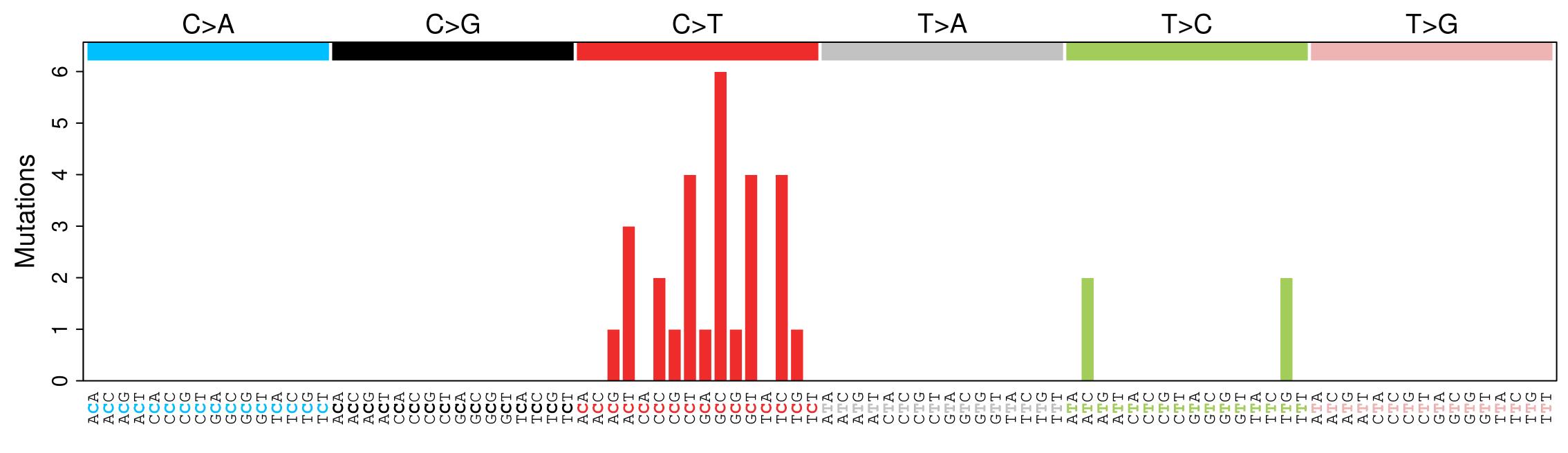
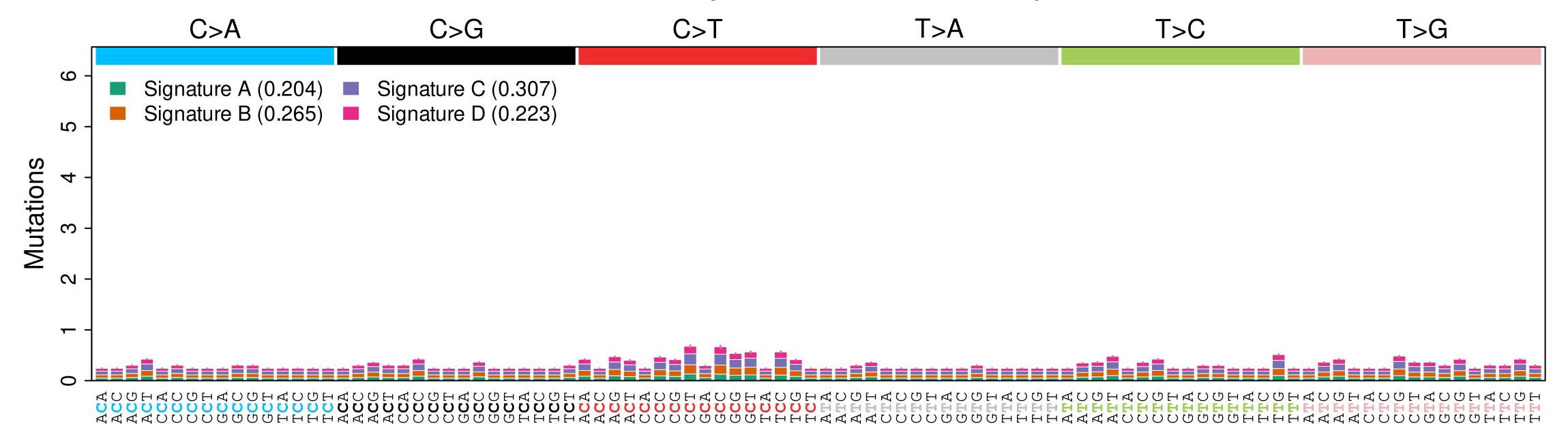
### CATD0393a (32 mutations)

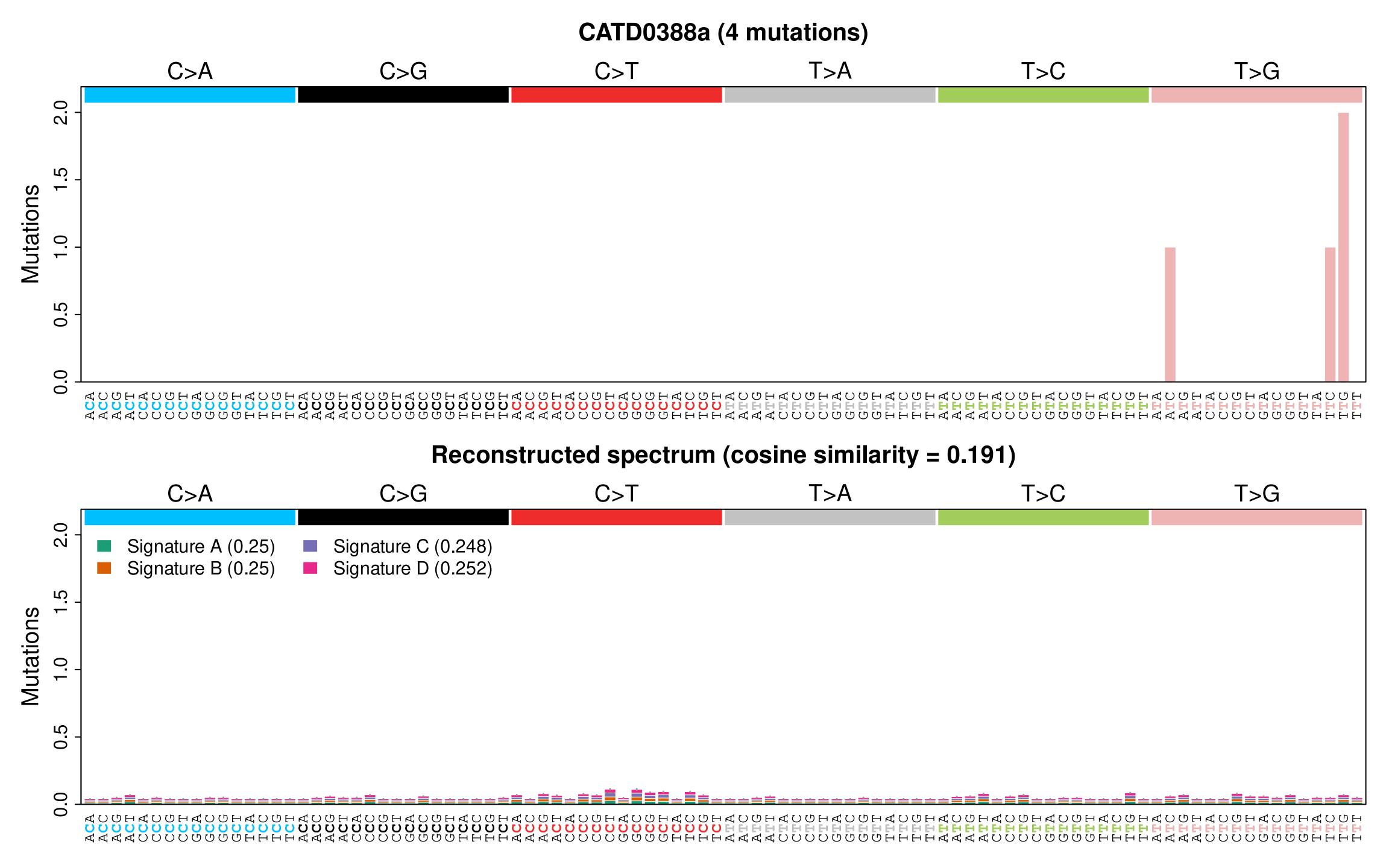


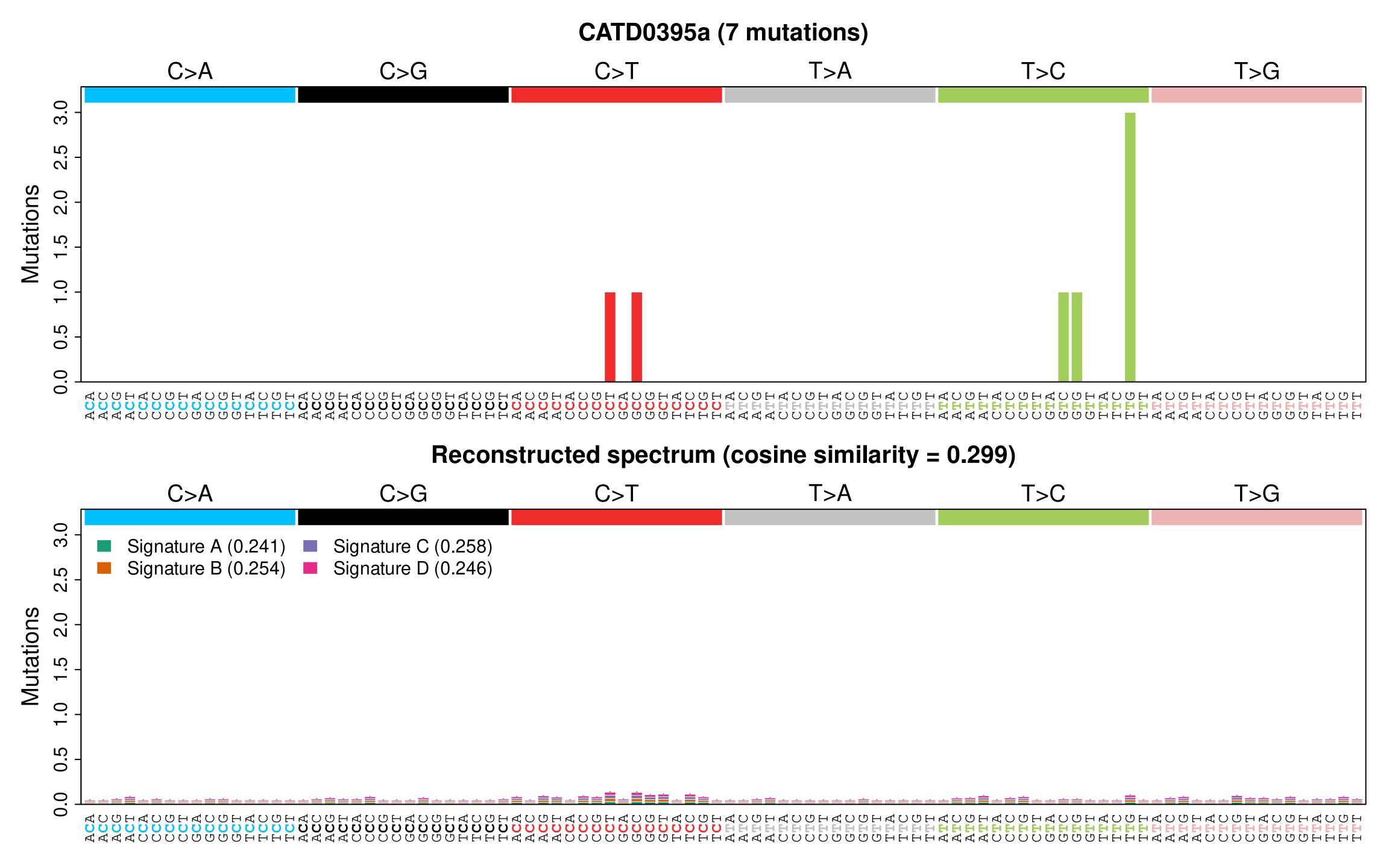
## Reconstructed spectrum (cosine similarity = 0.51)



