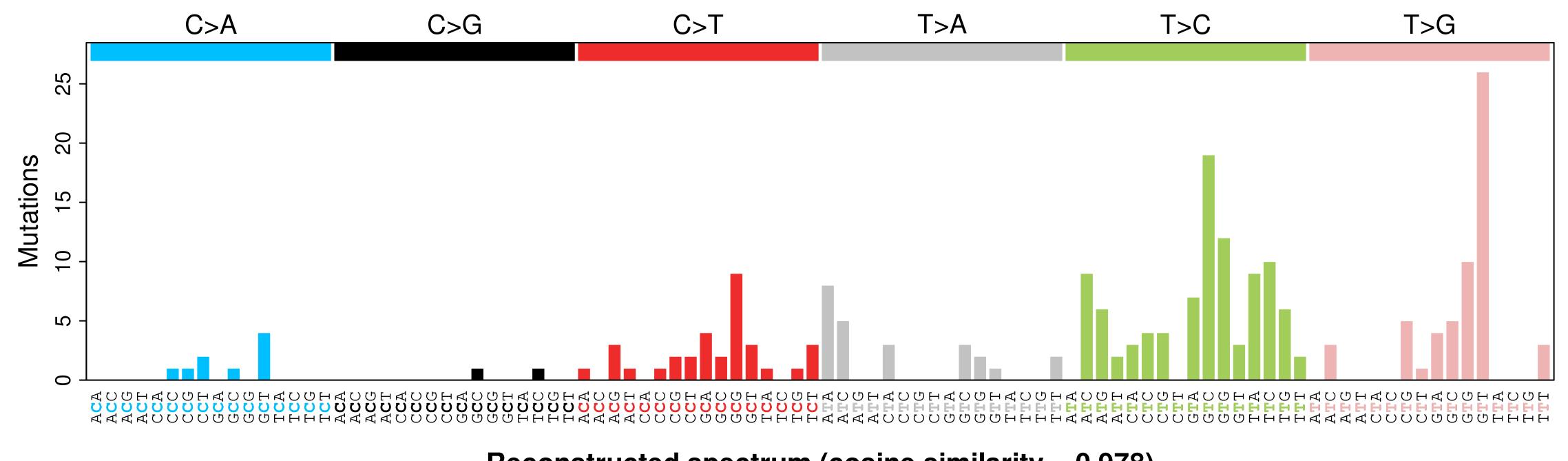
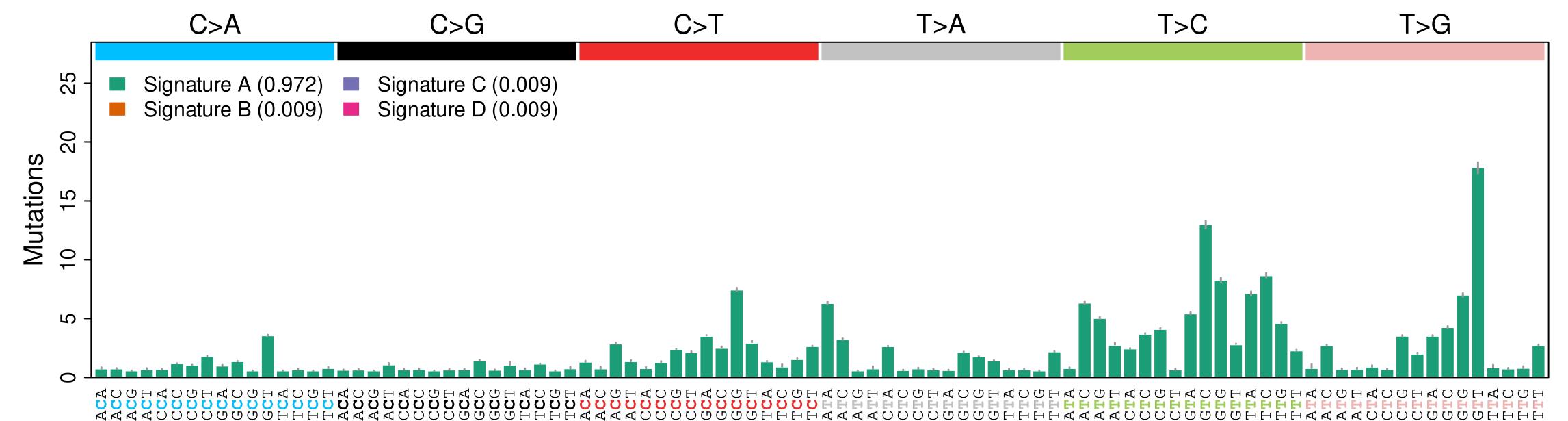
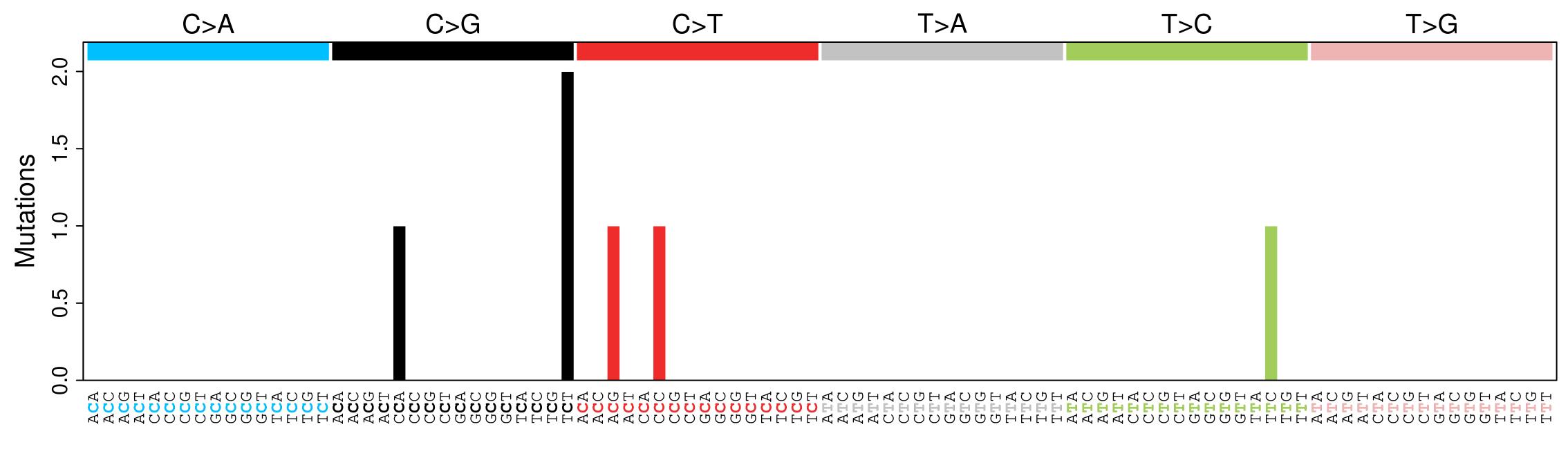
#### CATD0735a (221 mutations)



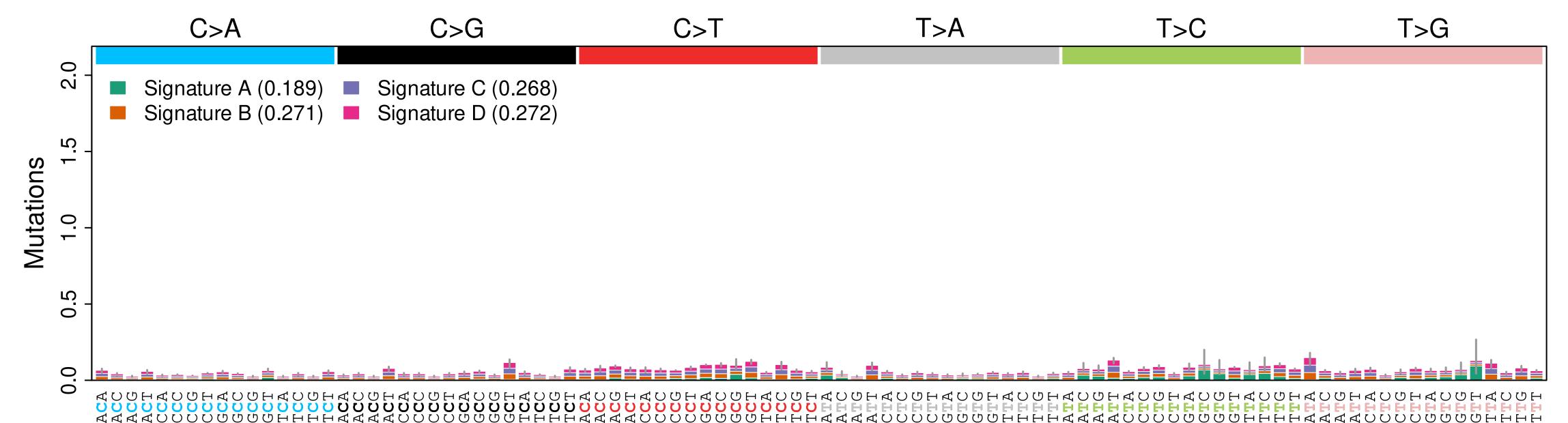
## Reconstructed spectrum (cosine similarity = 0.978)



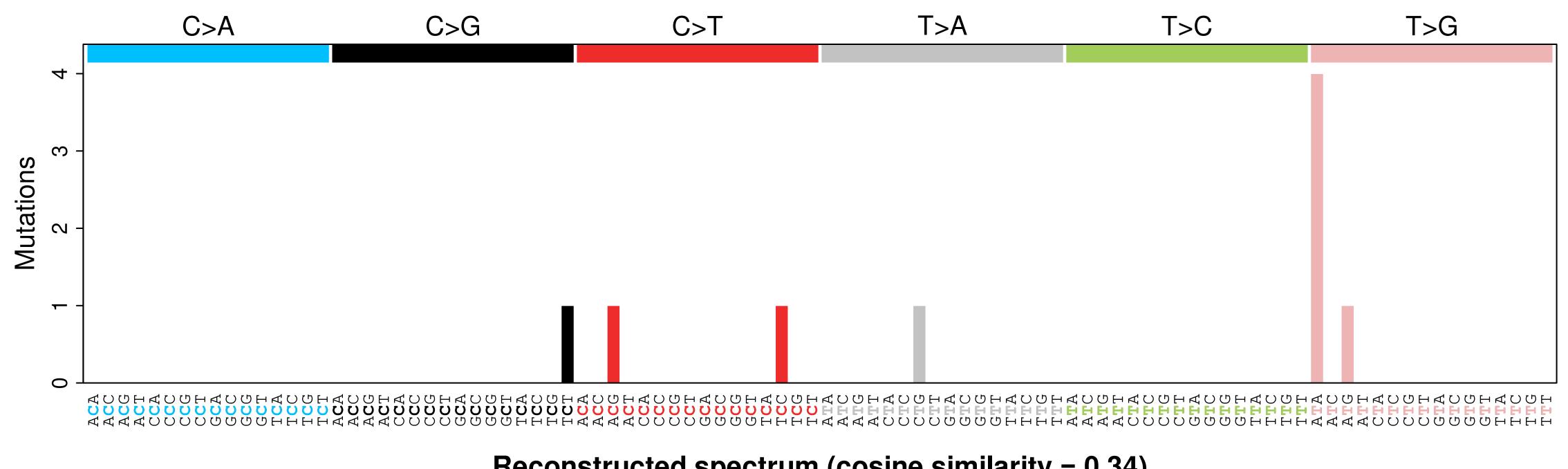
#### CATD0575a (6 mutations)



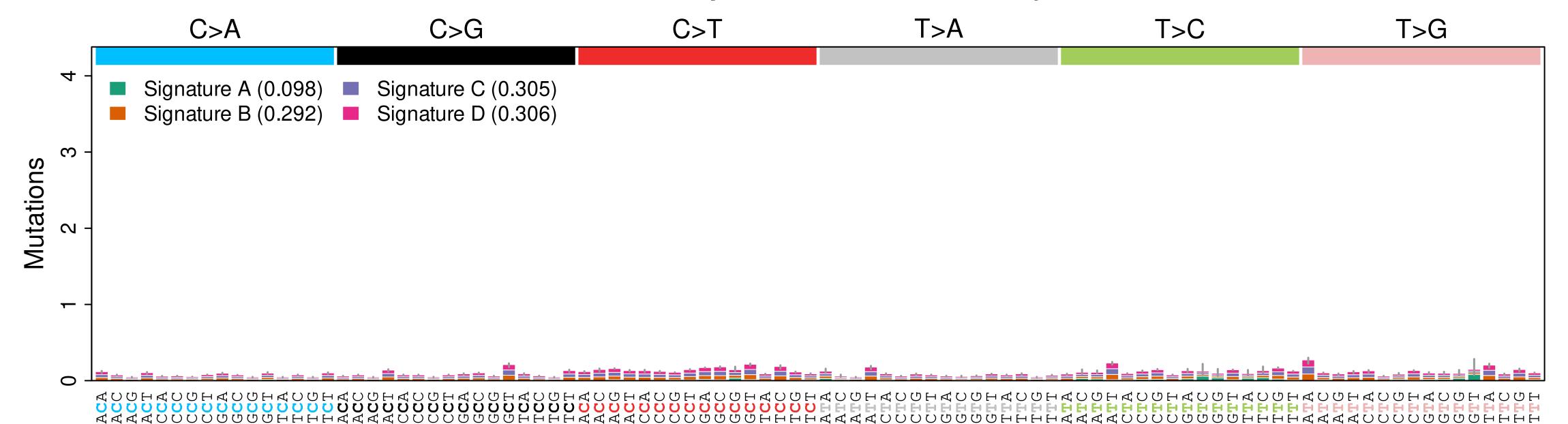
## Reconstructed spectrum (cosine similarity = 0.236)



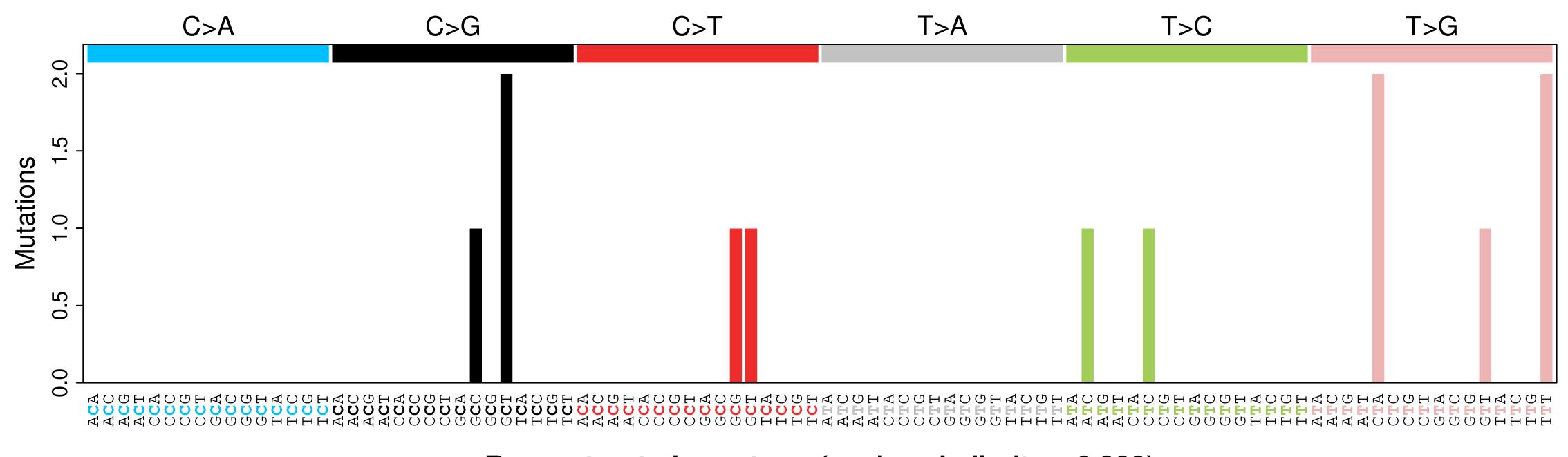
#### CATD0584a (9 mutations)



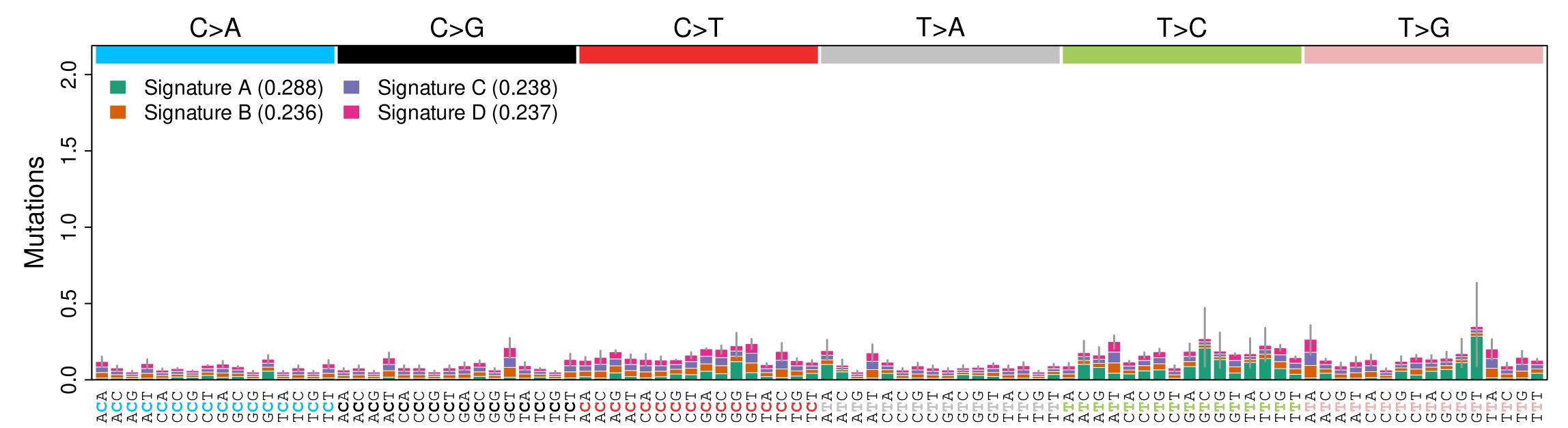
## **Reconstructed spectrum (cosine similarity = 0.34)**



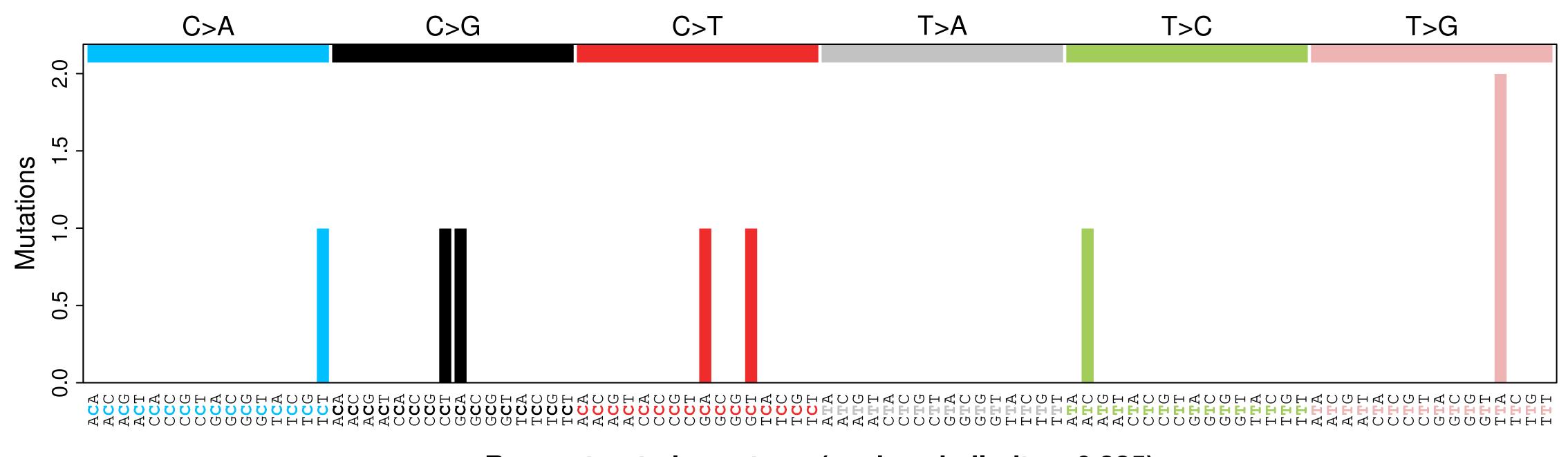
#### CATD0600a (12 mutations)



