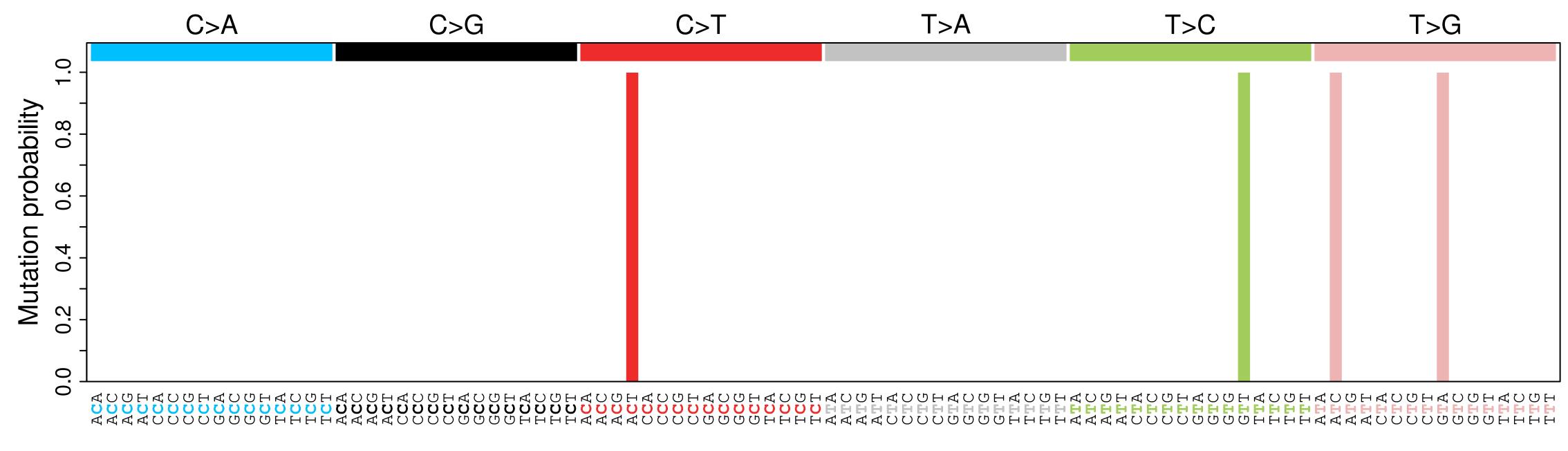
CATD258a (6 mutations)

