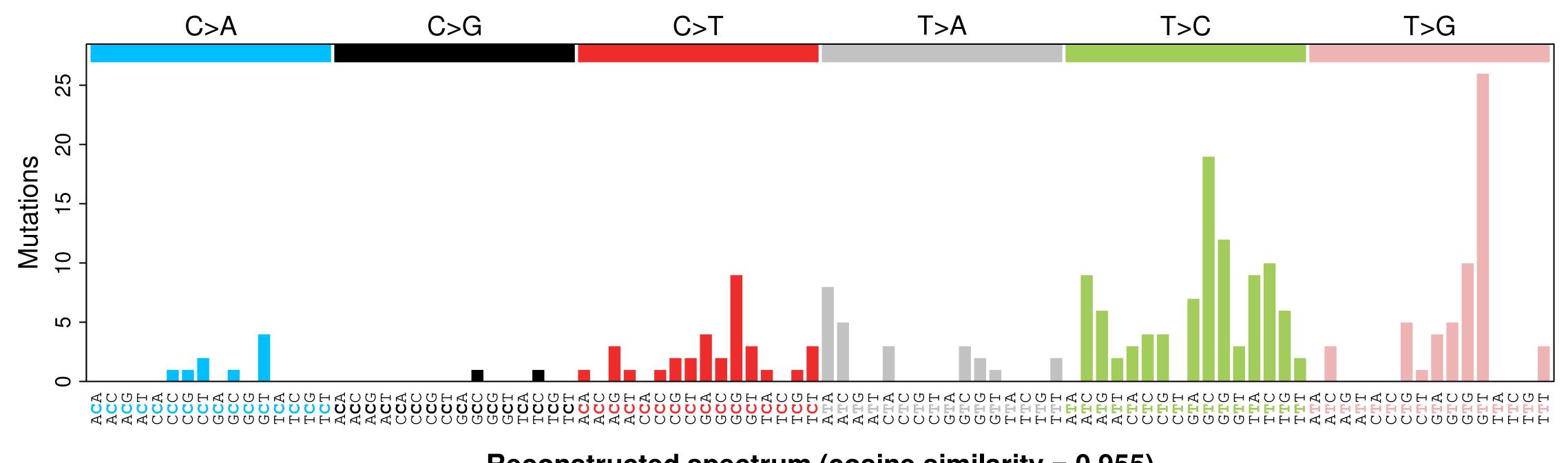
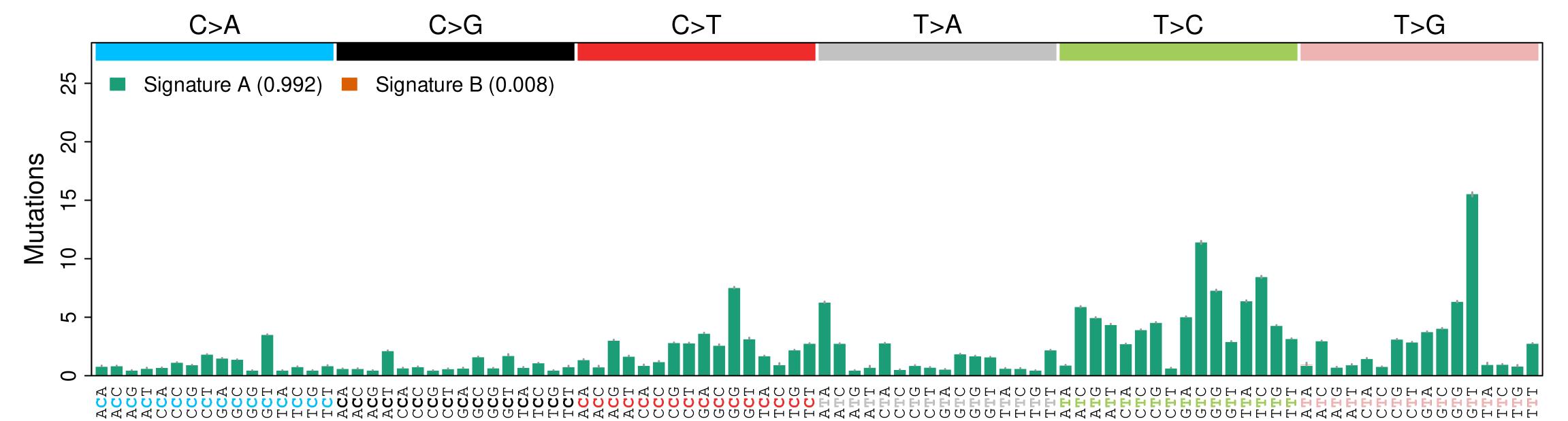
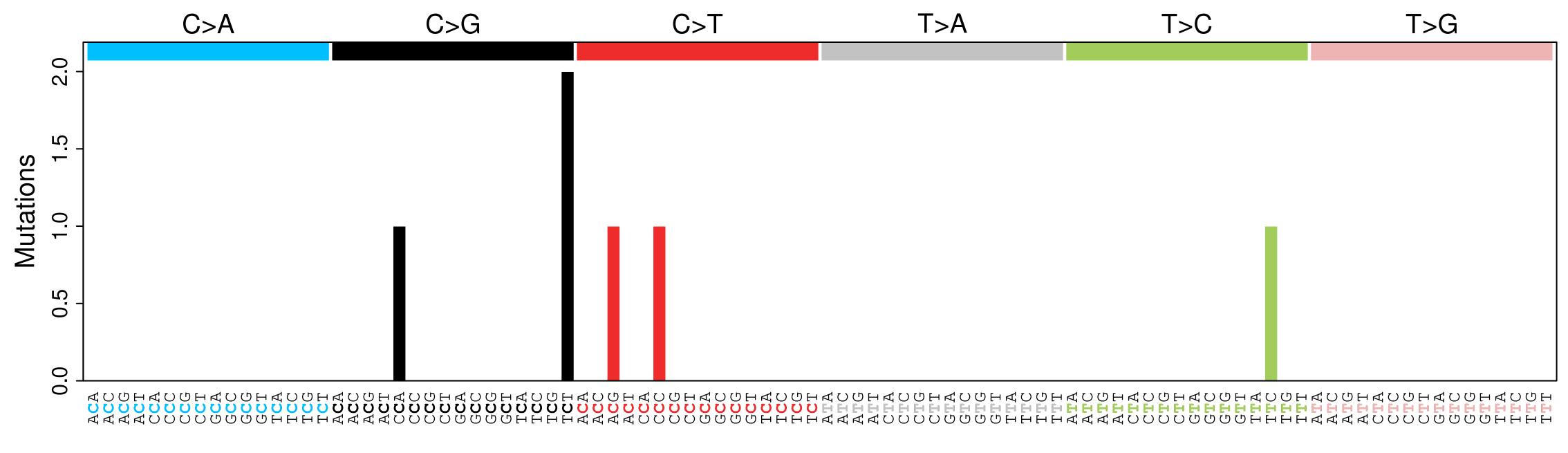
CATD0735a (221 mutations)



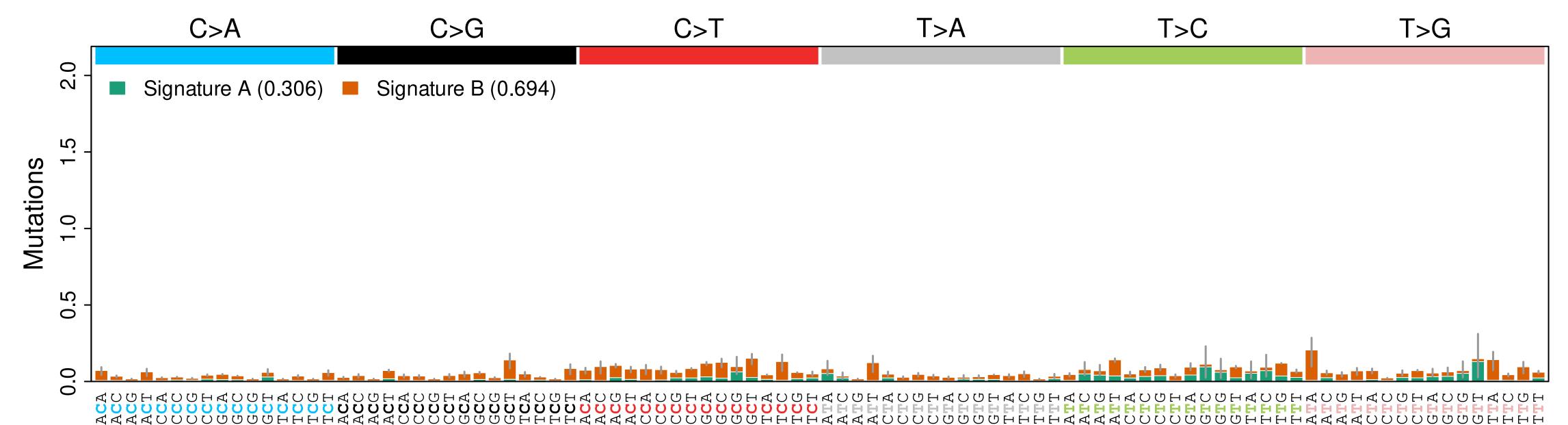
Reconstructed spectrum (cosine similarity = 0.955)



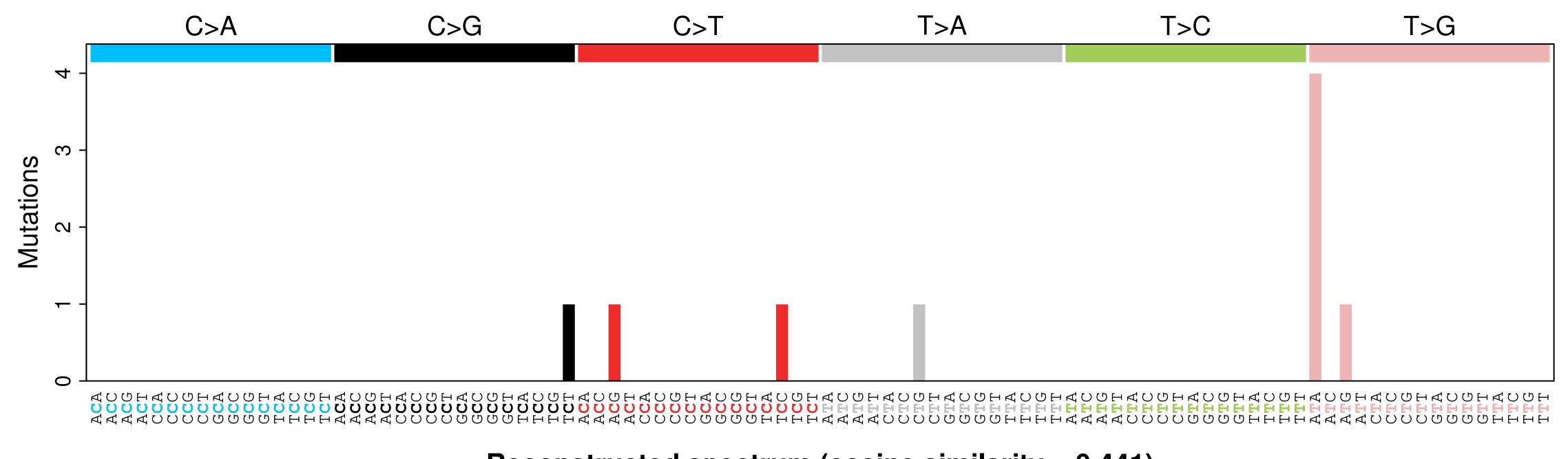
CATD0575a (6 mutations)



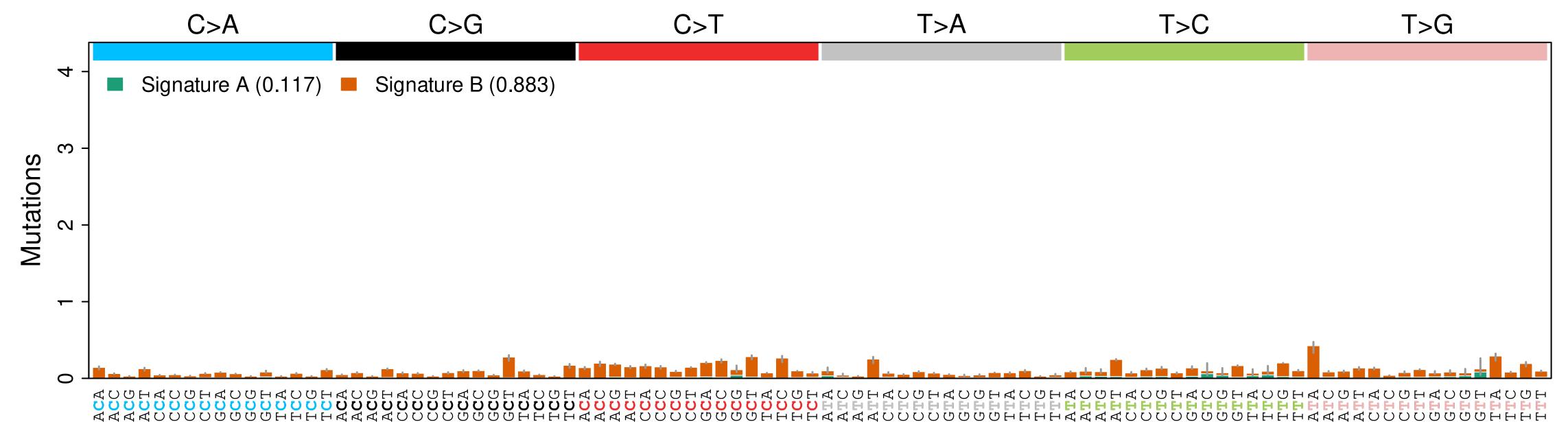




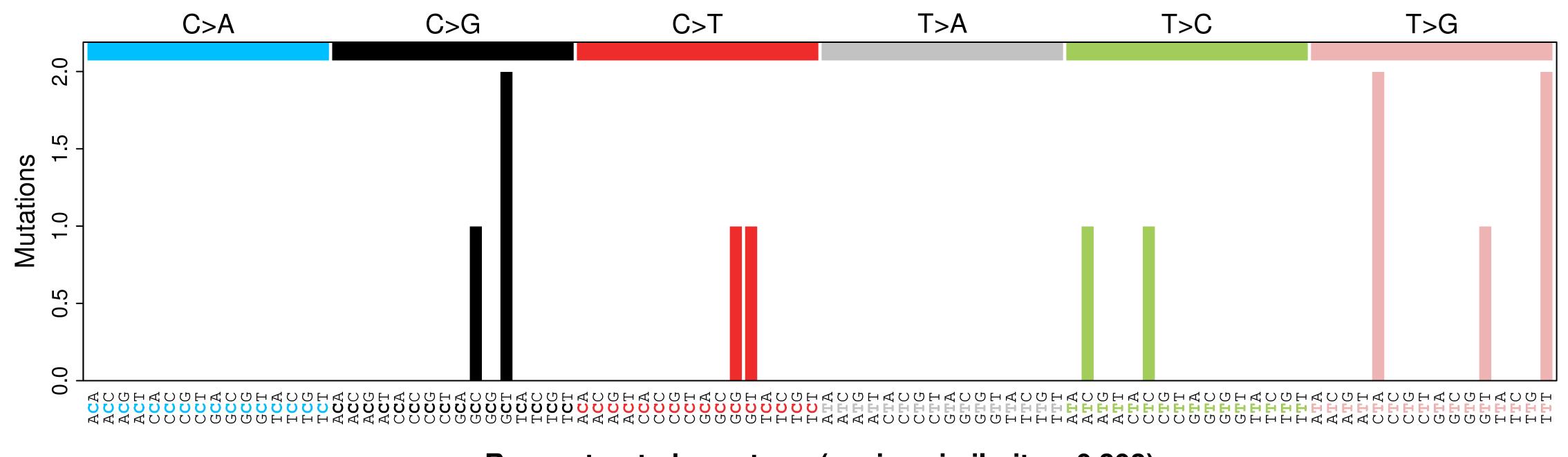
CATD0584a (9 mutations)



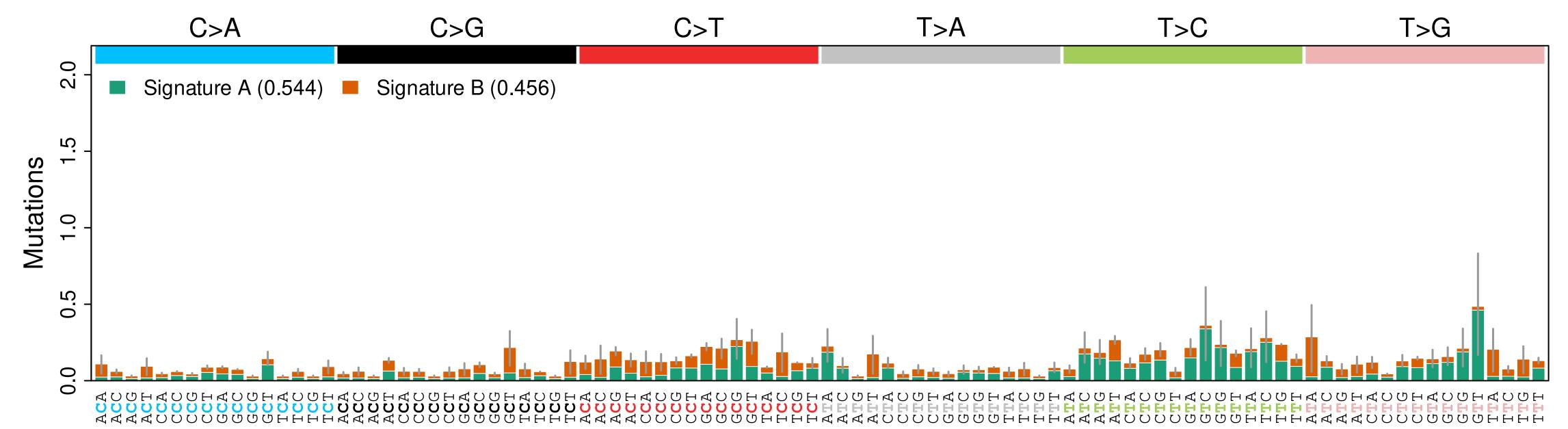
Reconstructed spectrum (cosine similarity = 0.441)



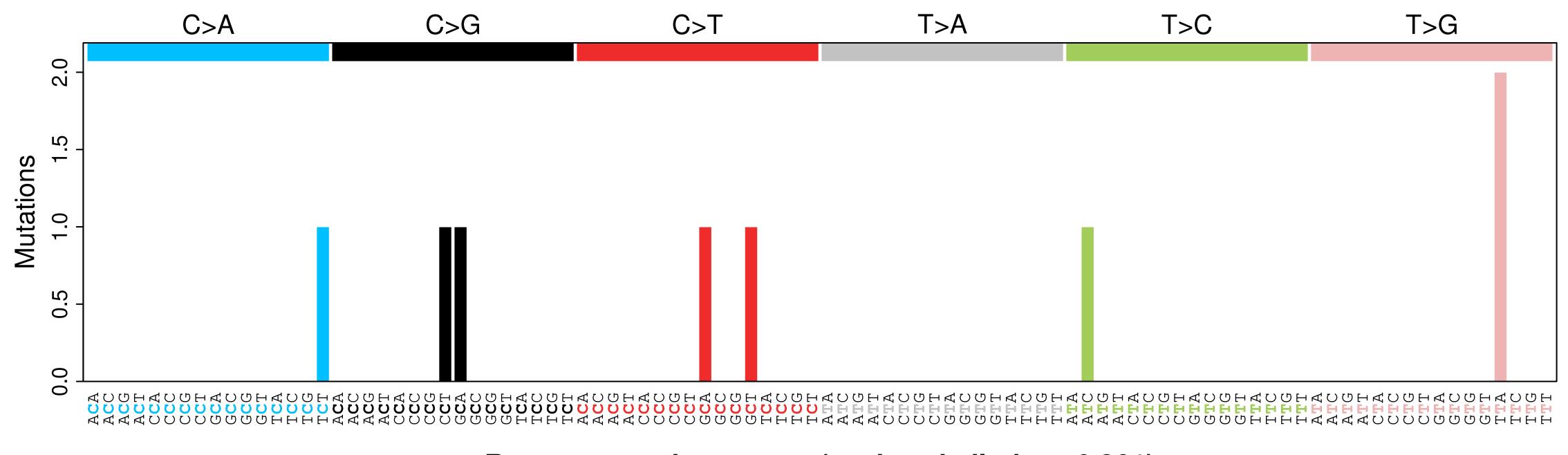
CATD0600a (12 mutations)

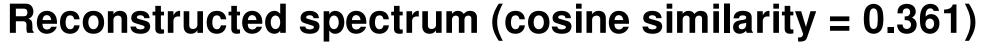


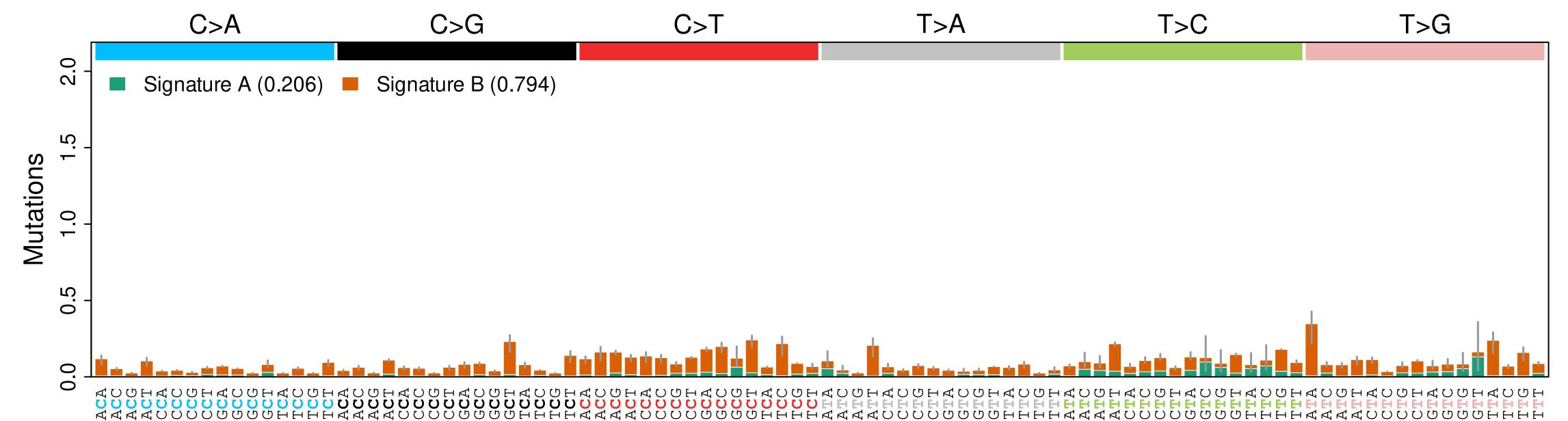




CATD0576a (8 mutations)

