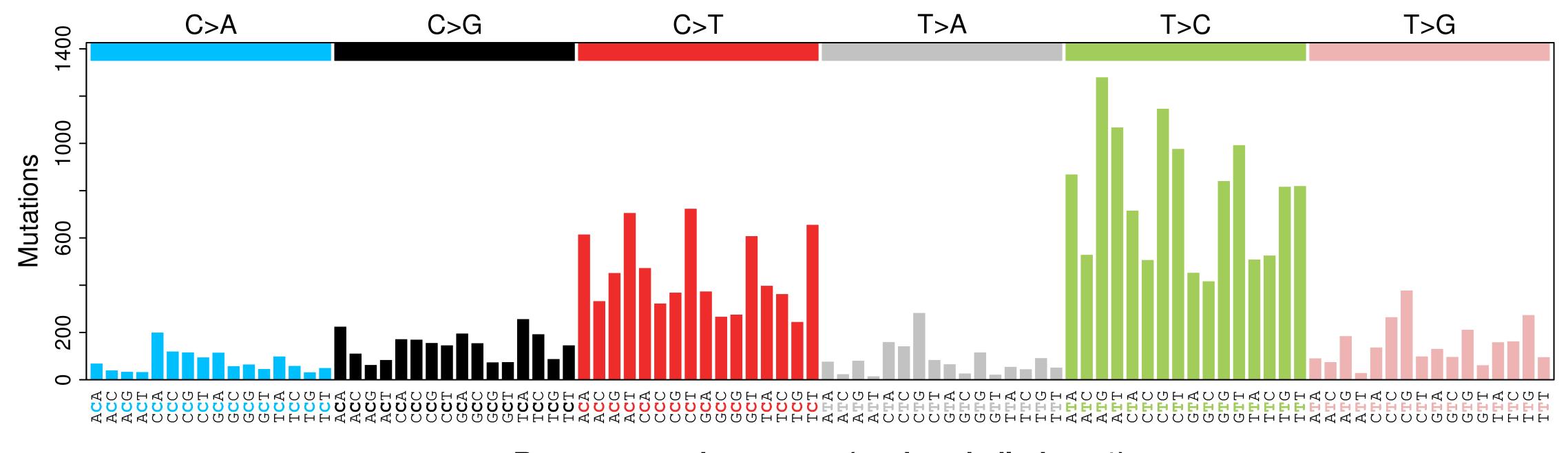
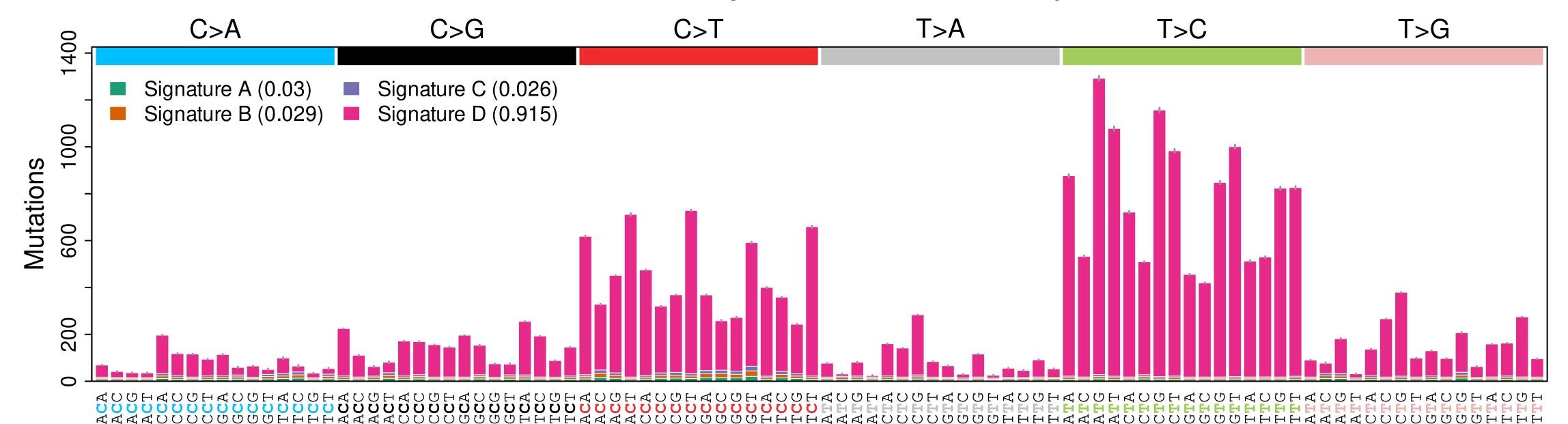
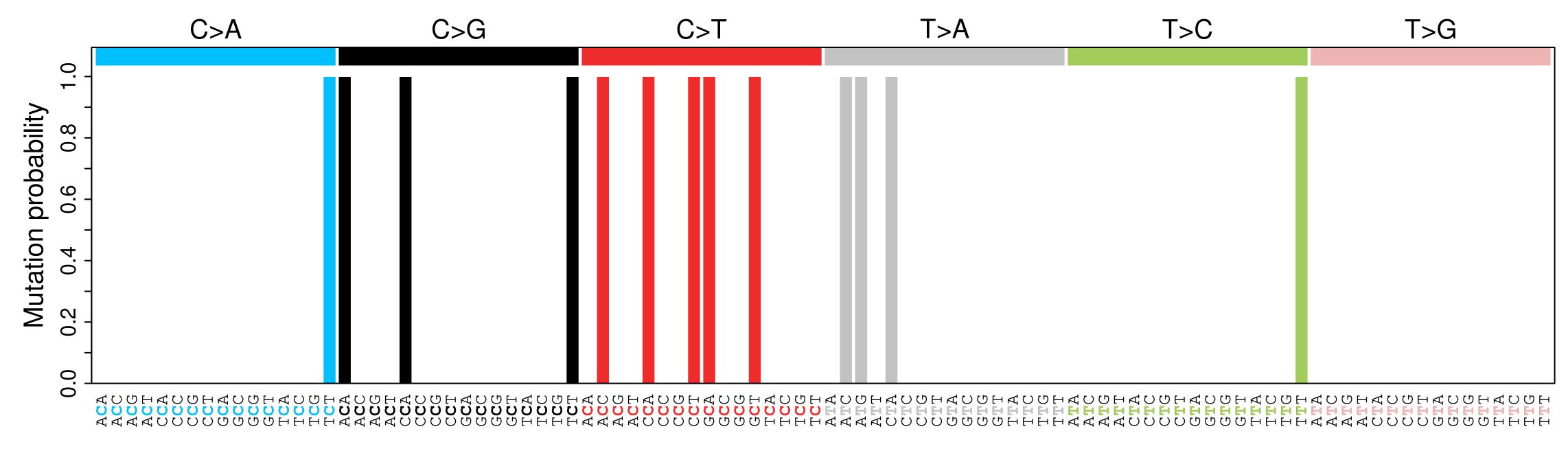
#### **CATD309a (27,083 mutations)**

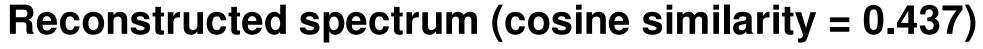


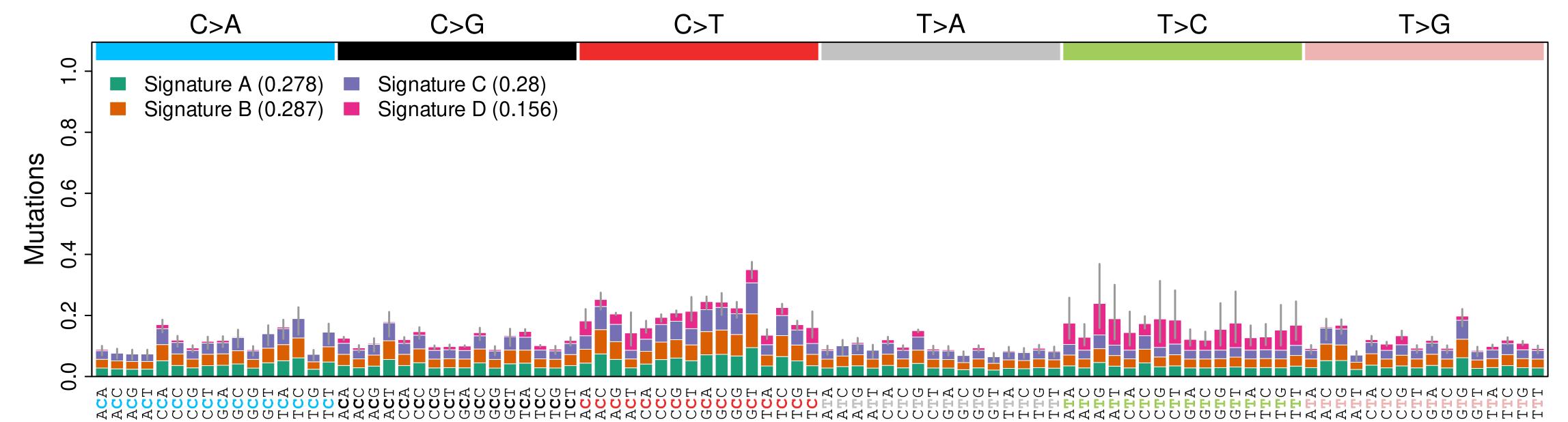
#### Reconstructed spectrum (cosine similarity = 1)