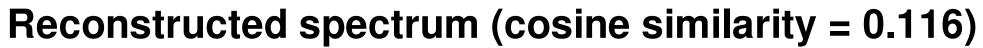


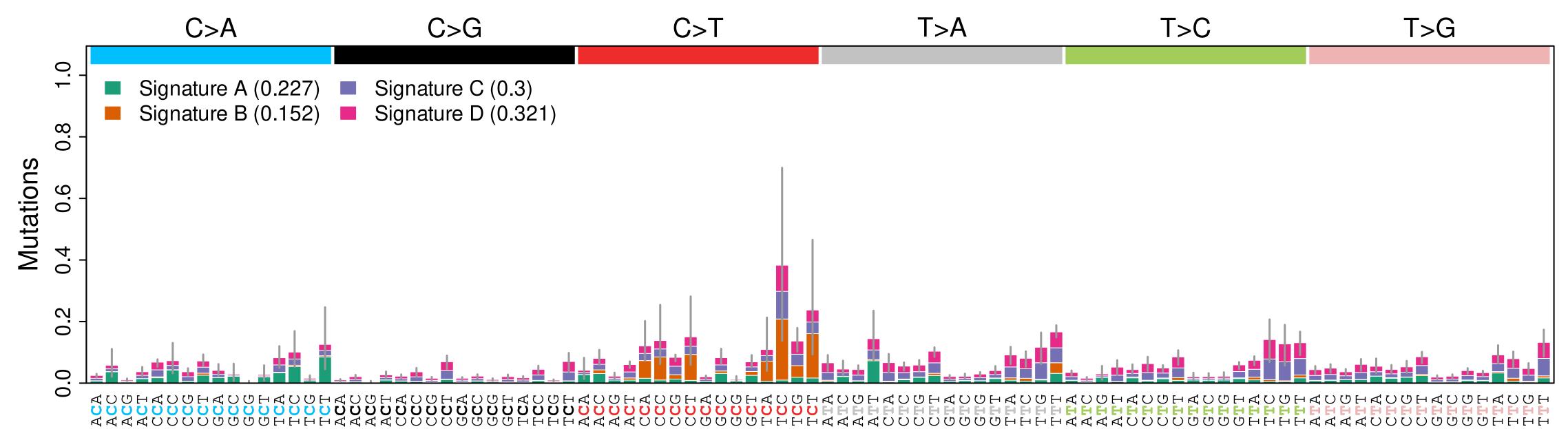




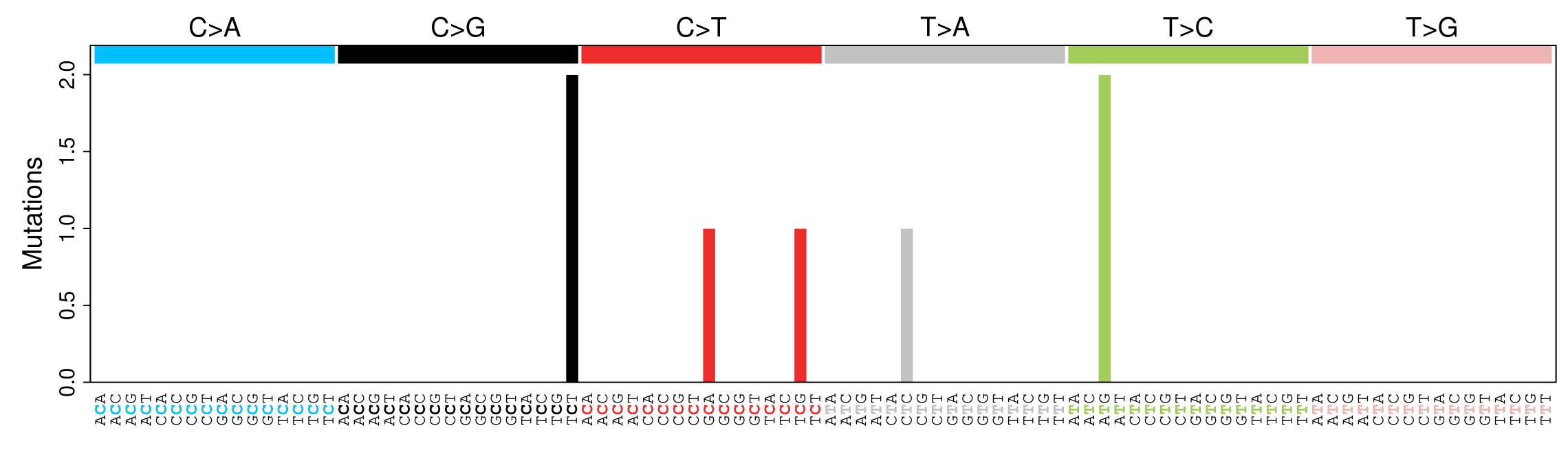
