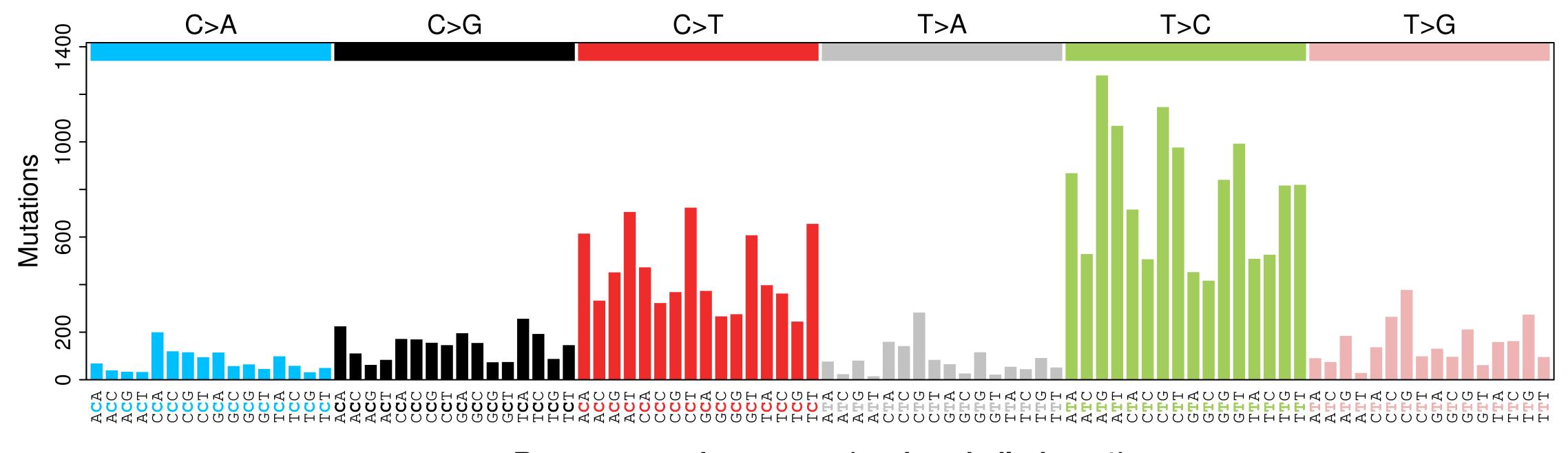
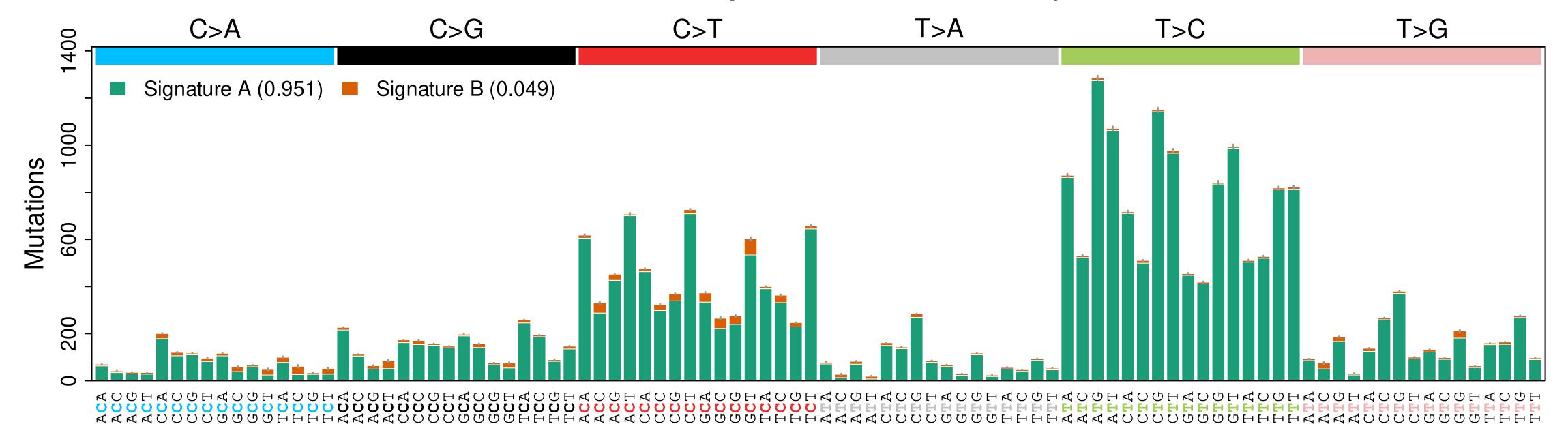
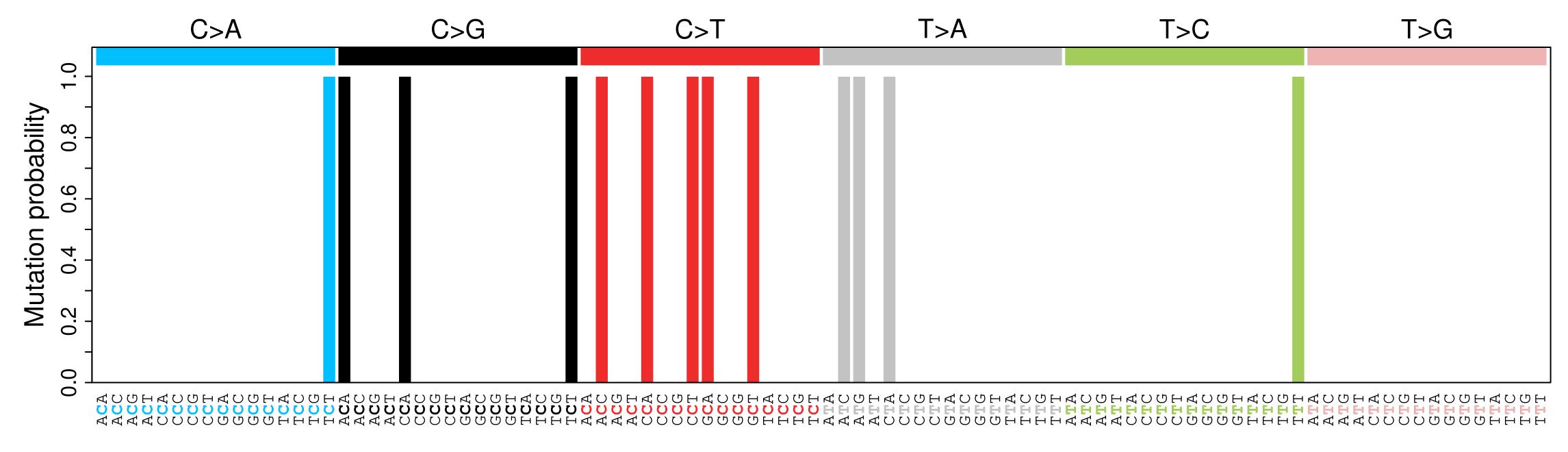
#### **CATD309a (27,083 mutations)**



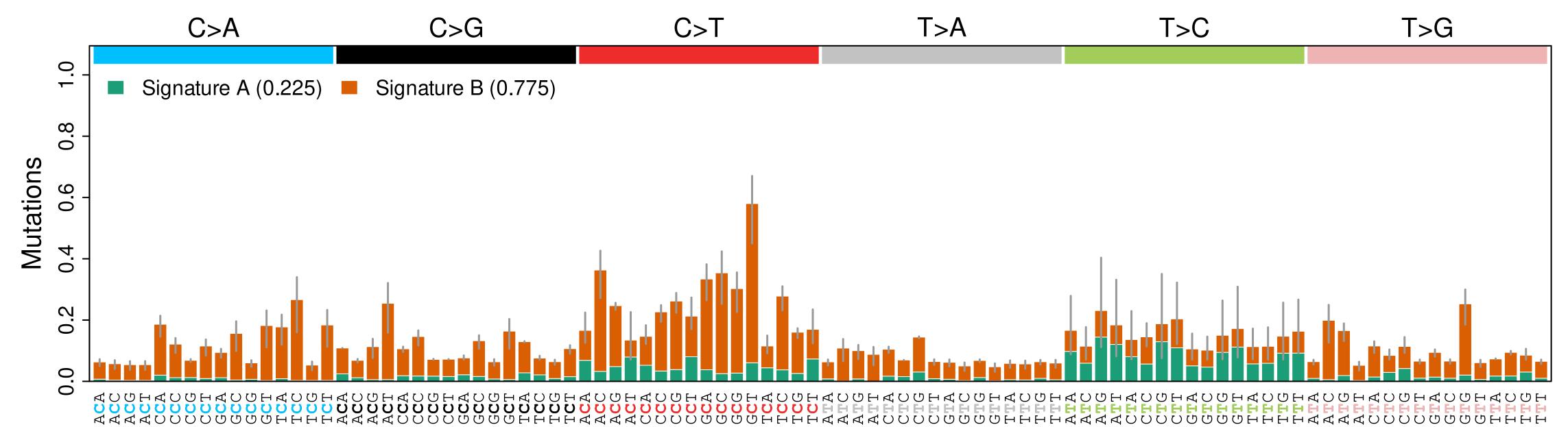
#### Reconstructed spectrum (cosine similarity = 1)