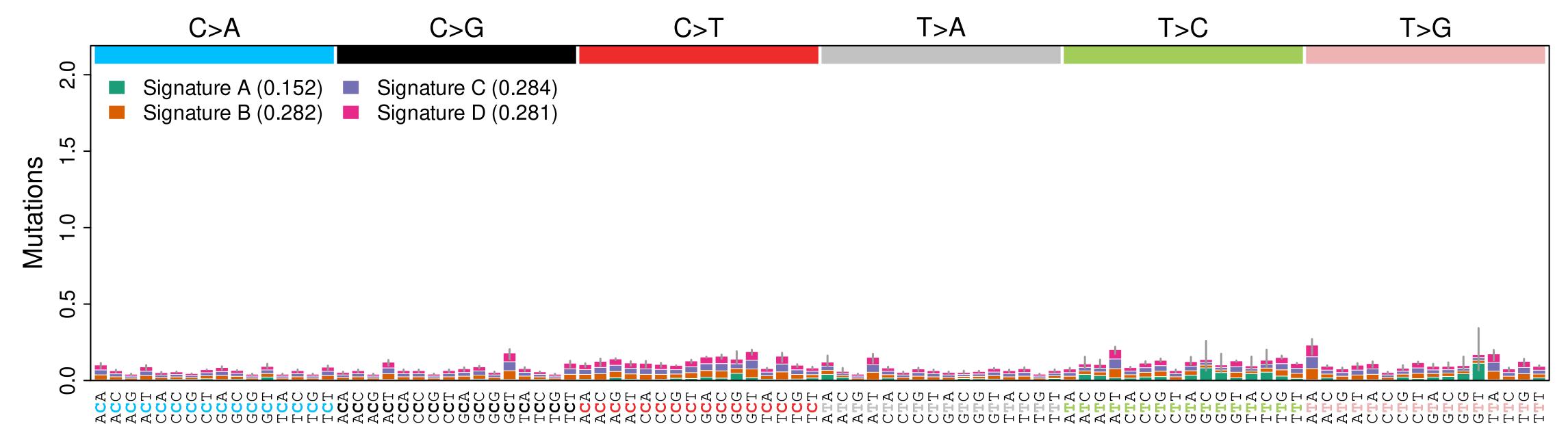




## CATD0576a (8 mutations)

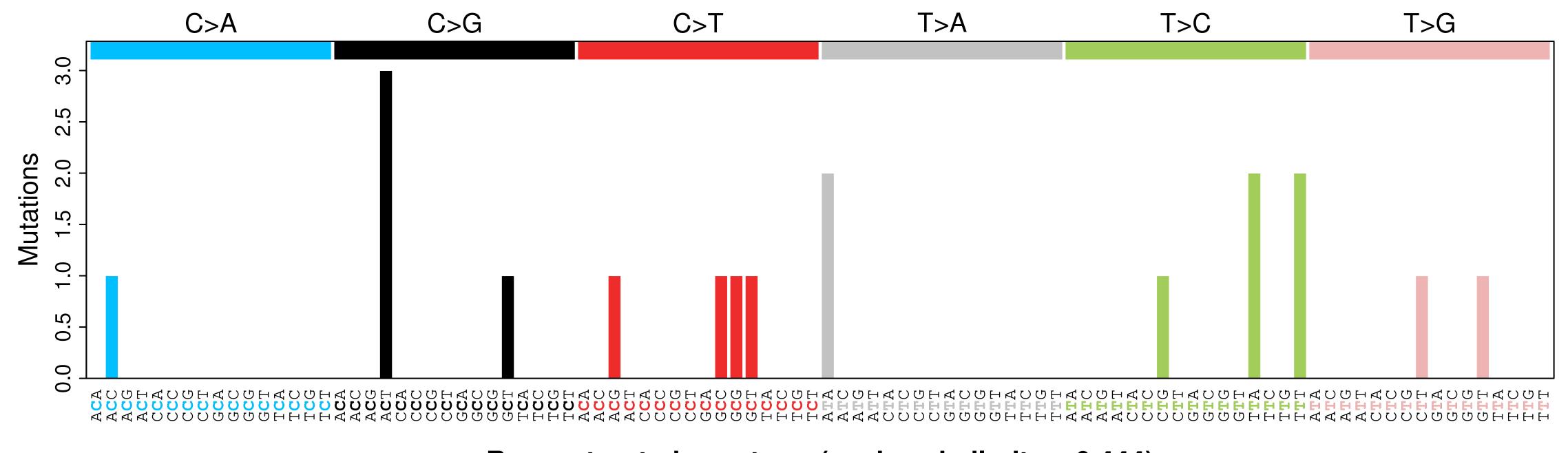




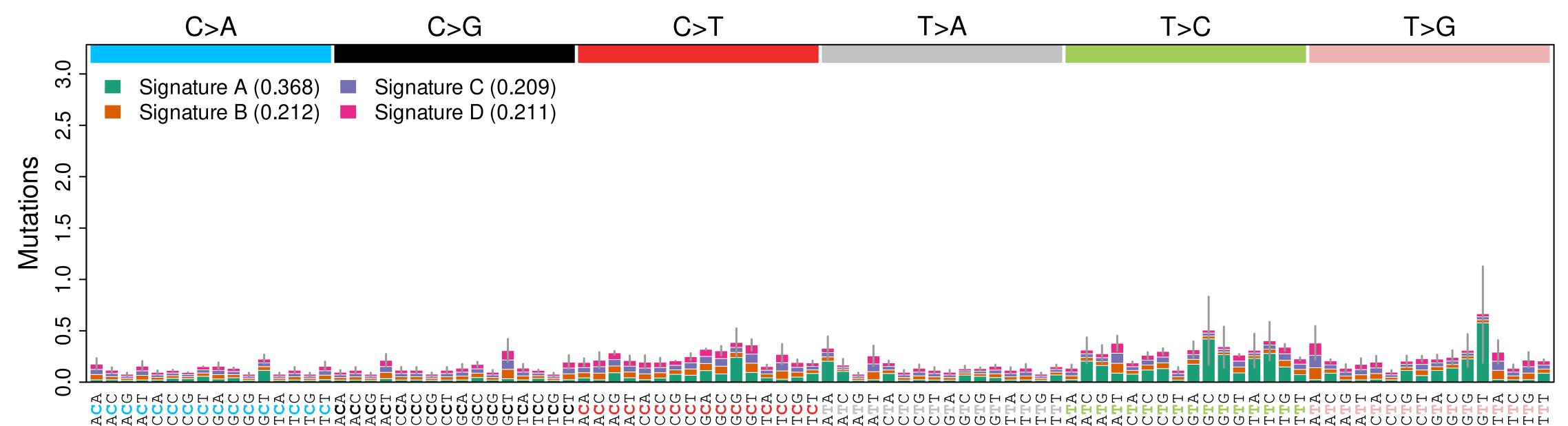


## CATD0679a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.307)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.193) Signature C (0.27) Signature B (0.269) Signature D (0.268) 5 Mutations 2 0

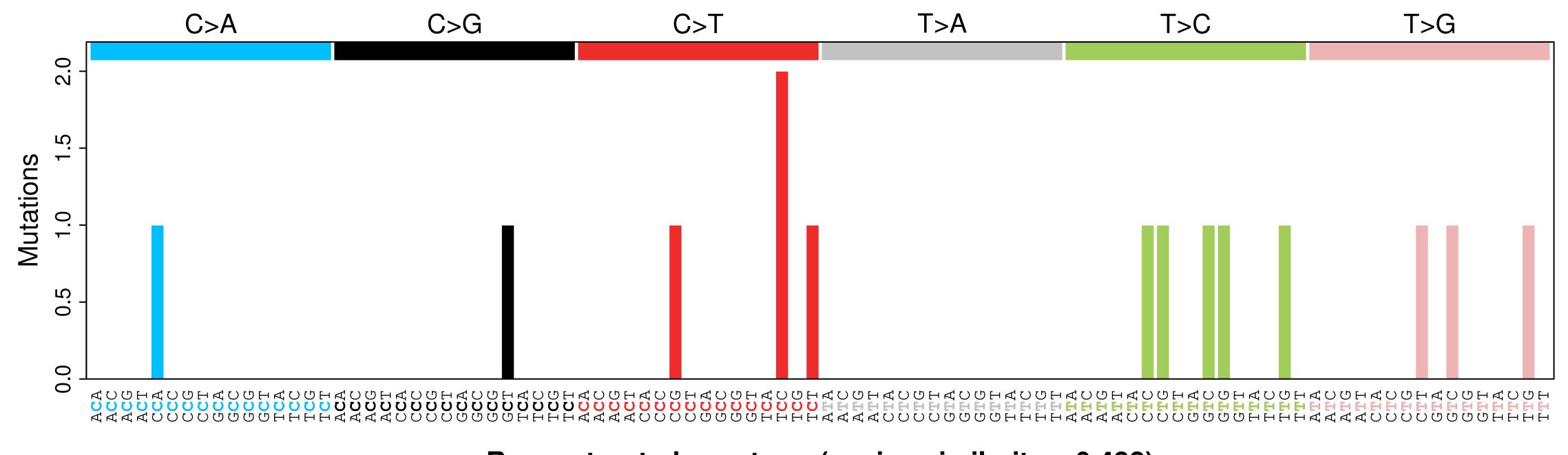
#### CATD0591a (18 mutations)



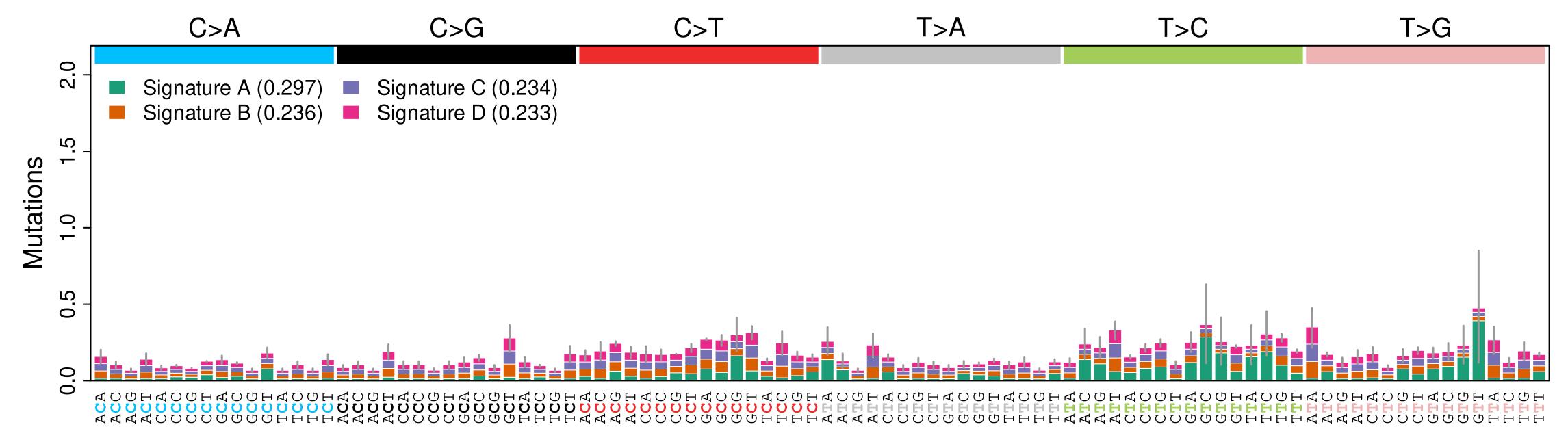
## Reconstructed spectrum (cosine similarity = 0.444)



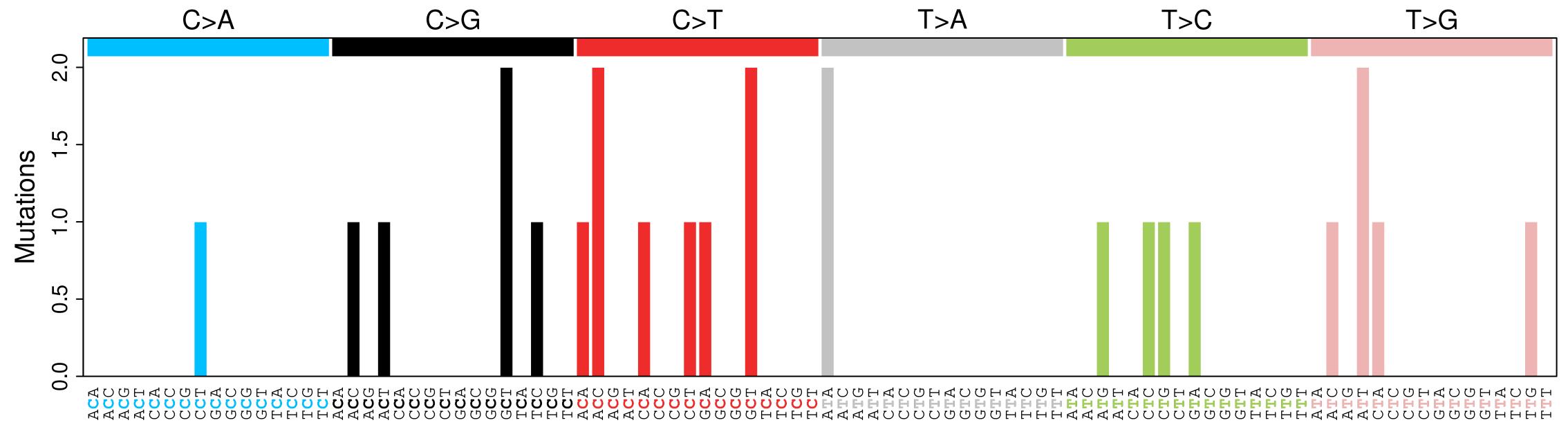
#### CATD0686a (14 mutations)

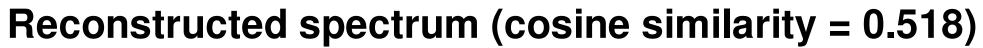


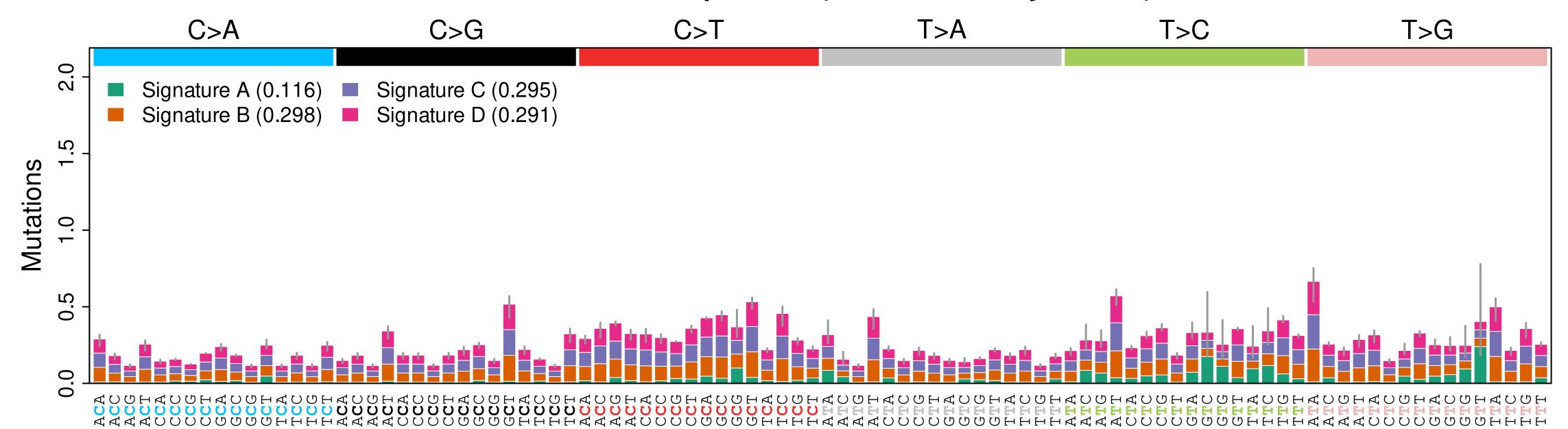
## **Reconstructed spectrum (cosine similarity = 0.432)**



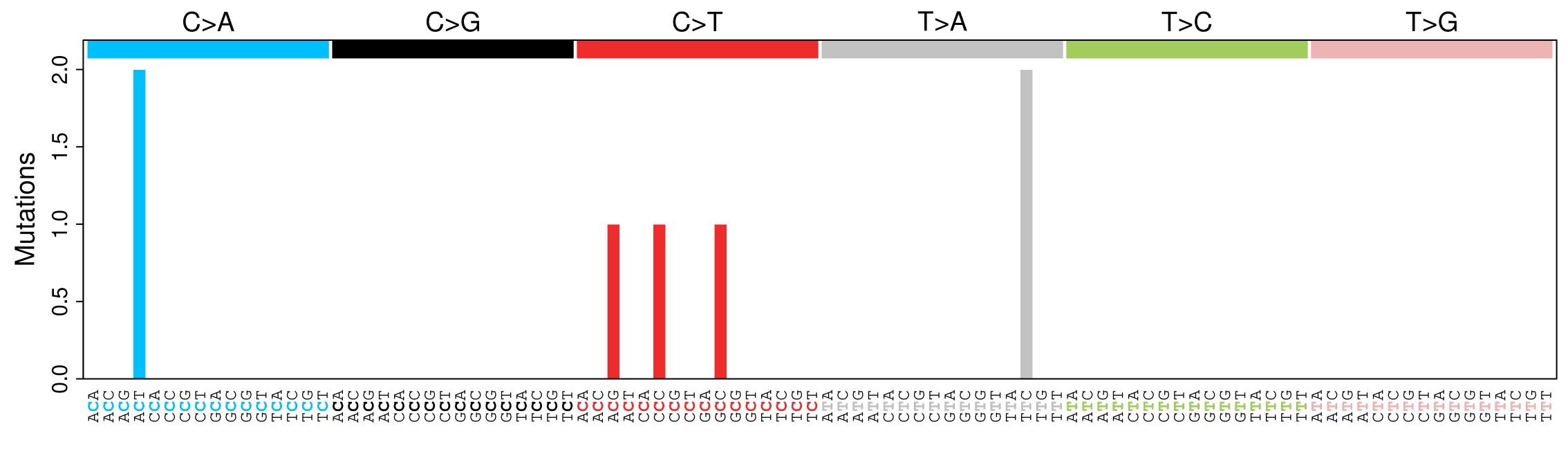
#### CATD0734a (25 mutations)



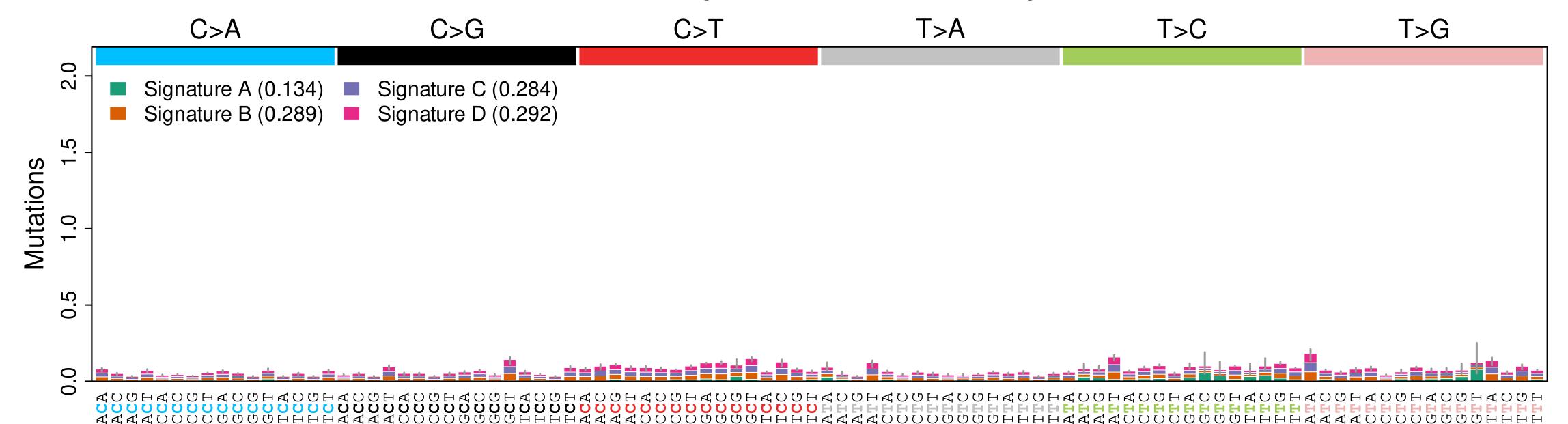




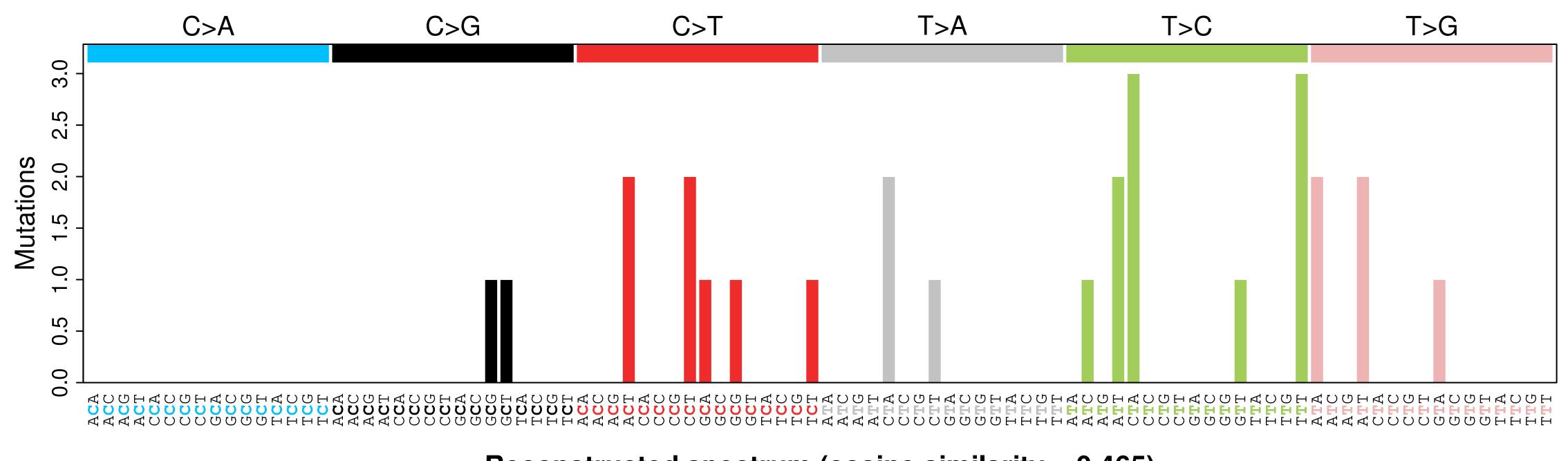
## CATD0678a (7 mutations)



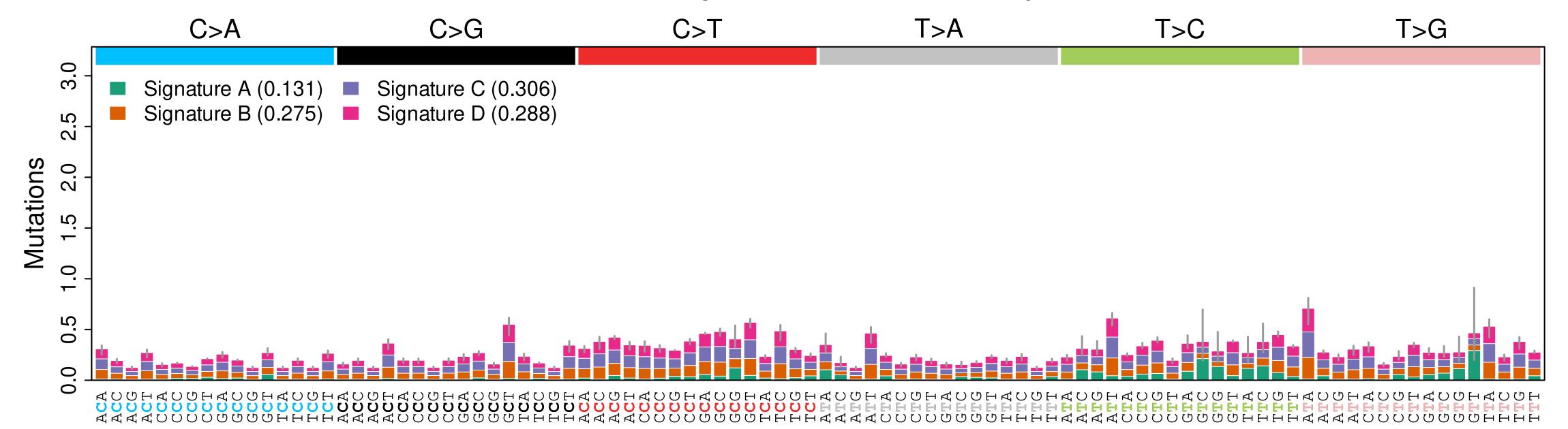
## **Reconstructed spectrum (cosine similarity = 0.225)**