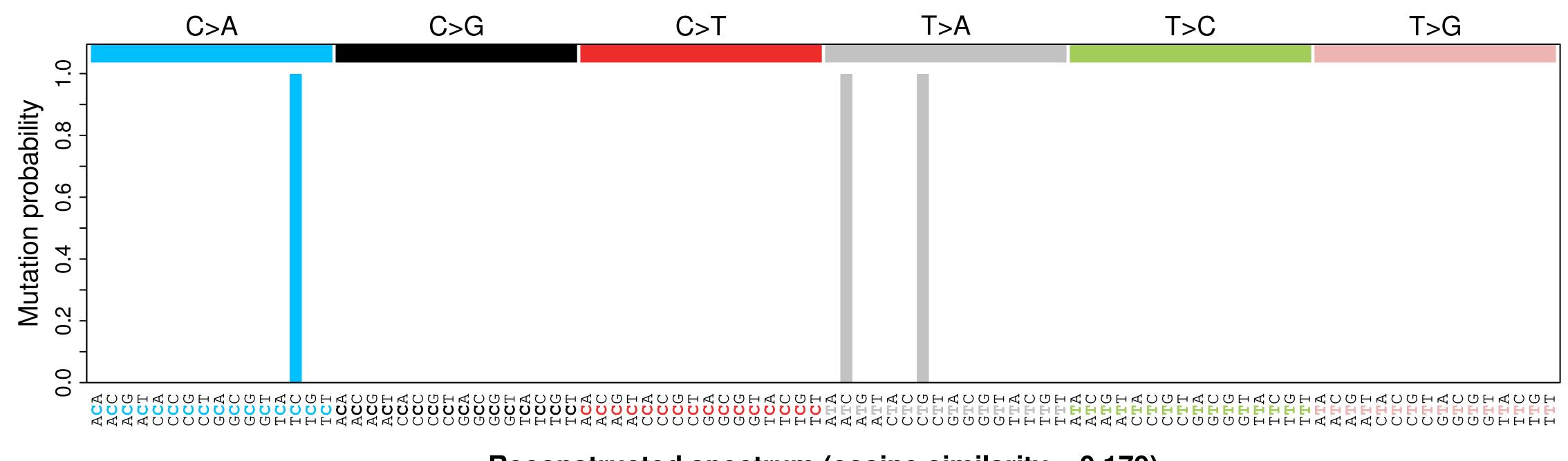
#### CATD319a

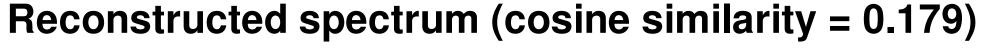


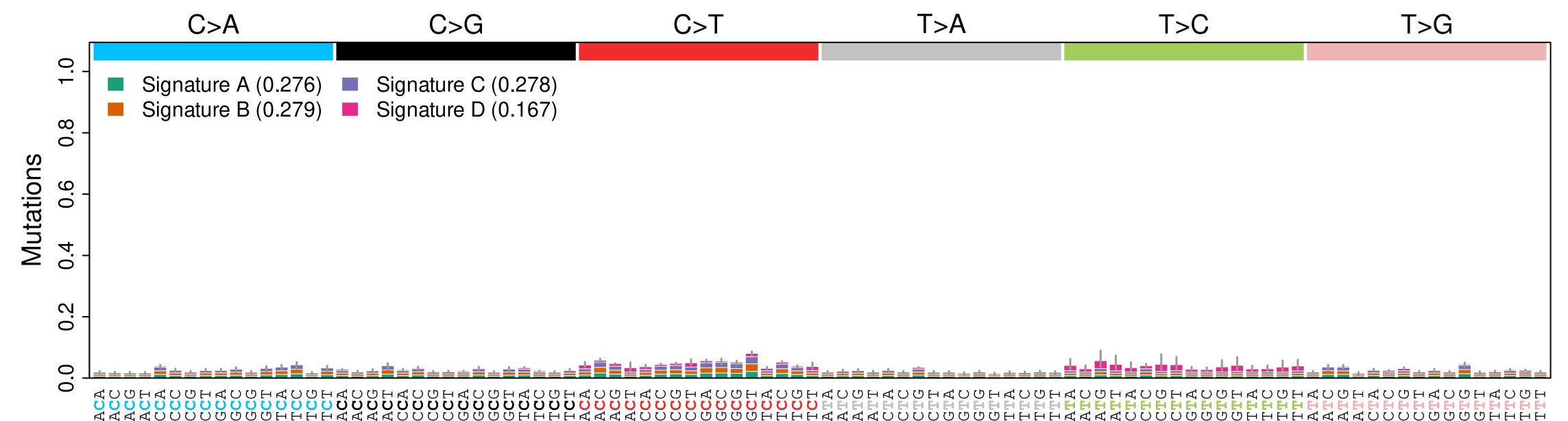




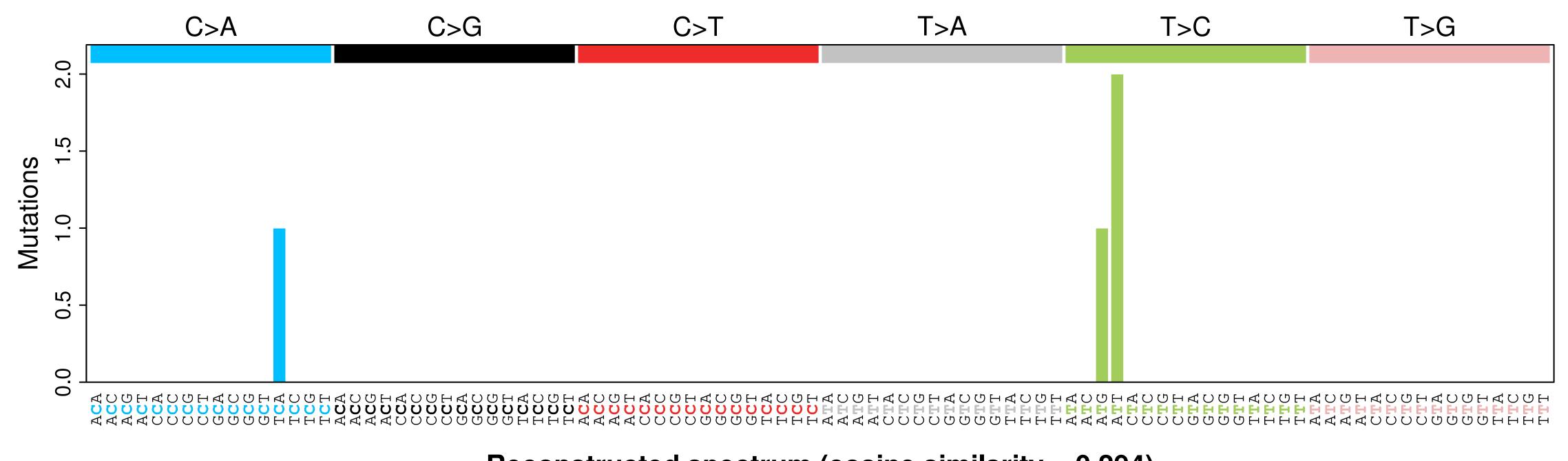




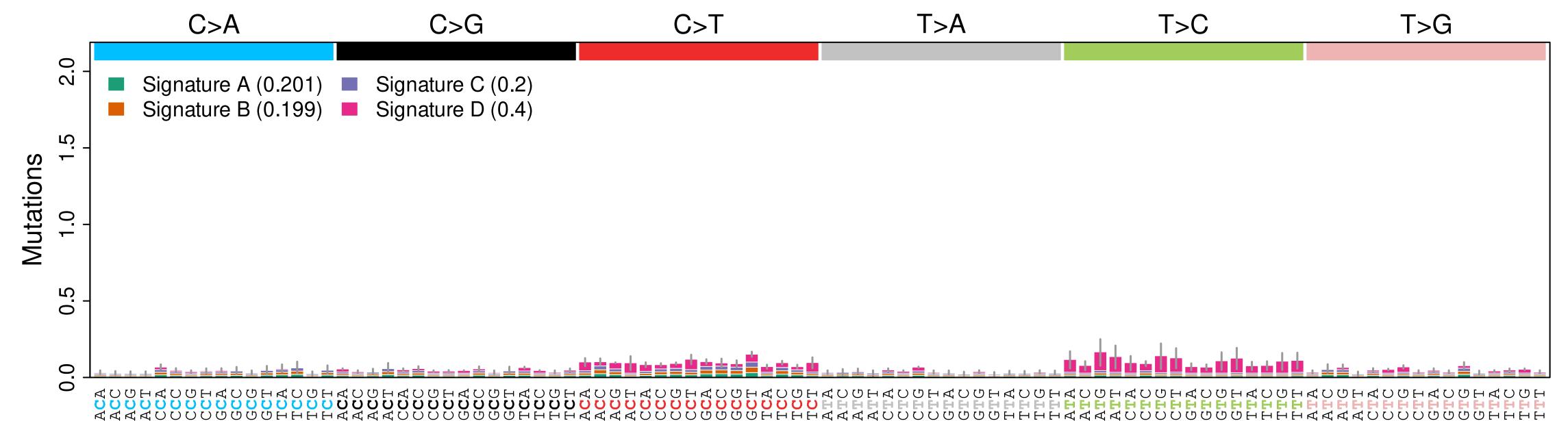




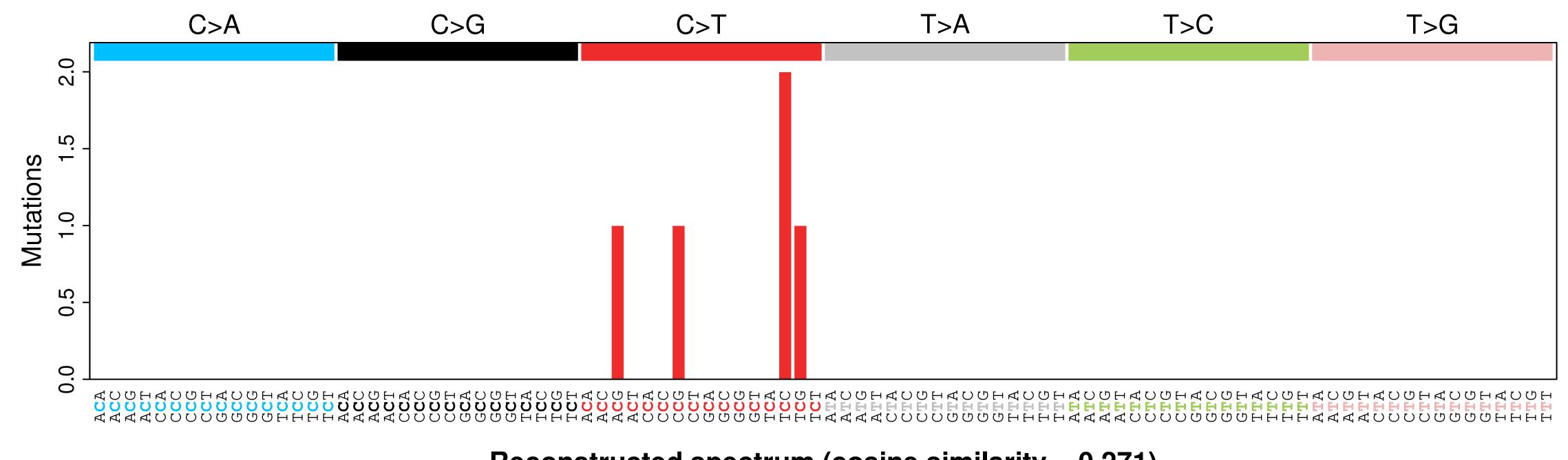
# CATD297a (4 mutations)



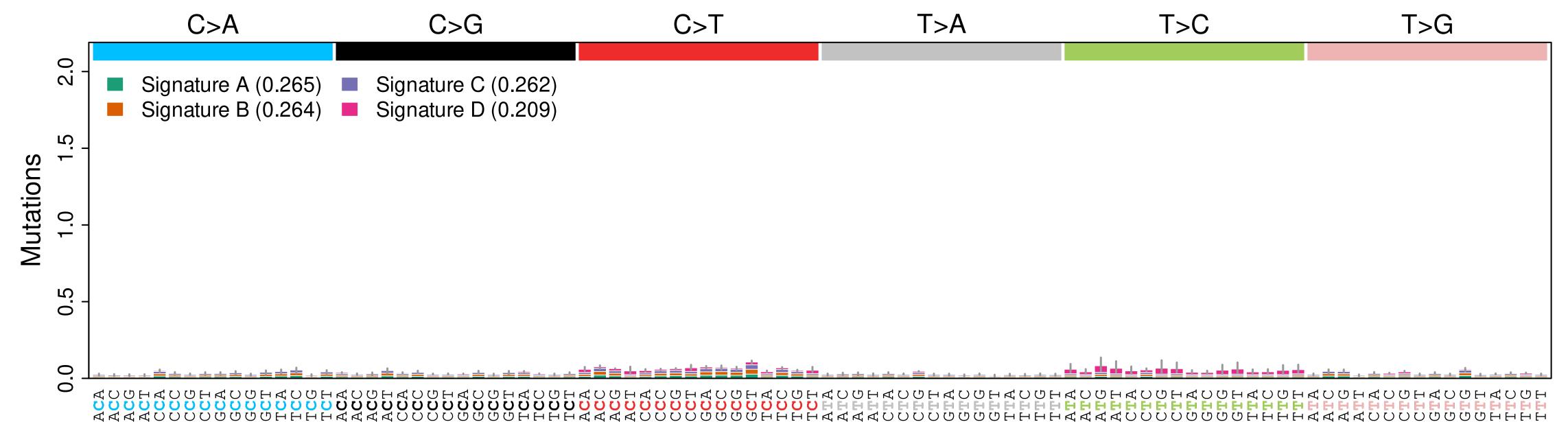
# Reconstructed spectrum (cosine similarity = 0.294)



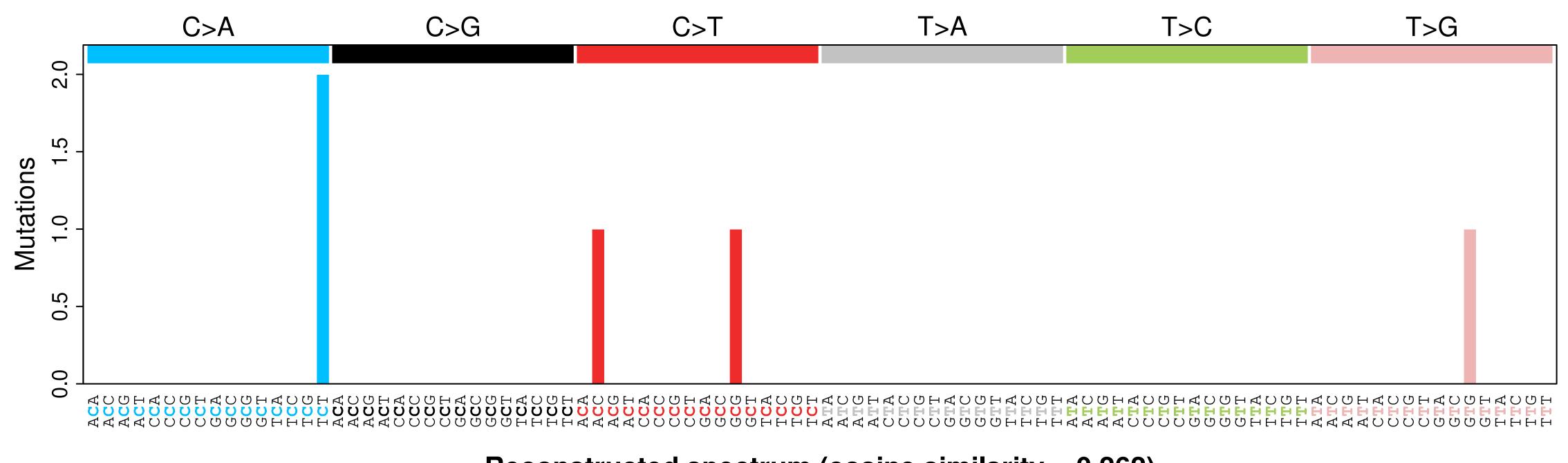
# CATD312a (5 mutations)



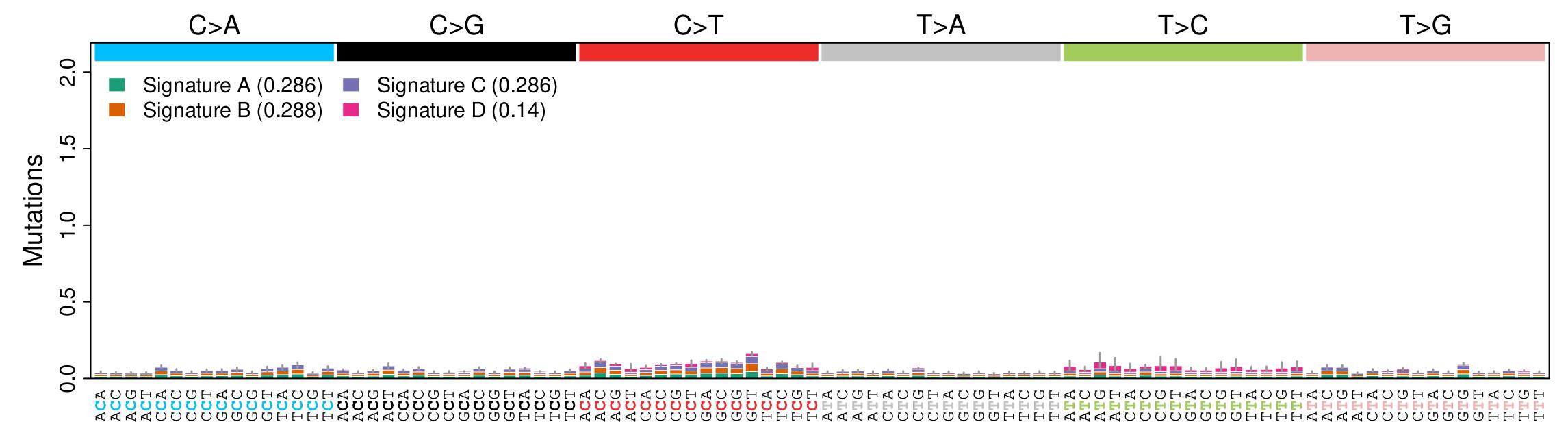
# Reconstructed spectrum (cosine similarity = 0.271)