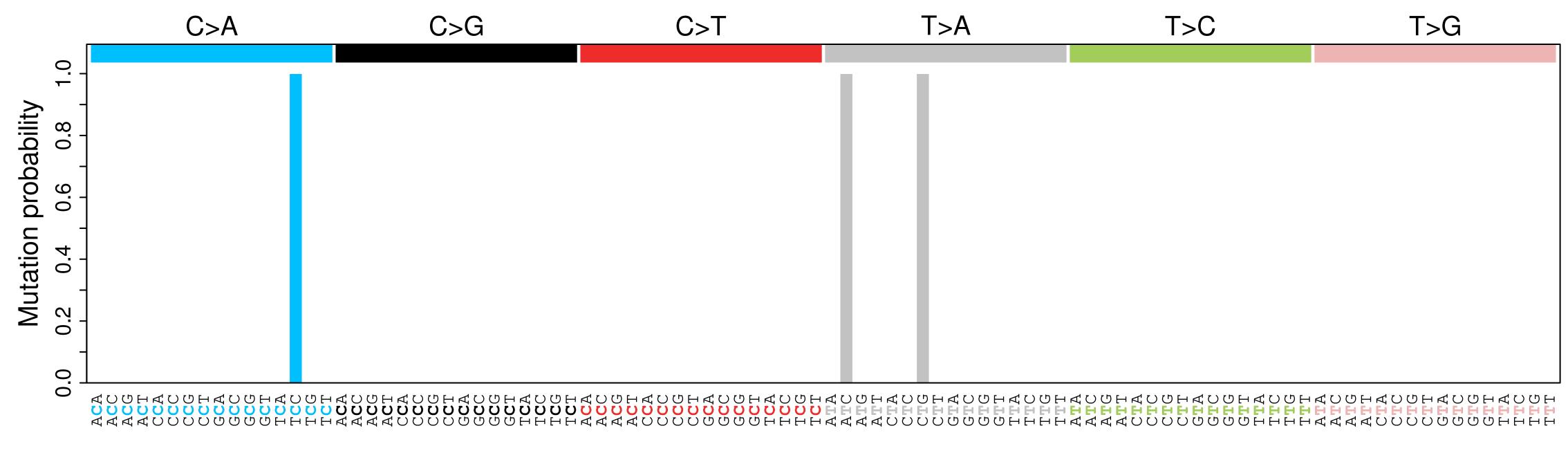
#### CATD319a



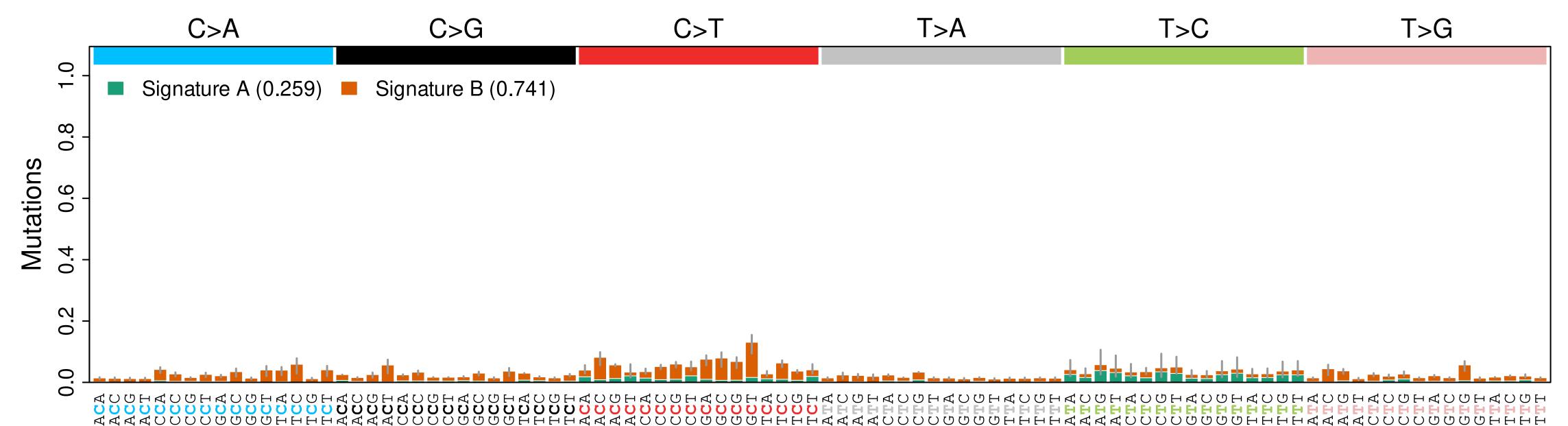
#### Reconstructed spectrum (cosine similarity = 0.462)





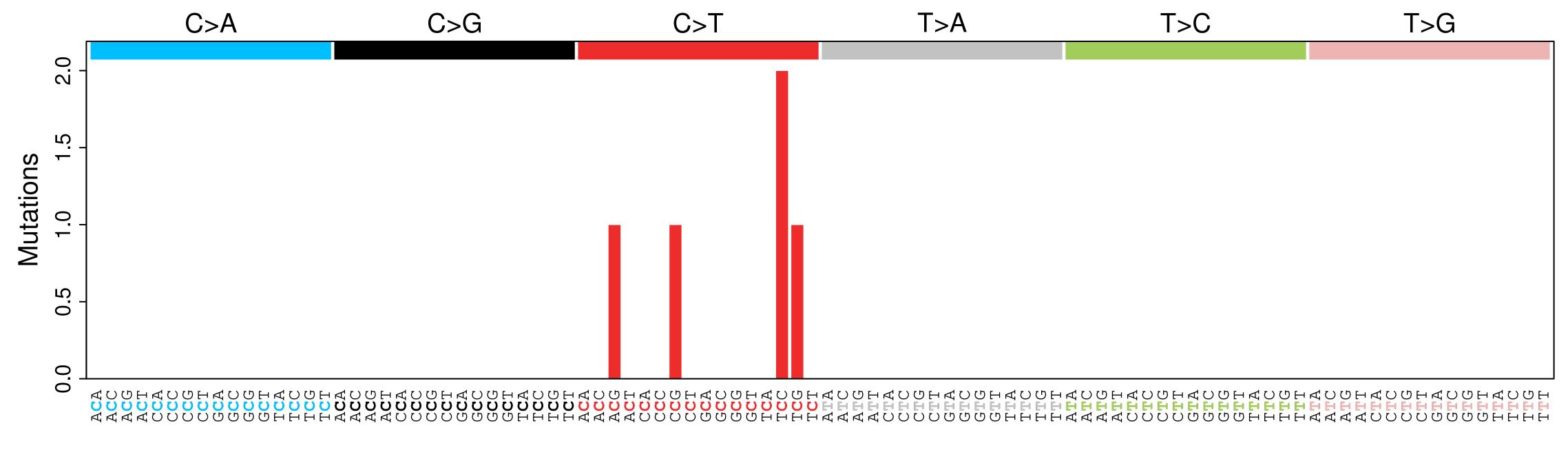


#### Reconstructed spectrum (cosine similarity = 0.186)

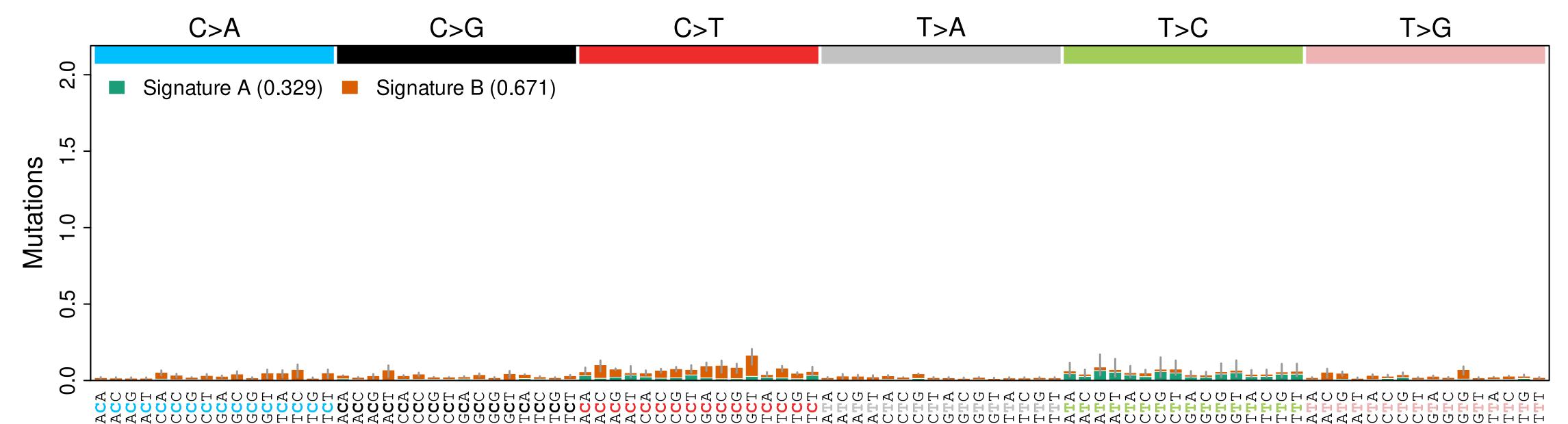


## CATD297a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.329)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.679) Signature B (0.321) 5 Mutations 2 0

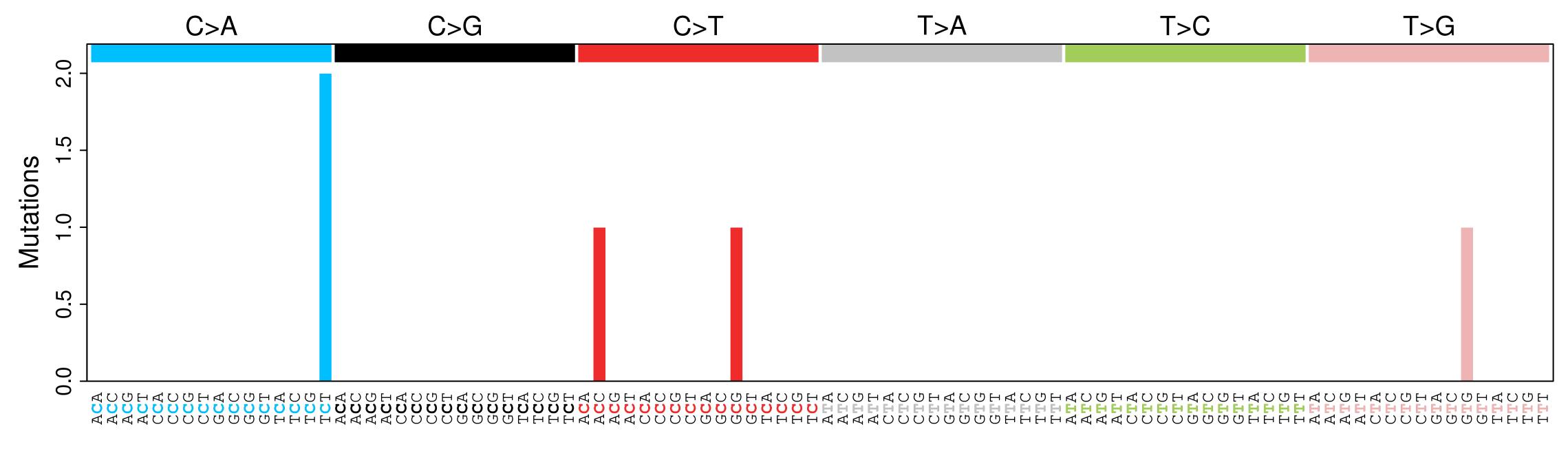
# CATD312a (5 mutations)



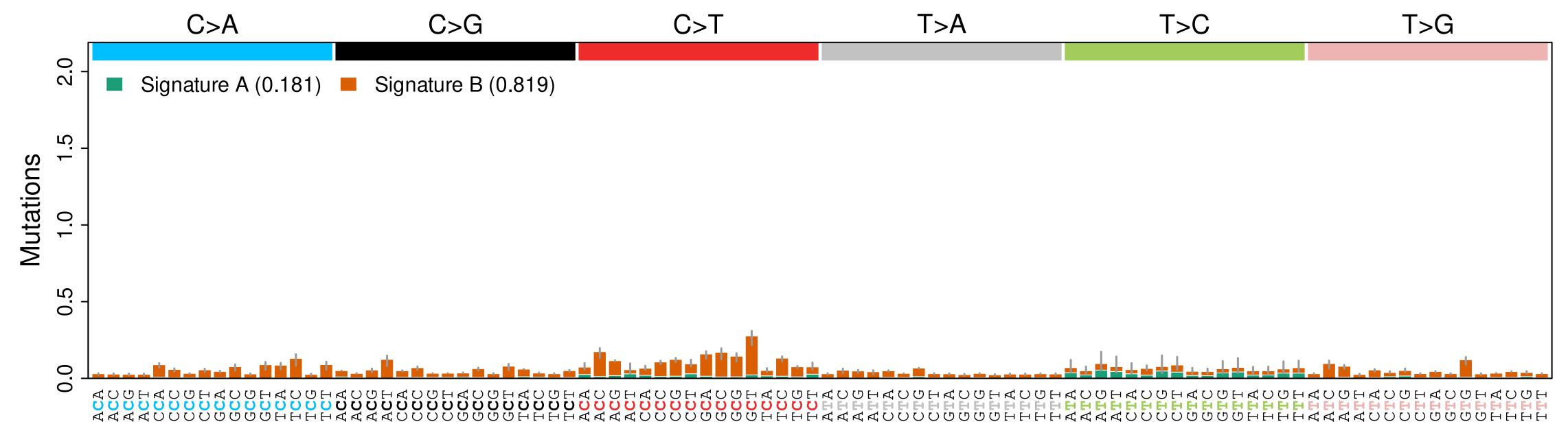
#### **Reconstructed spectrum (cosine similarity = 0.284)**



