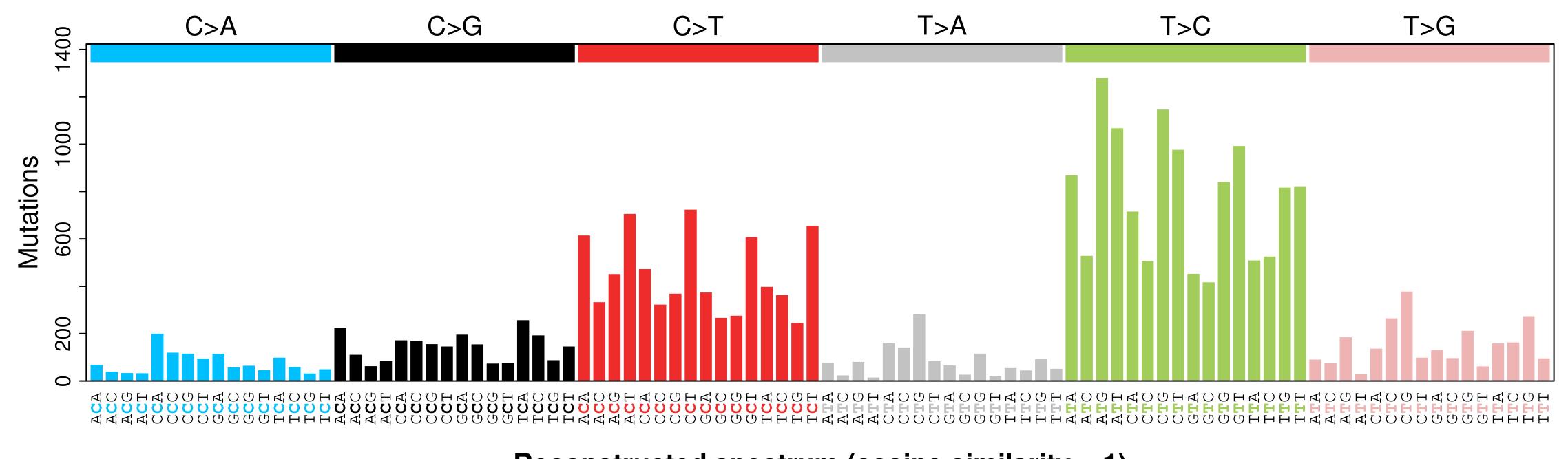
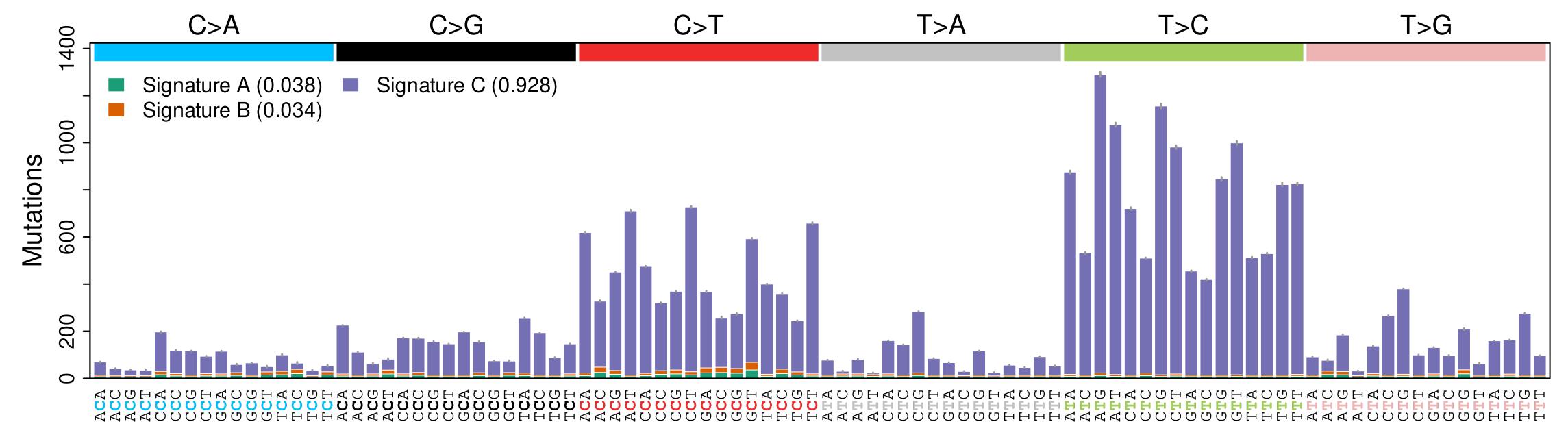
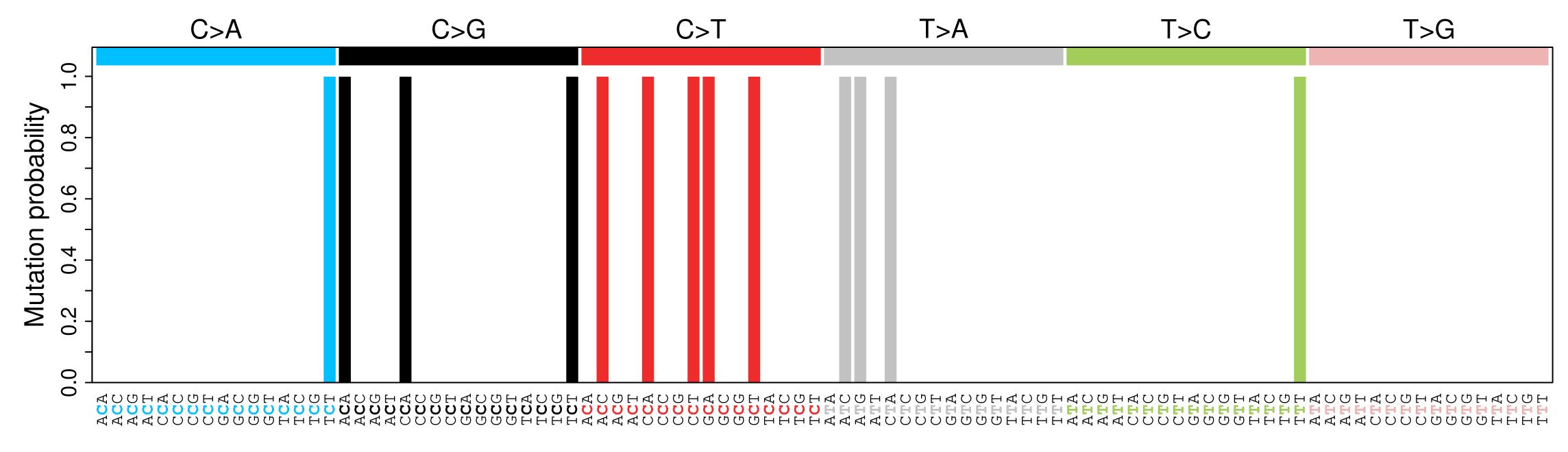
### **CATD309a (27,083 mutations)**

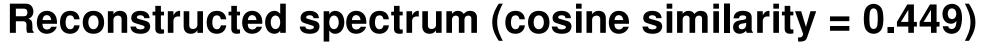


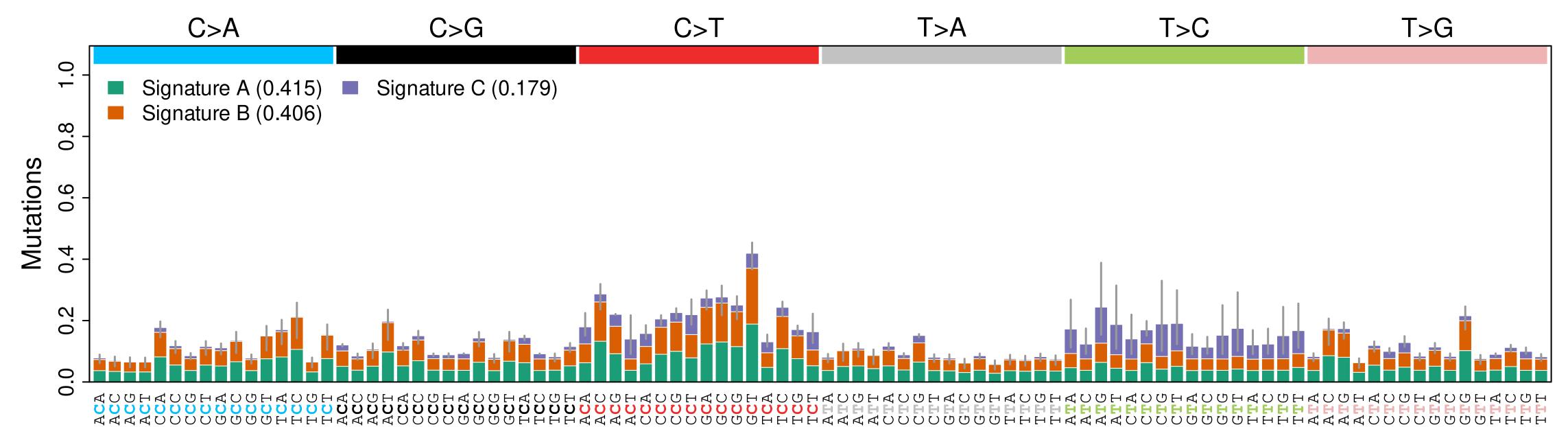
## Reconstructed spectrum (cosine similarity = 1)