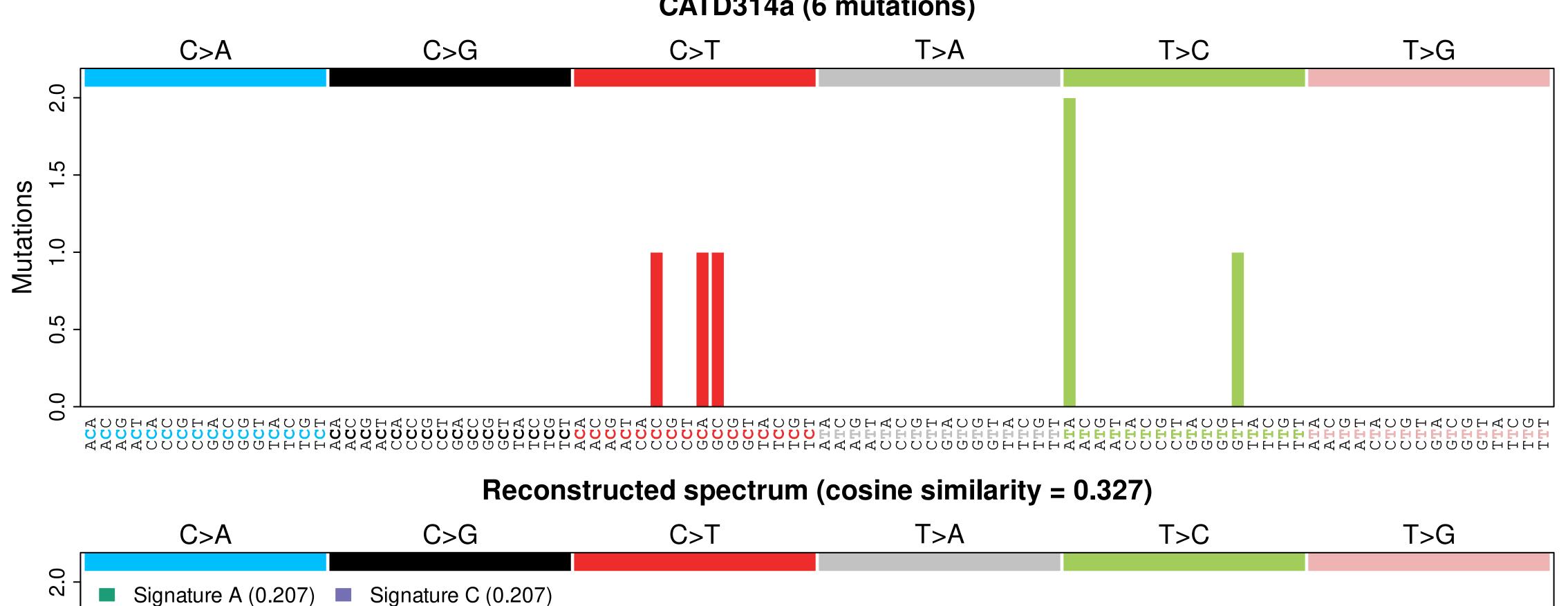
#### CATD323a (5 mutations)