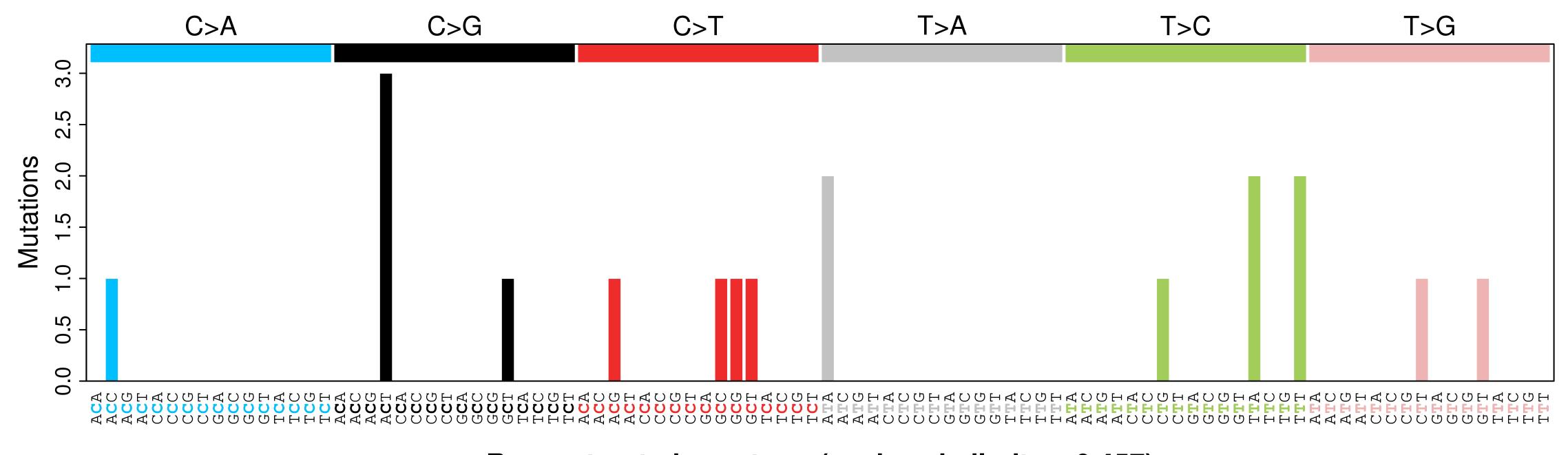


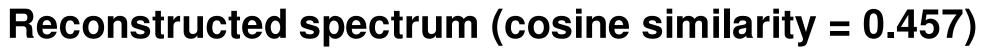


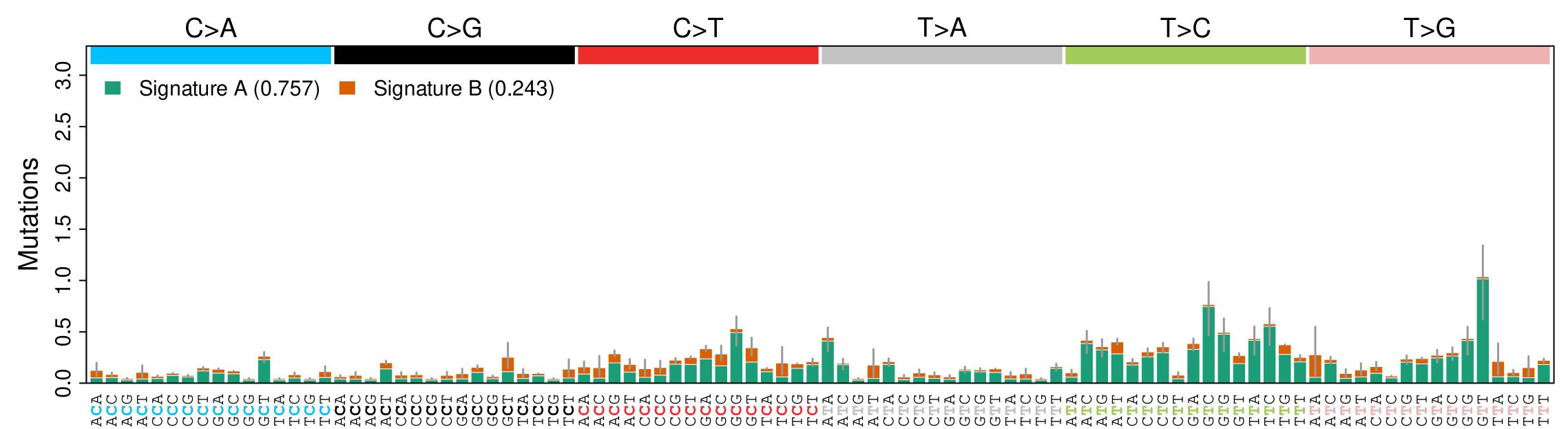


CATD0679a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 1.5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.341)** C>A T>G C>G T>A T>C C>T 2.0 Signature A (0.283) Signature B (0.717) 5 Mutations 2 0

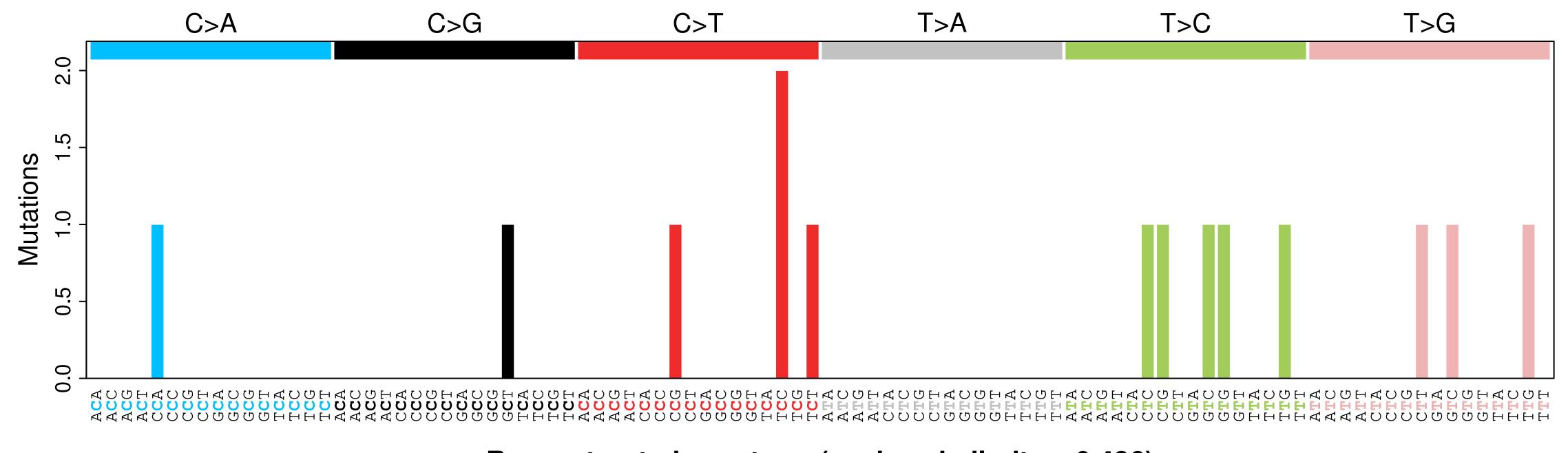
CATD0591a (18 mutations)



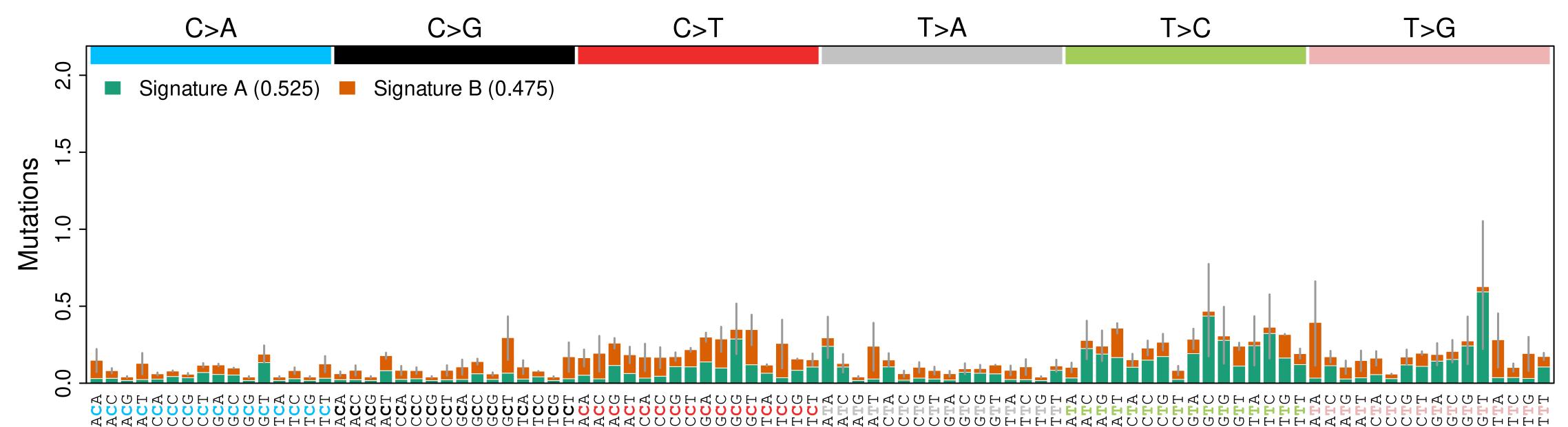




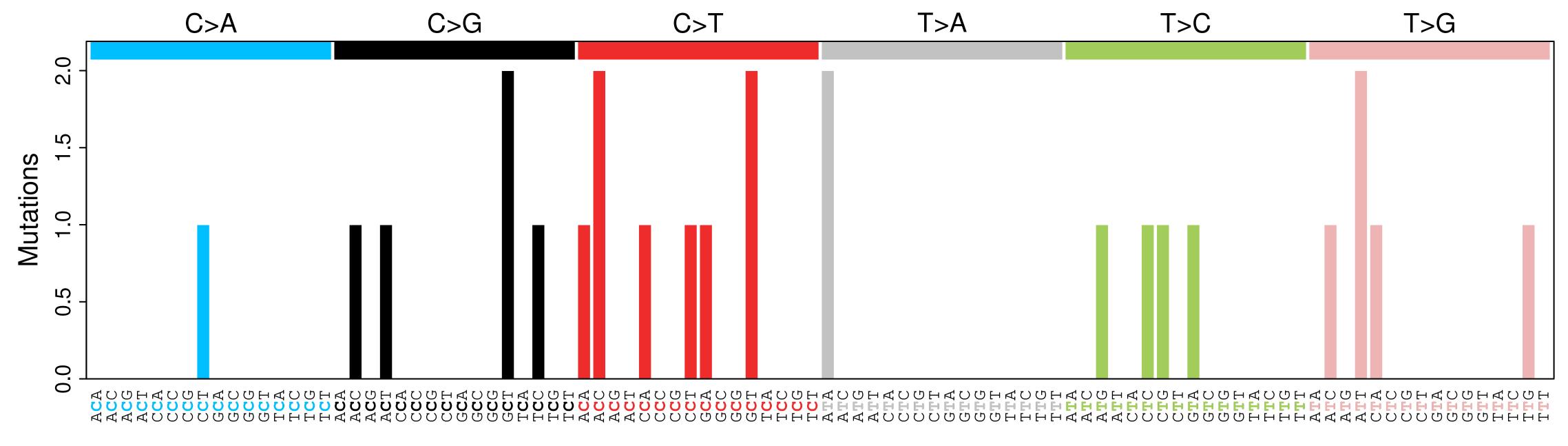
CATD0686a (14 mutations)



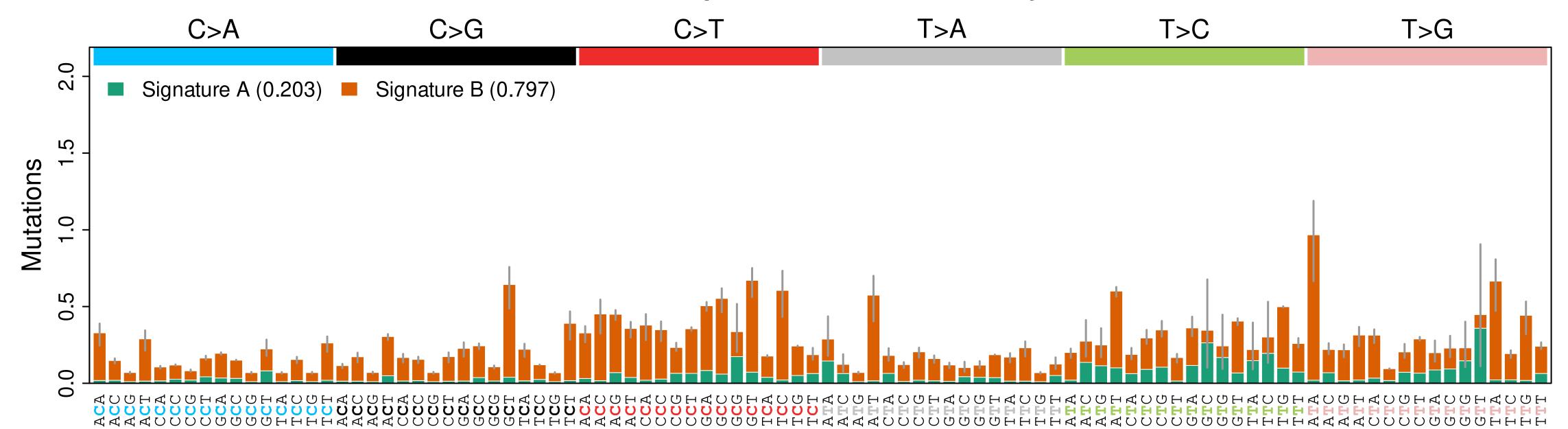
Reconstructed spectrum (cosine similarity = 0.436)



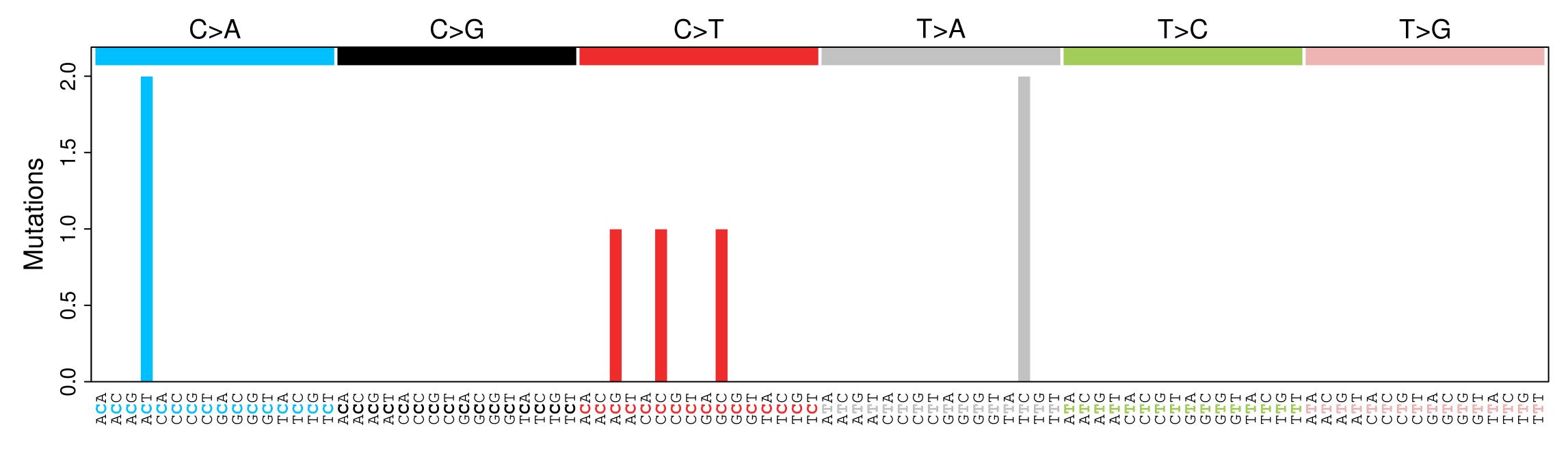
CATD0734a (25 mutations)



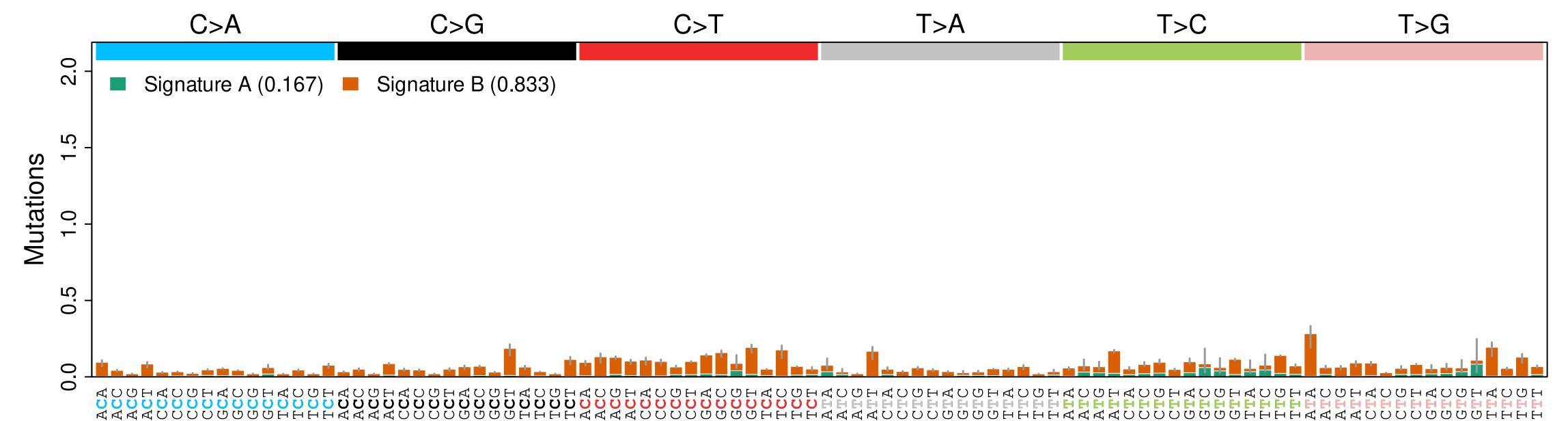
Reconstructed spectrum (cosine similarity = 0.521)



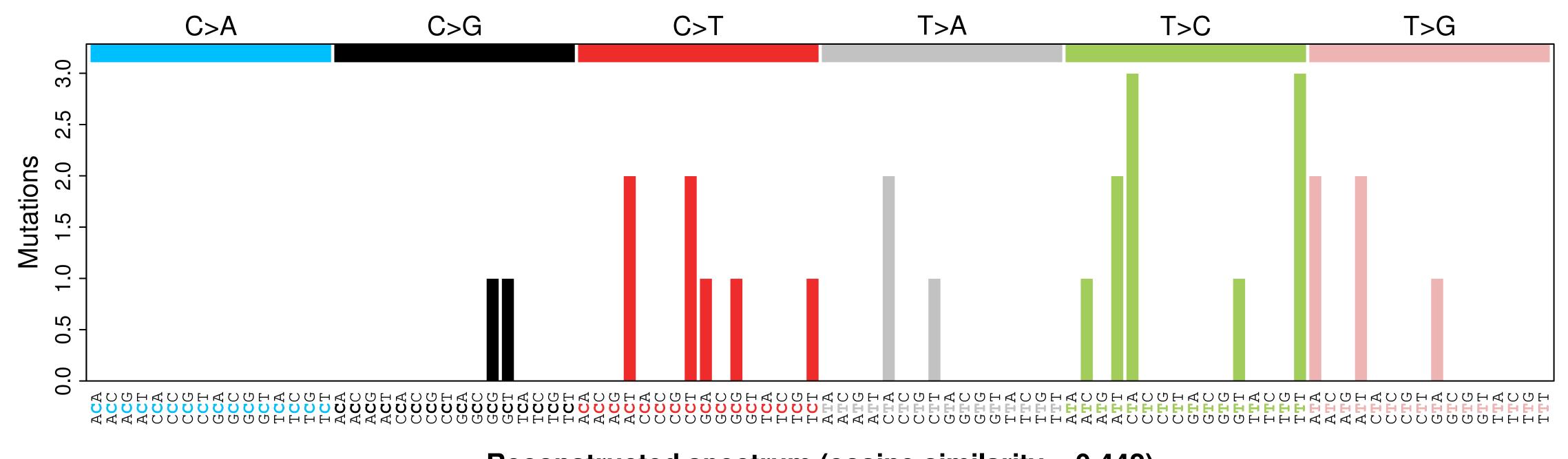
CATD0678a (7 mutations)



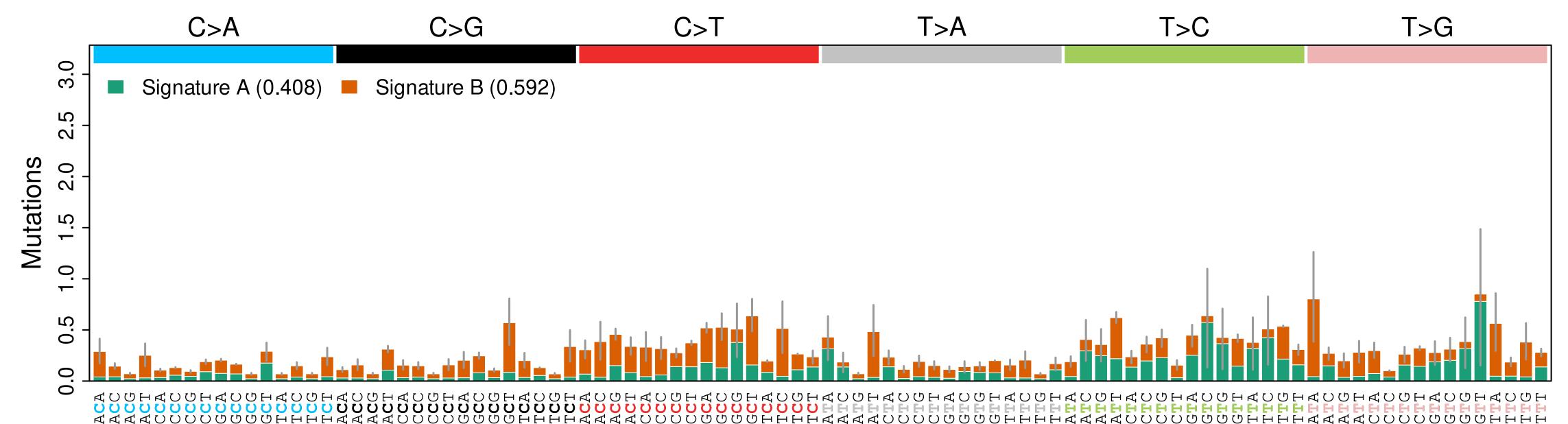
Reconstructed spectrum (cosine similarity = 0.243)