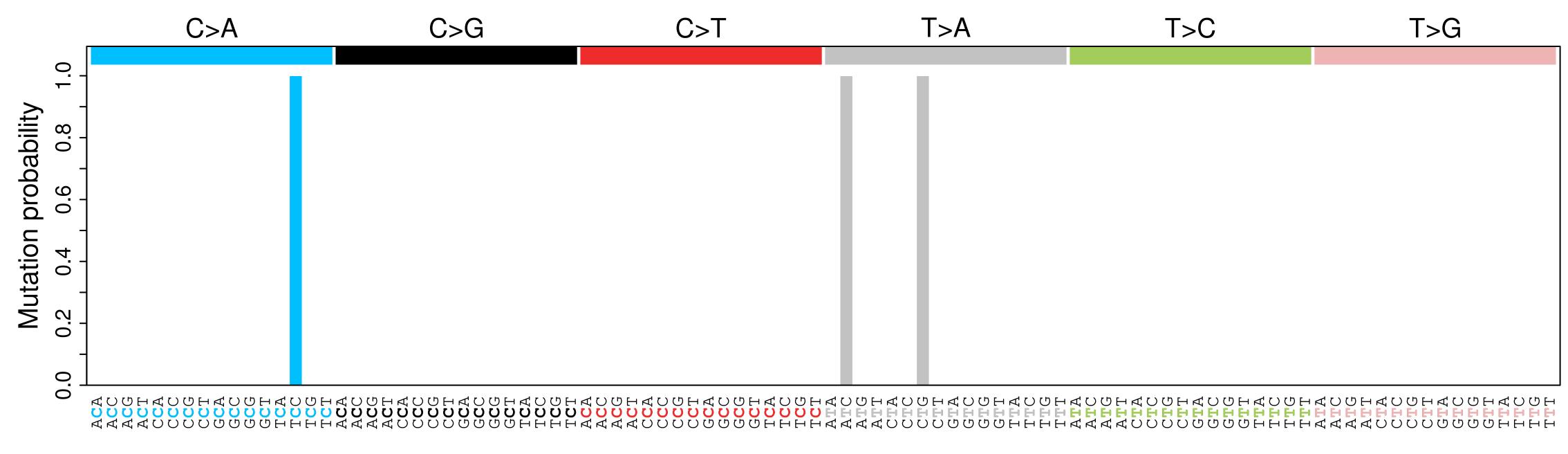
### CATD319a

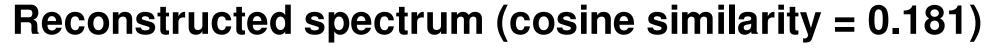


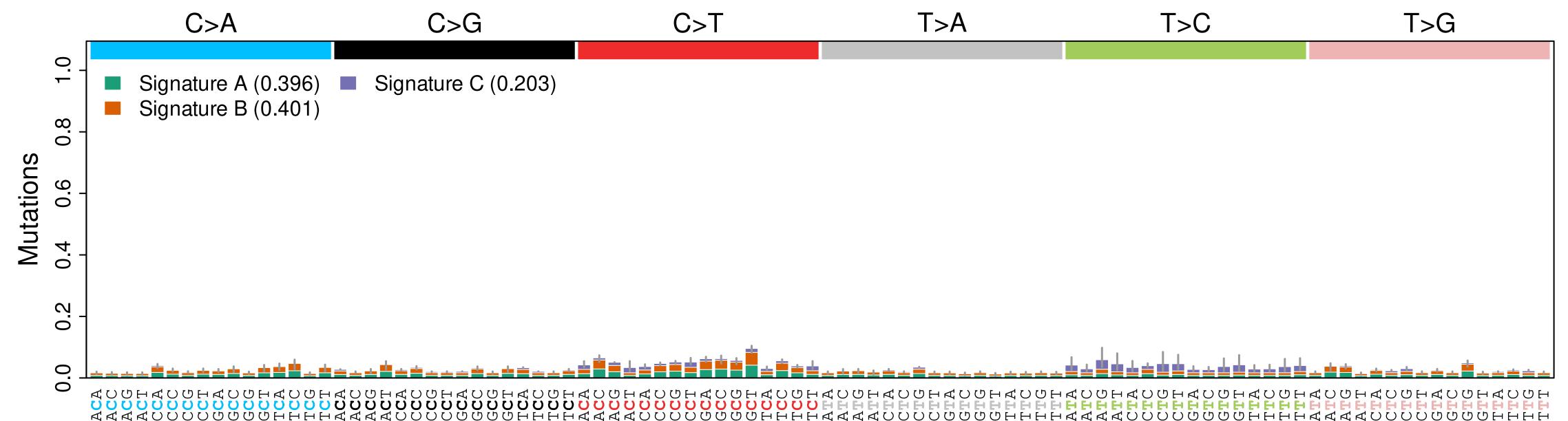




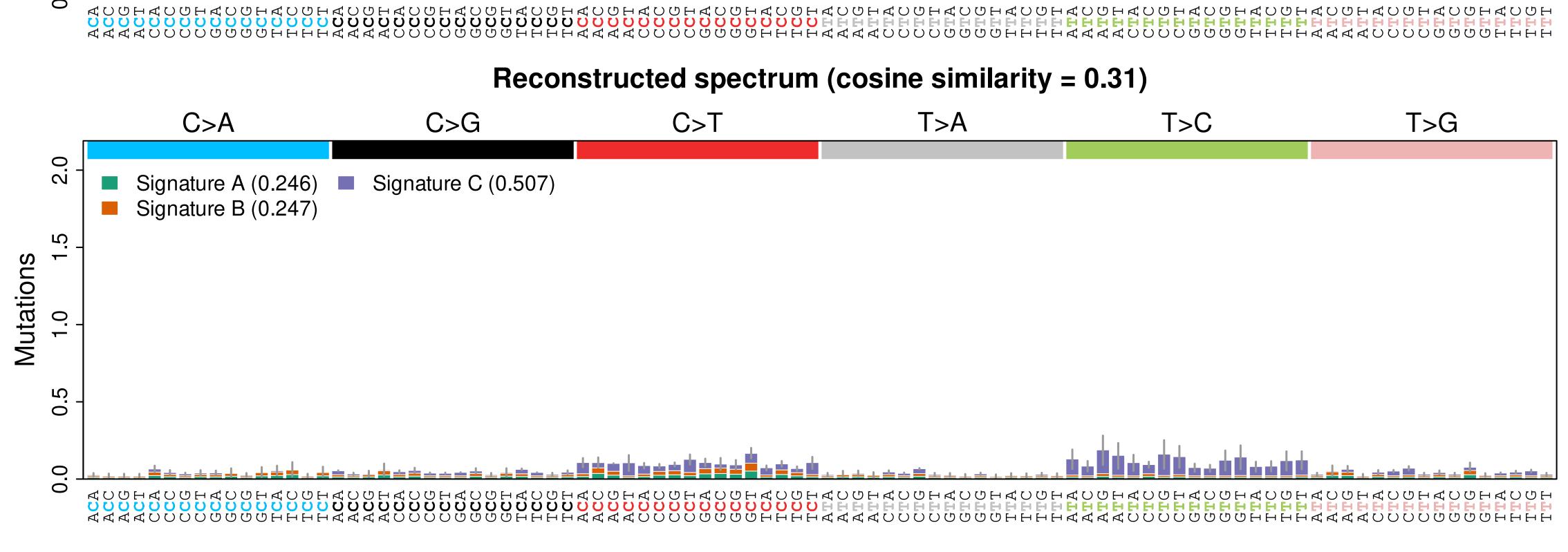




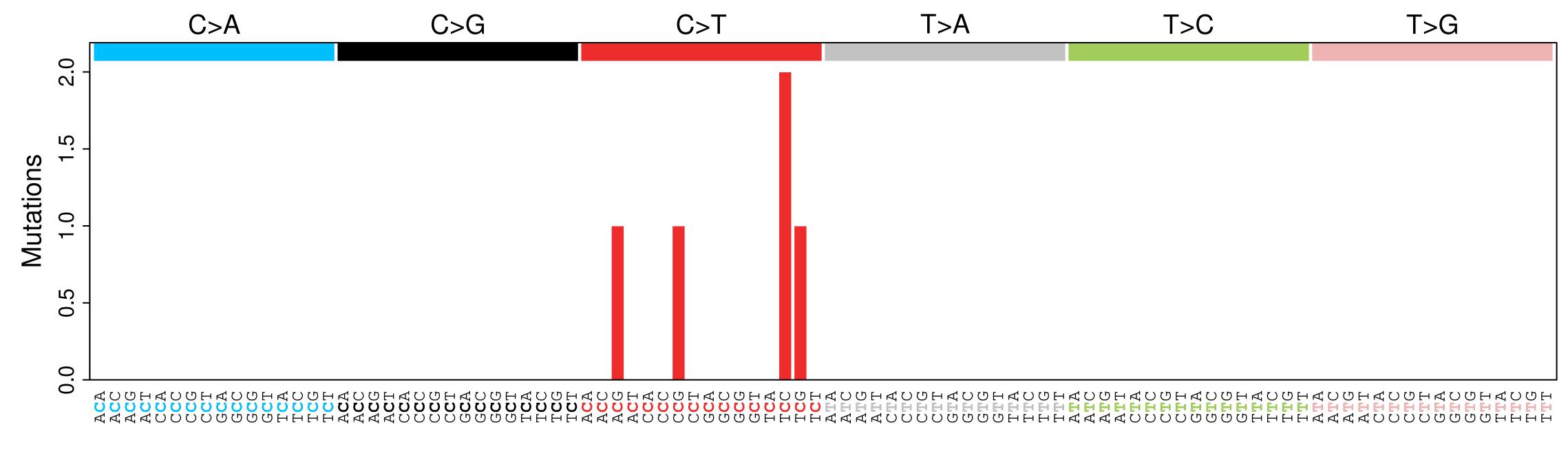




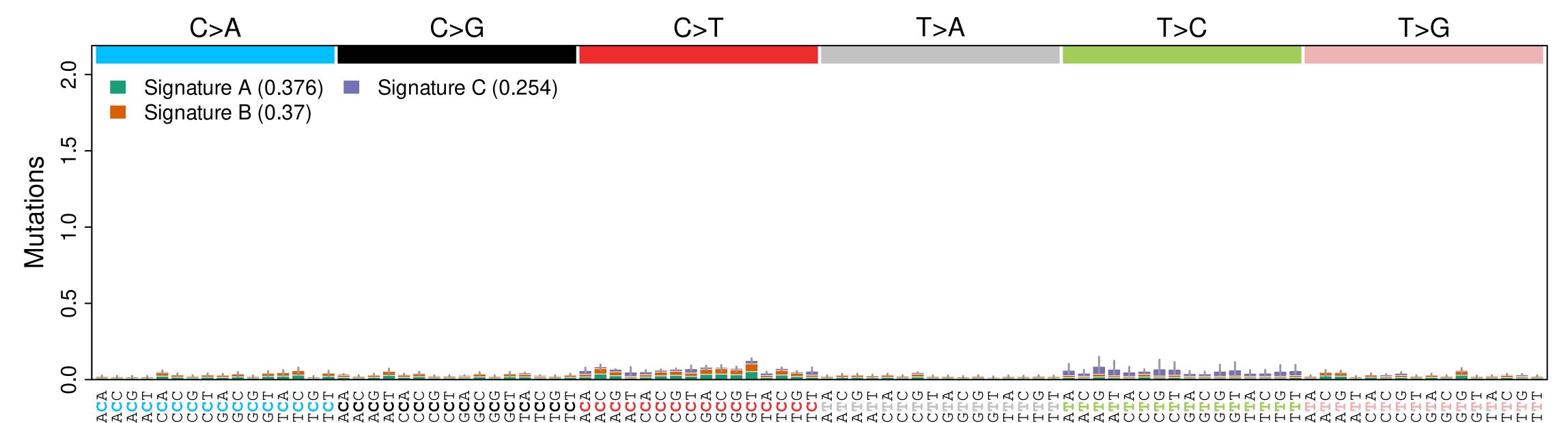
### CATD297a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.31)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.246) Signature C (0.507) Signature B (0.247) 5



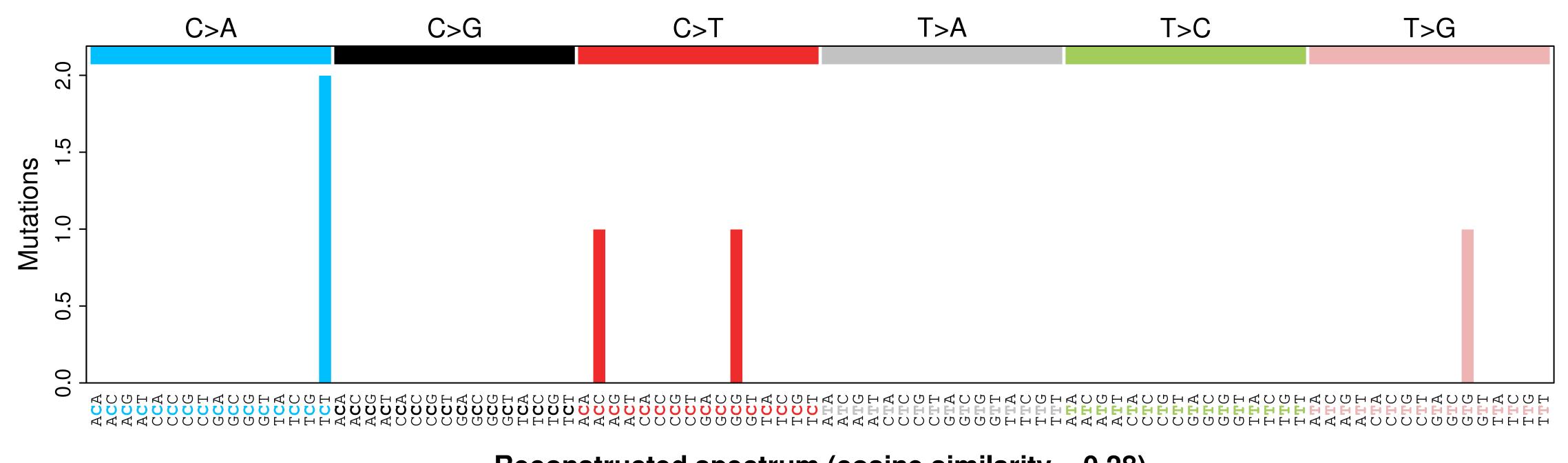
# CATD312a (5 mutations)