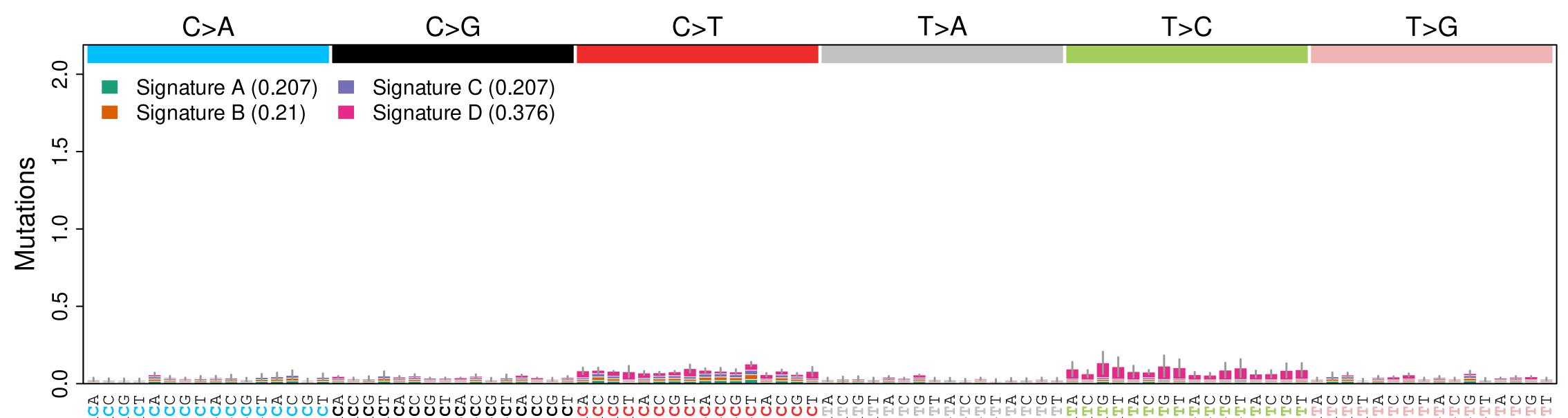


# Reconstructed spectrum (cosine similarity = 0.262)

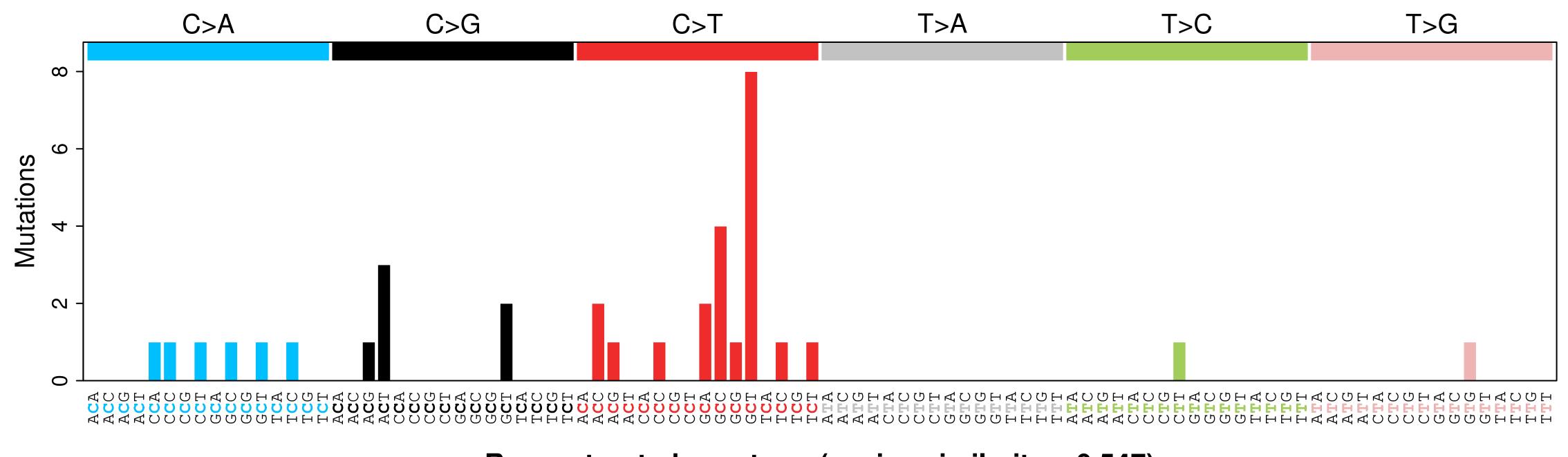


#### CATD314a (6 mutations)

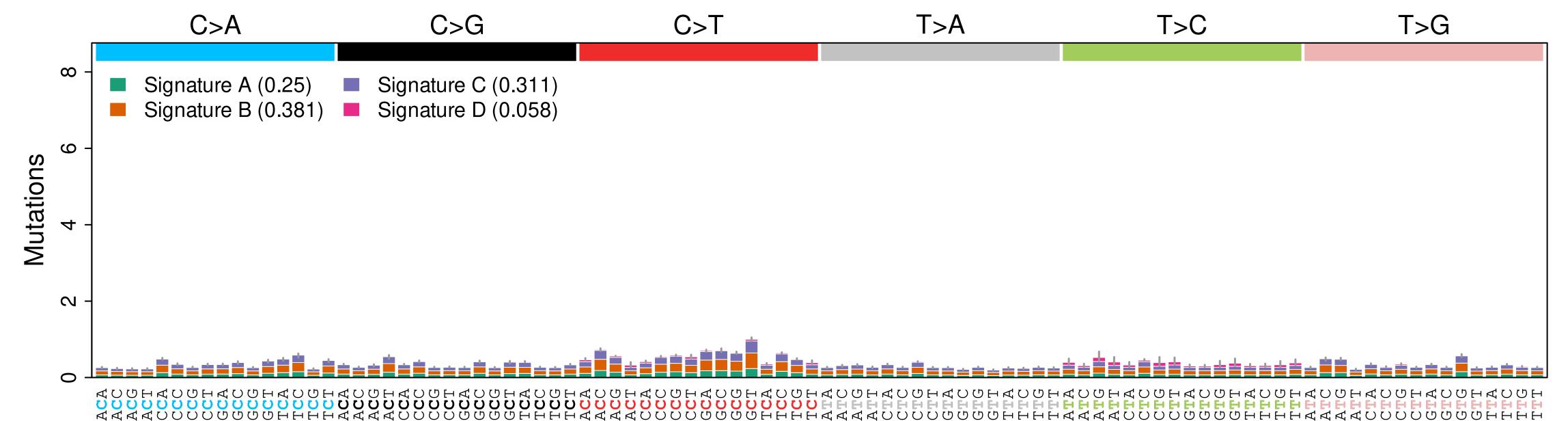


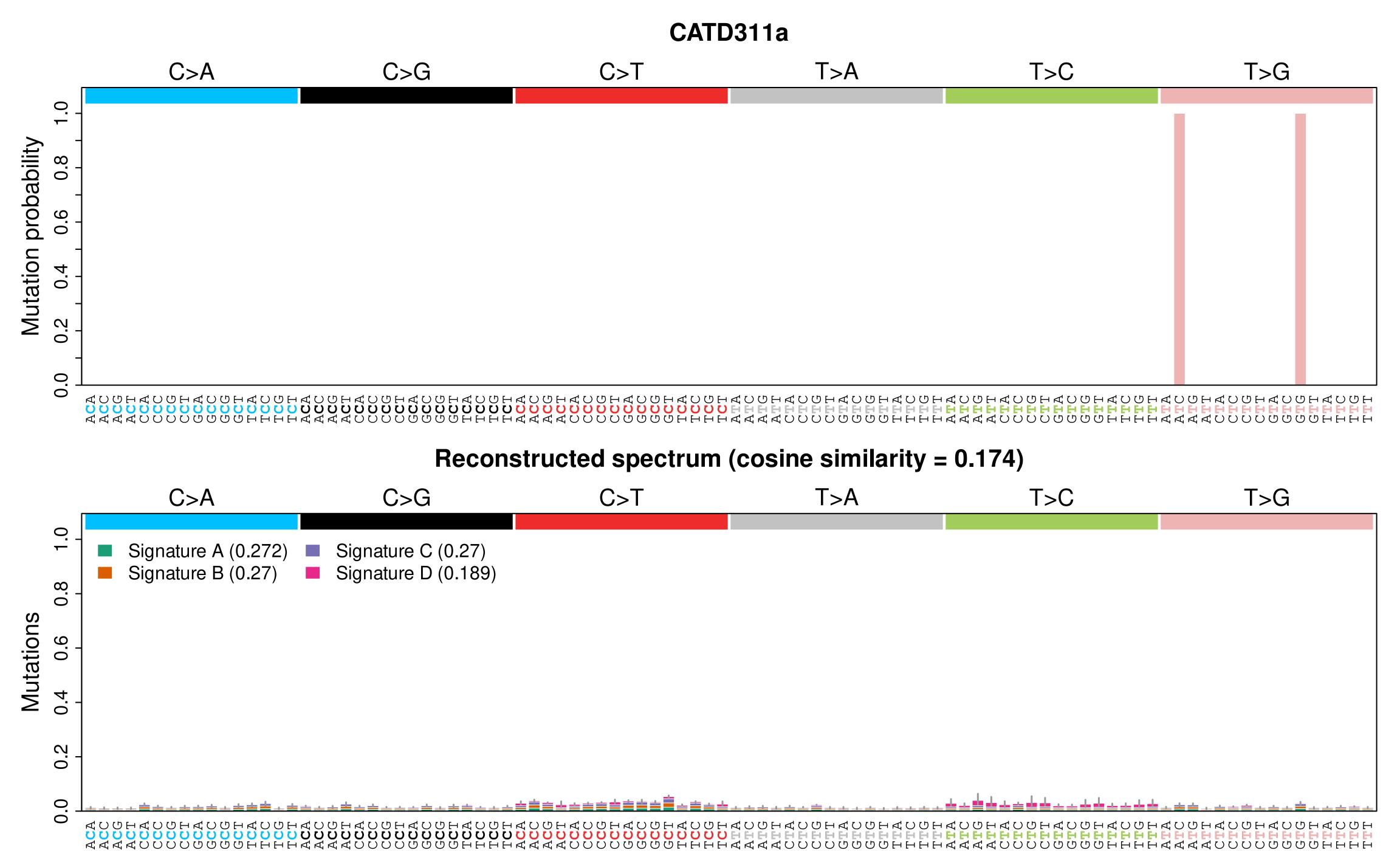


#### CATD329a (35 mutations)

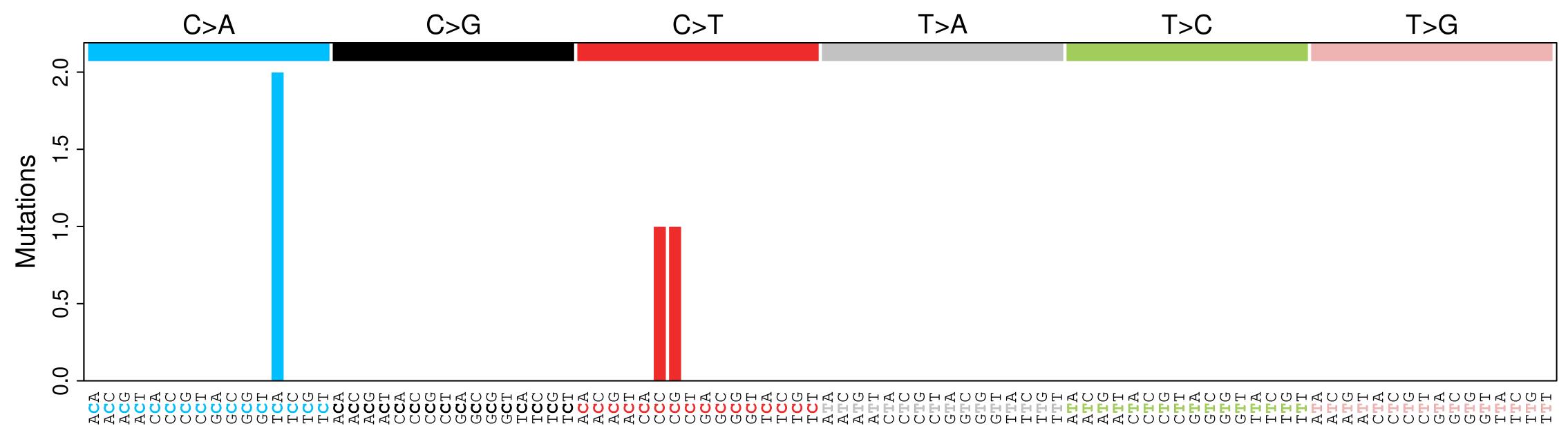


# Reconstructed spectrum (cosine similarity = 0.547)

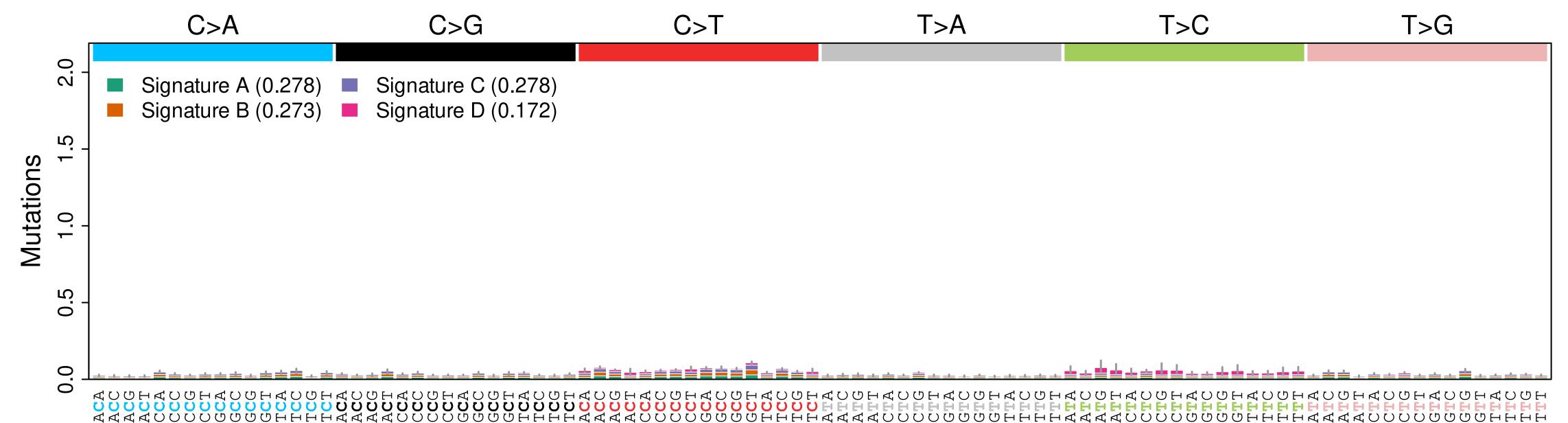




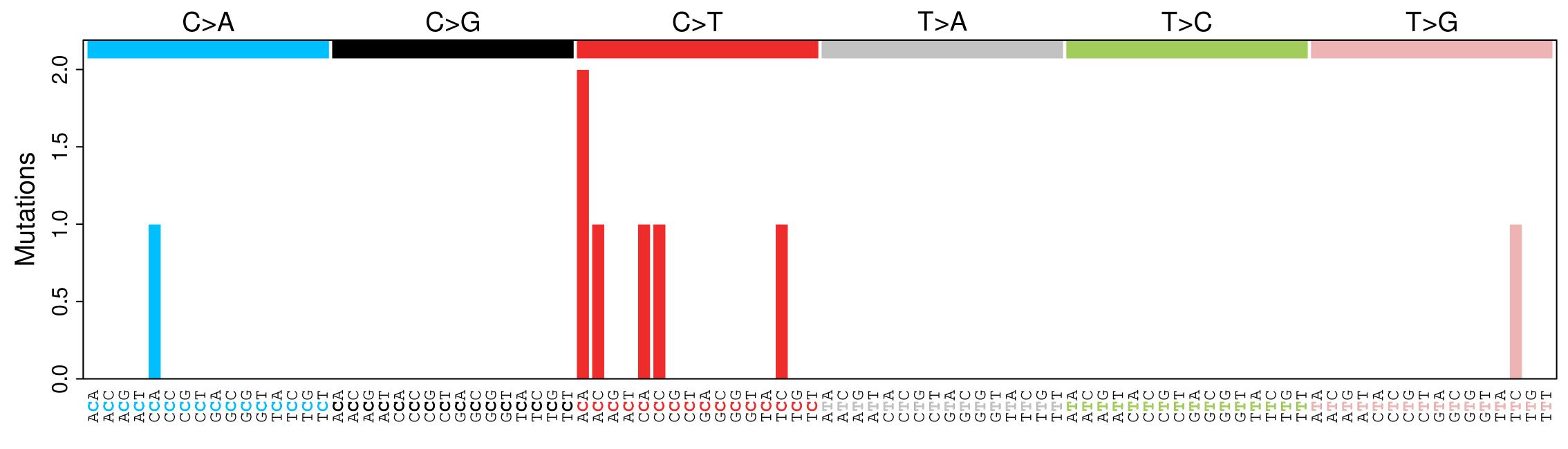
# CATD306a (4 mutations)



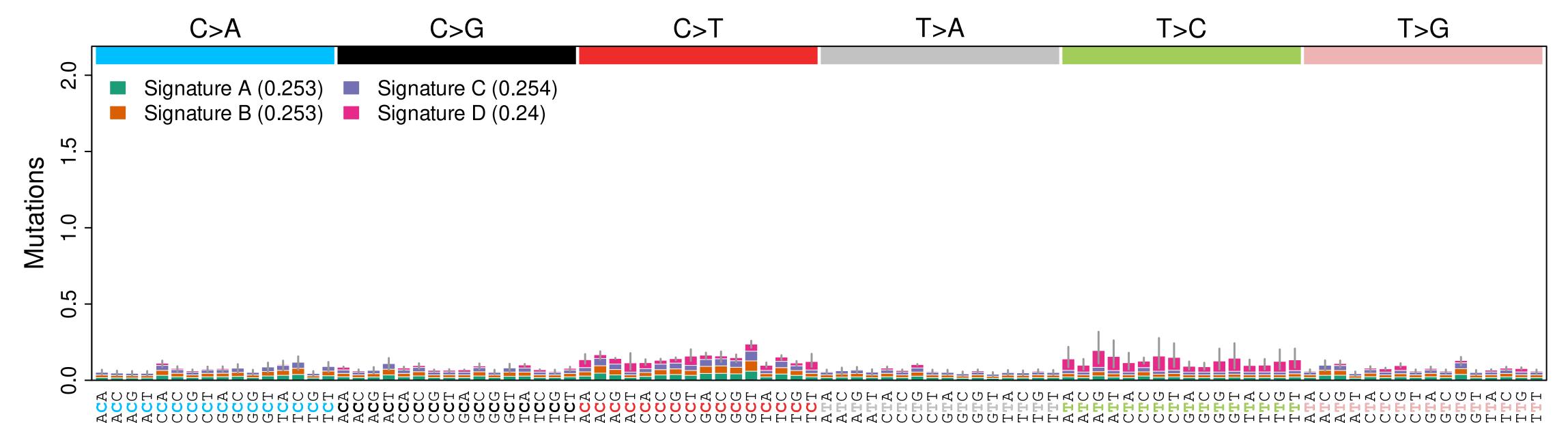
## Reconstructed spectrum (cosine similarity = 0.207)



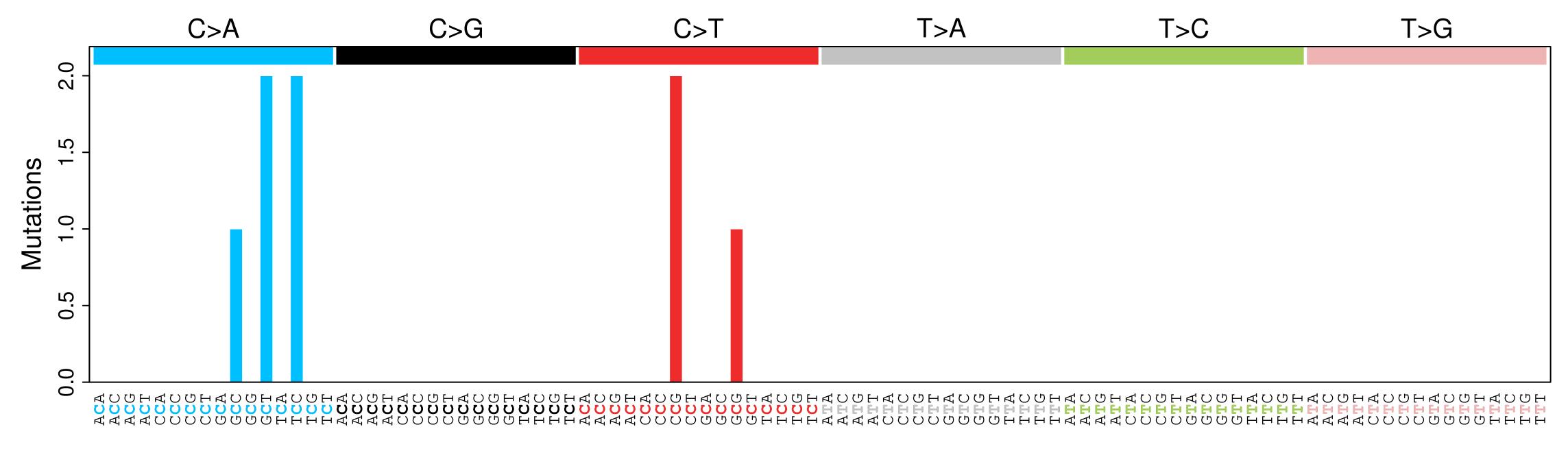
#### CATD320a (8 mutations)



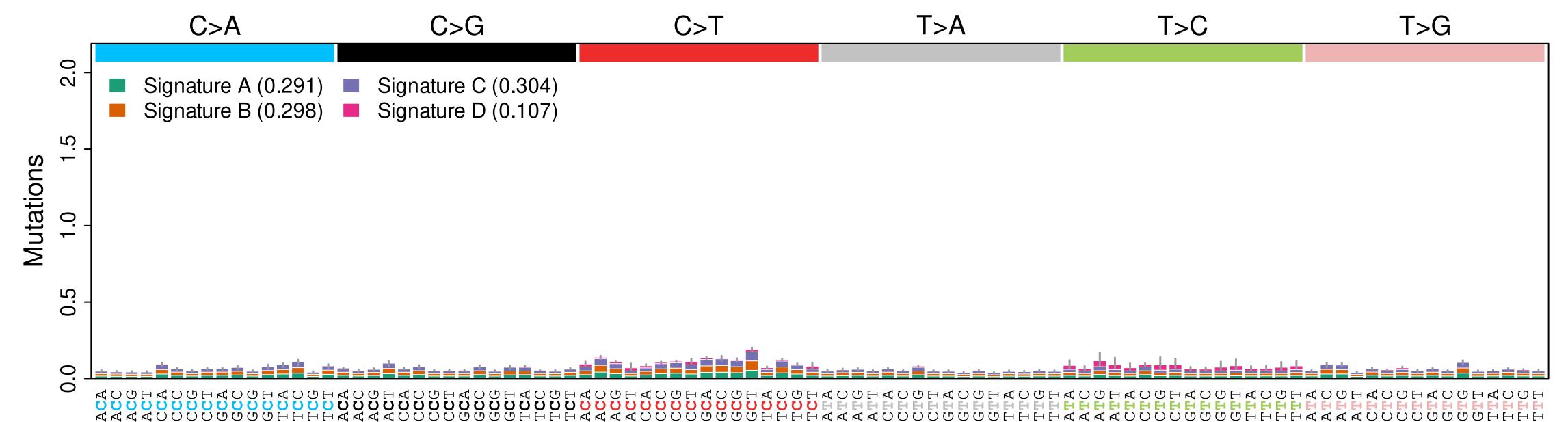
### **Reconstructed spectrum (cosine similarity = 0.327)**



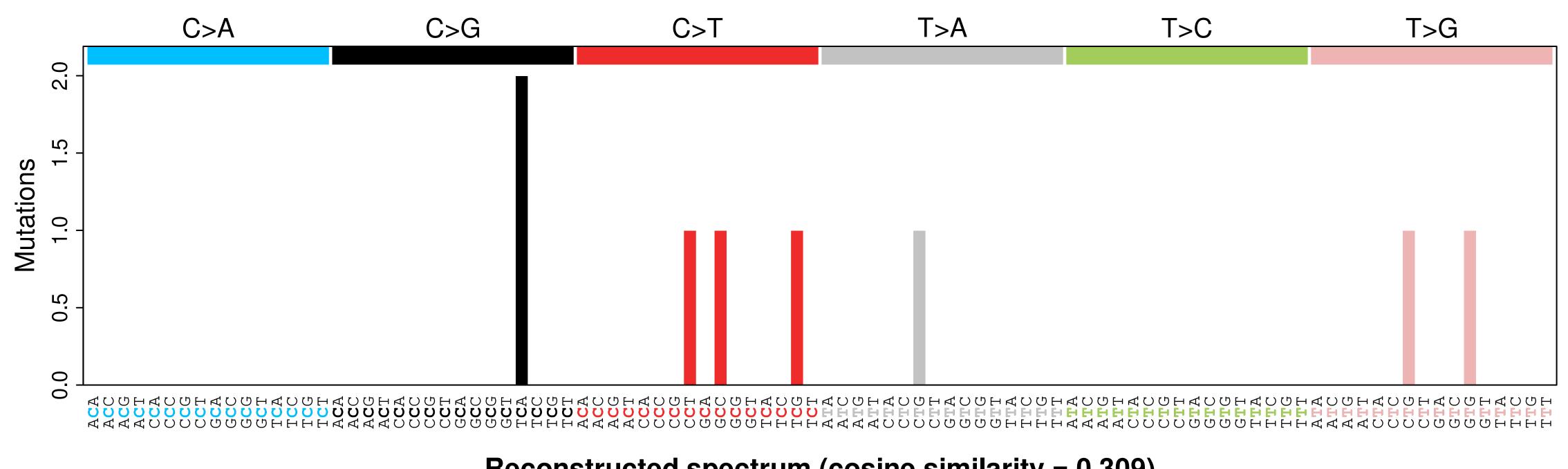
# CATD300a (8 mutations)