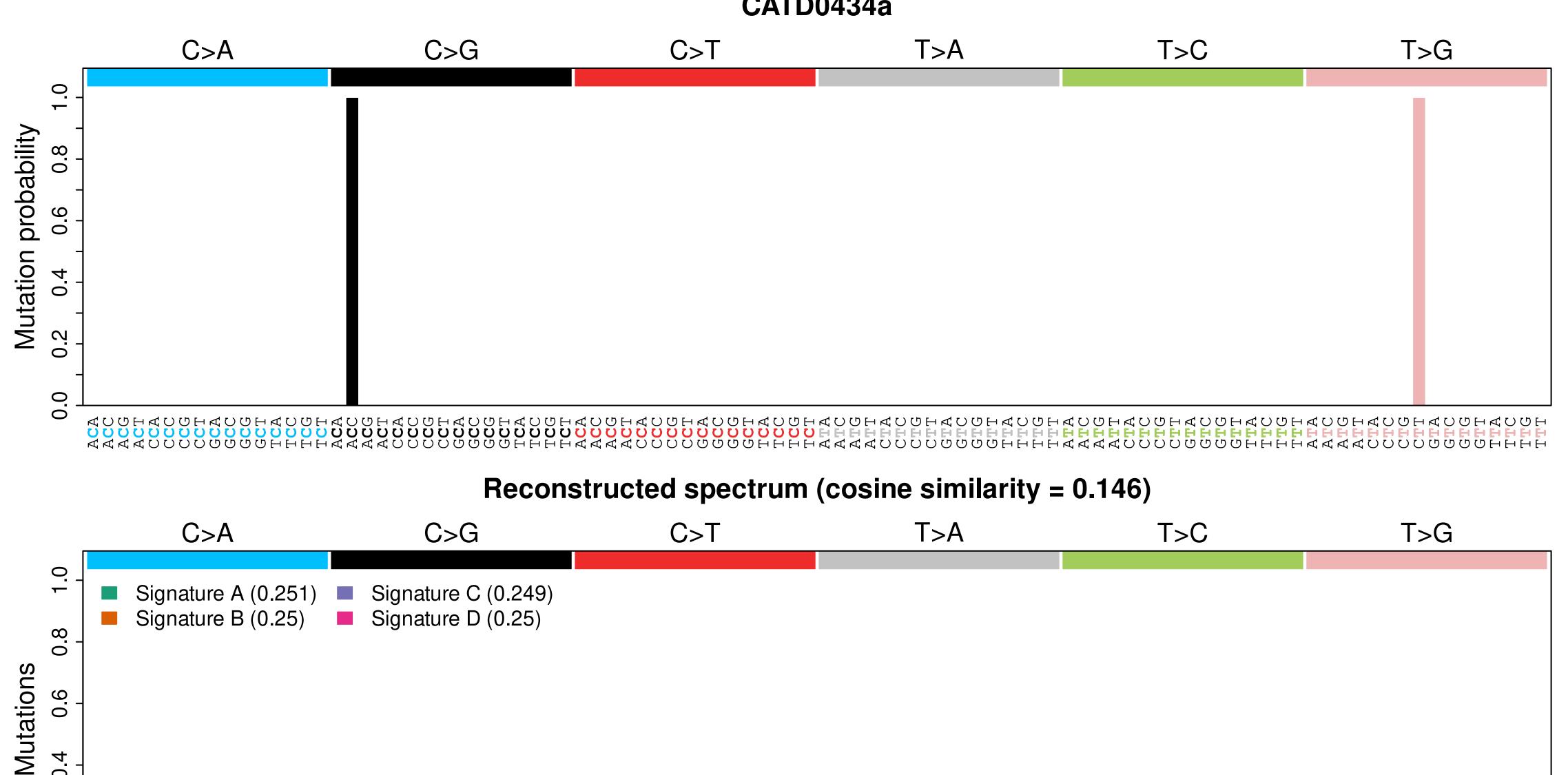
#### CATD0657a (7 mutations) T>G C>A C>G C>T T>A T>C 3.0 2.5 Mutations 2.0 1.5 0.5 0 **Reconstructed spectrum (cosine similarity = 0.294)** T>A T>C T>G C>A C>G C>T 3.0 Signature A (0.249) Signature C (0.25) Signature B (0.251) Signature D (0.249) 5 S Mutations 2.0 1.5

