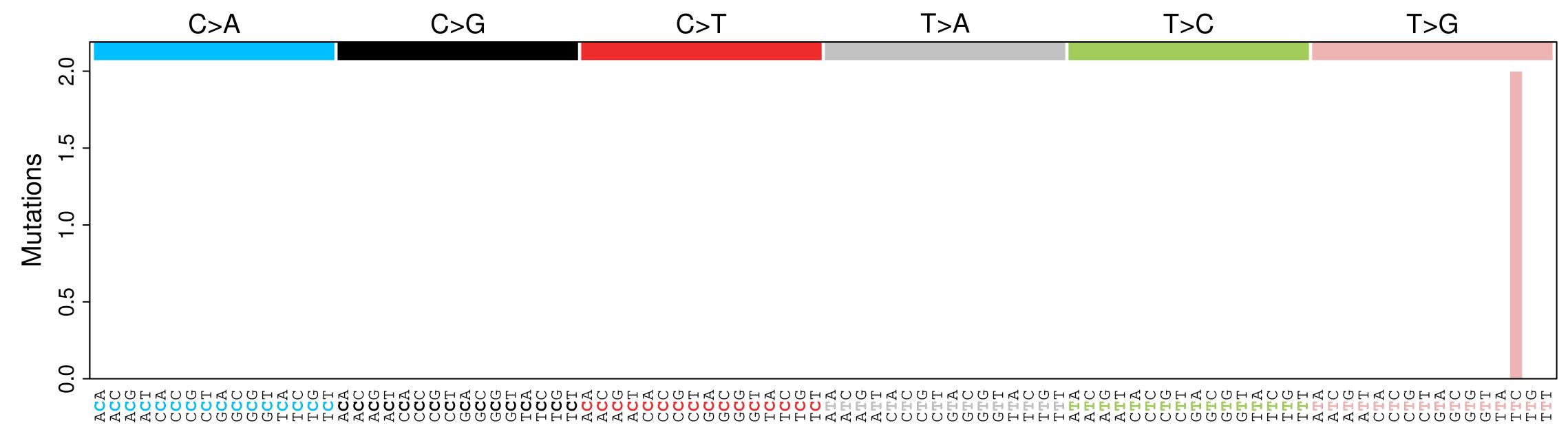
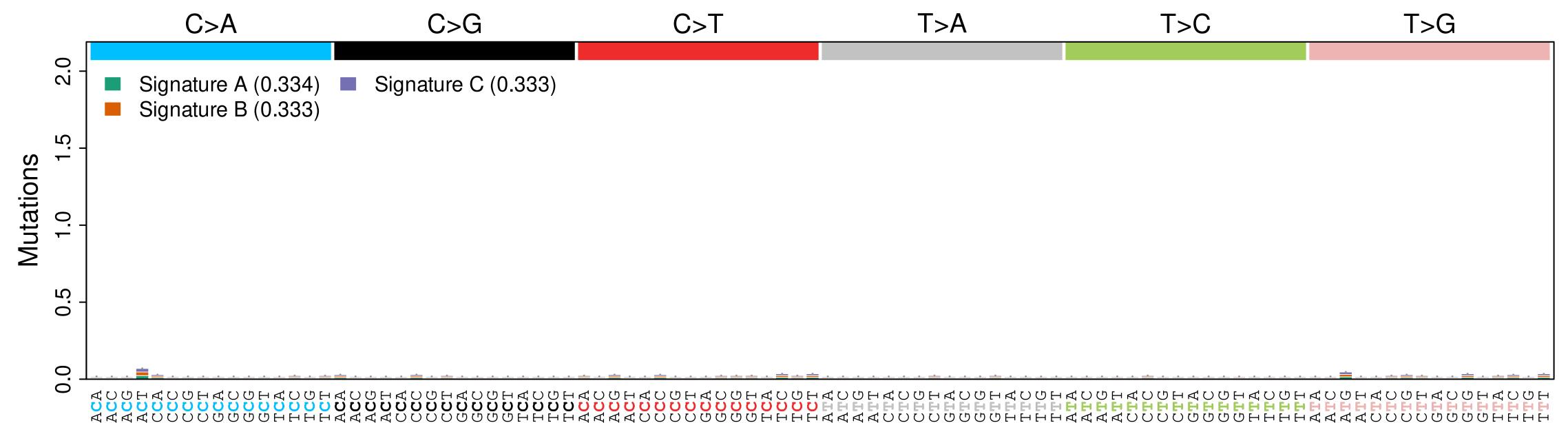
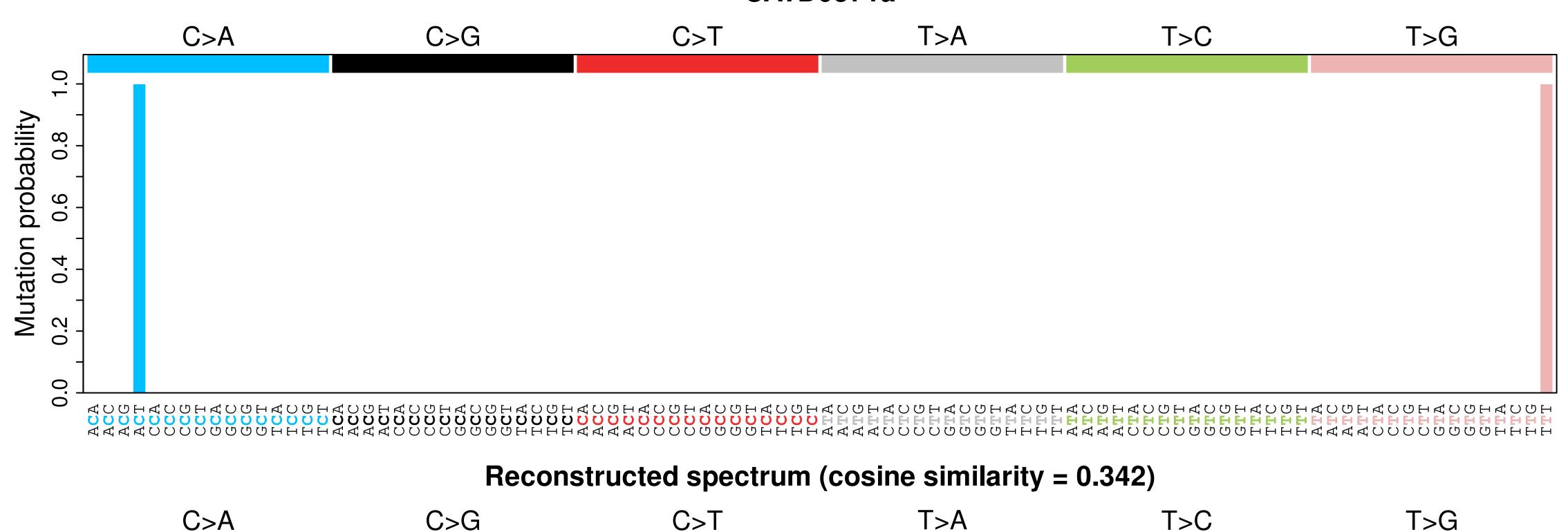
CATD0161a (2 mutations)

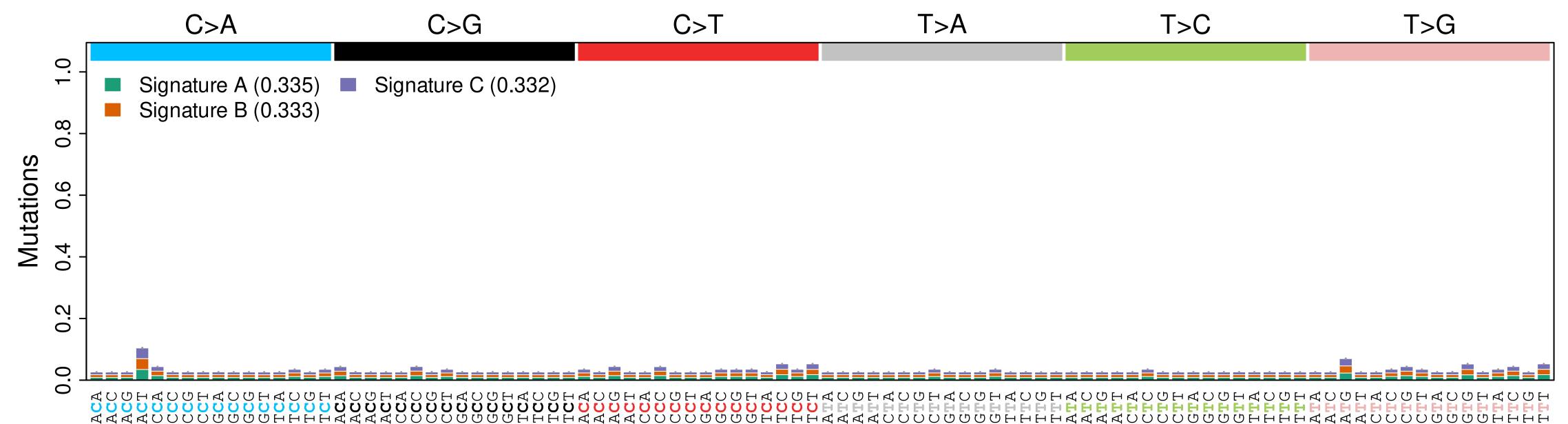


Reconstructed spectrum (cosine similarity = 0.135)

