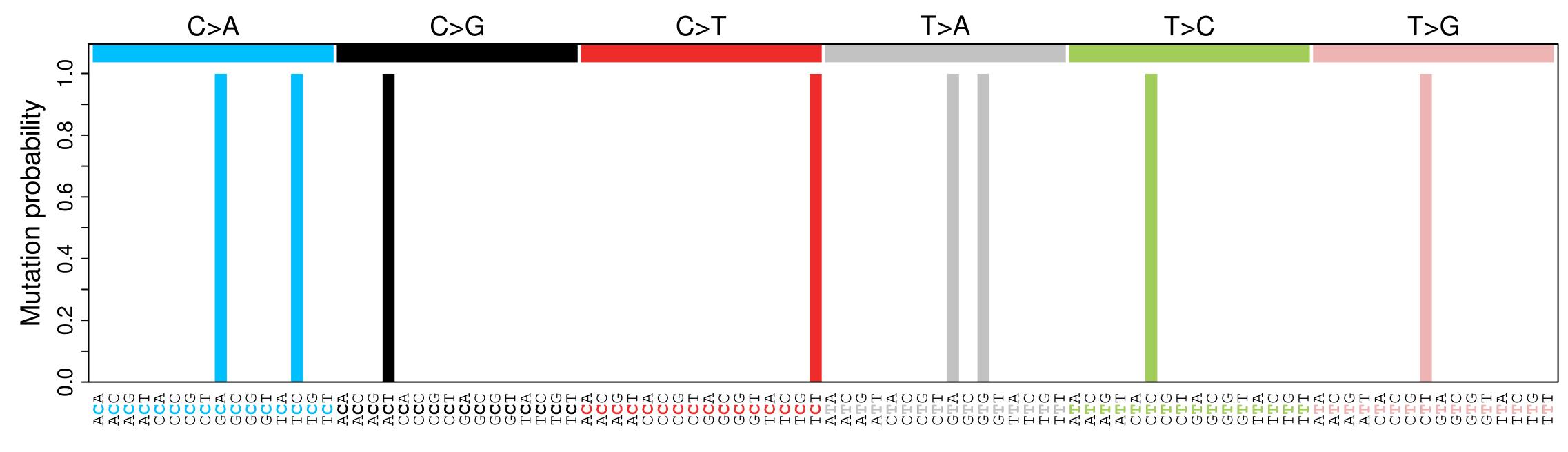
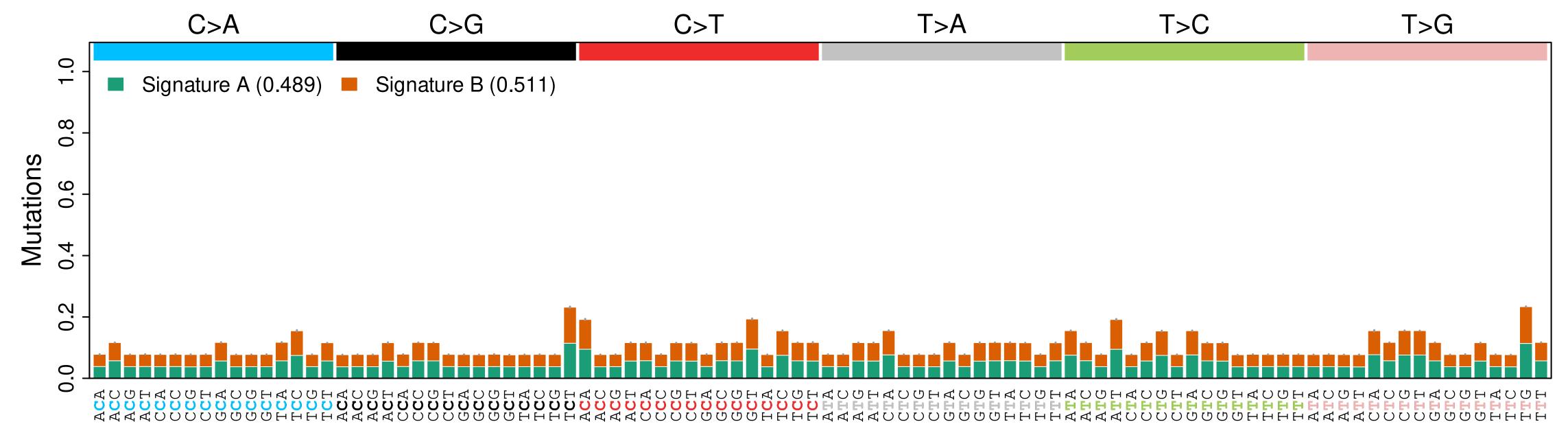