0.5



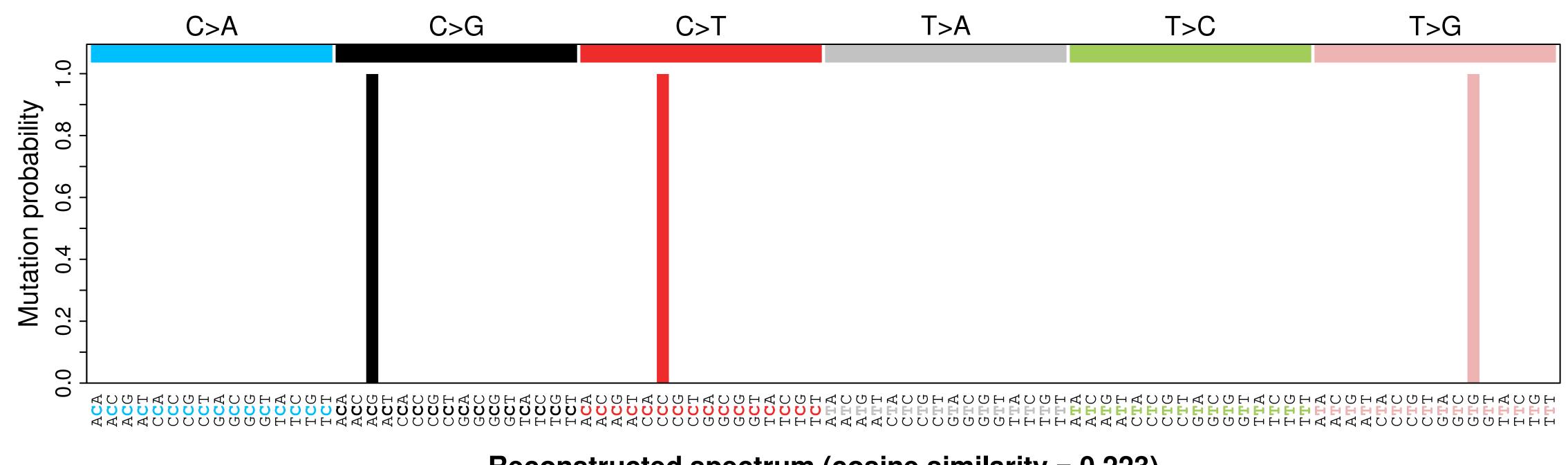


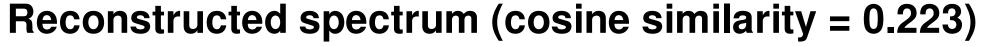


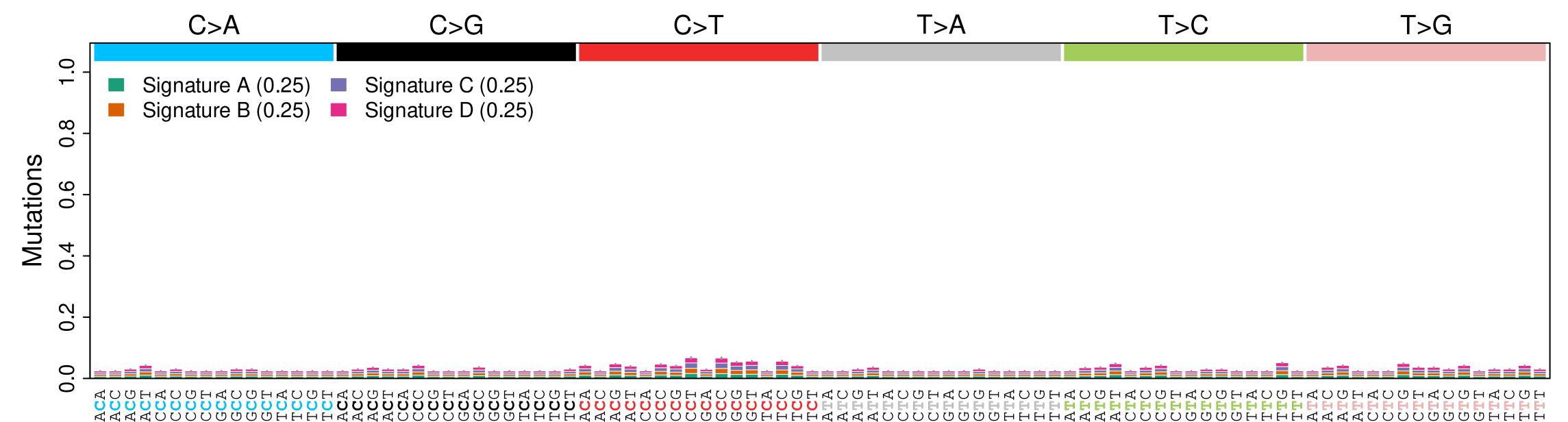


 $\mathcal{O}$ 0



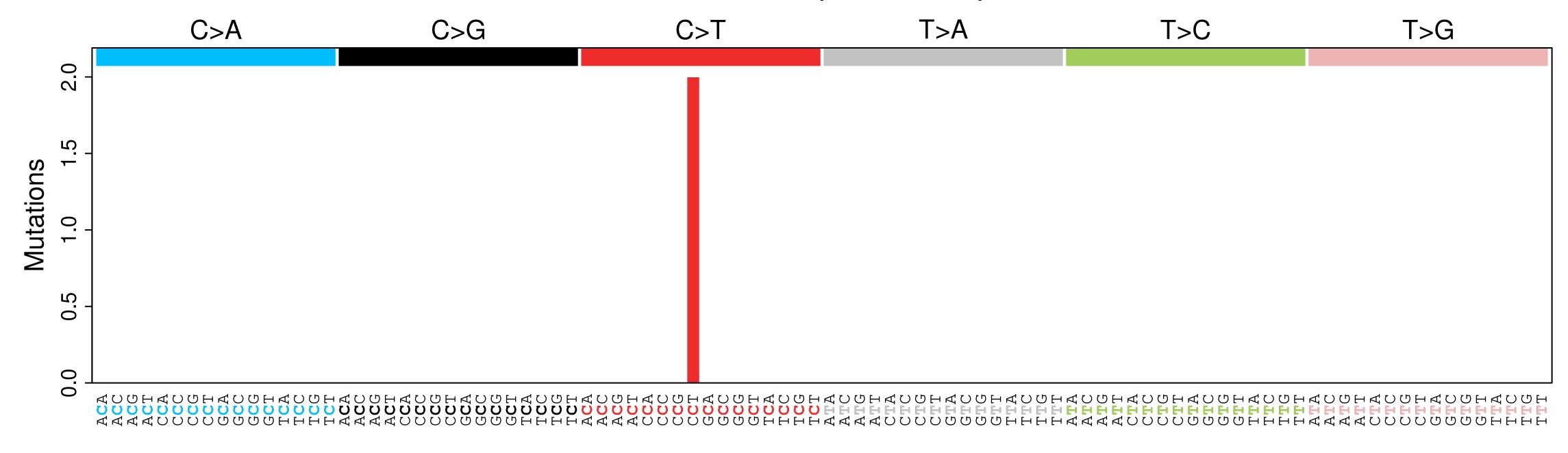




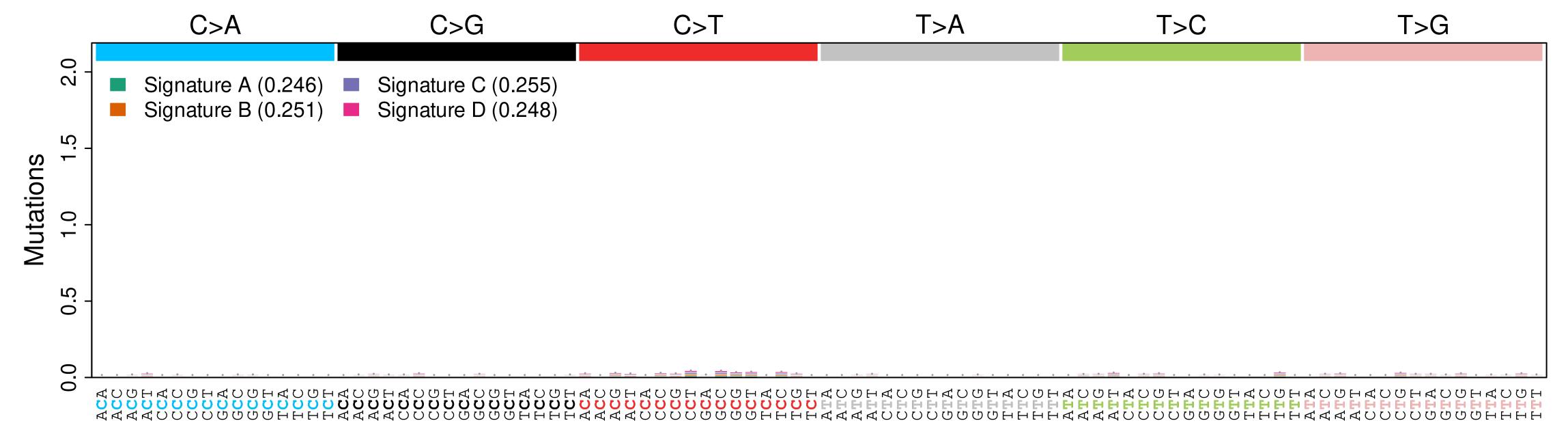


## CATD0391a (2 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.15)** T>A T>C T>G C>A C>G C>T 2.0 Signature A (0.25) Signature C (0.25) Signature B (0.251) Signature D (0.249) 5 Mutations 5 0

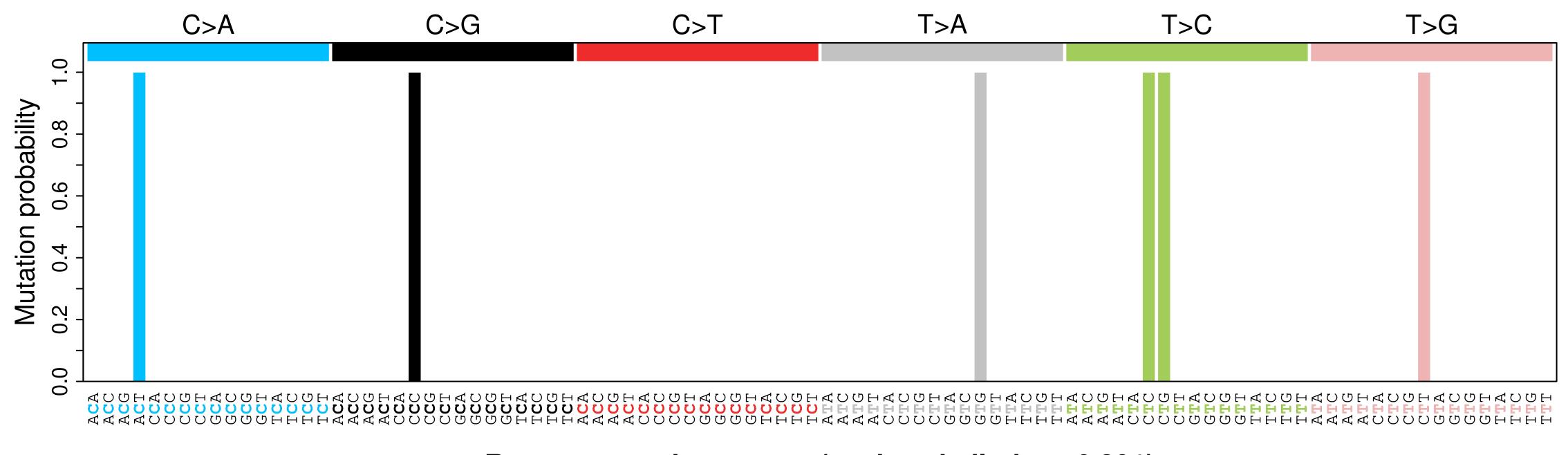
## CATD0387a (2 mutations)

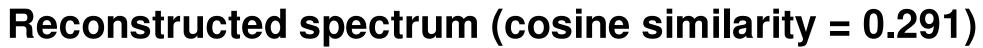


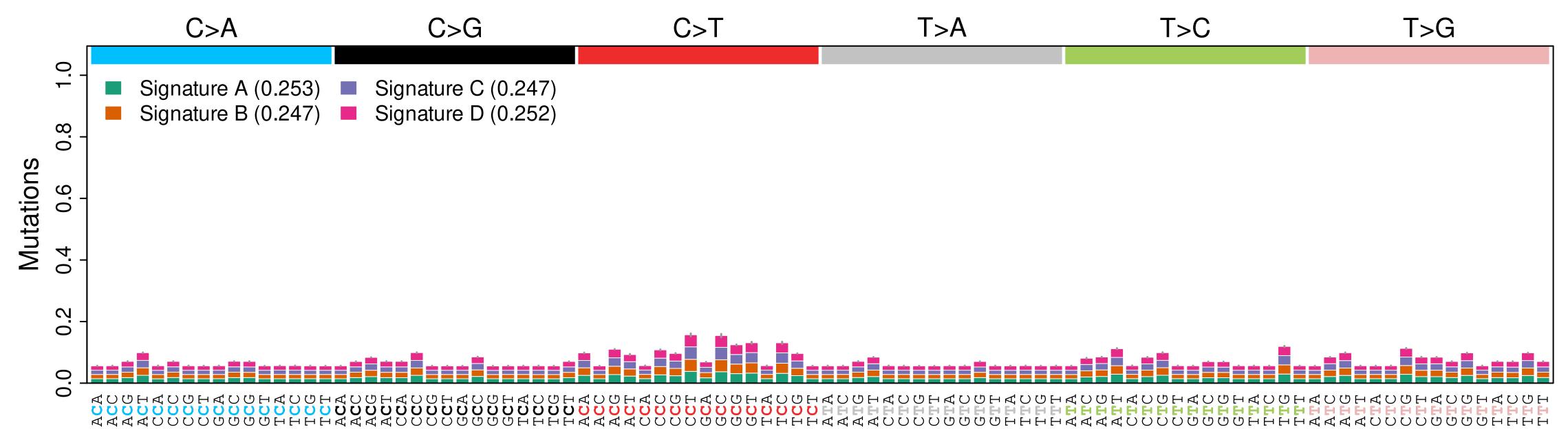
# Reconstructed spectrum (cosine similarity = 0.209)