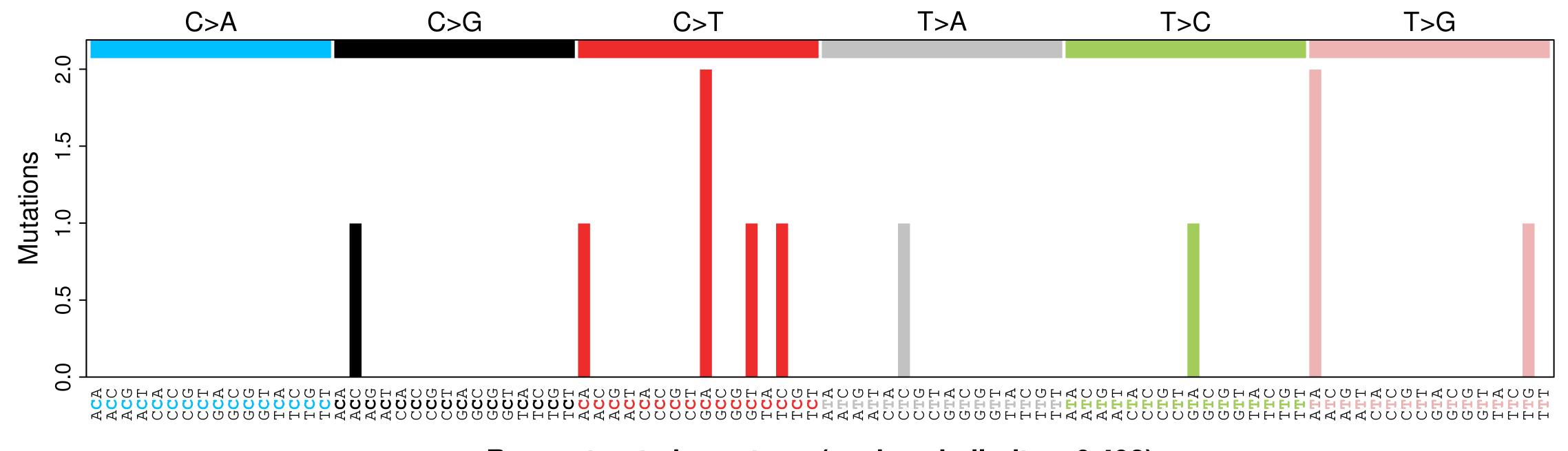
CATD0729a (27 mutations)



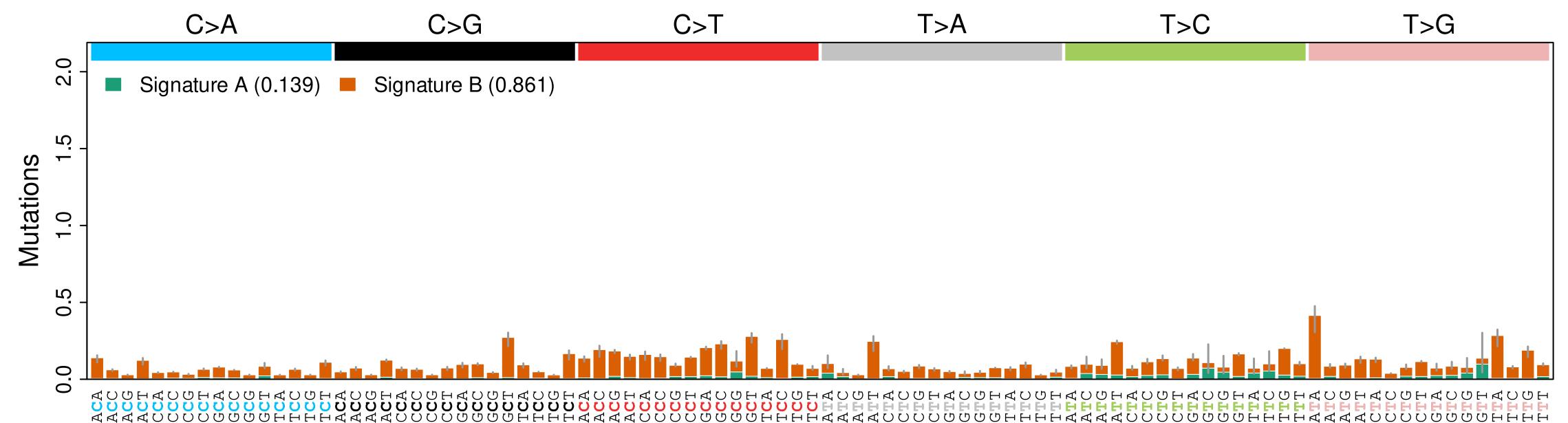
Reconstructed spectrum (cosine similarity = 0.442)



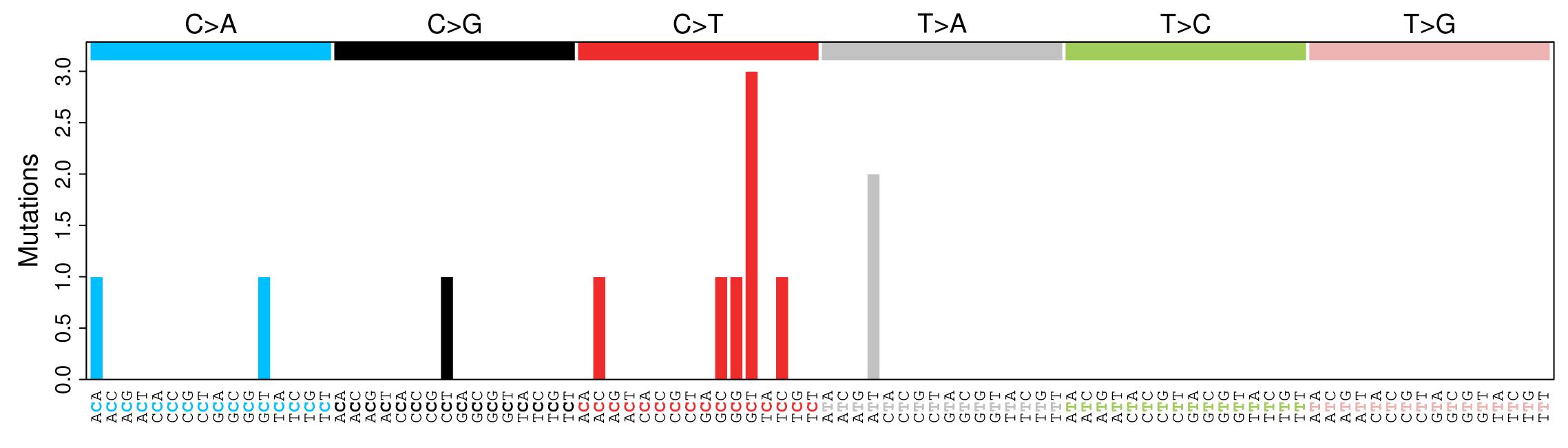
CATD0609a (11 mutations)



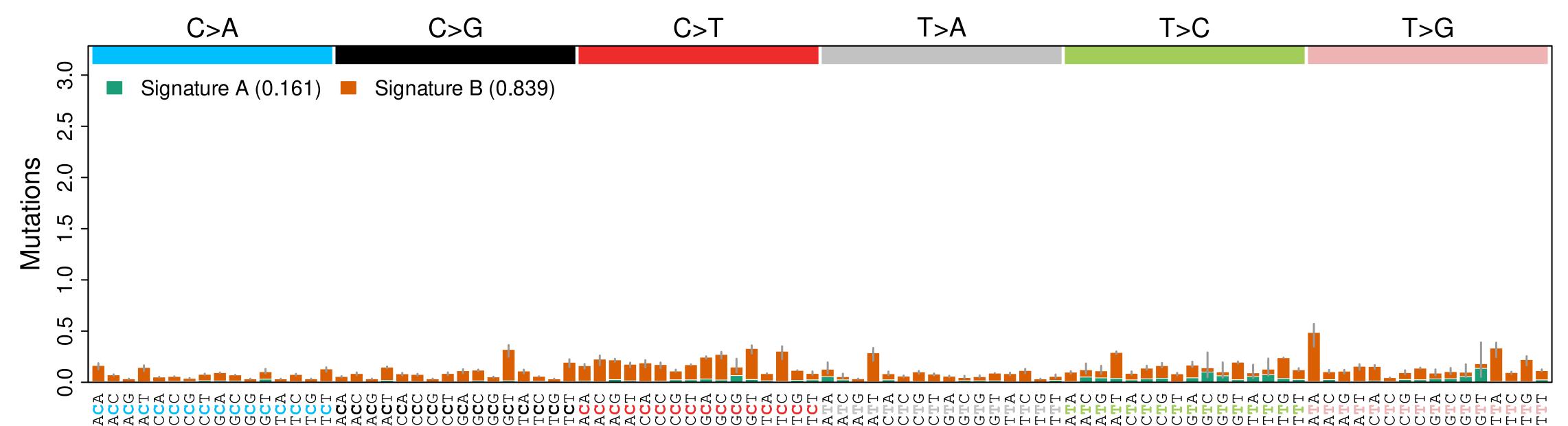
Reconstructed spectrum (cosine similarity = 0.498)



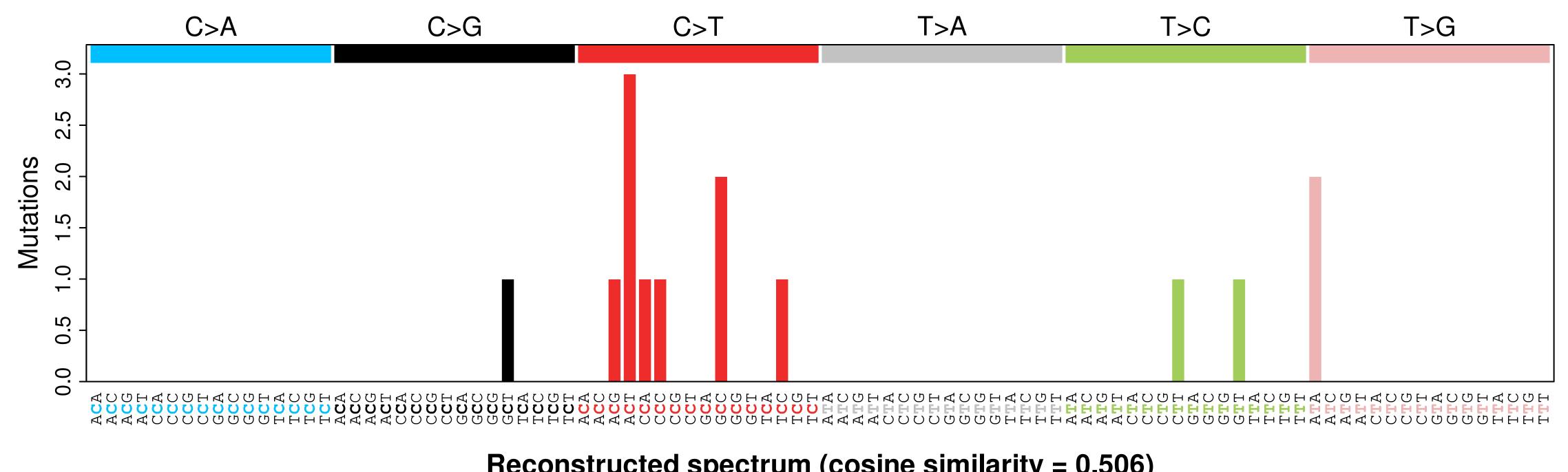
CATD0601a (12 mutations)



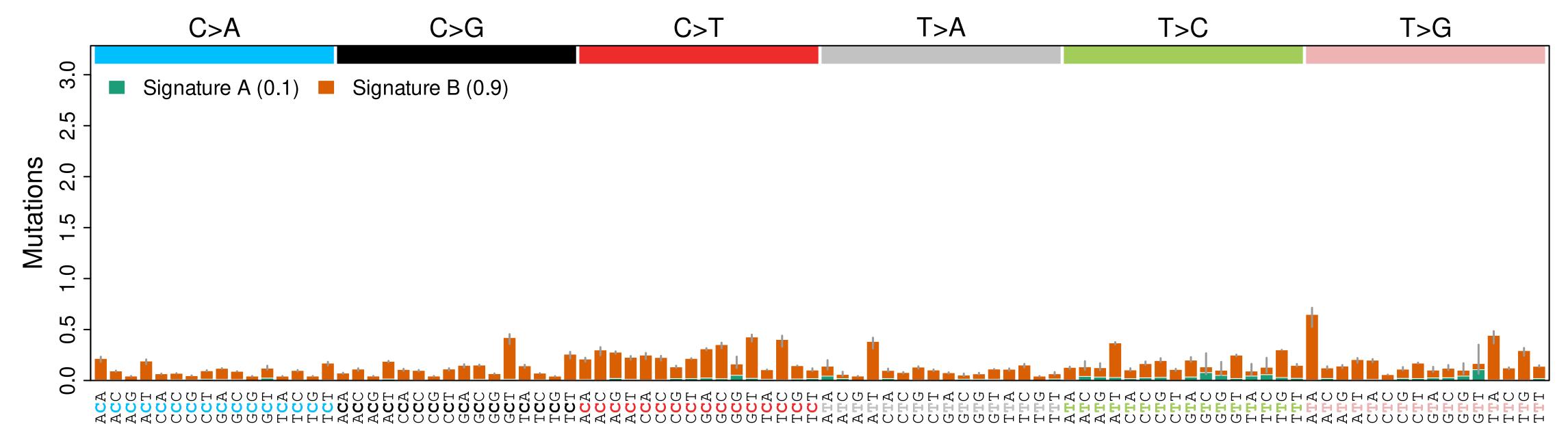
Reconstructed spectrum (cosine similarity = 0.439)



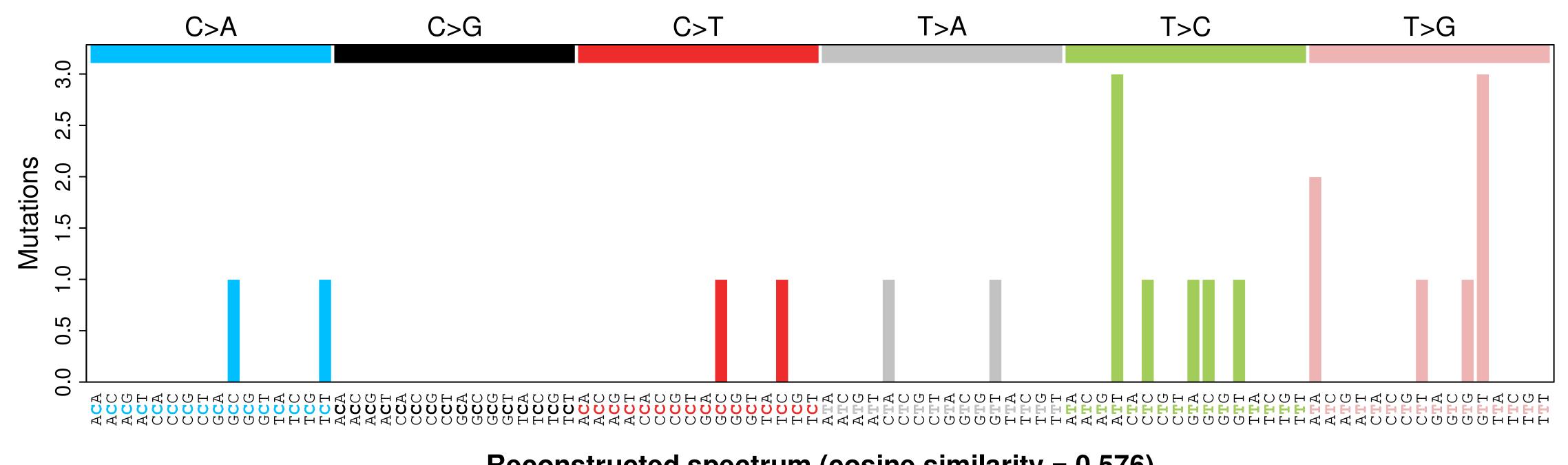
CATD0731a (14 mutations)



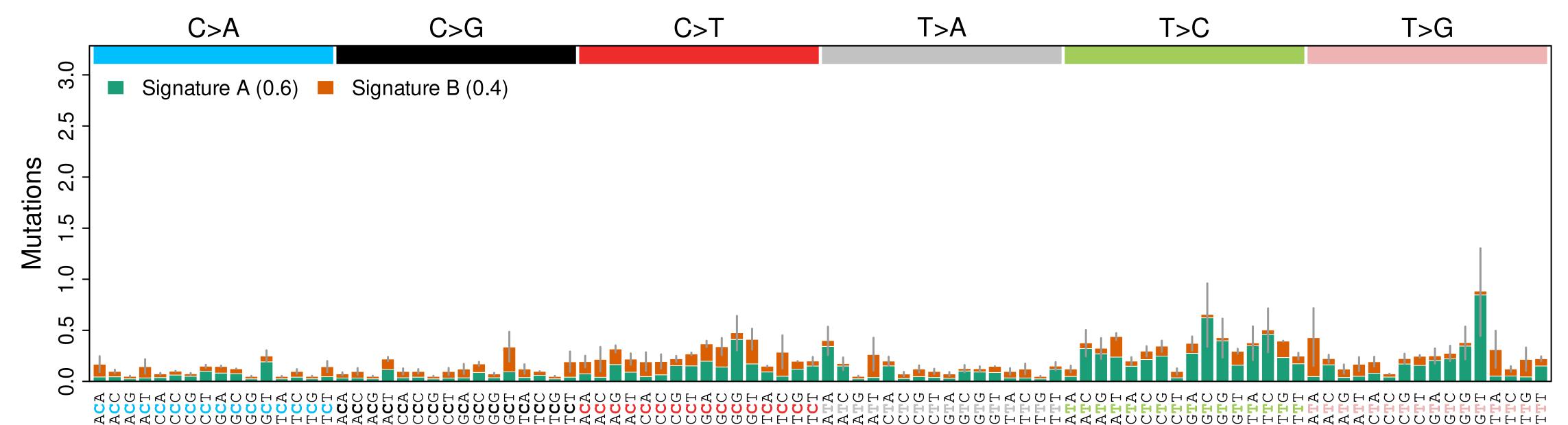
Reconstructed spectrum (cosine similarity = 0.506)



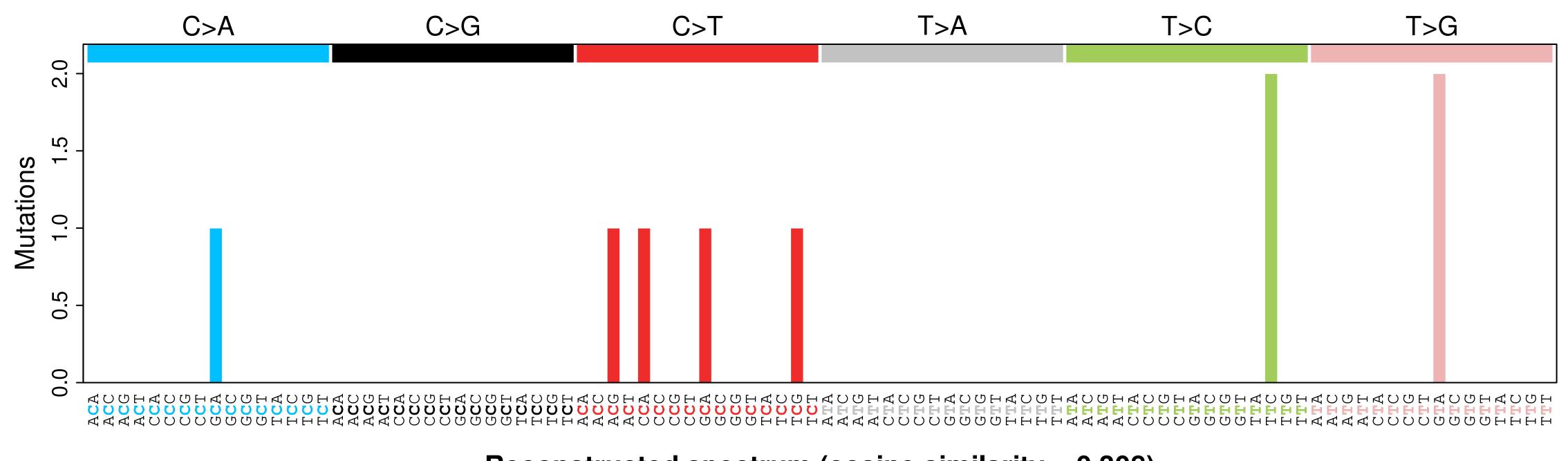
CATD0723a (20 mutations)