#### CATD323a (5 mutations)

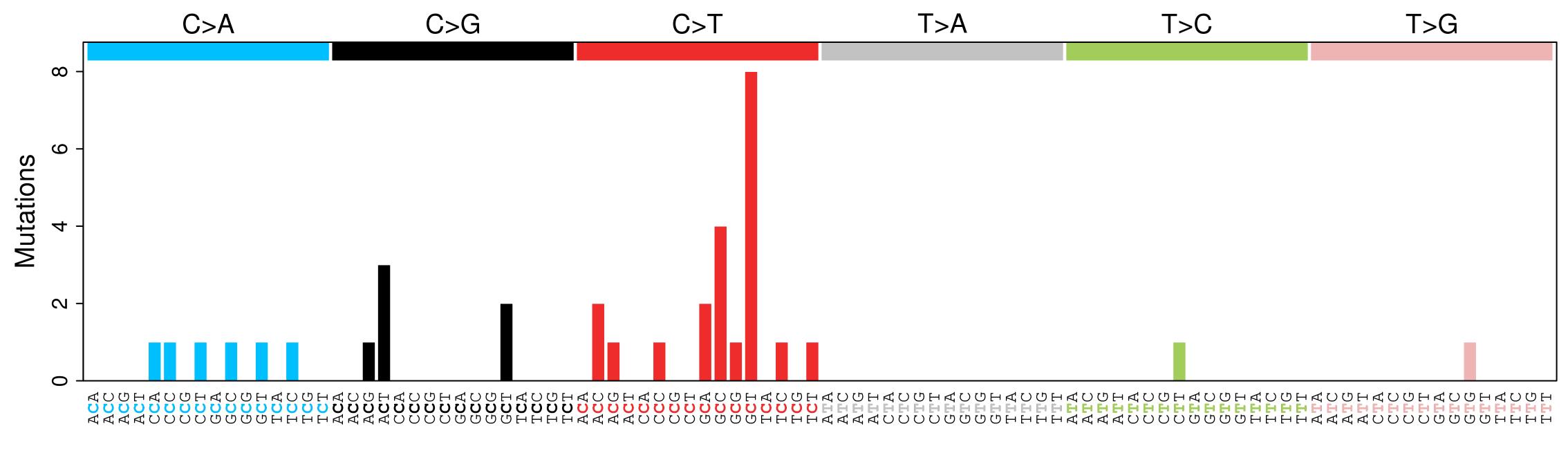


#### Reconstructed spectrum (cosine similarity = 0.319)

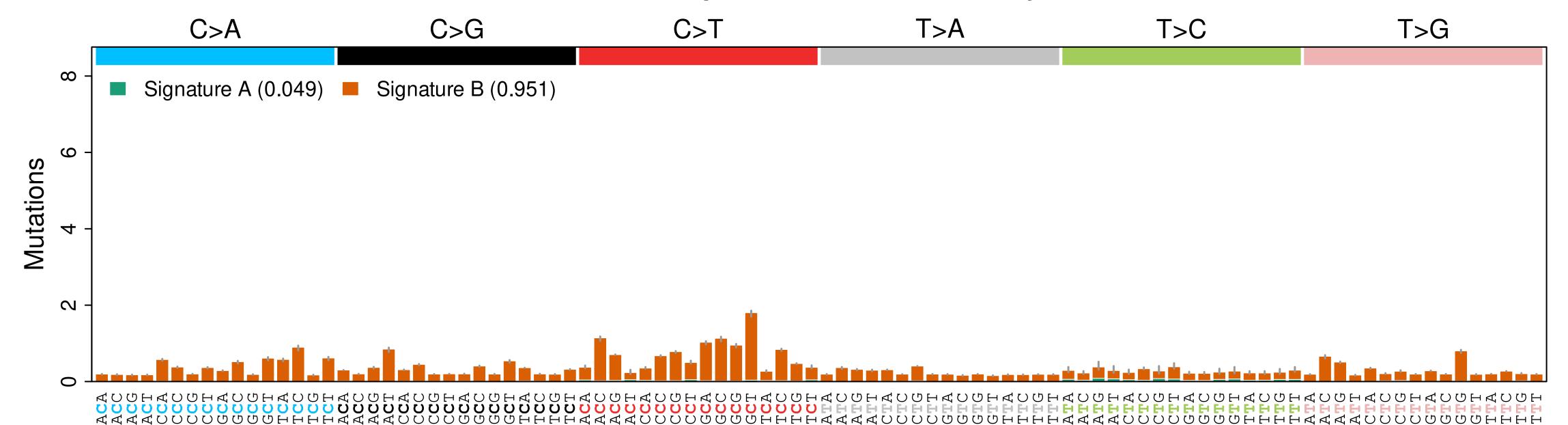


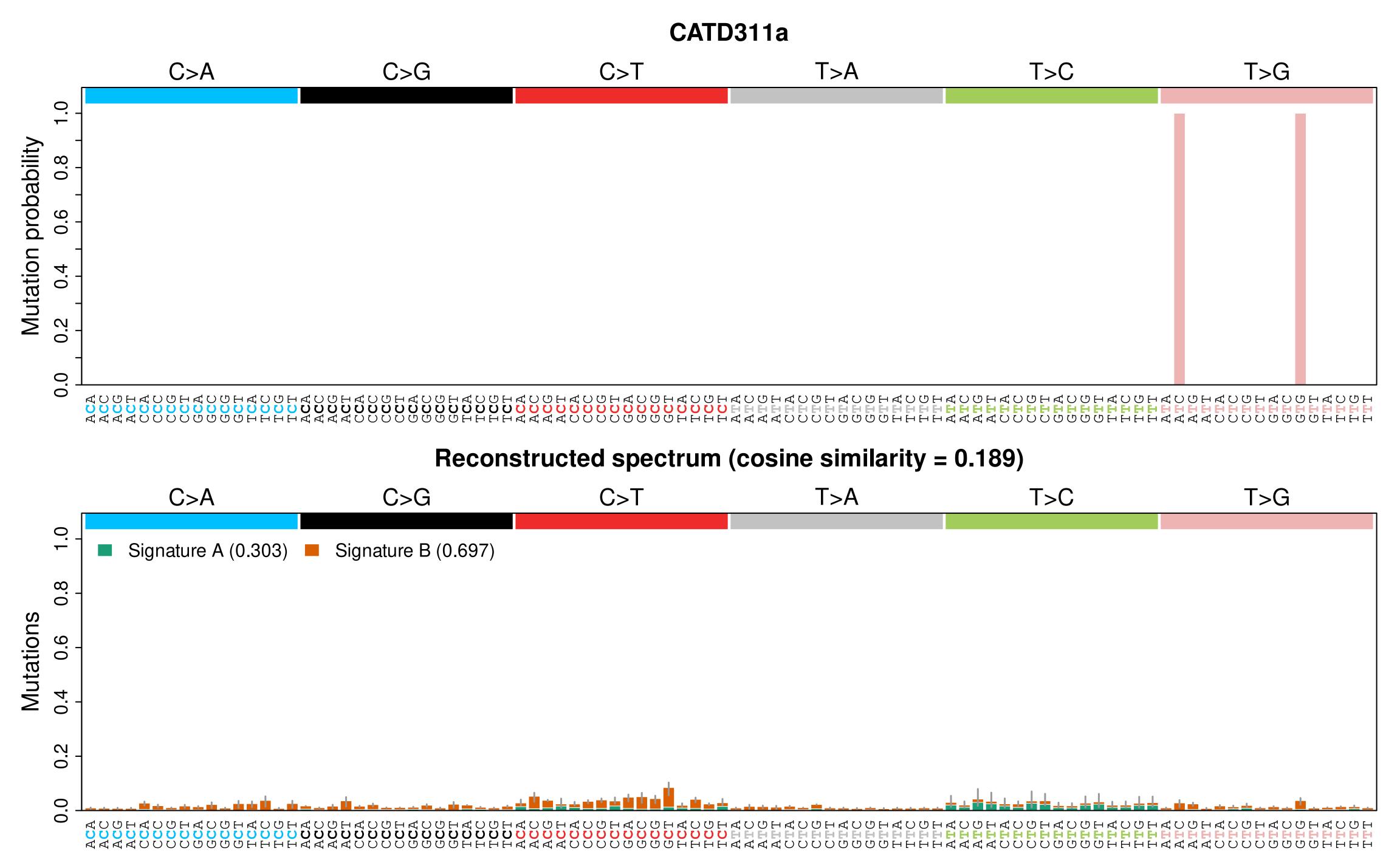
### CATD314a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.348)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.618) Signature B (0.382) 5 Mutations 2 0

#### CATD329a (35 mutations)



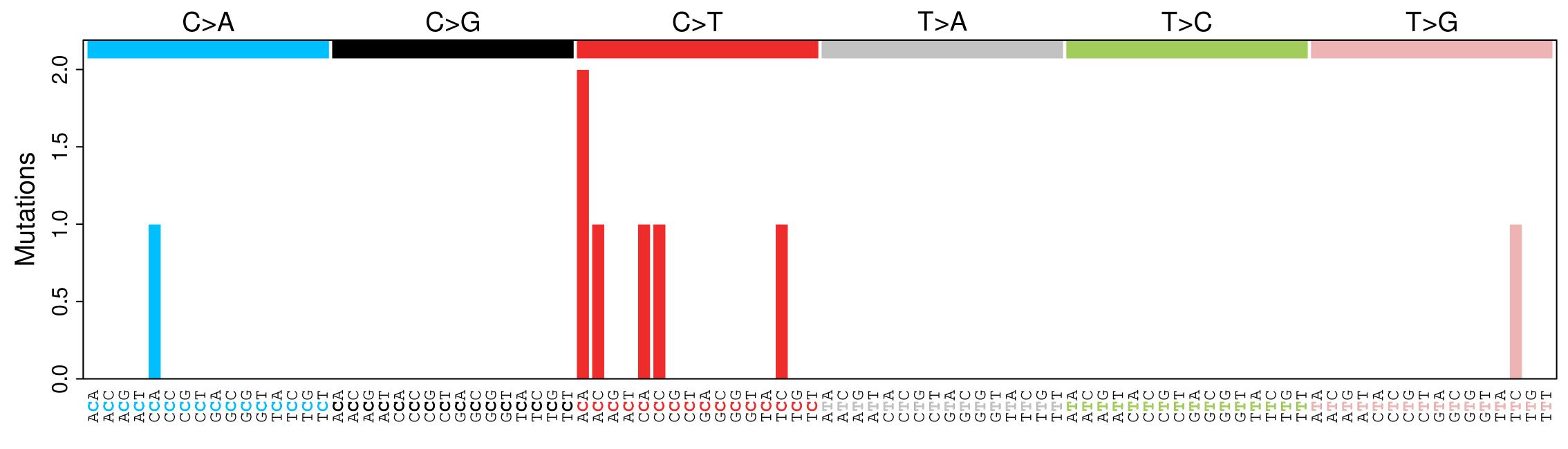
#### **Reconstructed spectrum (cosine similarity = 0.727)**