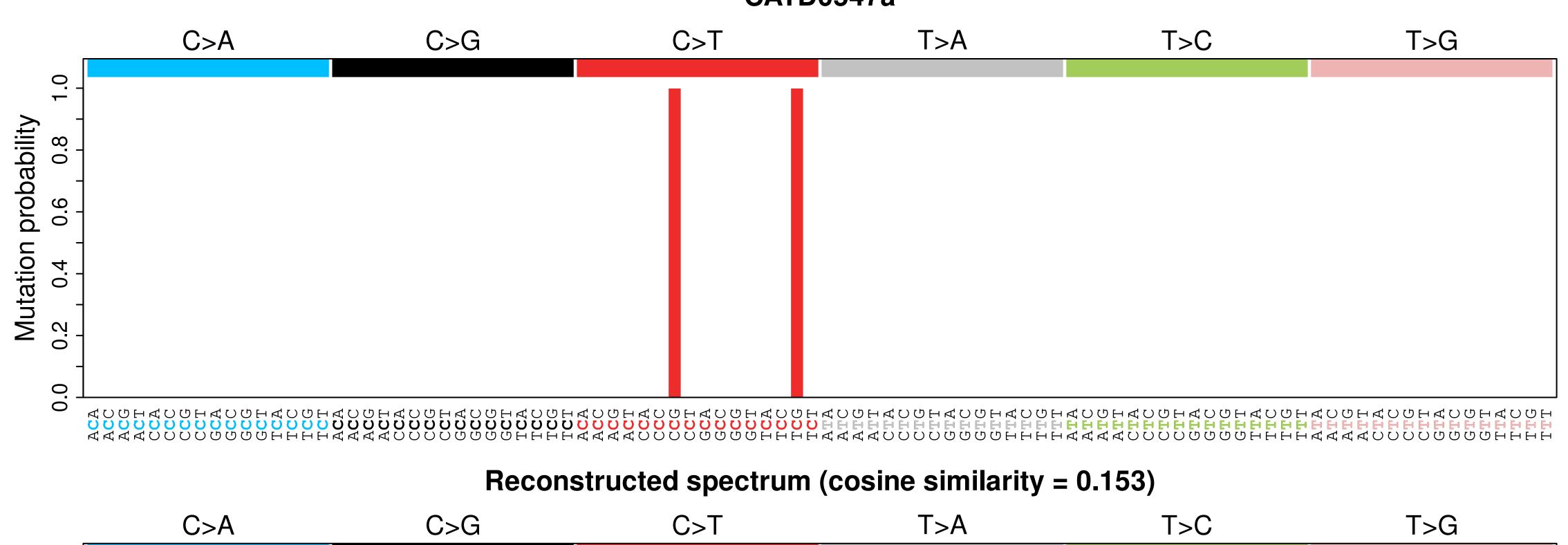
#### CATD336a

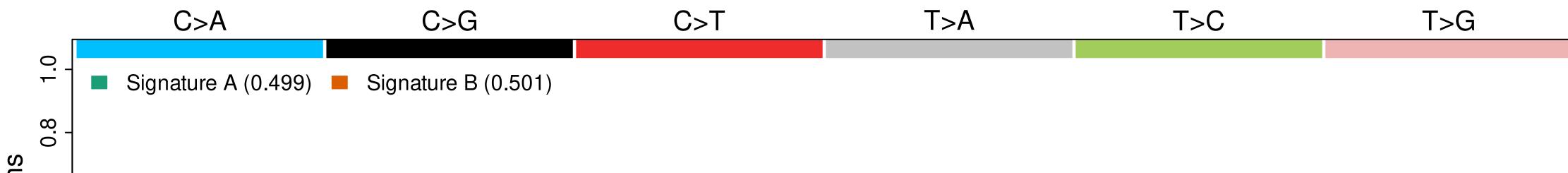


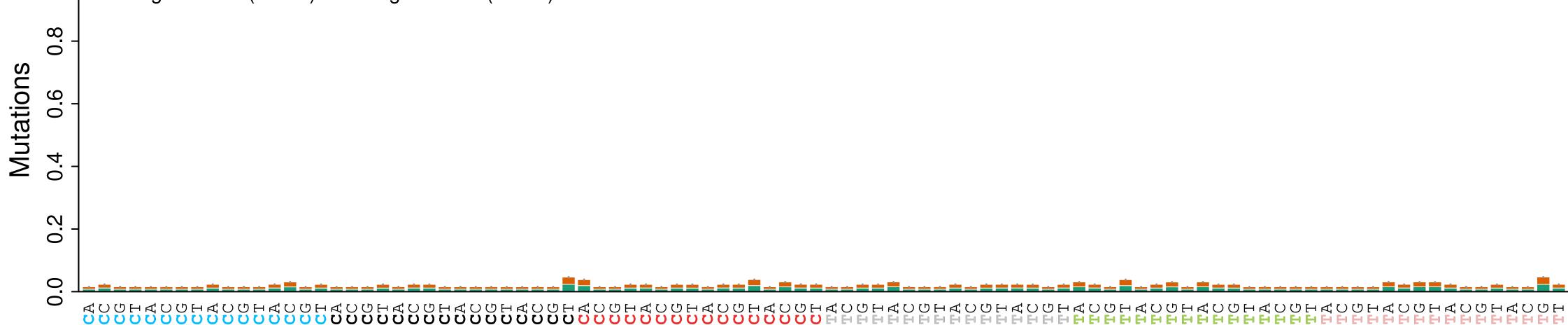
# Reconstructed spectrum (cosine similarity = 0.331)