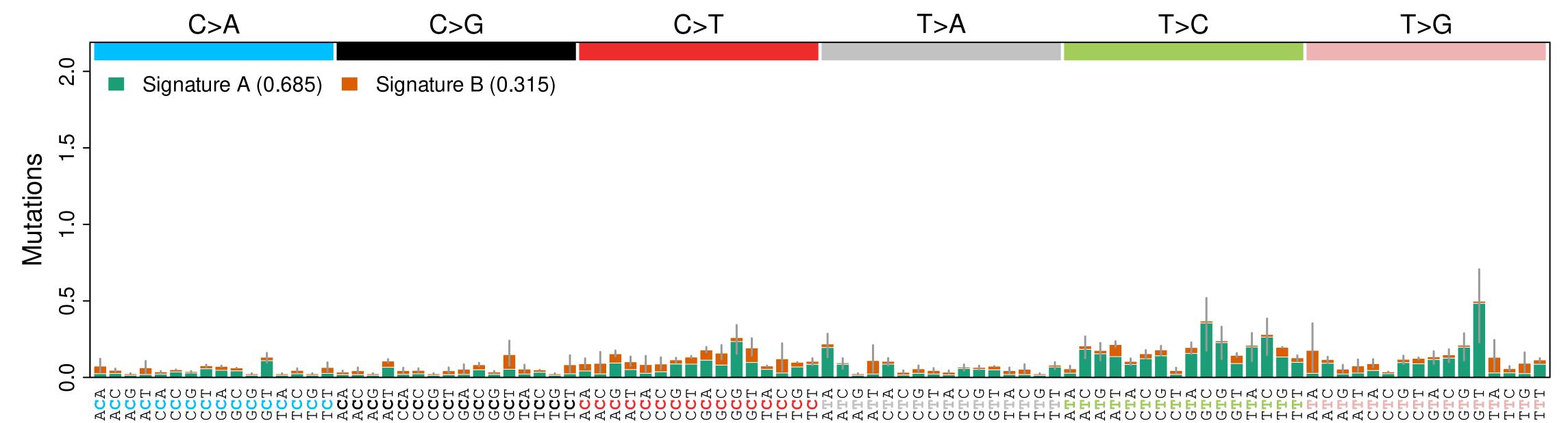




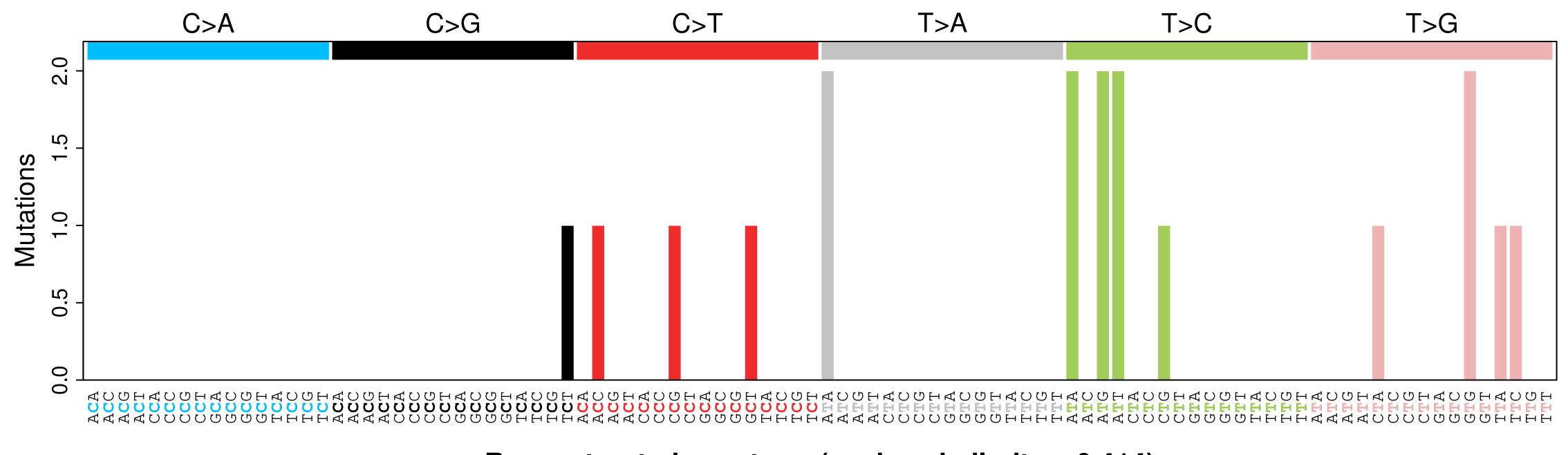
CATD0730a (9 mutations)



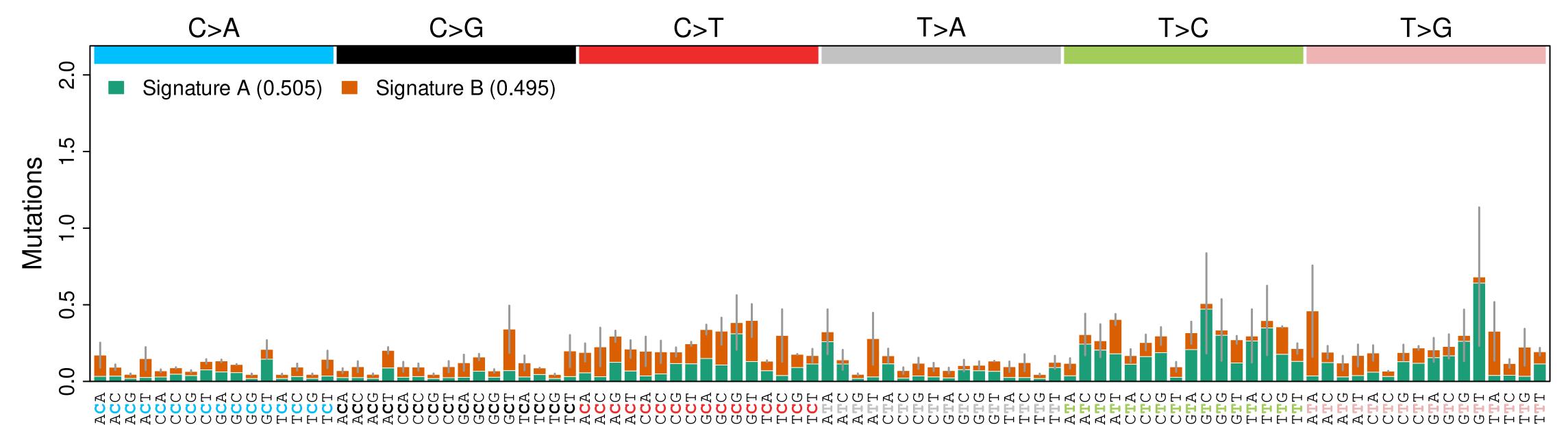
Reconstructed spectrum (cosine similarity = 0.308)



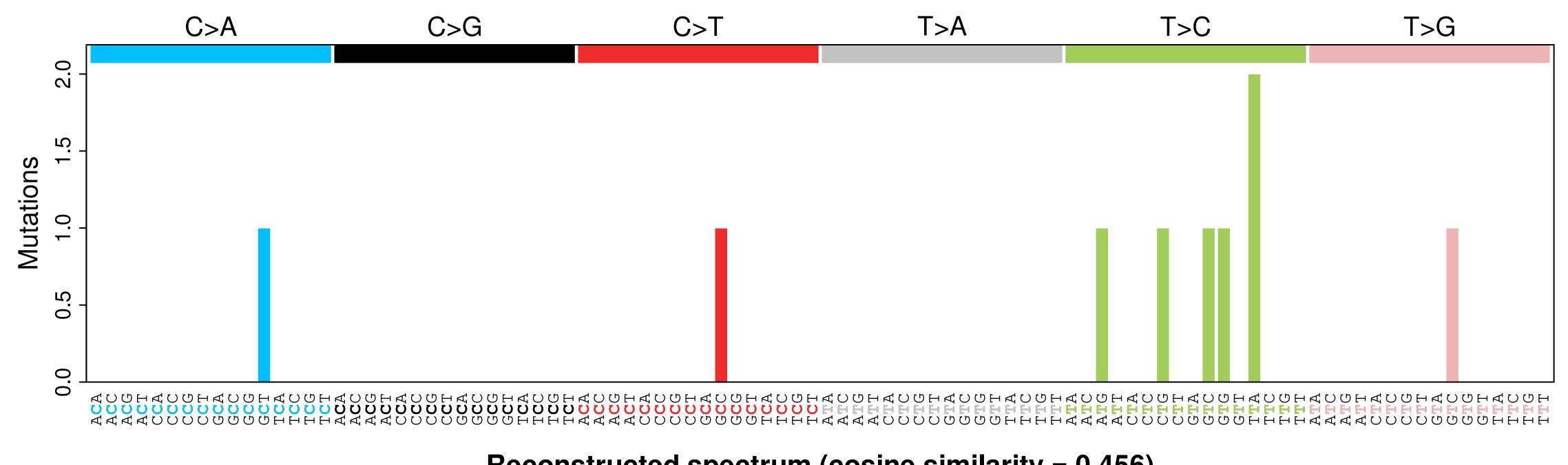
CATD0586a (18 mutations)

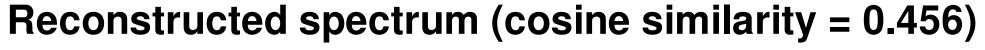


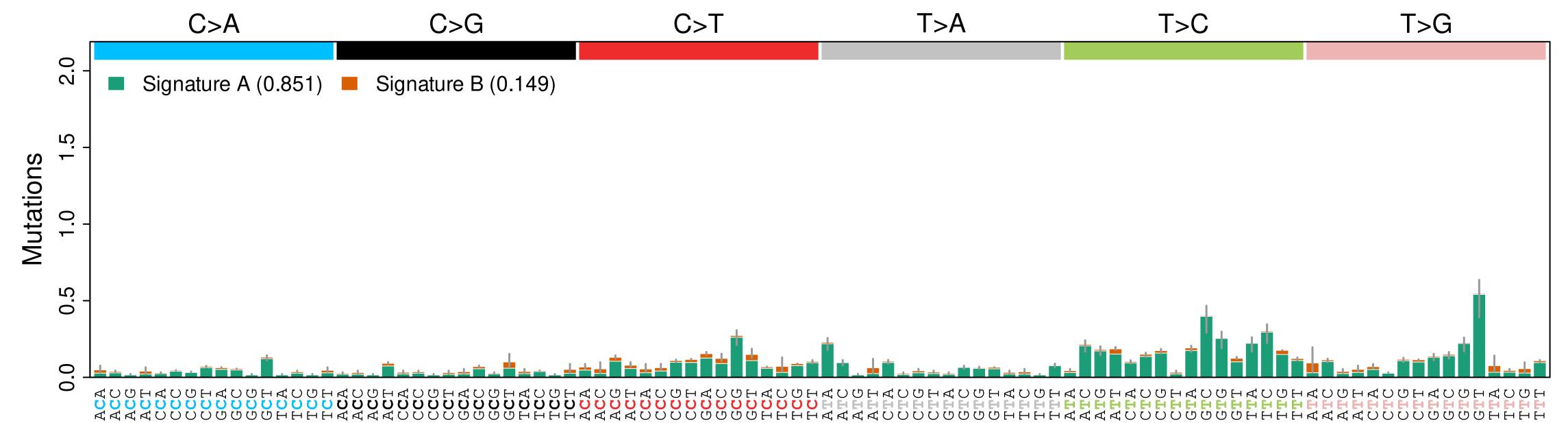
Reconstructed spectrum (cosine similarity = 0.414)



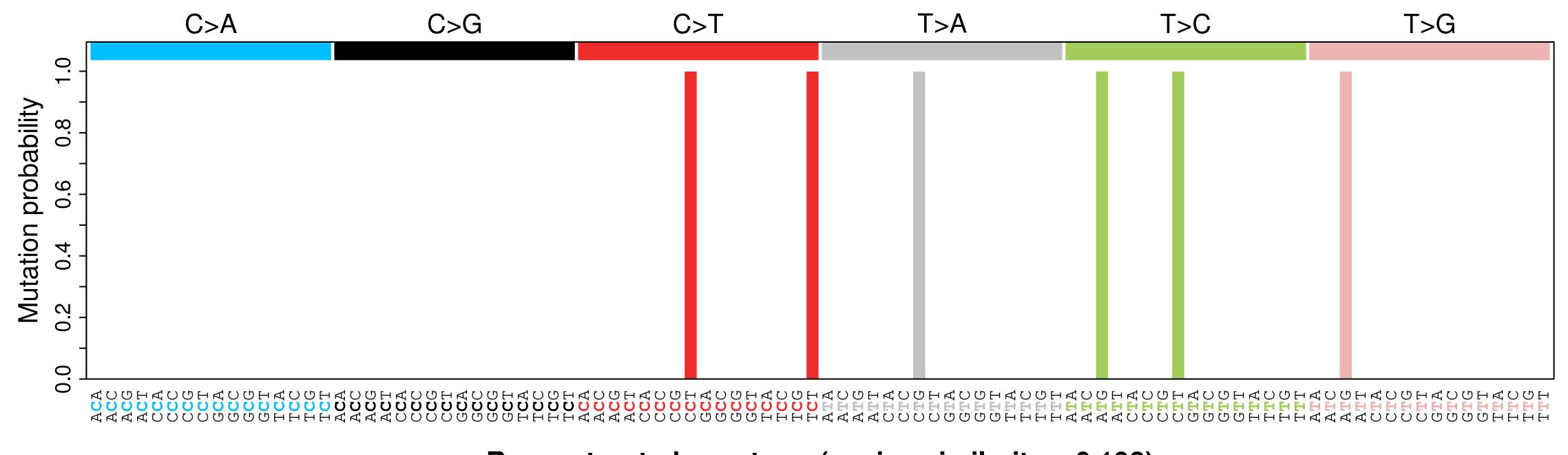
CATD0733a (9 mutations)

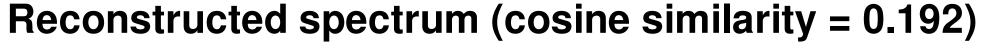


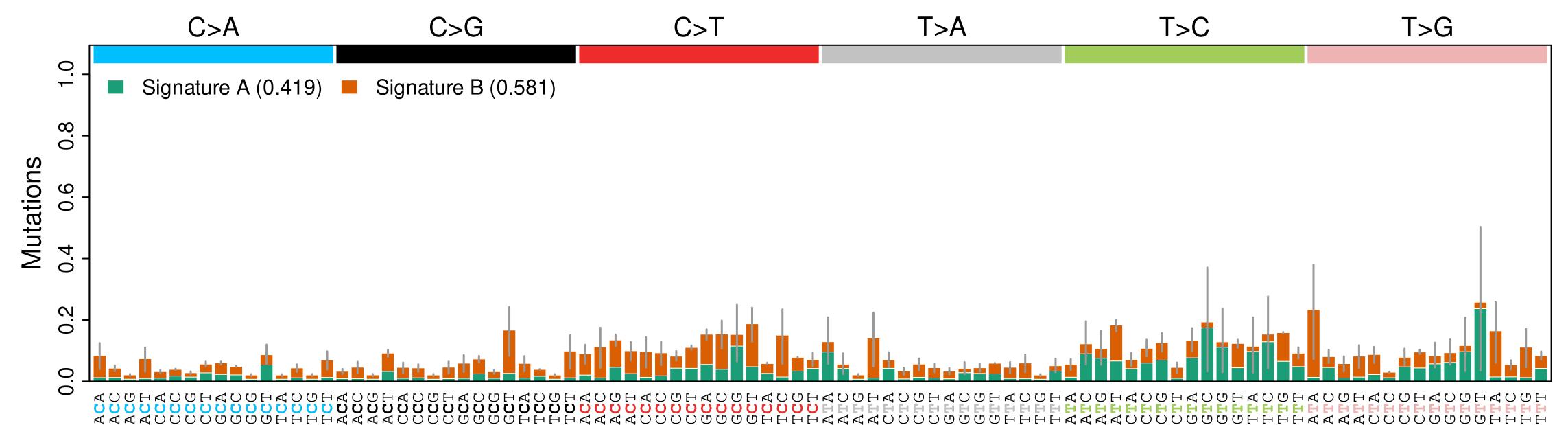




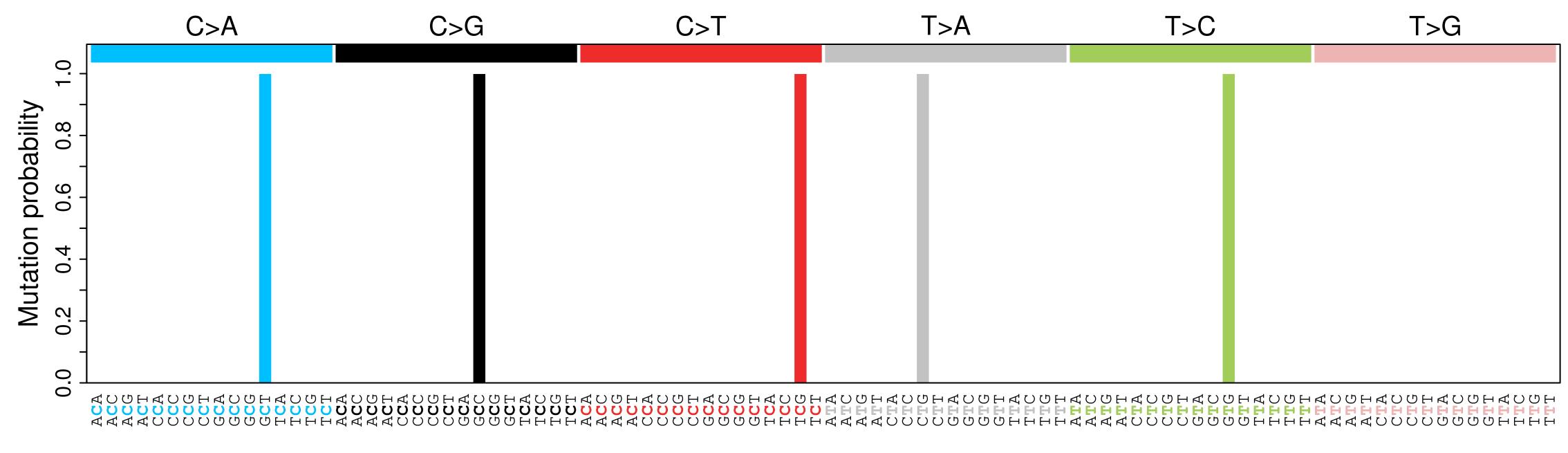
CATD0687a

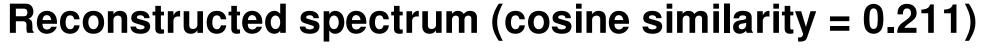


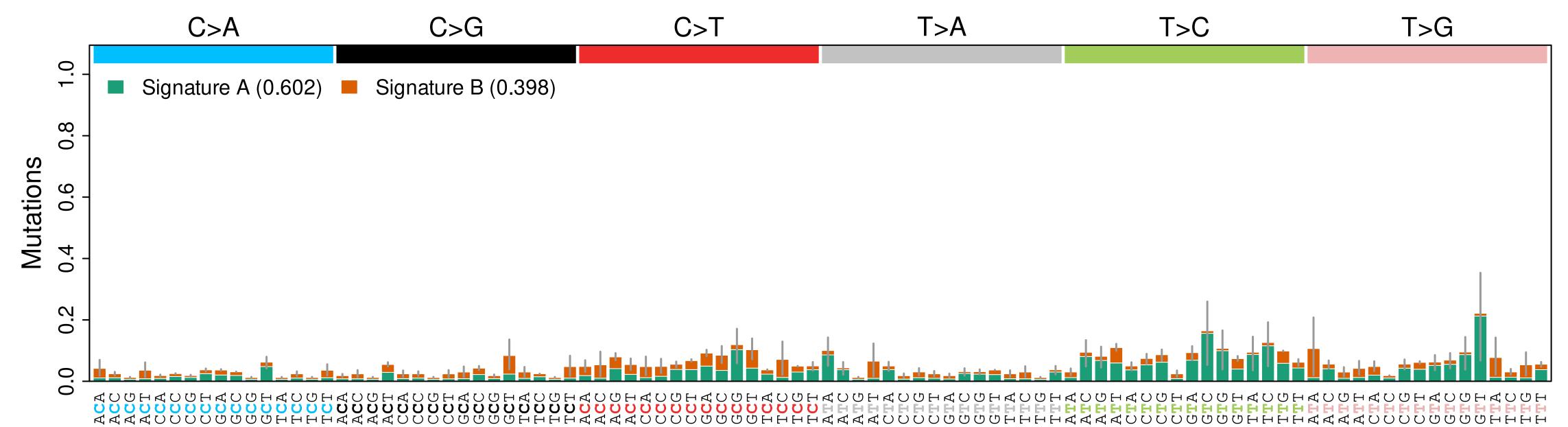




CATD0578a

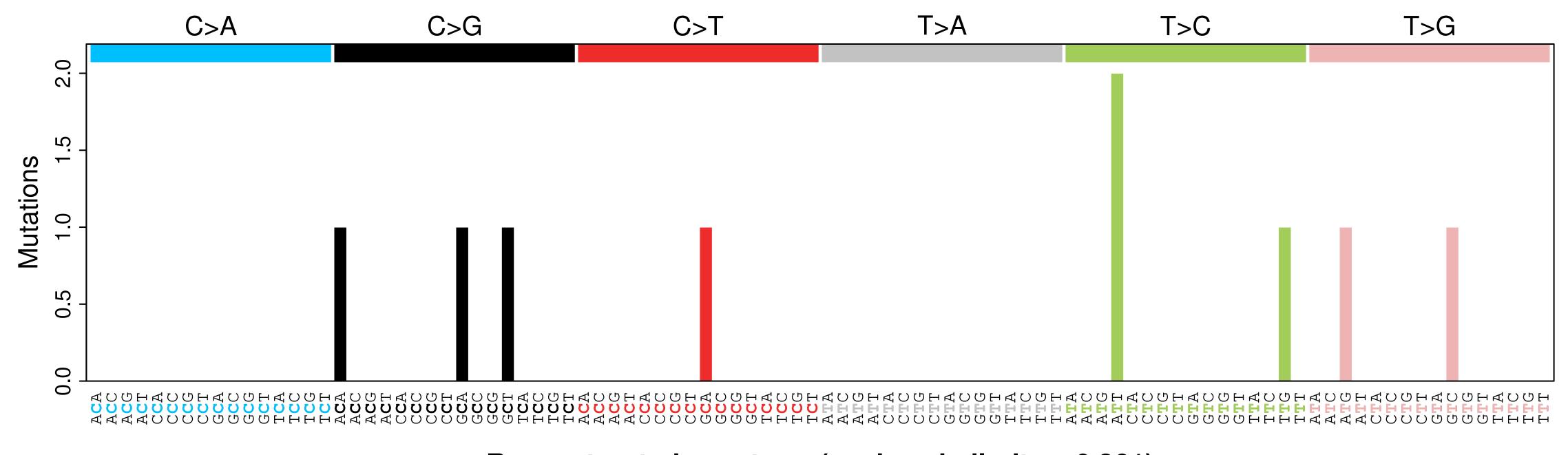


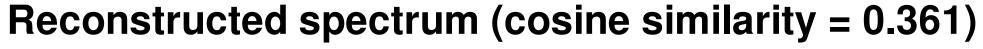


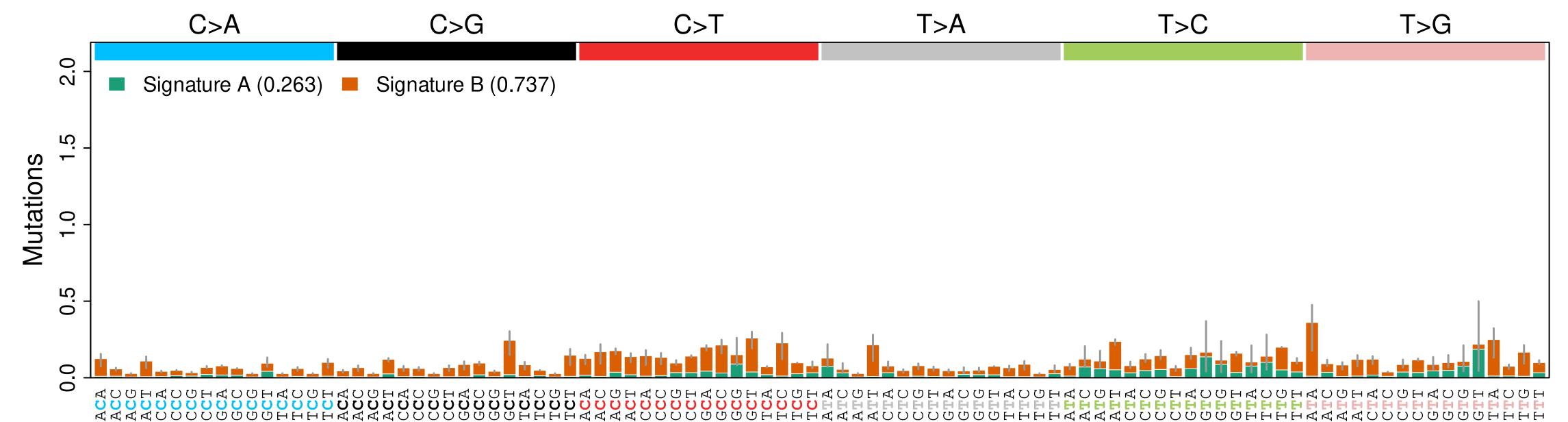


CATD0587a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.161)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.621) Signature B (0.379) 5 Mutations 2 0