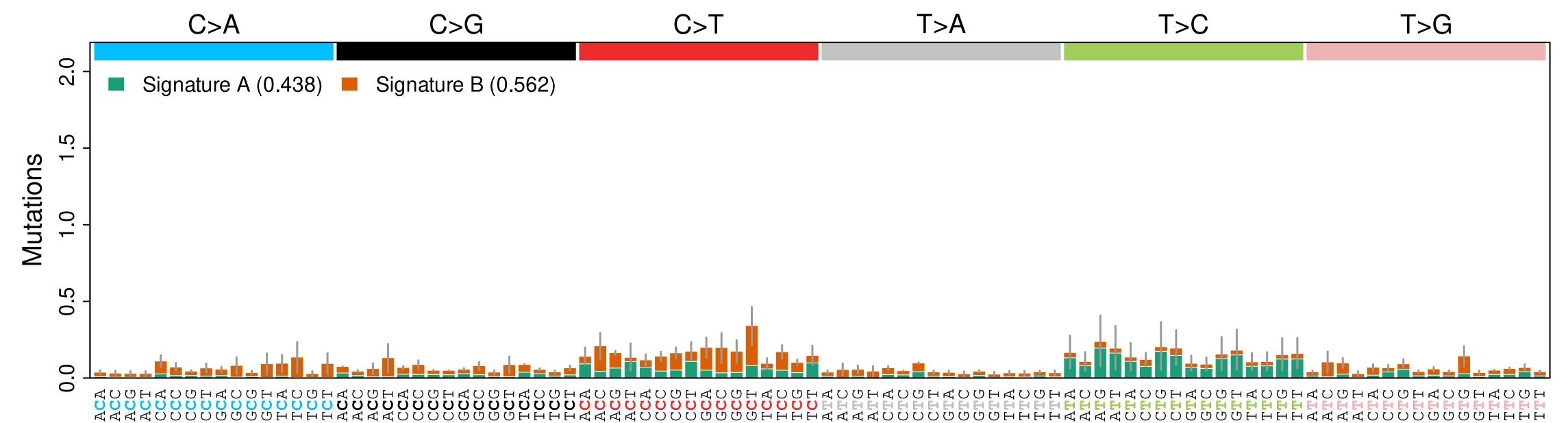


## CATD306a (4 mutations) C>A T>G C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.215)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.255) Signature B (0.745) 5 Mutations 2 0

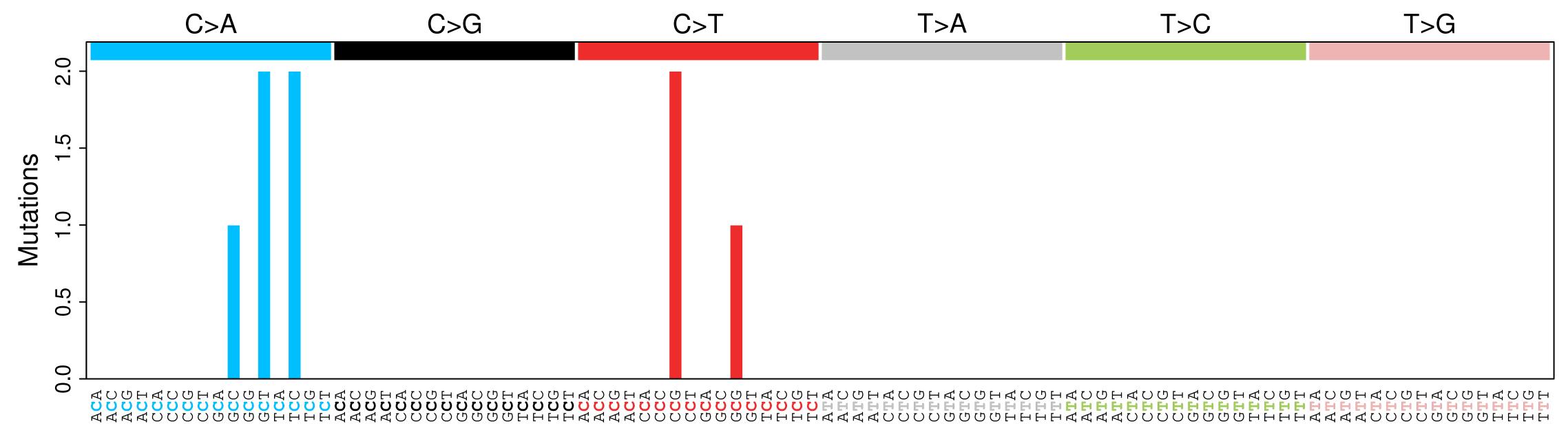
#### CATD320a (8 mutations)



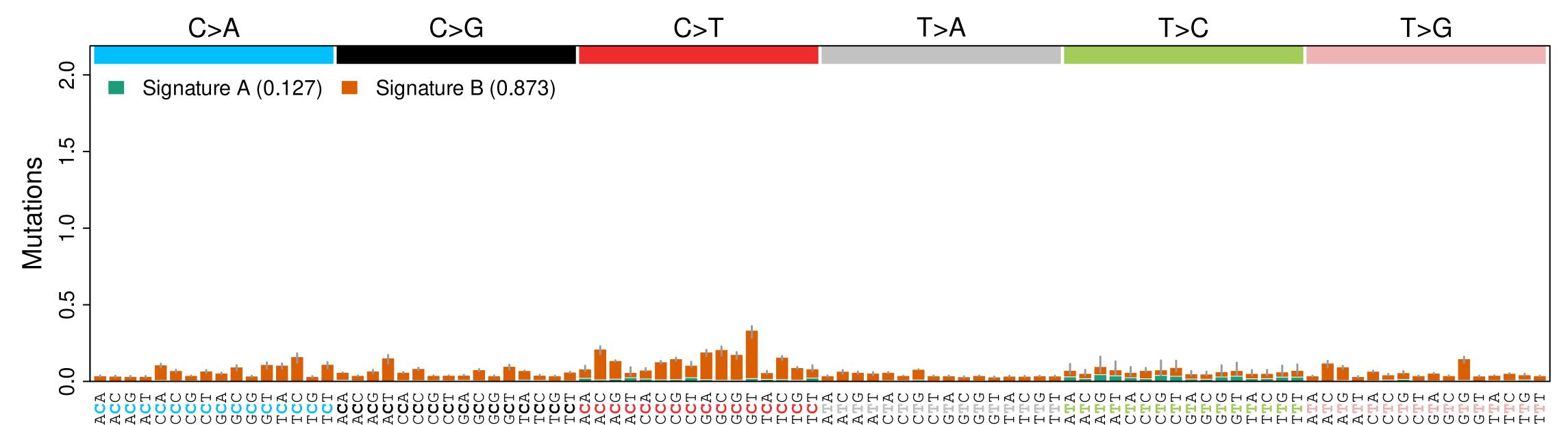
### Reconstructed spectrum (cosine similarity = 0.319)



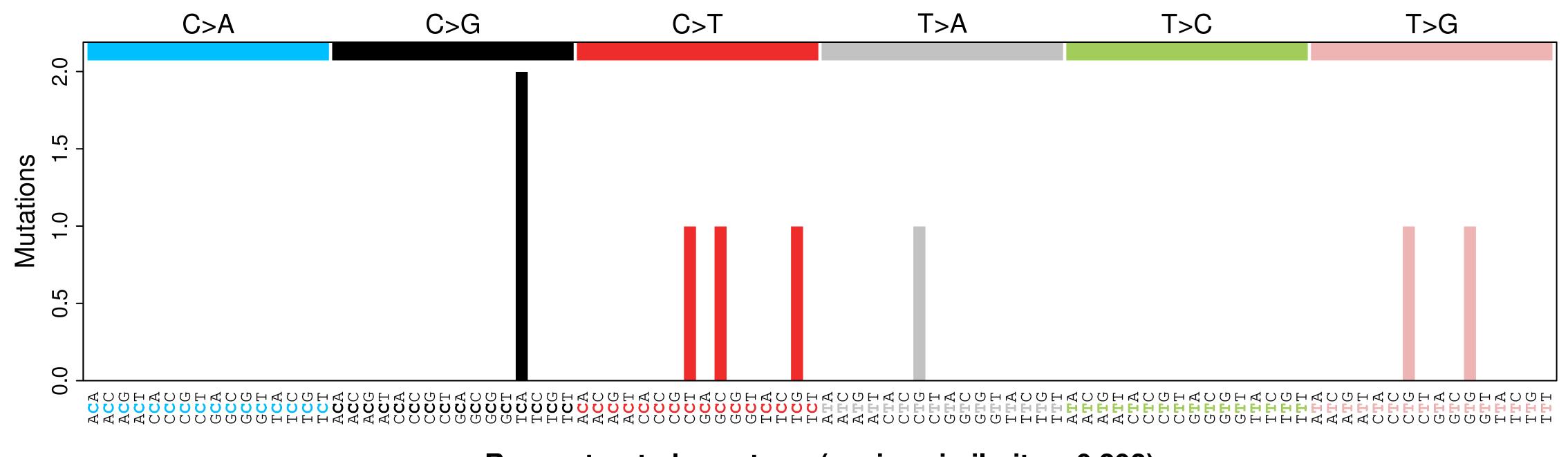
# CATD300a (8 mutations)



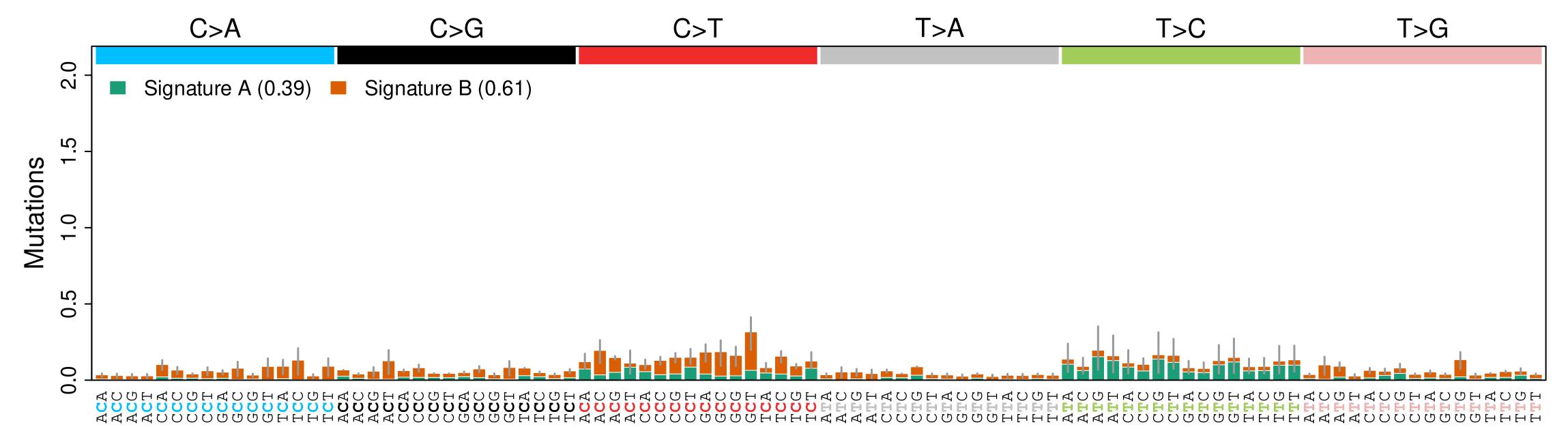
#### **Reconstructed spectrum (cosine similarity = 0.342)**