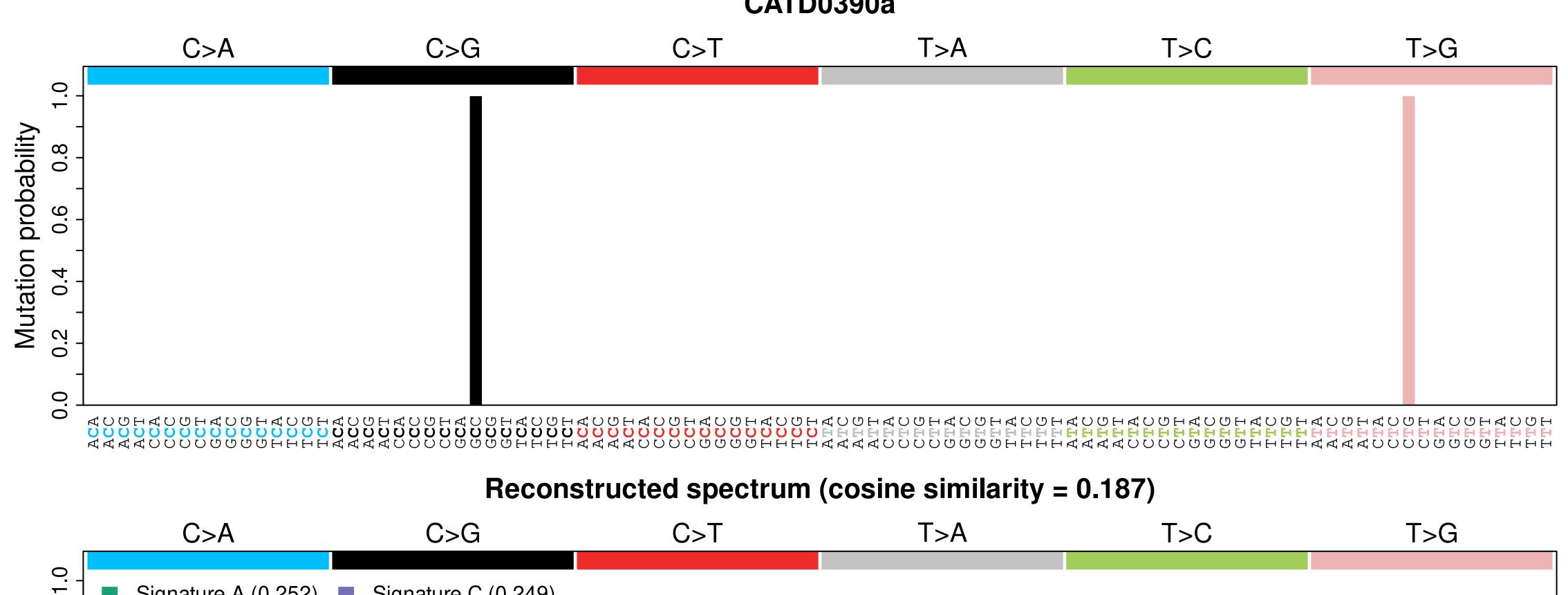
#### **CATD**0381a

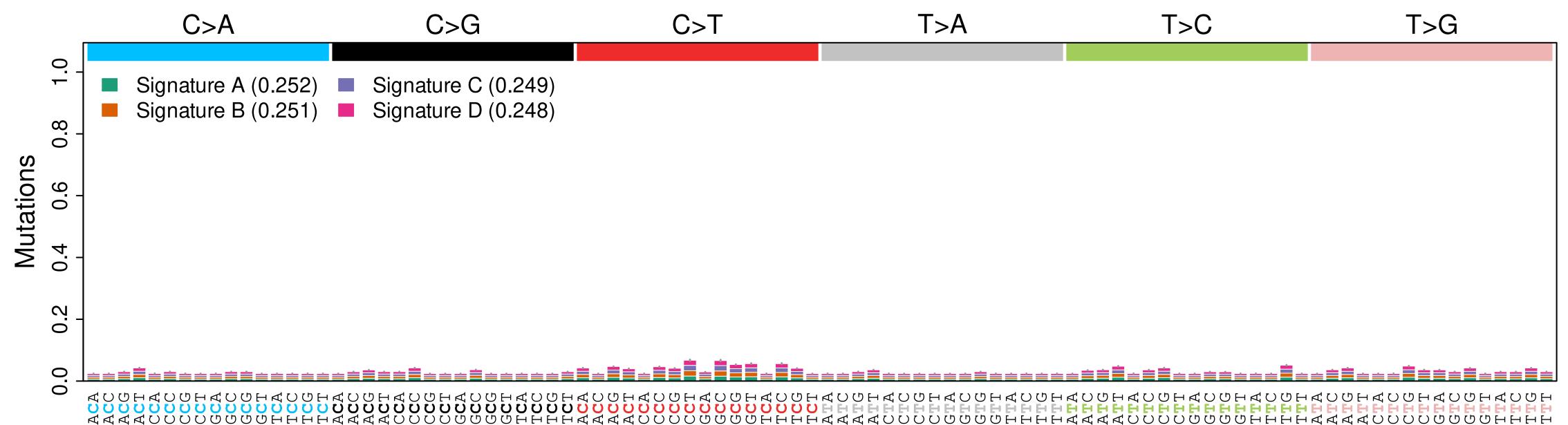




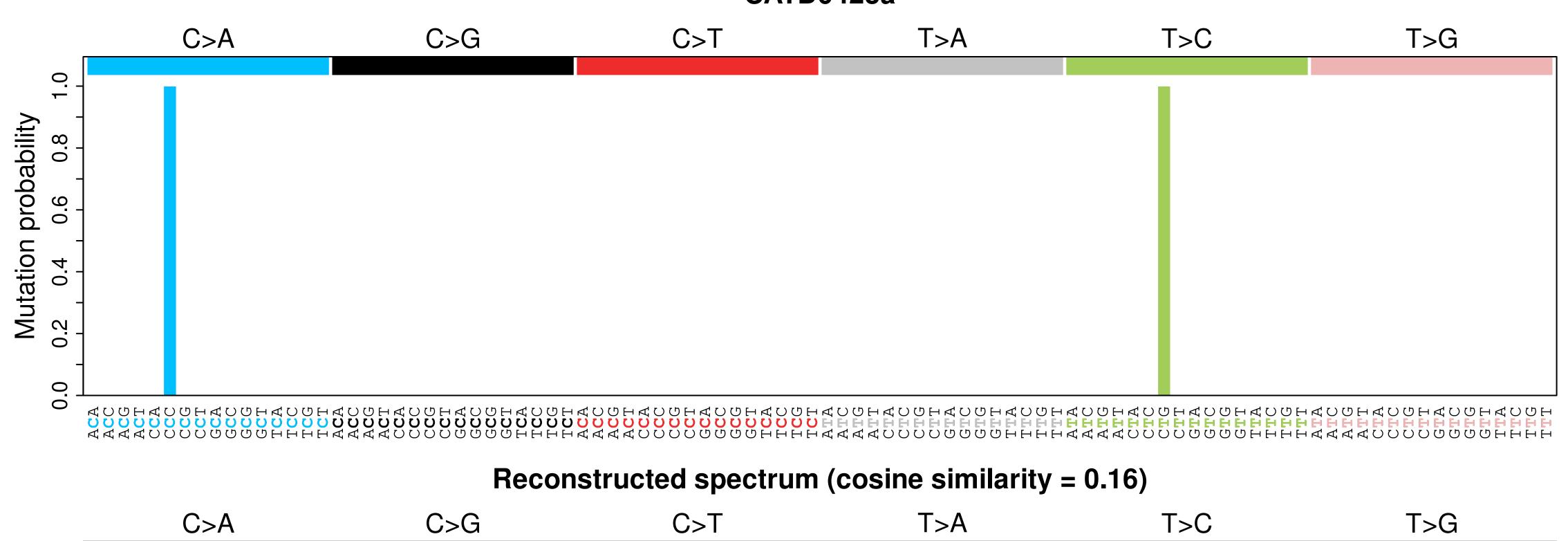


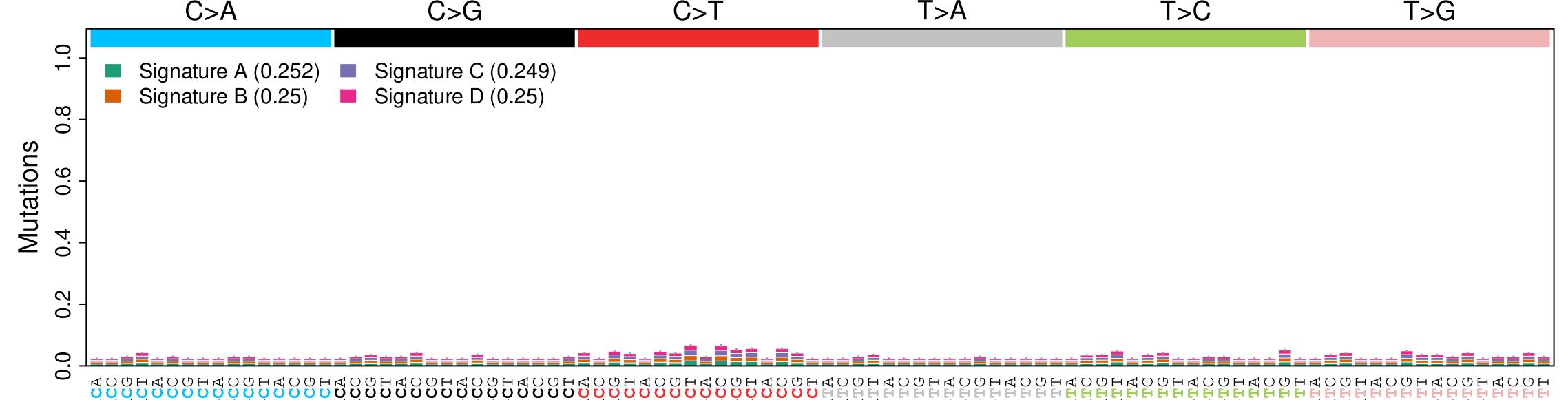




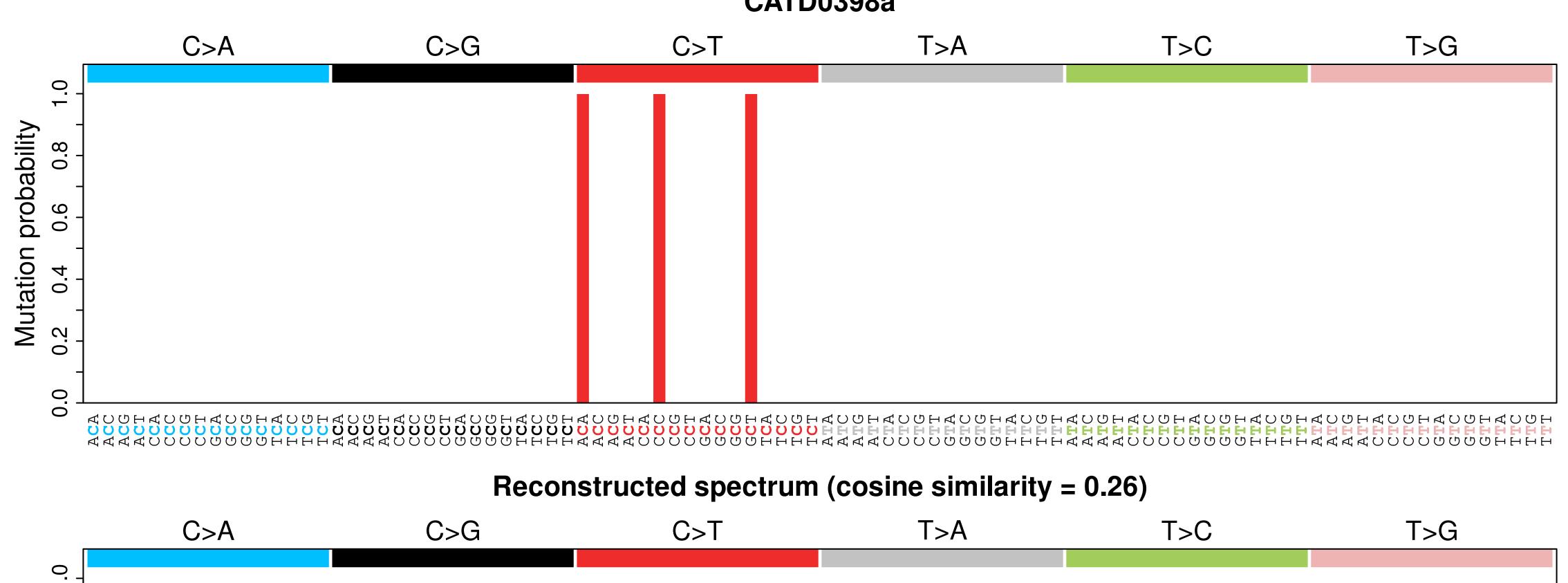


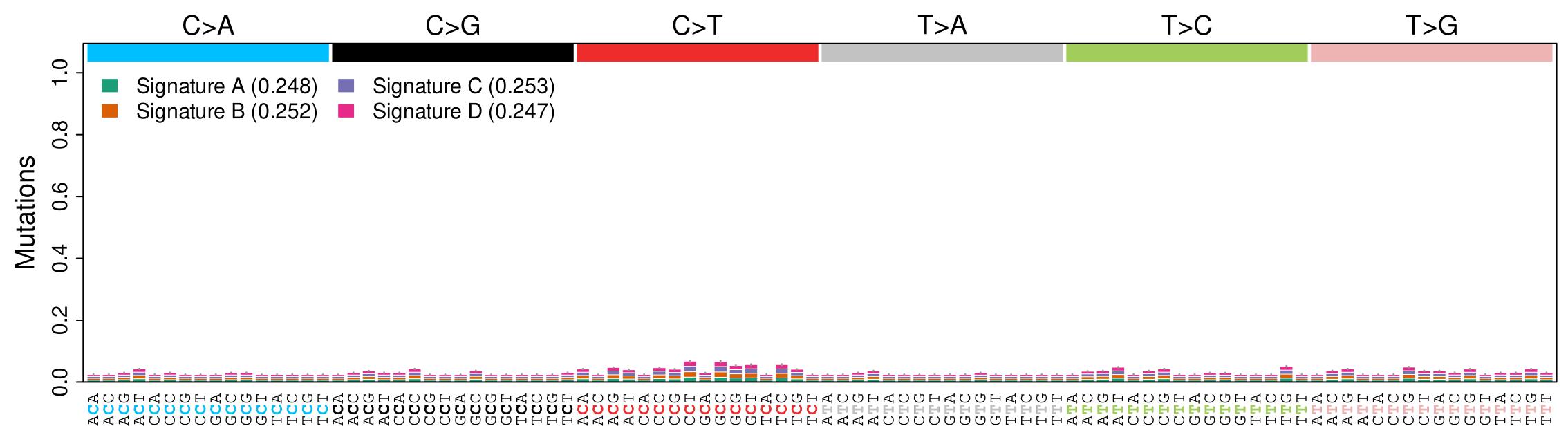