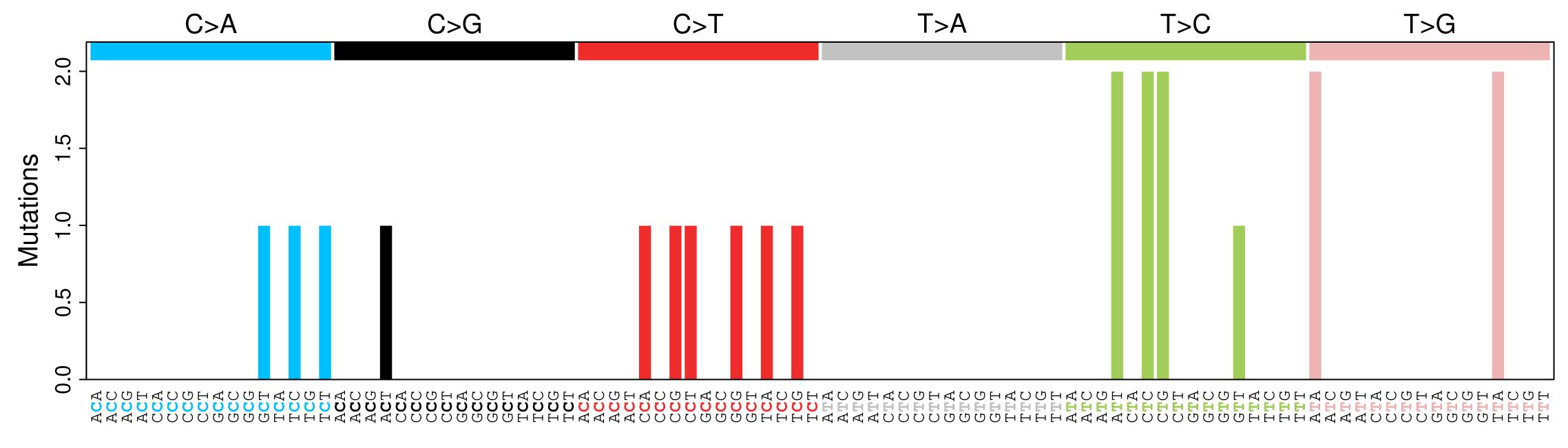
CATD0589a (9 mutations)



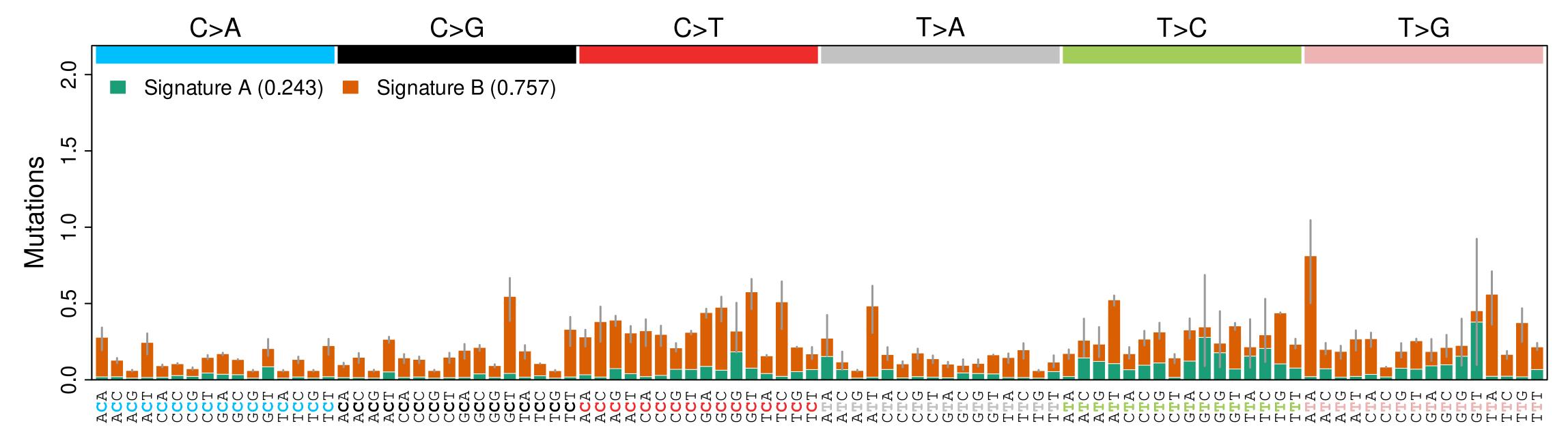




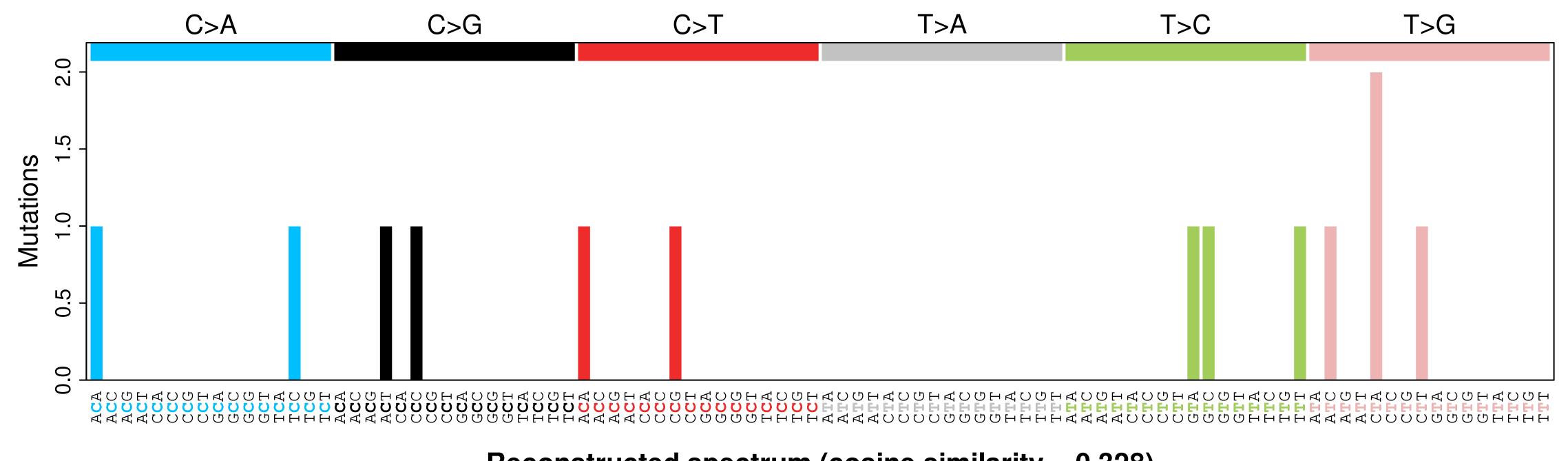
CATD0590a (21 mutations)

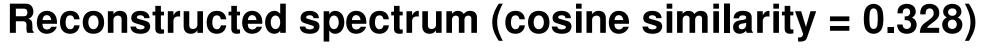


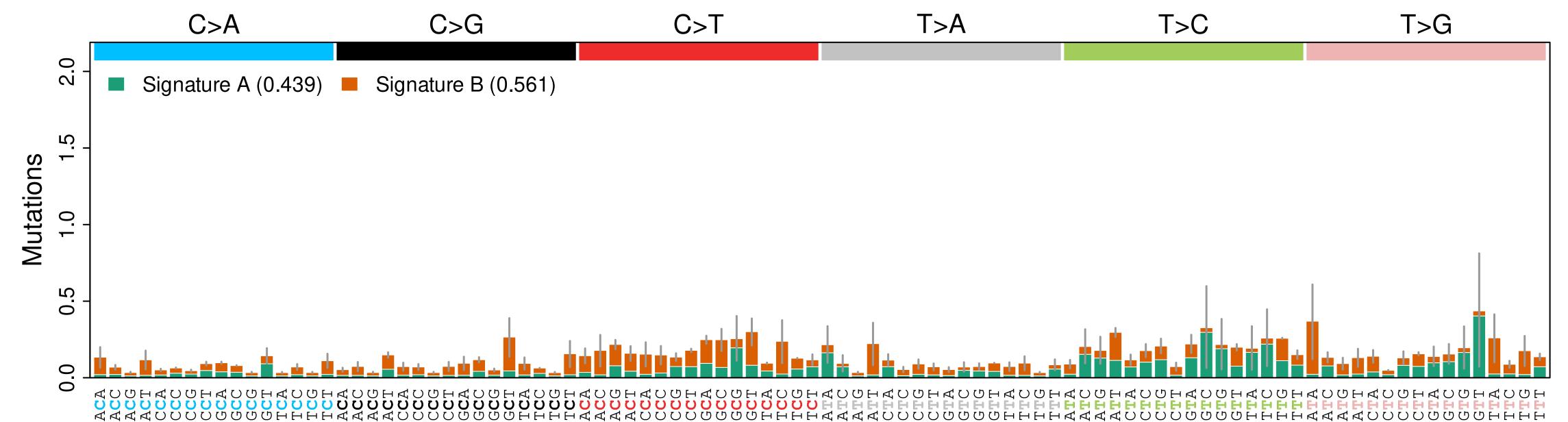
Reconstructed spectrum (cosine similarity = 0.523)



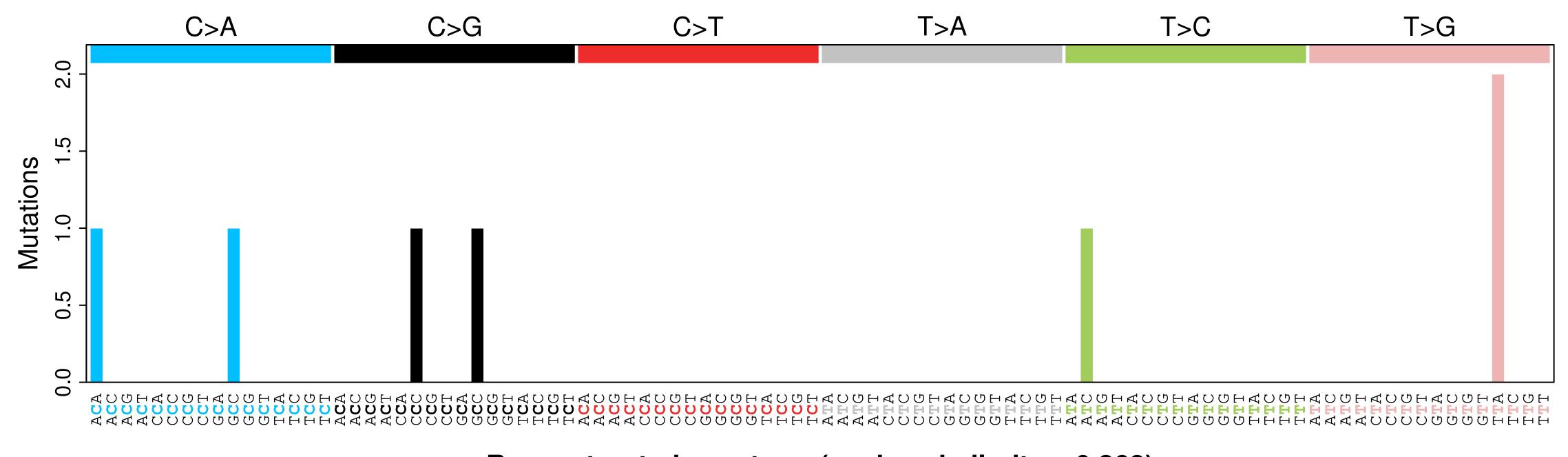
CATD0727a (13 mutations)



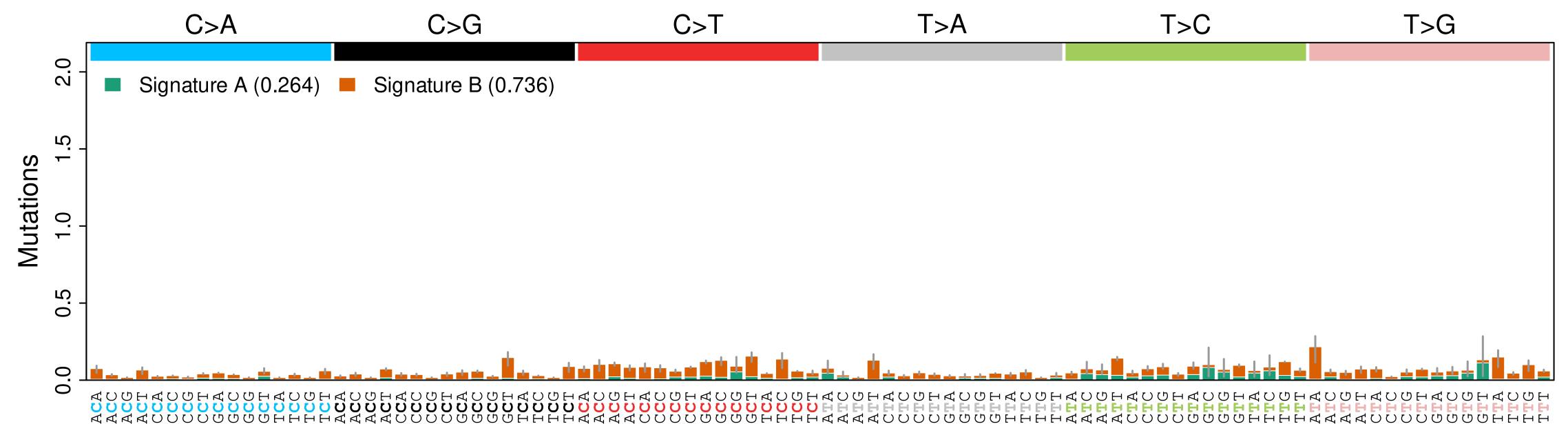




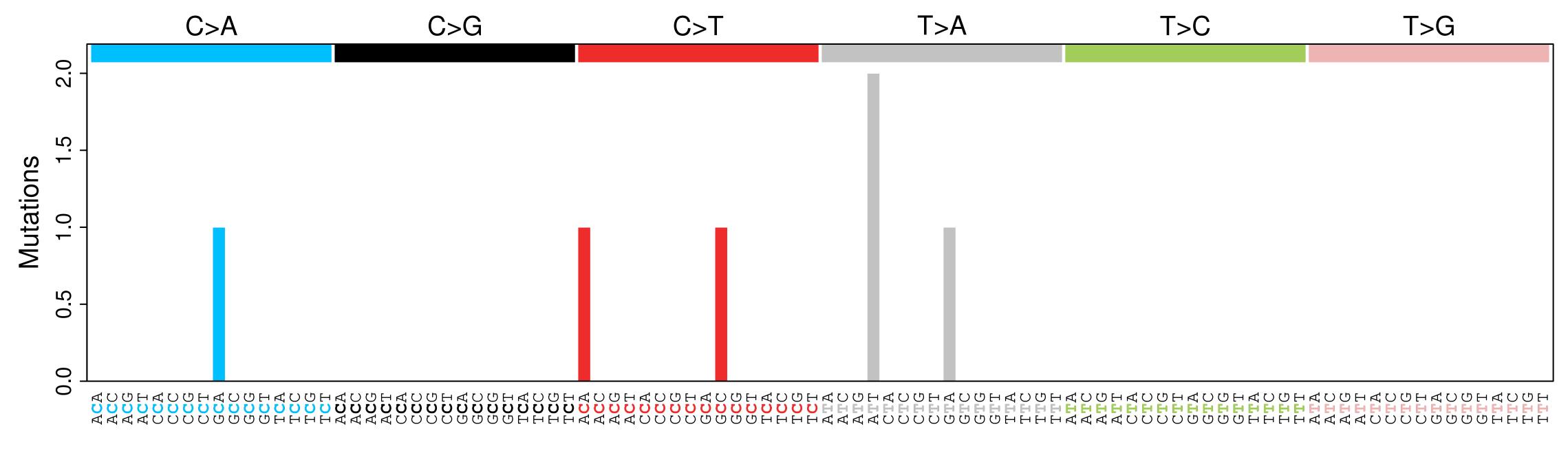
CATD0583a (7 mutations)



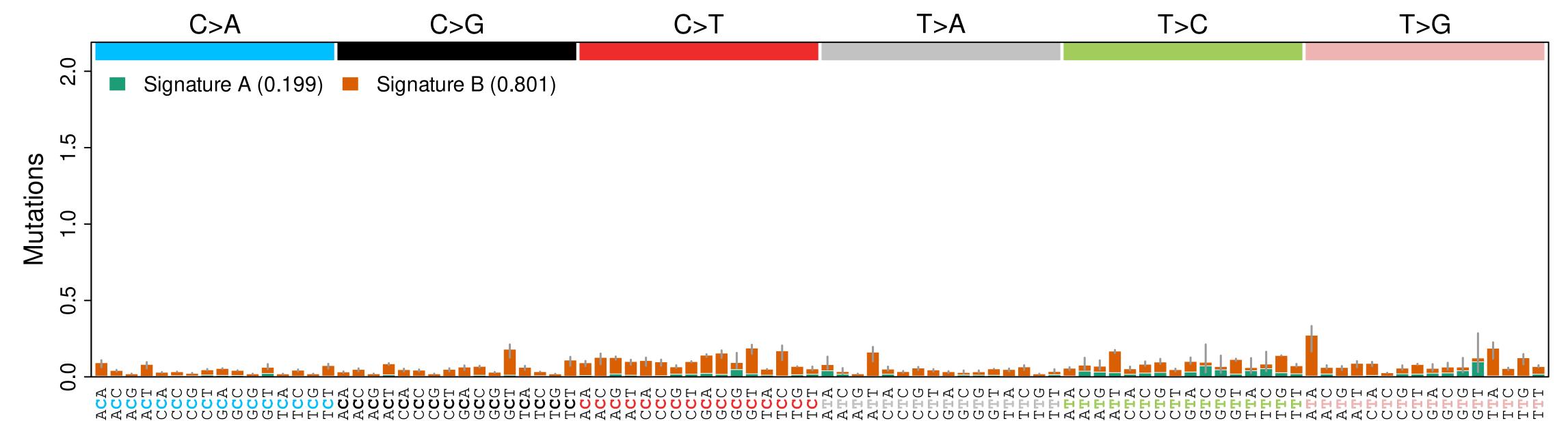




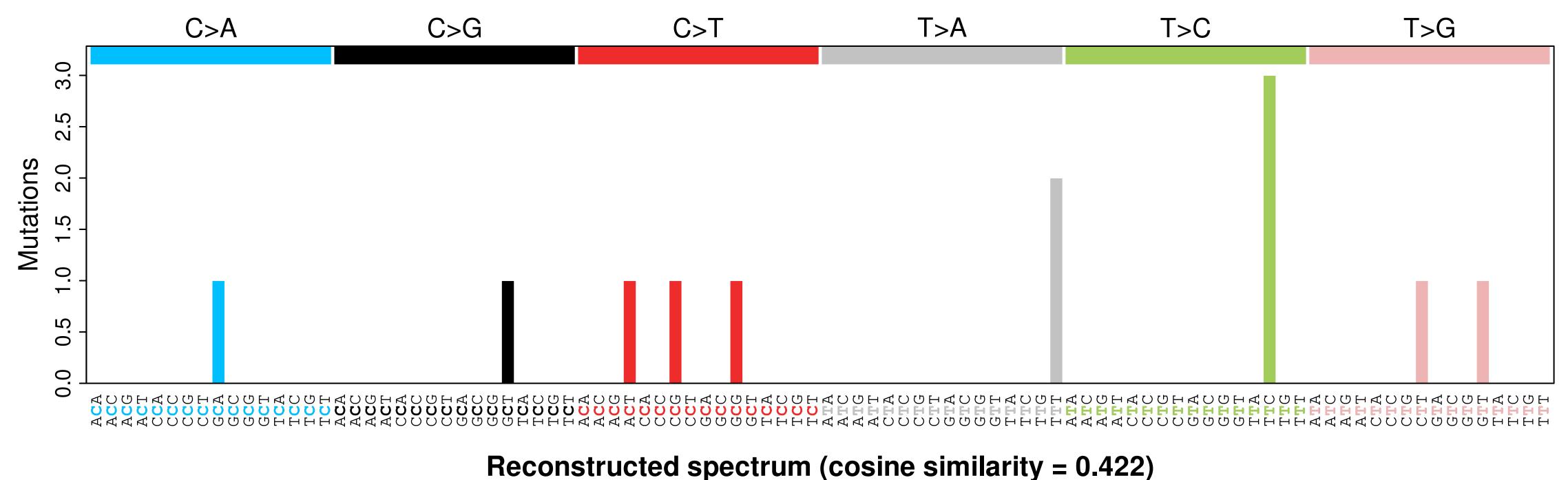
CATD0732a (6 mutations)