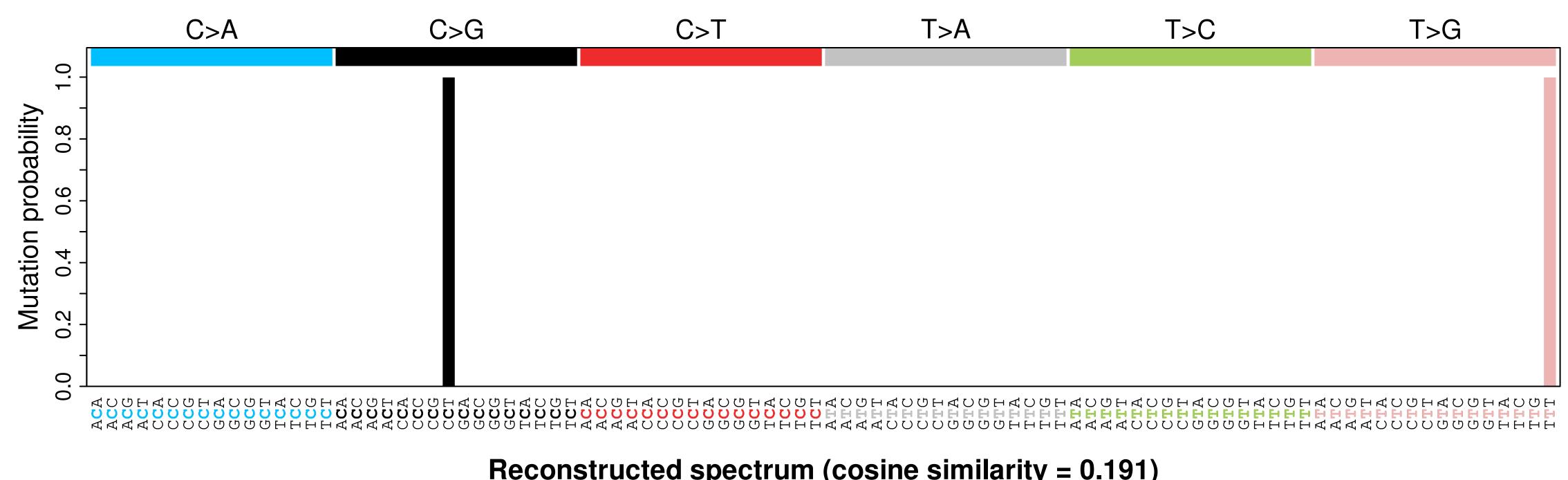


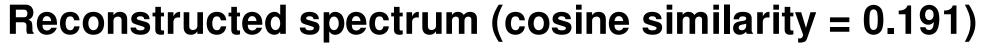


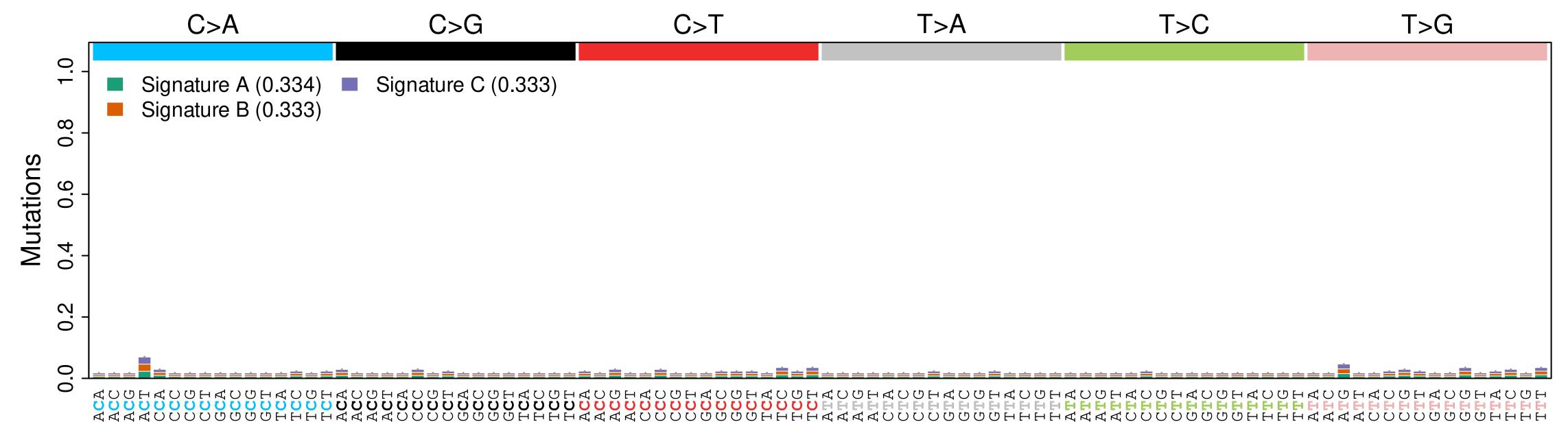




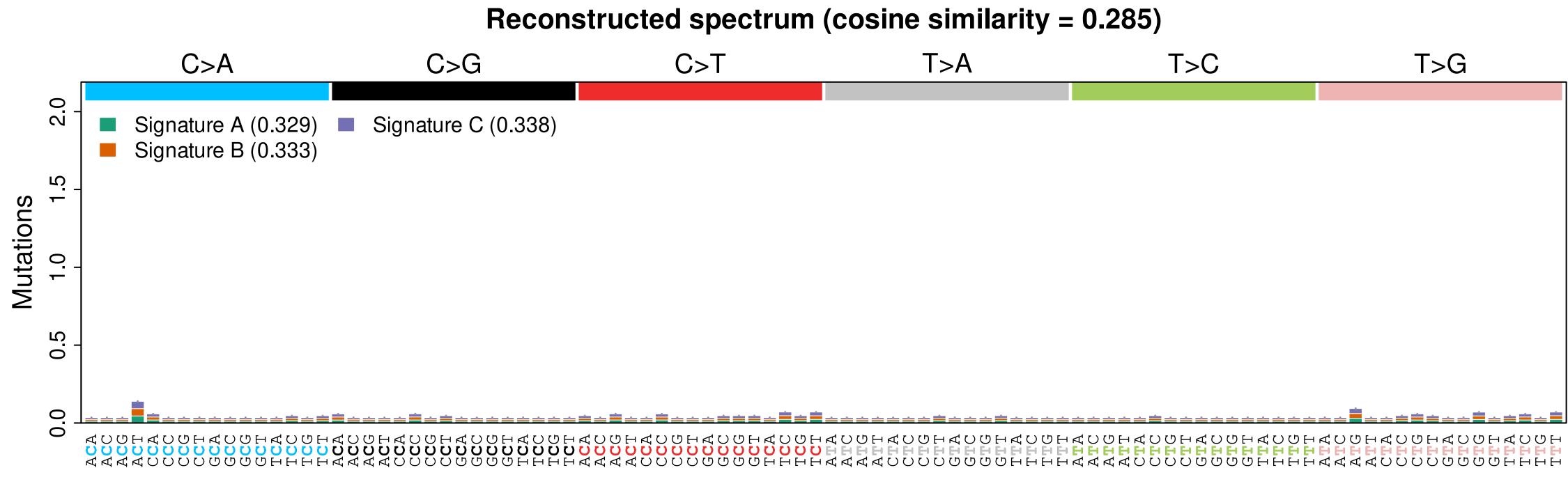




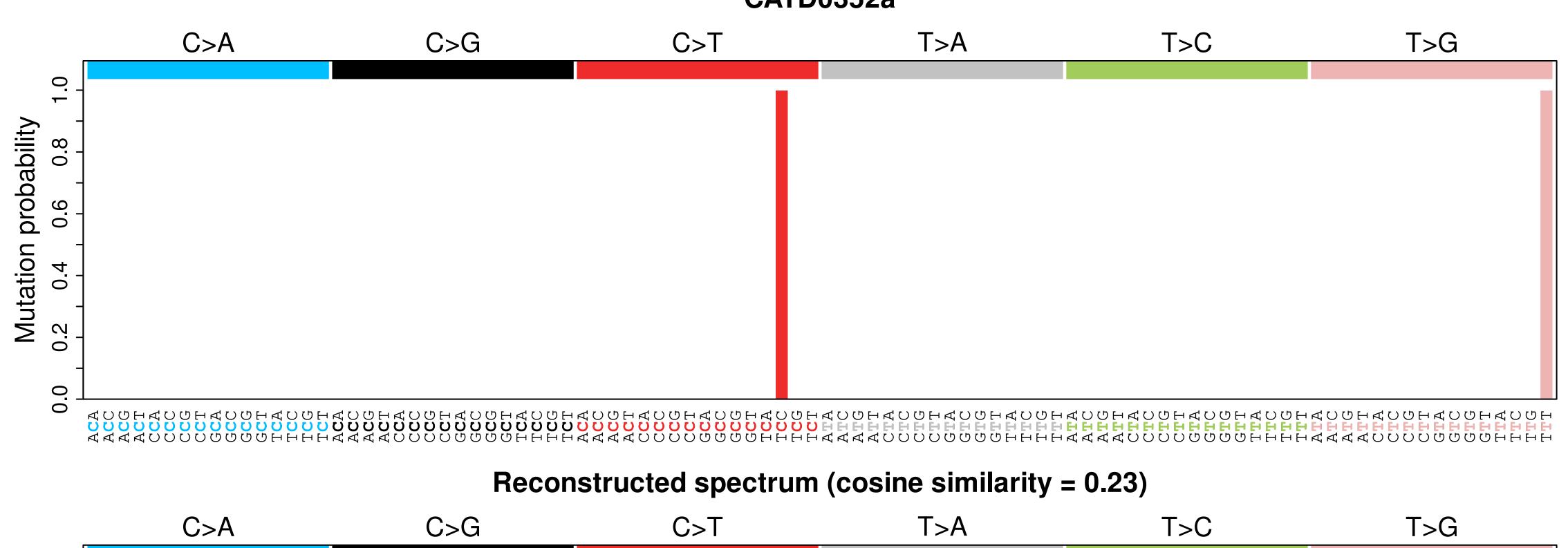


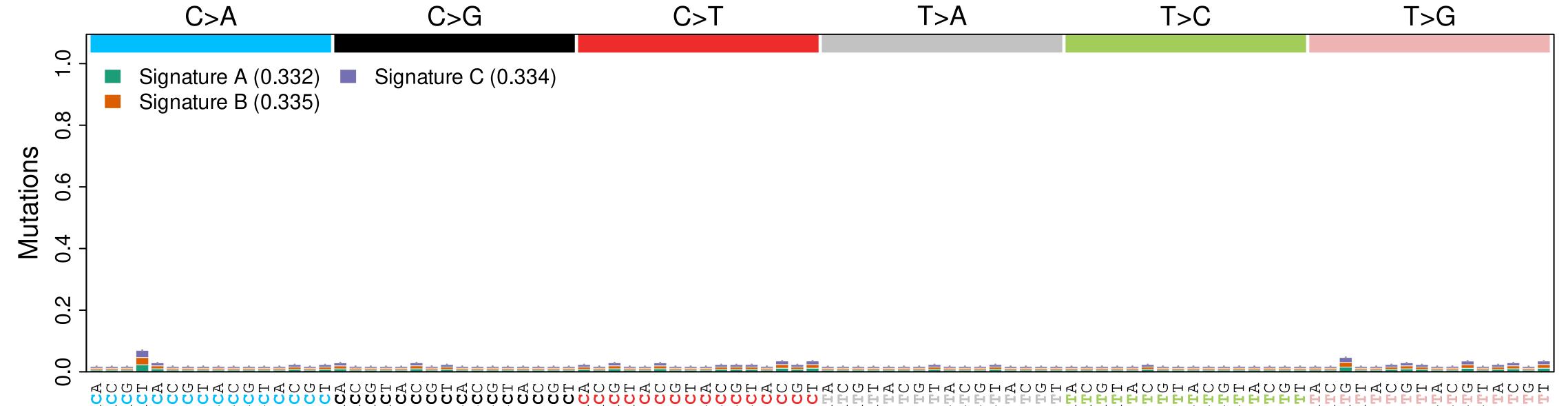


CATD0372a (4 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.285)** C>A C>G T>A T>C T>G C>T 2.0 Signature A (0.329) Signature C (0.338) Signature B (0.333) 5