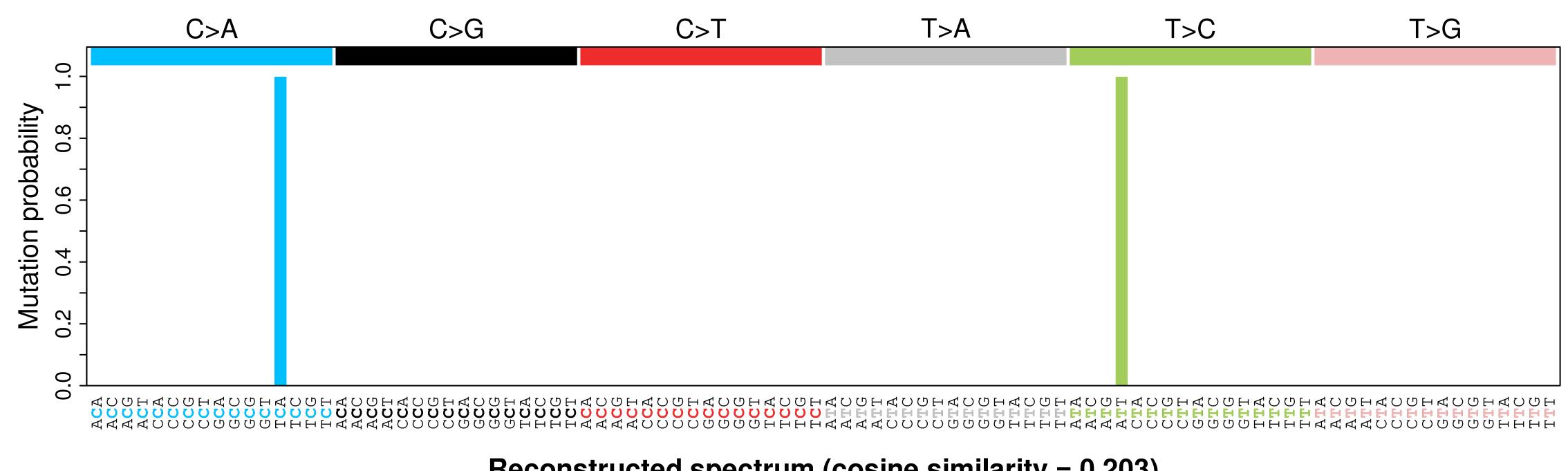


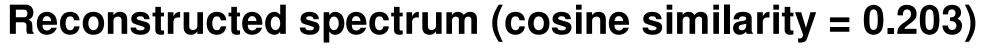


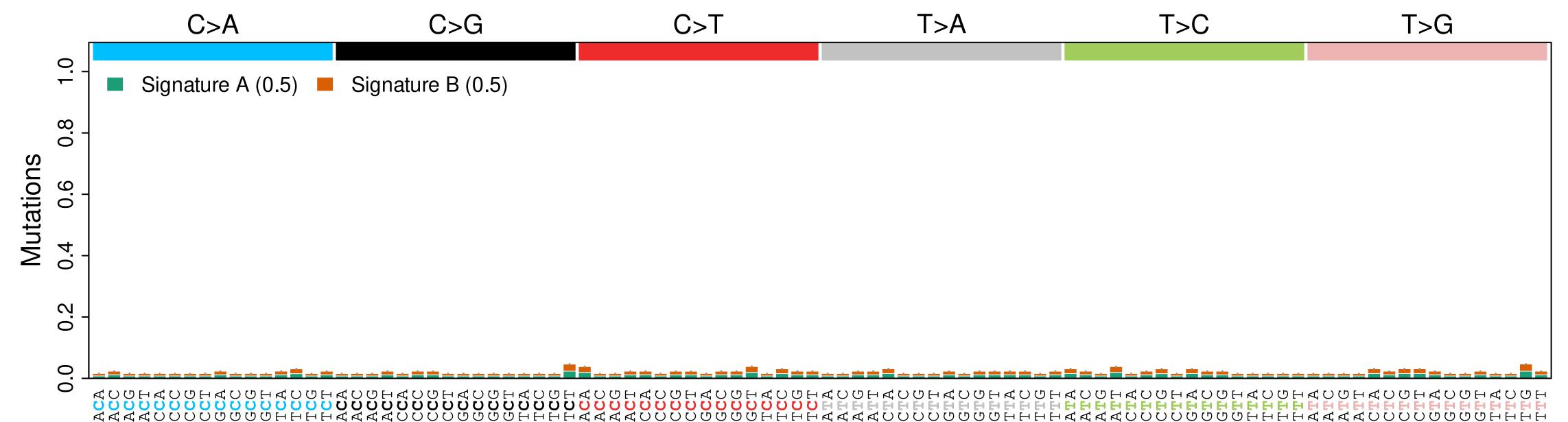


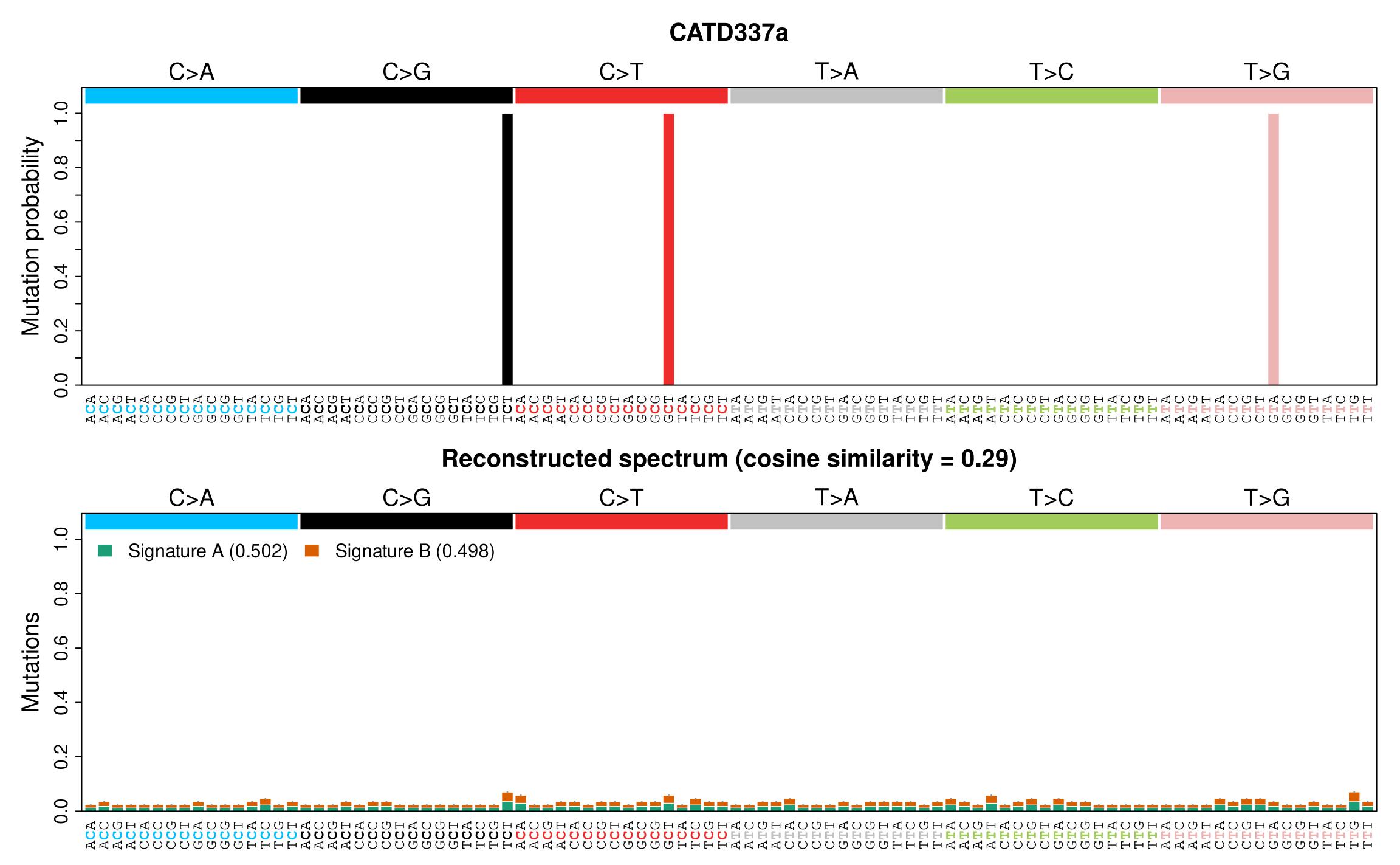








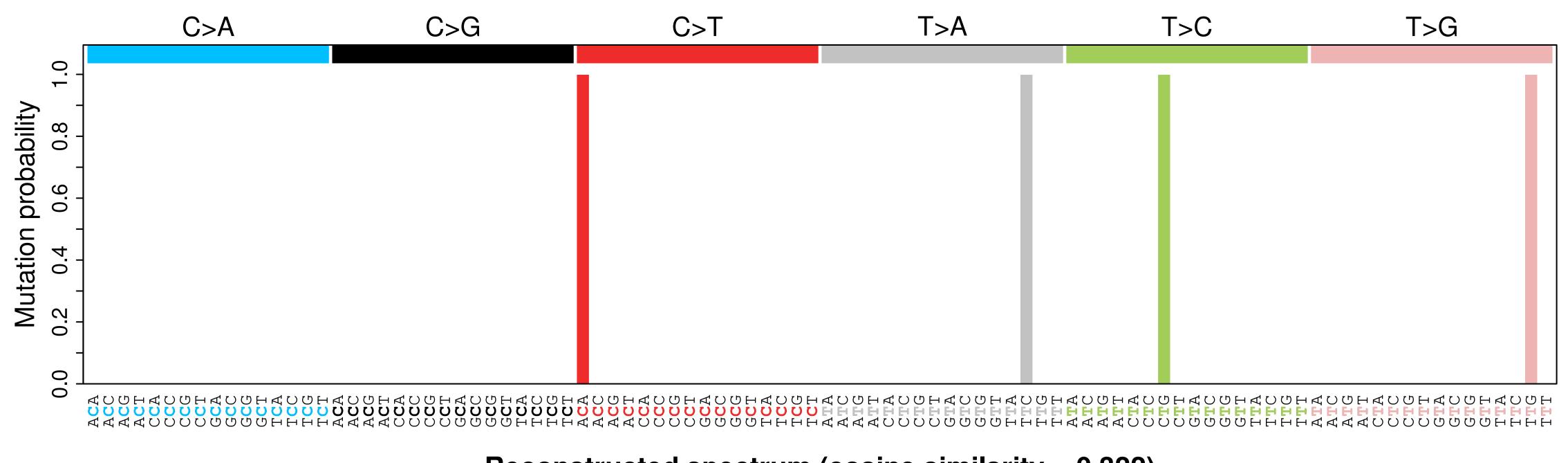




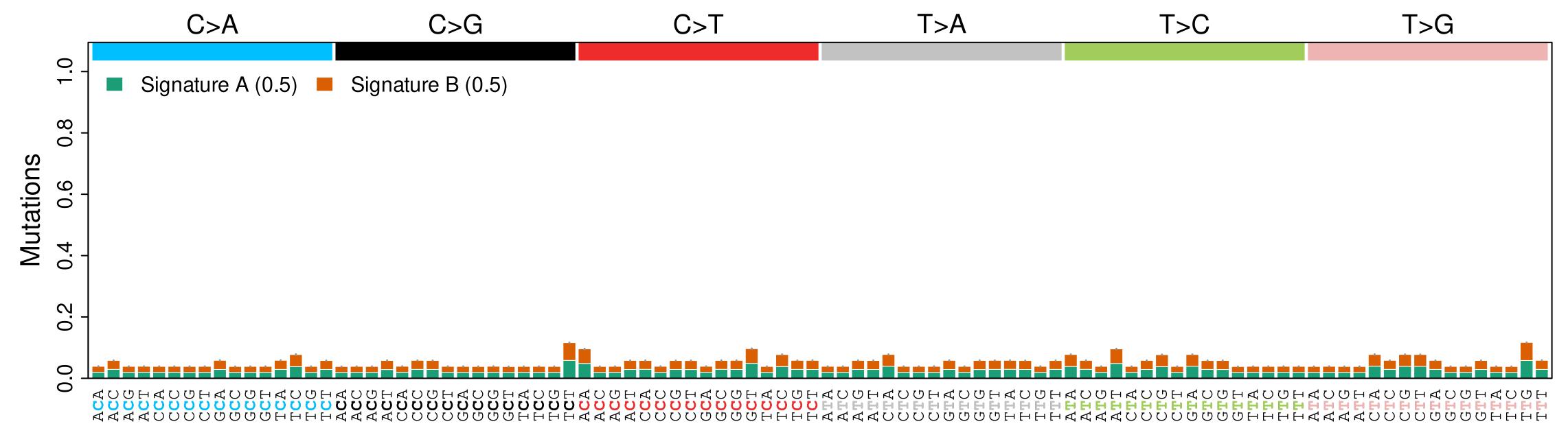
# CATD331a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.177)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.502) Signature B (0.498) 5 Mutations 5 0

# CATD0550a (3 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 = 0.177)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.498) Signature B (0.502) 5 Mutations 5 0