CATD257a



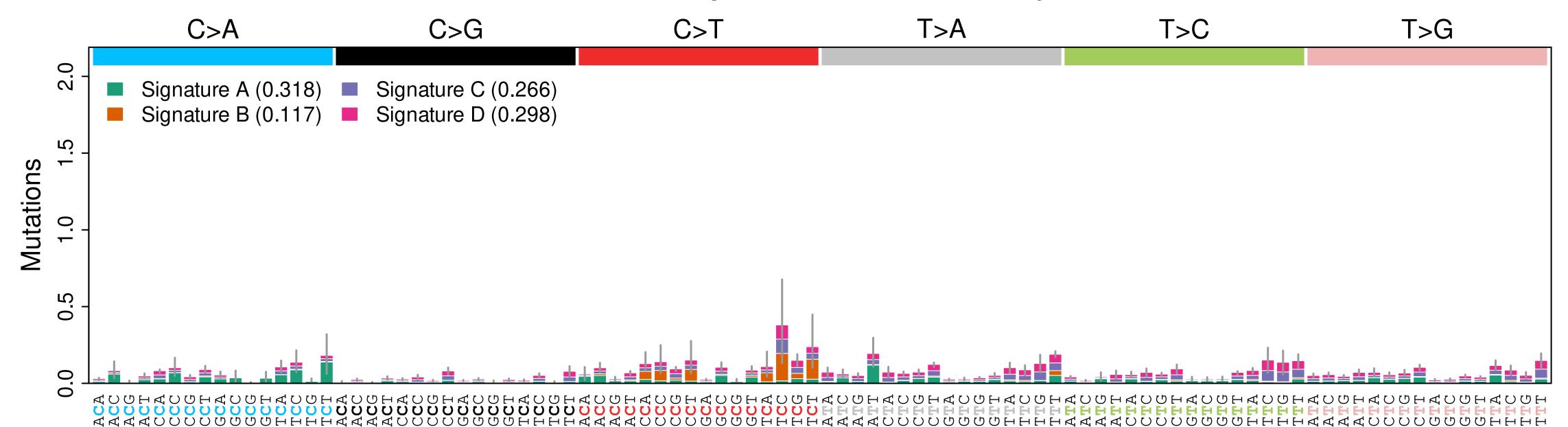




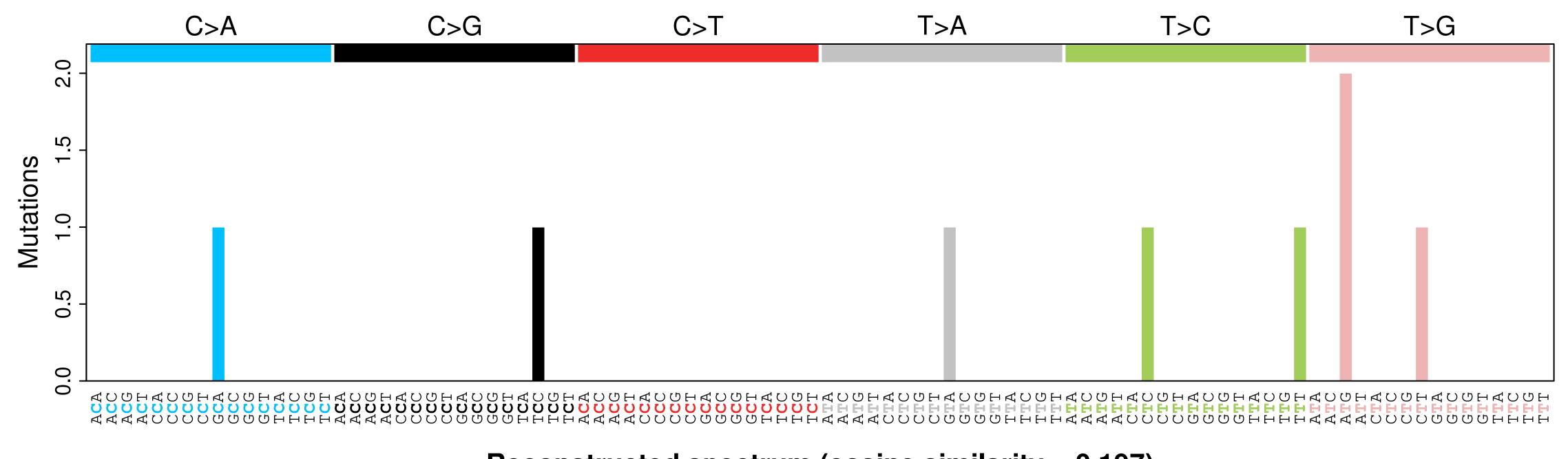
CATD0139a (7 mutations)