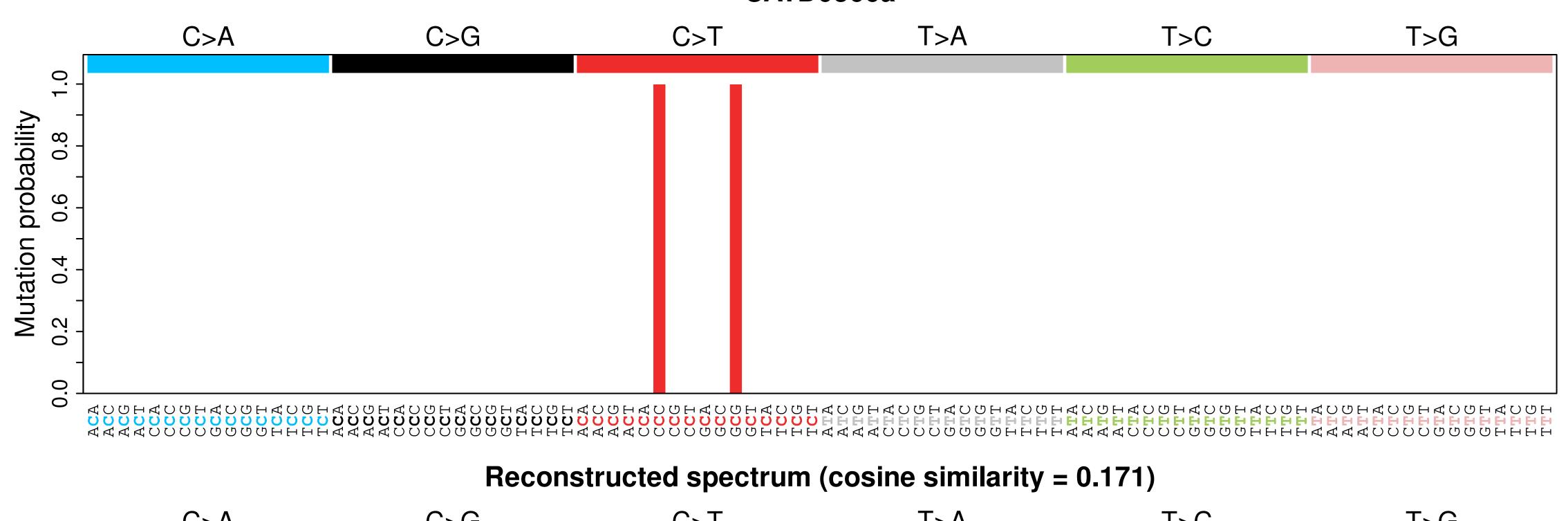


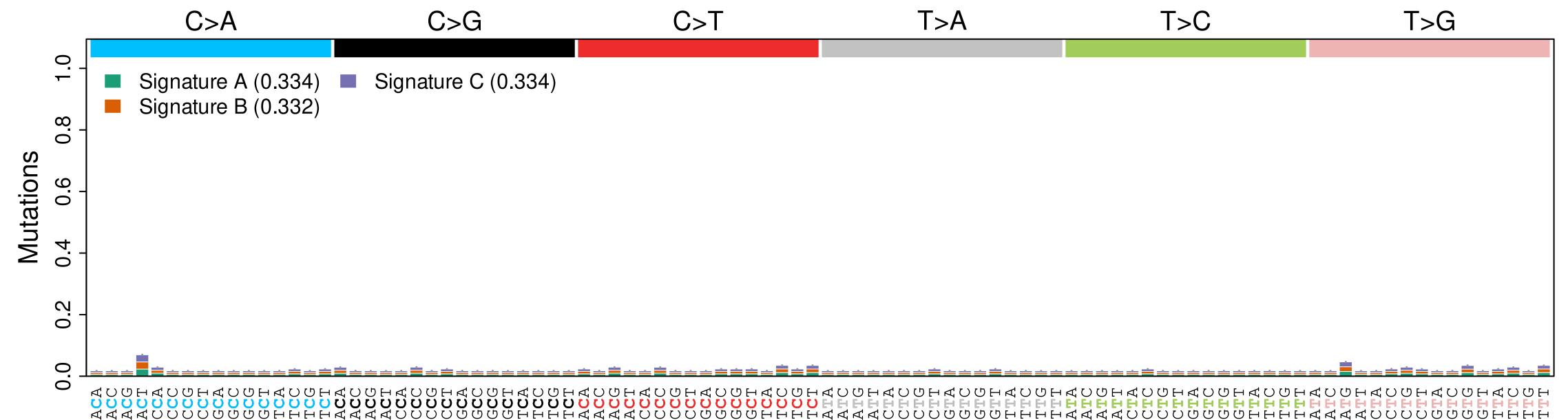




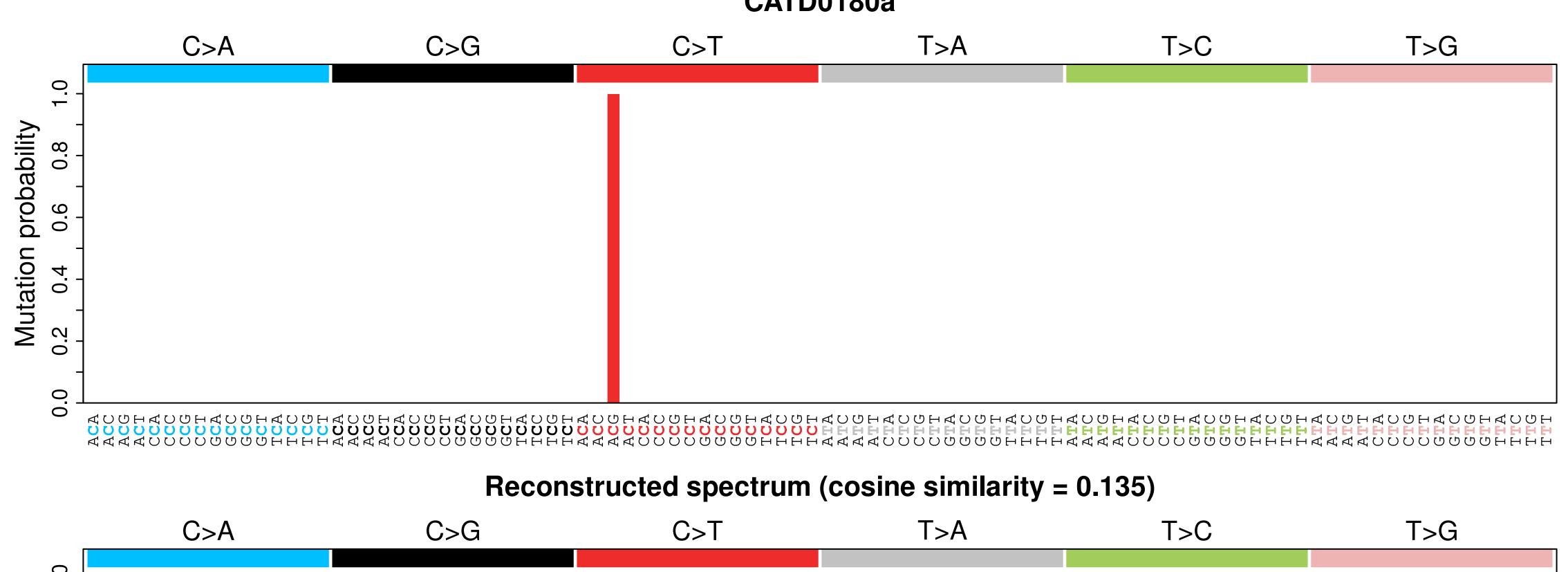


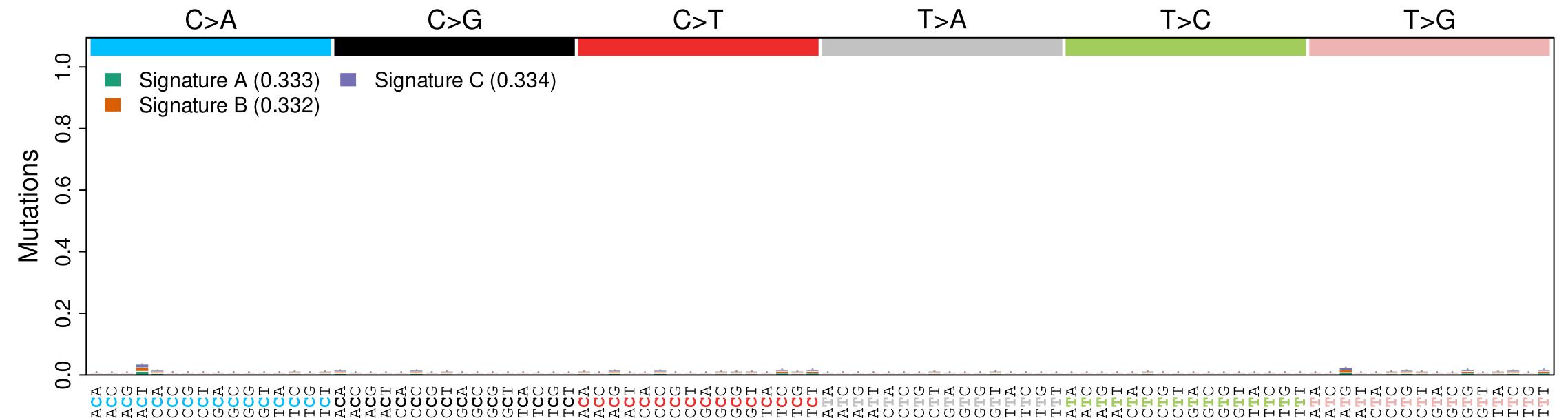




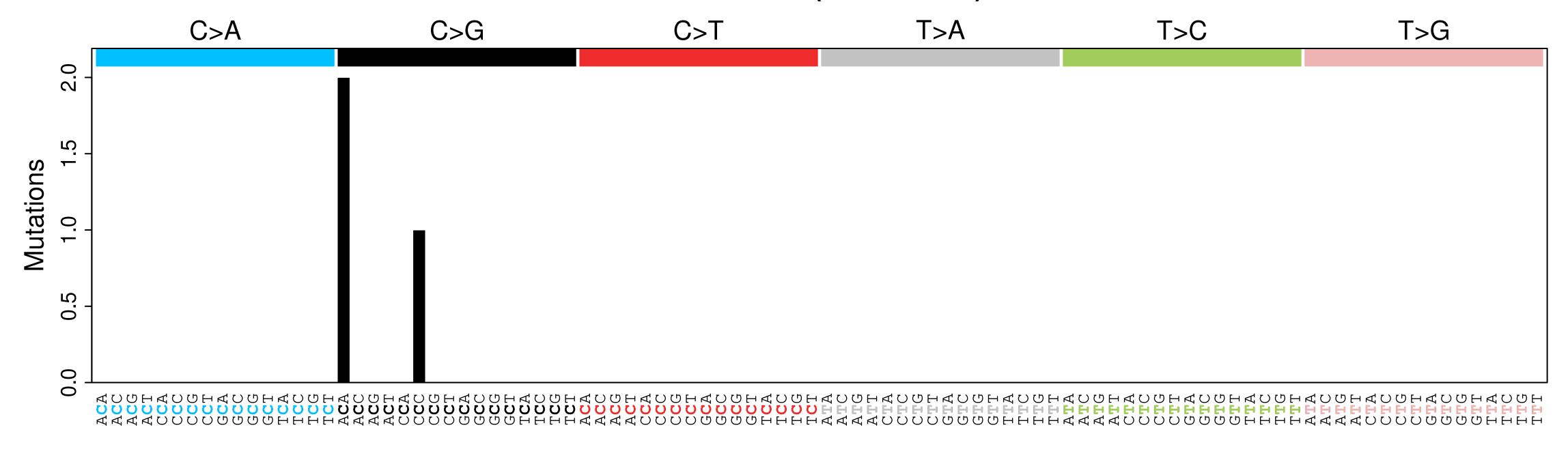




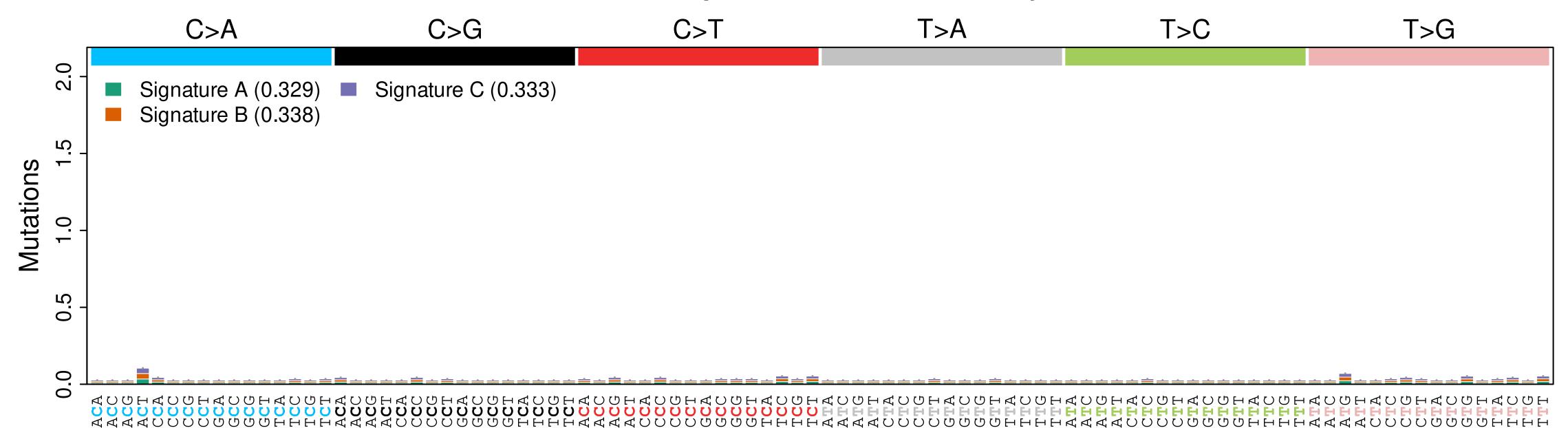




CATD0375a (3 mutations)



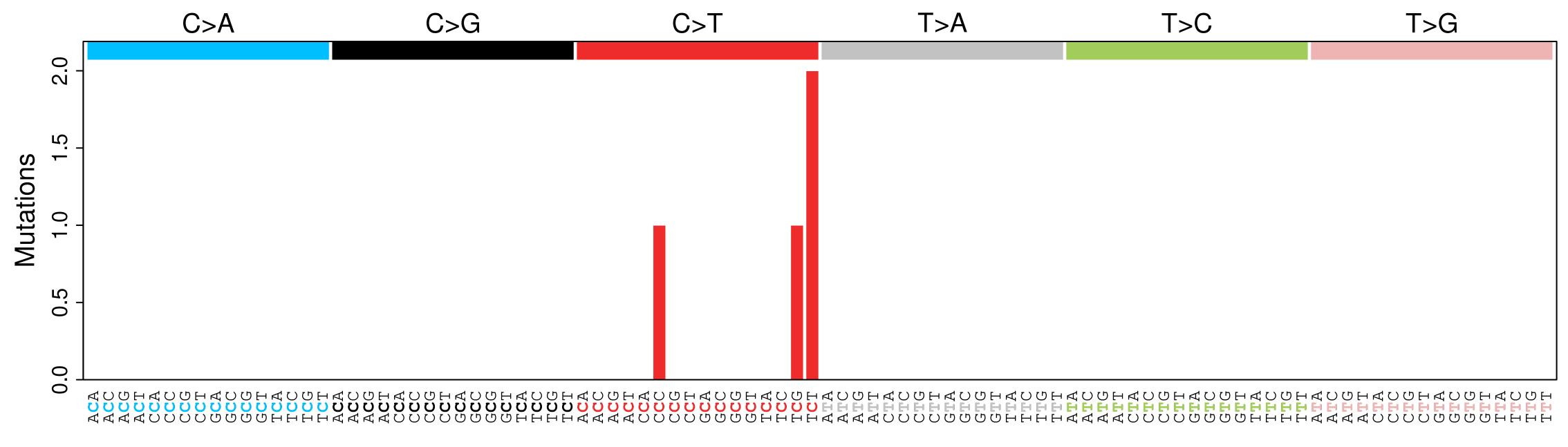
Reconstructed spectrum (cosine similarity = 0.181)



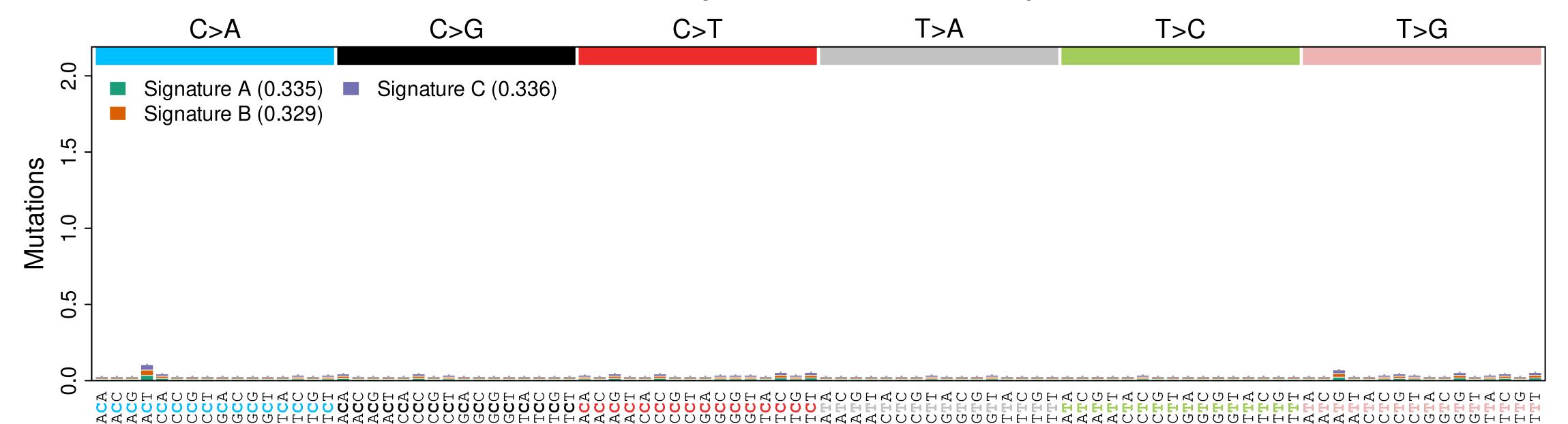
CATD0351a (2 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0.0 **Reconstructed spectrum (cosine similarity = 0.135)** C>A C>G T>C T>G T>A C>T 2.0 Signature A (0.332) Signature C (0.335) Signature B (0.333) 5 Mutations 5 0

CATD0182a (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 = 0.192)** C>A C>G T>C T>G T>A C>T 2.0 Signature A (0.331) Signature C (0.339) Signature B (0.331) 5 Mutations 5 0