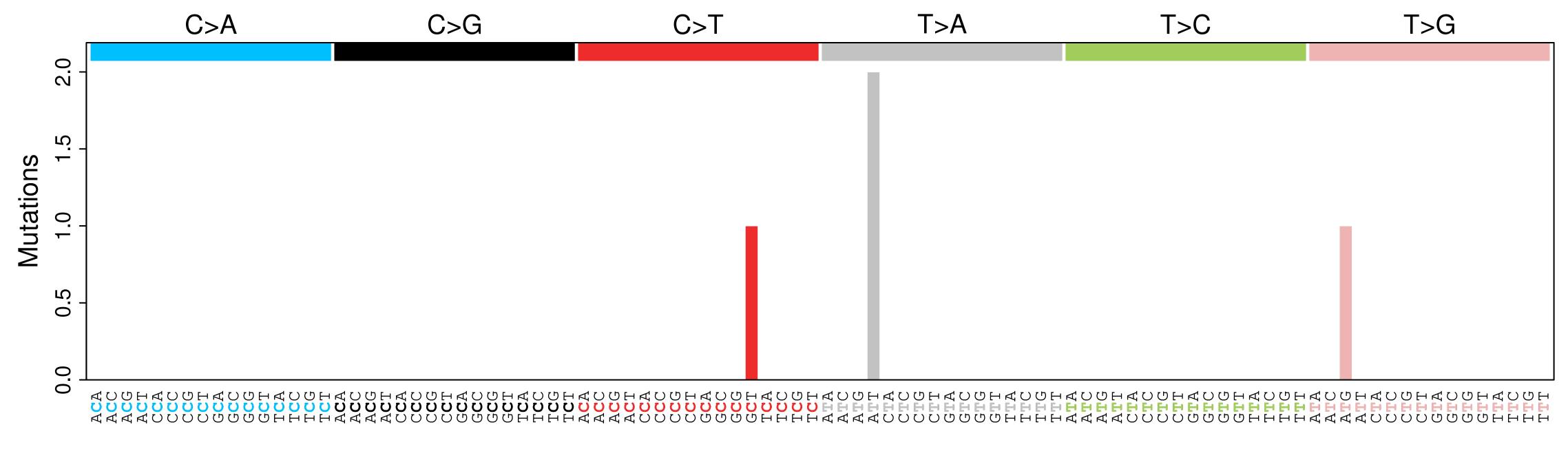




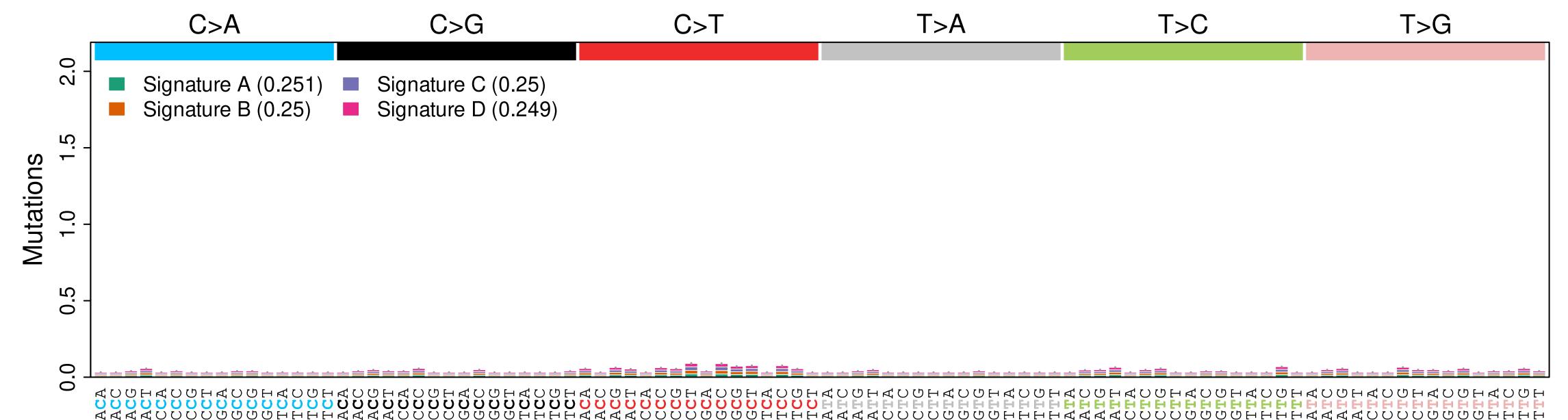




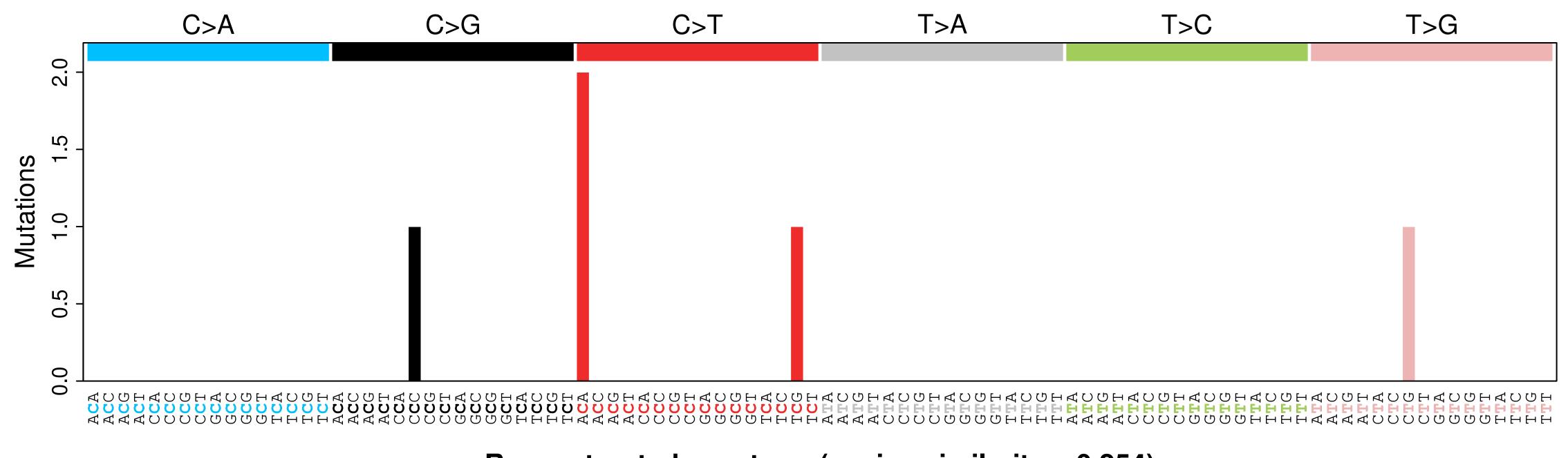
# CATD0428a (4 mutations)



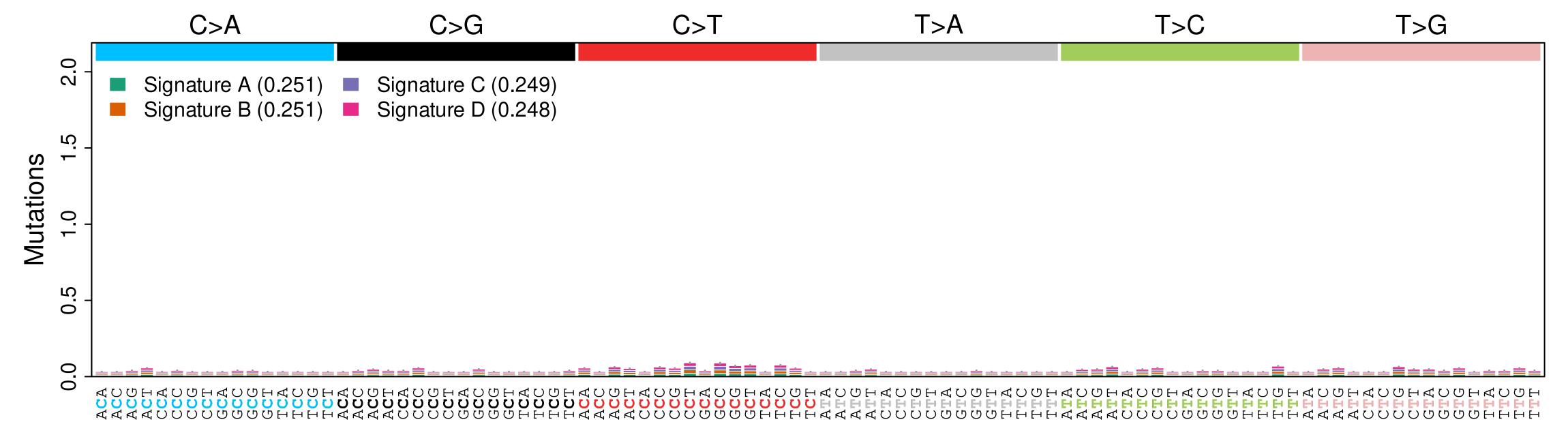
# Reconstructed spectrum (cosine similarity = 0.217)