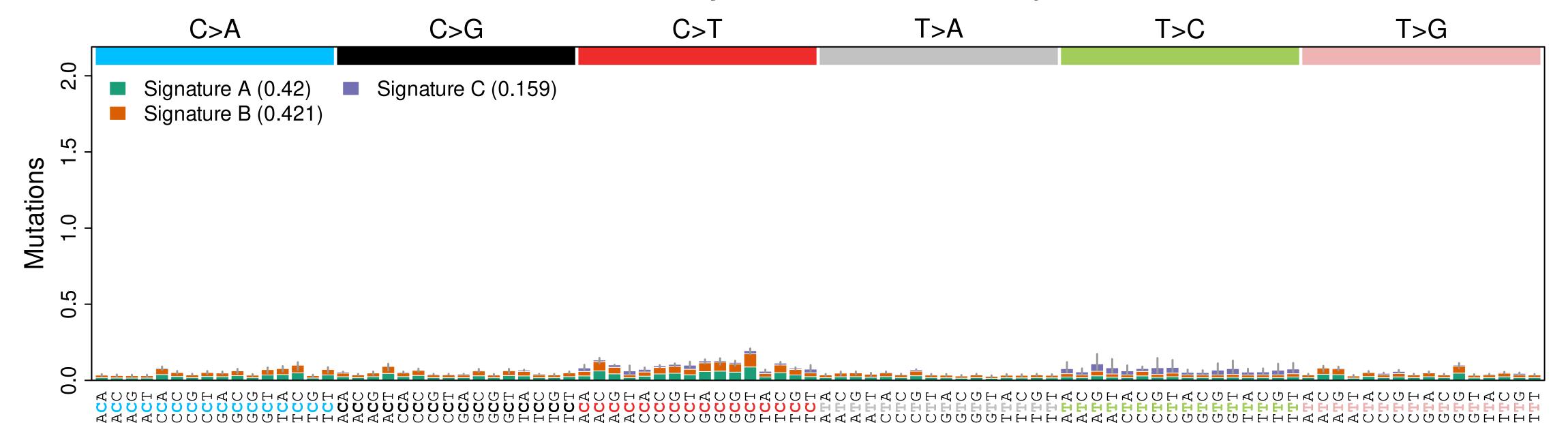
## Reconstructed spectrum (cosine similarity = 0.278)



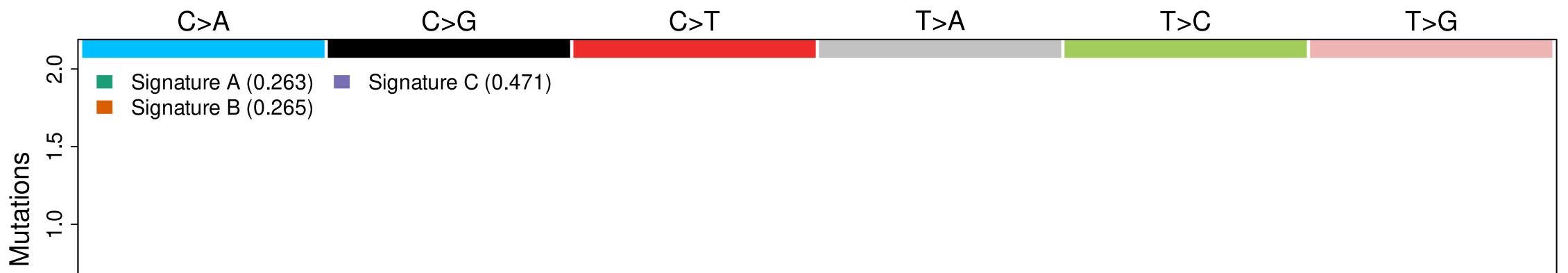
## CATD323a (5 mutations)



## Reconstructed spectrum (cosine similarity = 0.28)

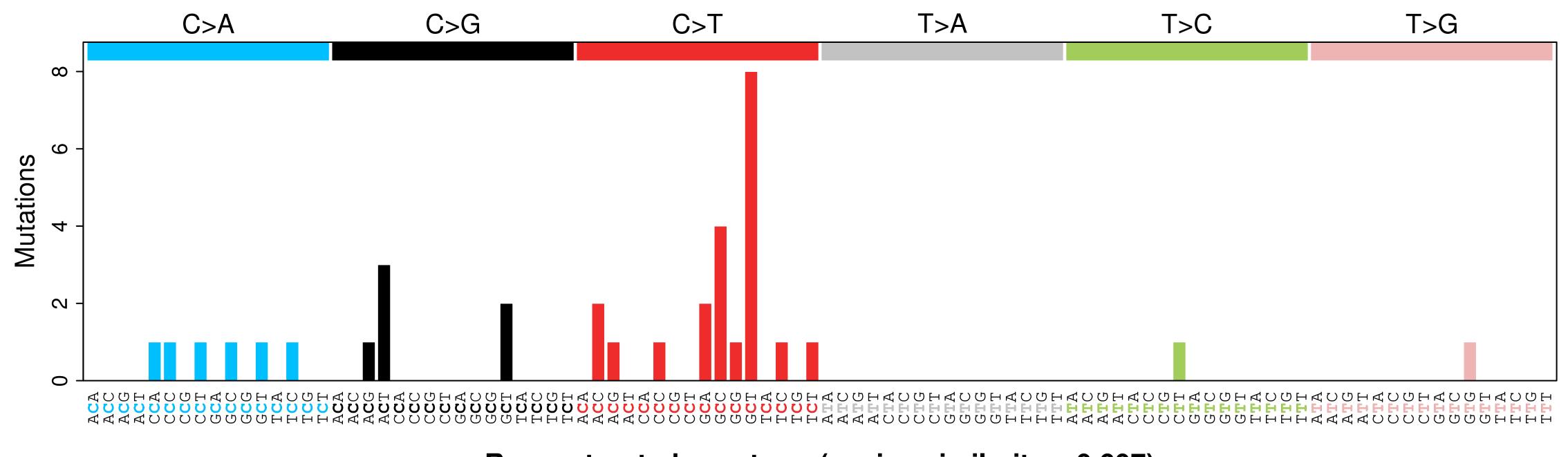


# CATD314a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.337)**

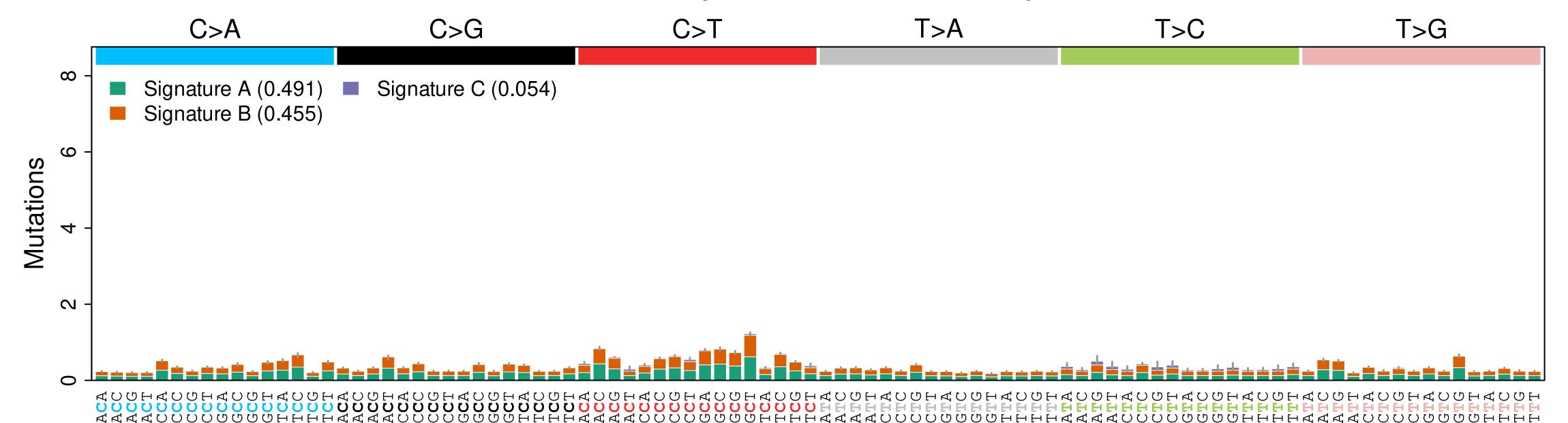


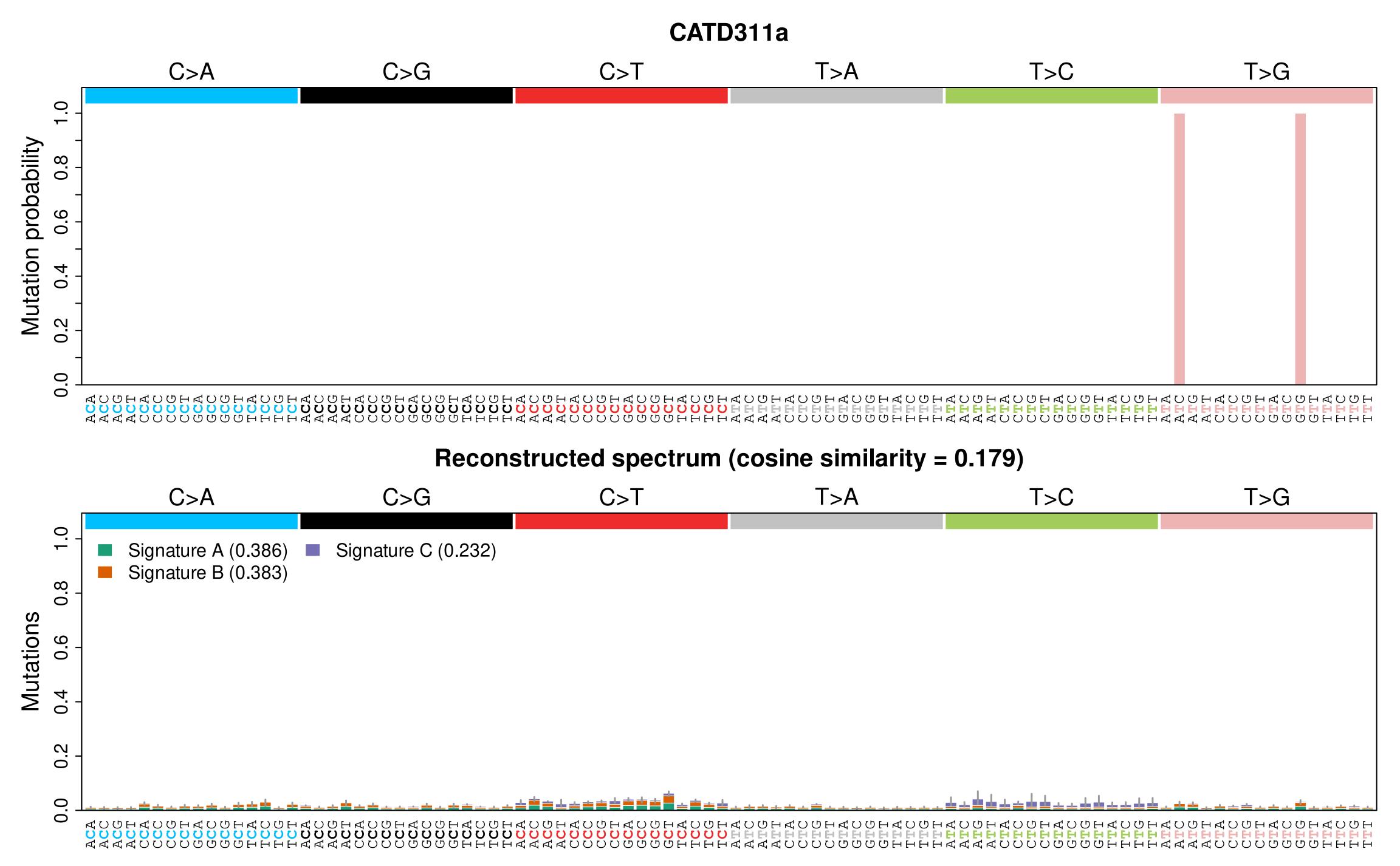
0.5

### CATD329a (35 mutations)



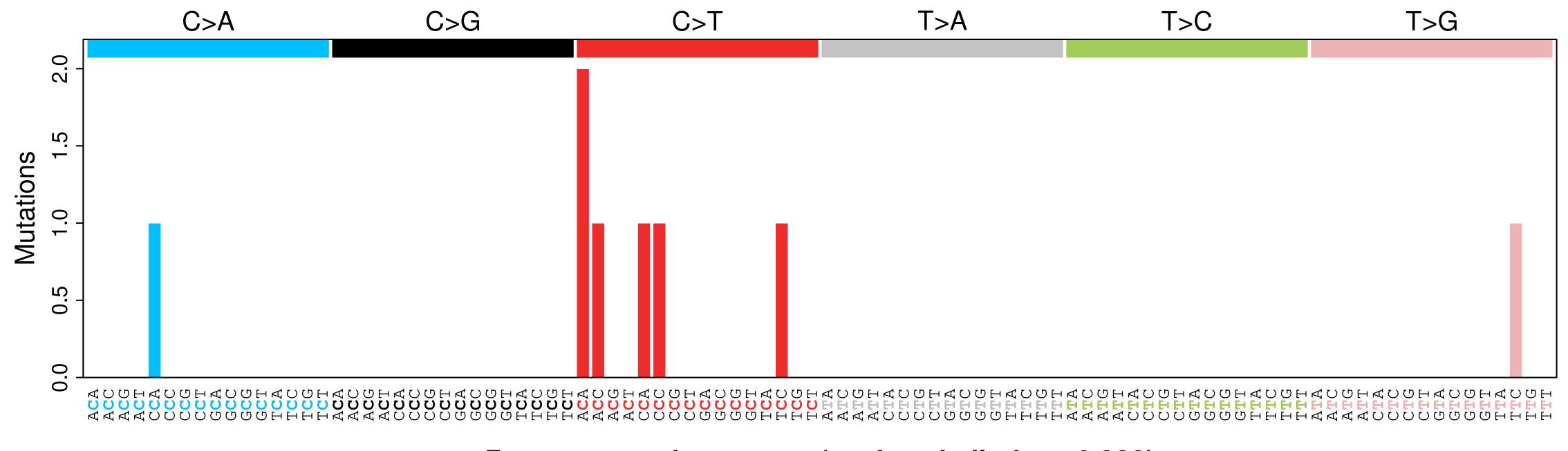
## **Reconstructed spectrum (cosine similarity = 0.607)**