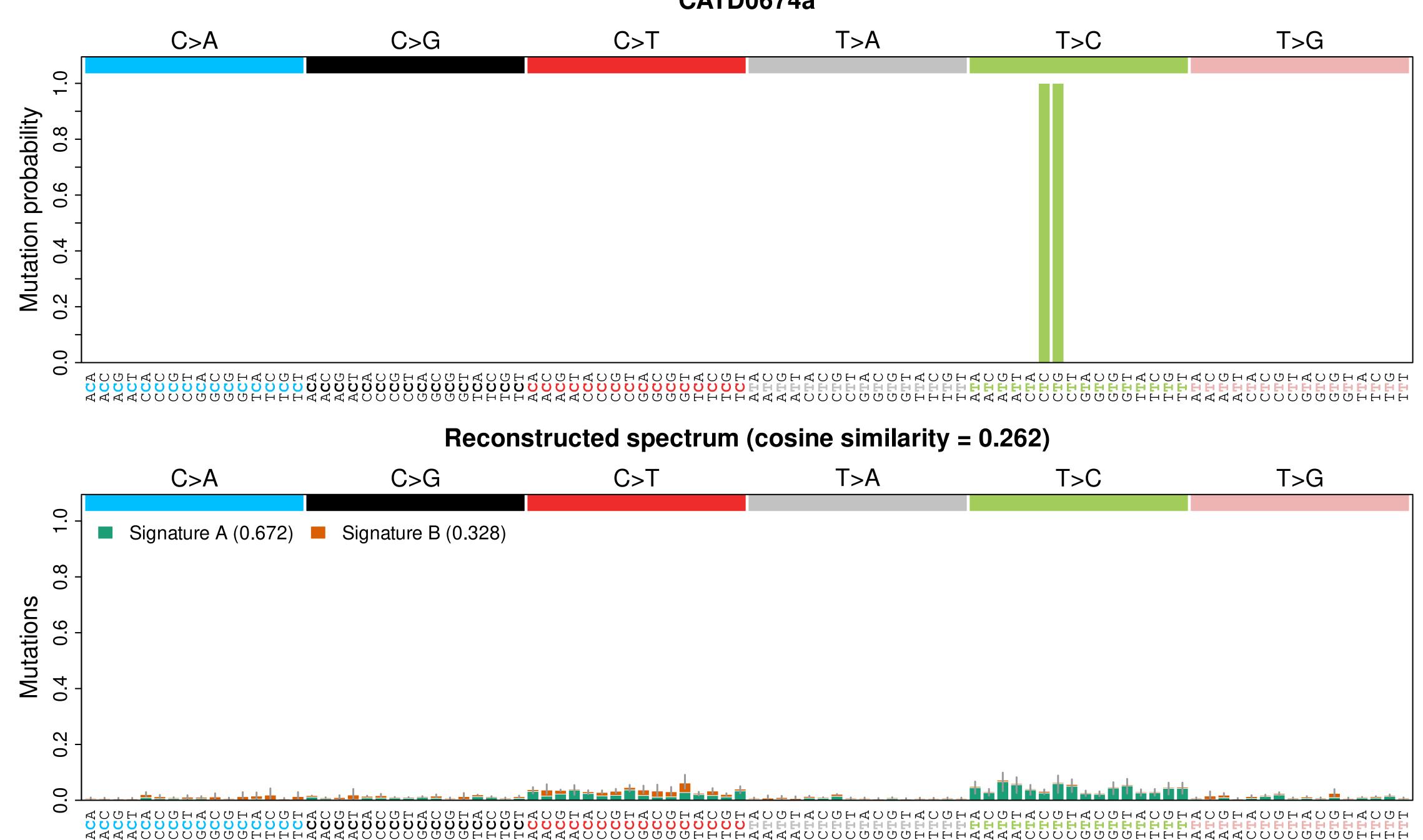
#### CATD328a (8 mutations)



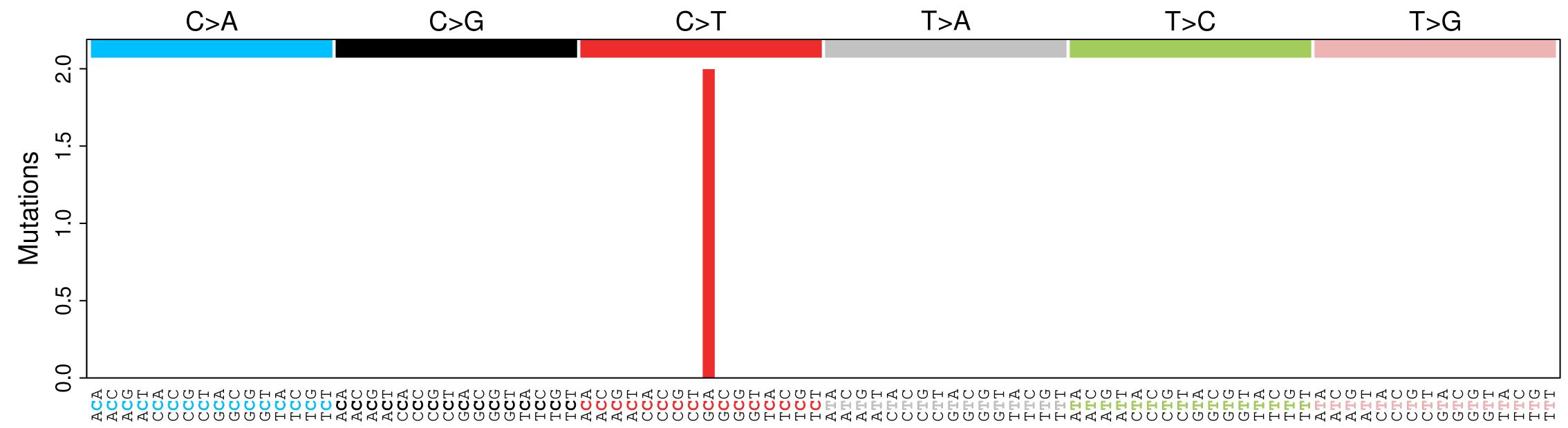
#### Reconstructed spectrum (cosine similarity = 0.292)

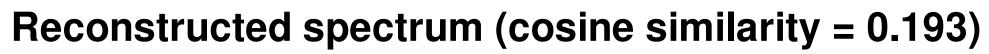


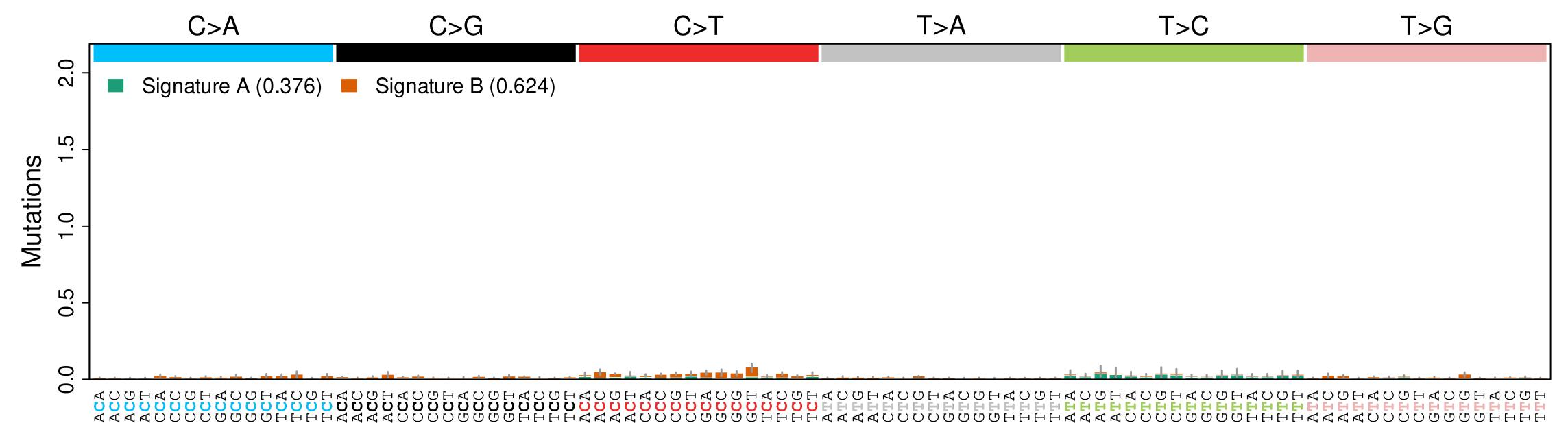




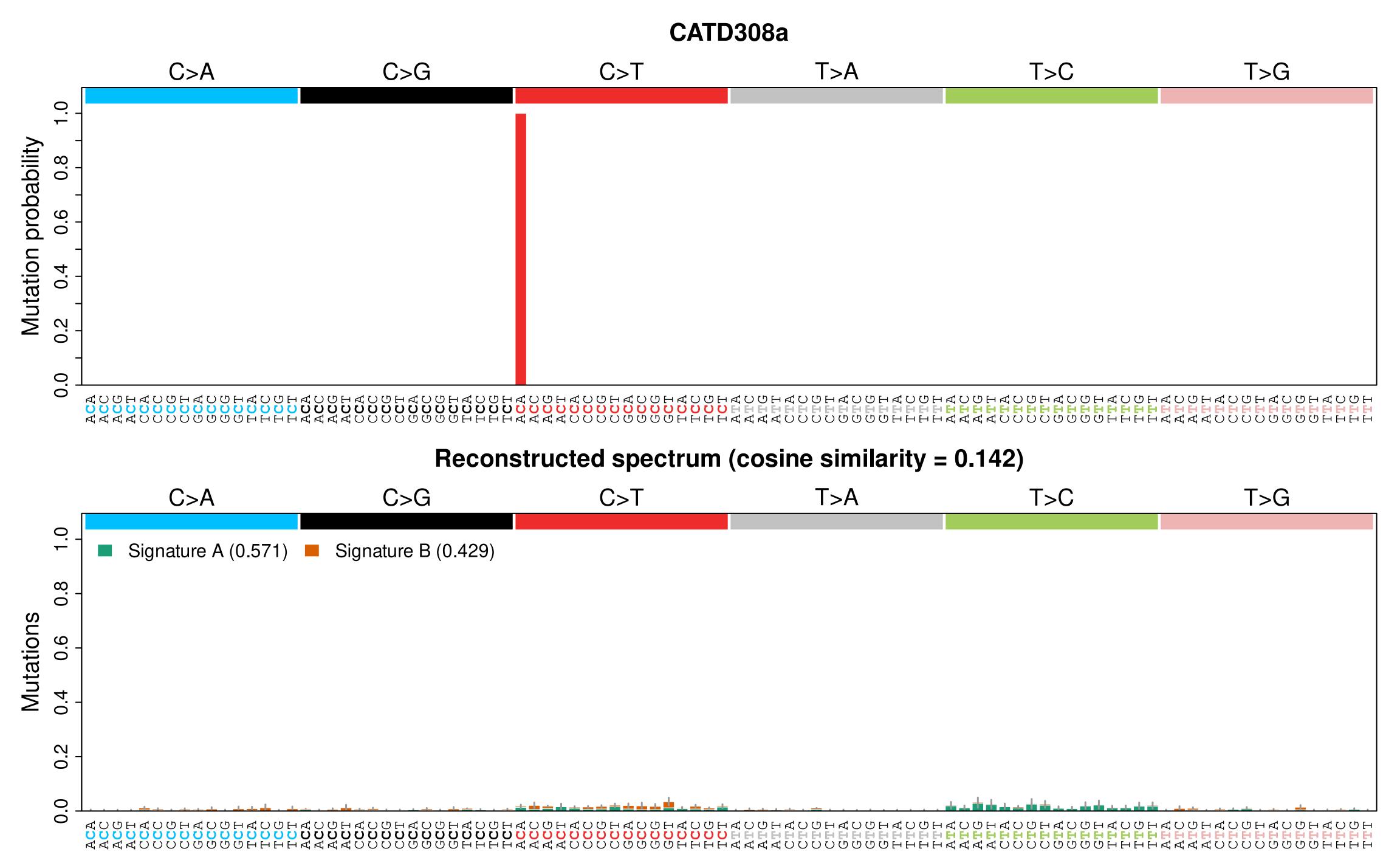
# CATD318a (2 mutations) C>A C>G C>T T>A