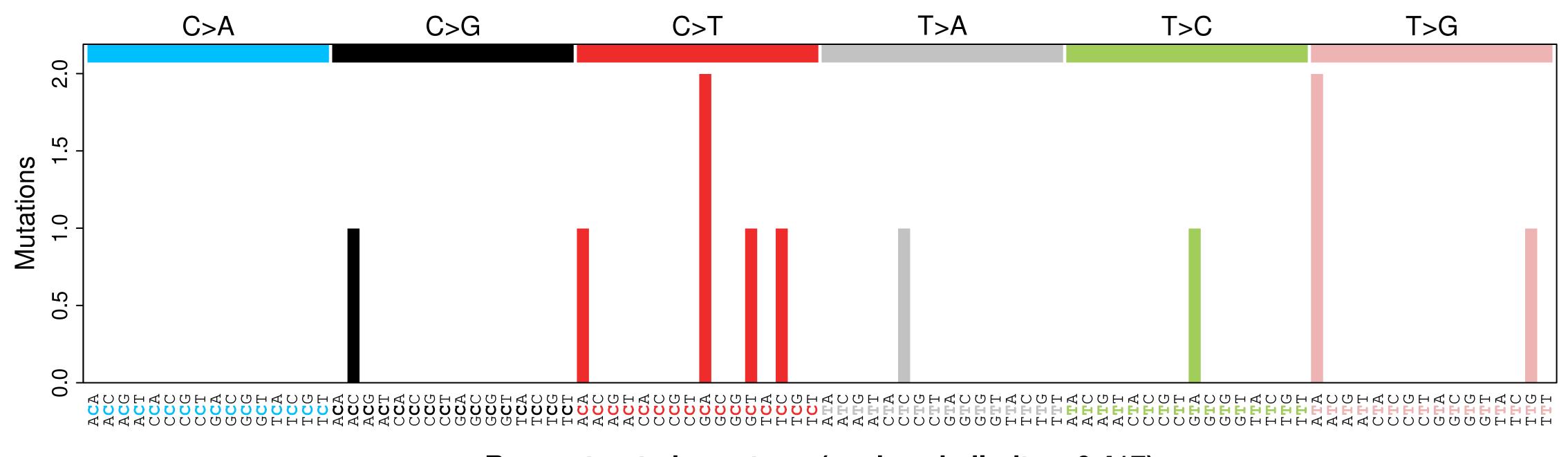
#### CATD0729a (27 mutations)

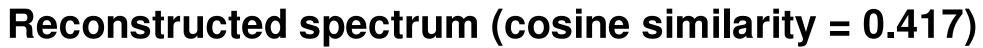


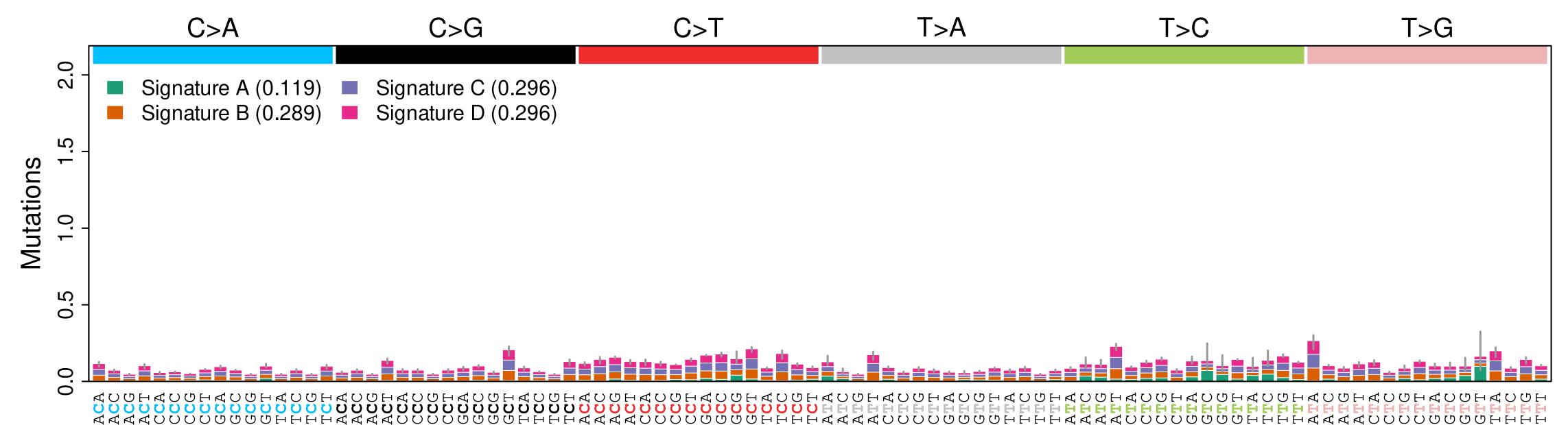
## **Reconstructed spectrum (cosine similarity = 0.465)**



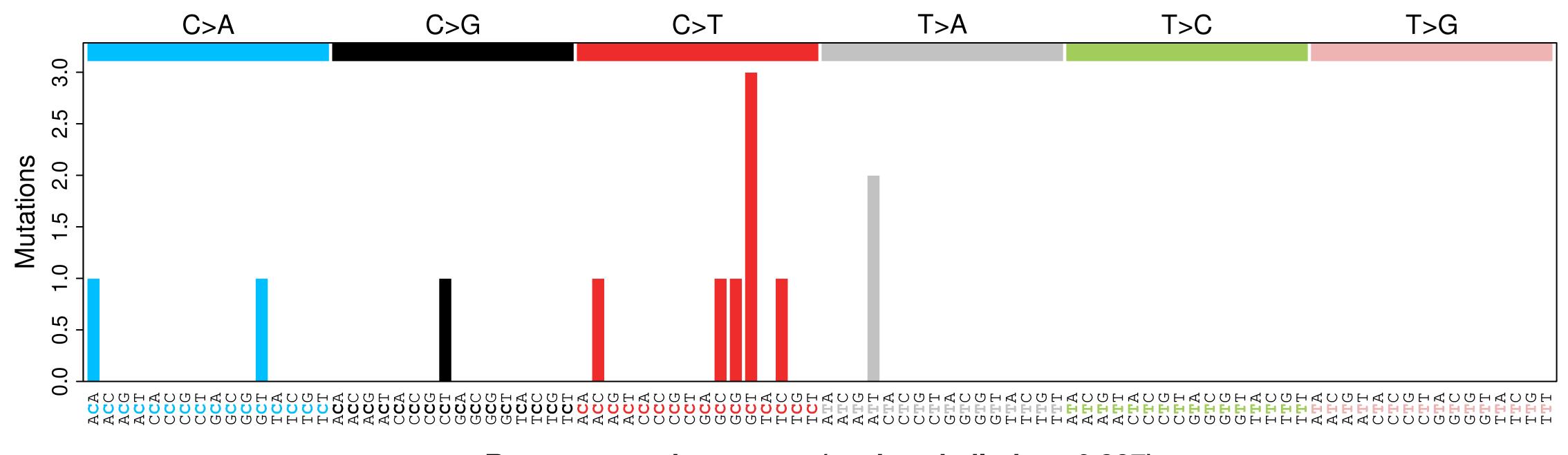
#### CATD0609a (11 mutations)

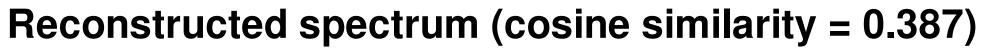


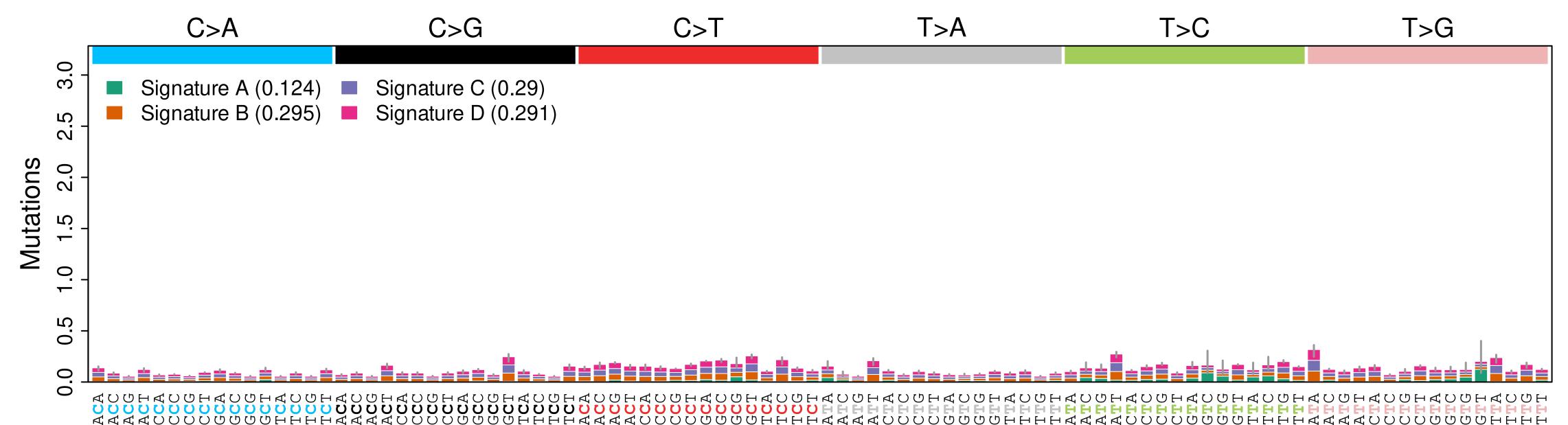




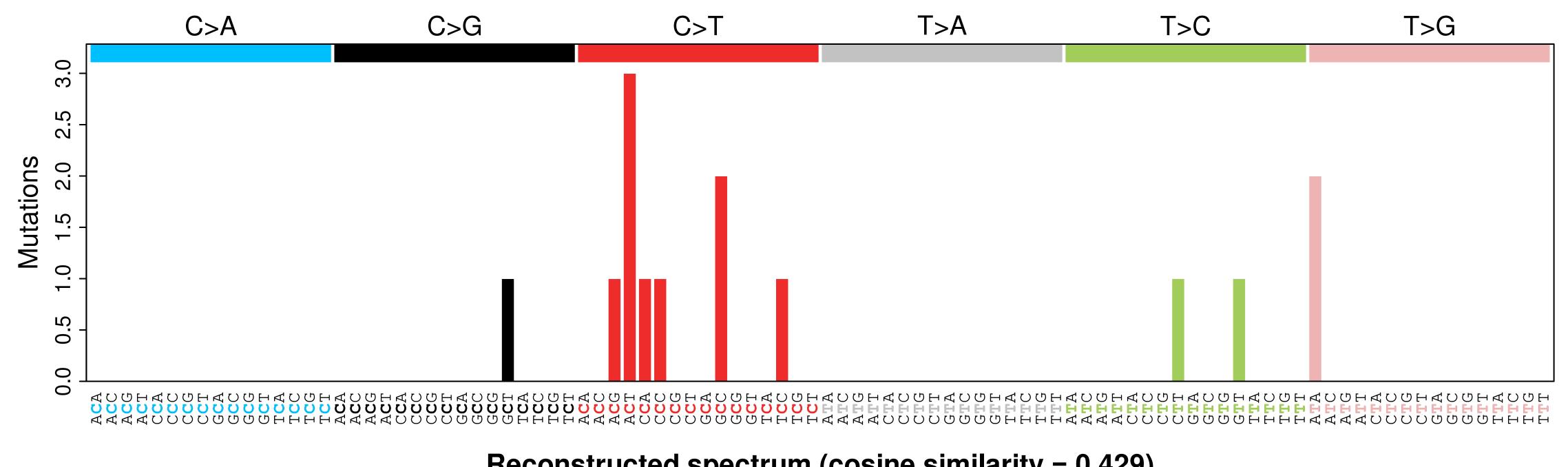
#### CATD0601a (12 mutations)



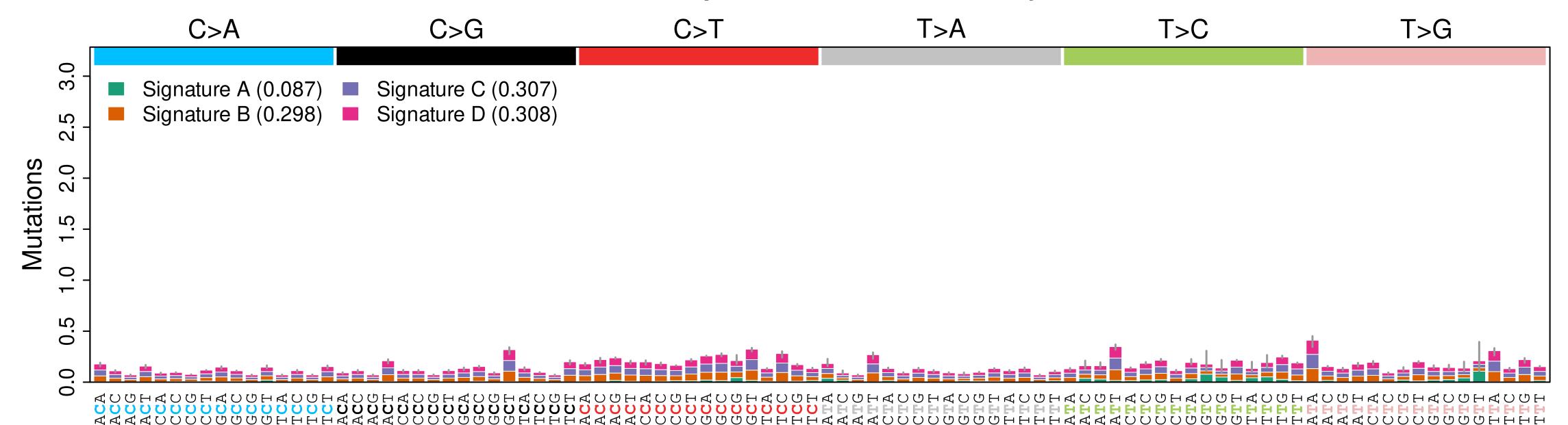




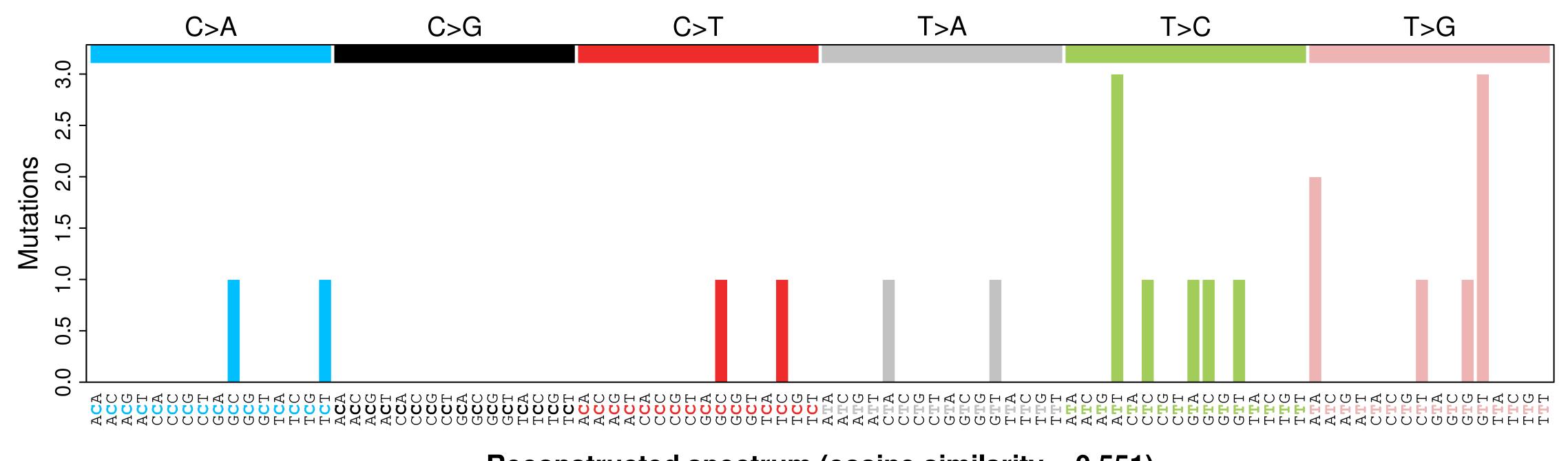
#### CATD0731a (14 mutations)

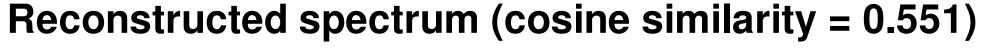


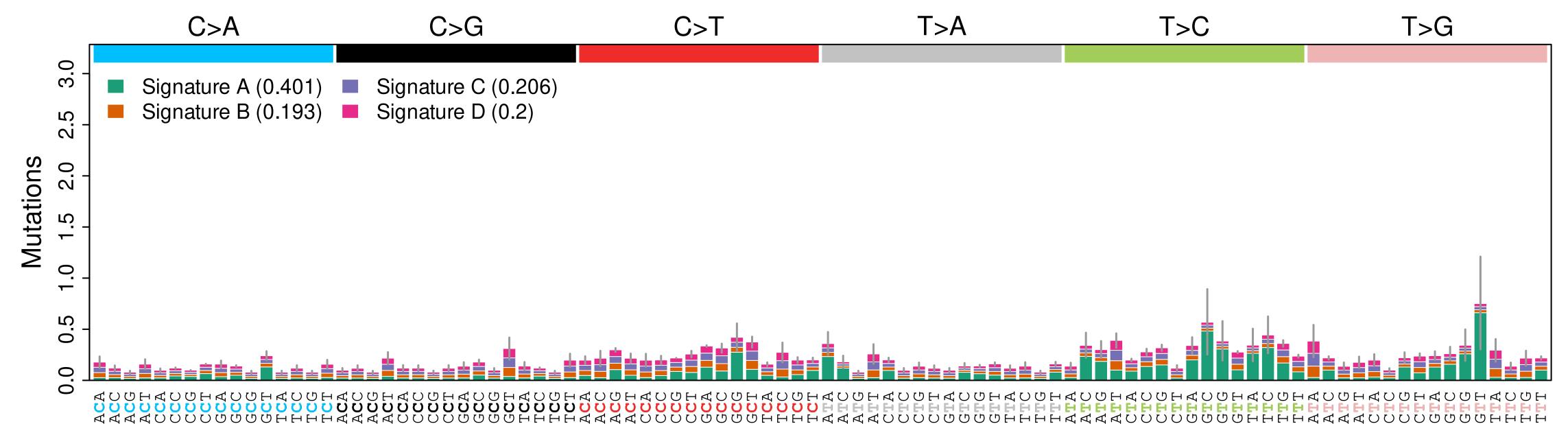
## **Reconstructed spectrum (cosine similarity = 0.429)**



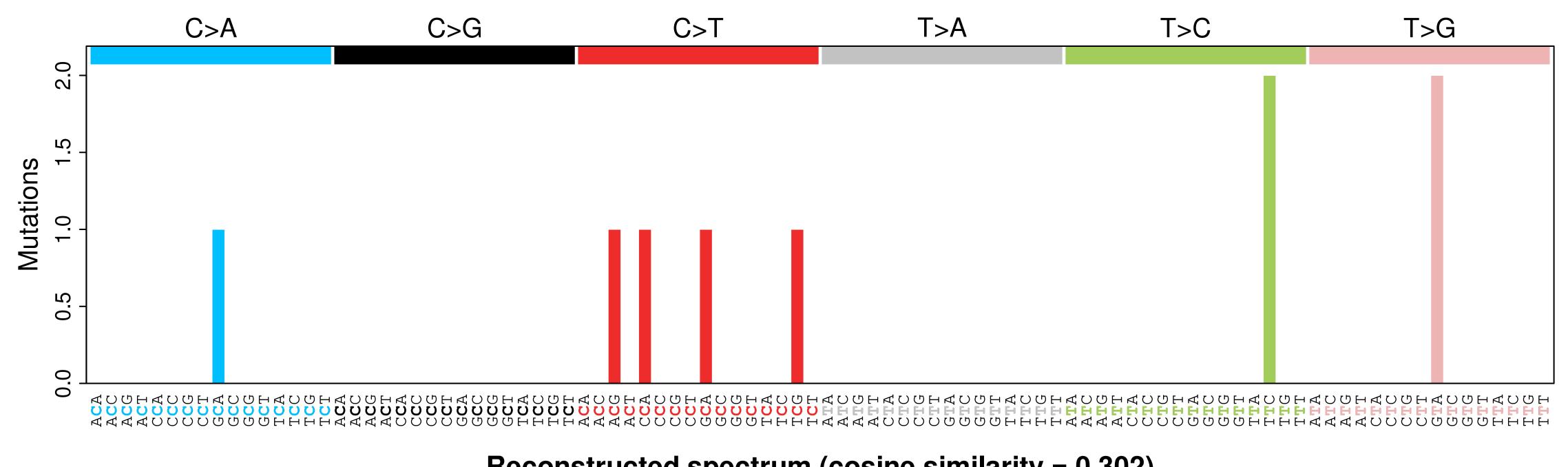
#### CATD0723a (20 mutations)