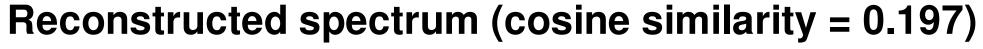


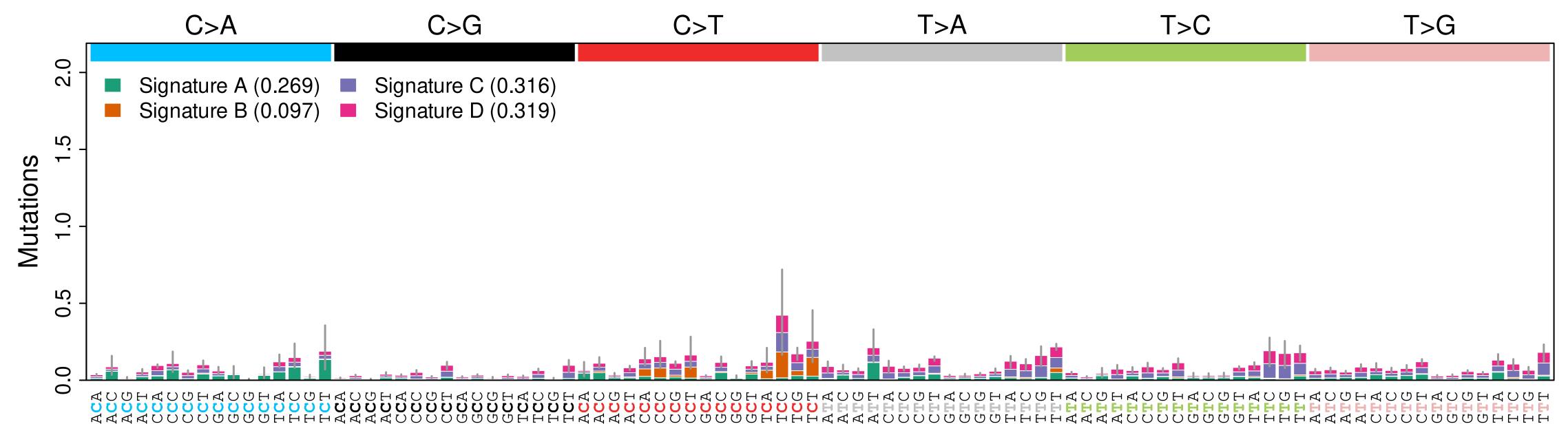
Reconstructed spectrum (cosine similarity = 0.16)



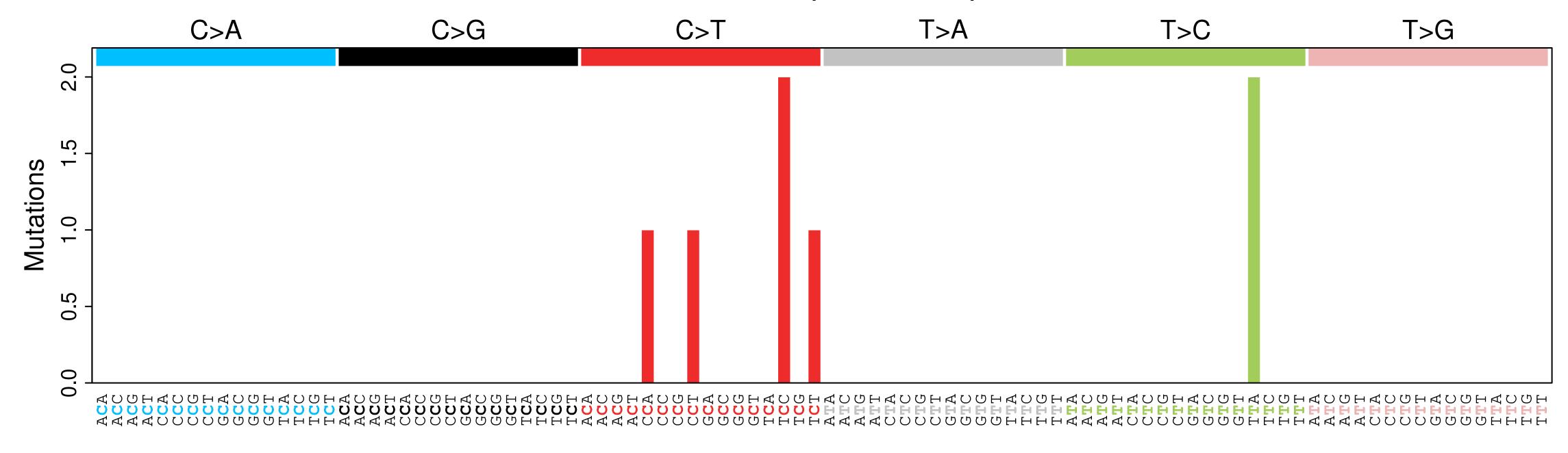
CATD0137a (8 mutations)