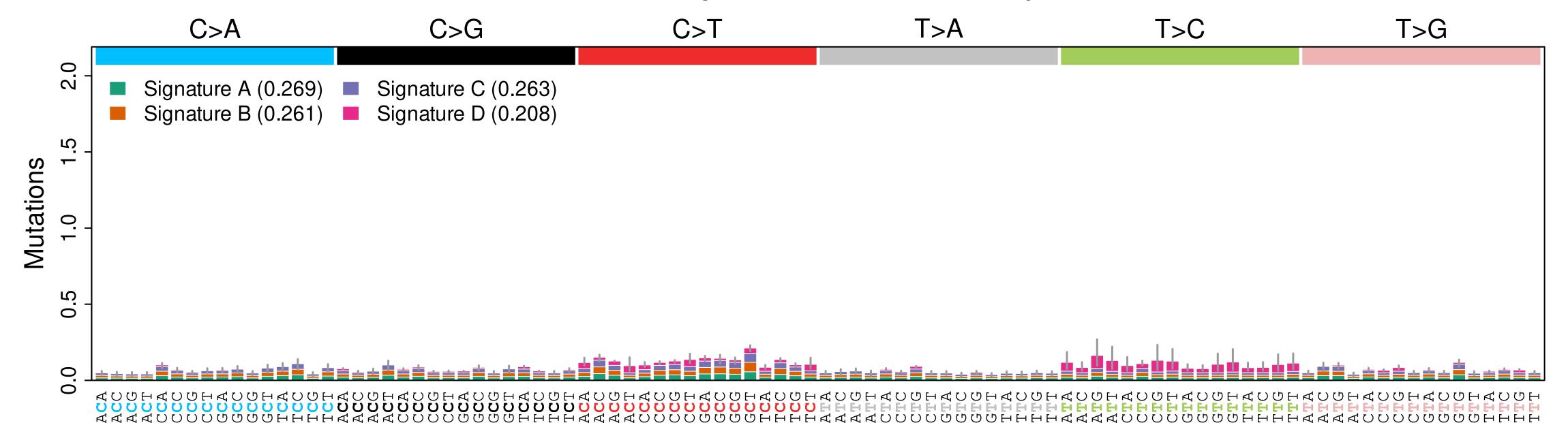
#### Reconstructed spectrum (cosine similarity = 0.282)



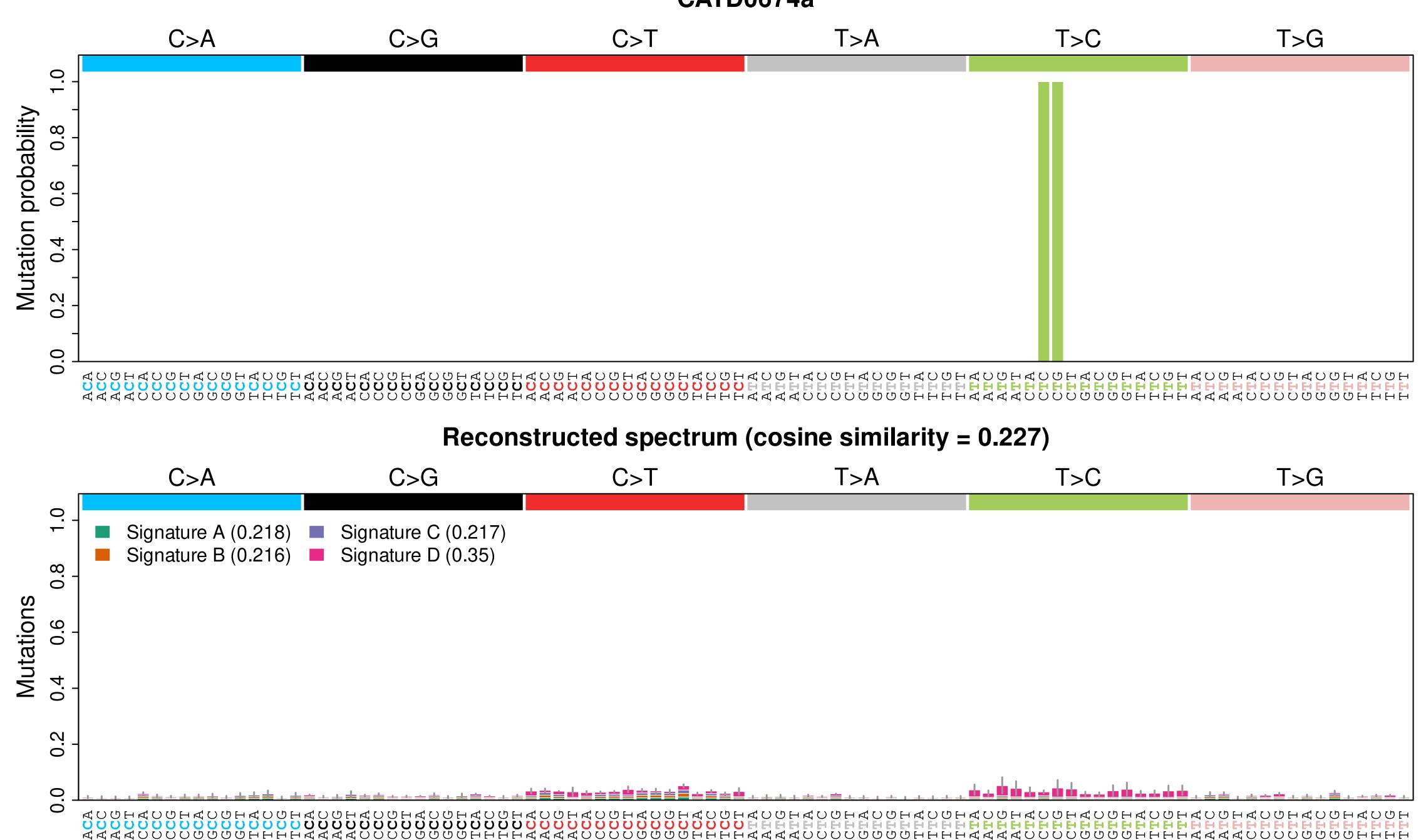
#### CATD328a (8 mutations)



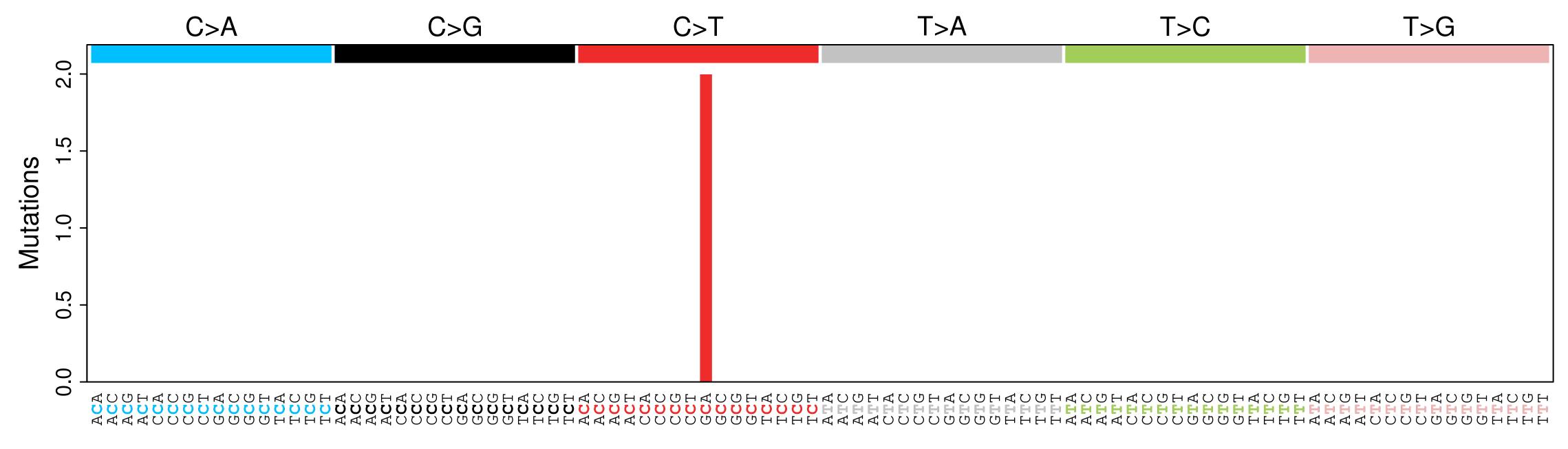
#### **Reconstructed spectrum (cosine similarity = 0.309)**



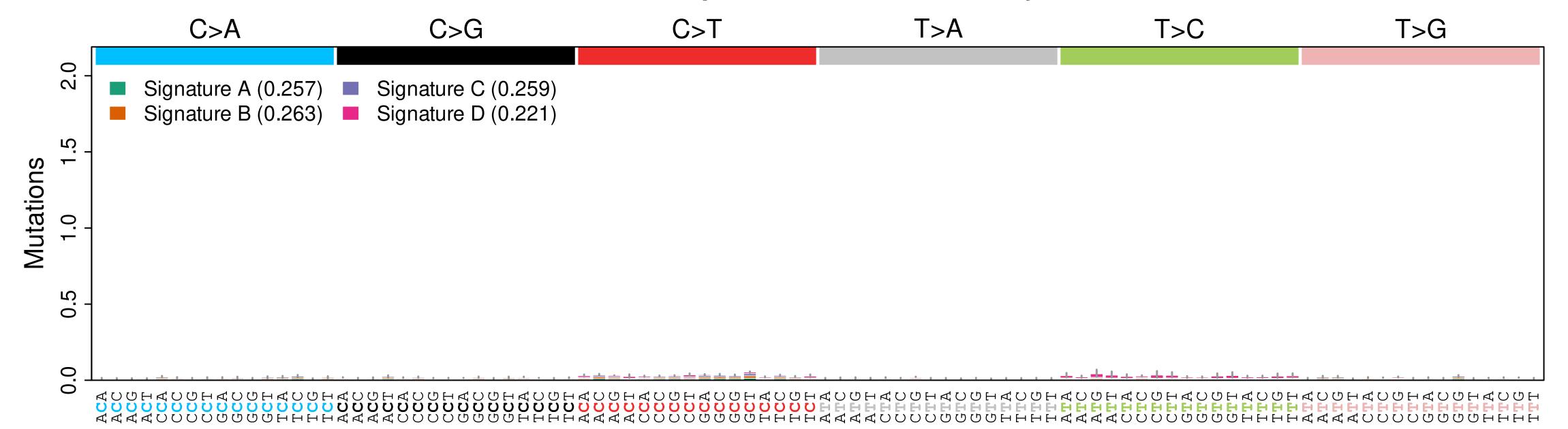




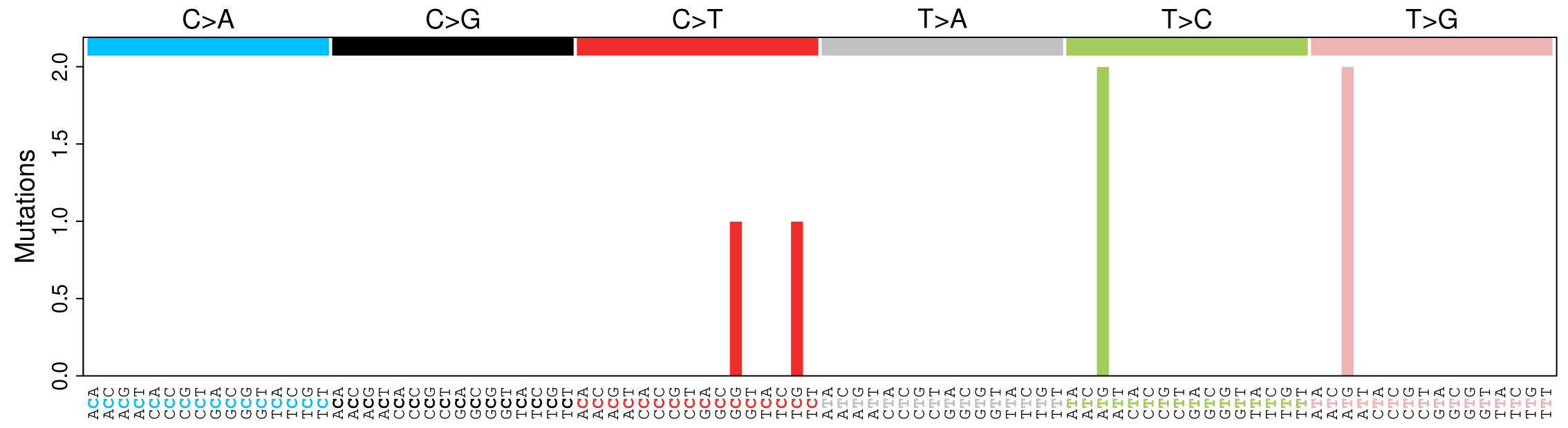
#### CATD318a (2 mutations)



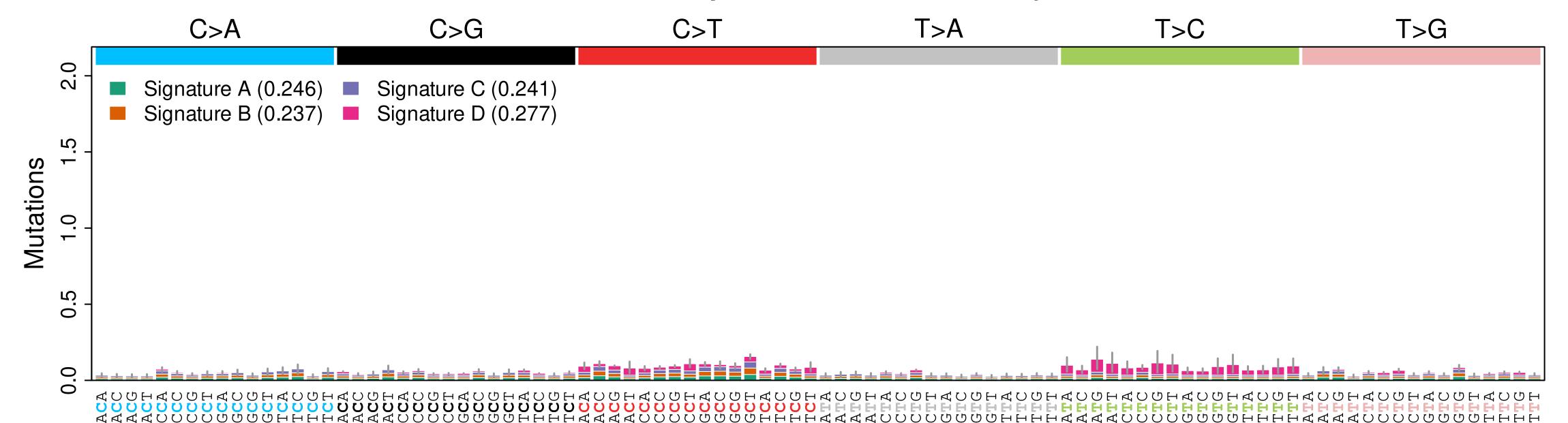
#### **Reconstructed spectrum (cosine similarity = 0.168)**