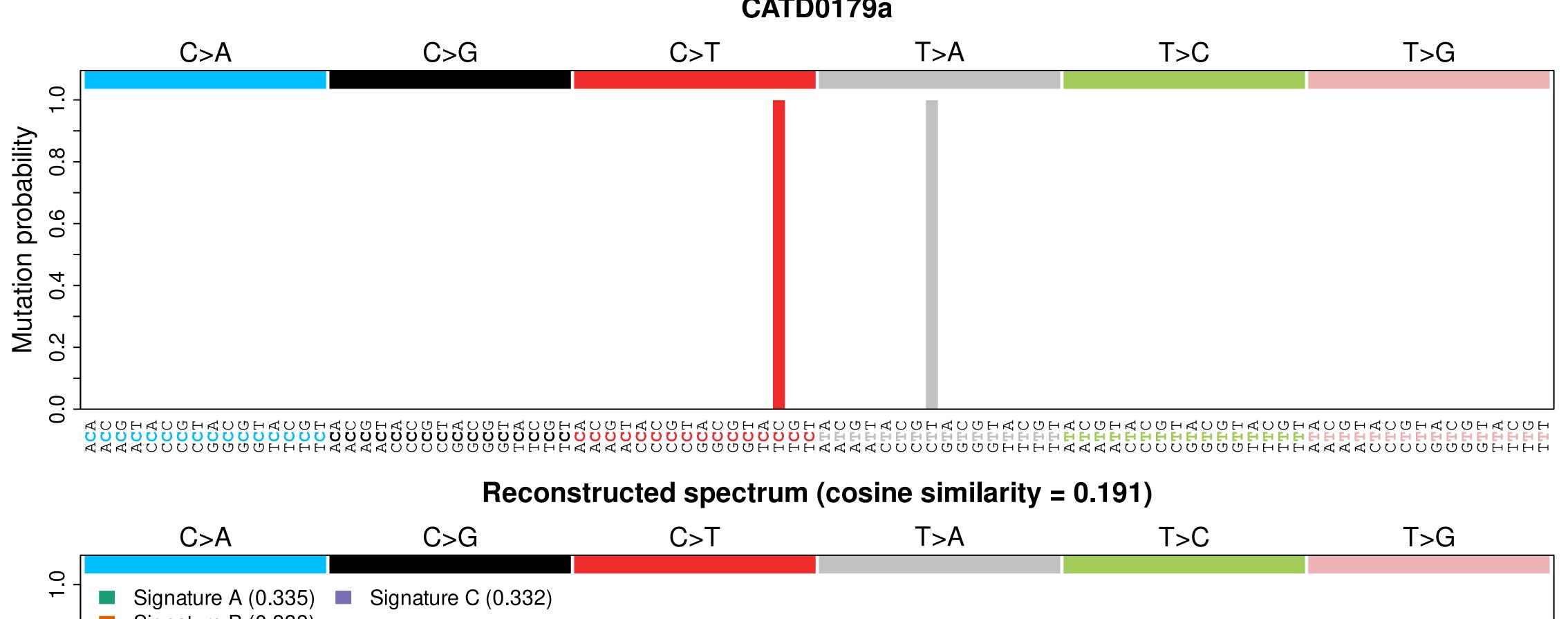
CATD0184a (4 mutations)

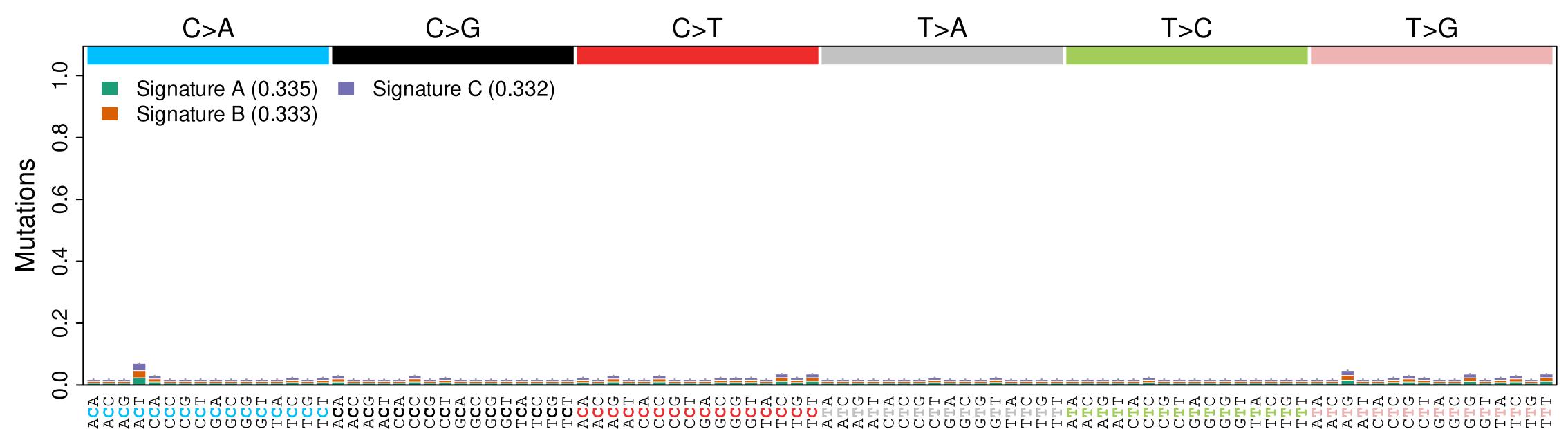


Reconstructed spectrum (cosine similarity = 0.231)