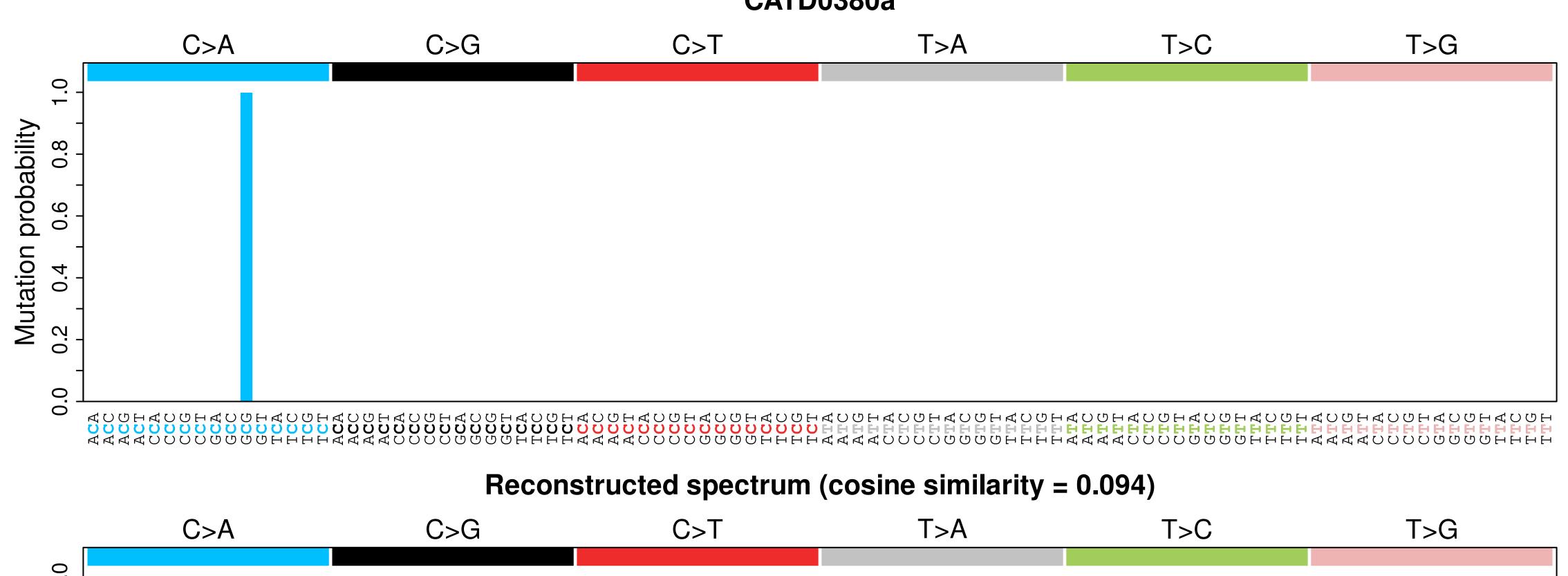
## CATD0378a (5 mutations)