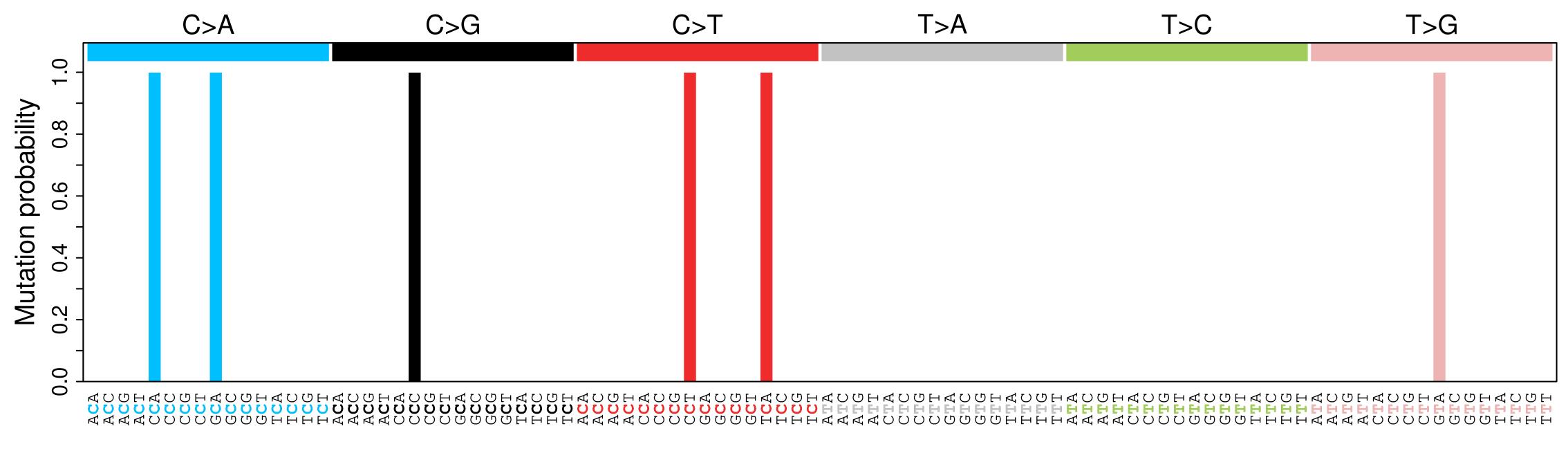


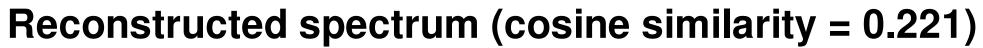


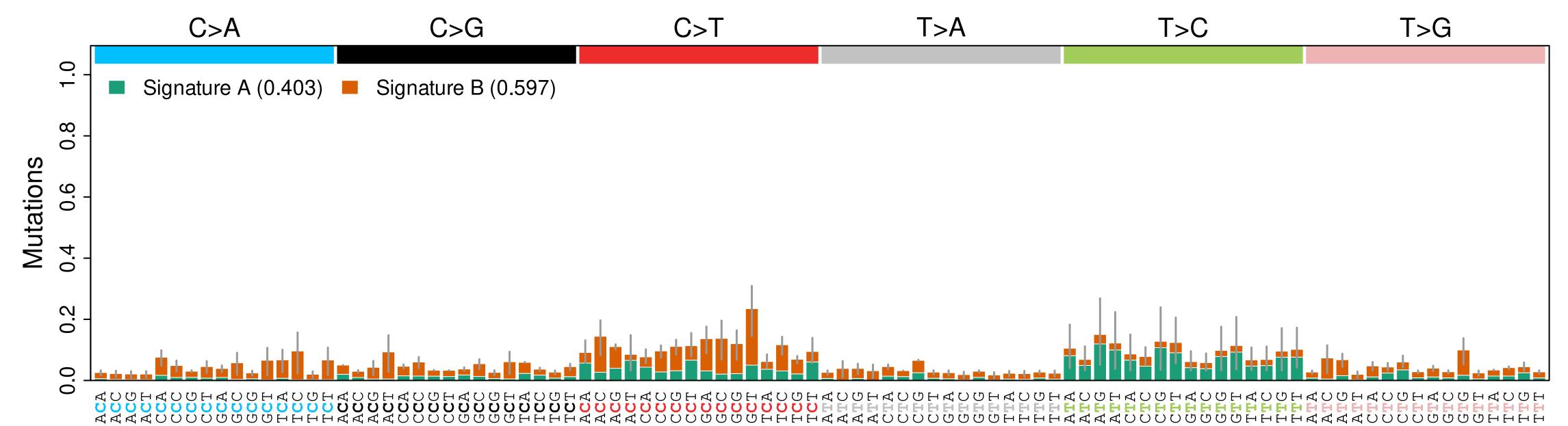
### CATD301a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.281)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.507) Signature B (0.493) 5 Mutations 2 0