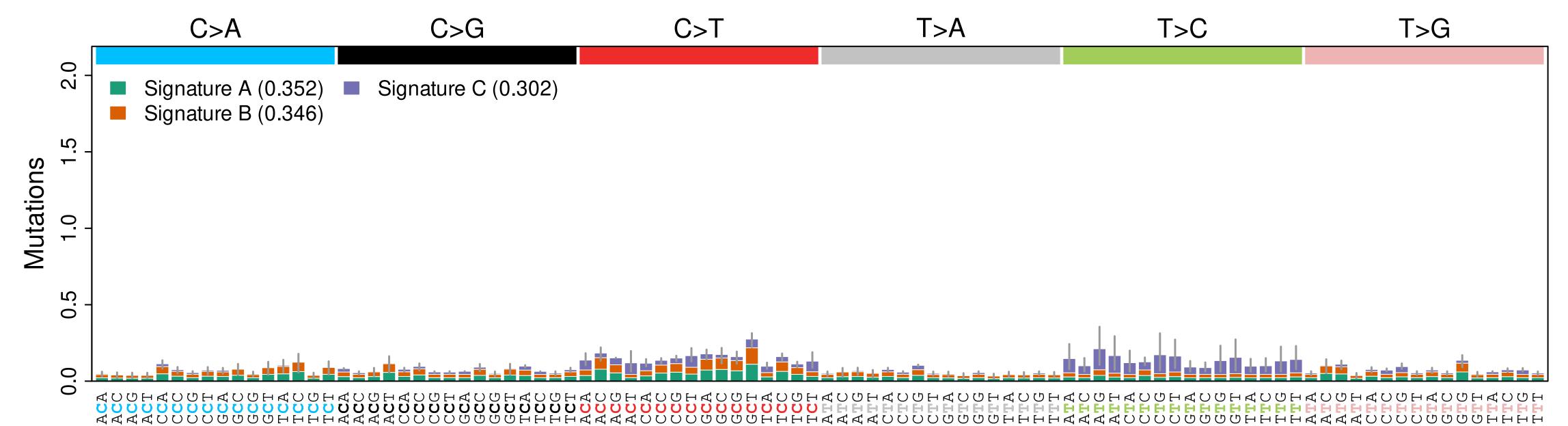


## CATD306a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.212)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.394) Signature C (0.205) Signature B (0.4) 5 Mutations 2 0

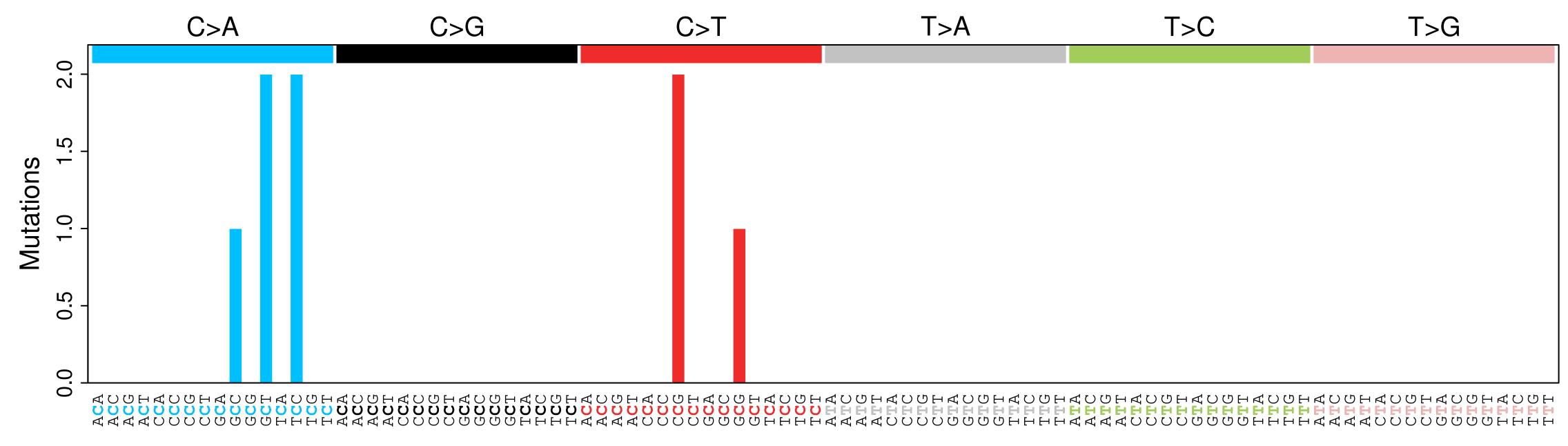
### CATD320a (8 mutations)



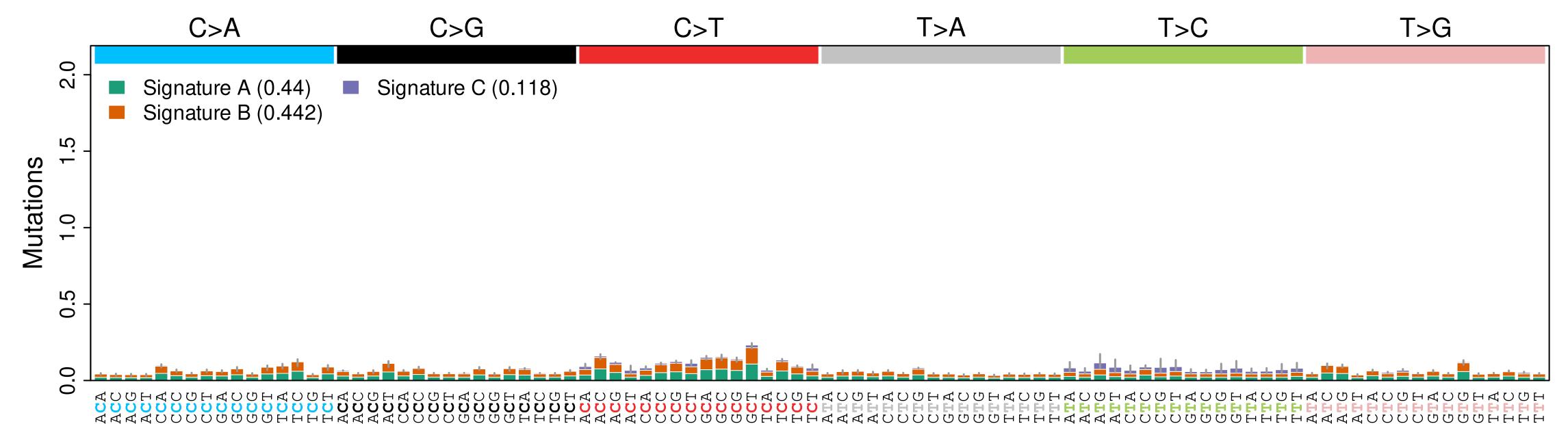
## **Reconstructed spectrum (cosine similarity = 0.328)**



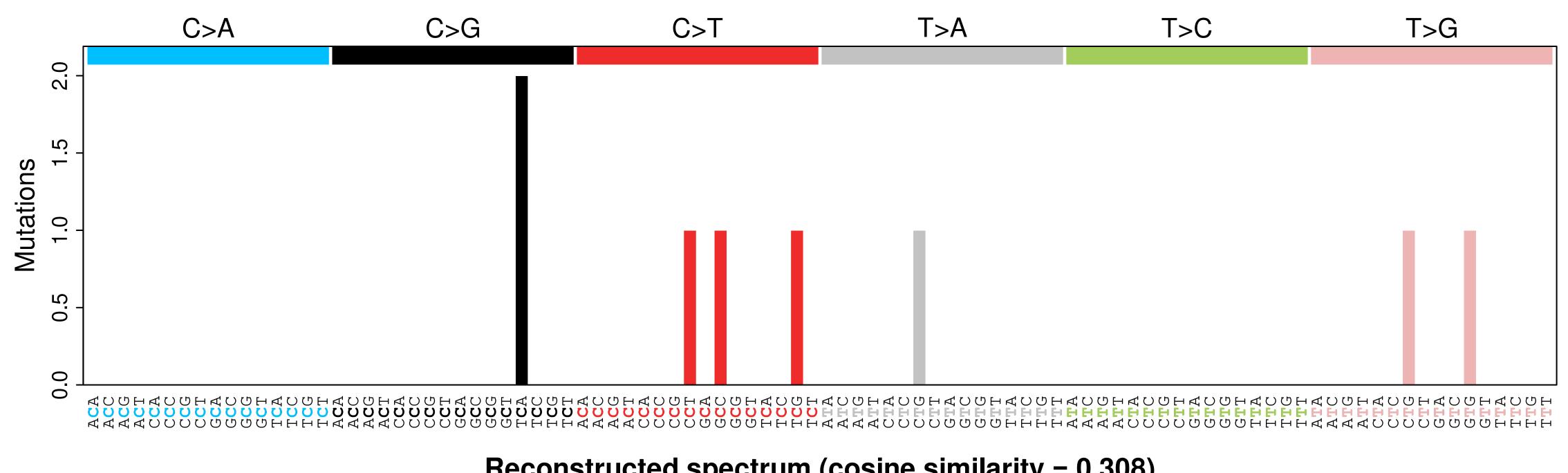
# CATD300a (8 mutations)

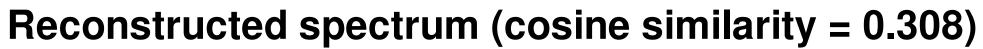


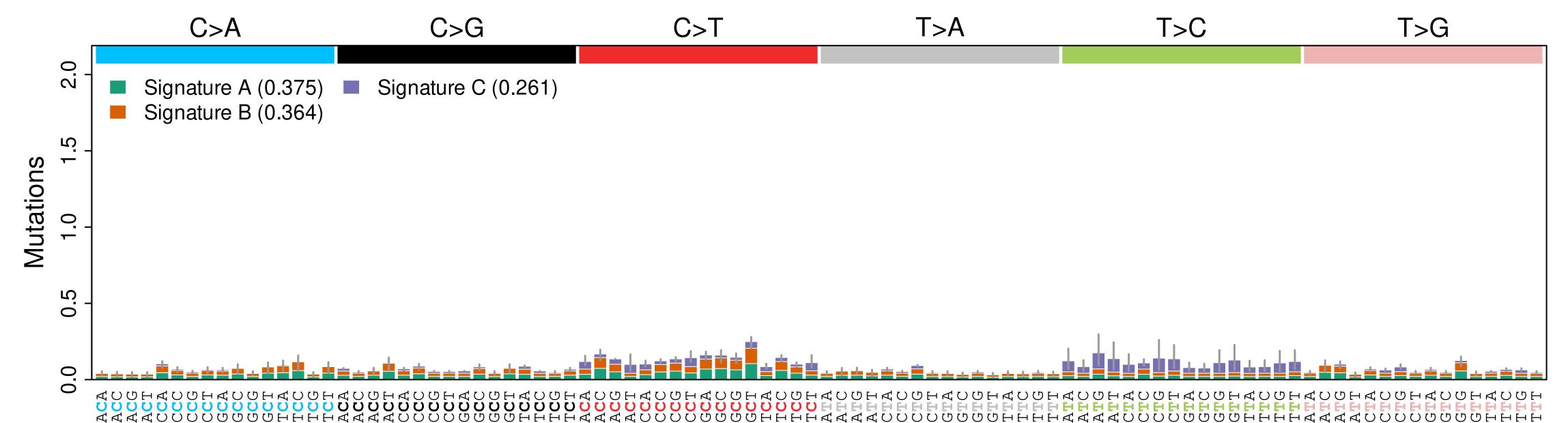
## **Reconstructed spectrum (cosine similarity = 0.301)**