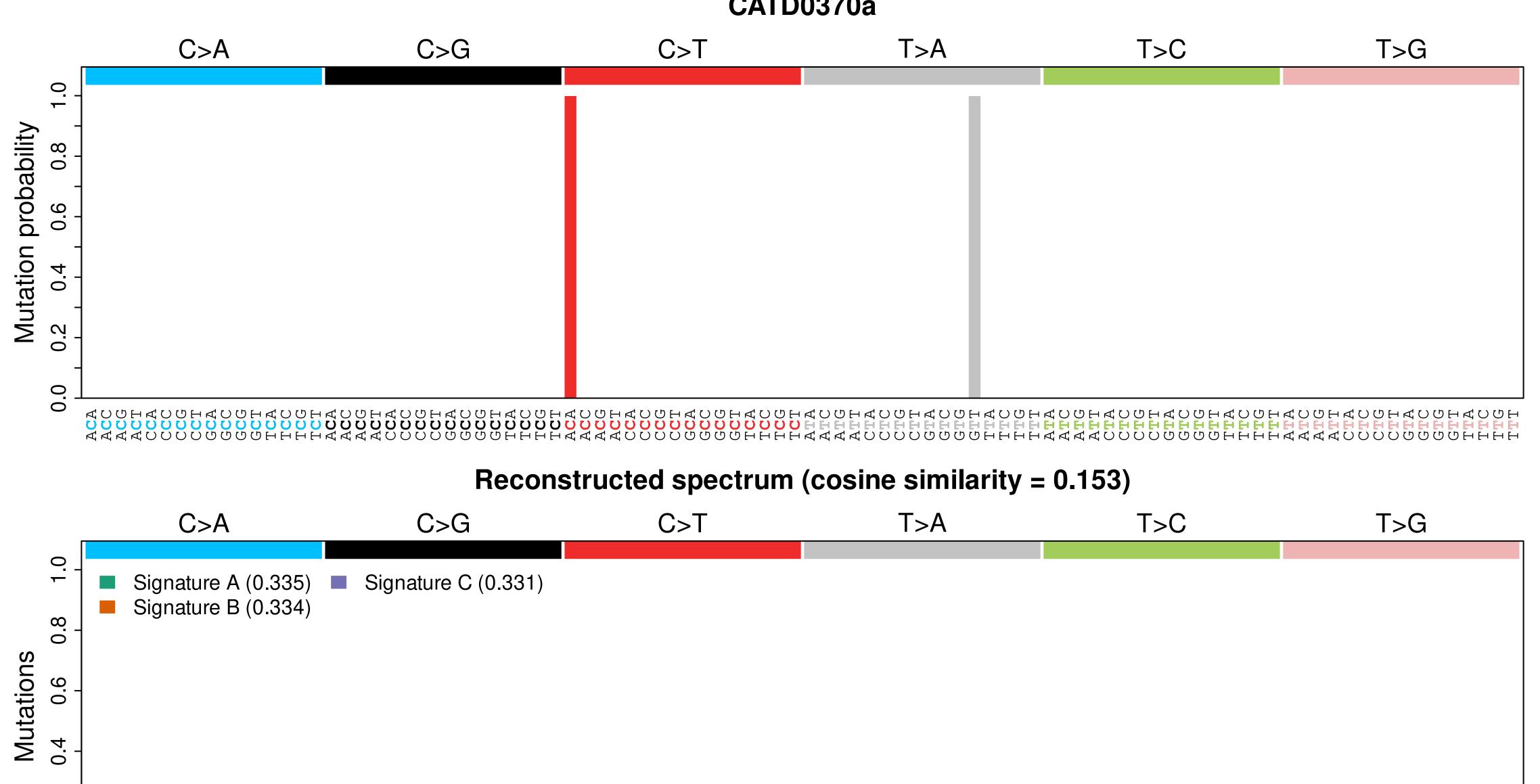






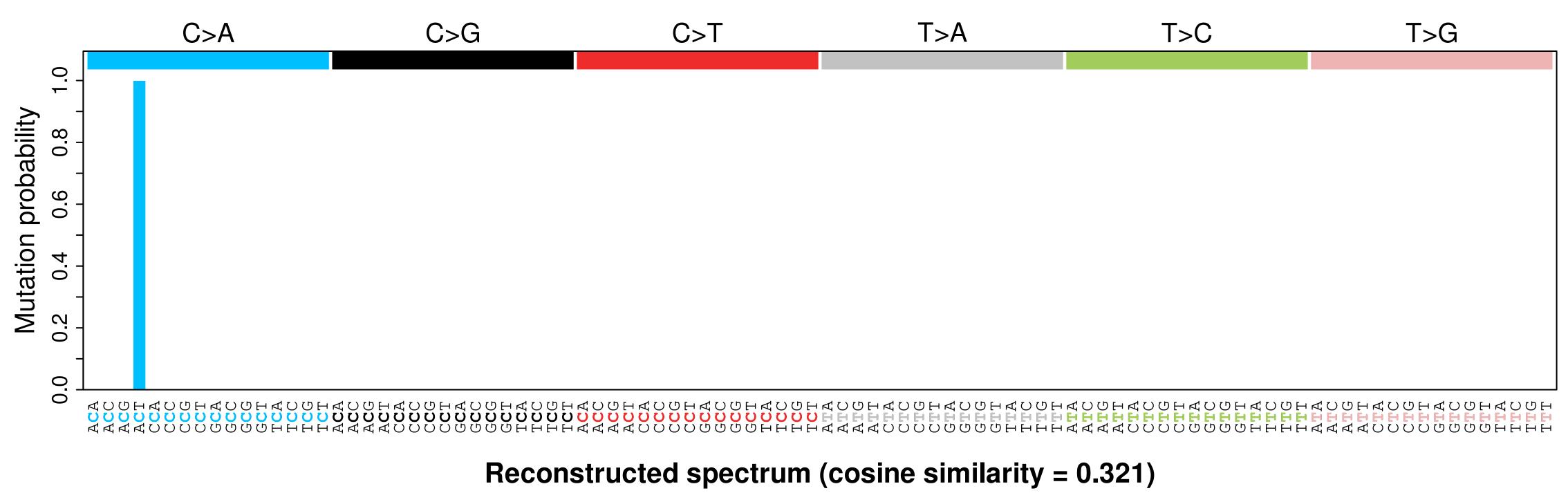


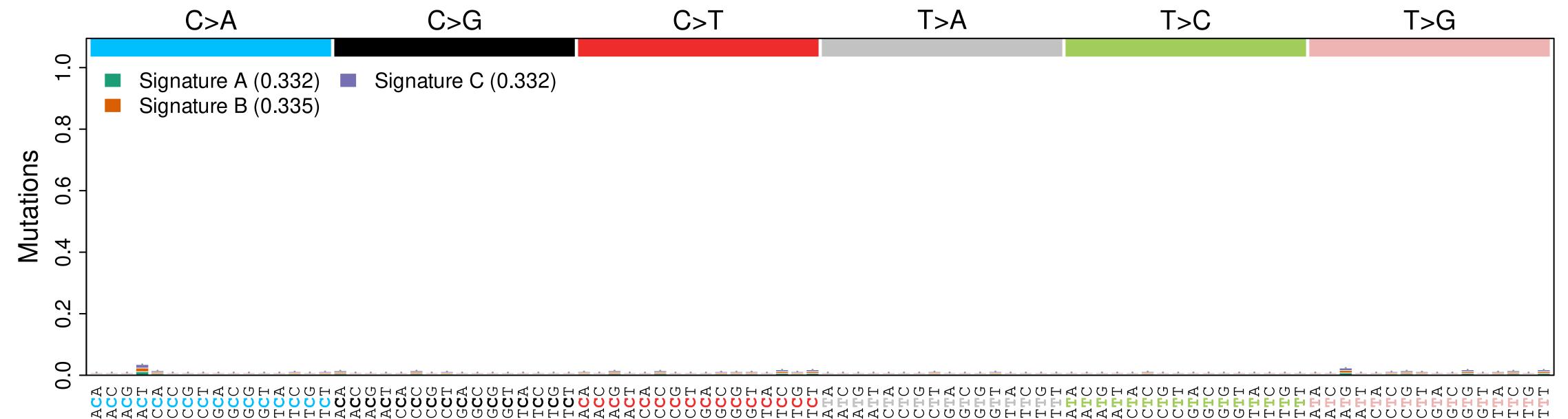




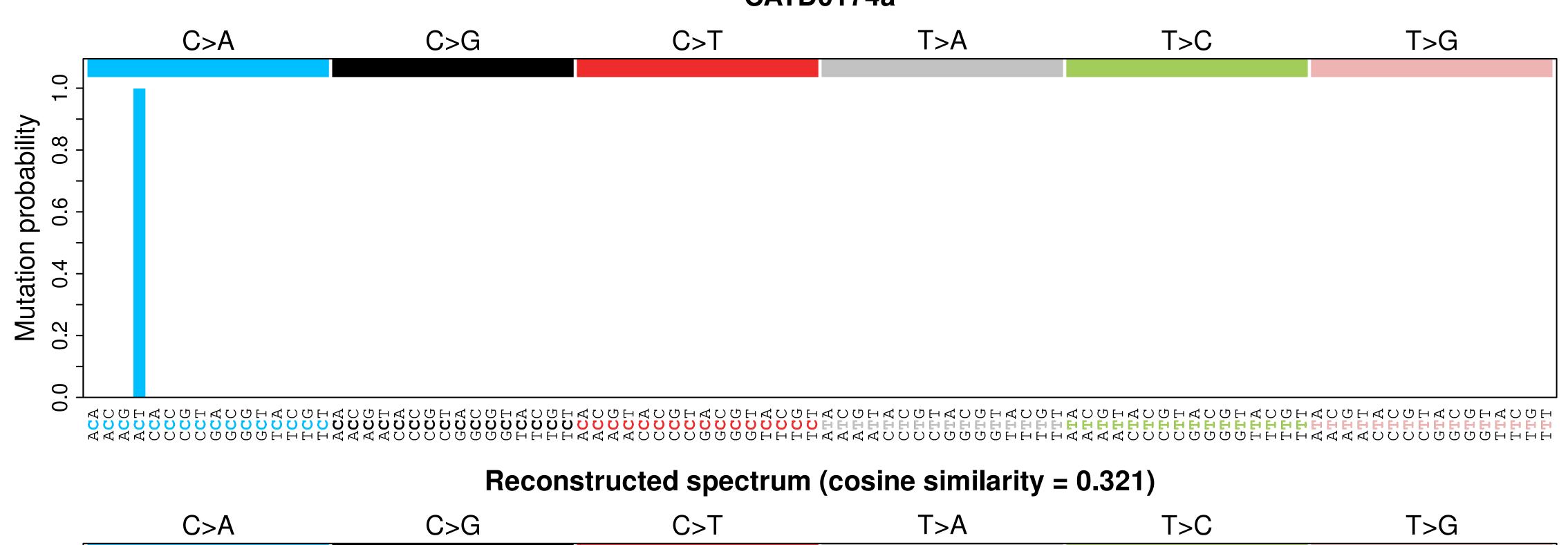
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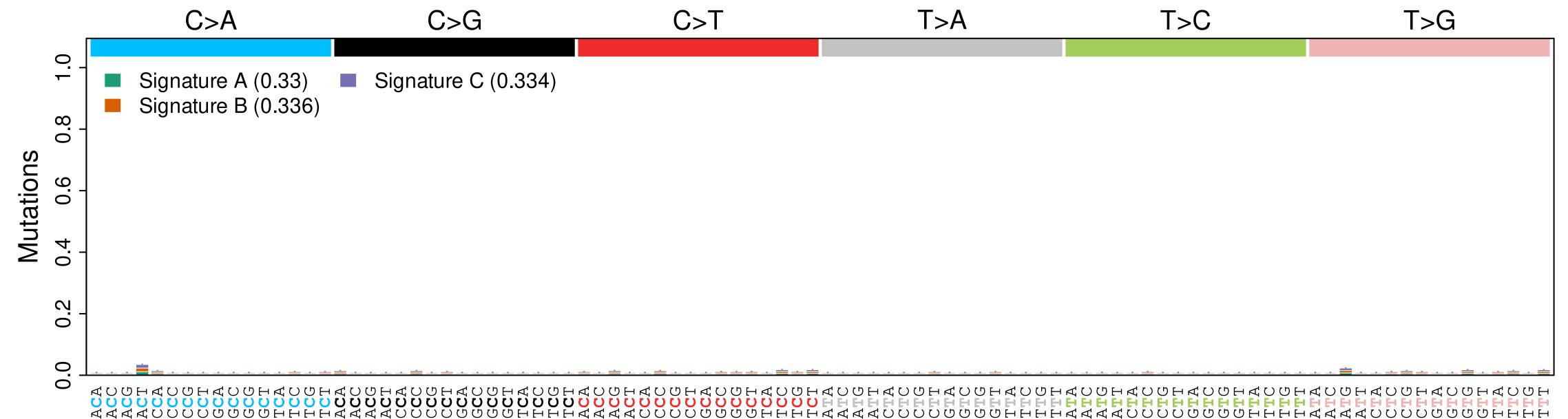