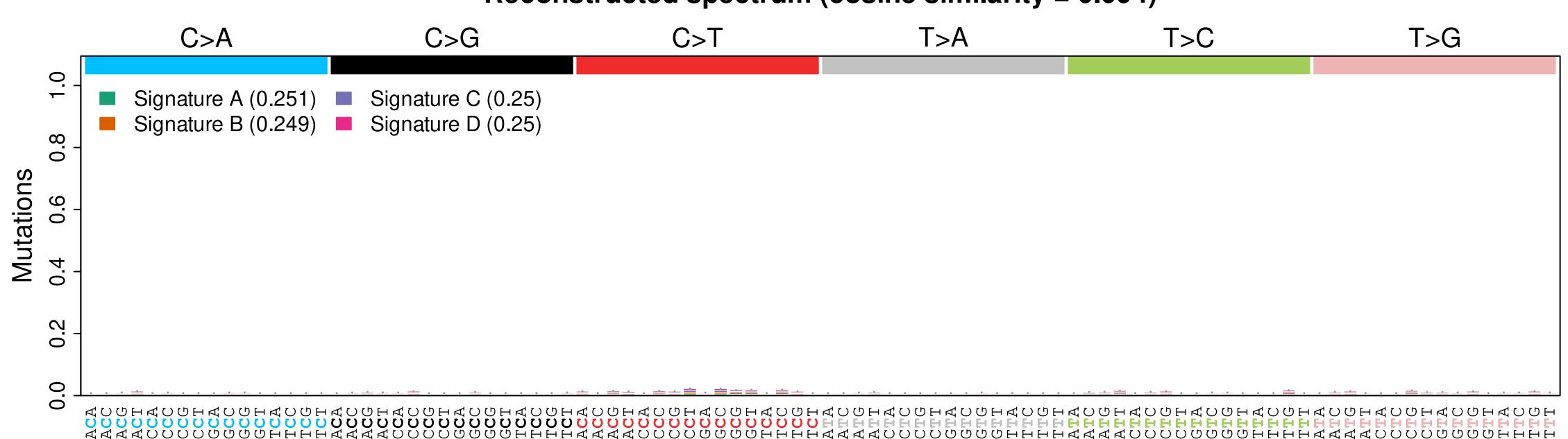


# Reconstructed spectrum (cosine similarity = 0.254)

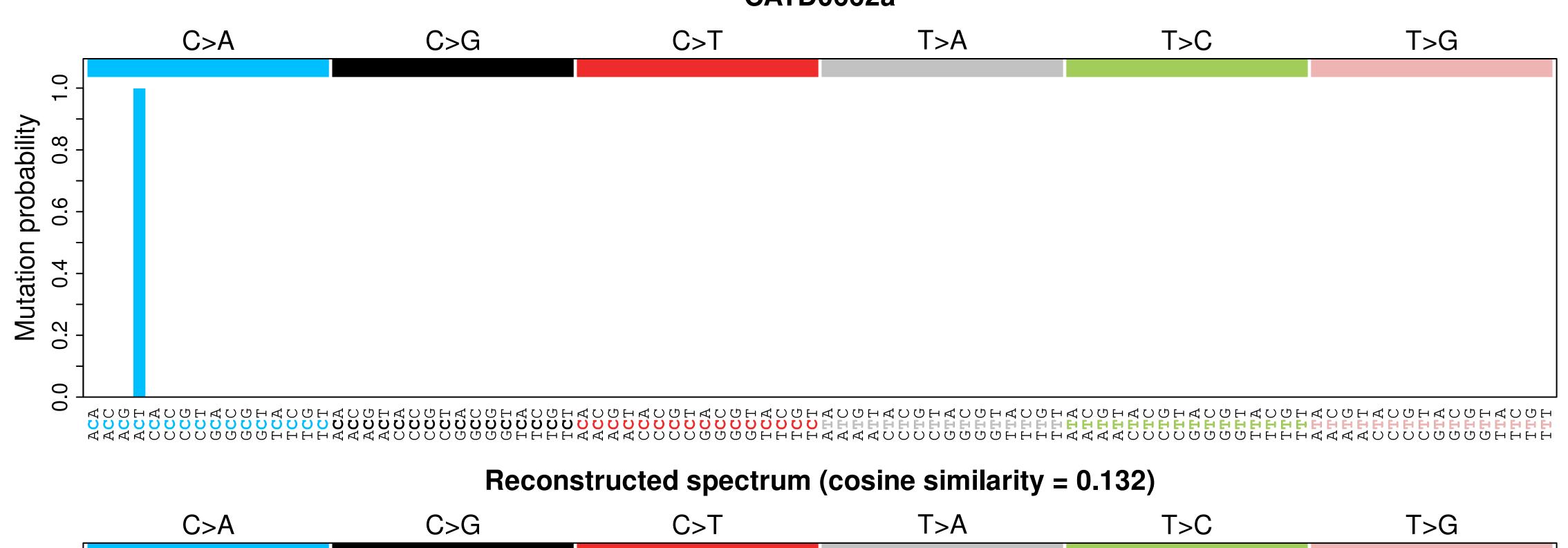




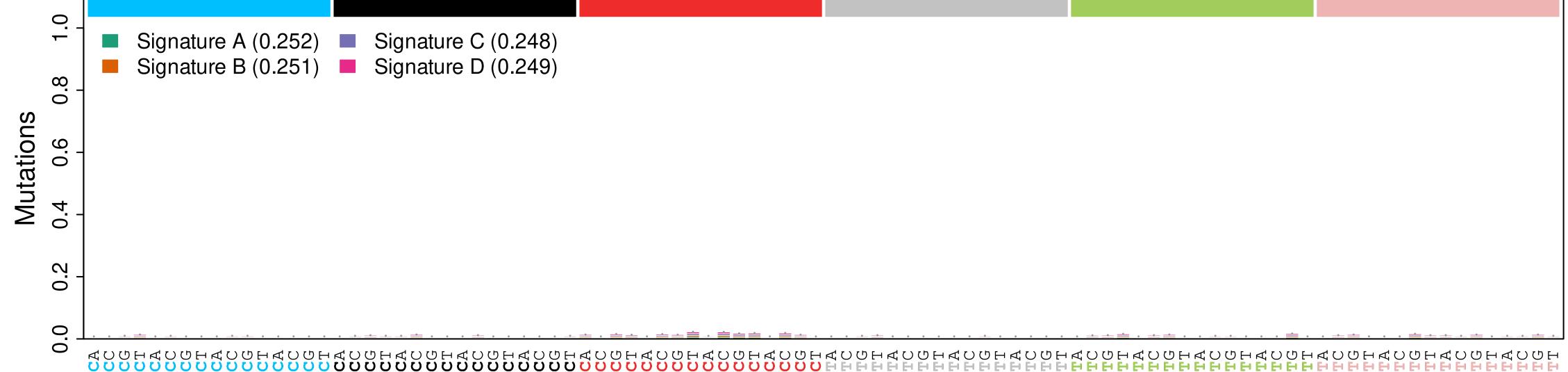




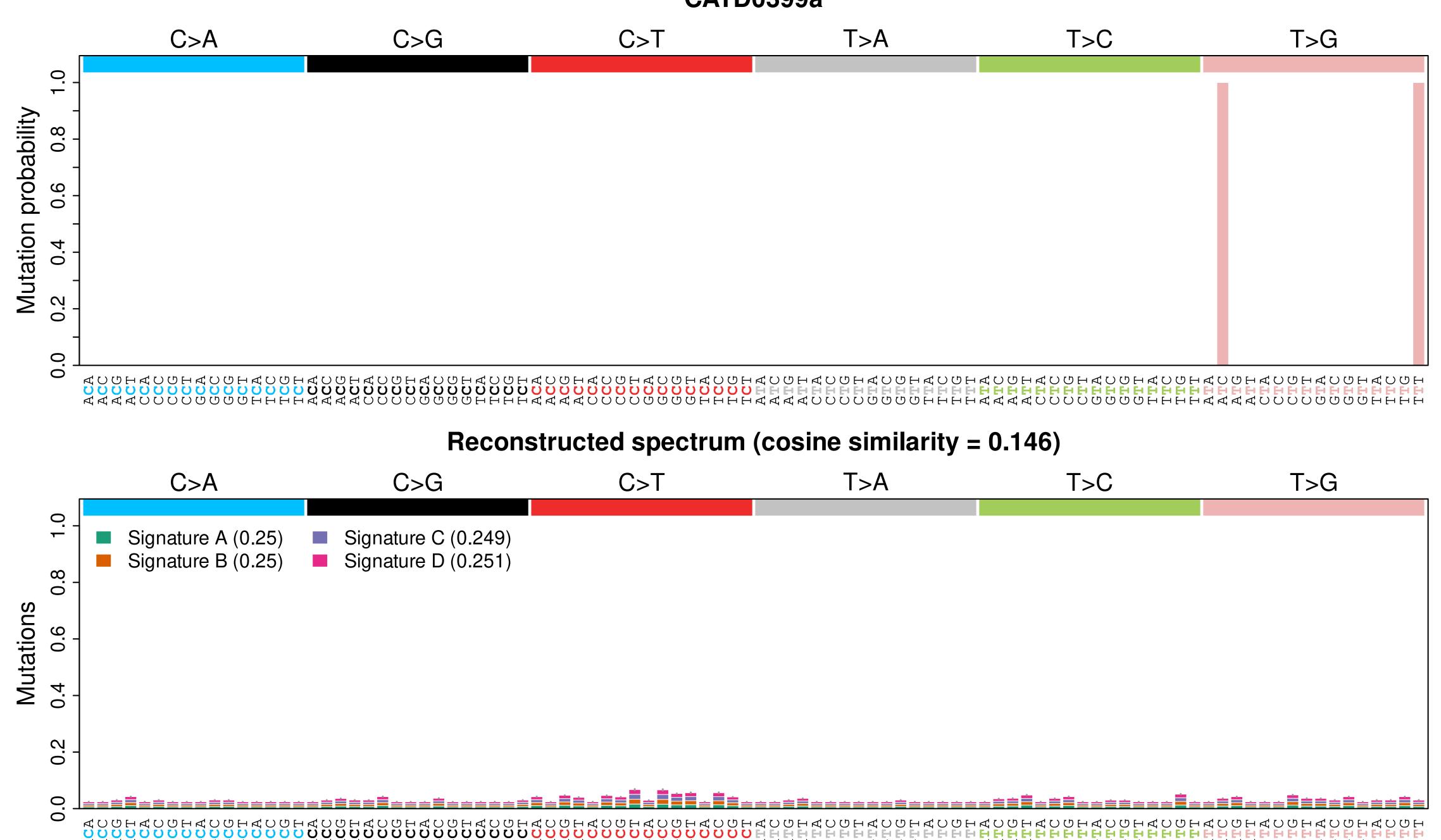




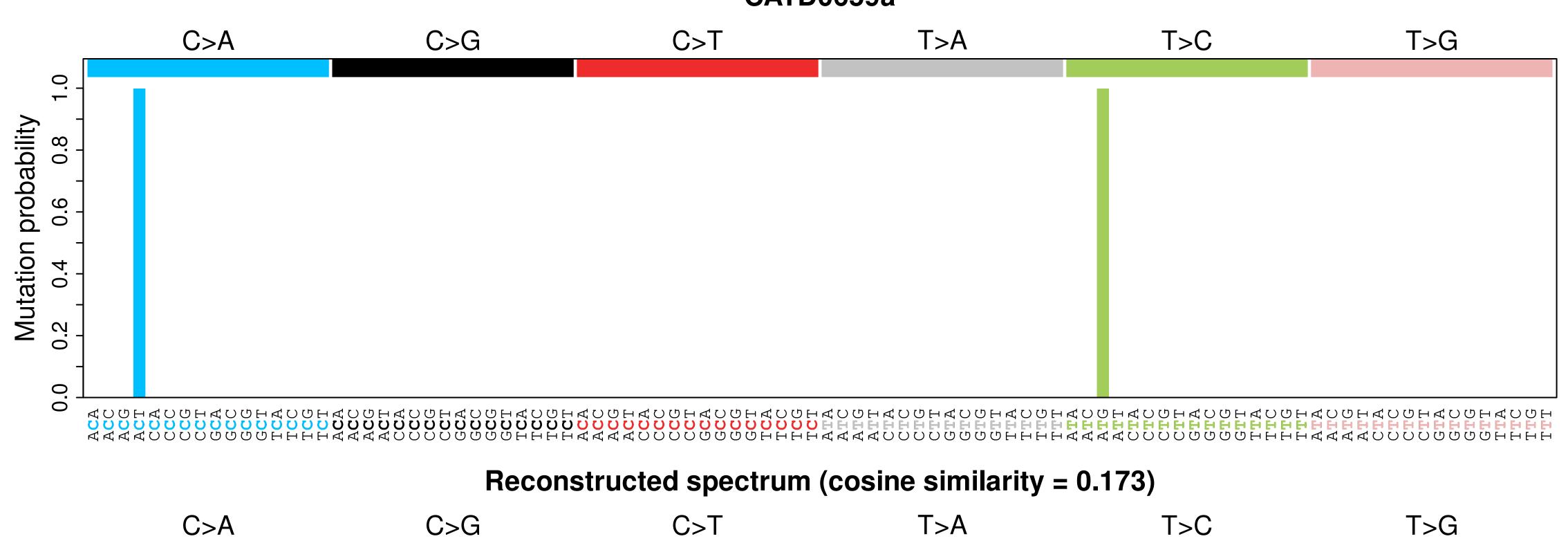


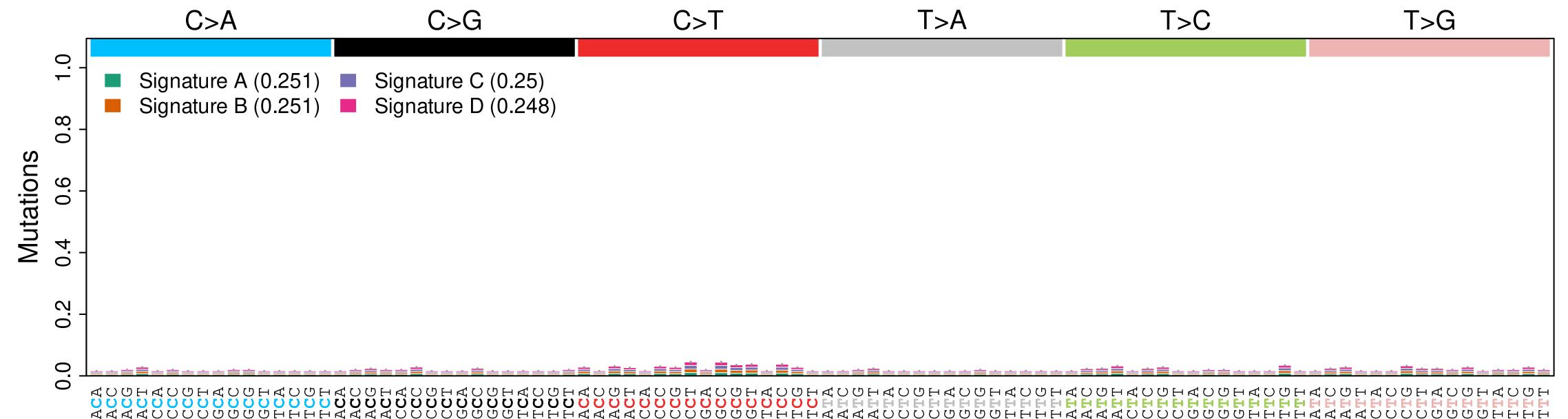




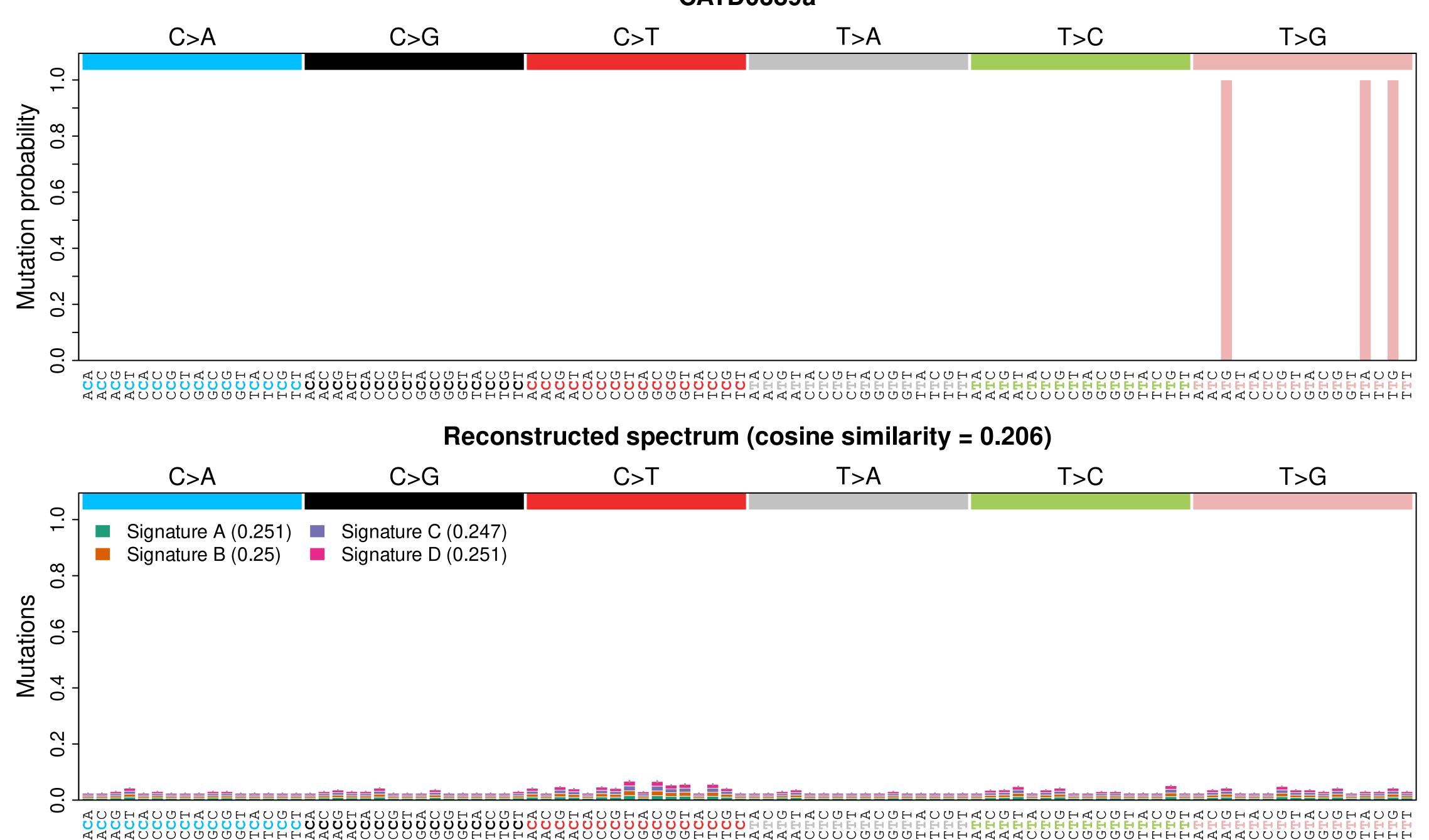