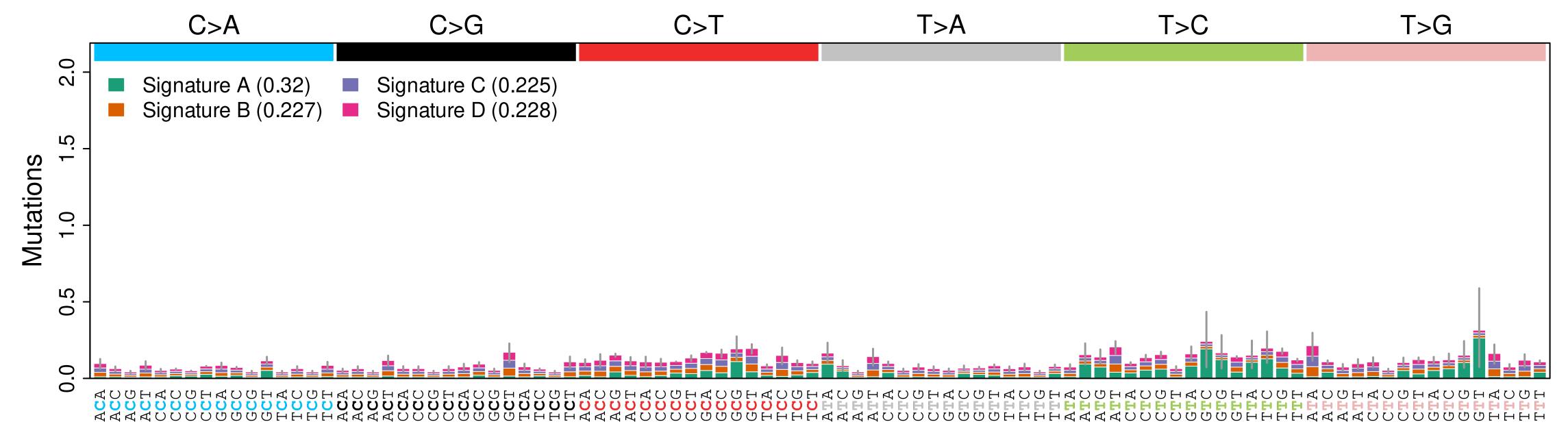




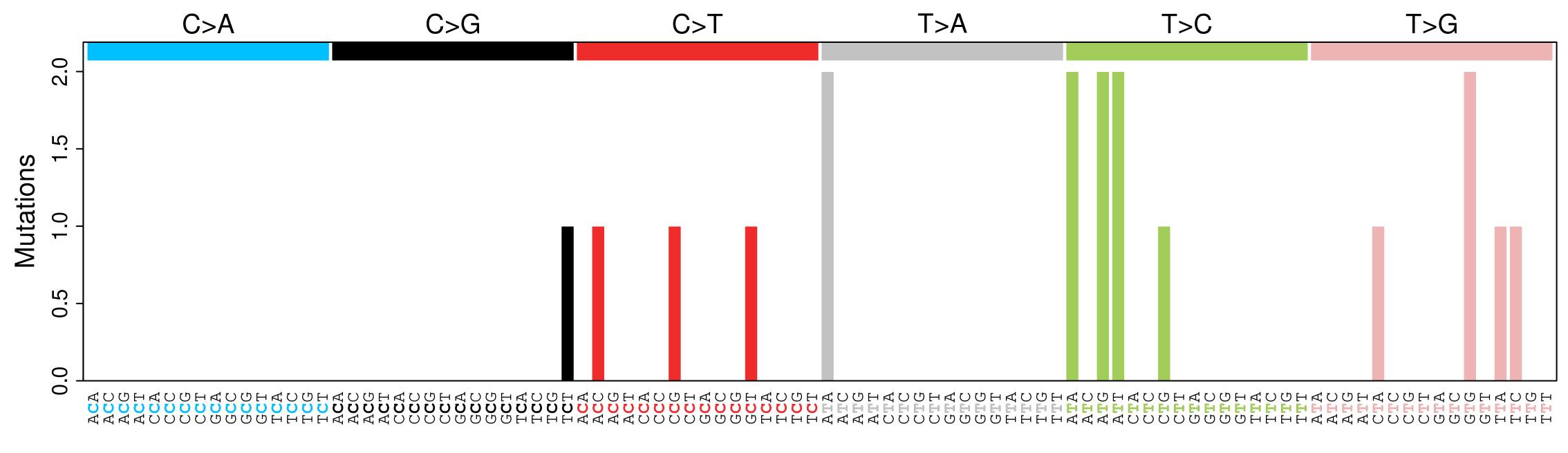
#### CATD0730a (9 mutations)

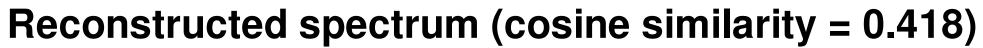


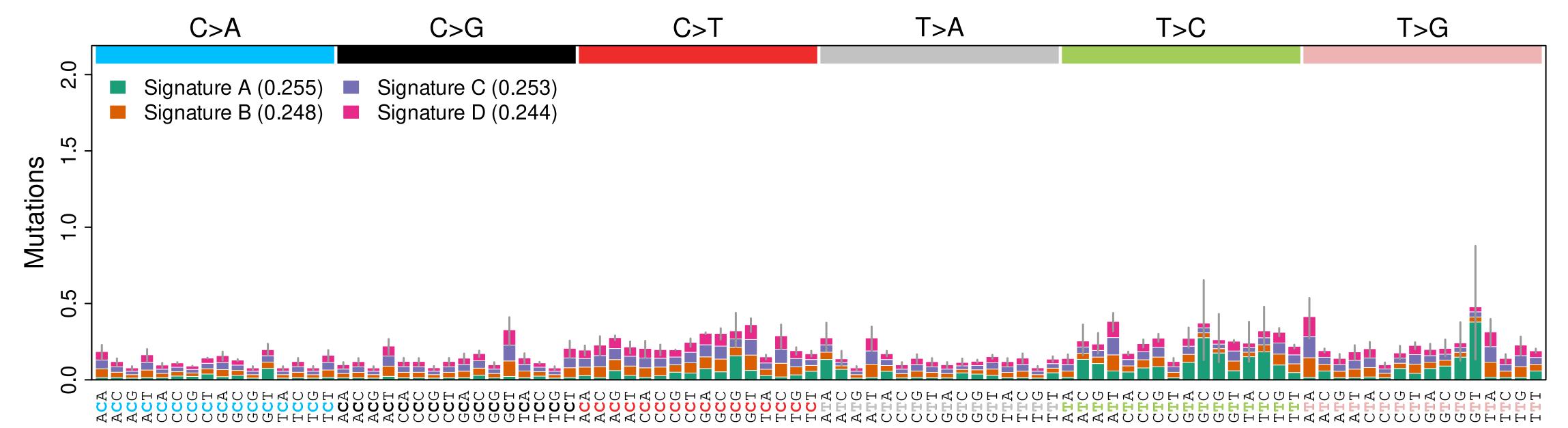
## Reconstructed spectrum (cosine similarity = 0.302)



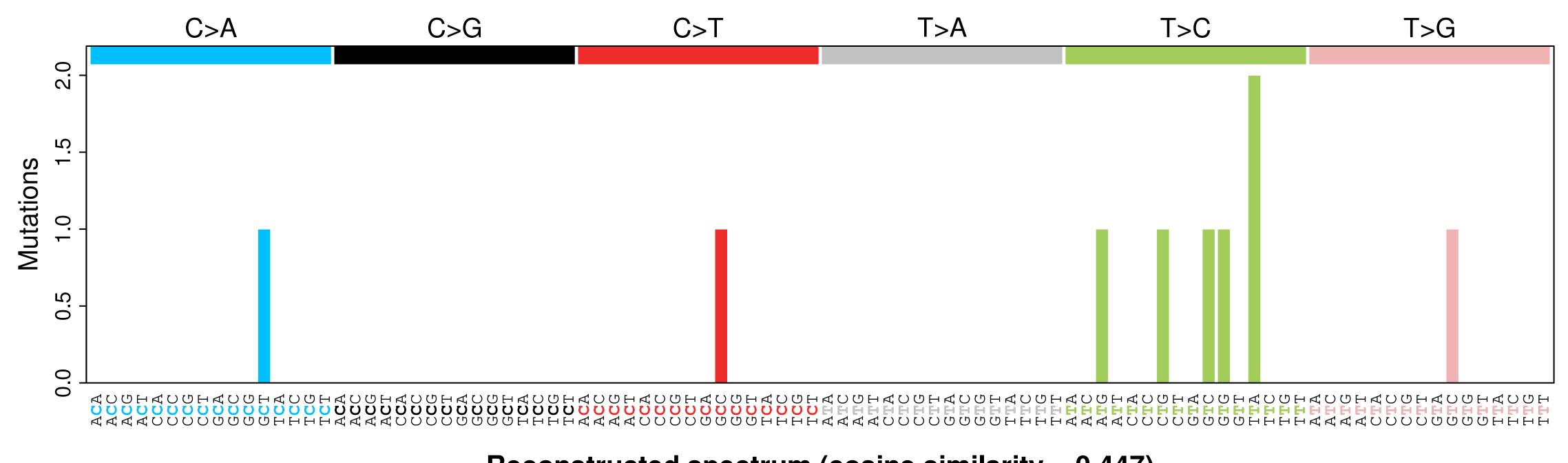
#### CATD0586a (18 mutations)



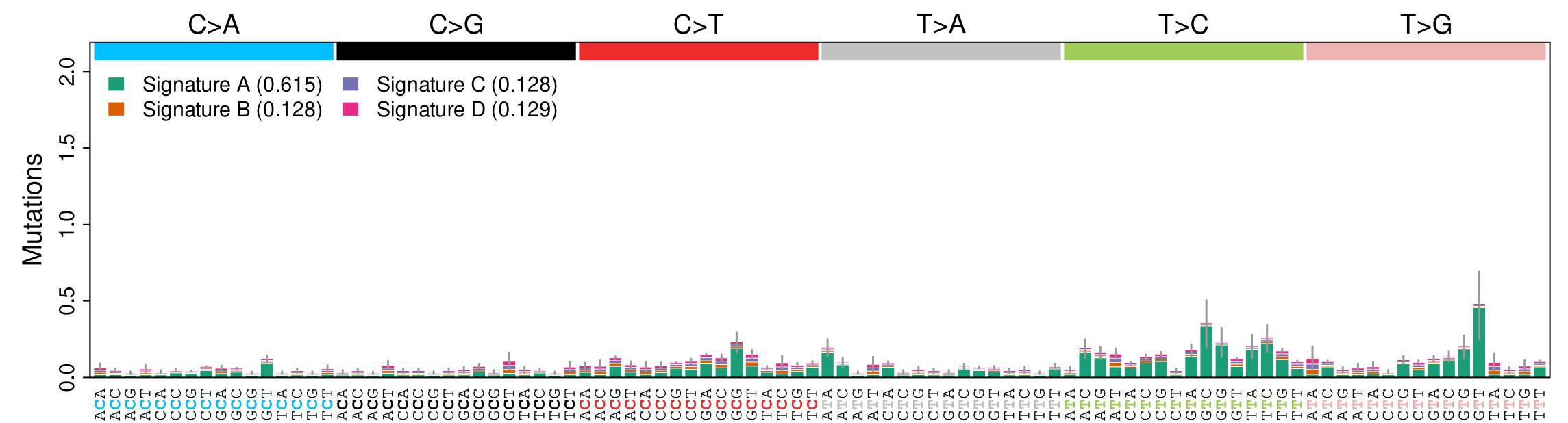




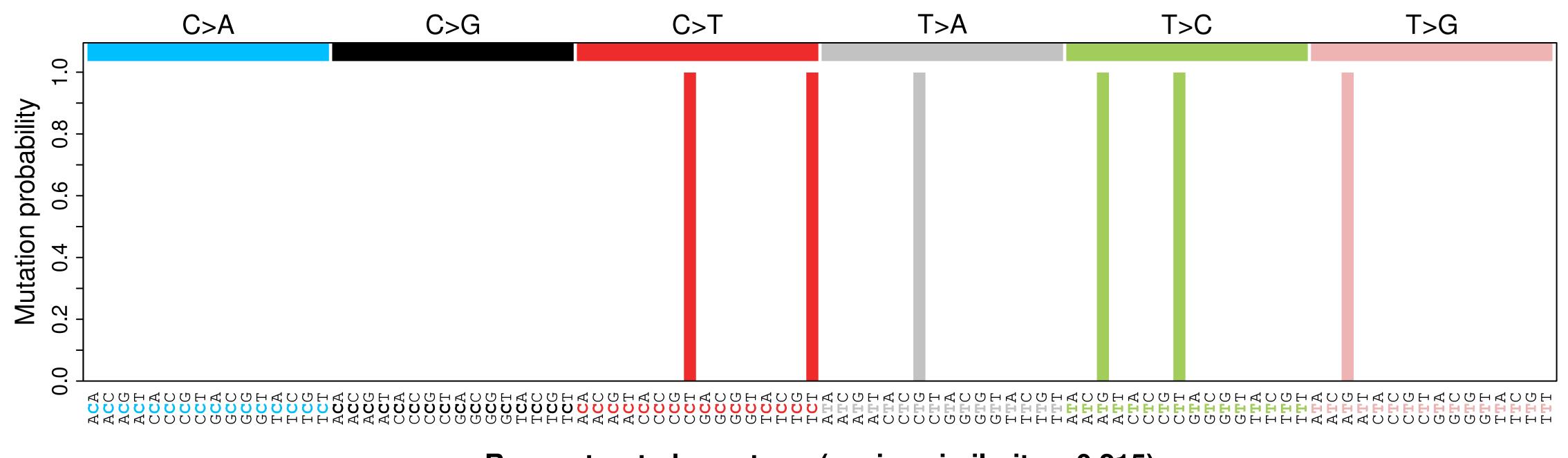
## CATD0733a (9 mutations)

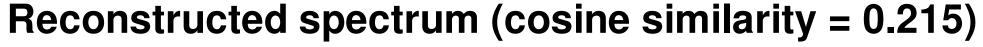


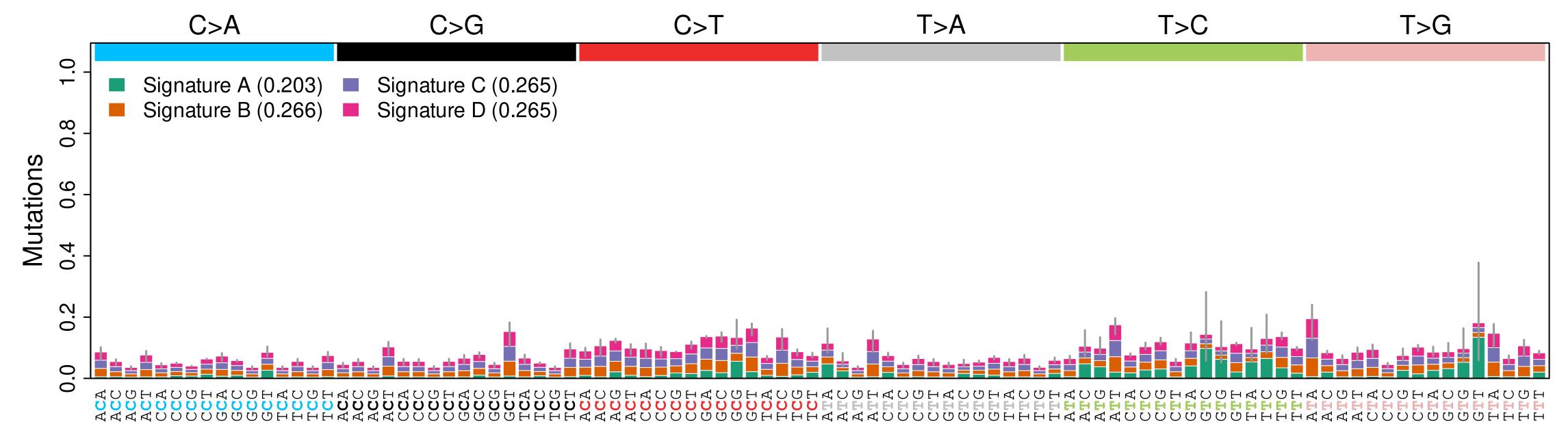
## Reconstructed spectrum (cosine similarity = 0.447)



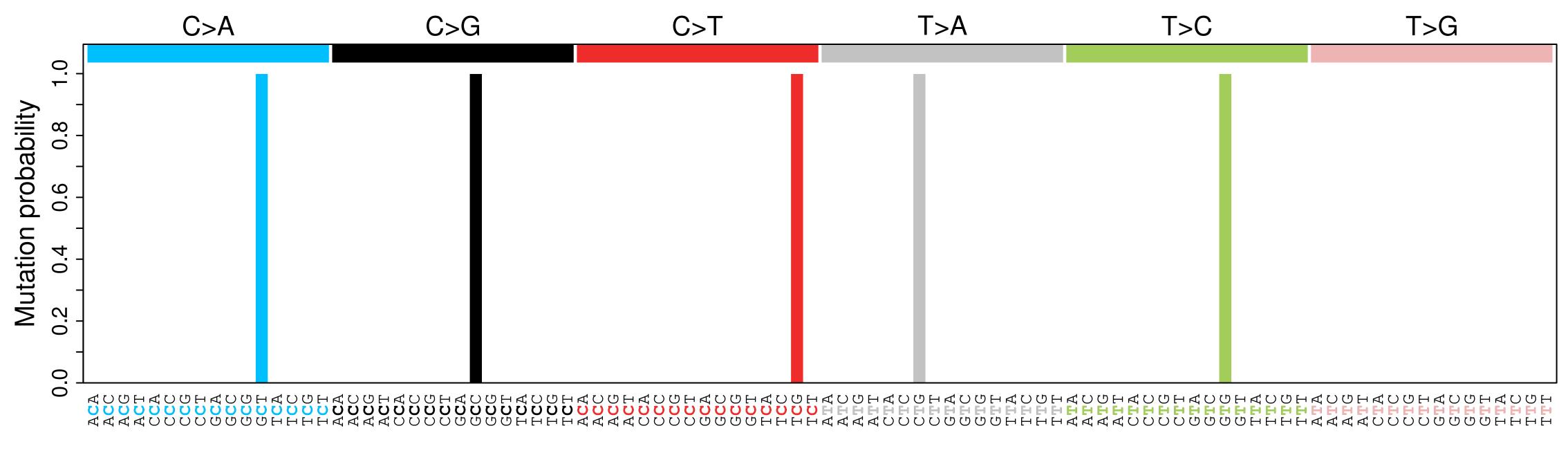
#### CATD0687a



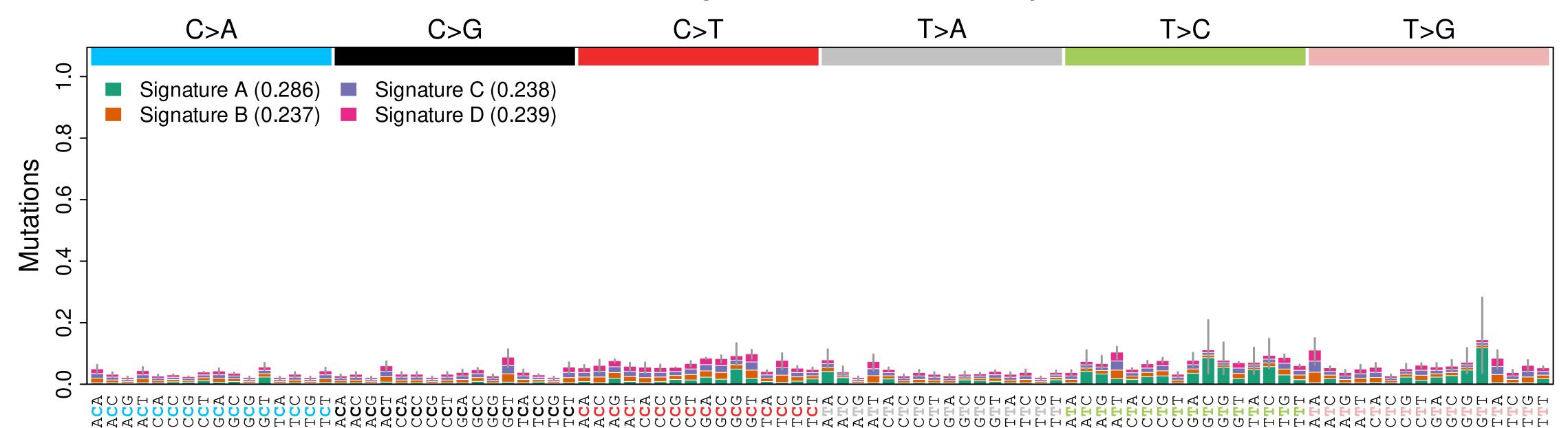




#### CATD0578a



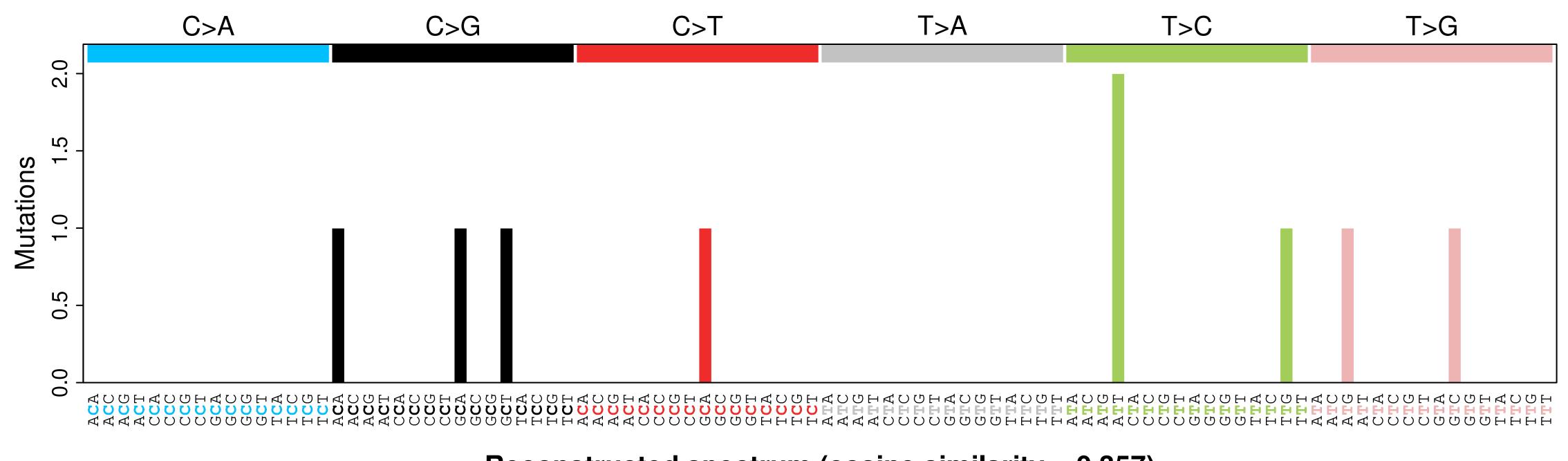




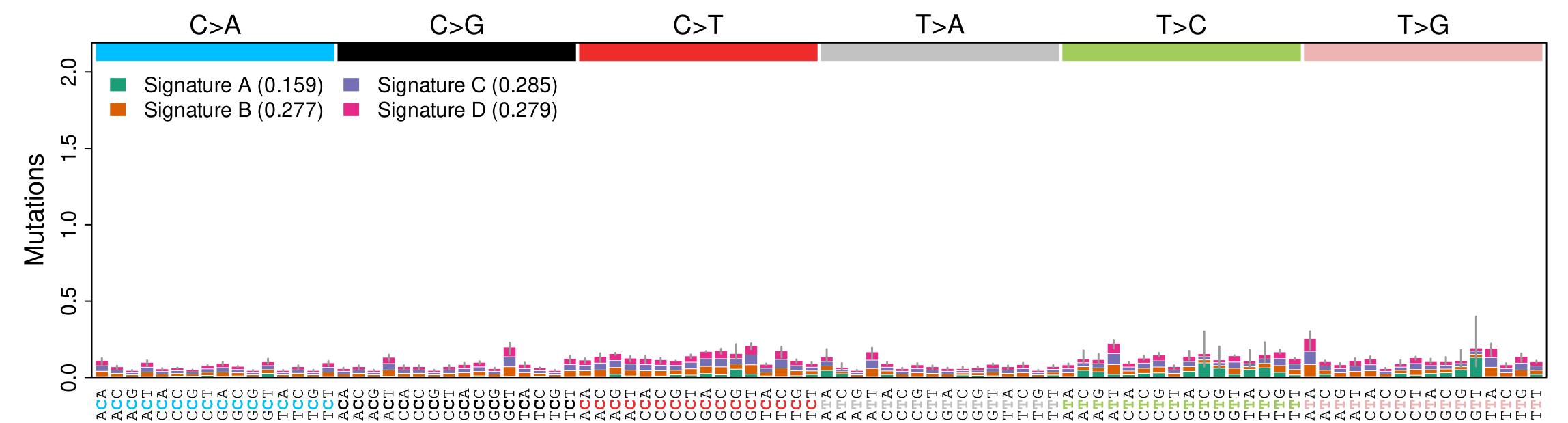
## CATD0587a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.164)** T>C T>G C>A C>G T>A C>T 2.0 Signature A (0.251) Signature C (0.25) Signature B (0.251) Signature D (0.248) 5 Mutations