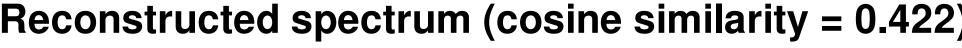


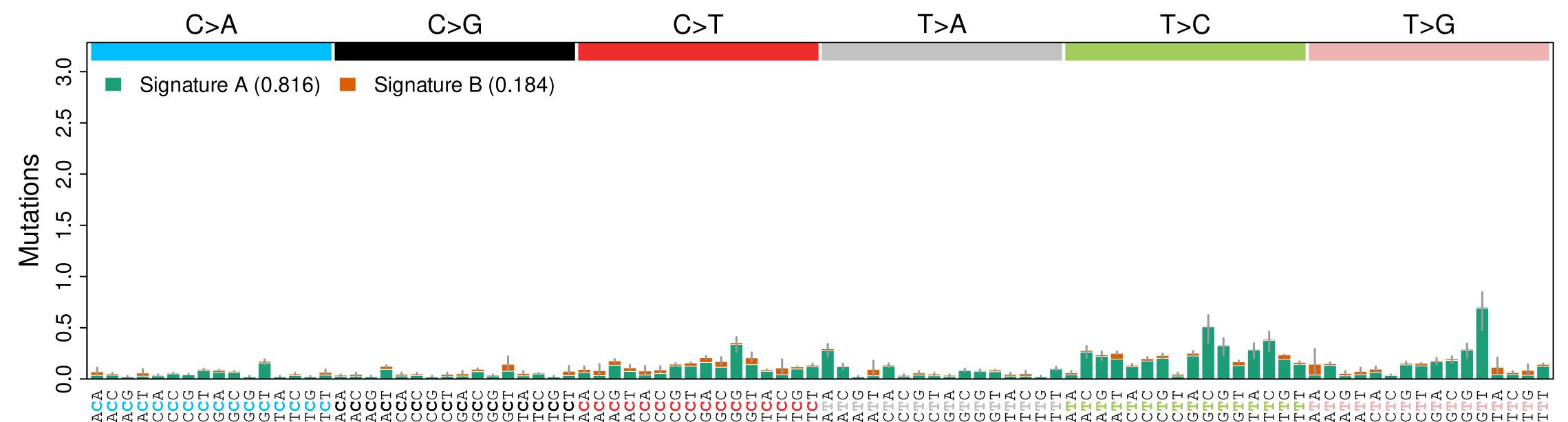




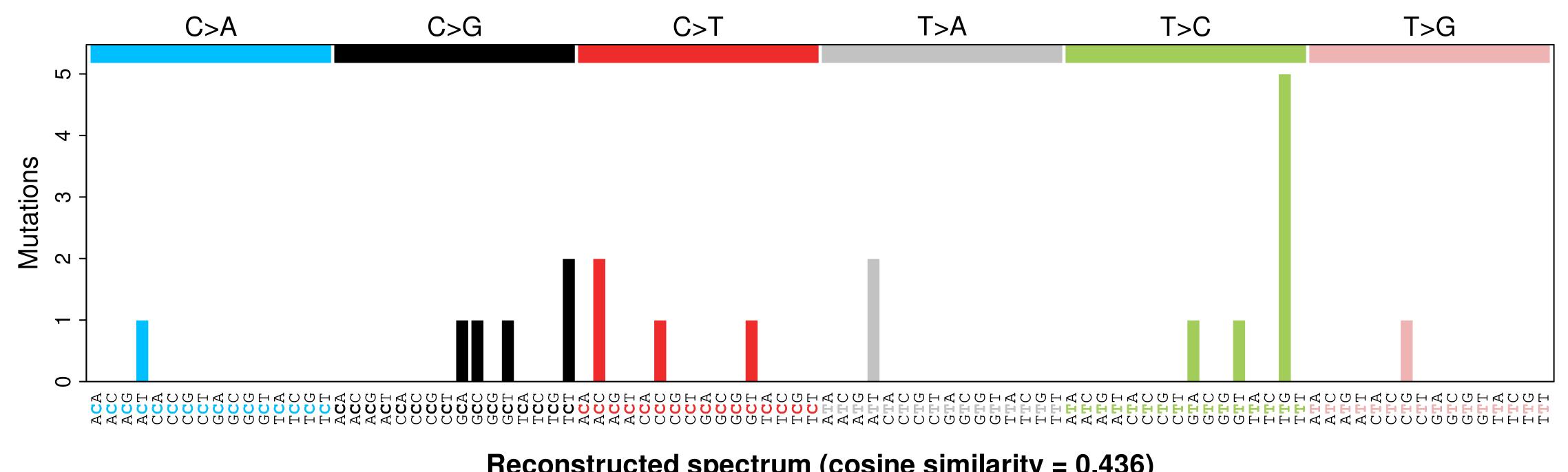
CATD0725a (12 mutations)



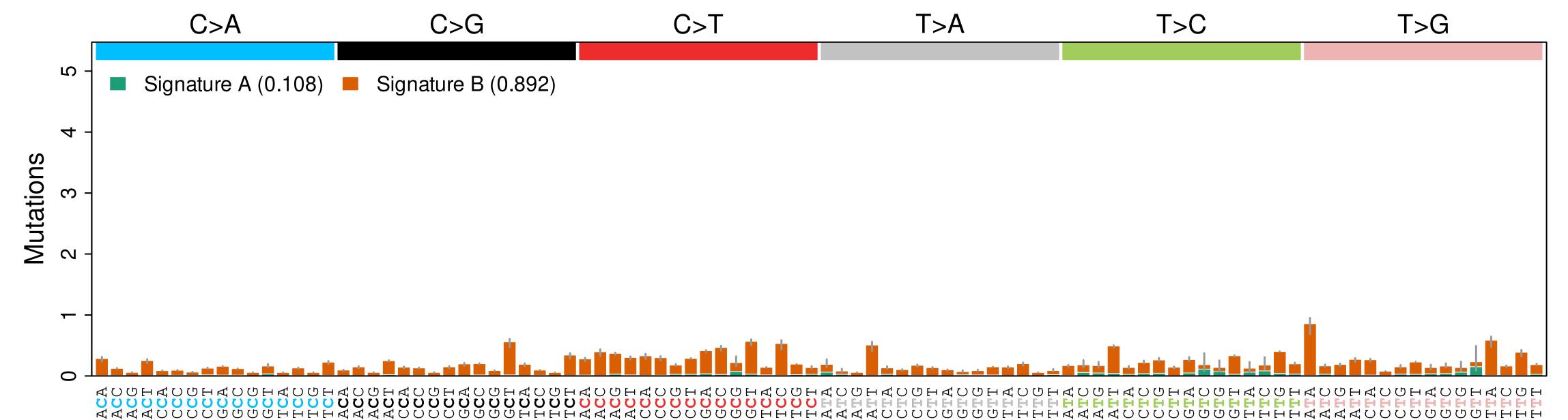




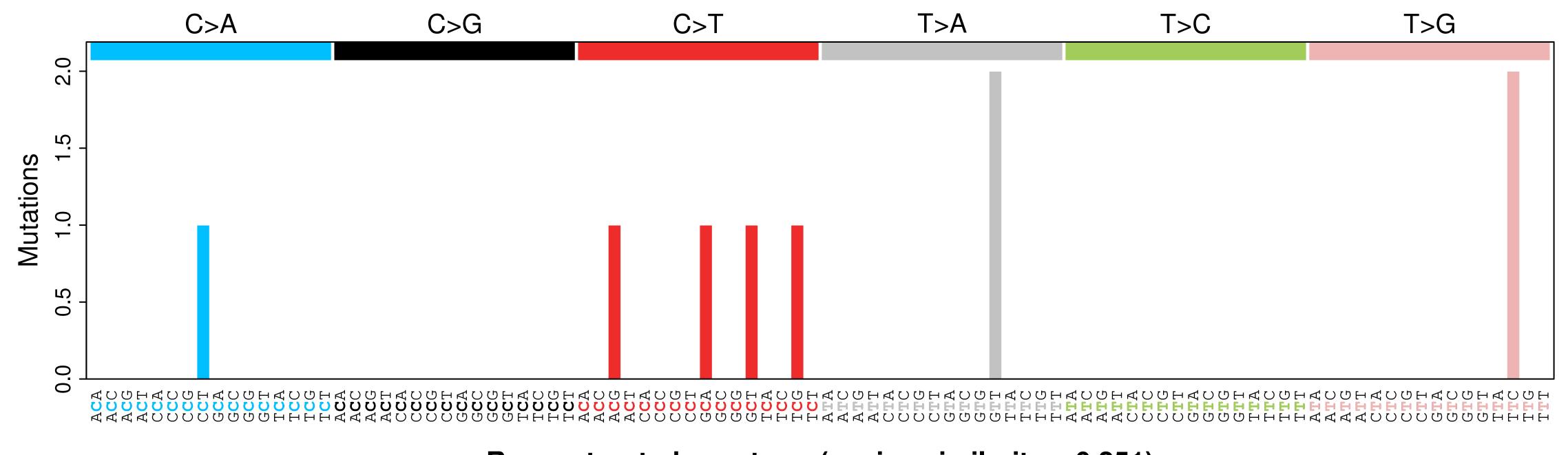
CATD0577a (20 mutations)



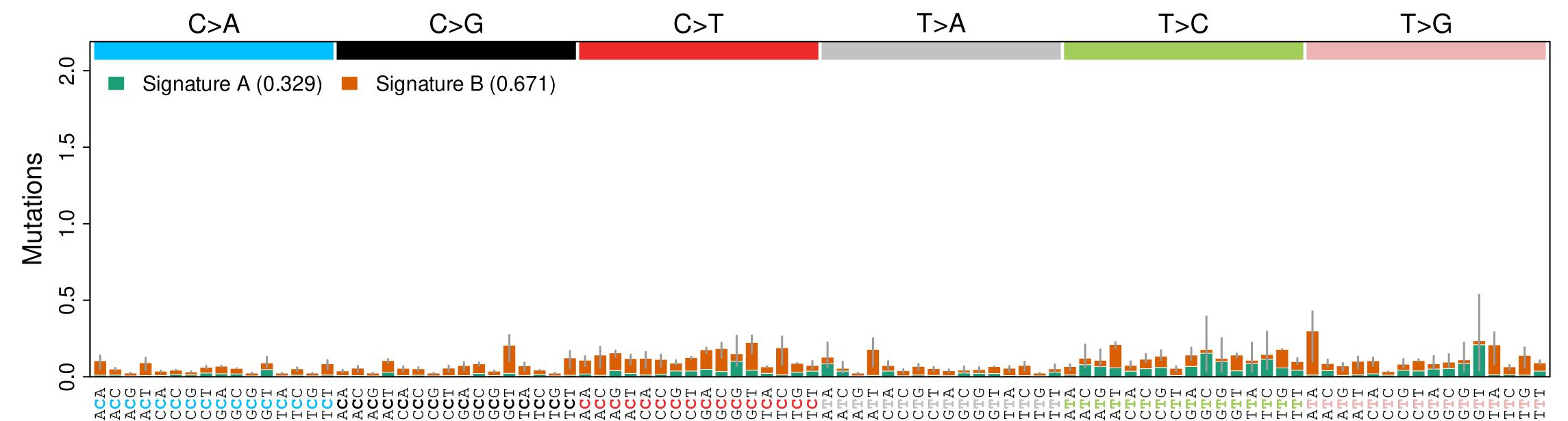
Reconstructed spectrum (cosine similarity = 0.436)



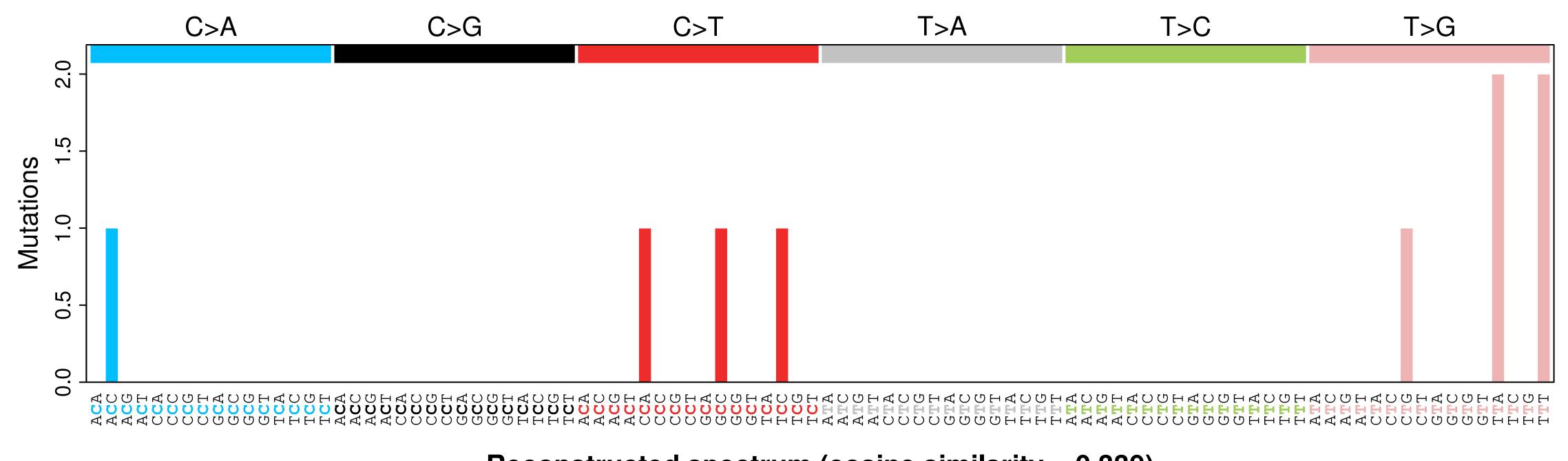
CATD0606a (9 mutations)



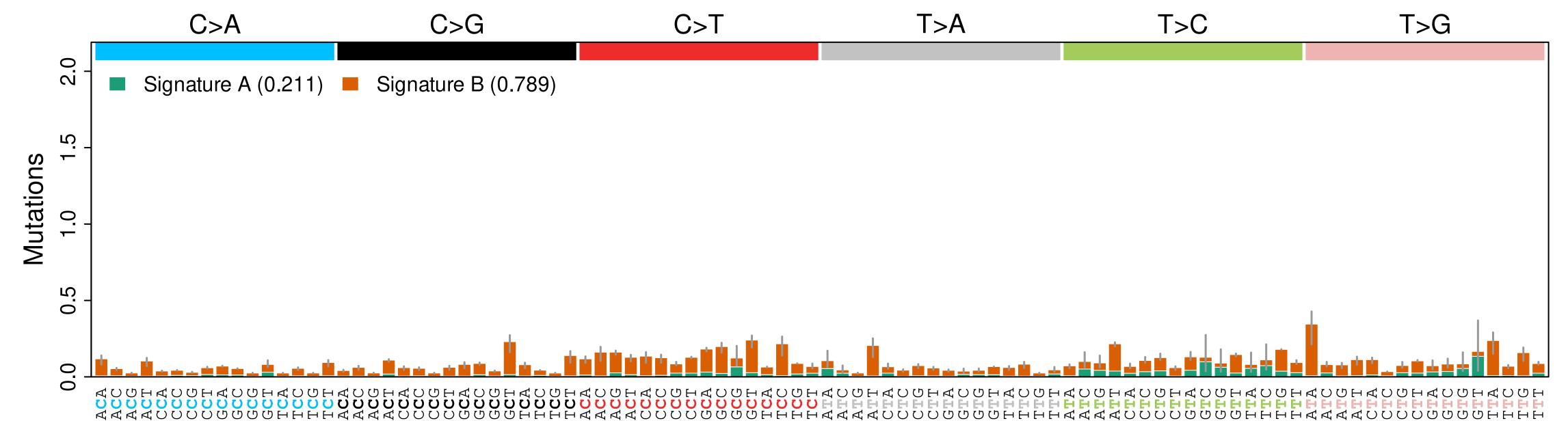
Reconstructed spectrum (cosine similarity = 0.251)



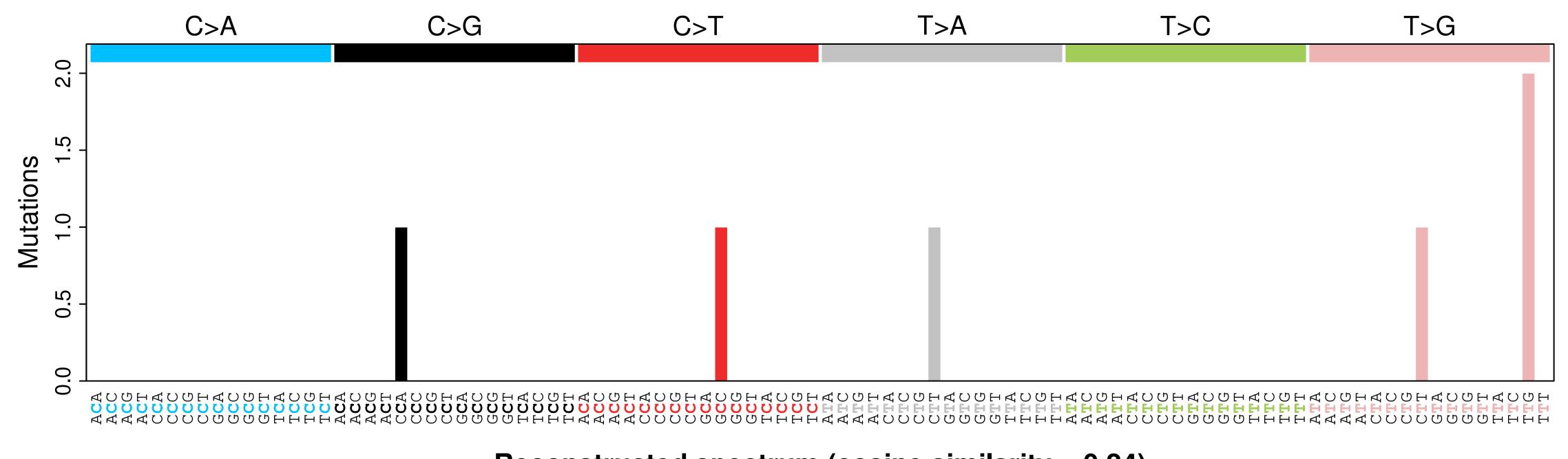
CATD0588a (9 mutations)



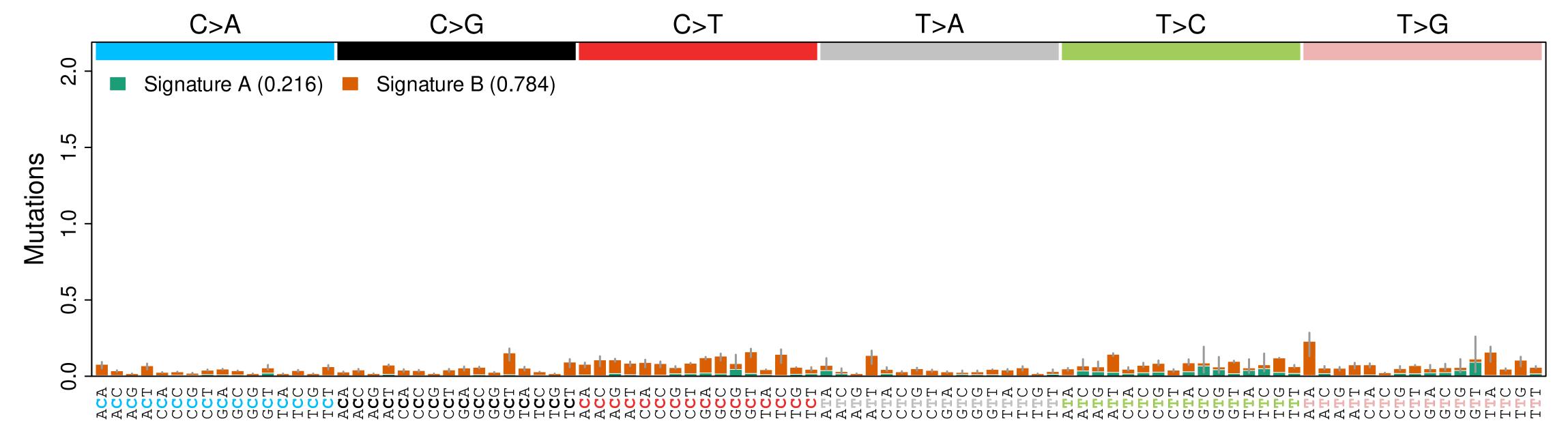
Reconstructed spectrum (cosine similarity = 0.339)



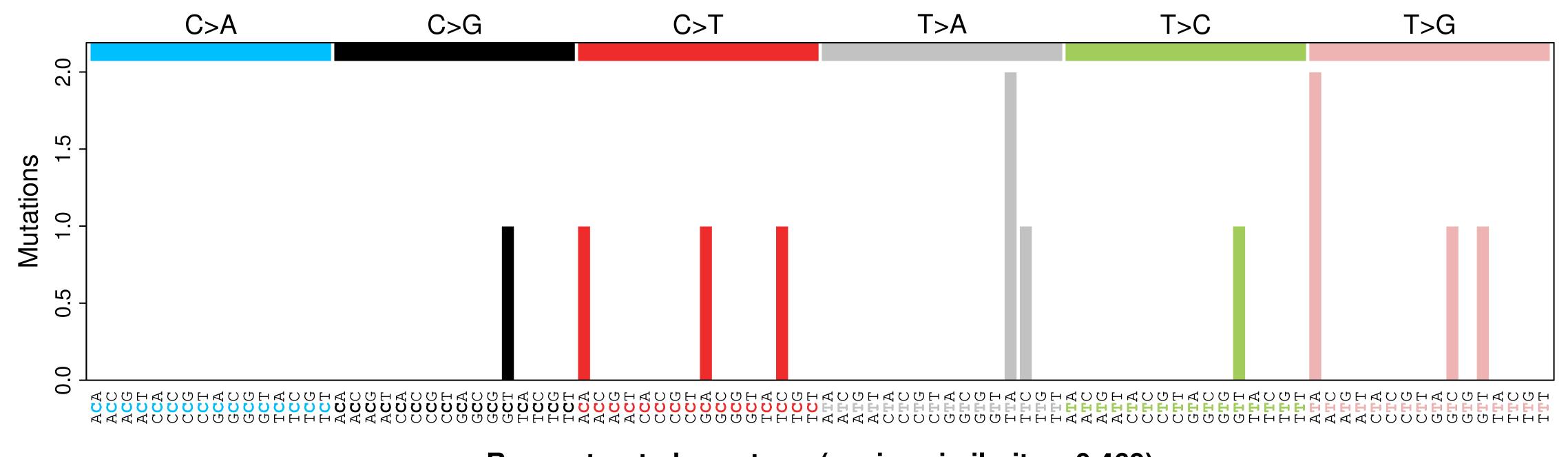
CATD0572a (6 mutations)