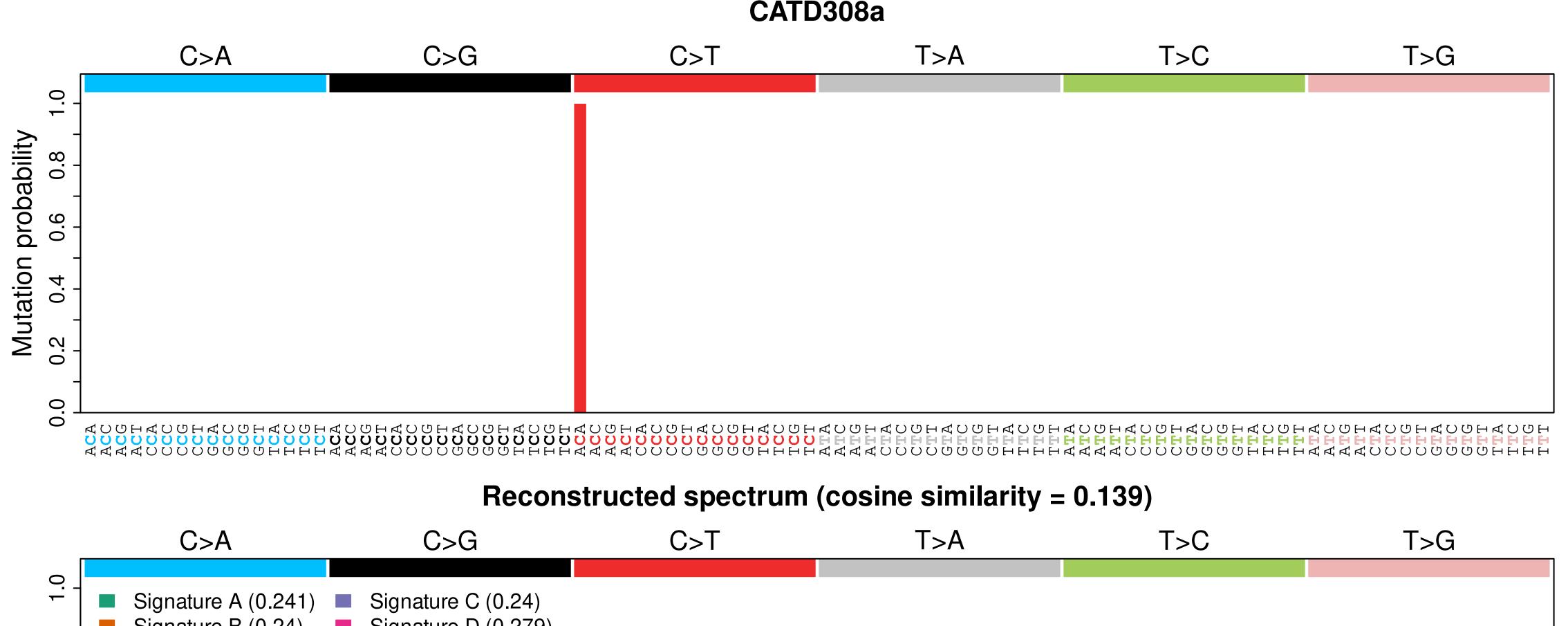
#### CATD301a (6 mutations) C>A C>G C>T T>A