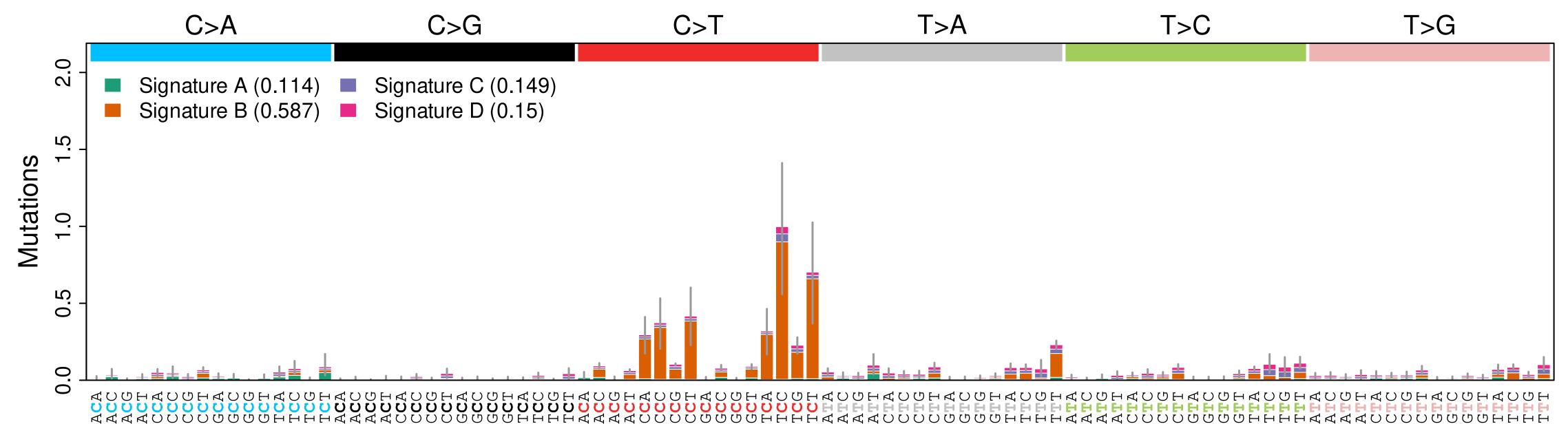




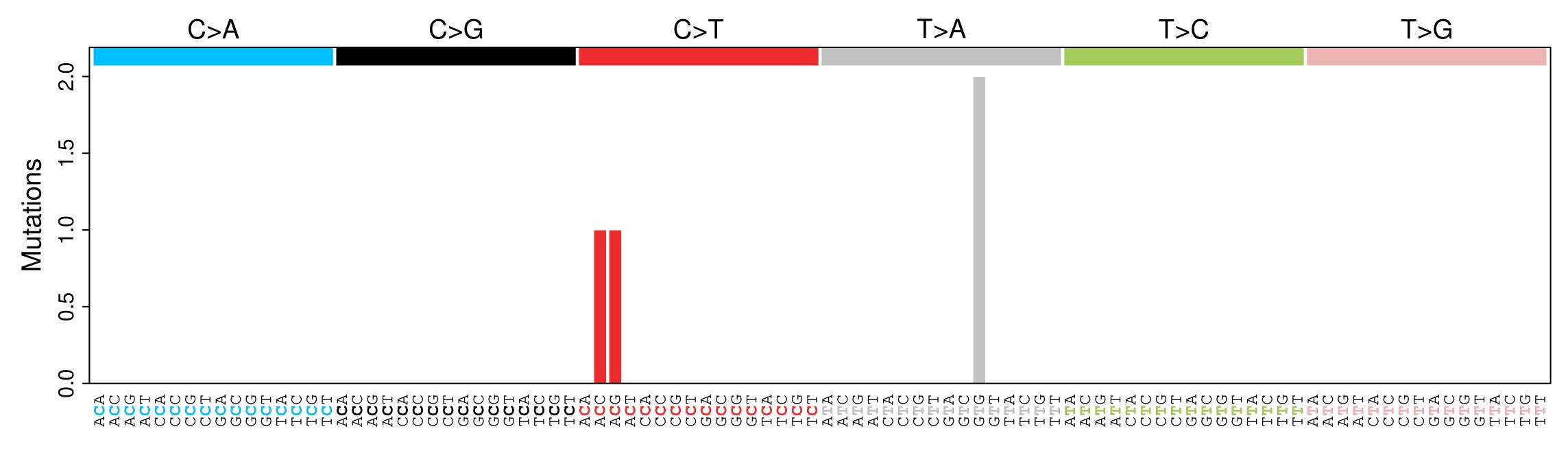
CATD249a (7 mutations)