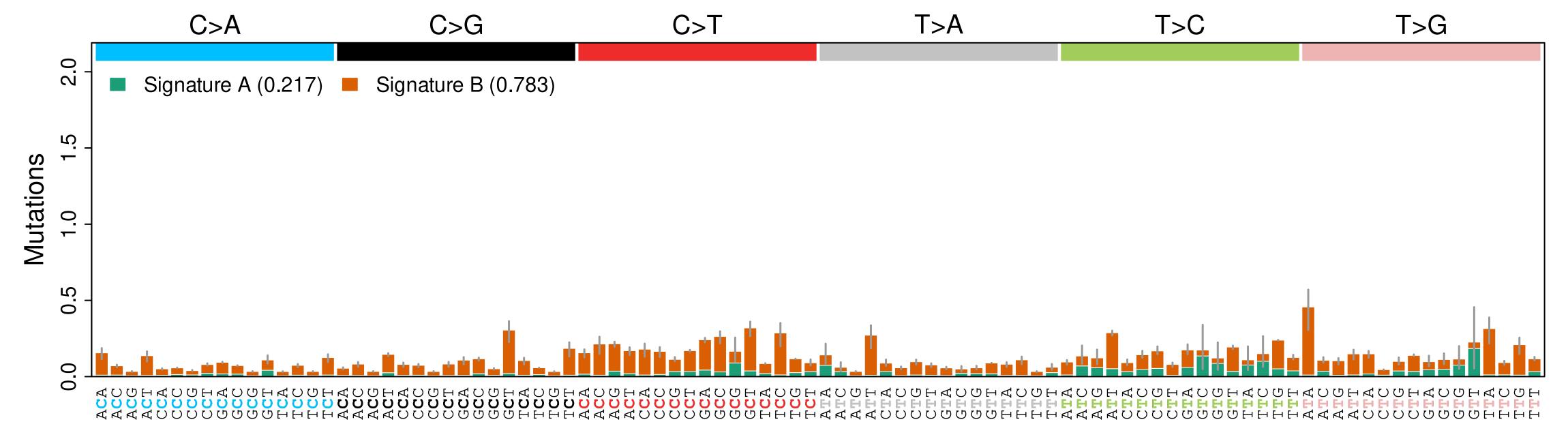
Reconstructed spectrum (cosine similarity = 0.24)



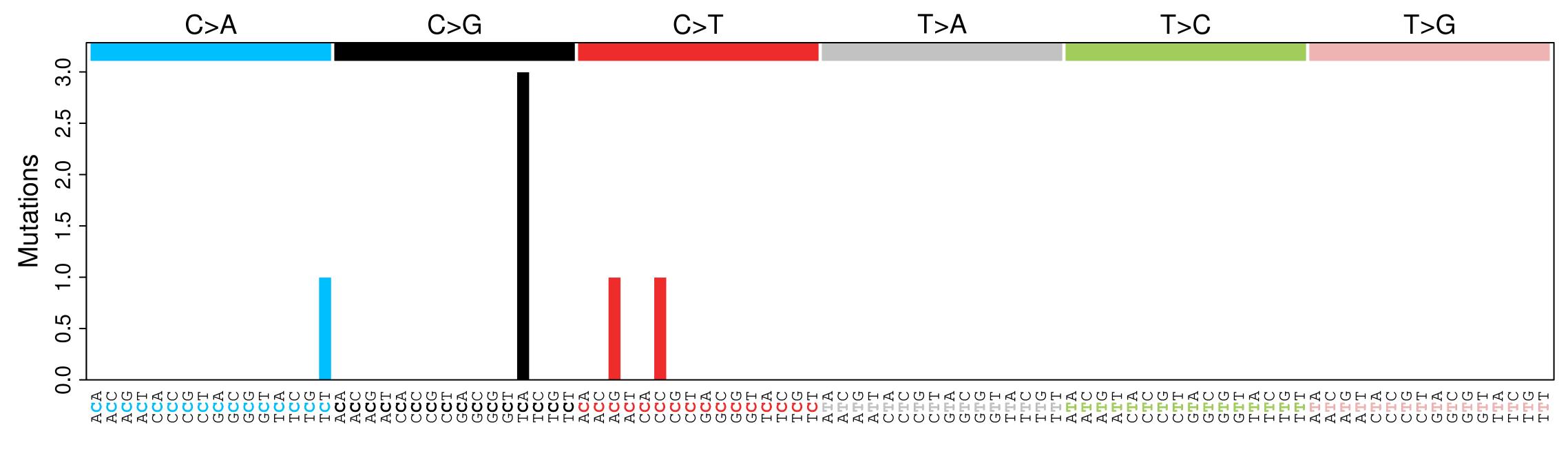
CATD0573a (12 mutations)

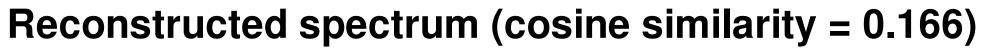


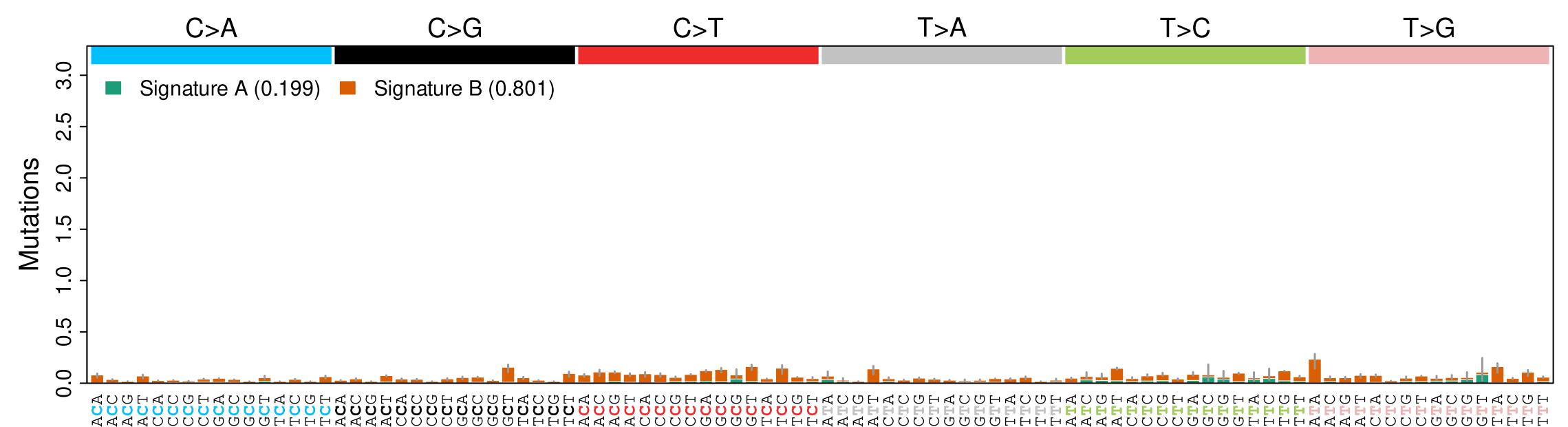
Reconstructed spectrum (cosine similarity = 0.469)



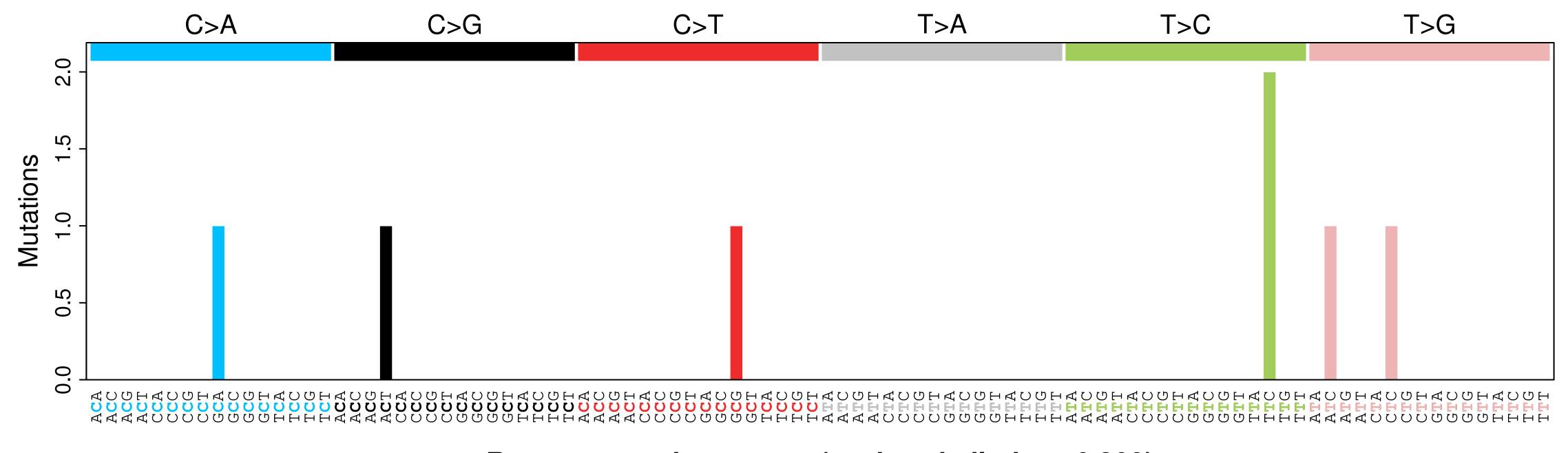
CATD0592a (6 mutations)

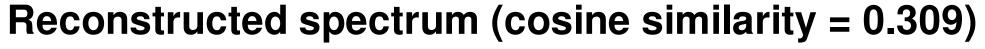


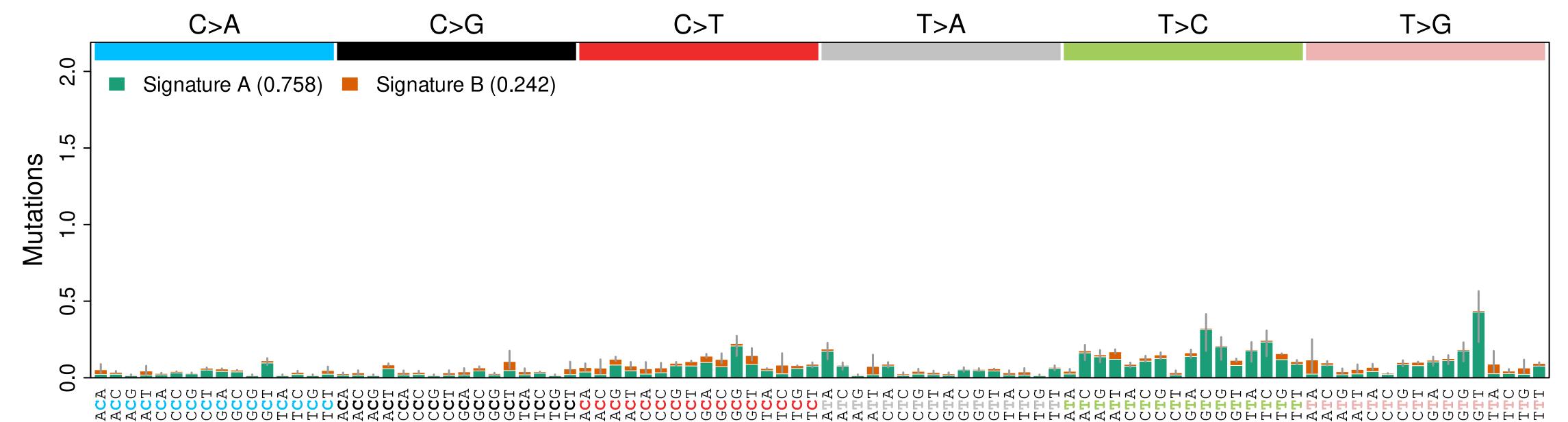




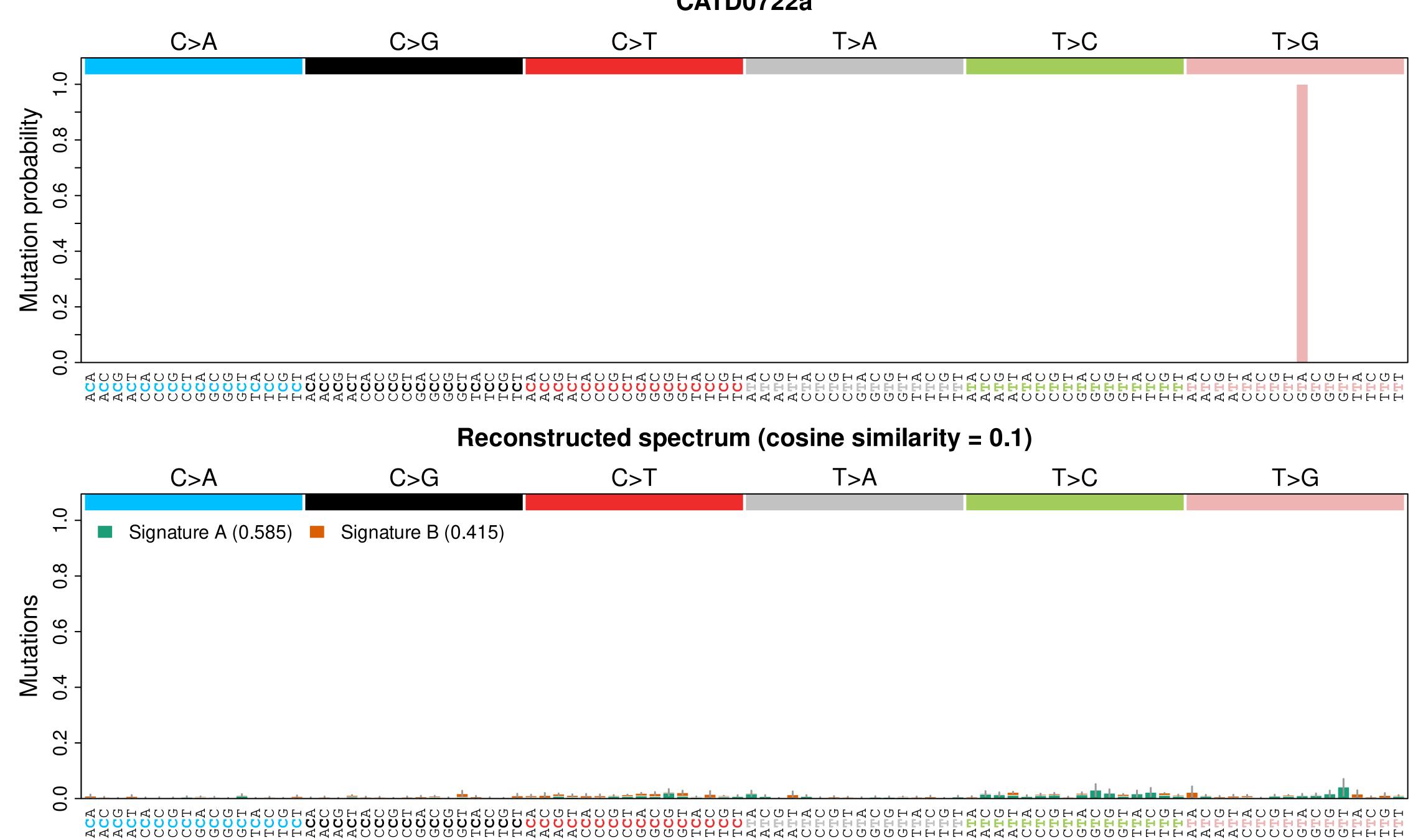
CATD0603a (7 mutations)