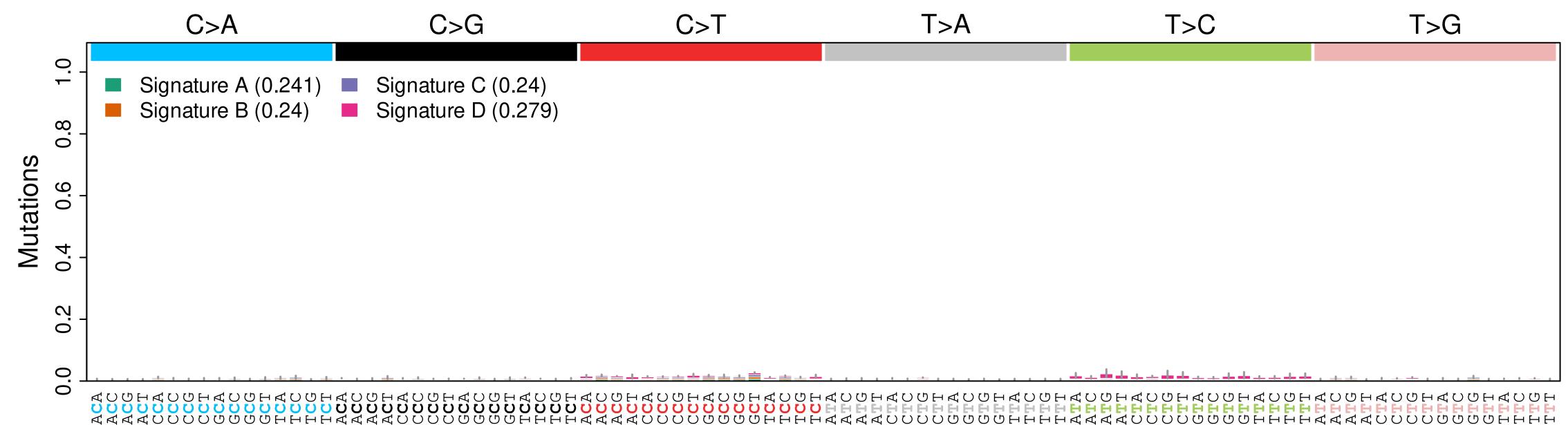


#### Reconstructed spectrum (cosine similarity = 0.28)

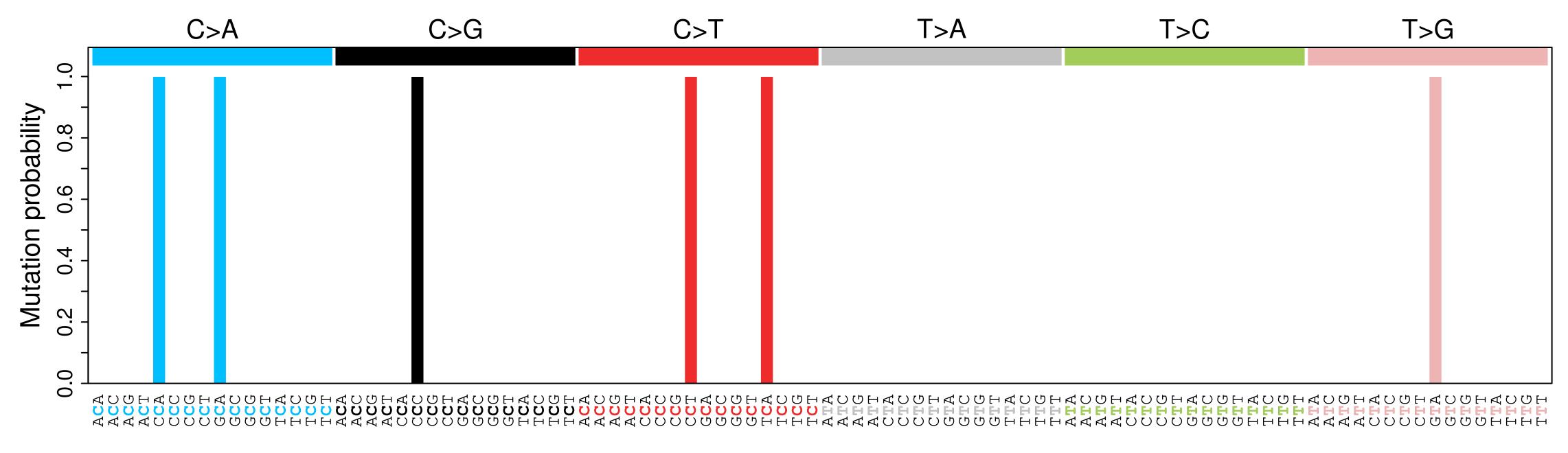


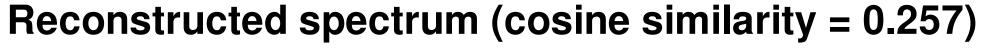


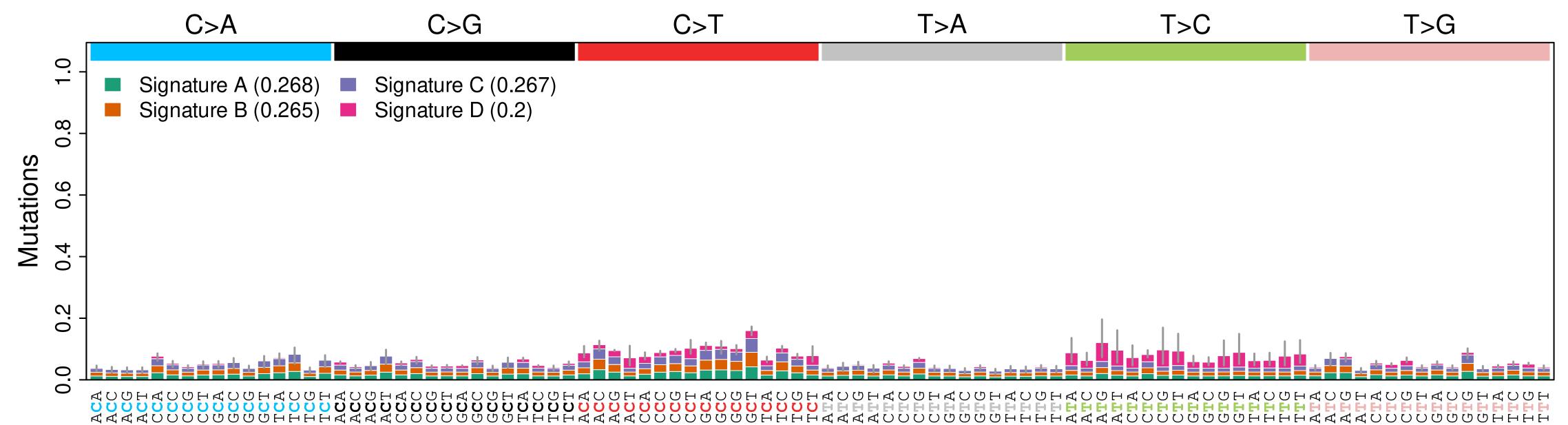




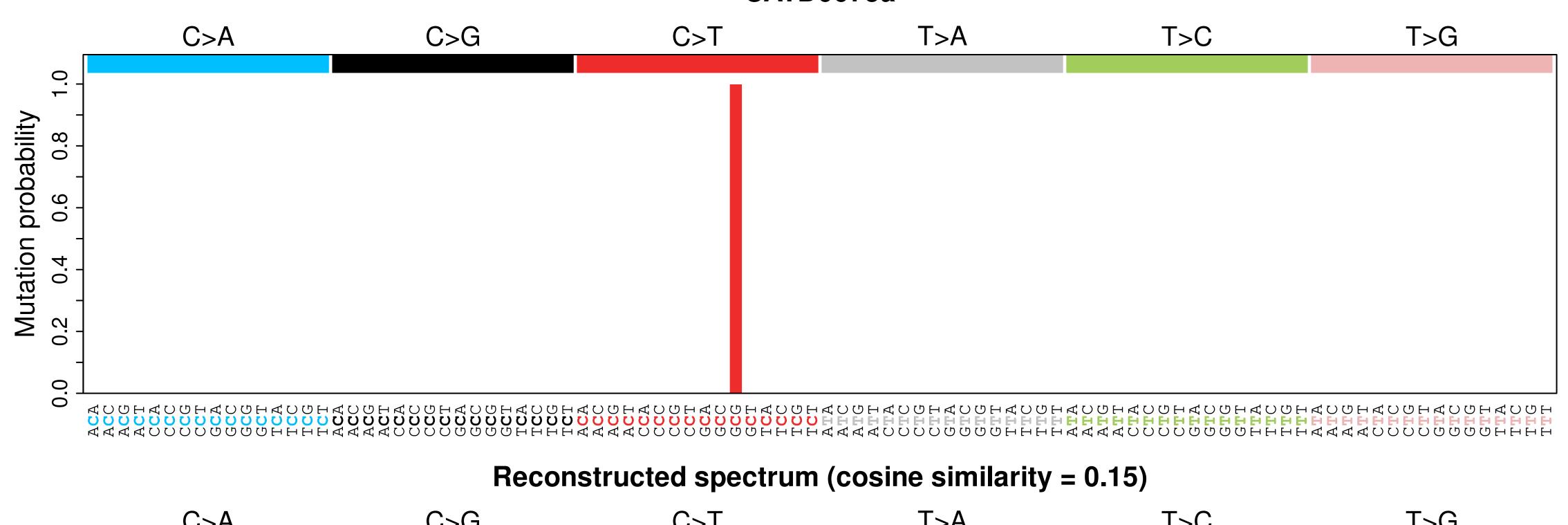
#### CATD296a

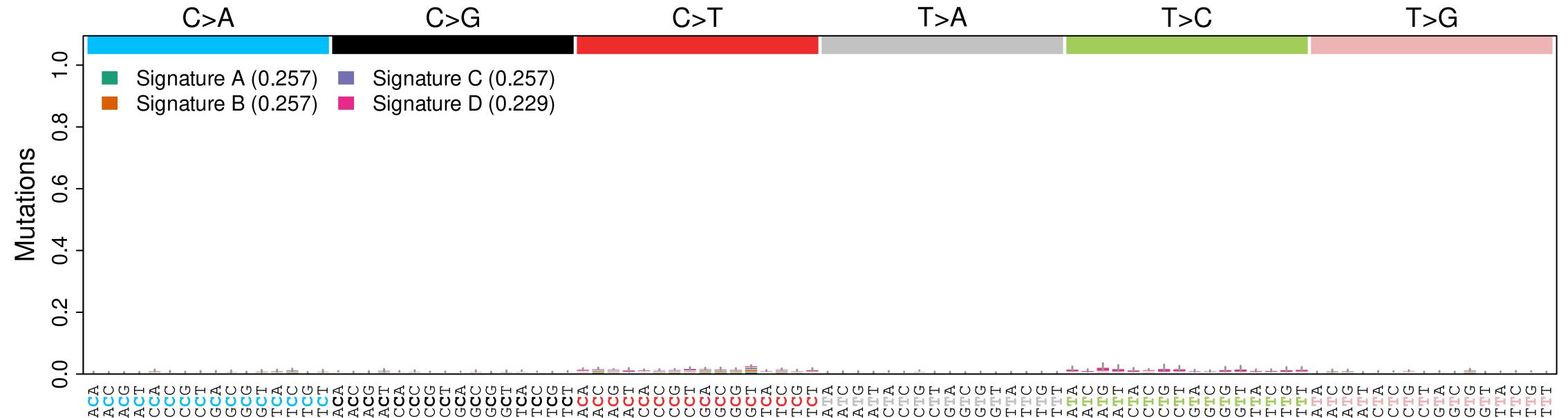




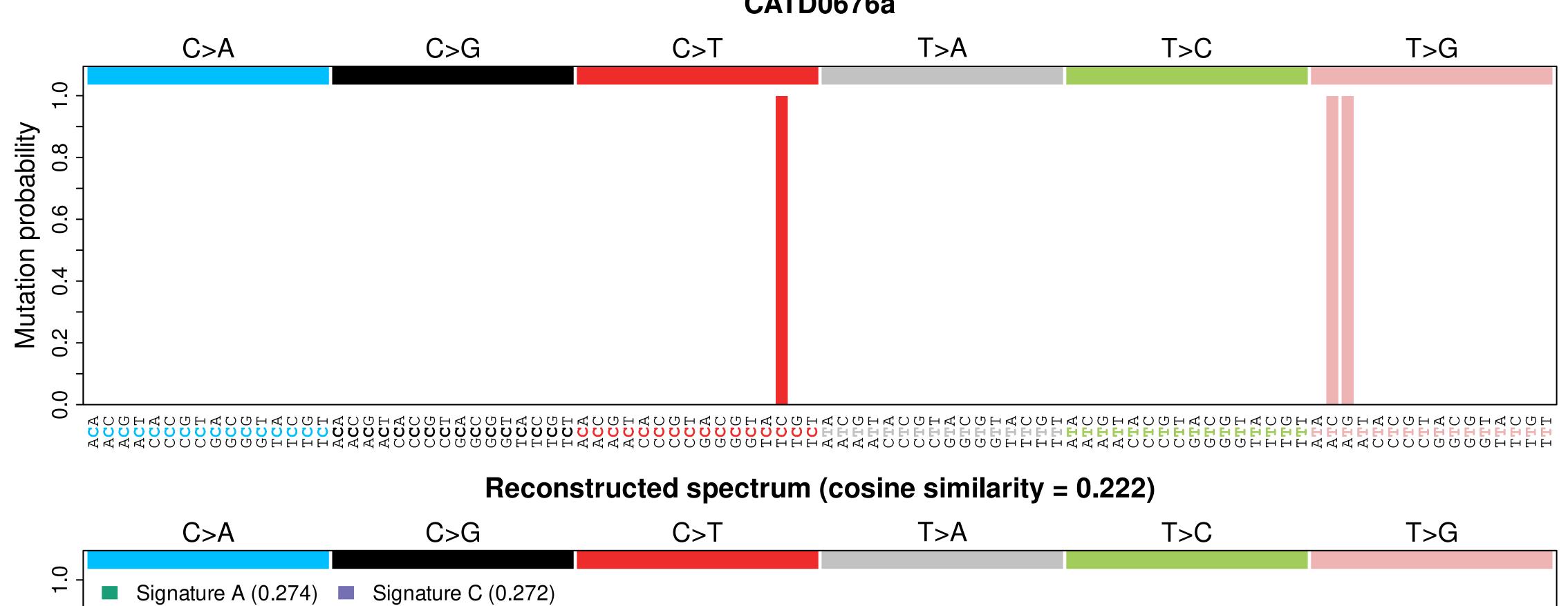


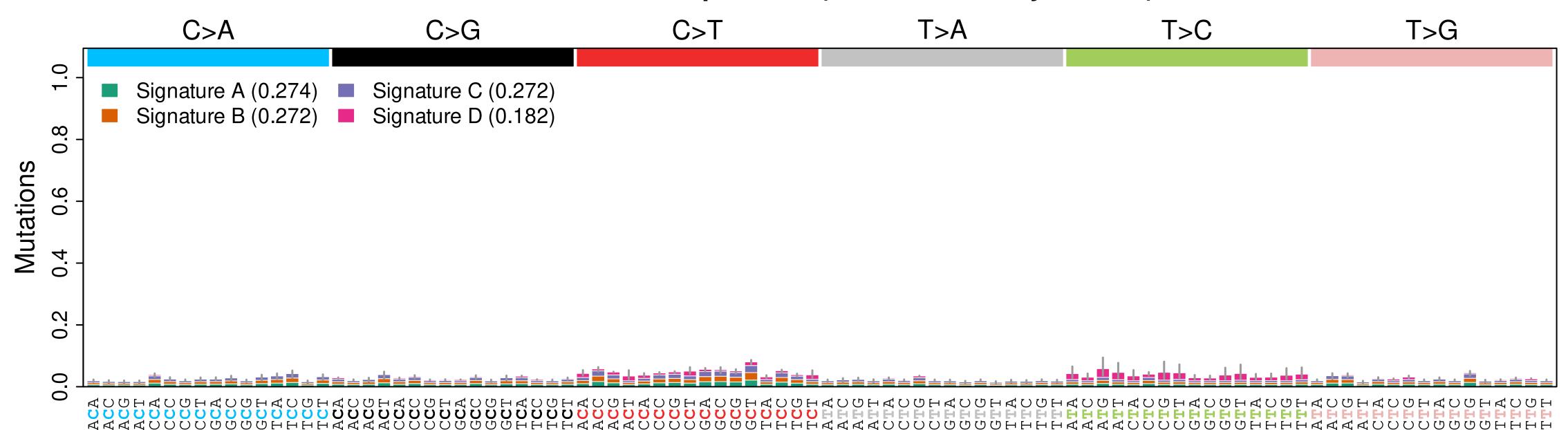




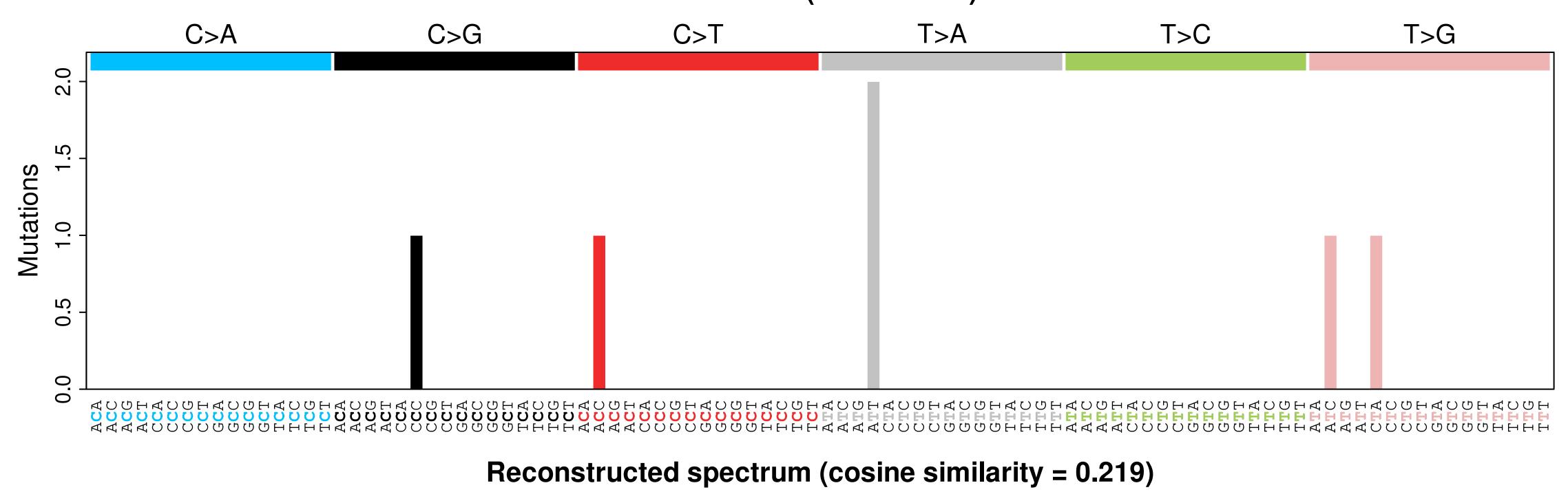


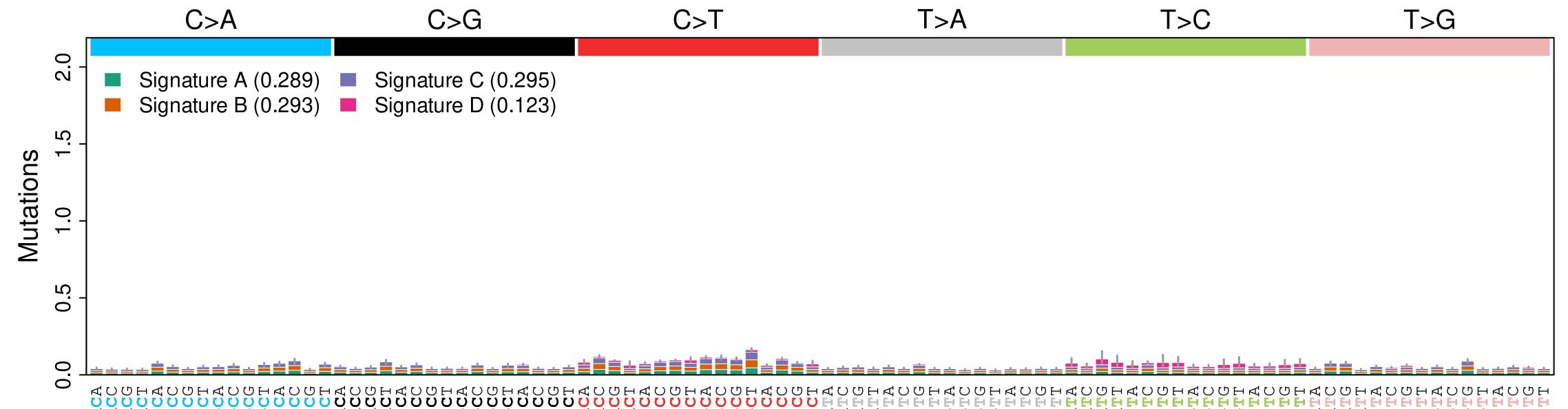




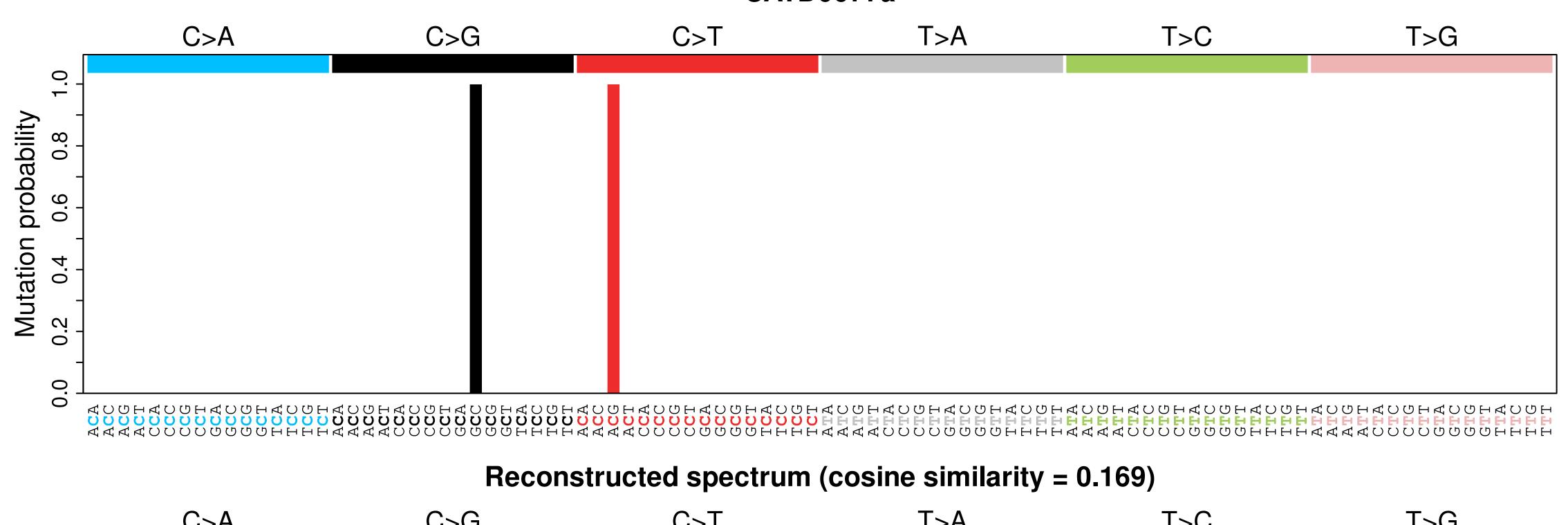


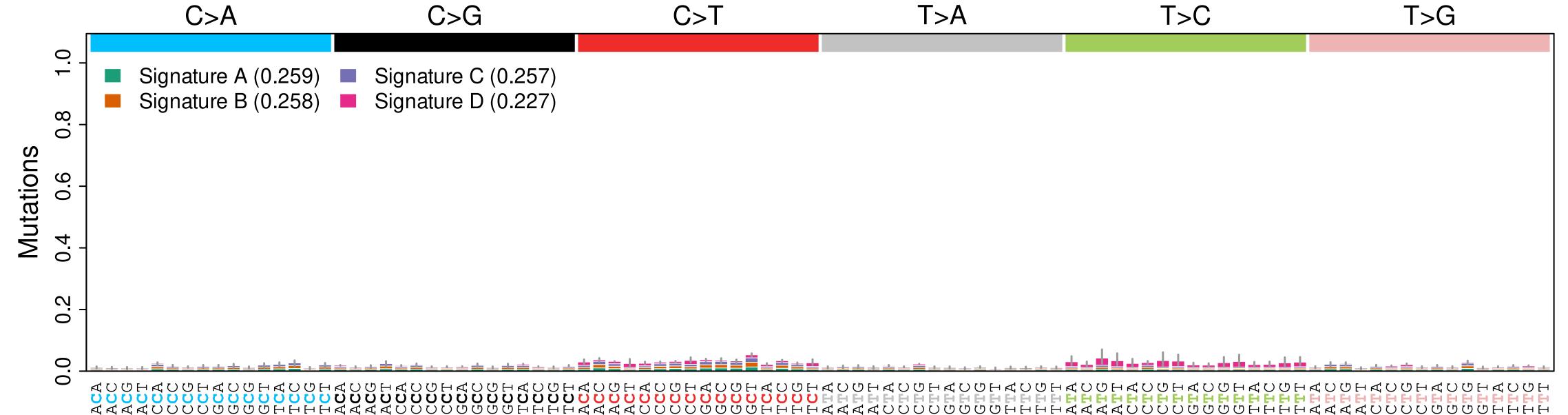
# CATD326a (6 mutations)