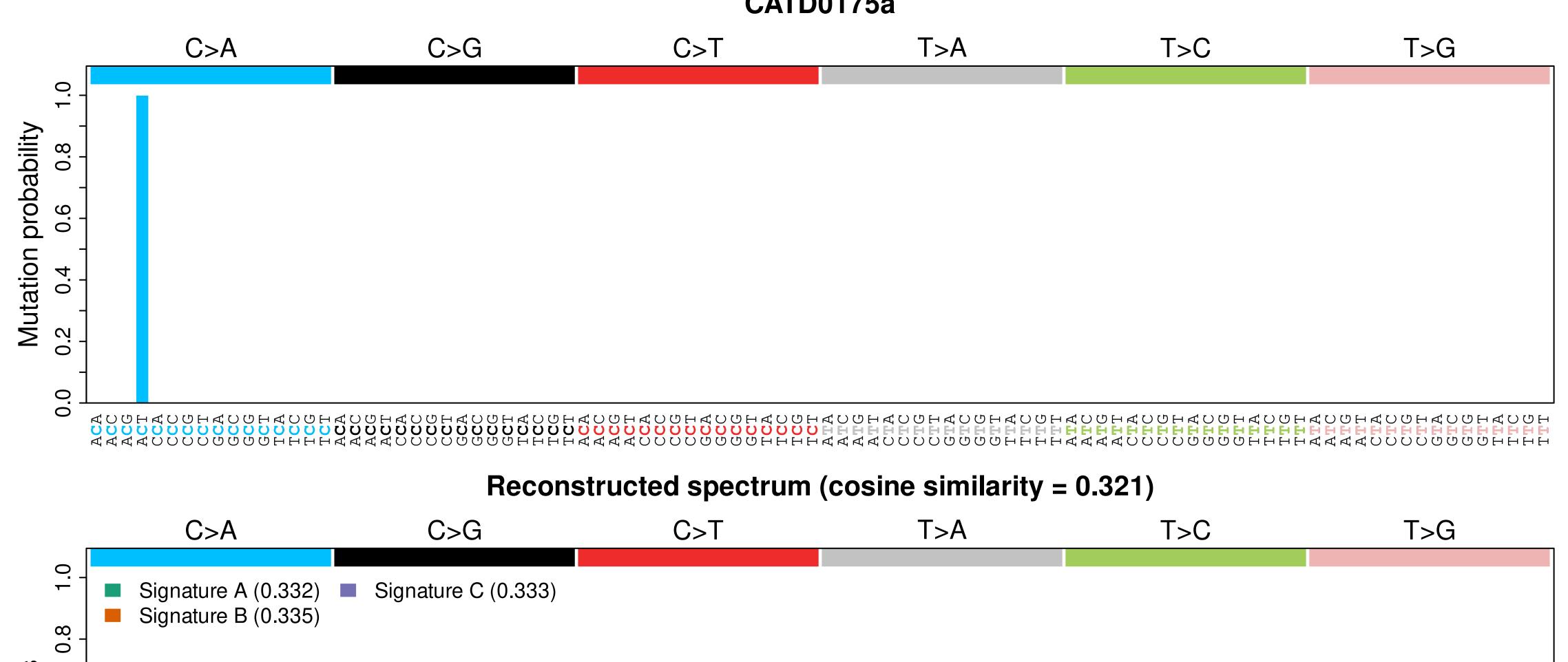


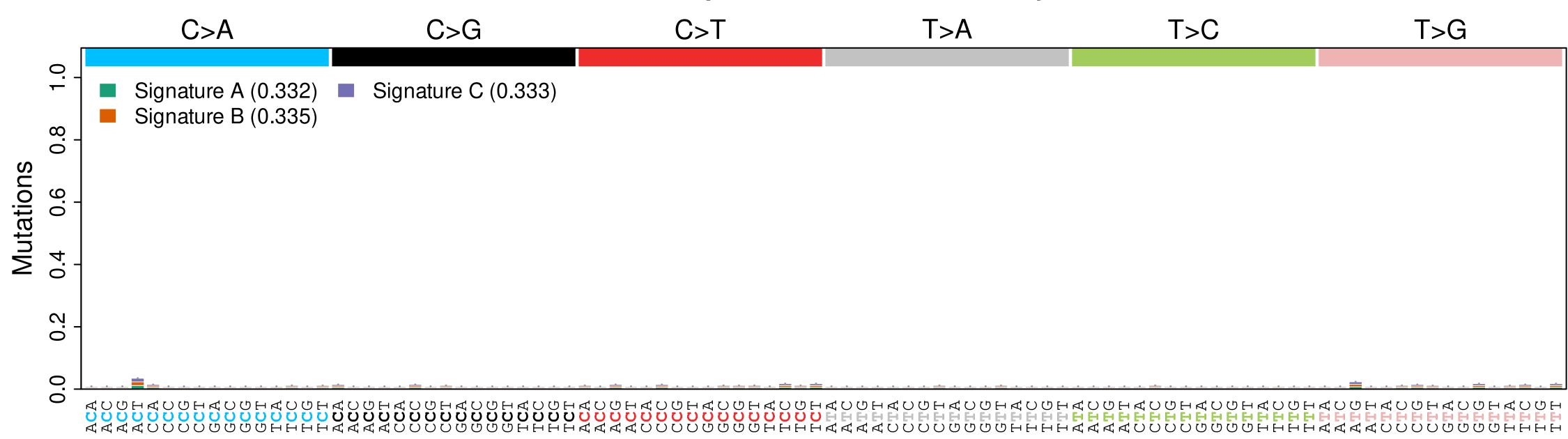




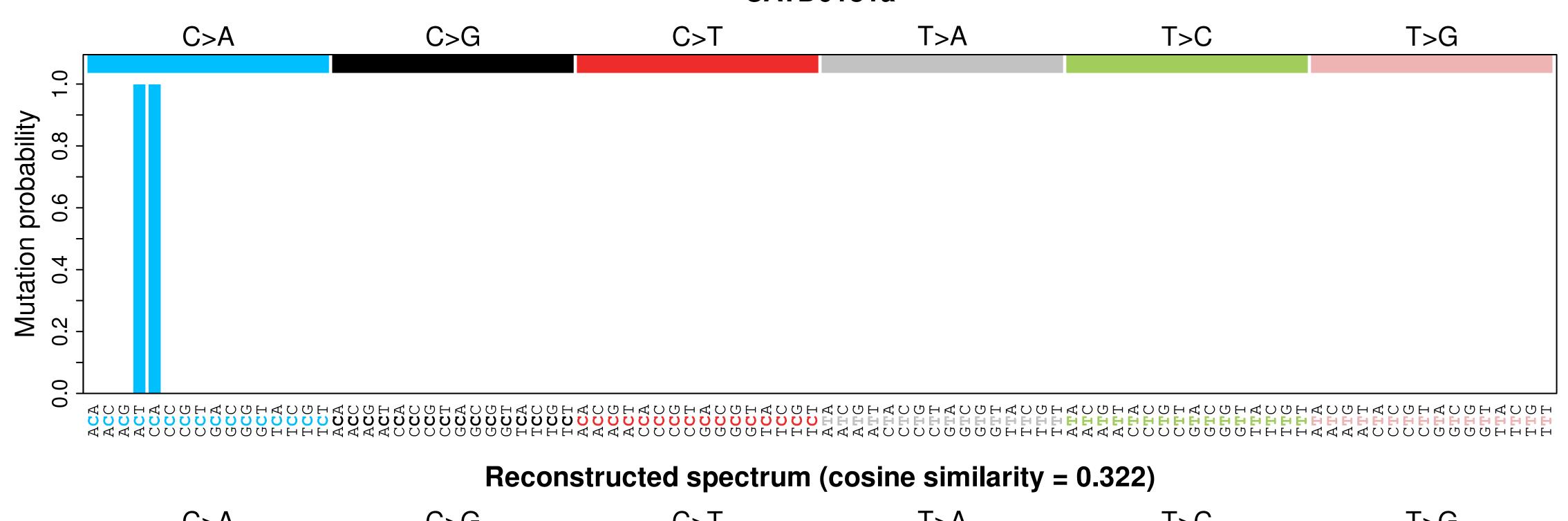


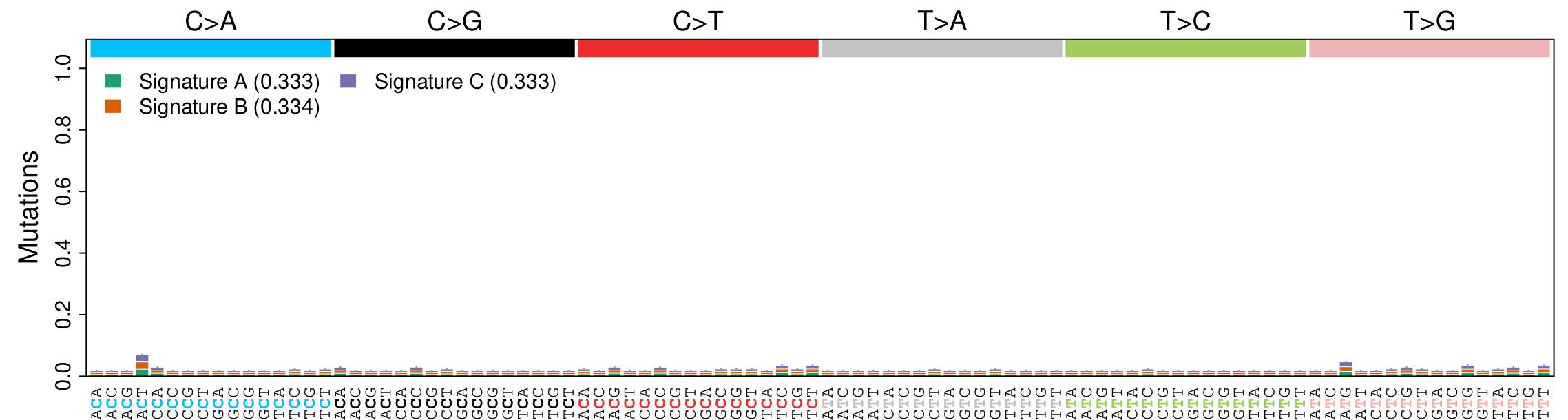




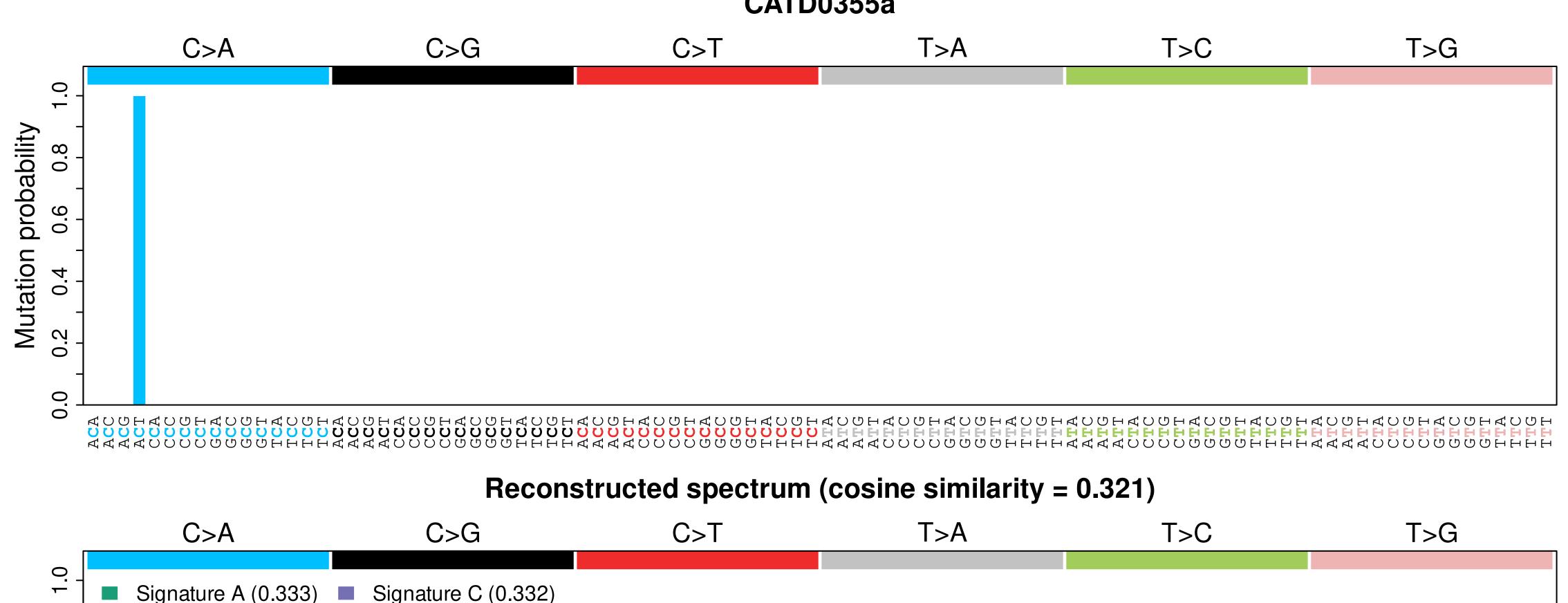