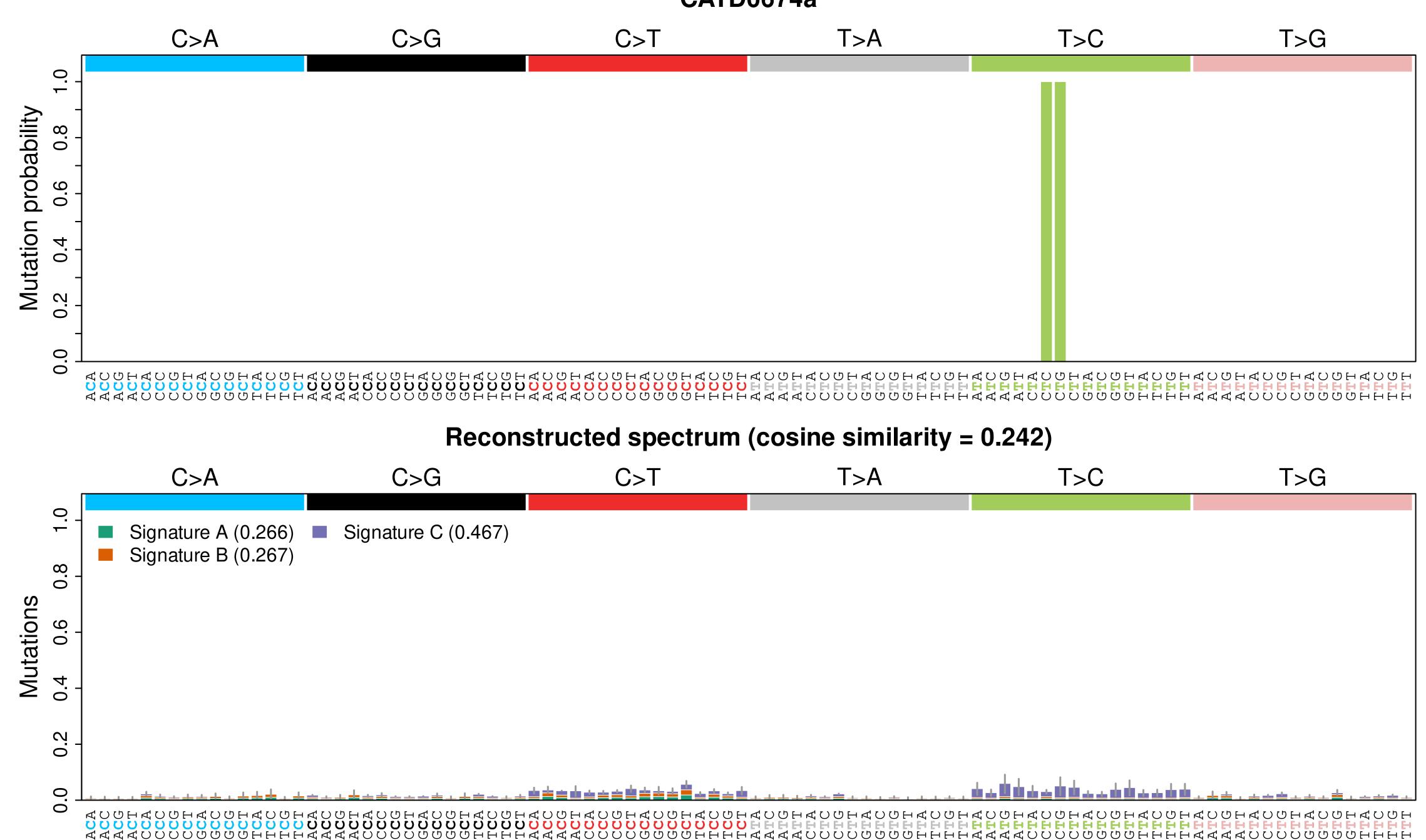
### CATD328a (8 mutations)



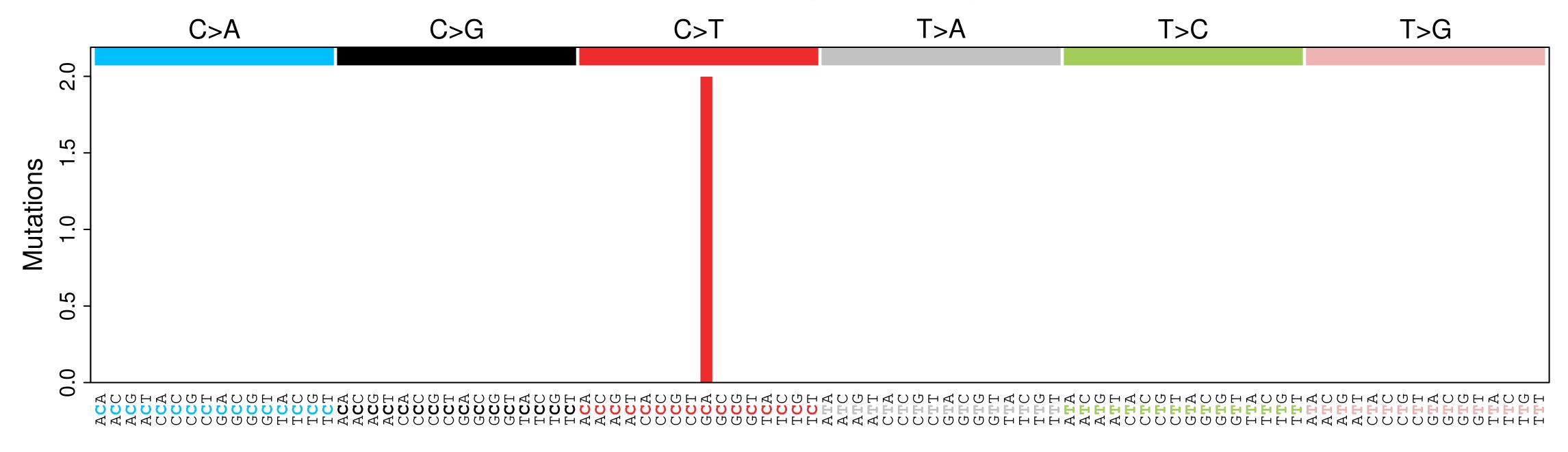




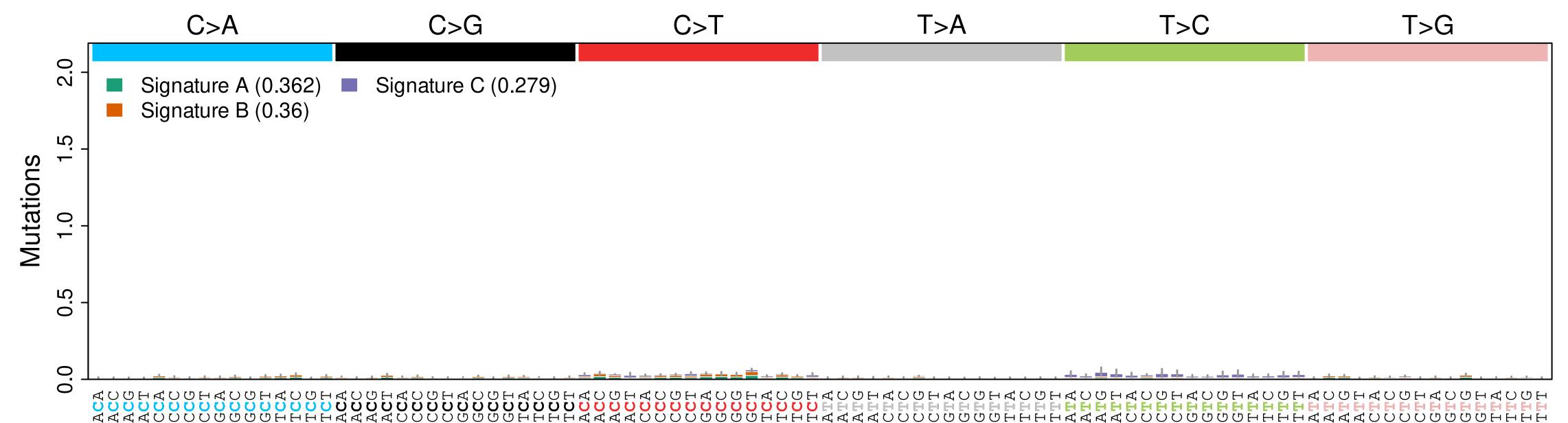




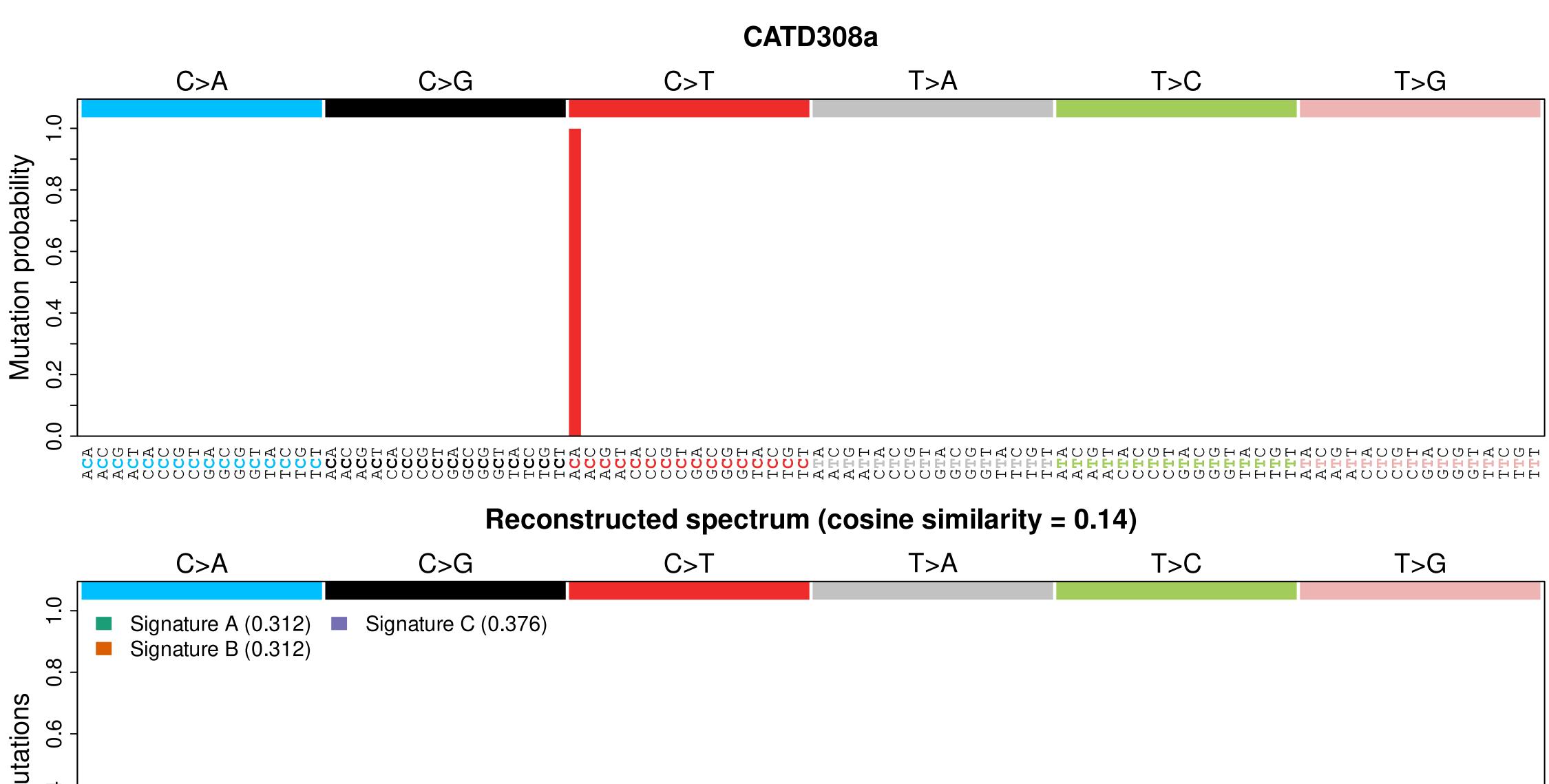
## CATD318a (2 mutations)