0.5

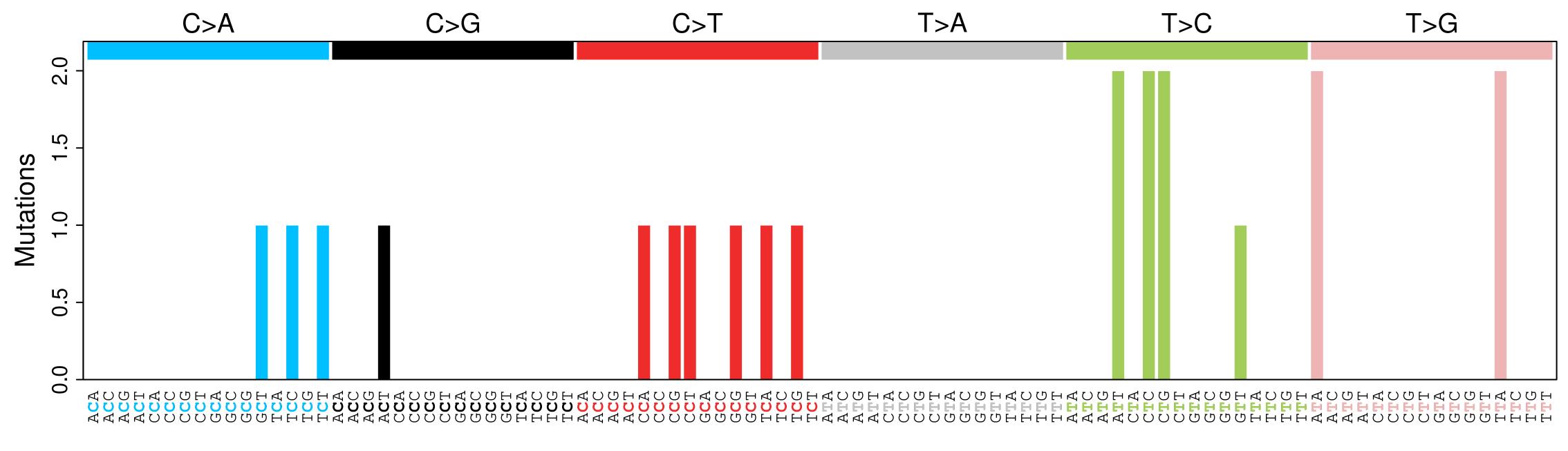
## CATD0589a (9 mutations)

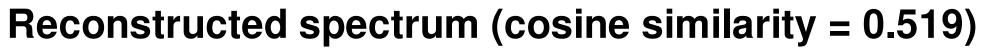


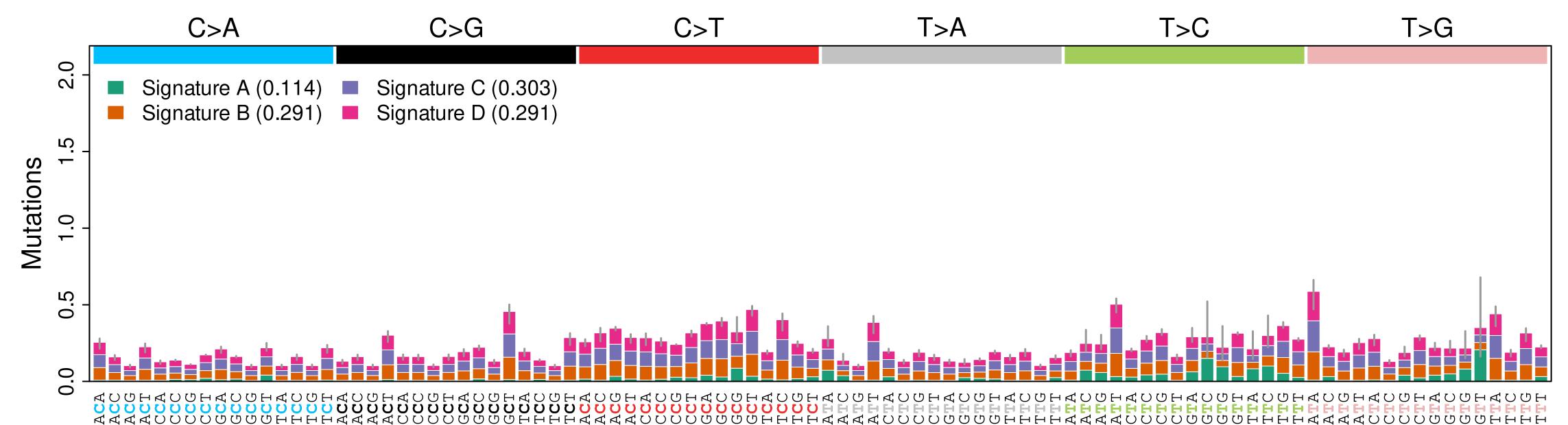
## Reconstructed spectrum (cosine similarity = 0.357)



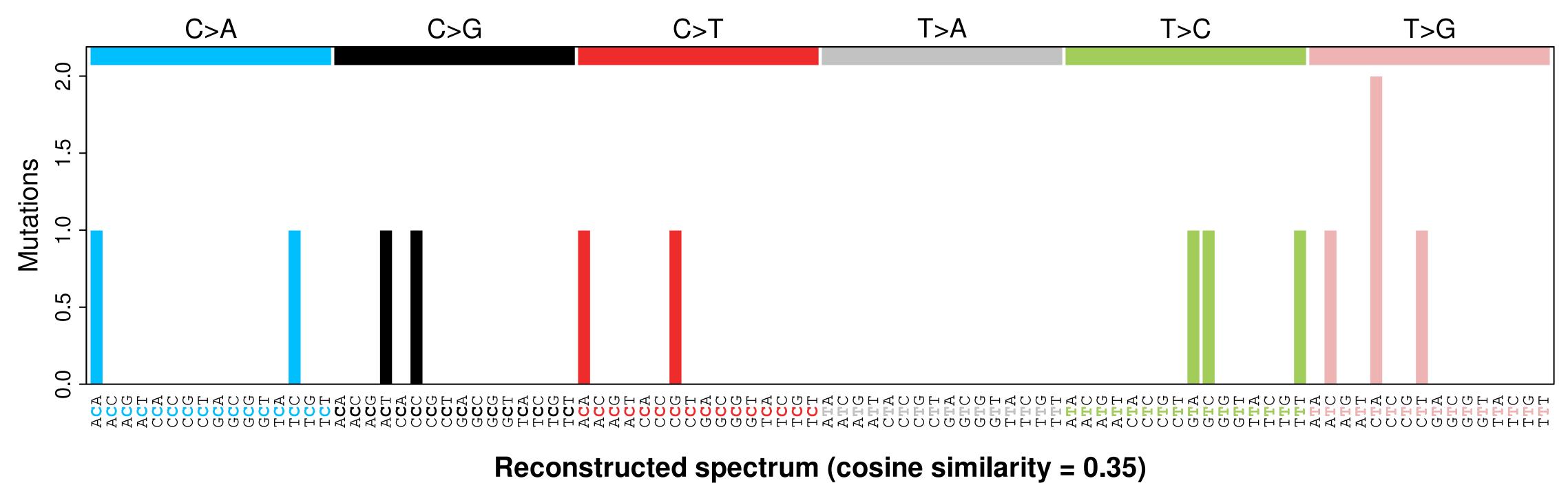
#### CATD0590a (21 mutations)



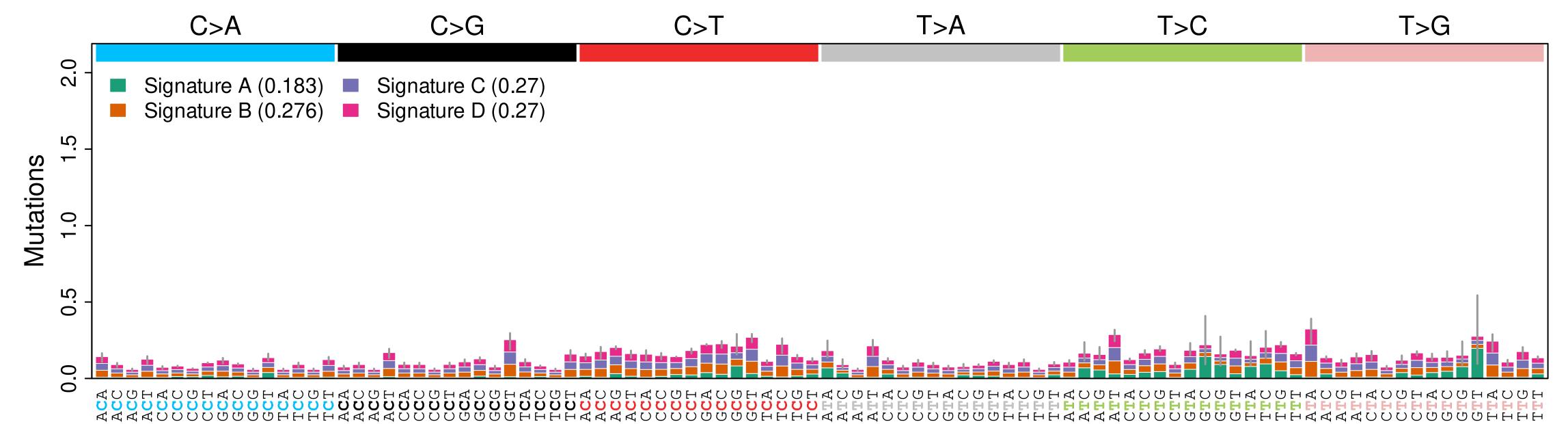




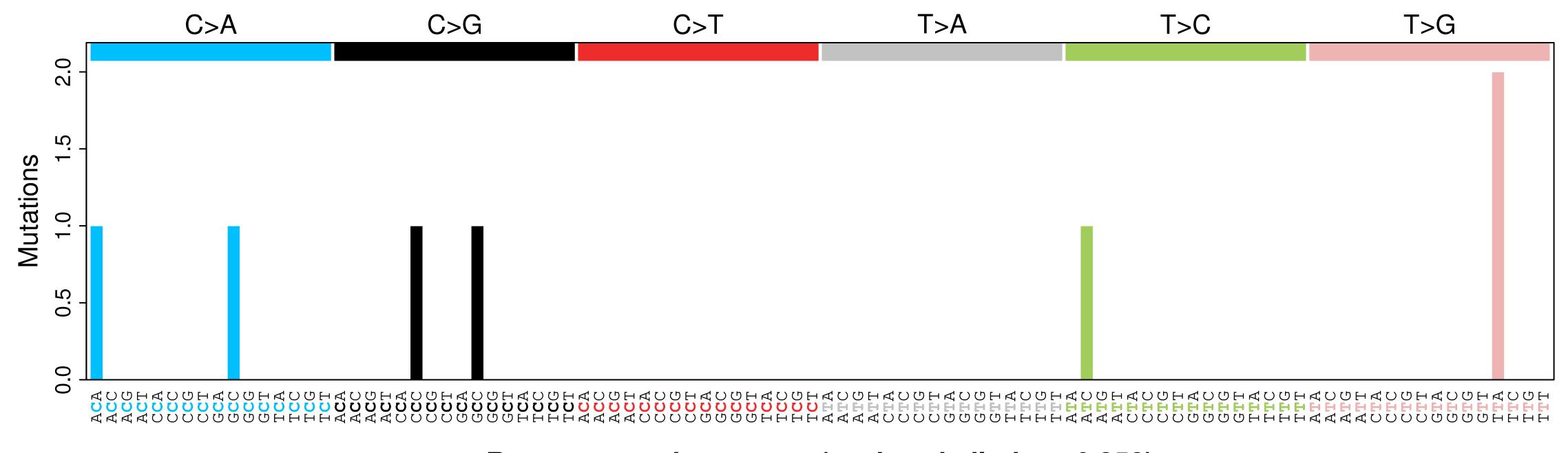
#### CATD0727a (13 mutations)



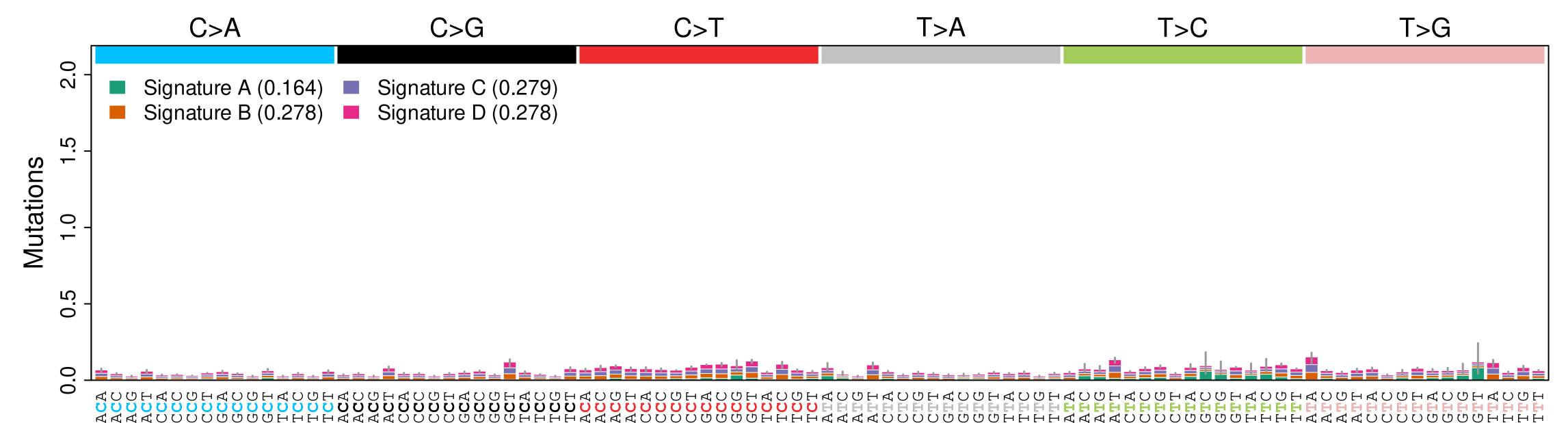




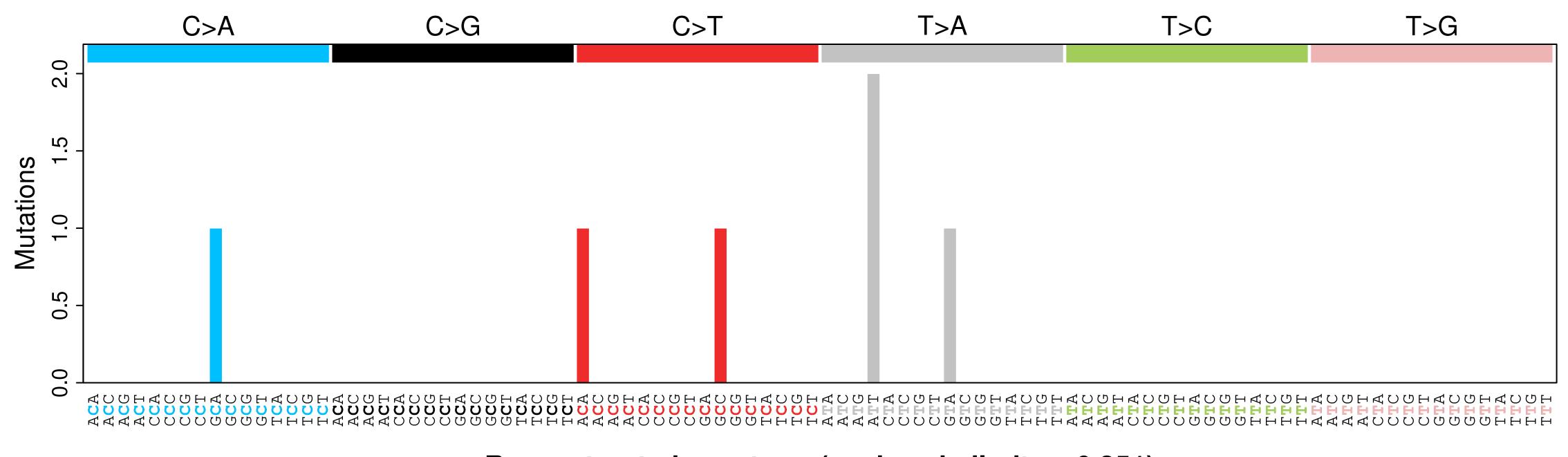
# CATD0583a (7 mutations)

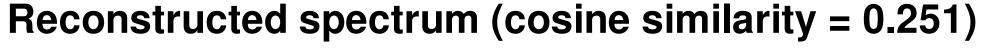


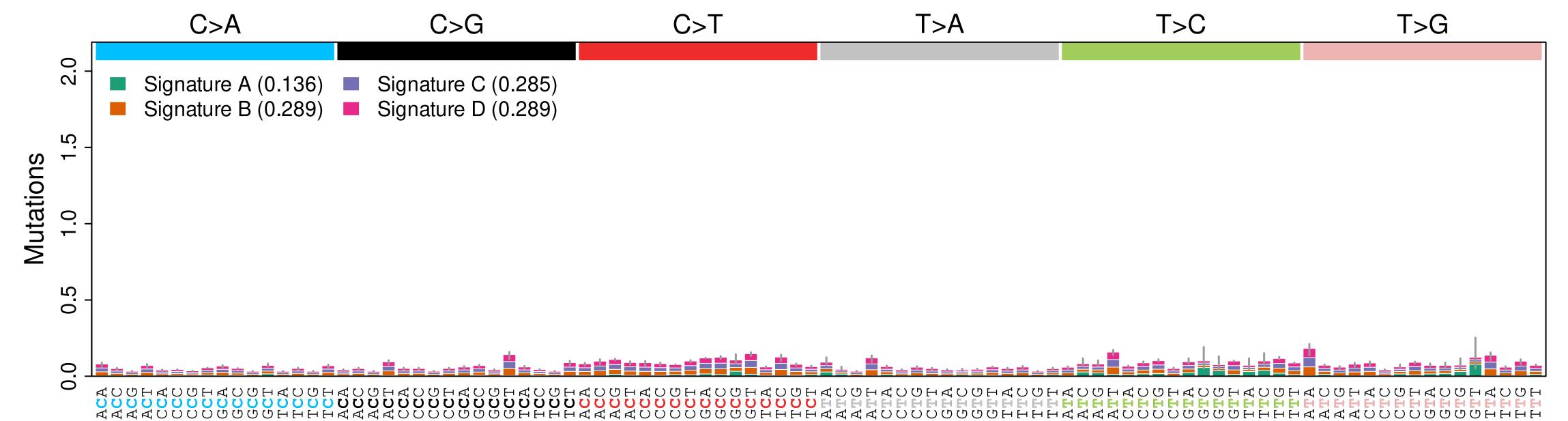
## **Reconstructed spectrum (cosine similarity = 0.258)**



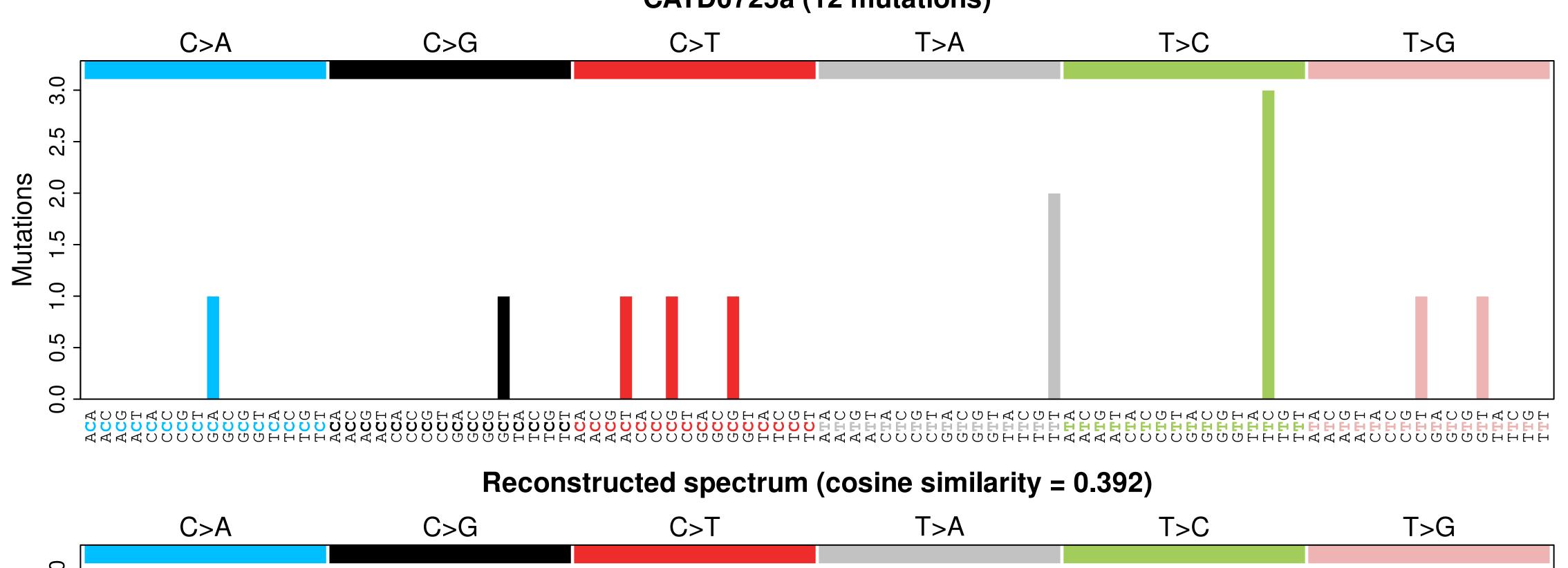
## CATD0732a (6 mutations)