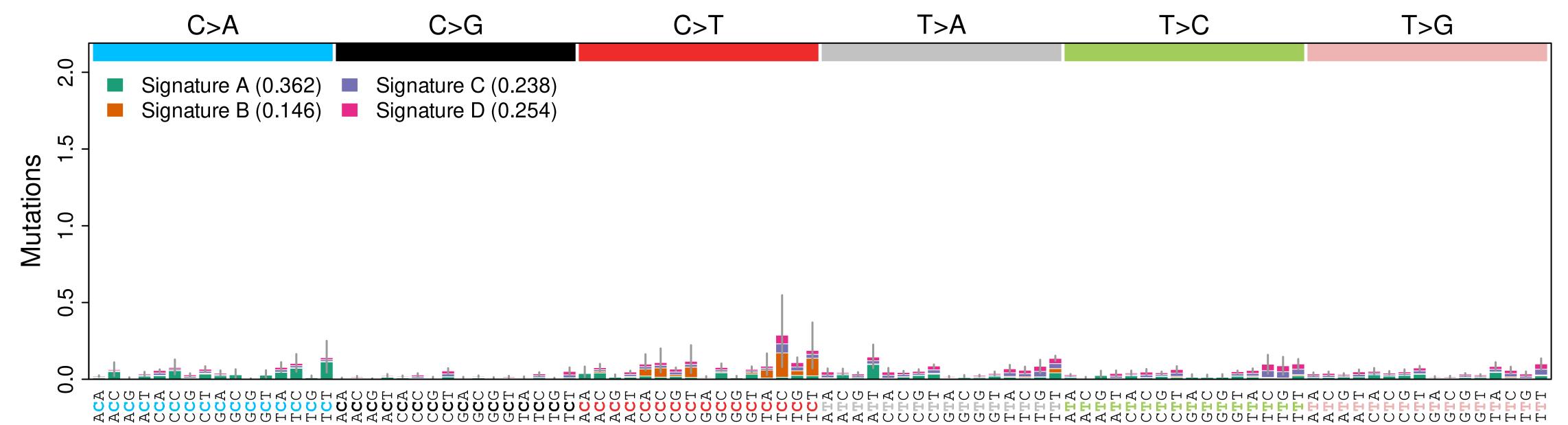
Reconstructed spectrum (cosine similarity = 0.707)