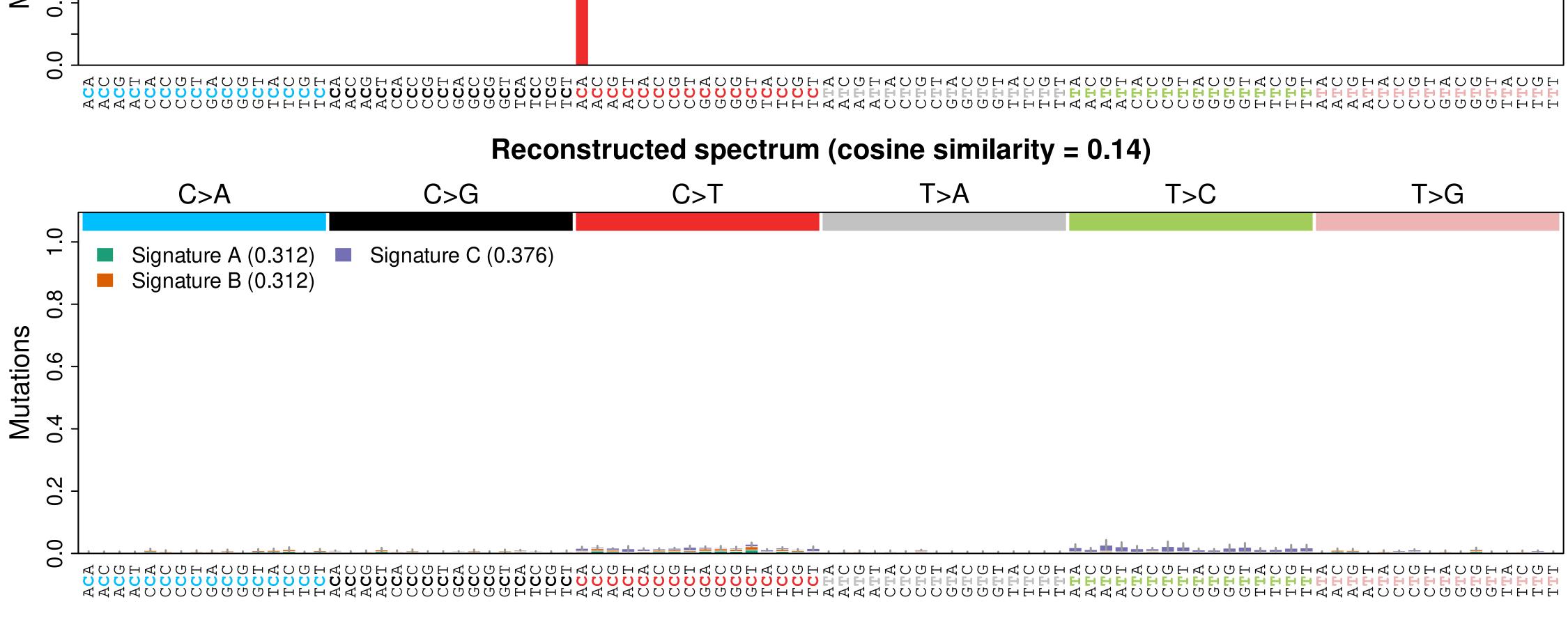


## Reconstructed spectrum (cosine similarity = 0.177)

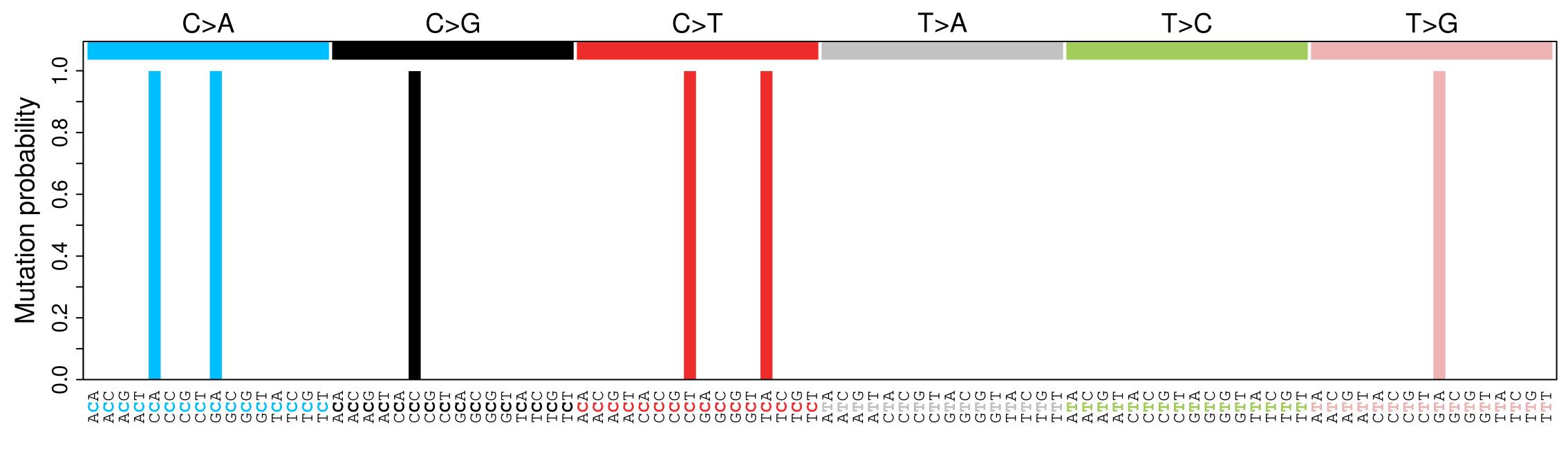


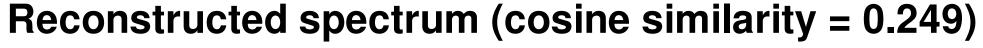
## CATD301a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.286)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.325) Signature C (0.348) Signature B (0.327) 5 Mutations 2 0