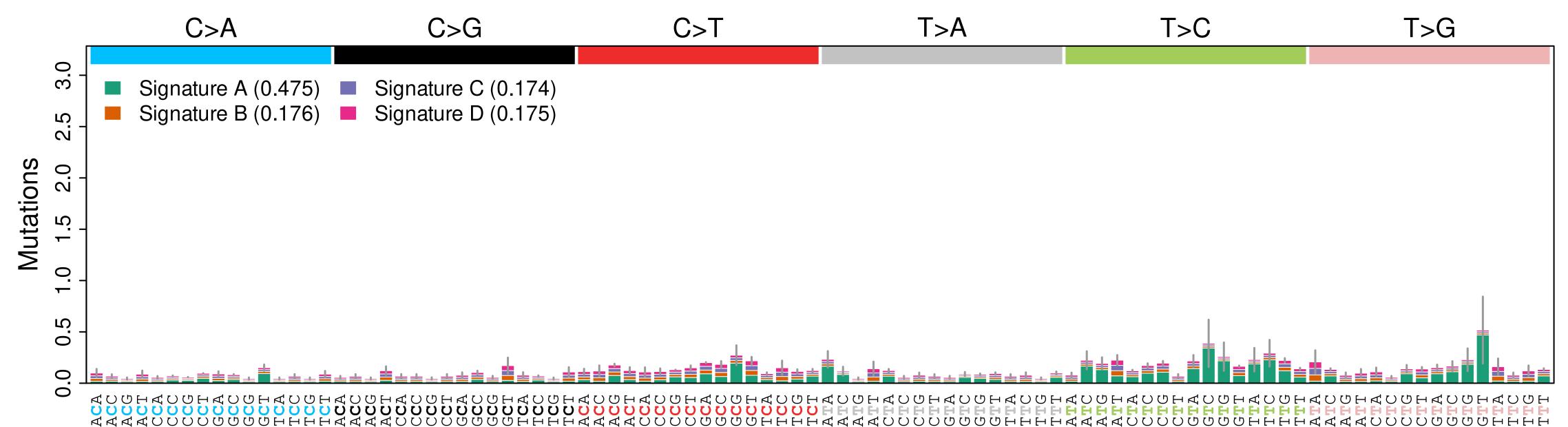




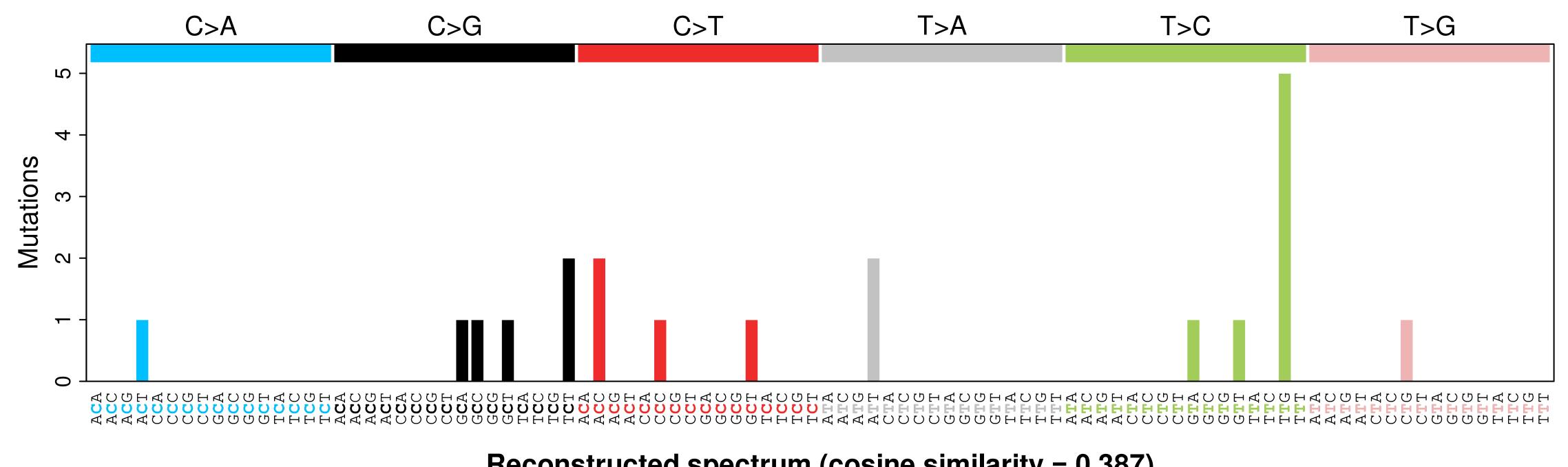


#### CATD0725a (12 mutations)

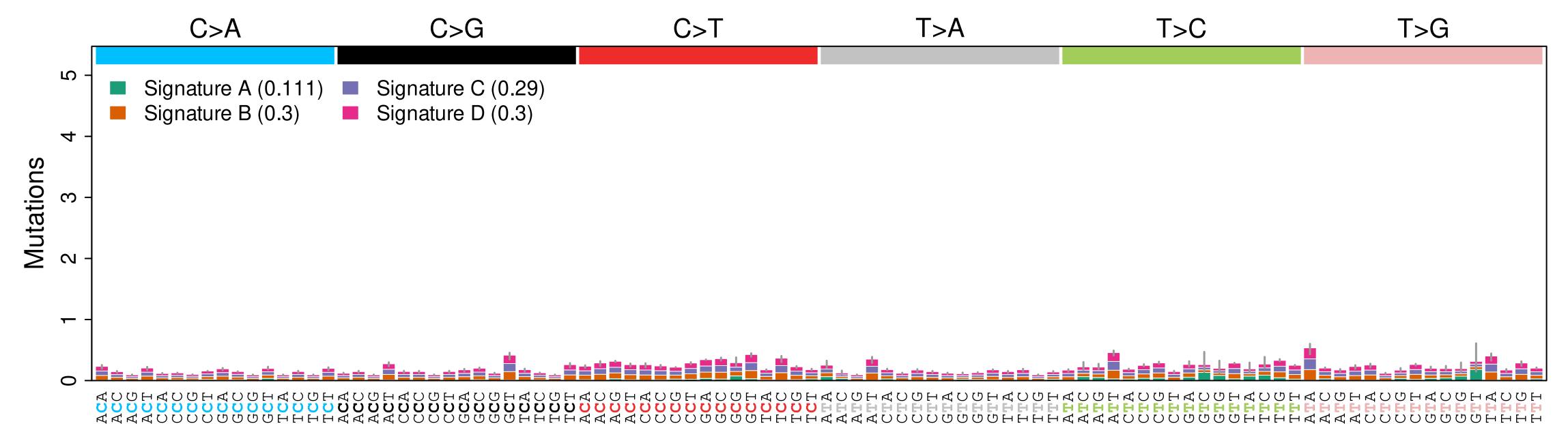




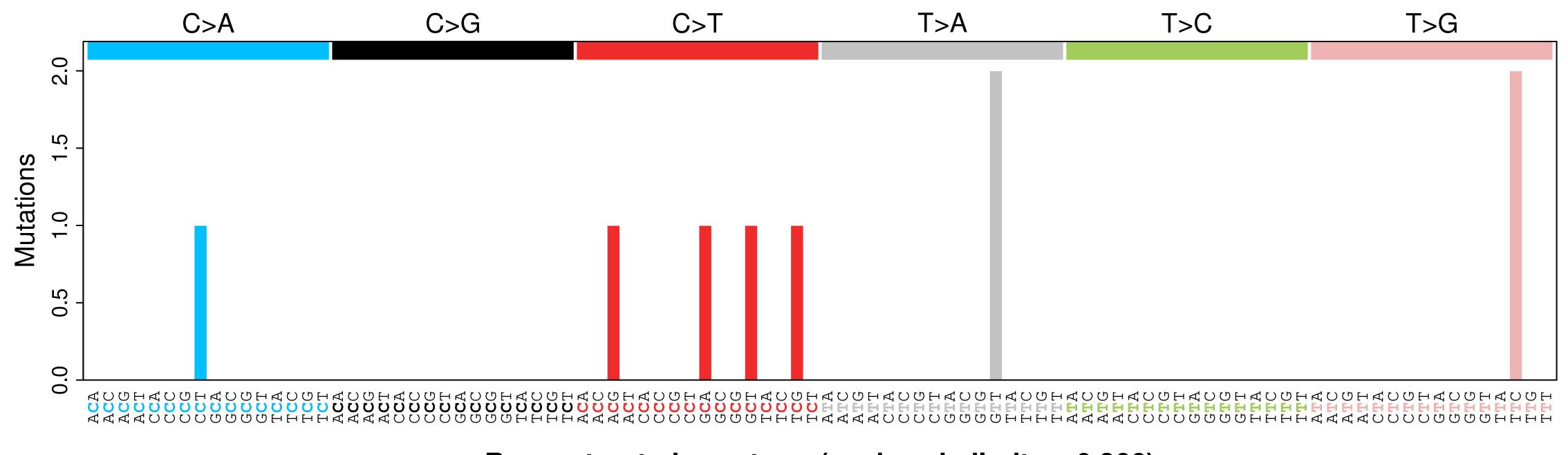
#### CATD0577a (20 mutations)



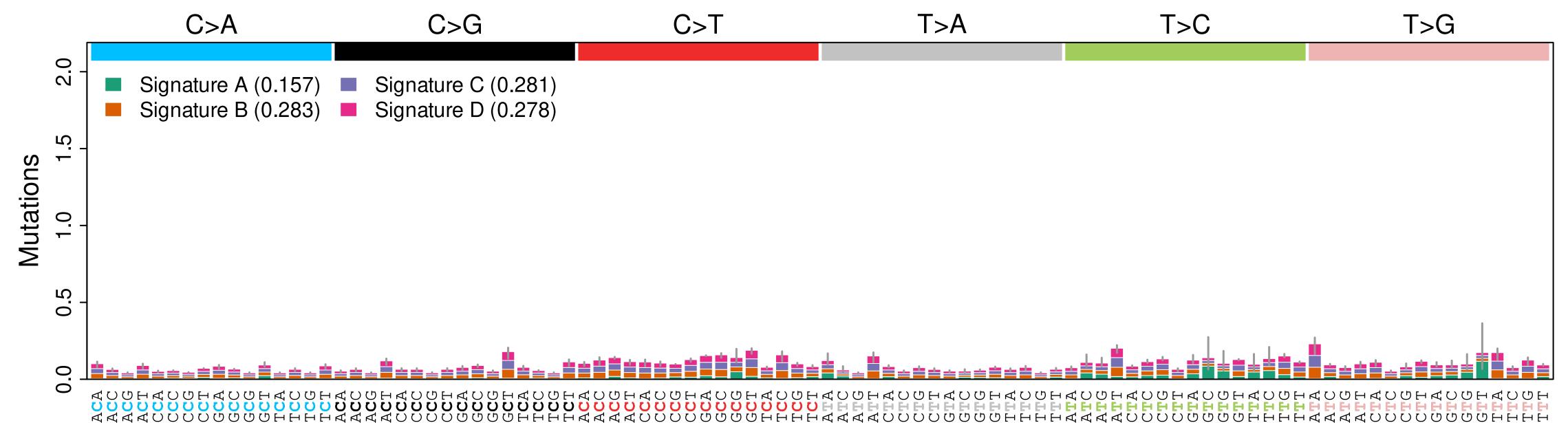
## Reconstructed spectrum (cosine similarity = 0.387)



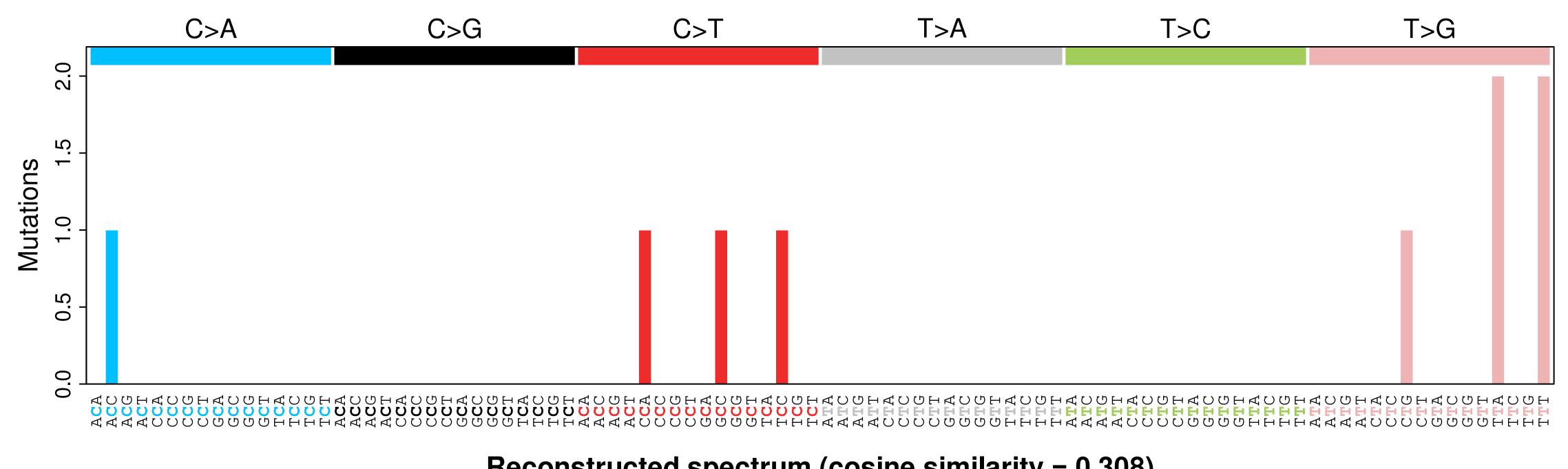
## CATD0606a (9 mutations)

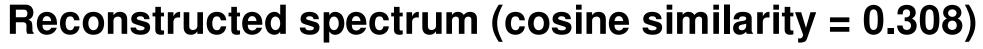


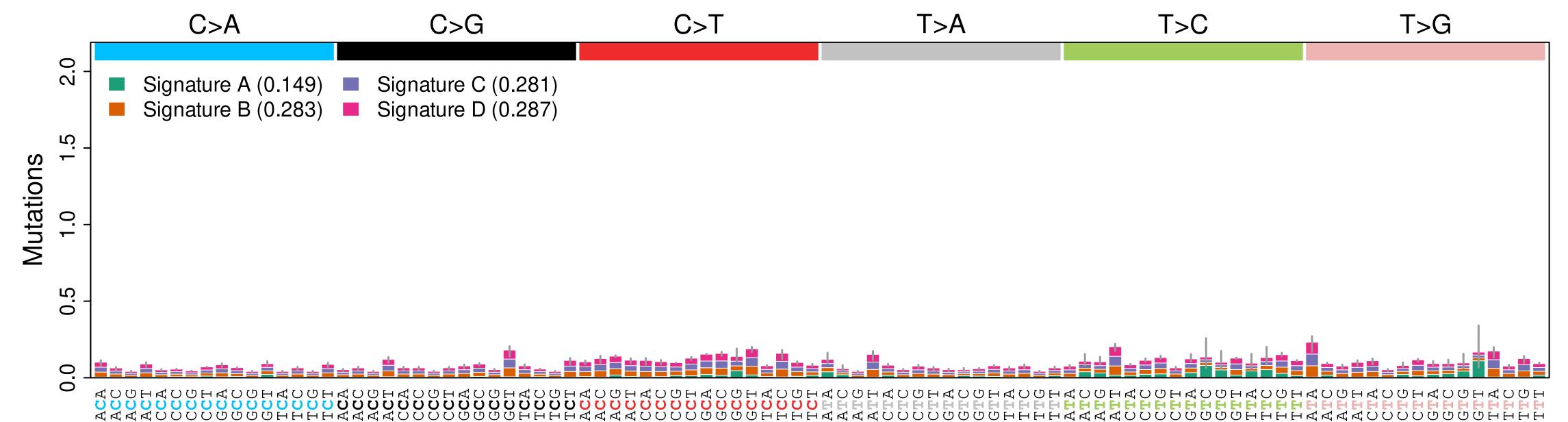
## Reconstructed spectrum (cosine similarity = 0.266)



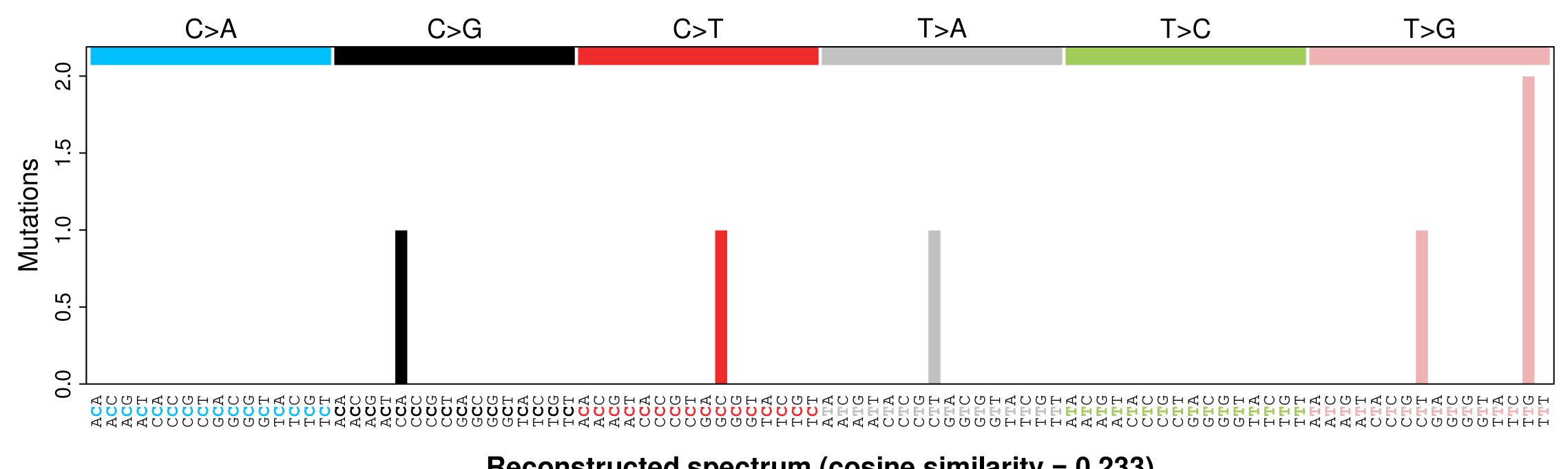
## CATD0588a (9 mutations)

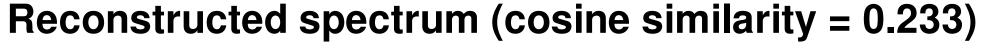


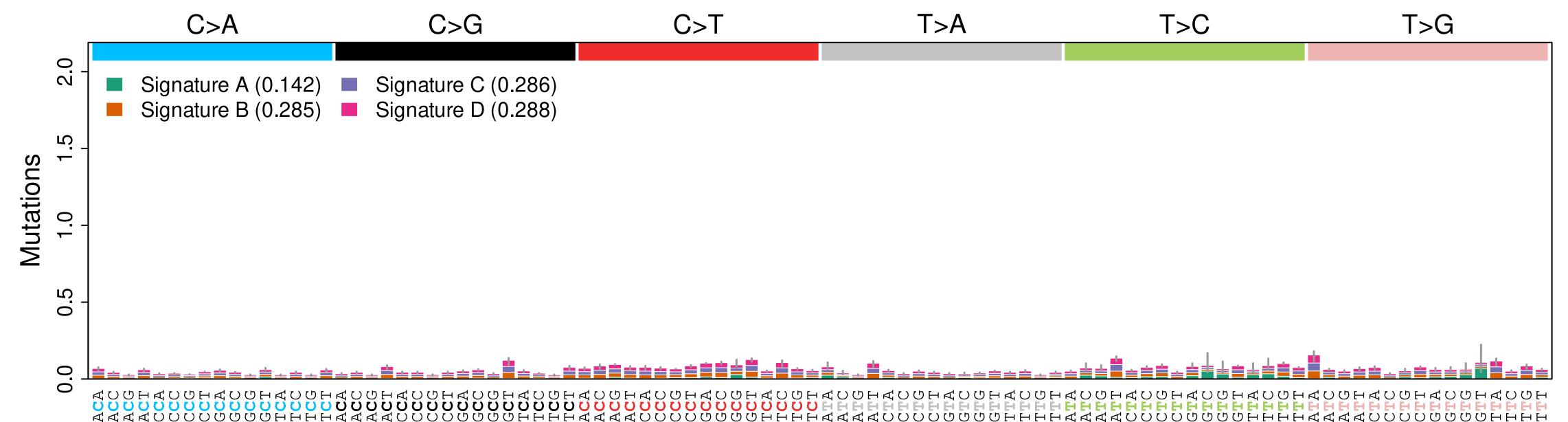




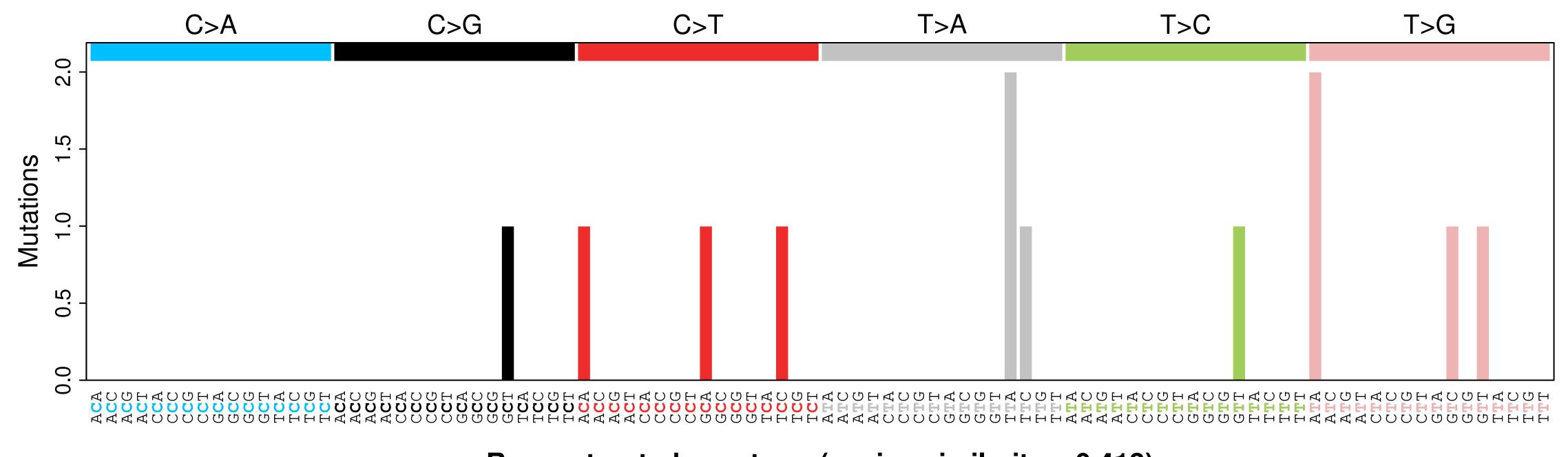
## CATD0572a (6 mutations)