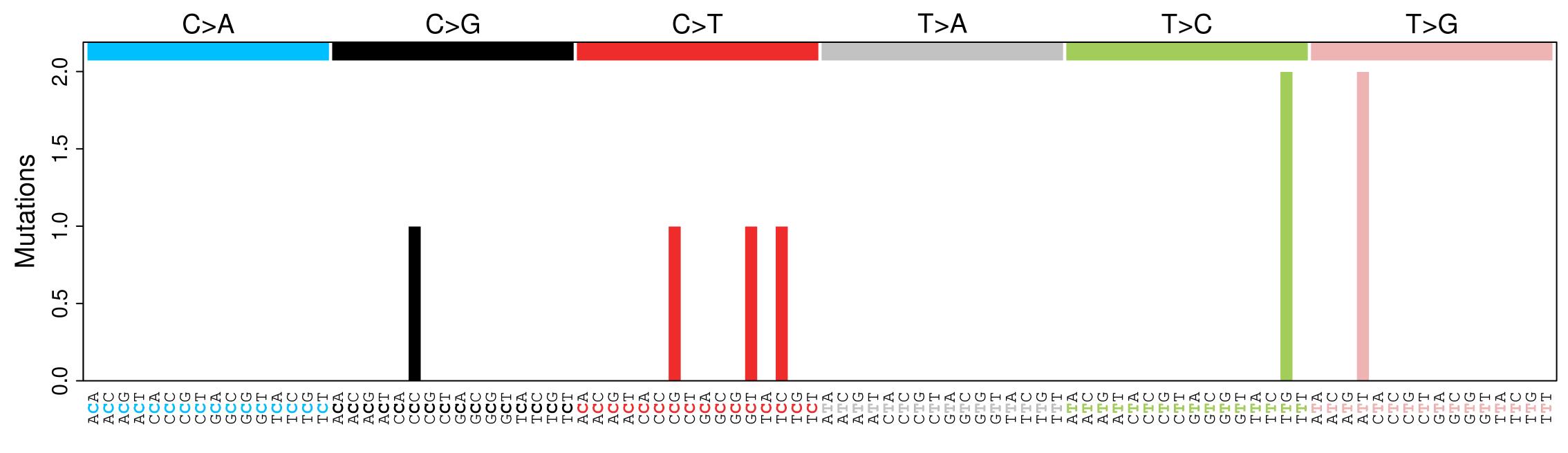
CATD271a (4 mutations)

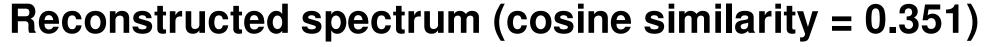


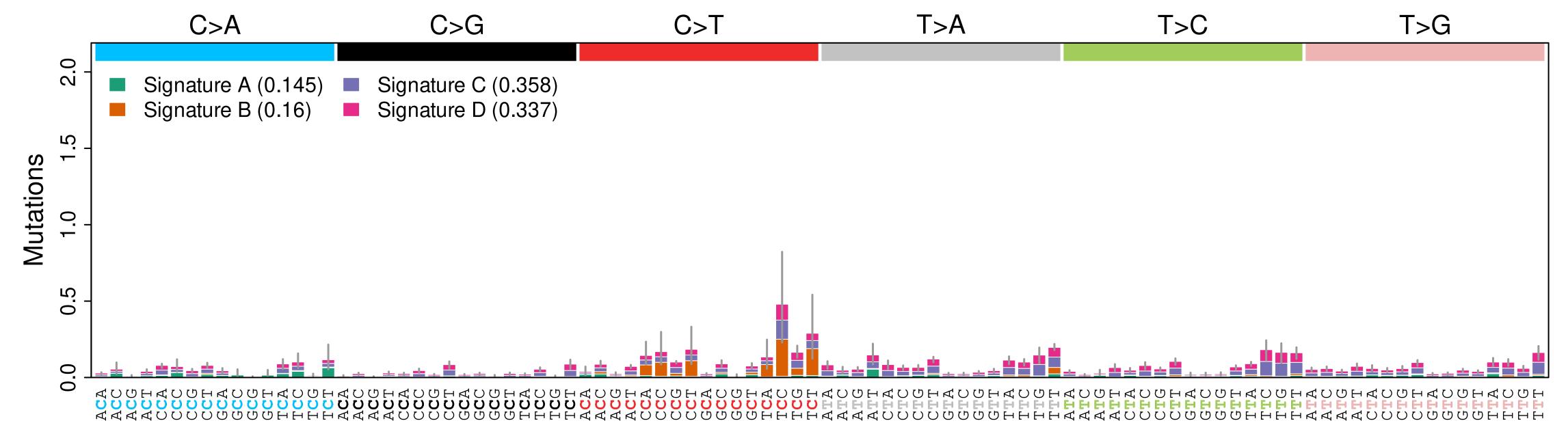
Reconstructed spectrum (cosine similarity = 0.091)



CATD259a (8 mutations)







CATD0127a (5 mutations)