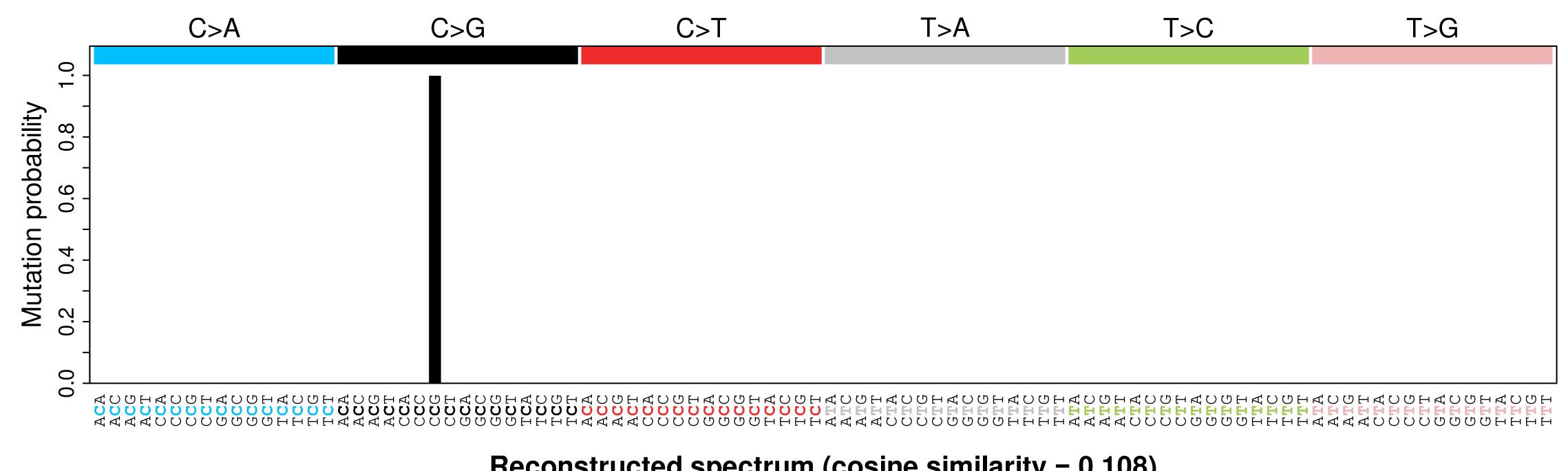


# Reconstructed spectrum (cosine similarity = 0.322)

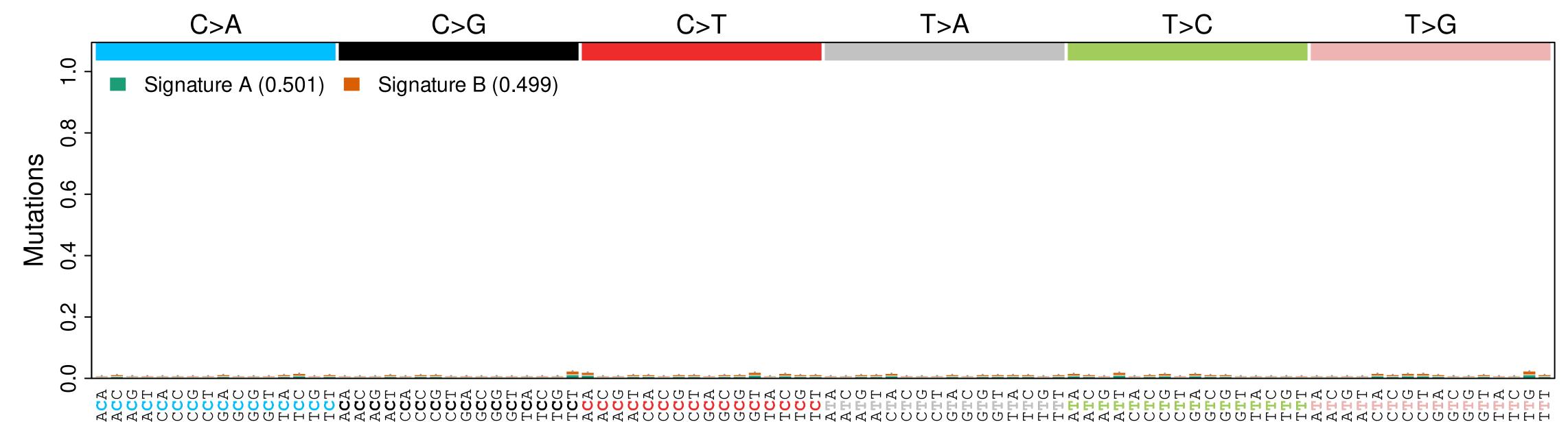


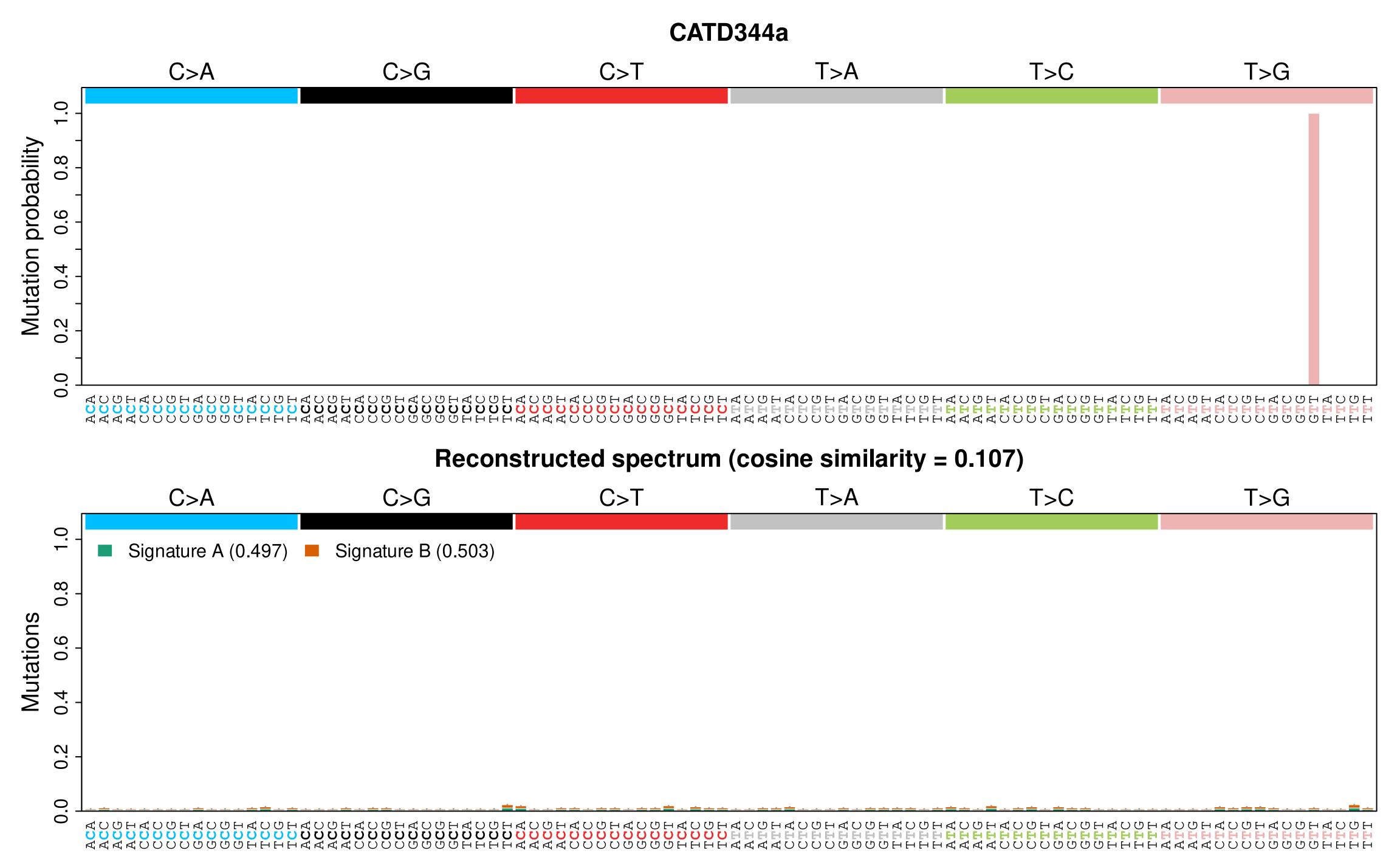
# CATD0557a (5 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.272)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.496) Signature B (0.504) 5 Mutations 2 0