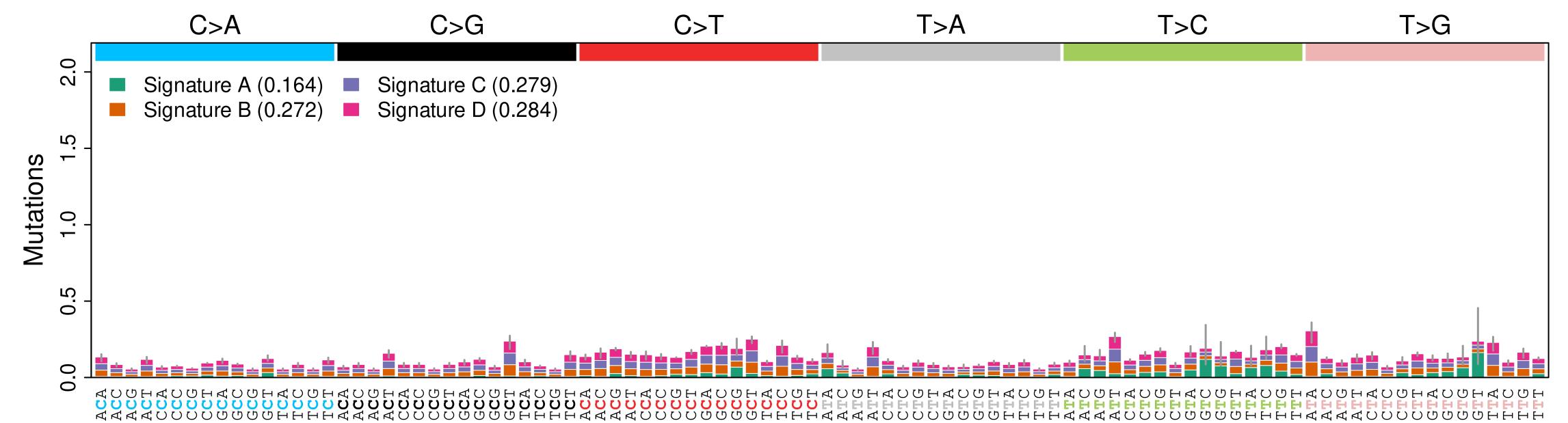




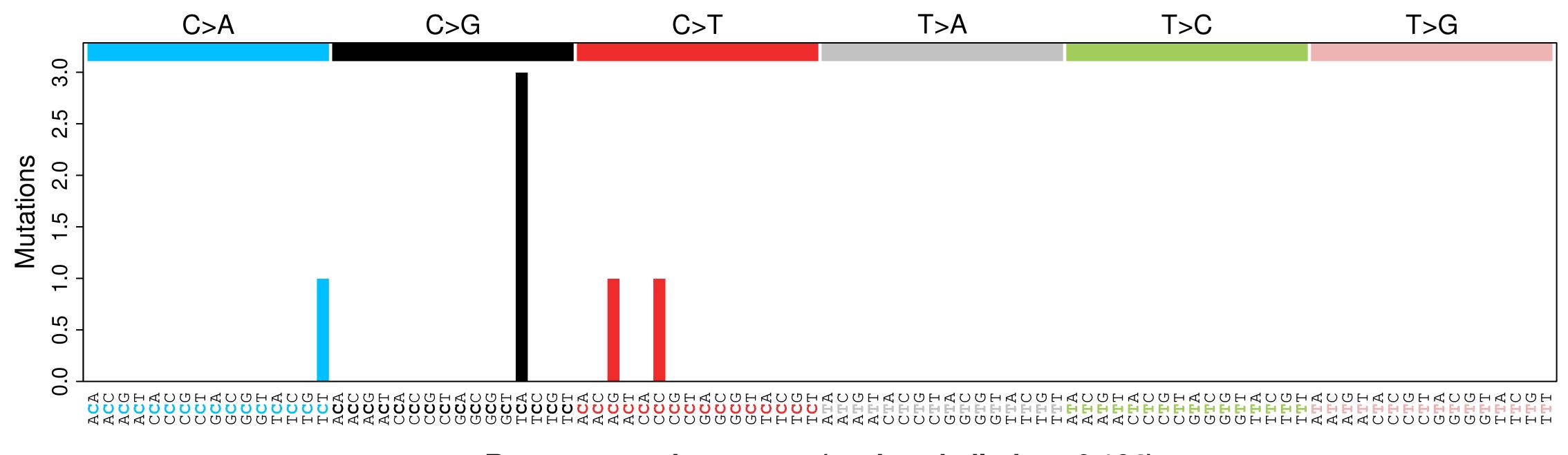
#### CATD0573a (12 mutations)



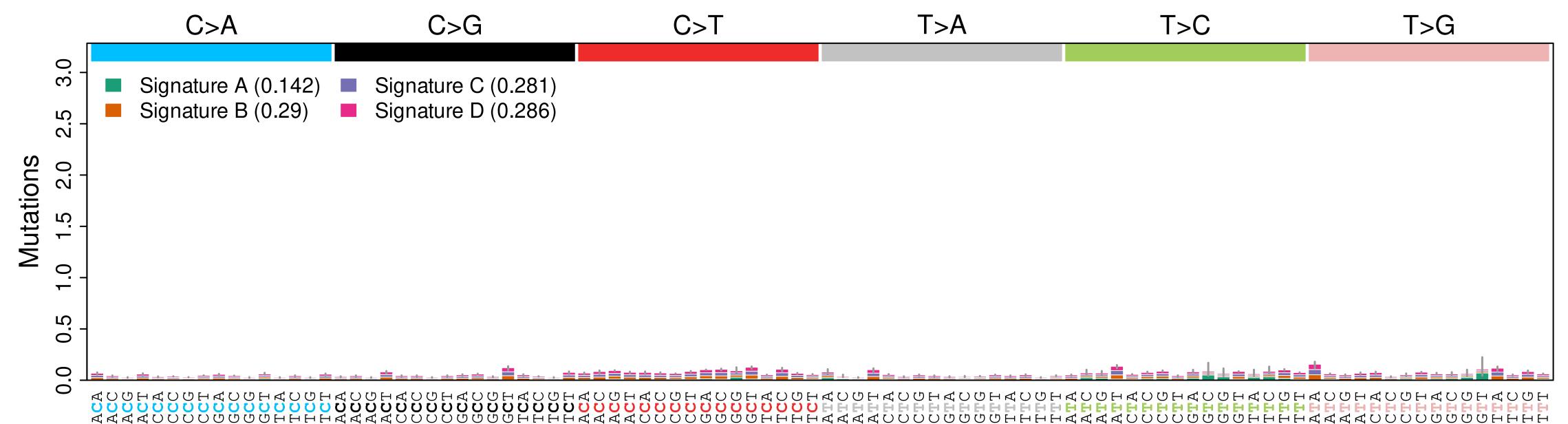
## Reconstructed spectrum (cosine similarity = 0.413)



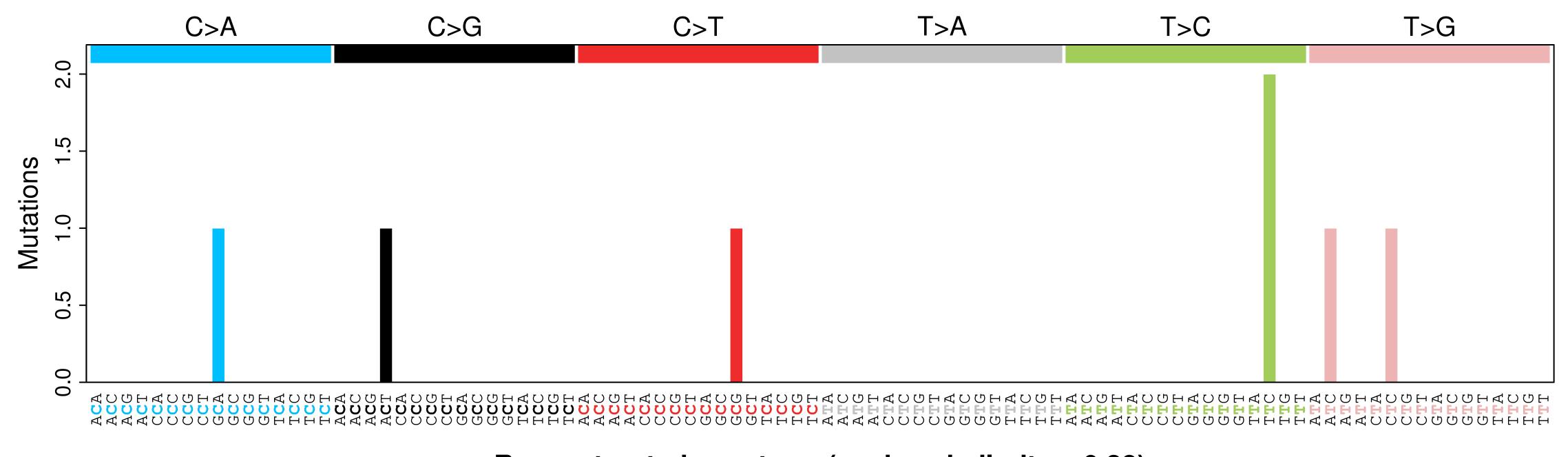
## CATD0592a (6 mutations)

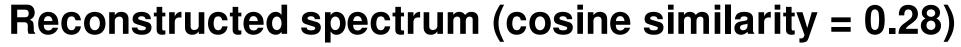


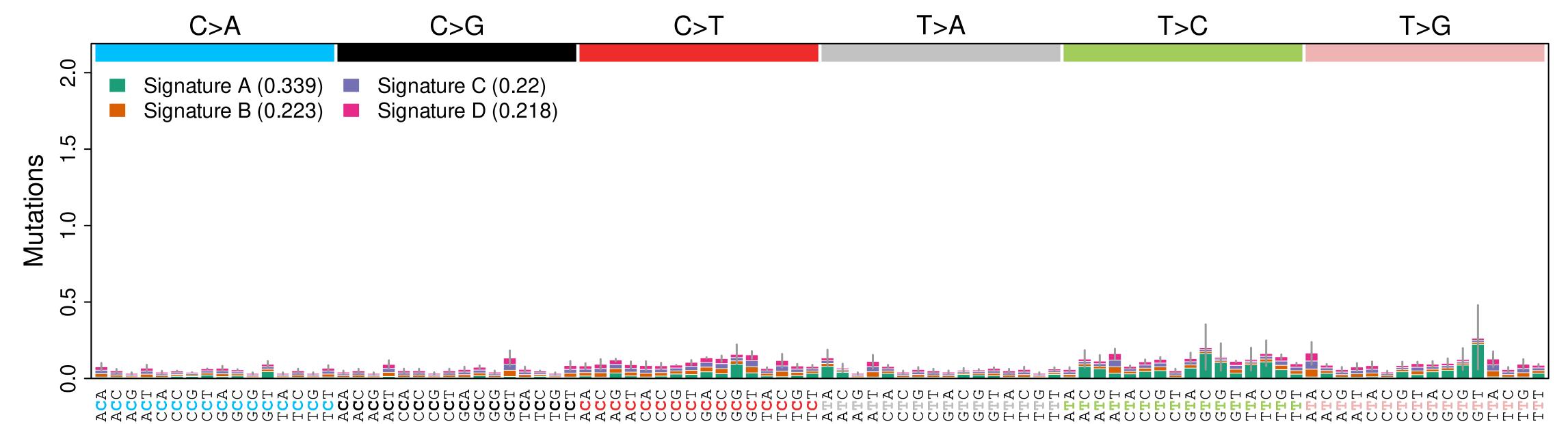
## Reconstructed spectrum (cosine similarity = 0.164)



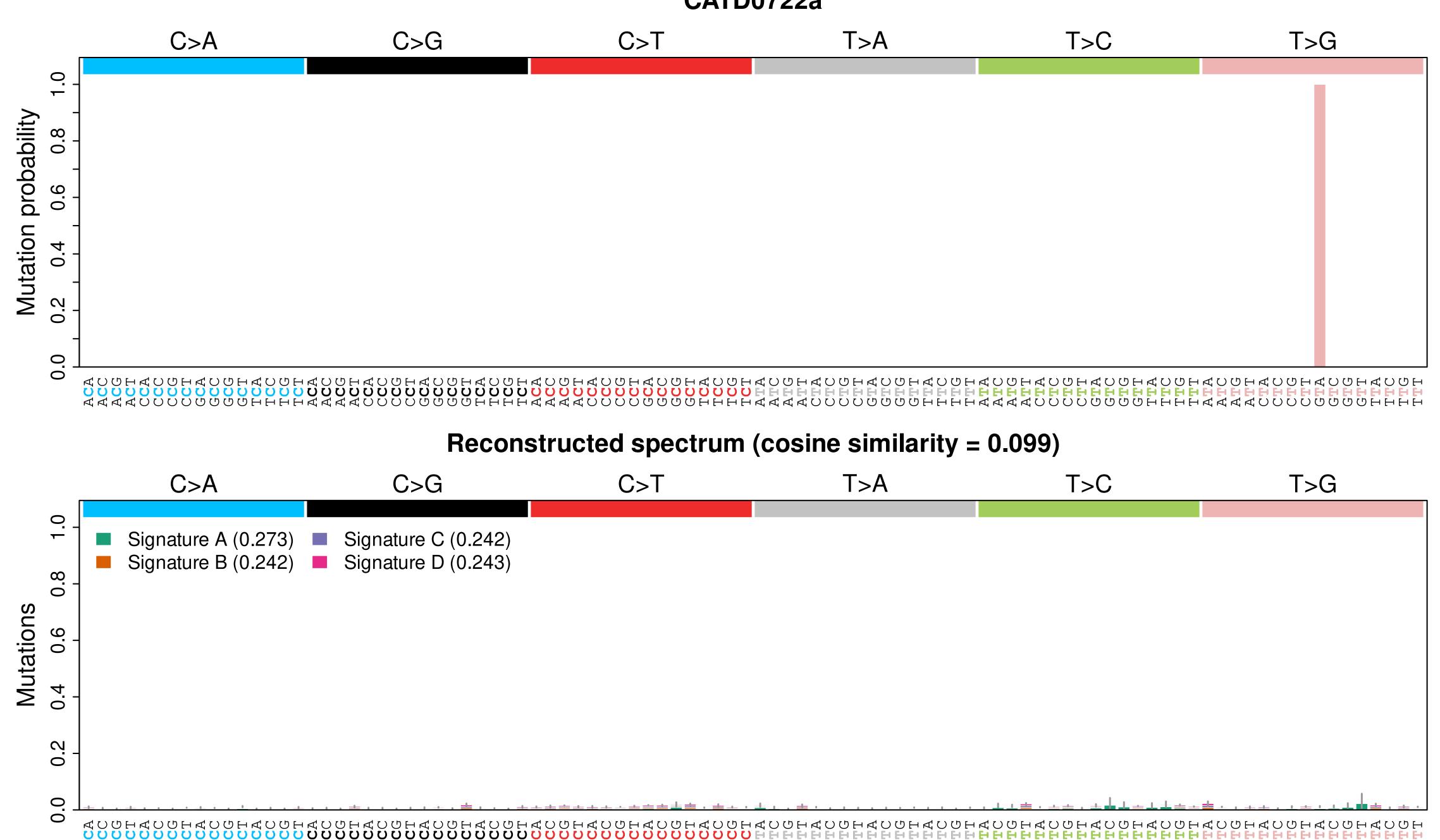
## CATD0603a (7 mutations)