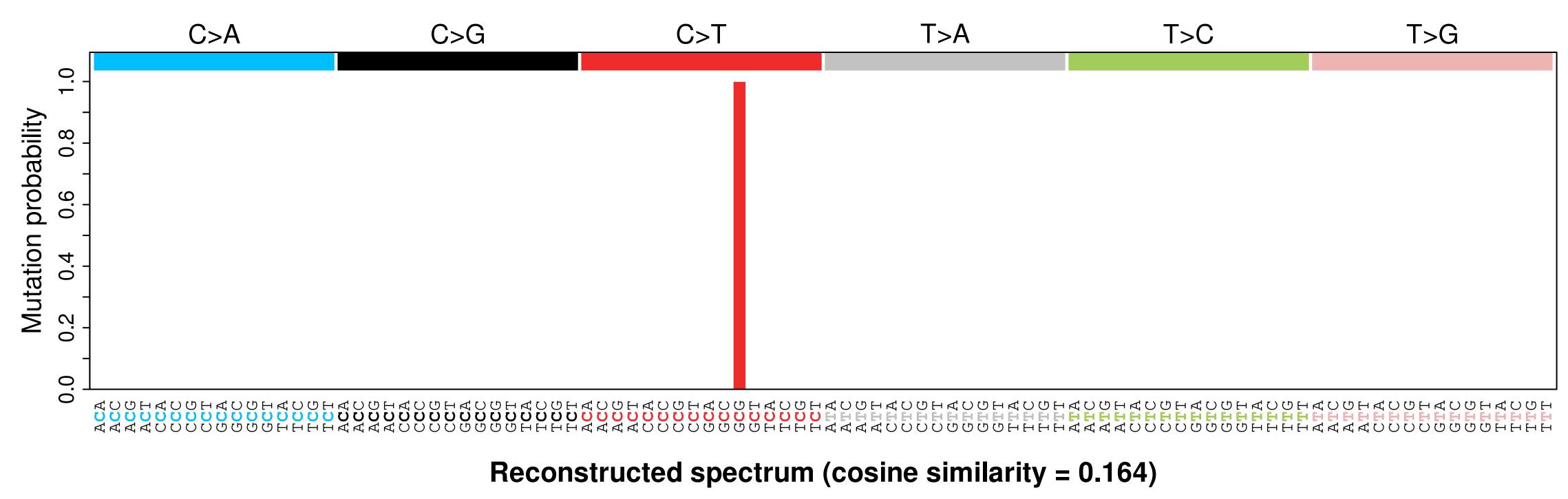
#### CATD296a

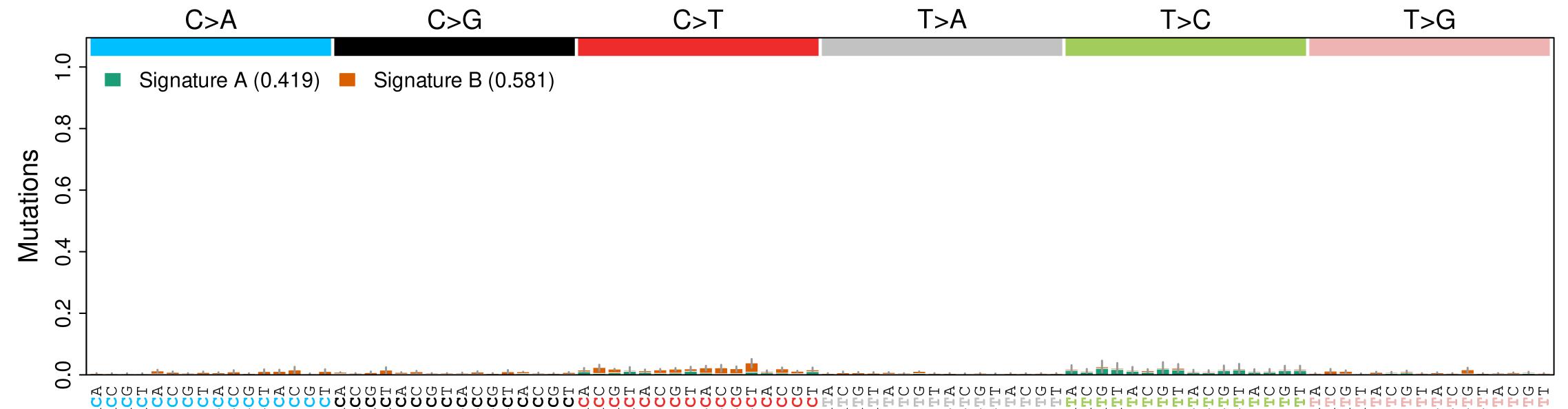




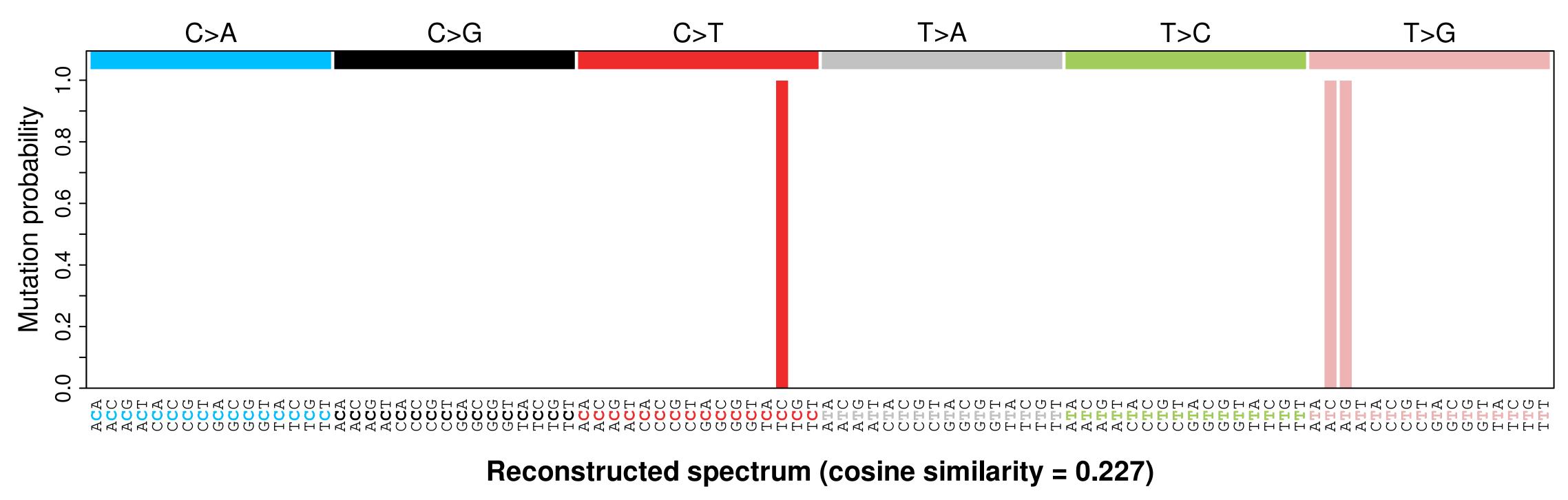


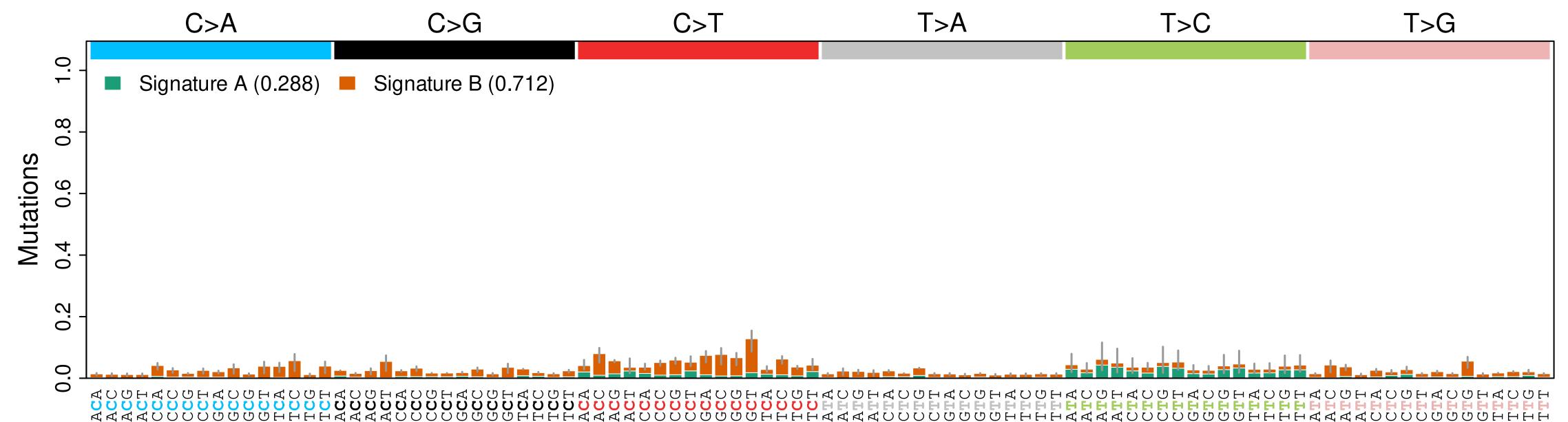








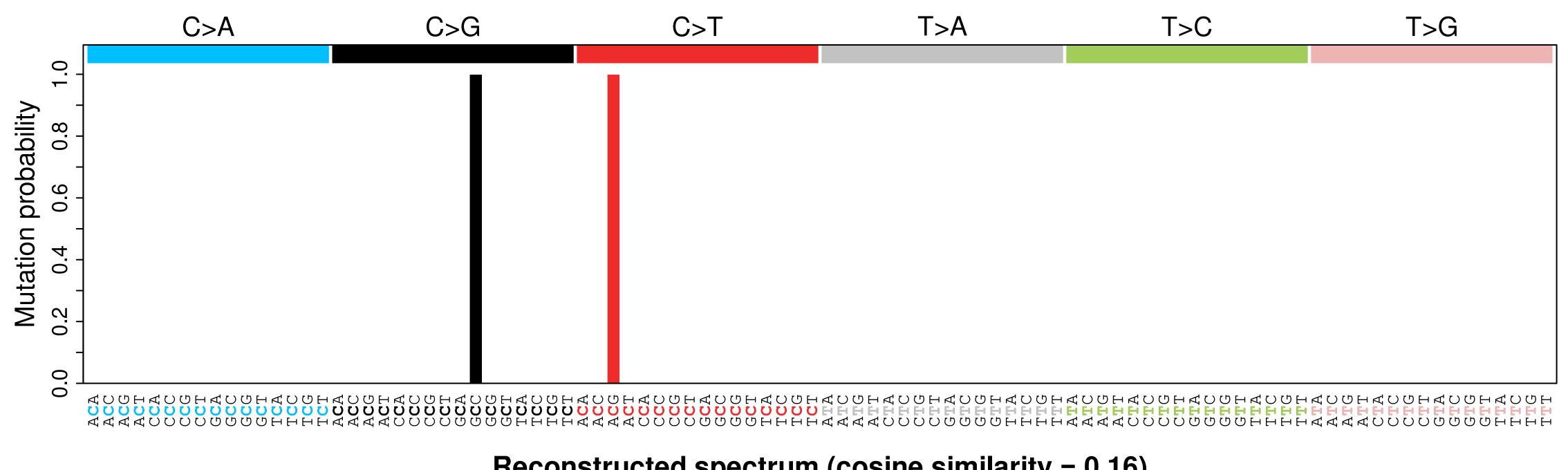


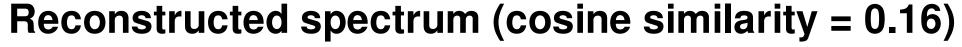


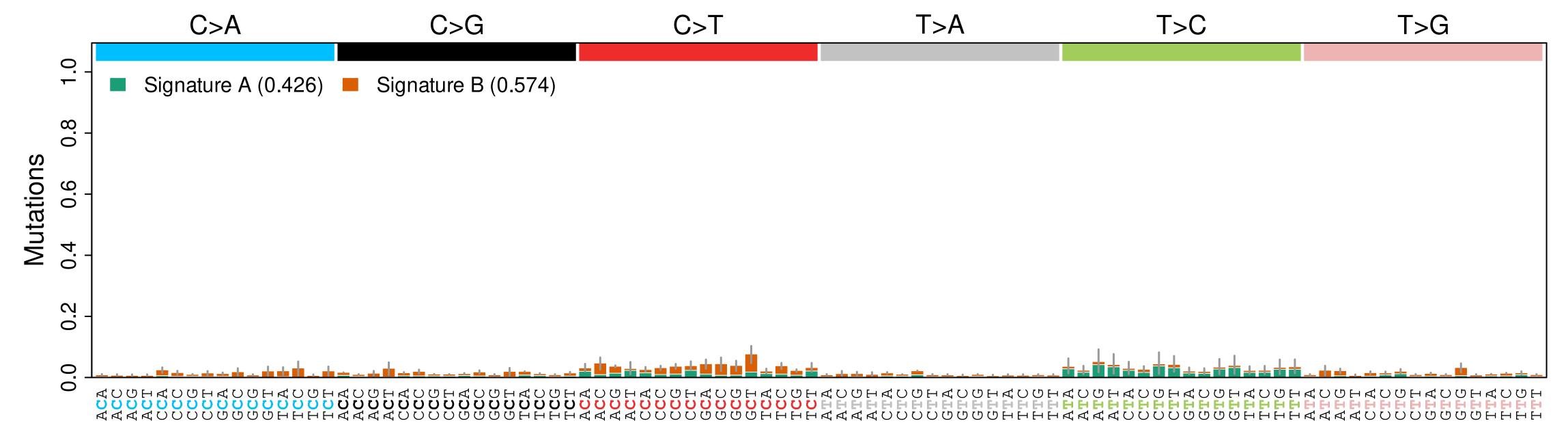
#### CATD326a (6 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.235)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.161) Signature B (0.839) 5 Mutations