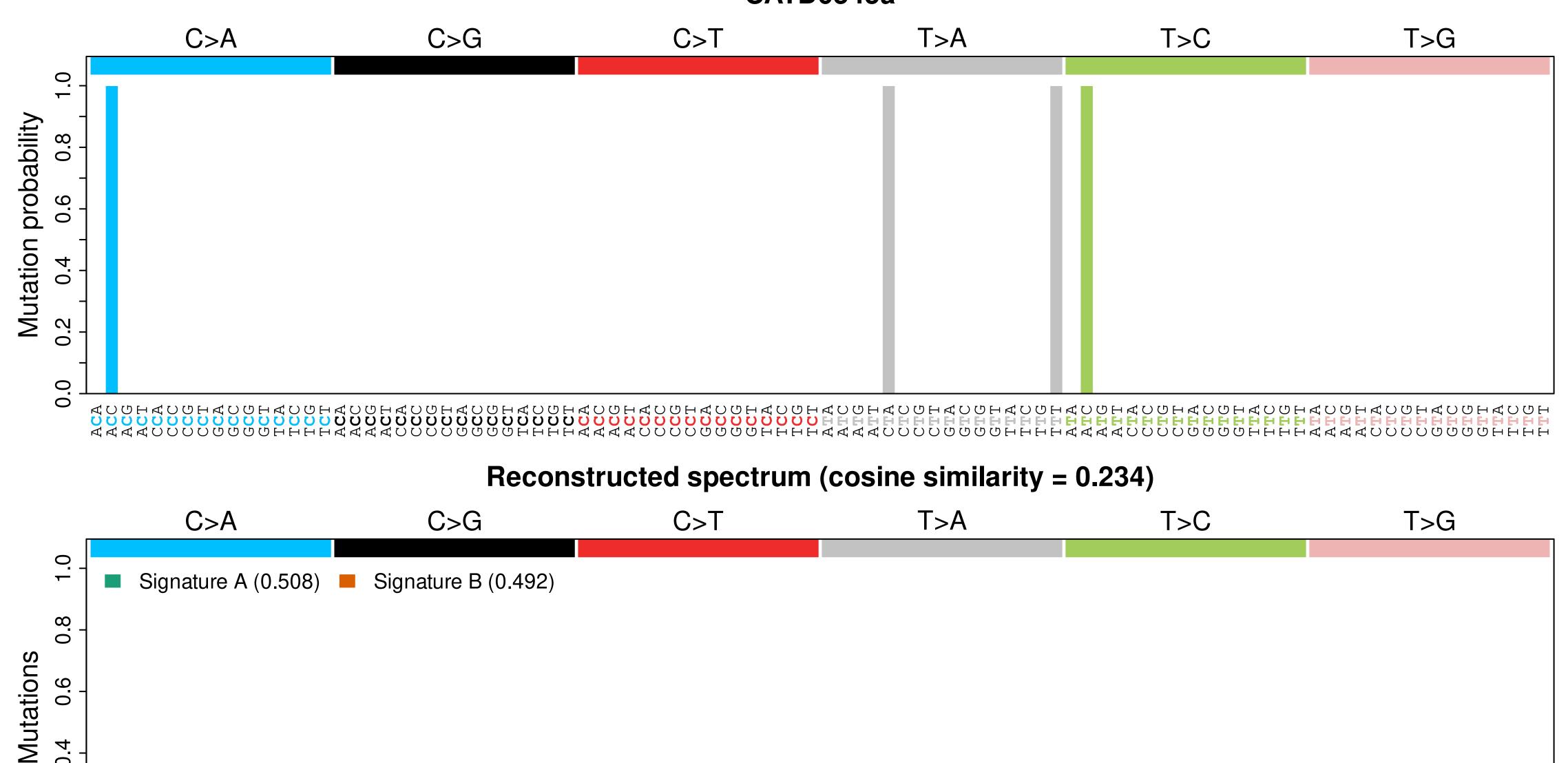


### Reconstructed spectrum (cosine similarity = 0.108)



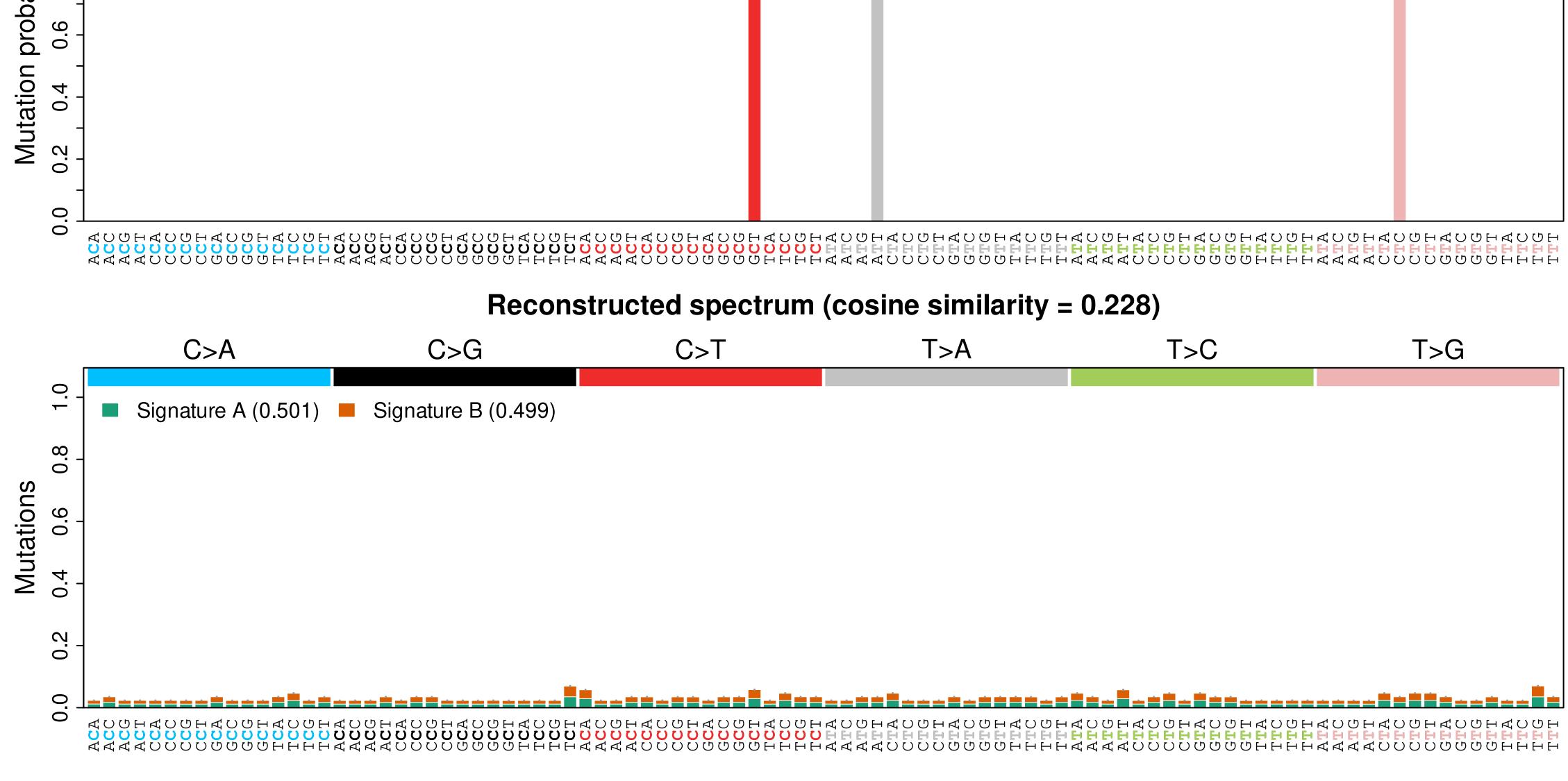




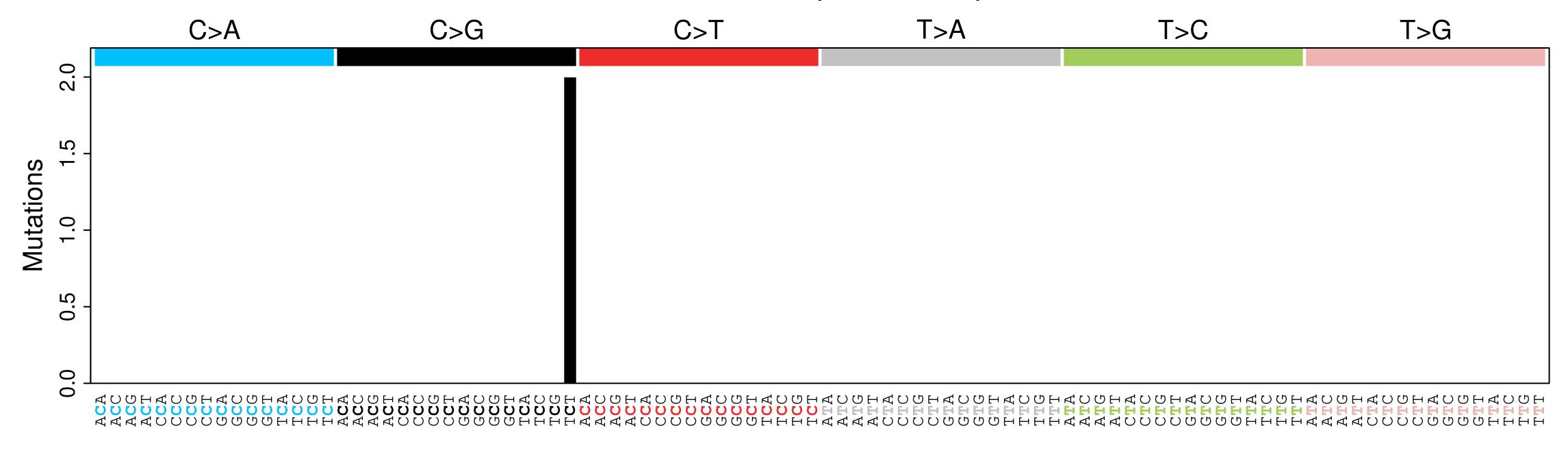


0.2

### CATD0554a C>G T>C T>G C>A C>T T>A 0 Mutation probability 0.8 0.4 0.2 0.0 Reconstructed spectrum (cosine similarity = 0.228) C>A C>G T>A T>C T>G C>T 1.0 Signature A (0.501) Signature B (0.499) 0.8 9.0



#### CATD0541a (2 mutations)



### **Reconstructed spectrum (cosine similarity = 0.215)**