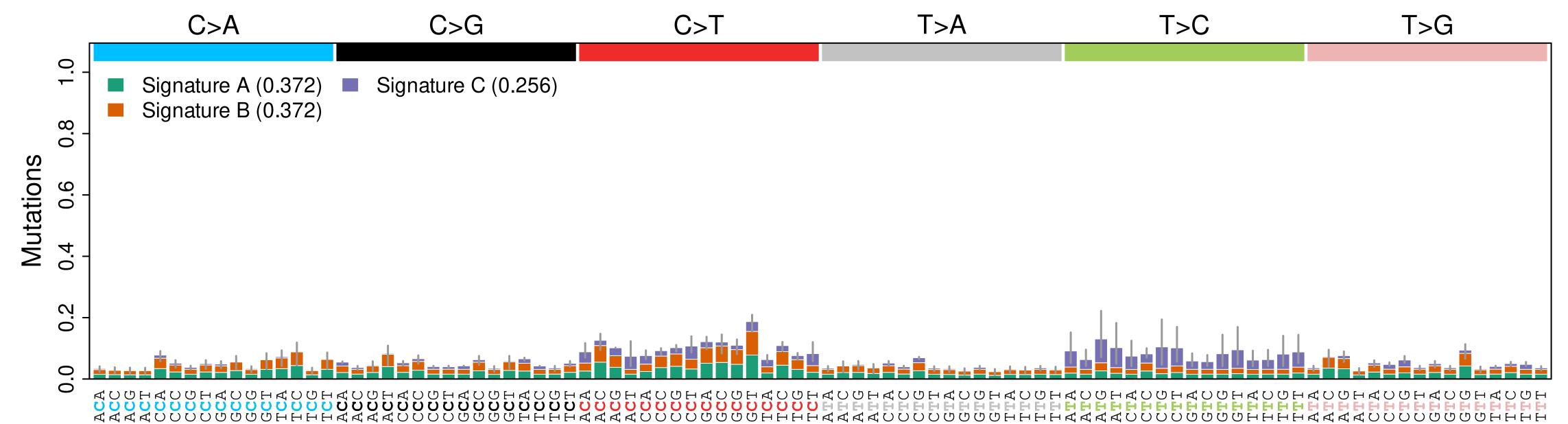




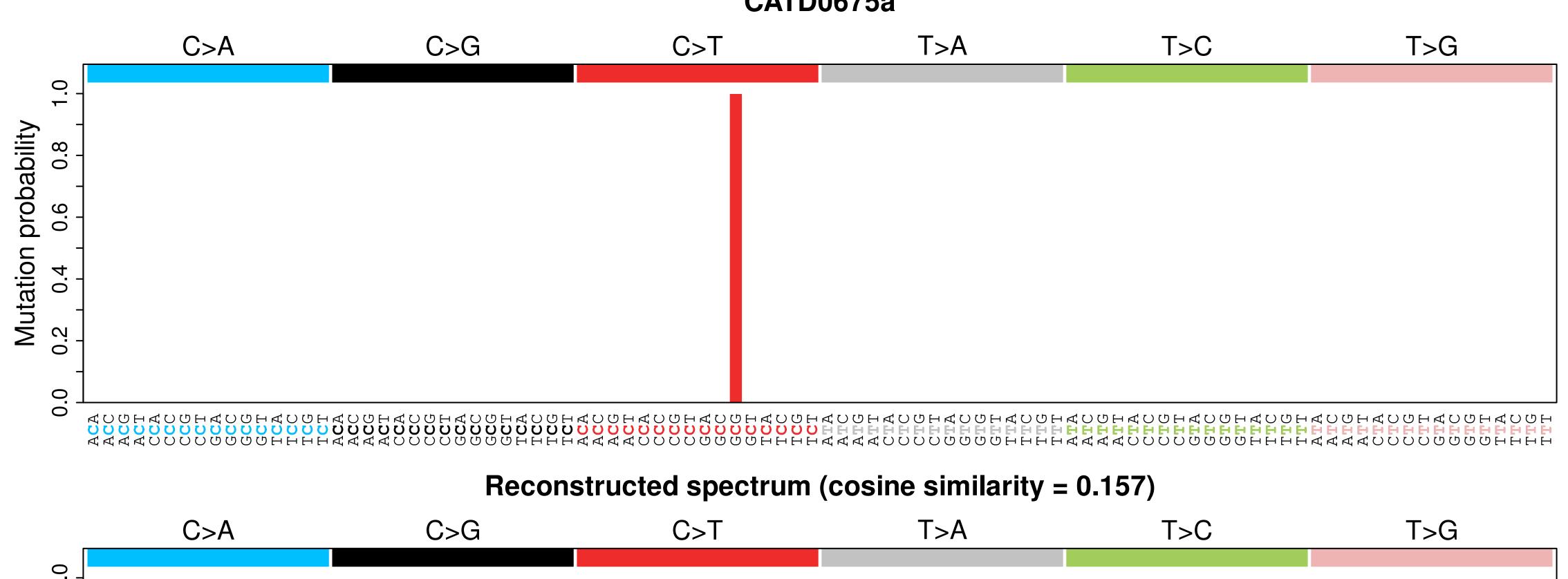
#### CATD296a

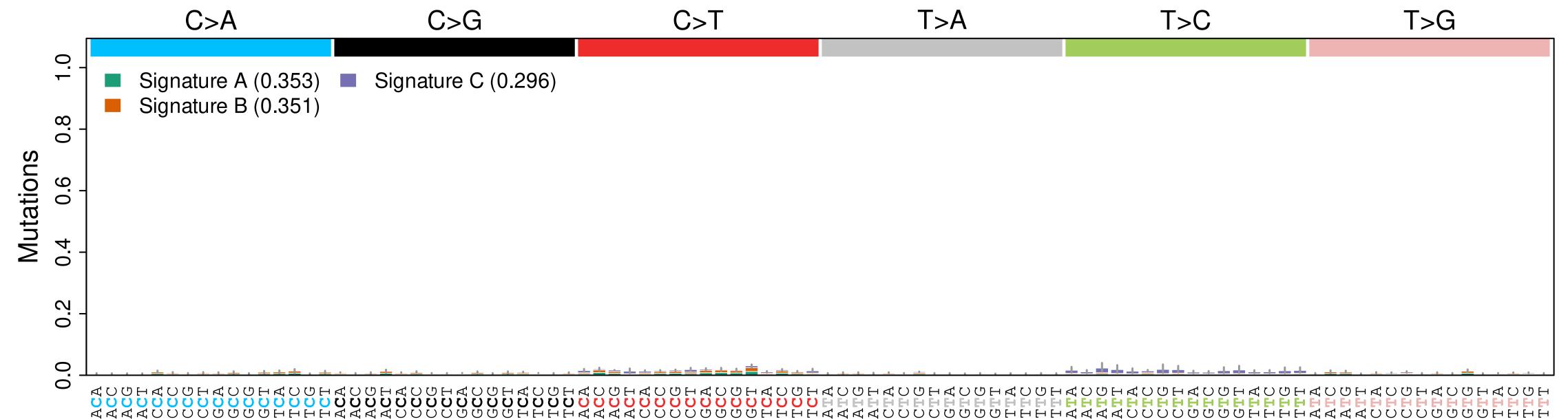








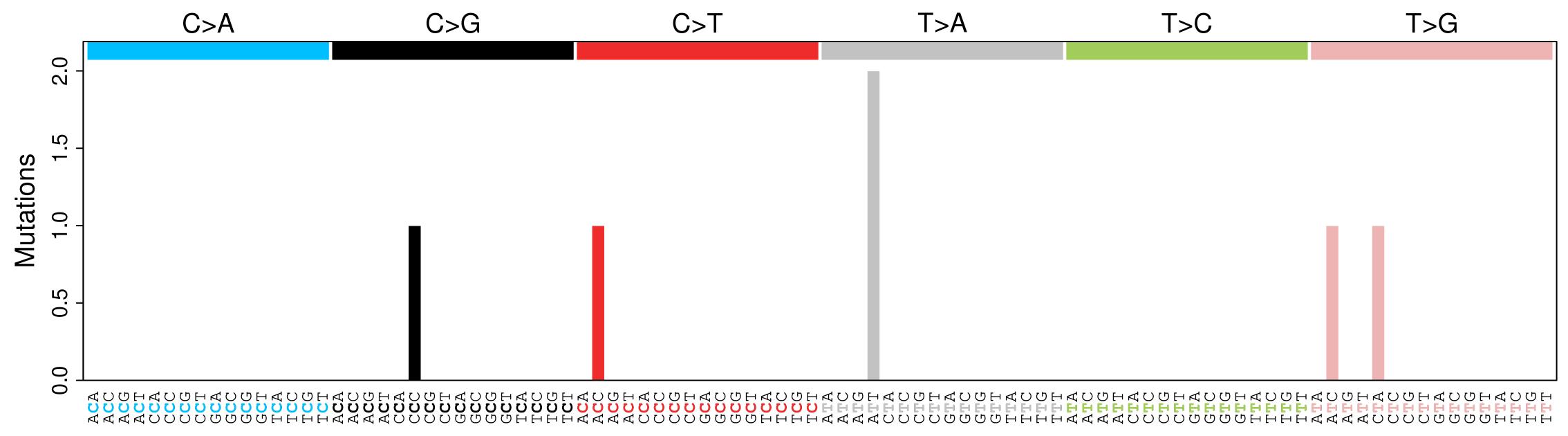




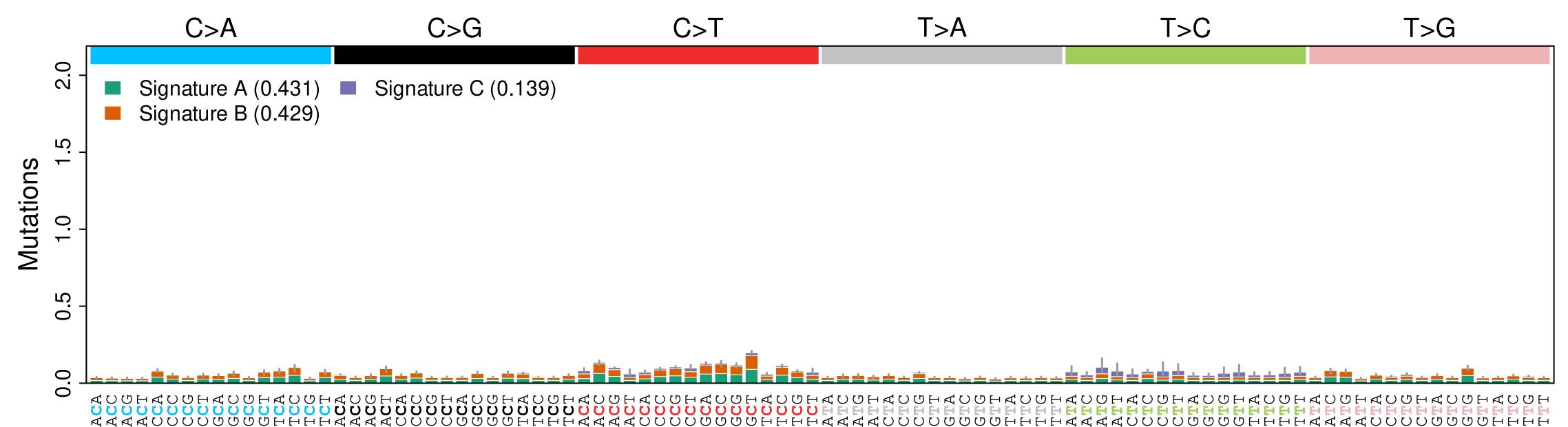
### CATD0676a C>A T>C T>G C>G C>T T>A 1.0 Mutation probability 0.8 9.0 0.4 0.2 0.0 **Reconstructed spectrum (cosine similarity = 0.227)** C>A C>G T>A T>C T>G C>T 1.0 Signature A (0.391) Signature C (0.22) Signature B (0.389) 0.8 Mutations 9.0

0.2

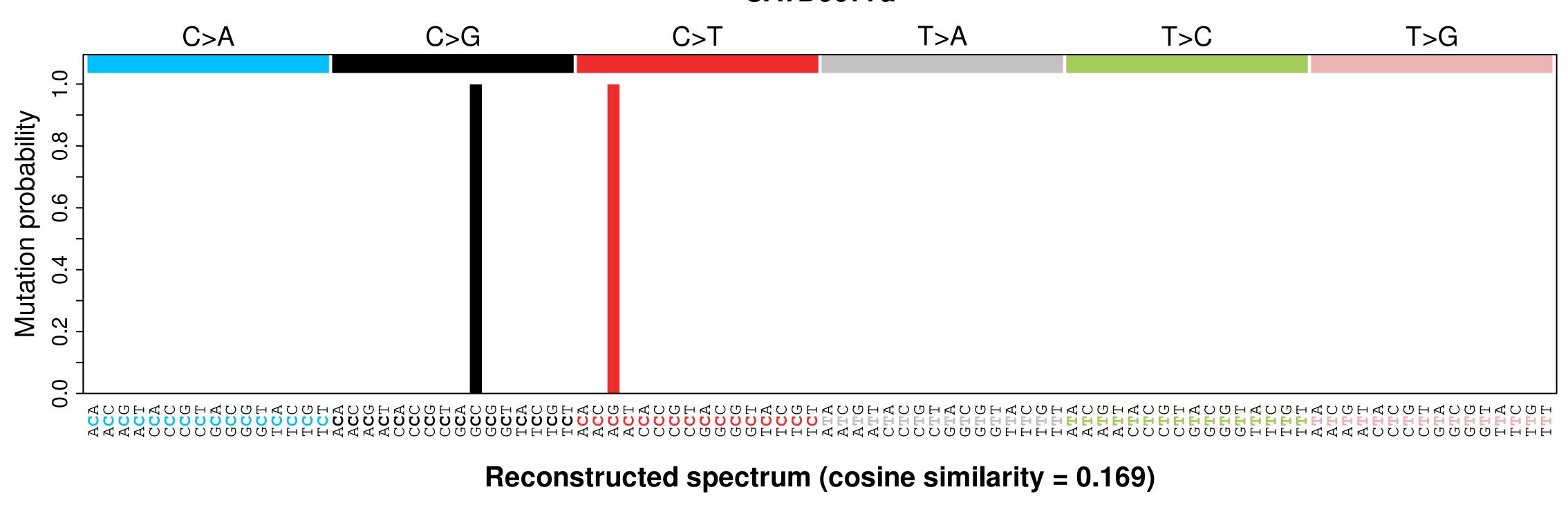
#### CATD326a (6 mutations) C>A C>G C>T T>A