0.5

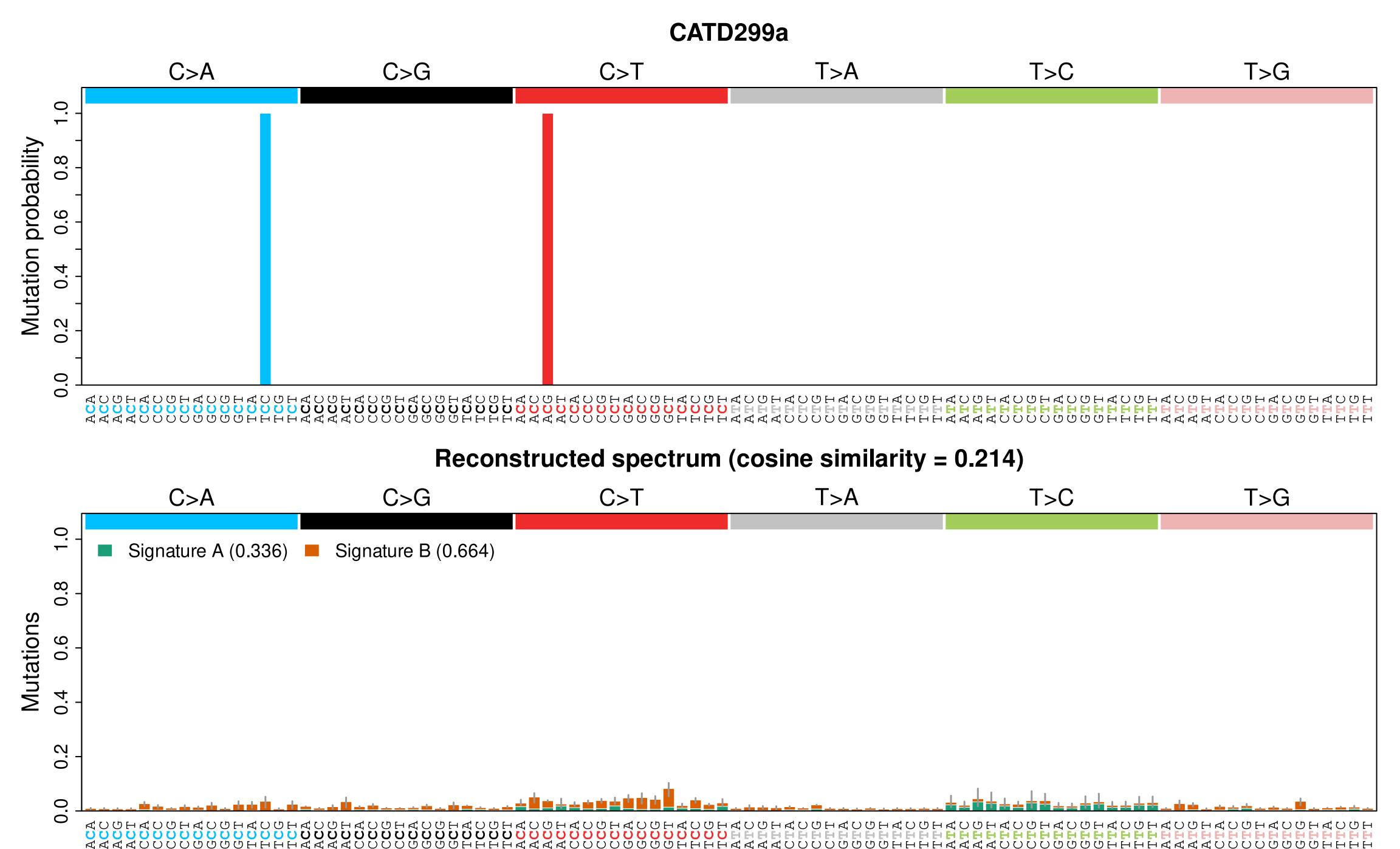


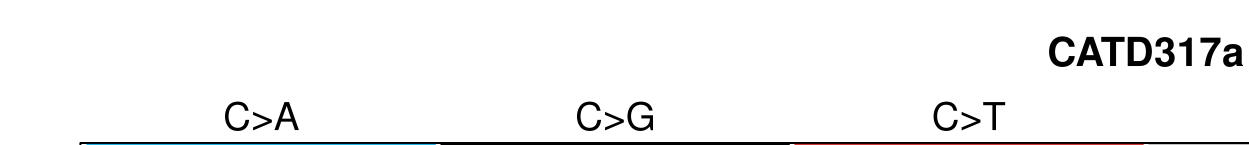


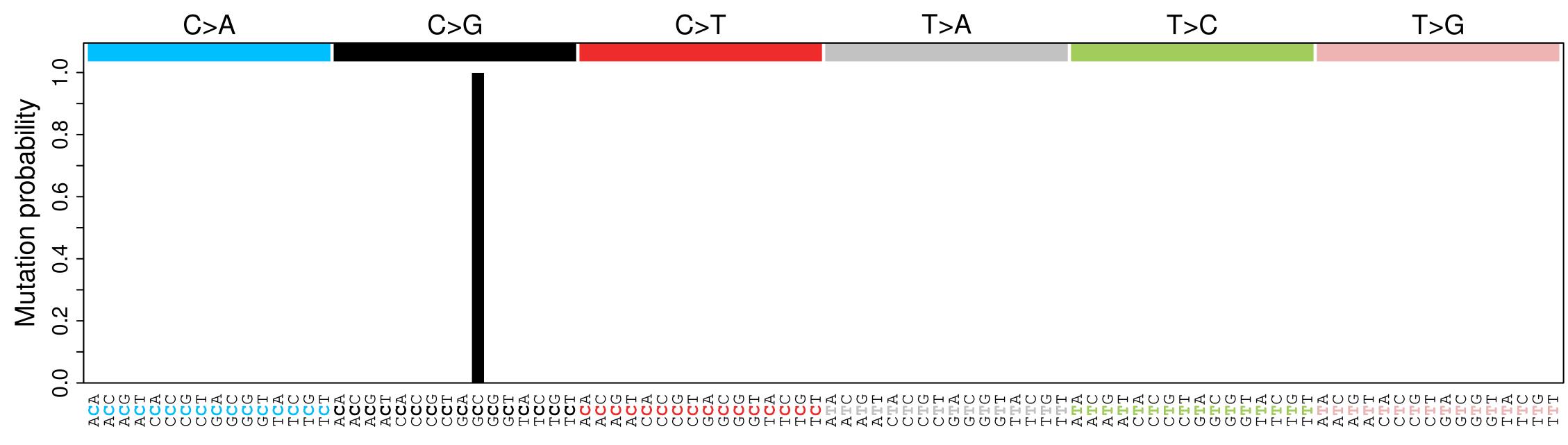




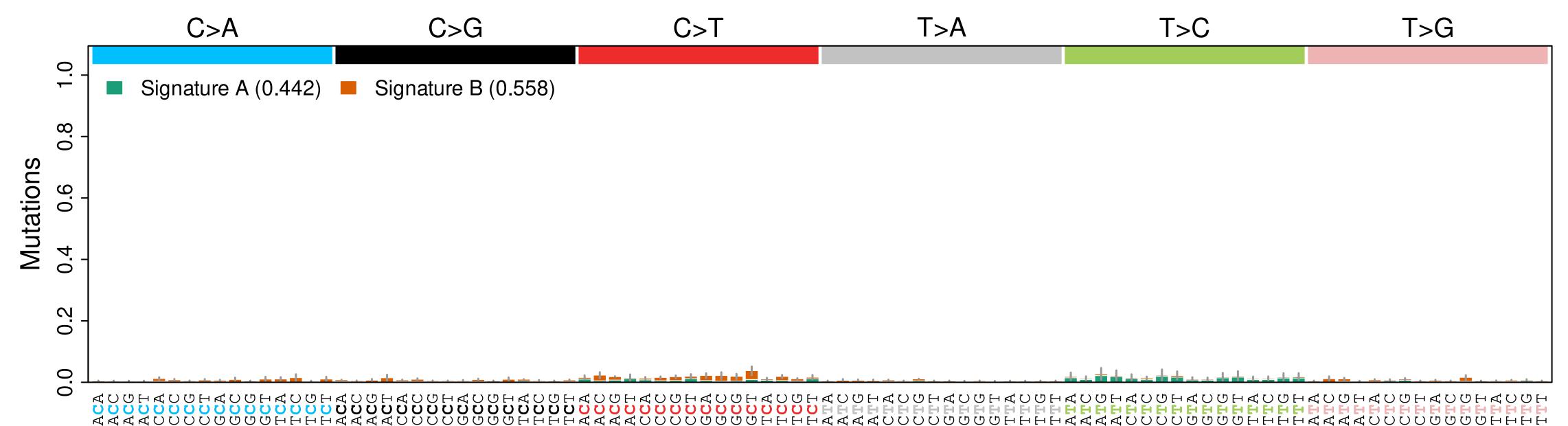
#### CATD304a (2 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.122)** C>G T>C T>G C>A T>A C>T 2.0 Signature A (0.62) Signature B (0.38) 5 Mutations 5 0 0 0

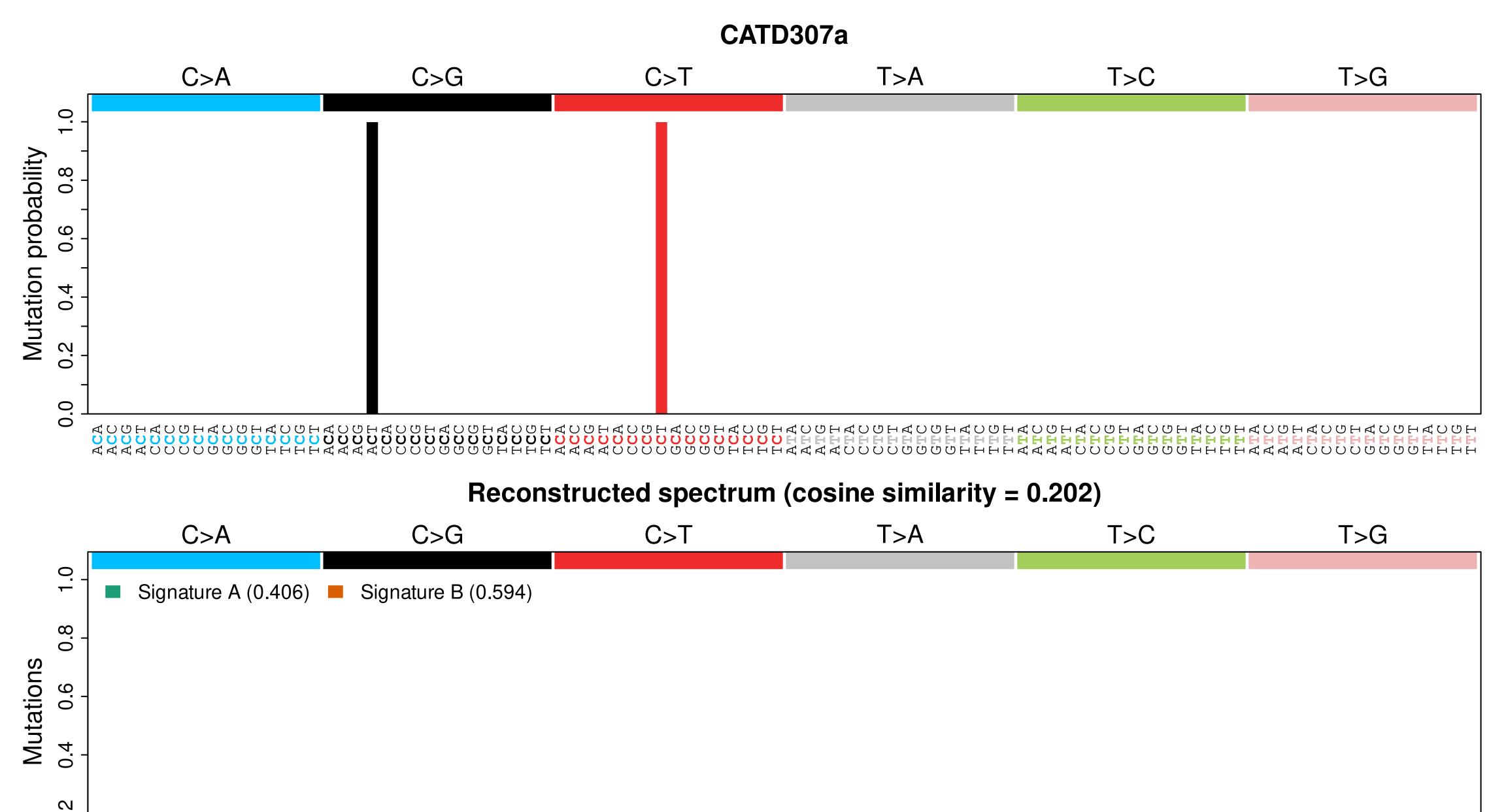






#### Reconstructed spectrum (cosine similarity = 0.073)





#### 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 = 0.287)** C>G T>A T>C T>G C>A C>T 2.0 Signature A (0.7) Signature B (0.3) 5 Mutations 5 0 0 0