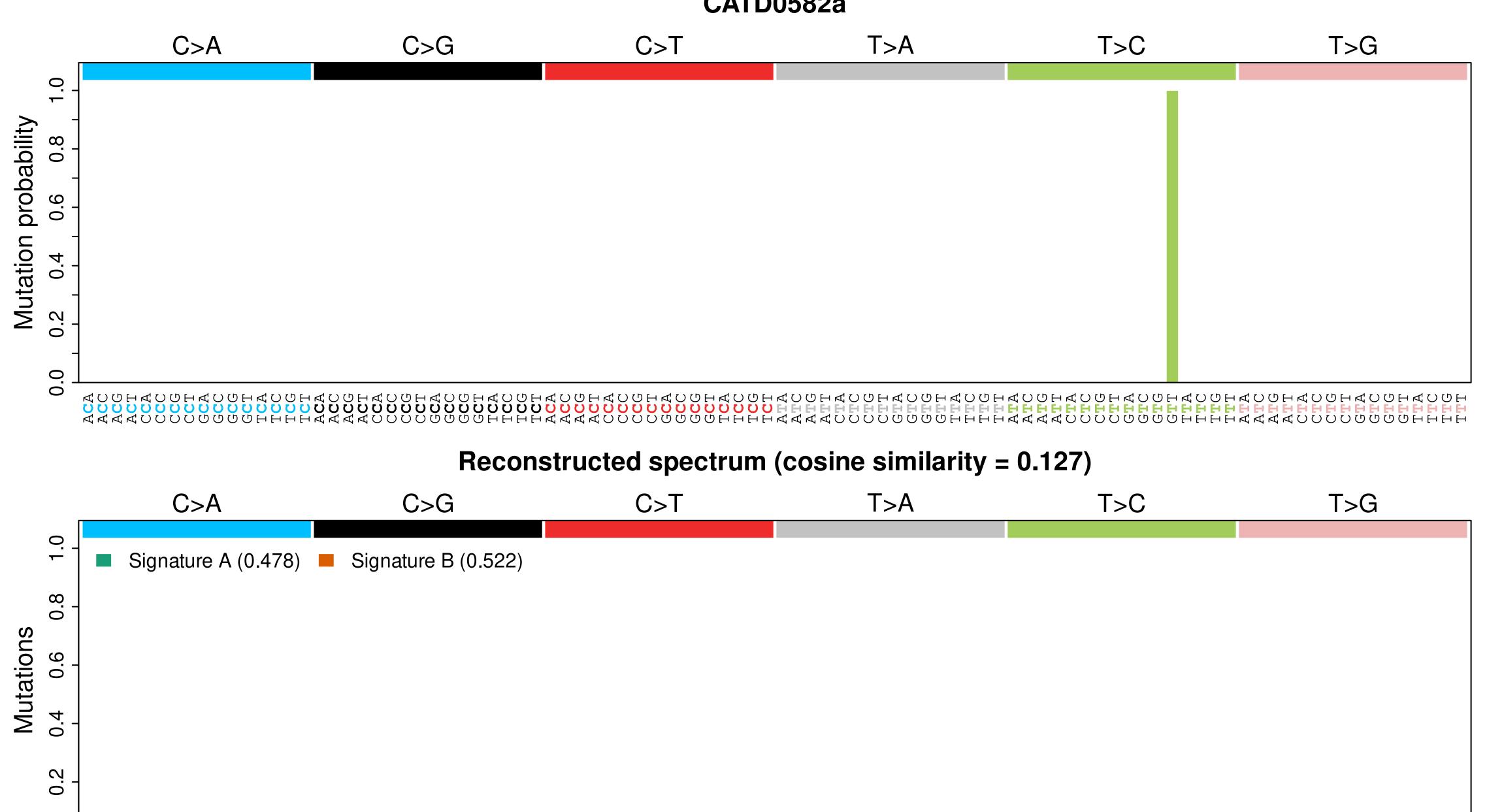




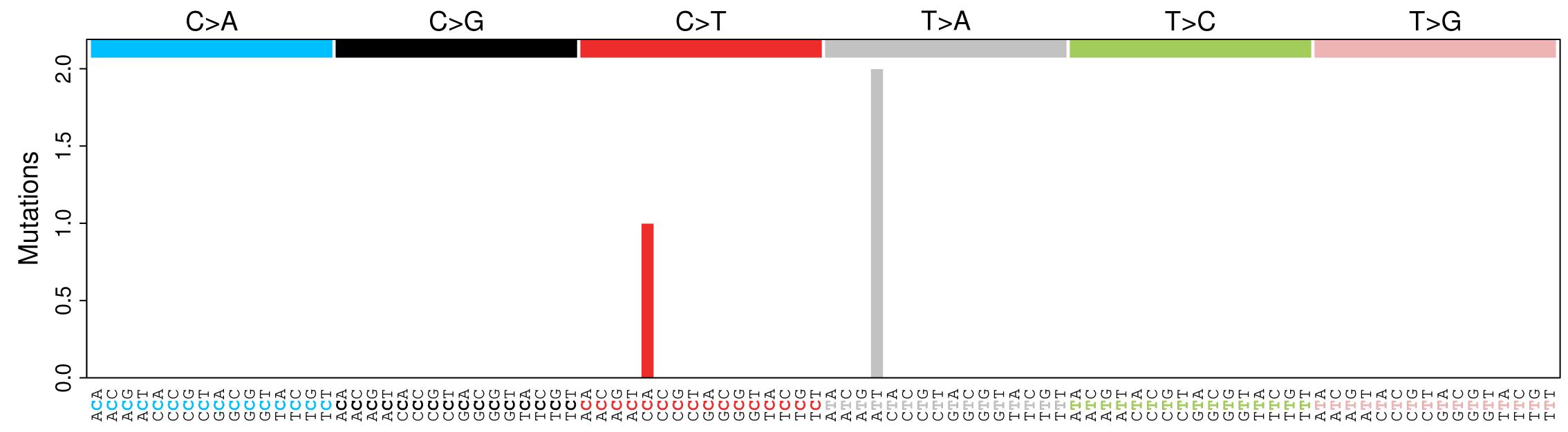




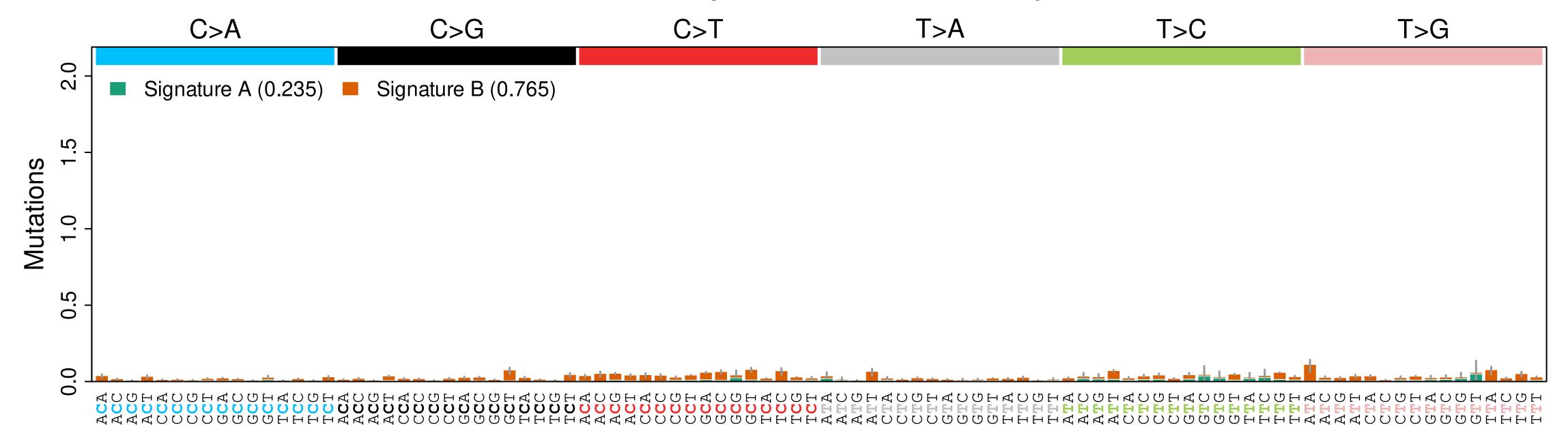




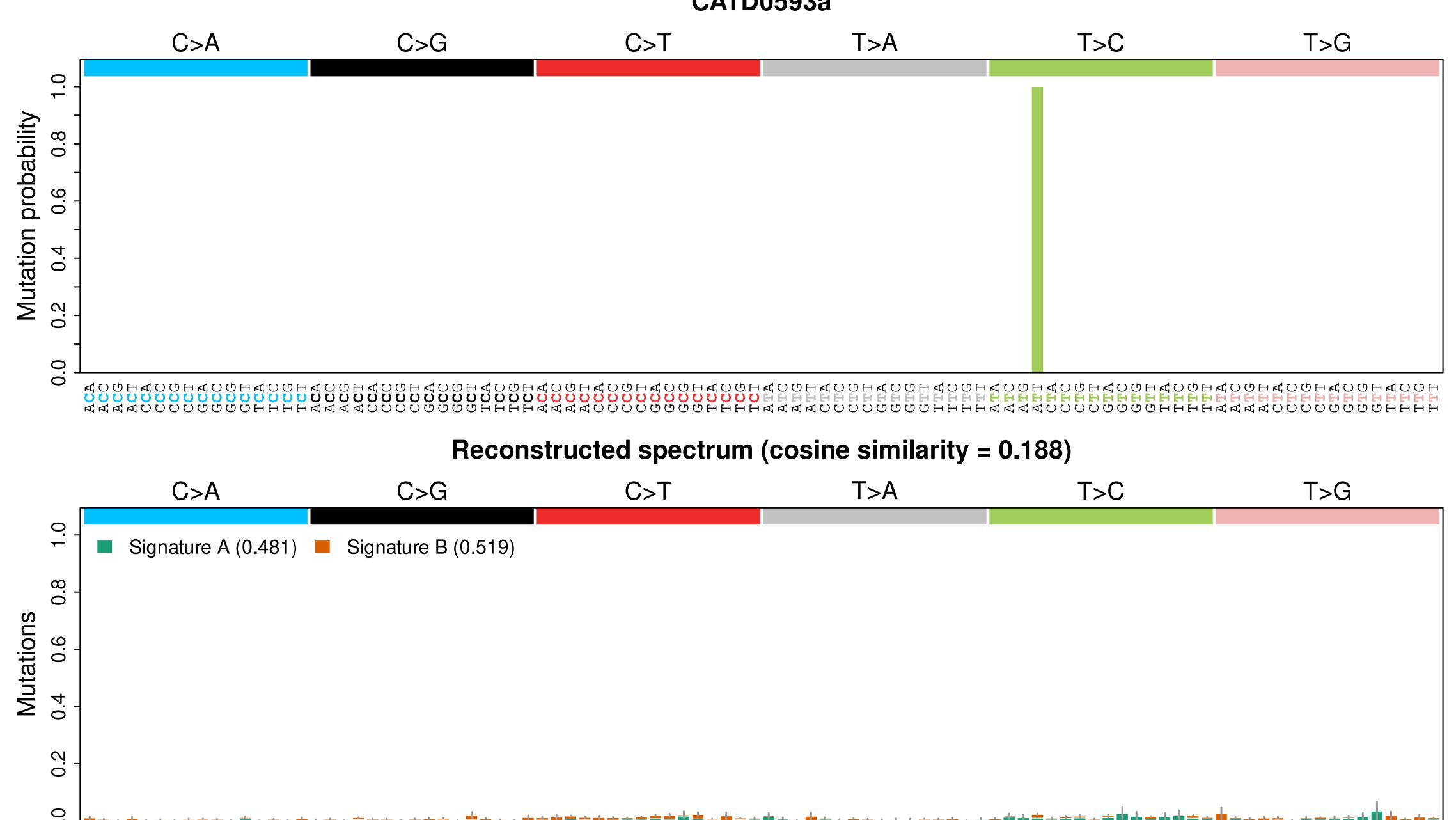
CATD0585a (3 mutations) C>A C>G C>T T>A



Reconstructed spectrum (cosine similarity = 0.22)





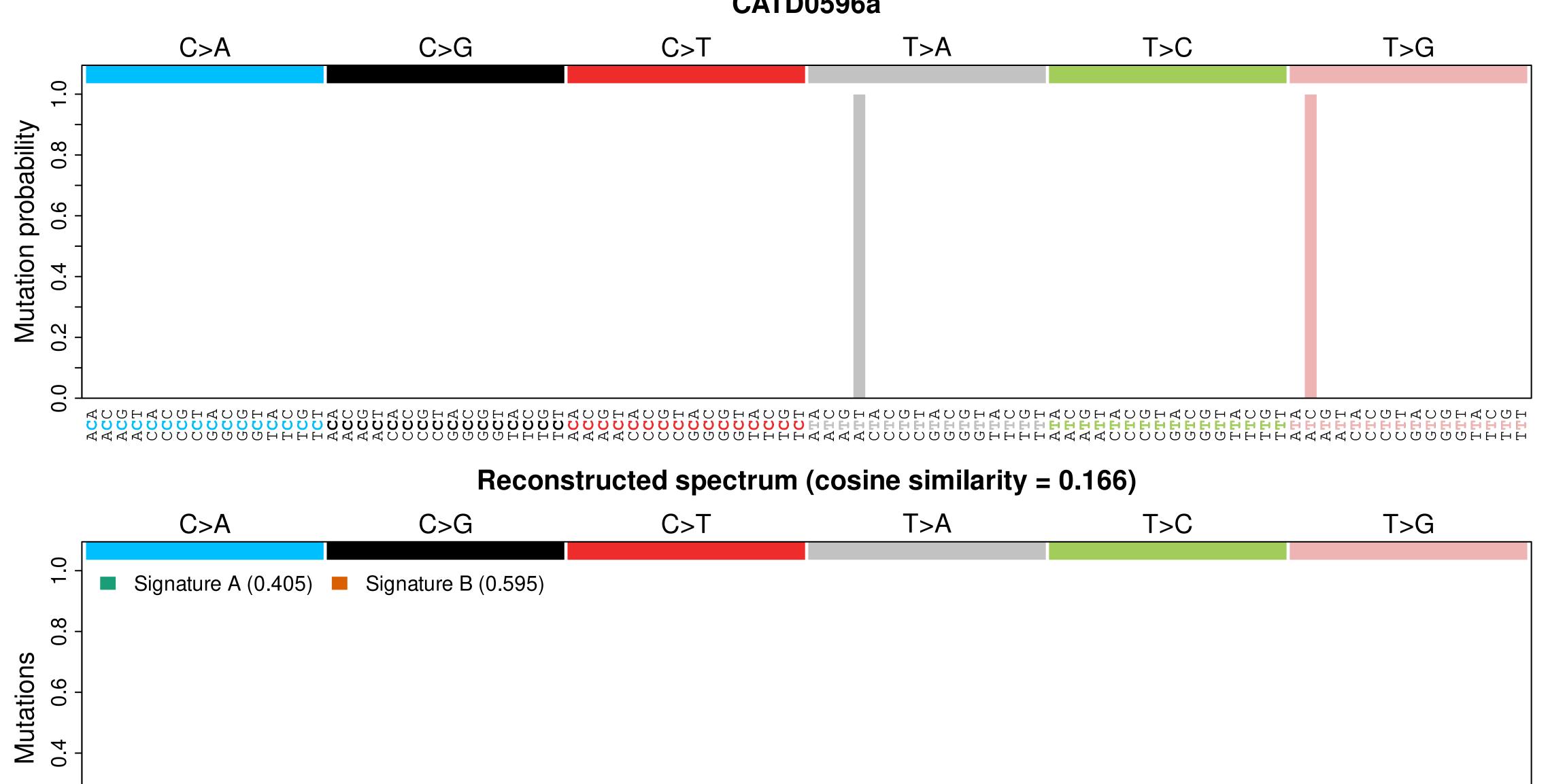


CATD0581a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 Mutations 0.0 **Reconstructed spectrum (cosine similarity = 0.158)** C>A T>G C>G T>A T>C C>T 2.0 Signature A (0.251) Signature B (0.749) 5 Mutations 5 0 0

CATD0736a (4 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 = 0.295)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.623) Signature B (0.377) 5 Mutations 2

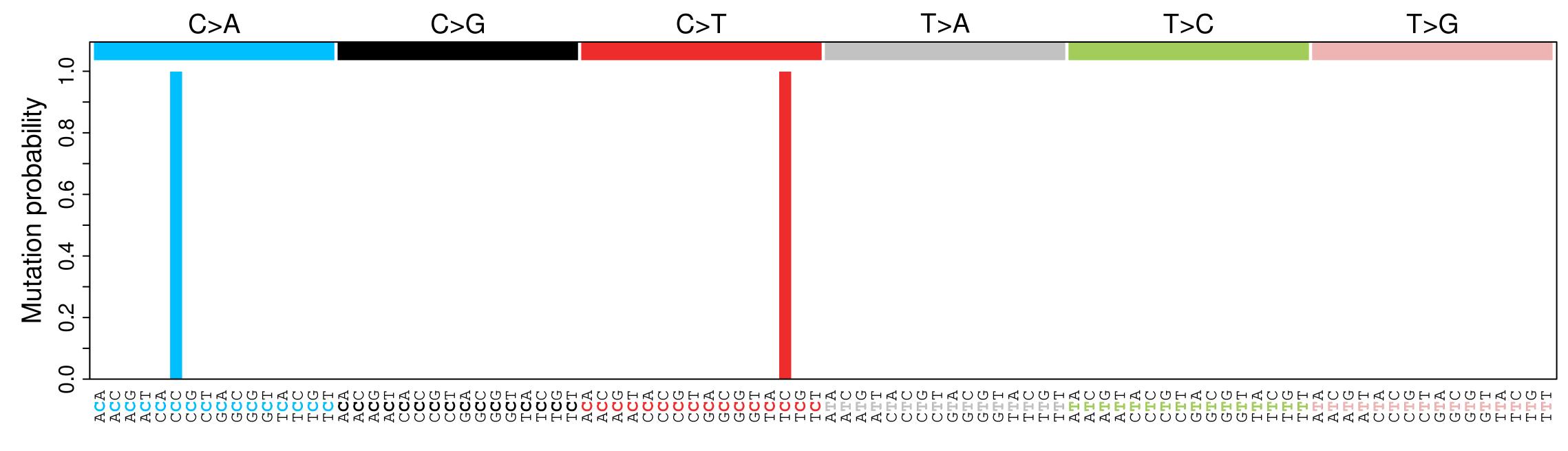
0



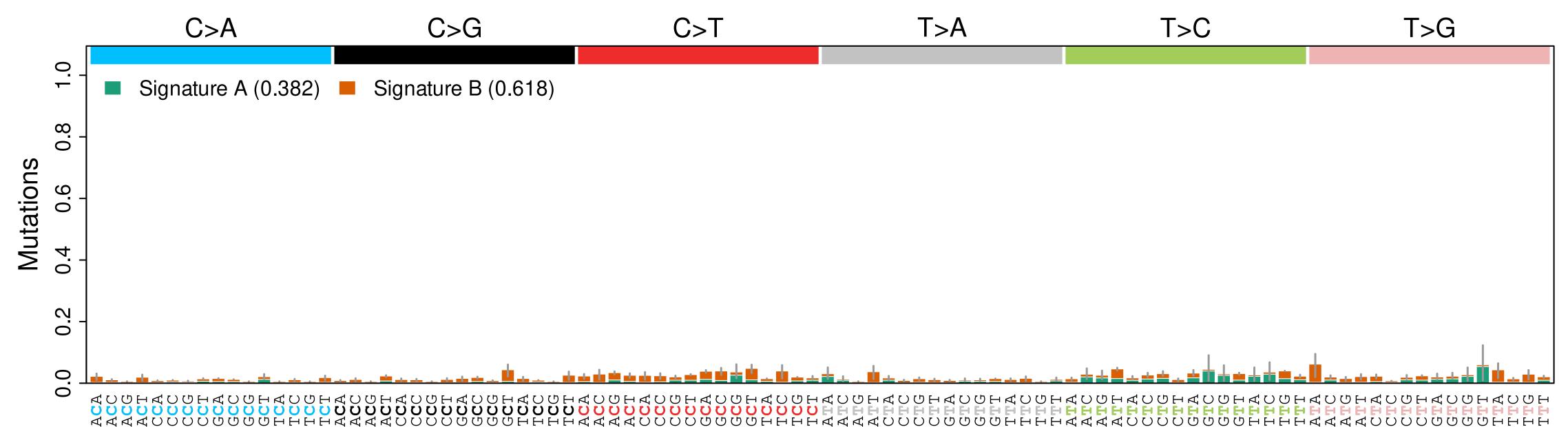


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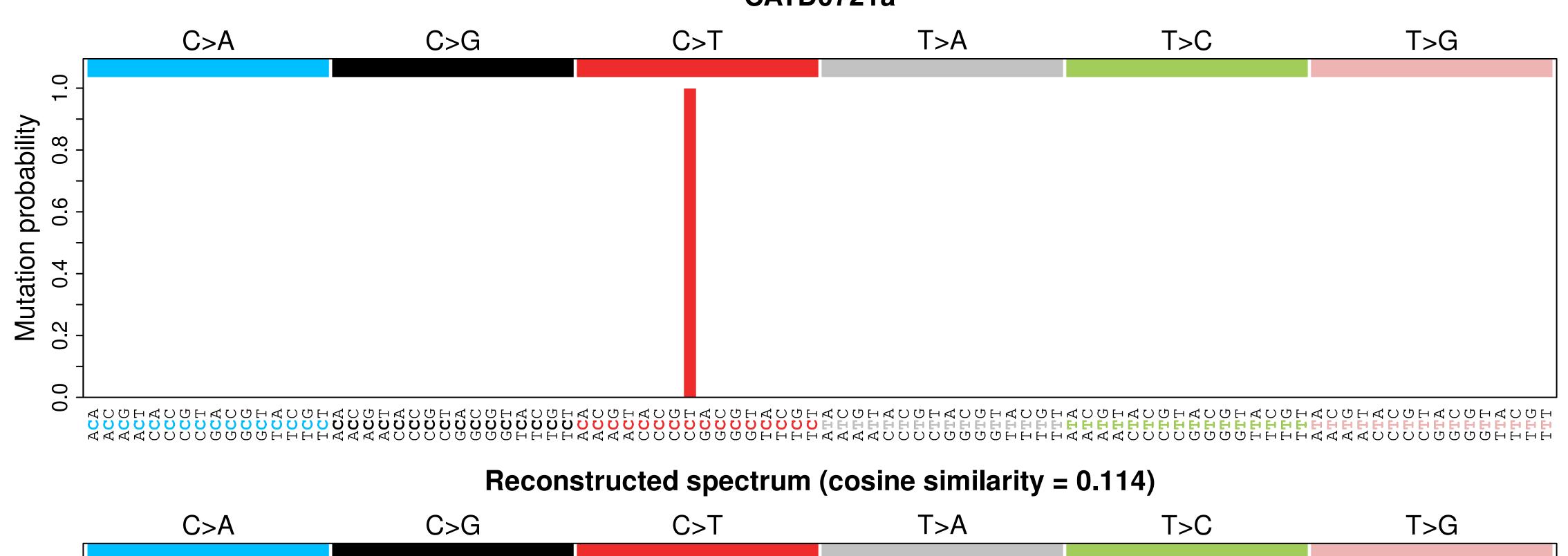


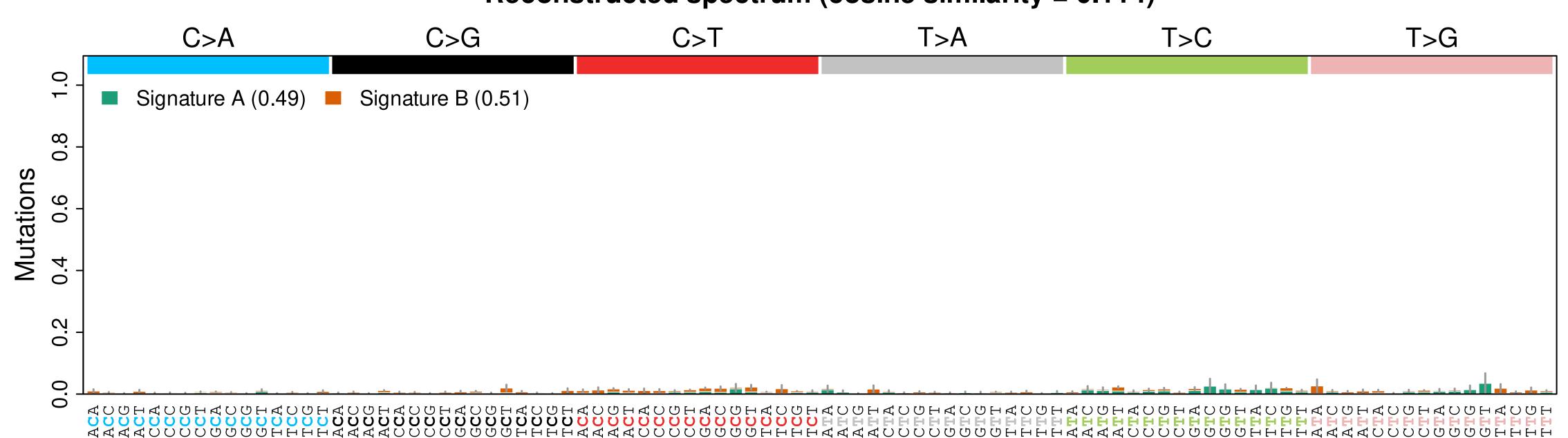


Reconstructed spectrum (cosine similarity = 0.146)

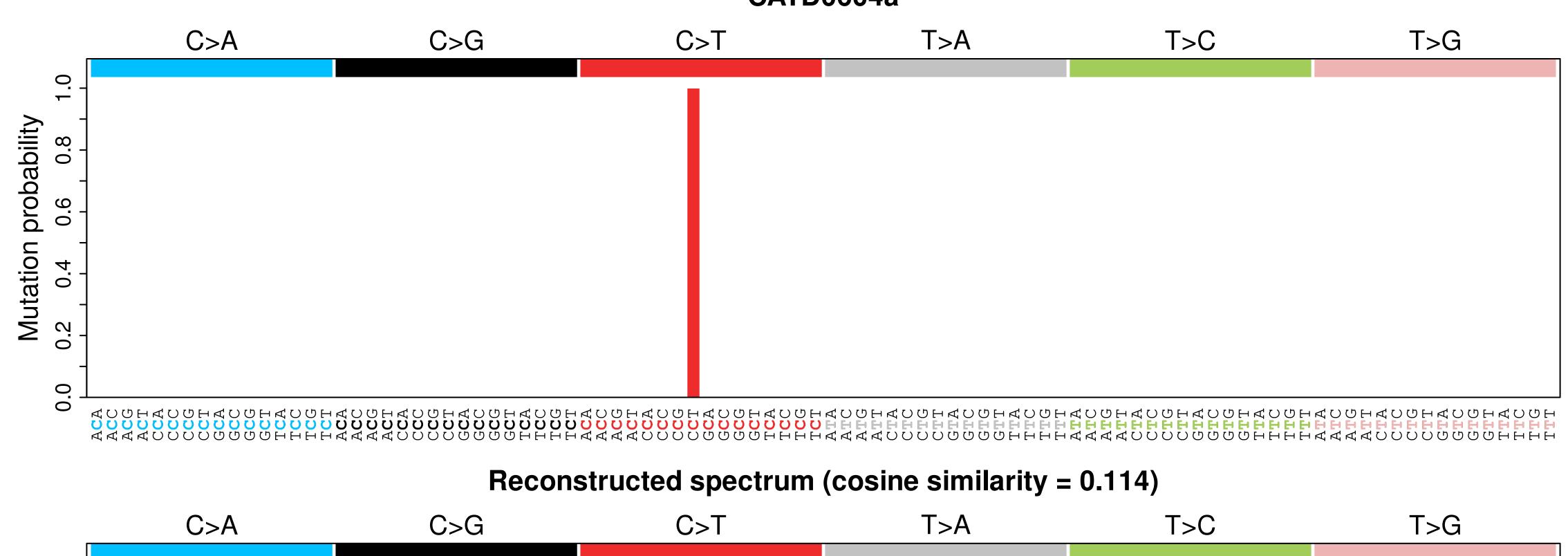


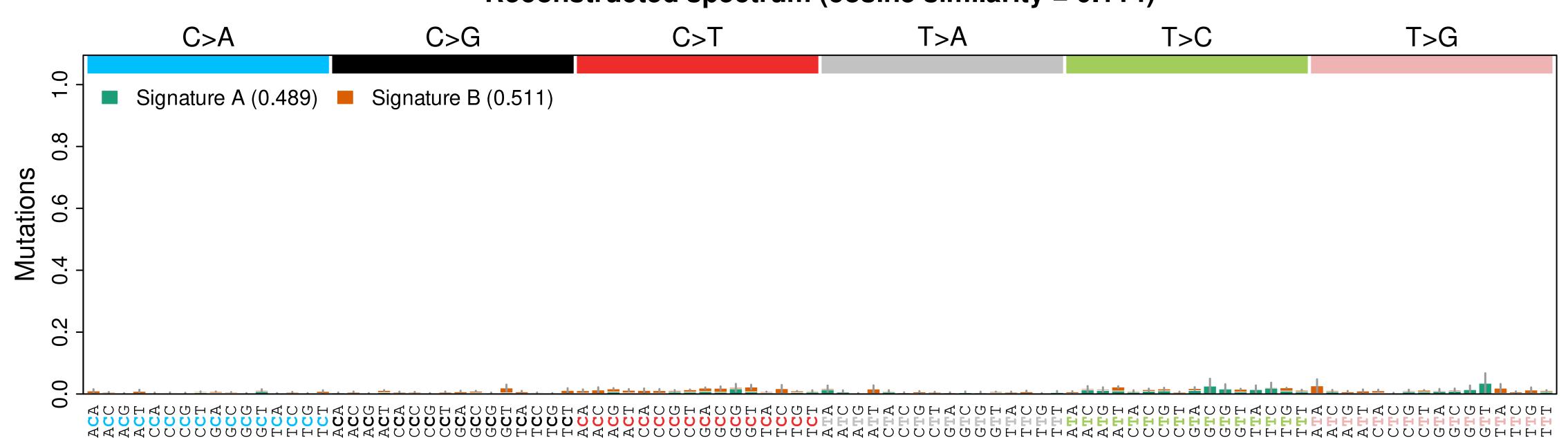












CATD0720a