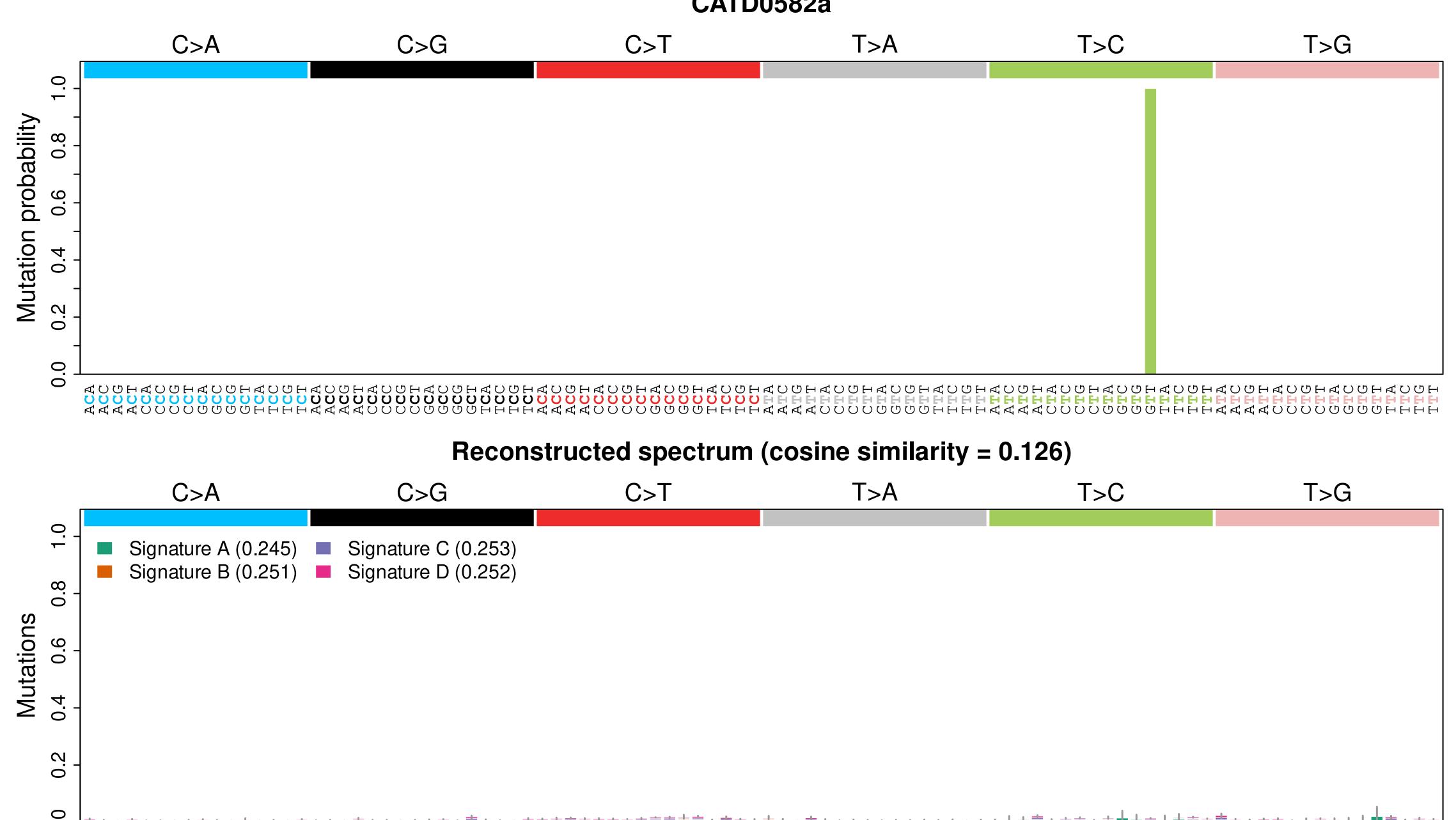




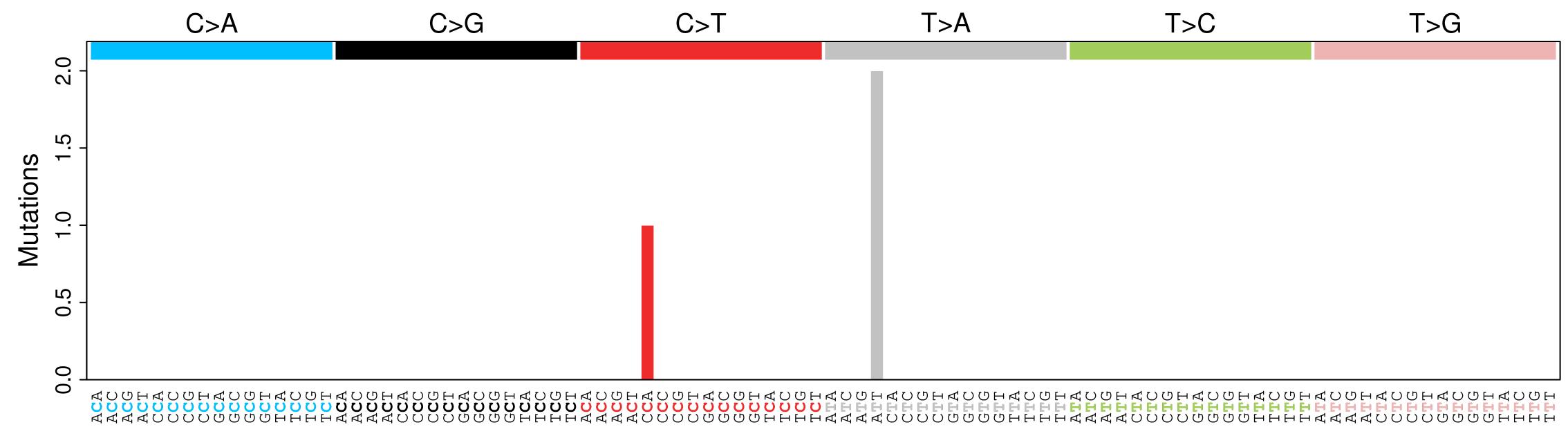




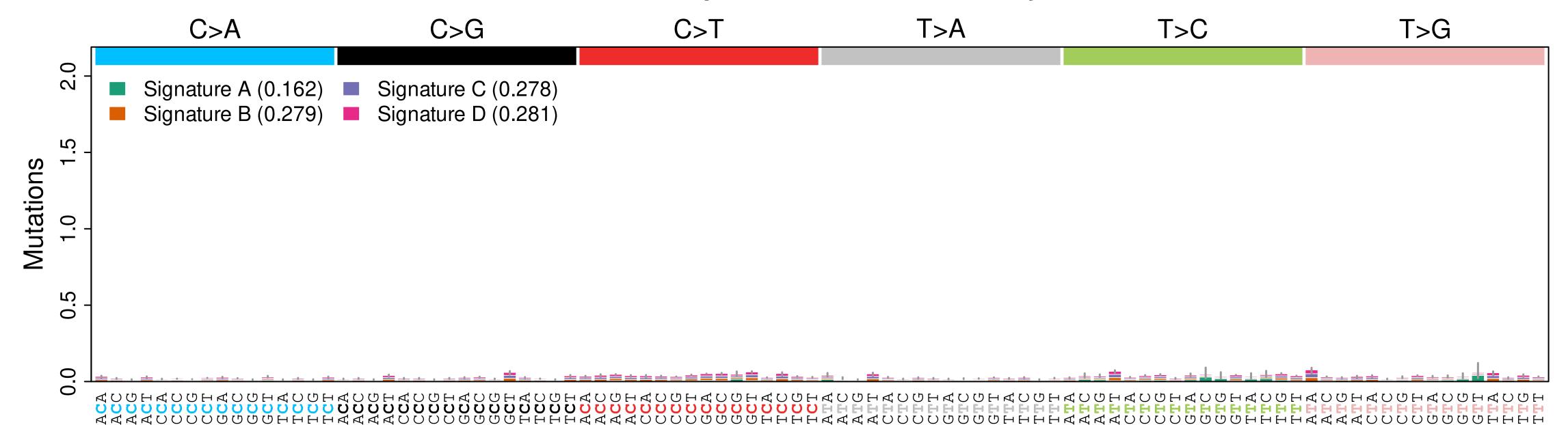




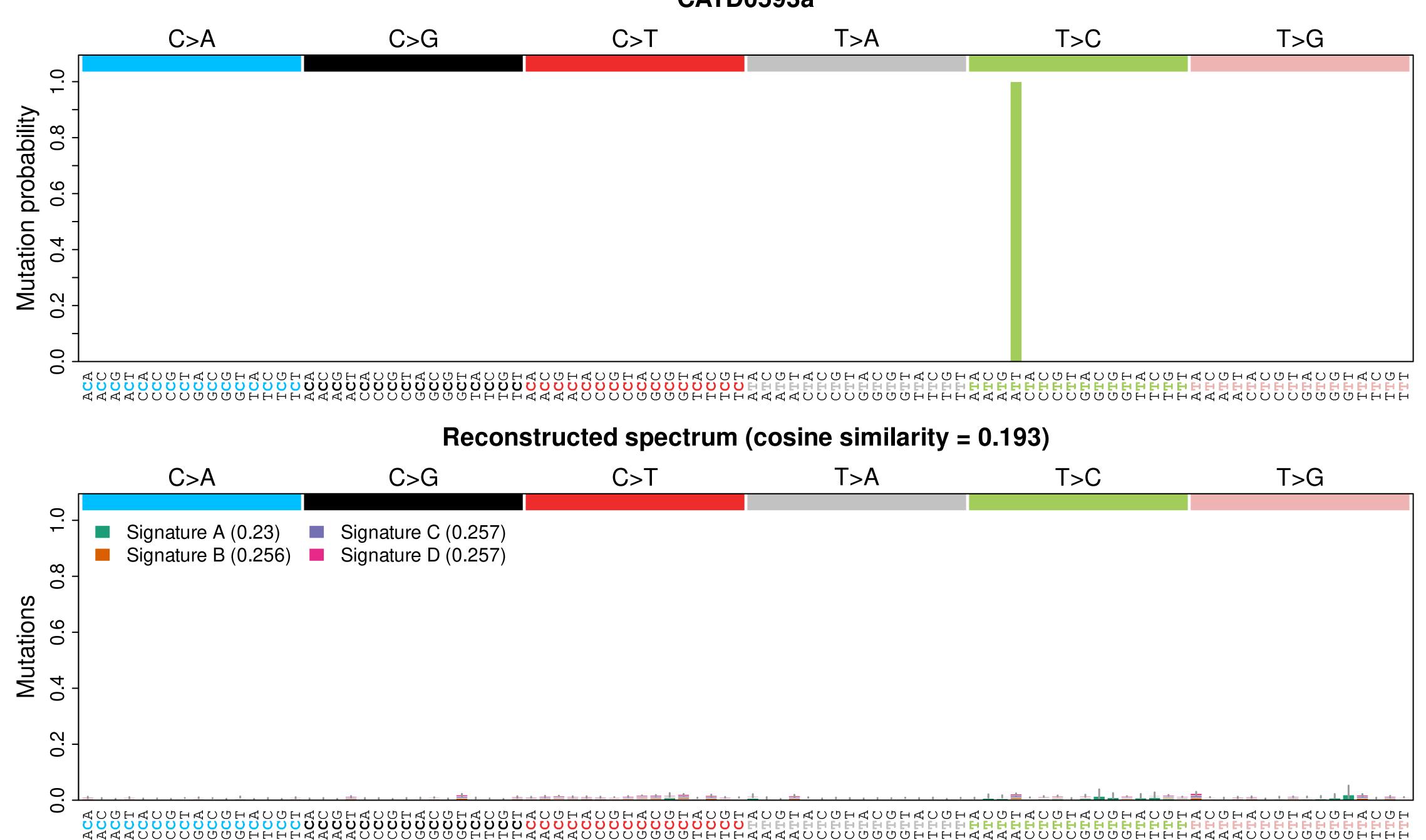
## CATD0585a (3 mutations)



## **Reconstructed spectrum (cosine similarity = 0.185)**



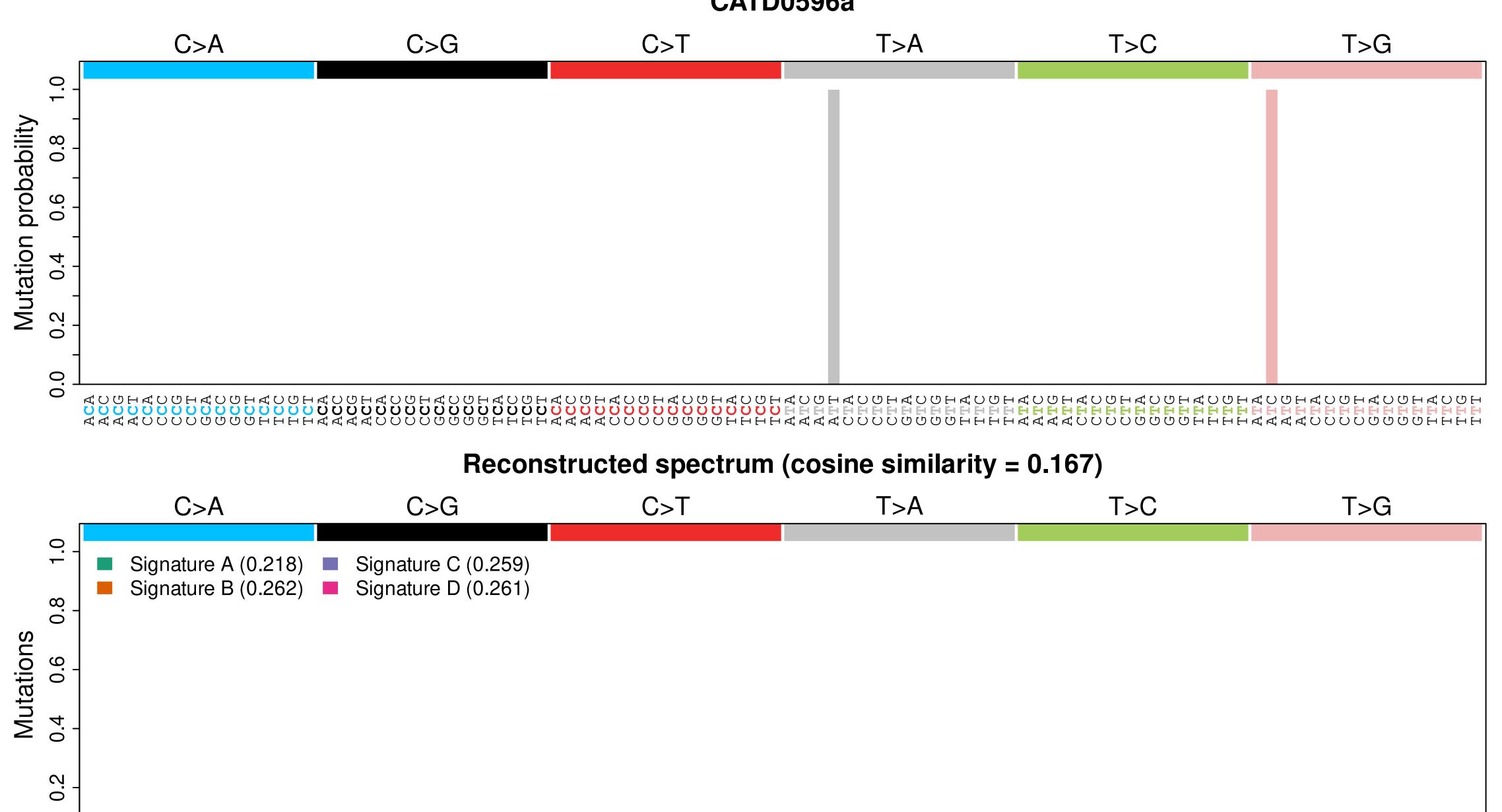




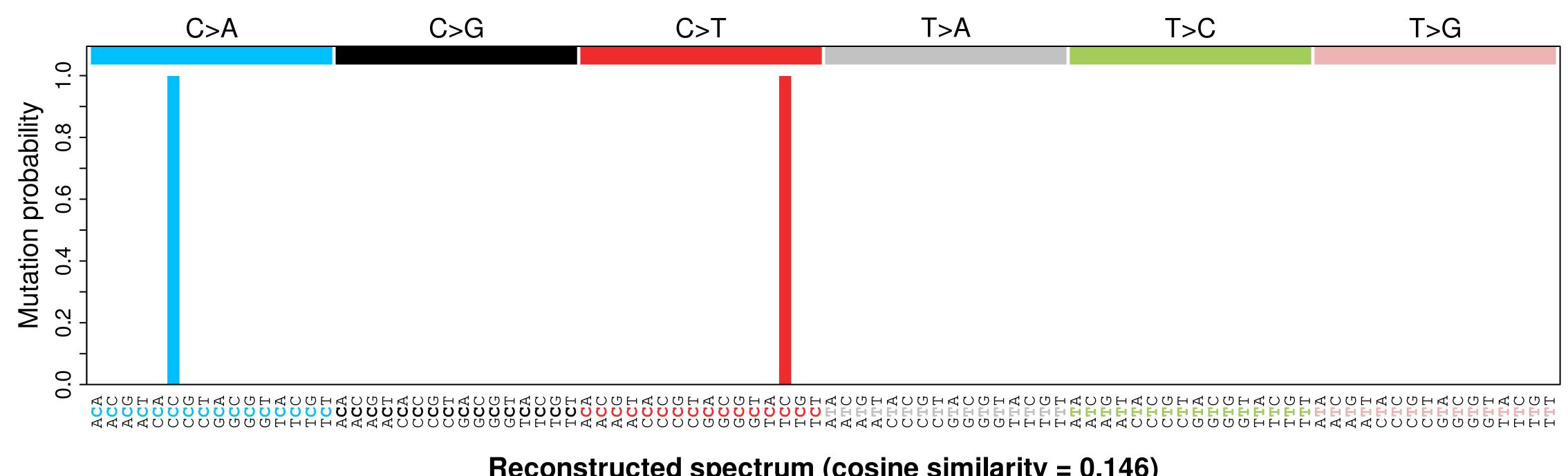
## CATD0581a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 1.5 Mutations 0.0 **Reconstructed spectrum (cosine similarity = 0.145)** T>A T>C T>G C>A C>G C>T 2.0 Signature A (0.166) Signature C (0.278) Signature B (0.279) Signature D (0.278) 5 Mutations 5 0 0

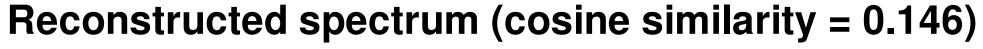
## CATD0736a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.277)** T>C T>G C>A C>G T>A C>T 2.0 Signature A (0.285) Signature C (0.242) Signature B (0.235) Signature D (0.238) 5 Mutations 2

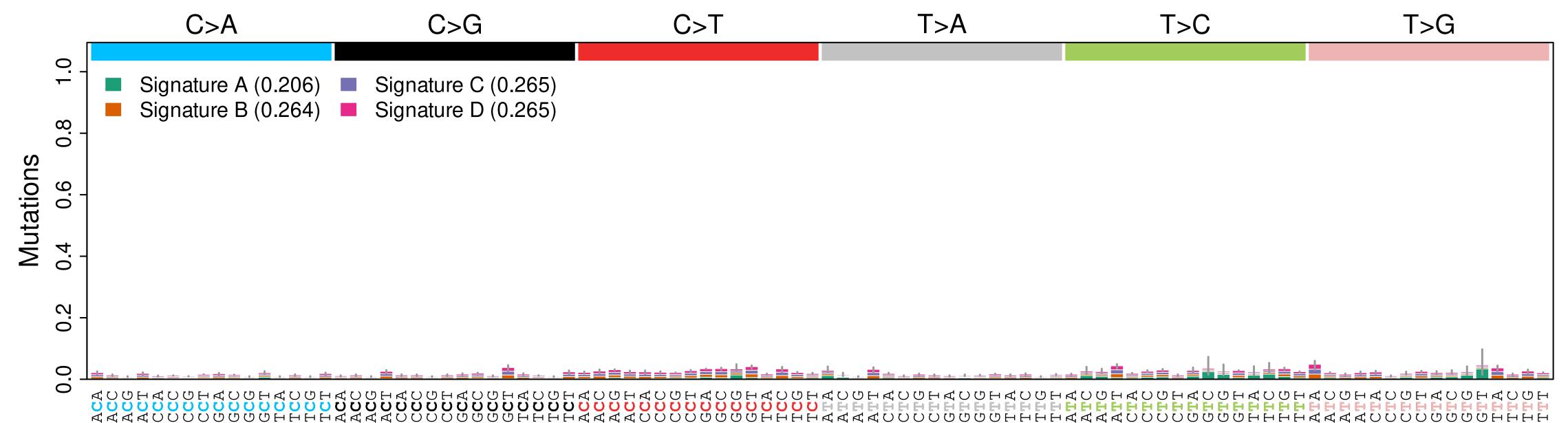




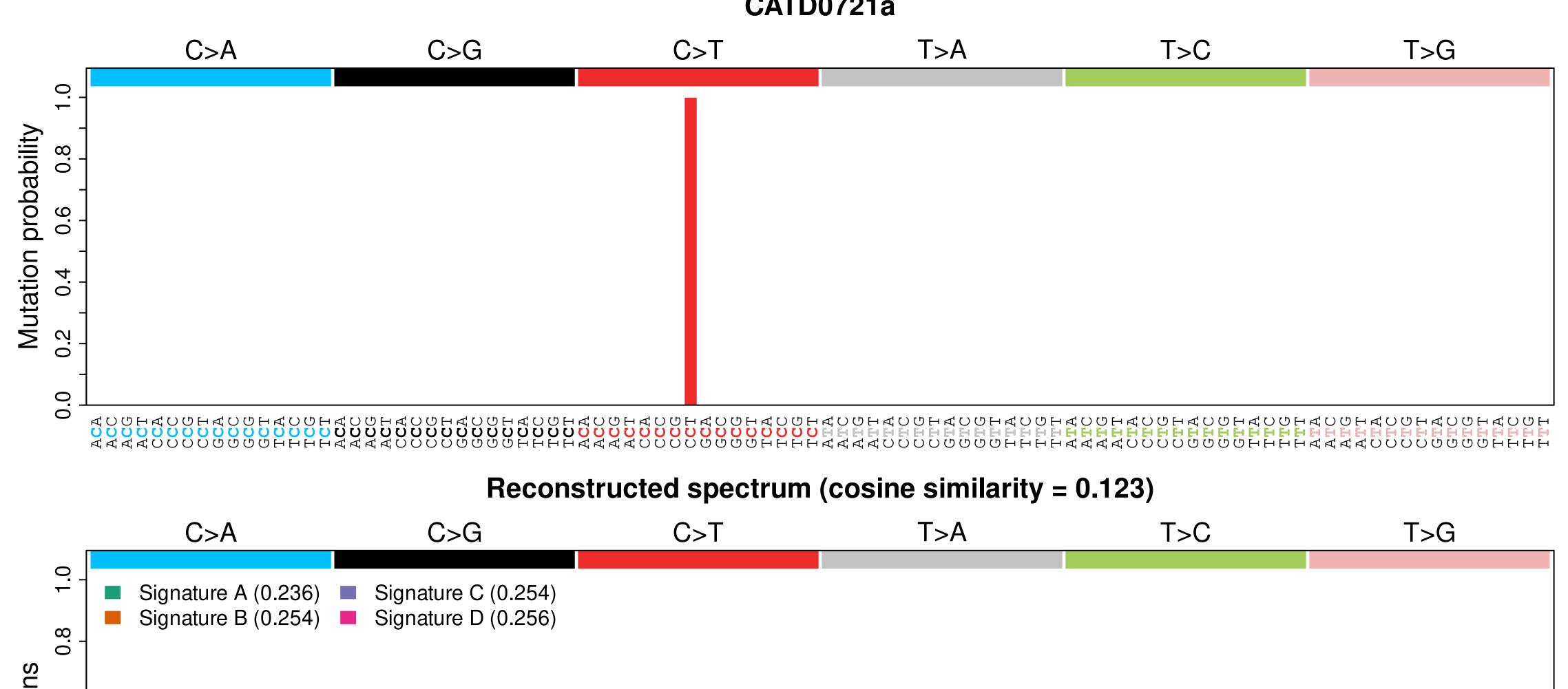


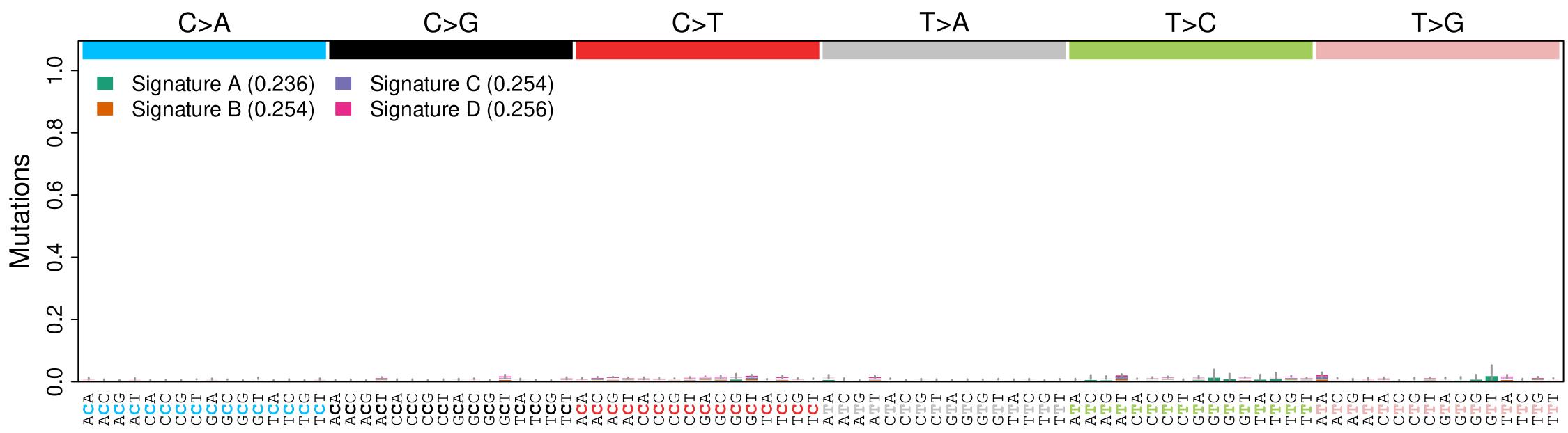




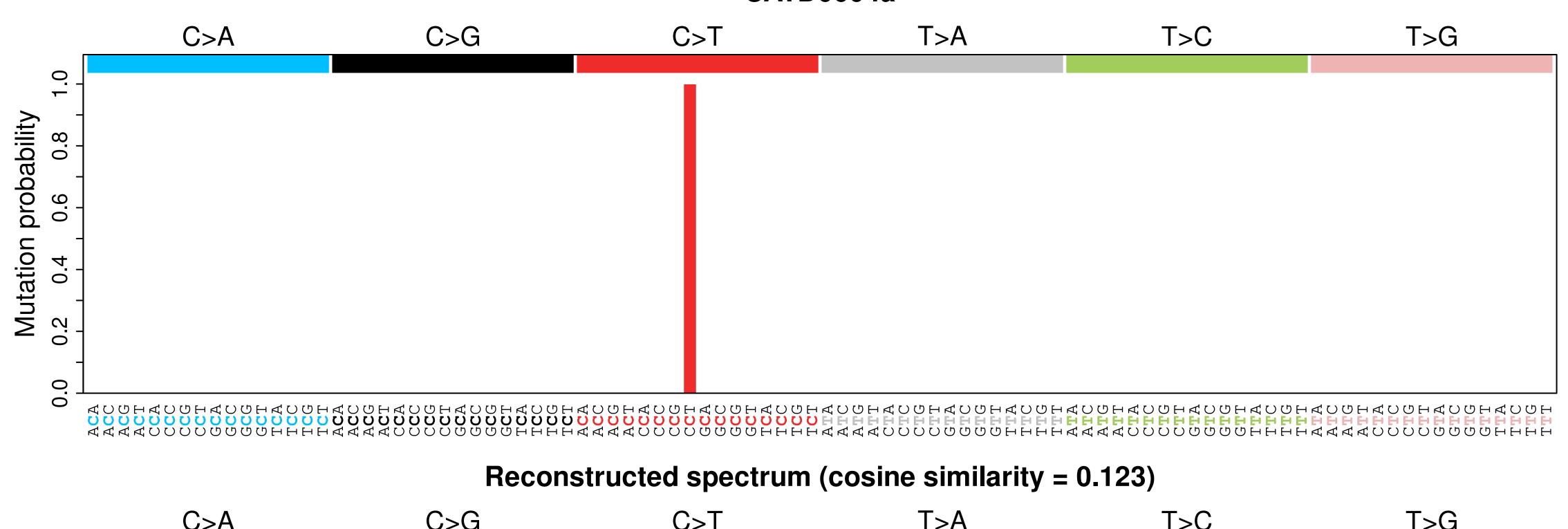


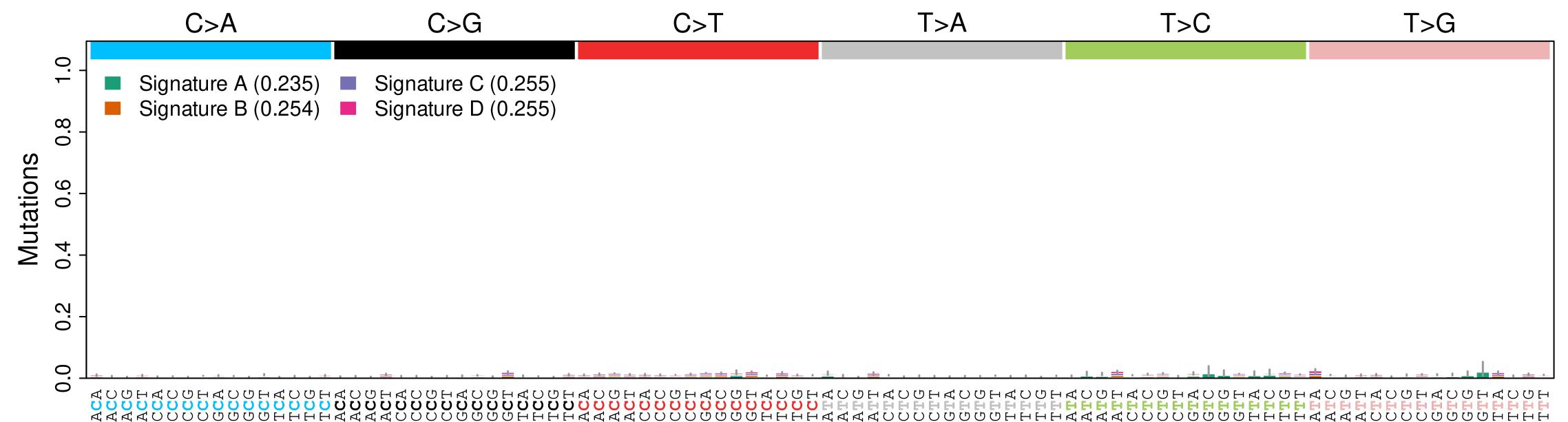












#### CATD0720a