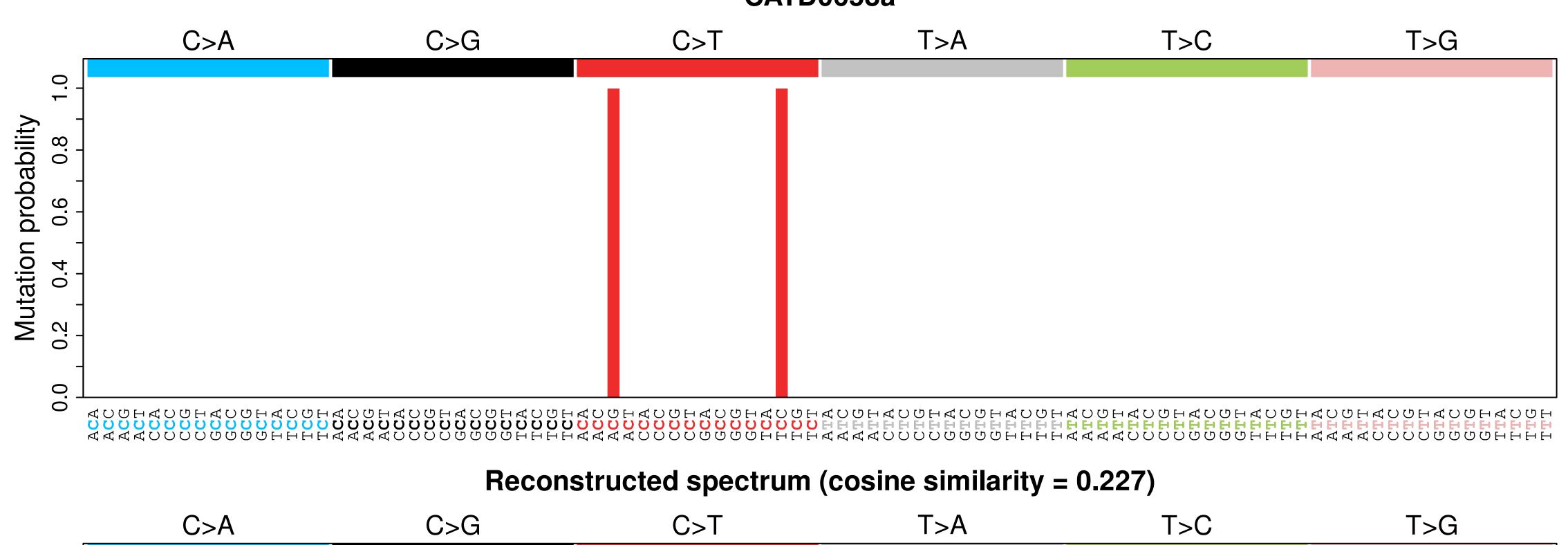


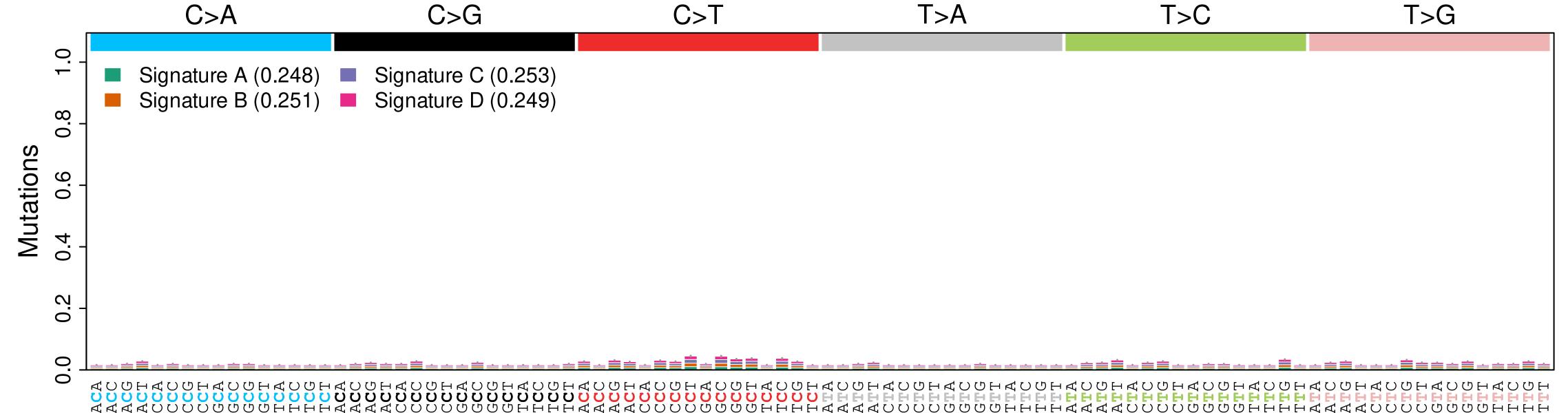






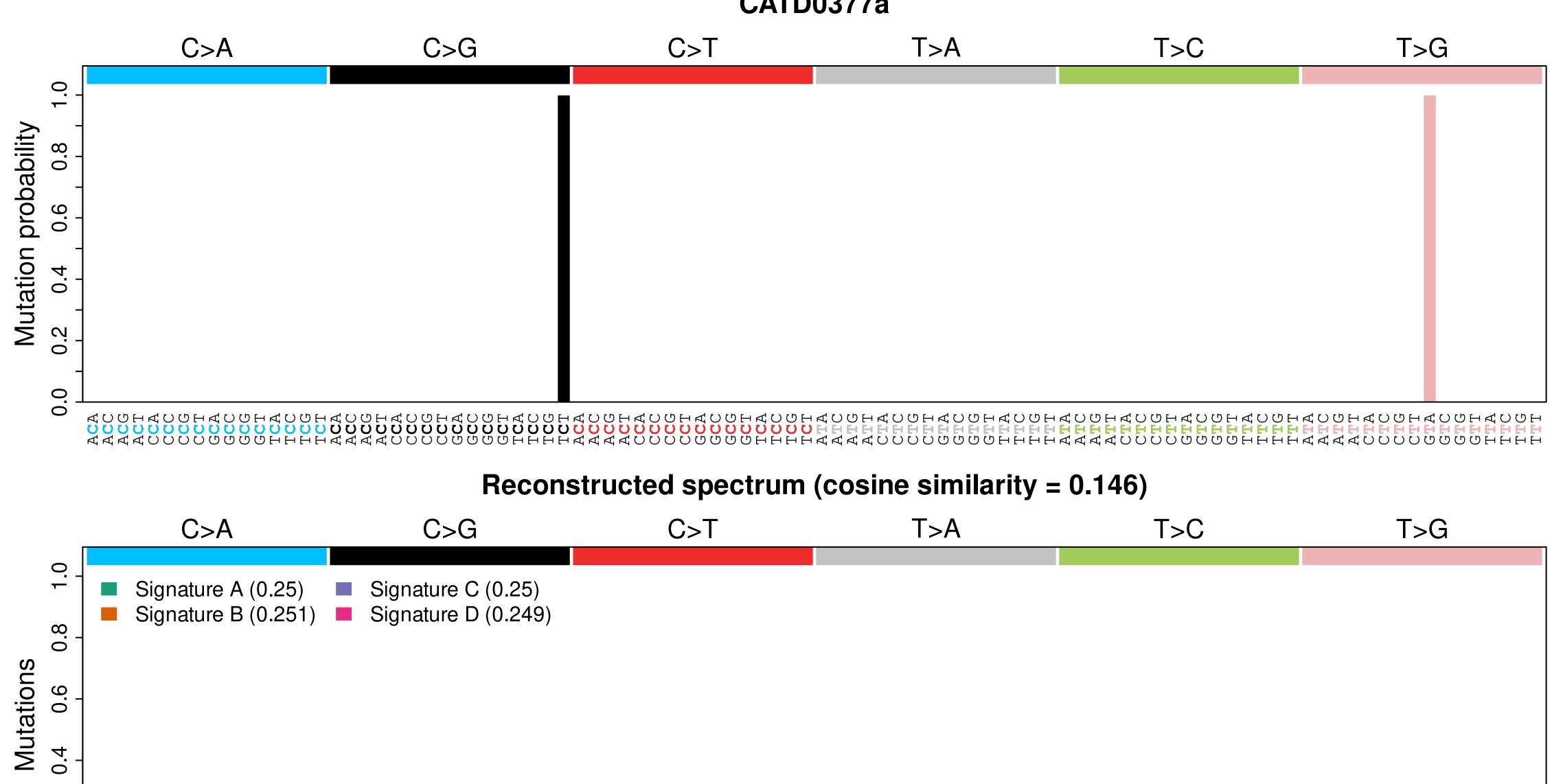






# CATD0665a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.227)** T>C T>G C>A C>G T>A C>T 2.0 Signature A (0.248) Signature C (0.249) Signature B (0.25) Signature D (0.253) 5 Mutations 5 0





 $\mathcal{O}$ 0