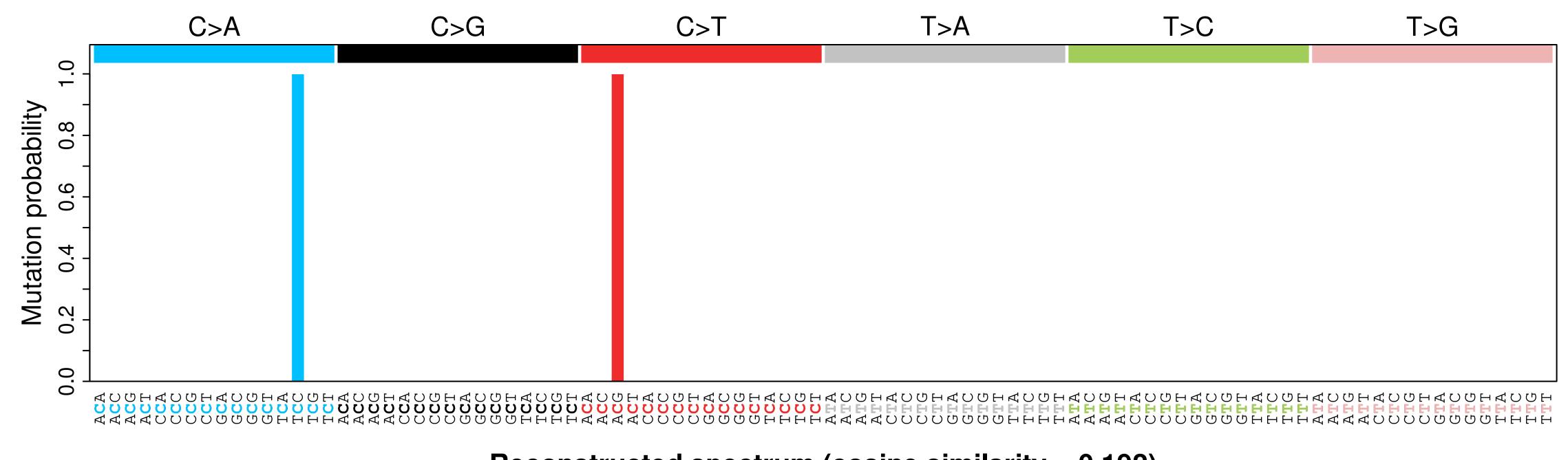


## CATD304a (2 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.128)** T>C T>G C>A C>G T>A C>T 2.0 Signature A (0.238) Signature C (0.236) Signature B (0.236) Signature D (0.29) 5 Mutations

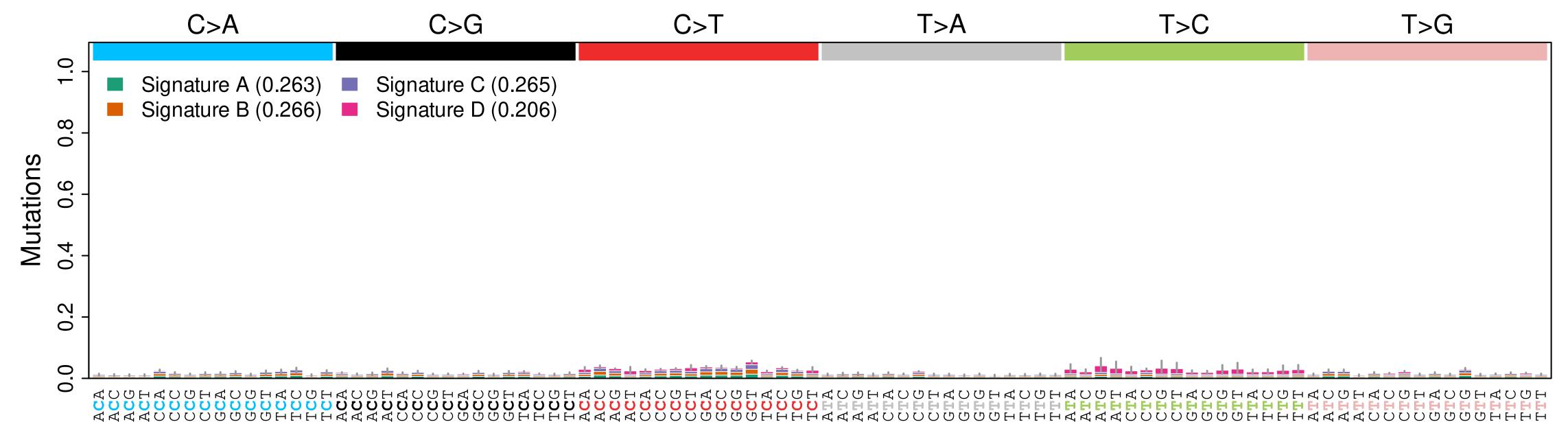
0.5

0.0

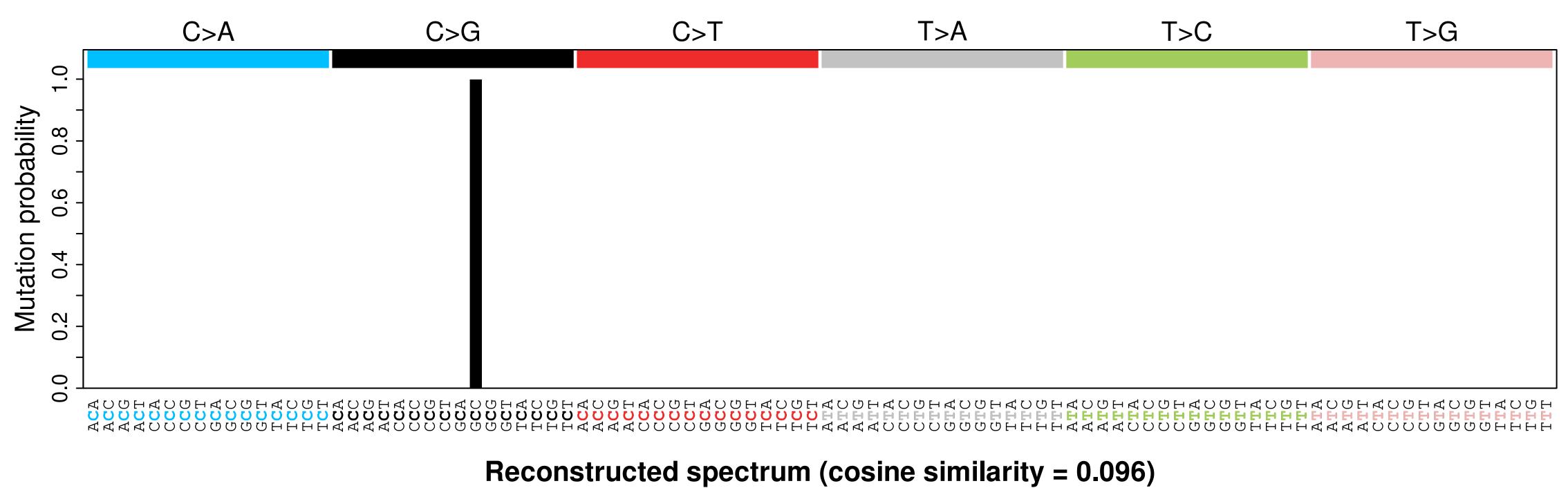


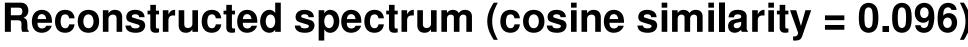


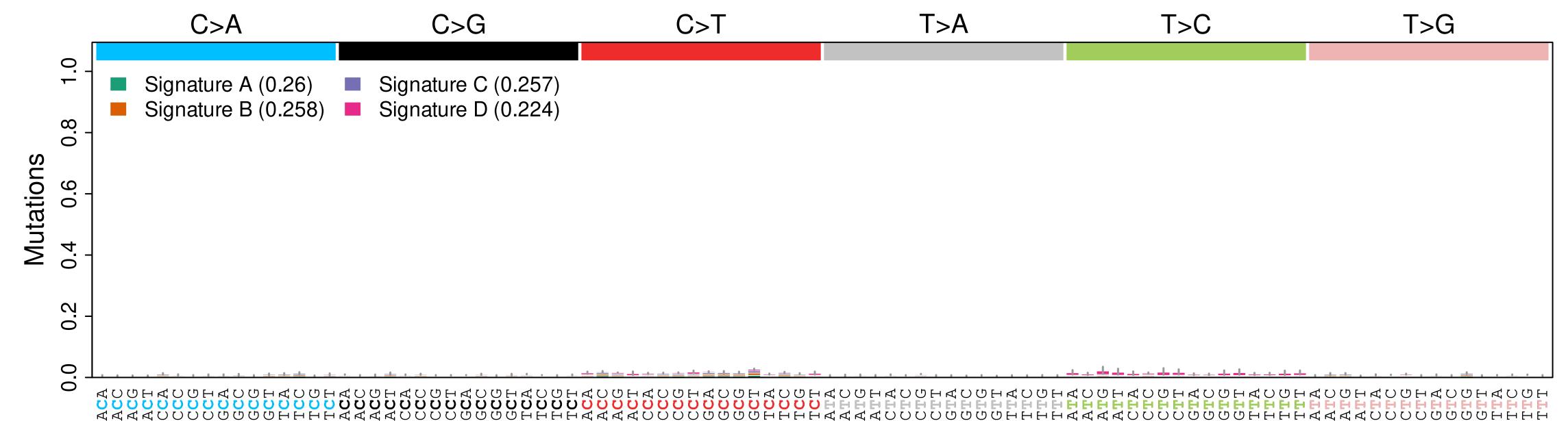
# Reconstructed spectrum (cosine similarity = 0.192)



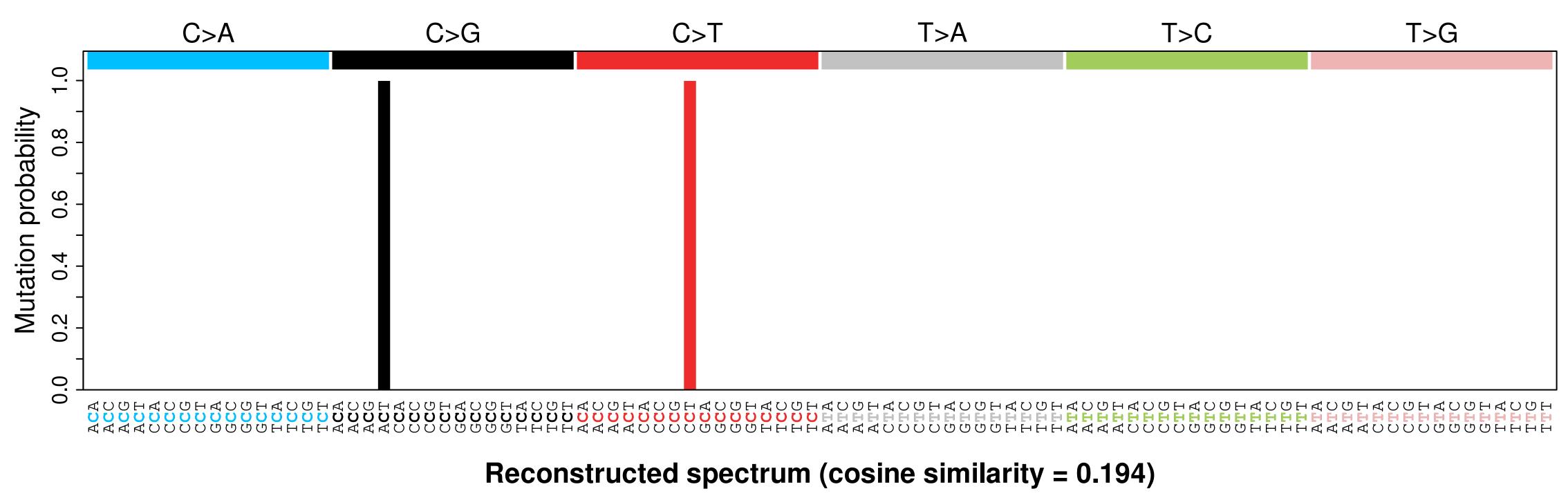


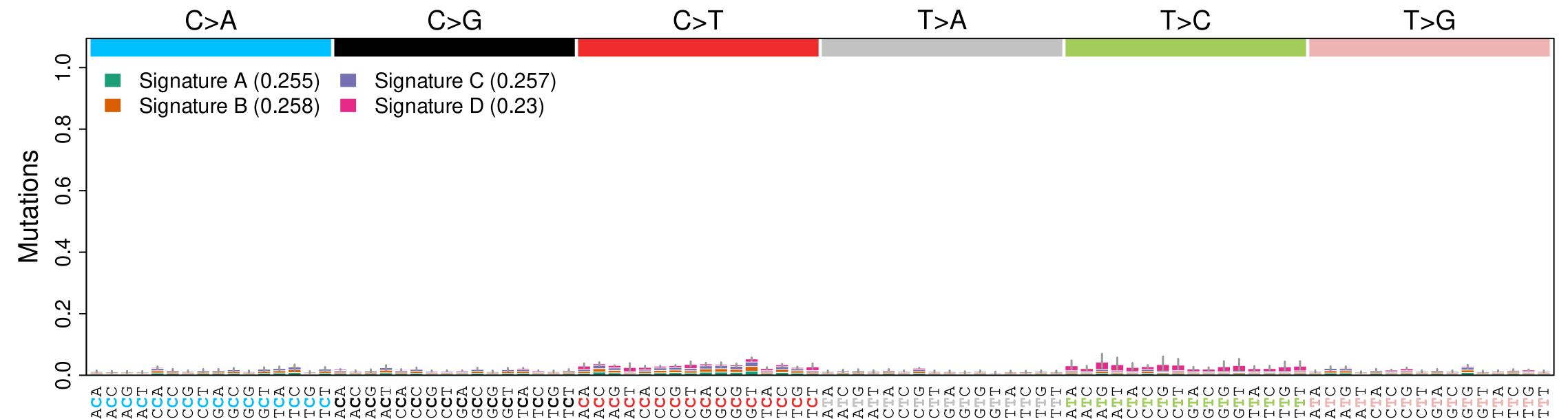












## CATD303a (2 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.238)** T>C T>G C>A C>G T>A C>T 2.0 Signature A (0.206) Signature C (0.205) Signature B (0.204) Signature D (0.386) 5 Mutations 5 0 0 0