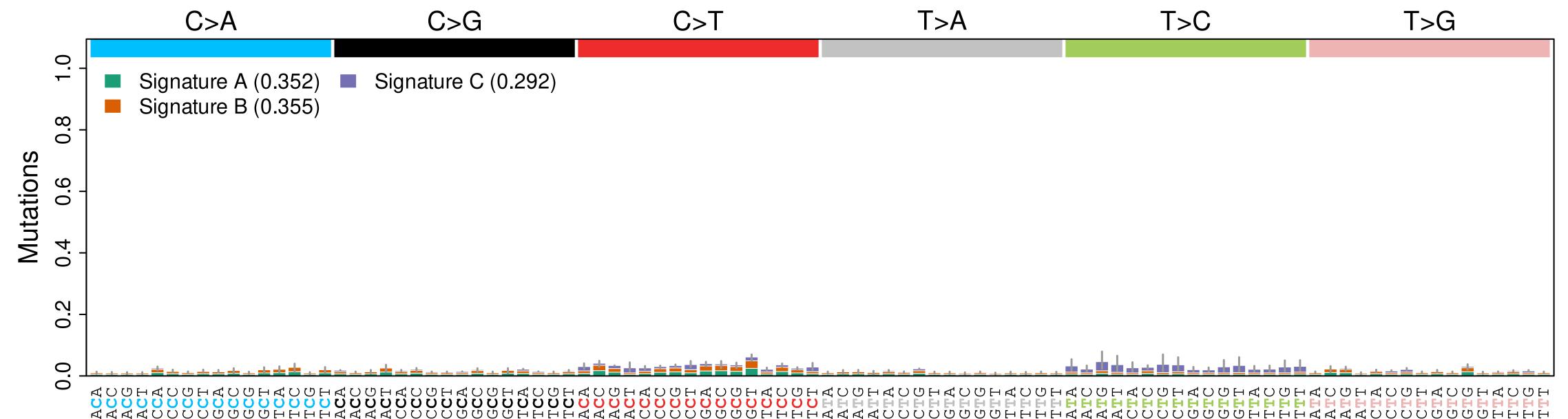


## **Reconstructed spectrum (cosine similarity = 0.226)**

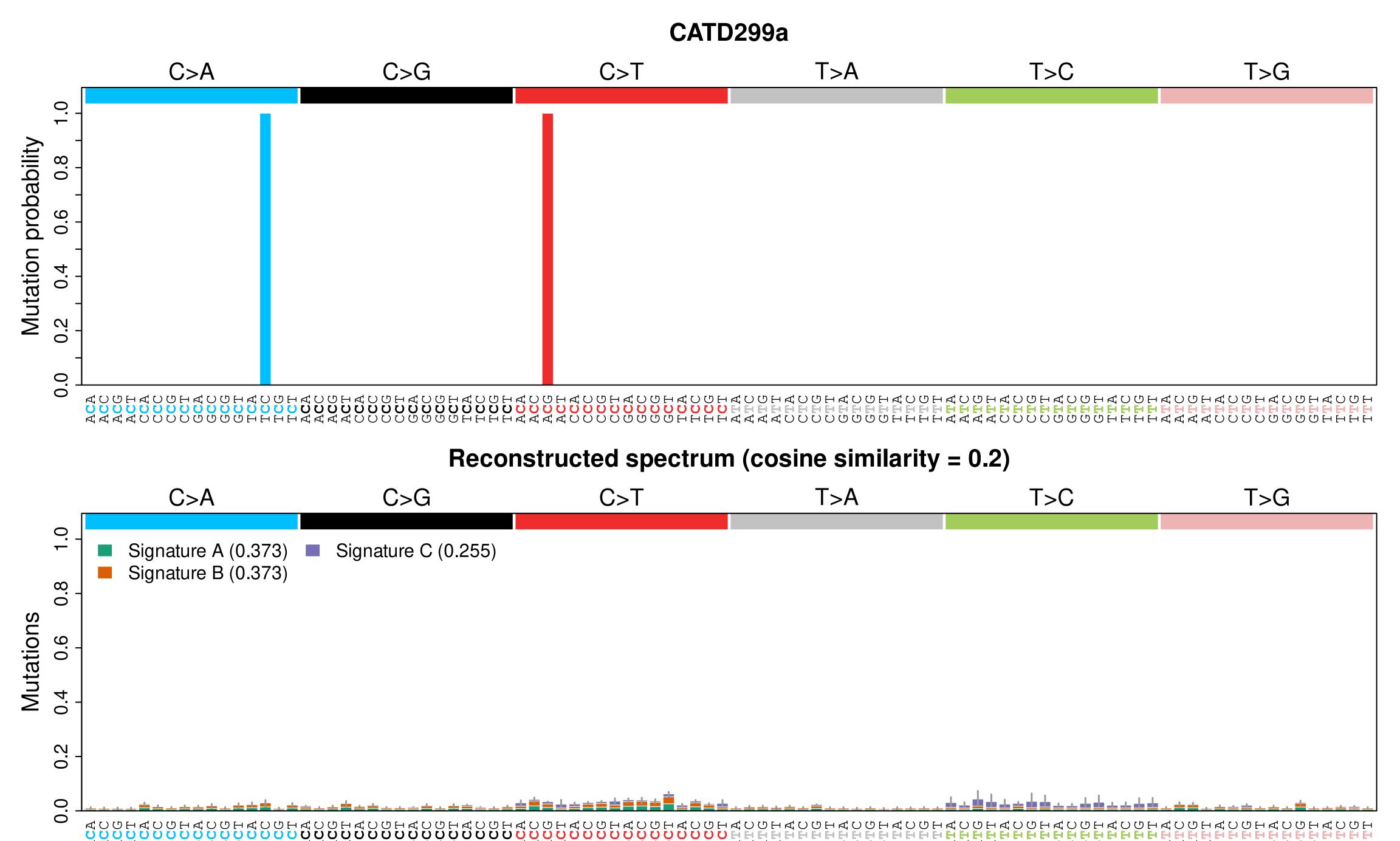




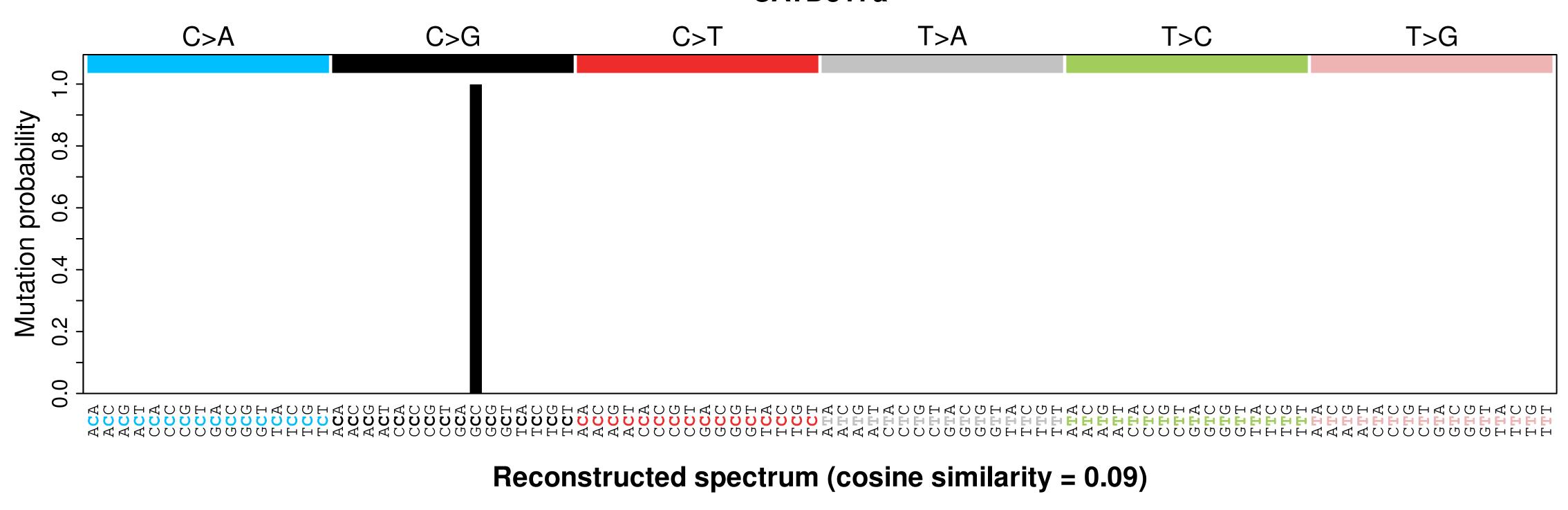


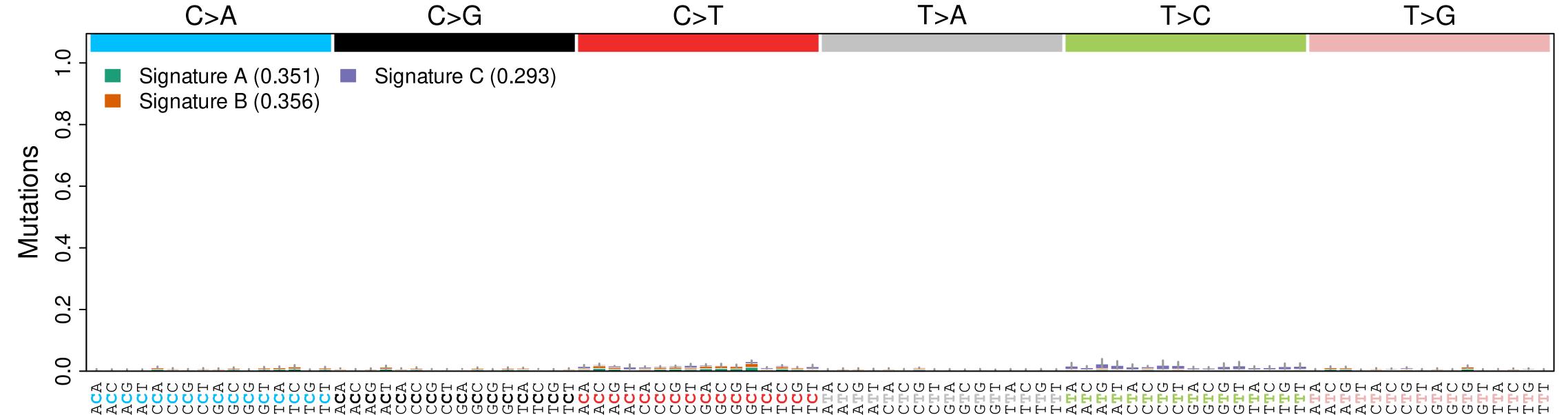


## CATD304a (2 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.127)** C>G T>C T>G C>A T>A C>T 2.0 Signature A (0.303) Signature C (0.395) Signature B (0.302) 5 Mutations 5 0 0 0

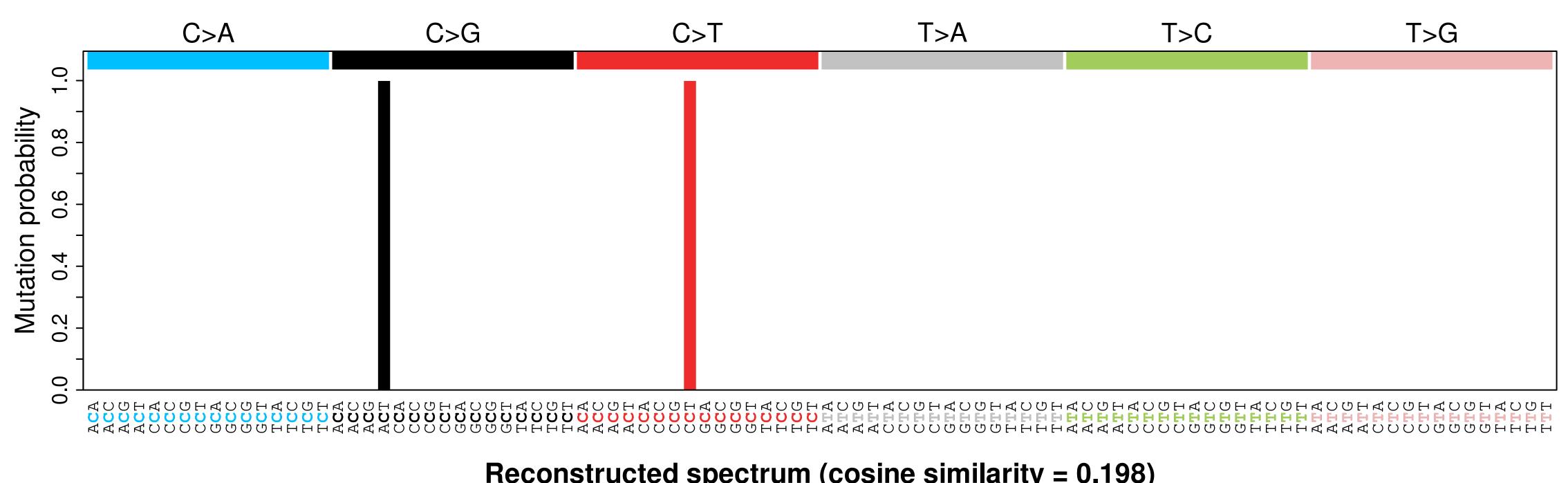




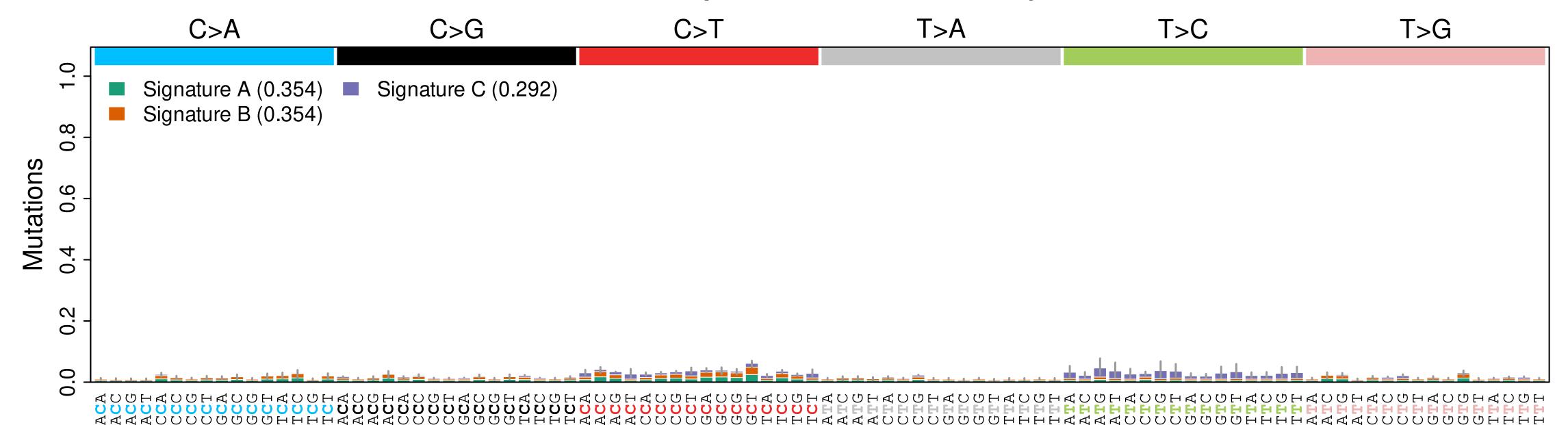












### CATD303a (2 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.26)** C>A C>G T>A T>C T>G C>T 2.0 Signature C (0.501) Signature A (0.25) Signature B (0.249) 5 Mutations 5 0 0 0