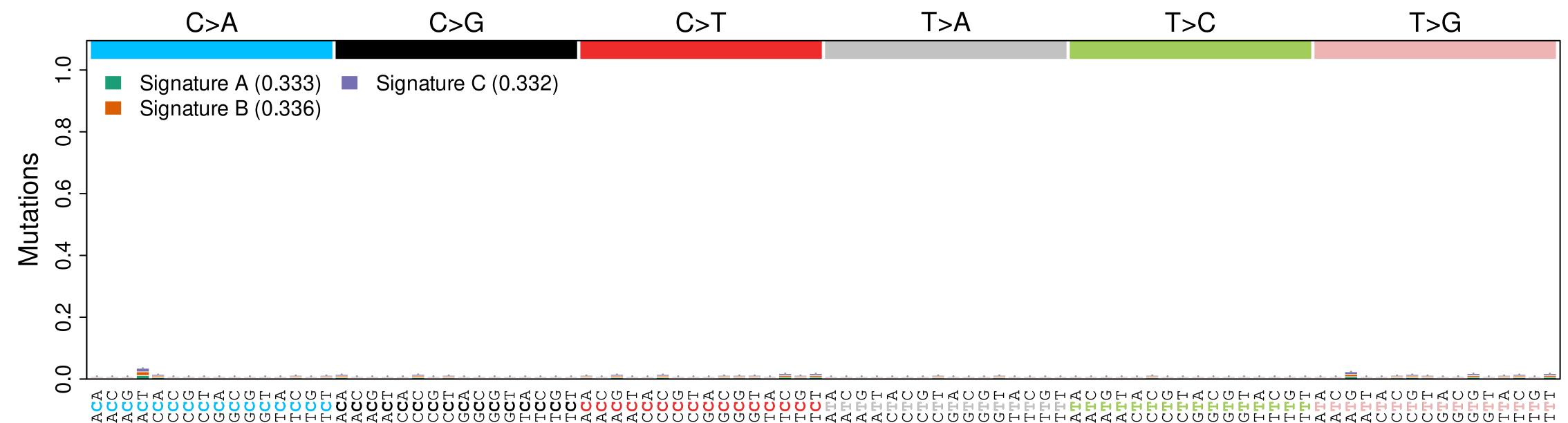




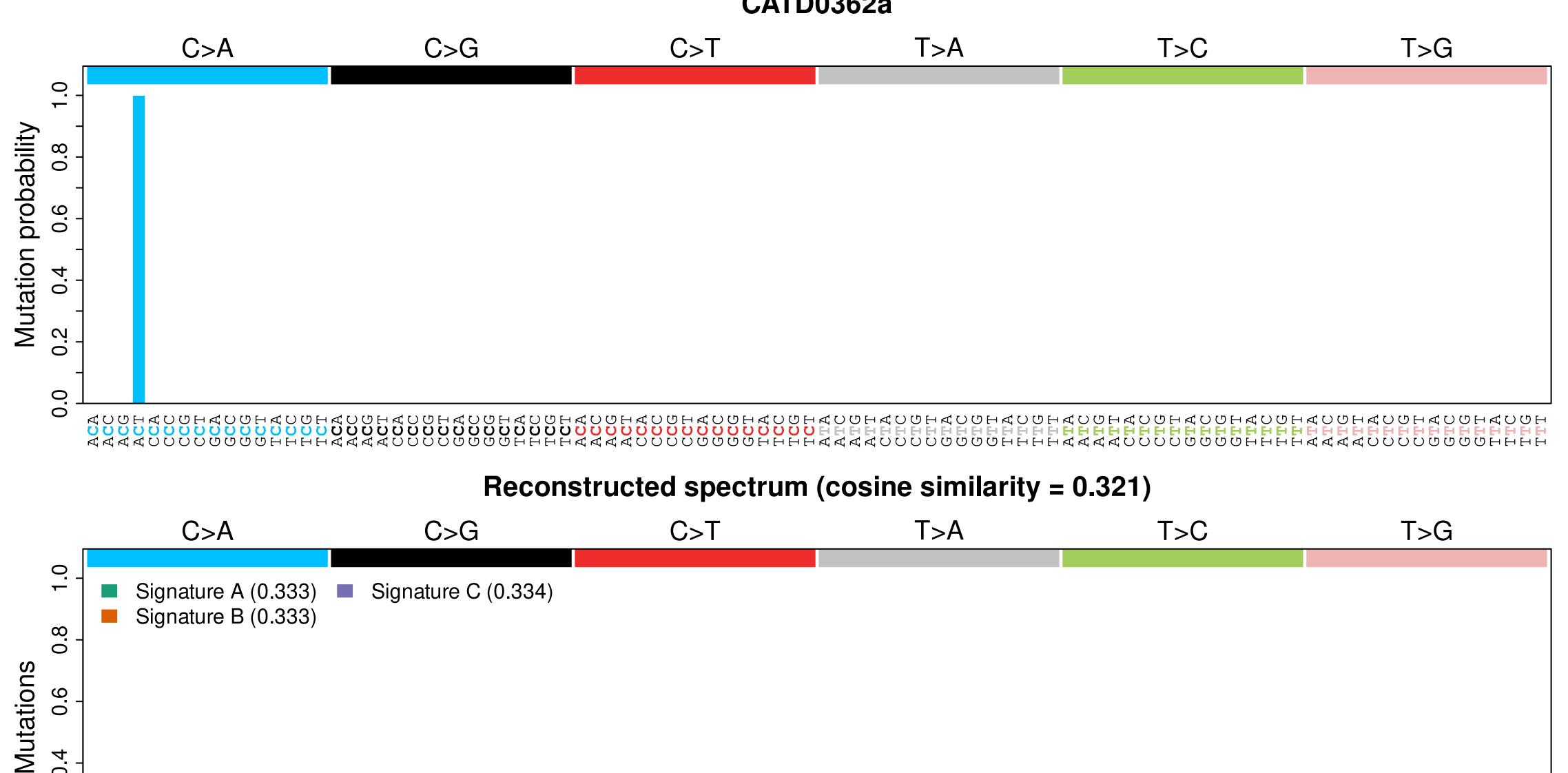






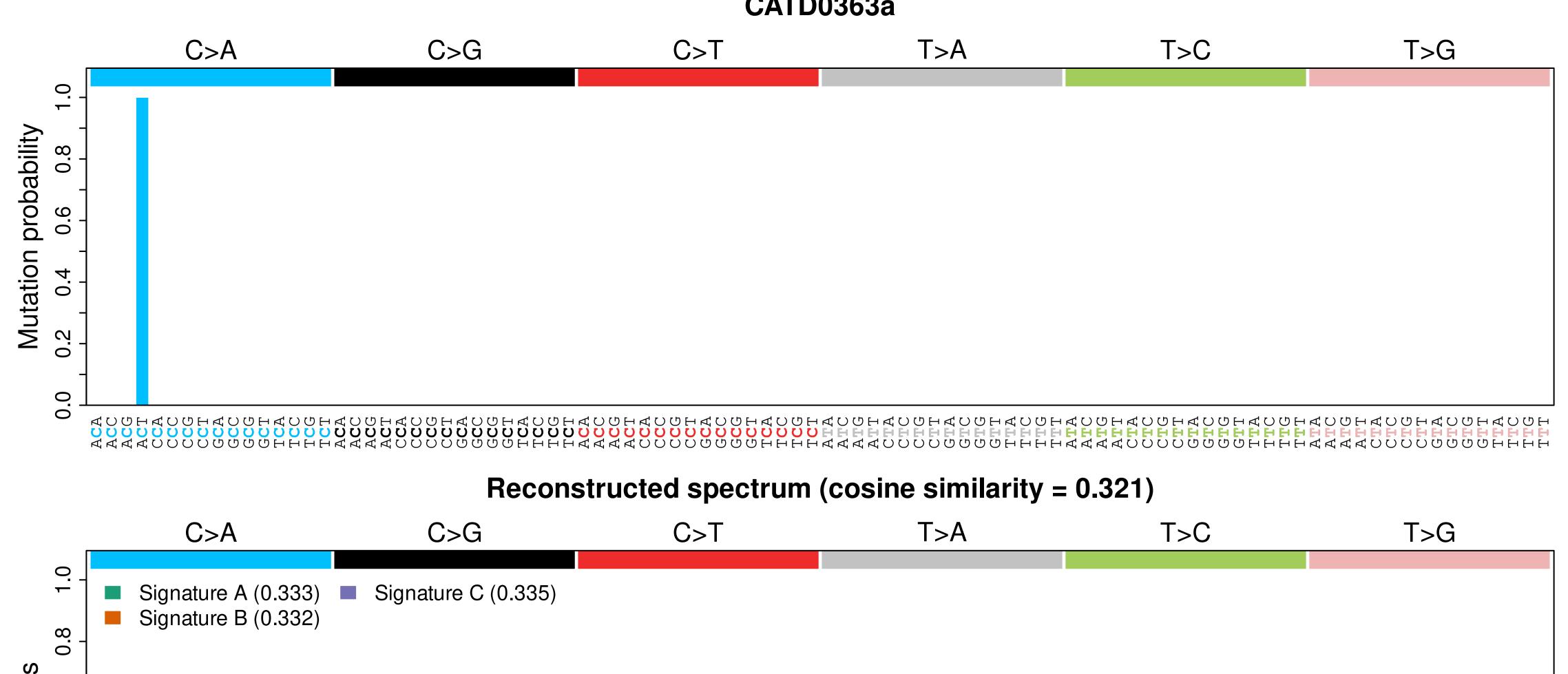


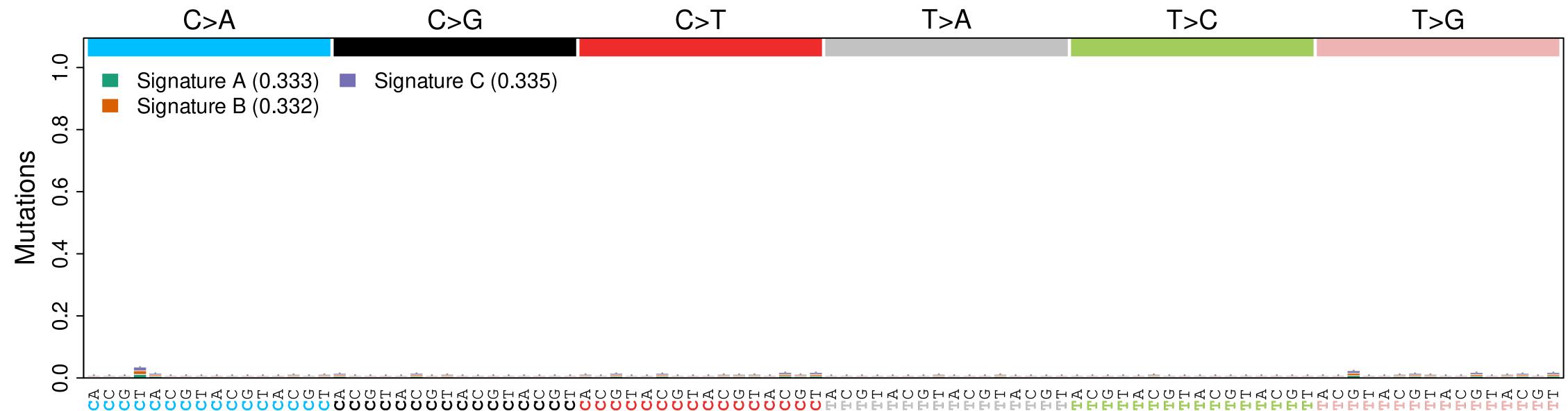




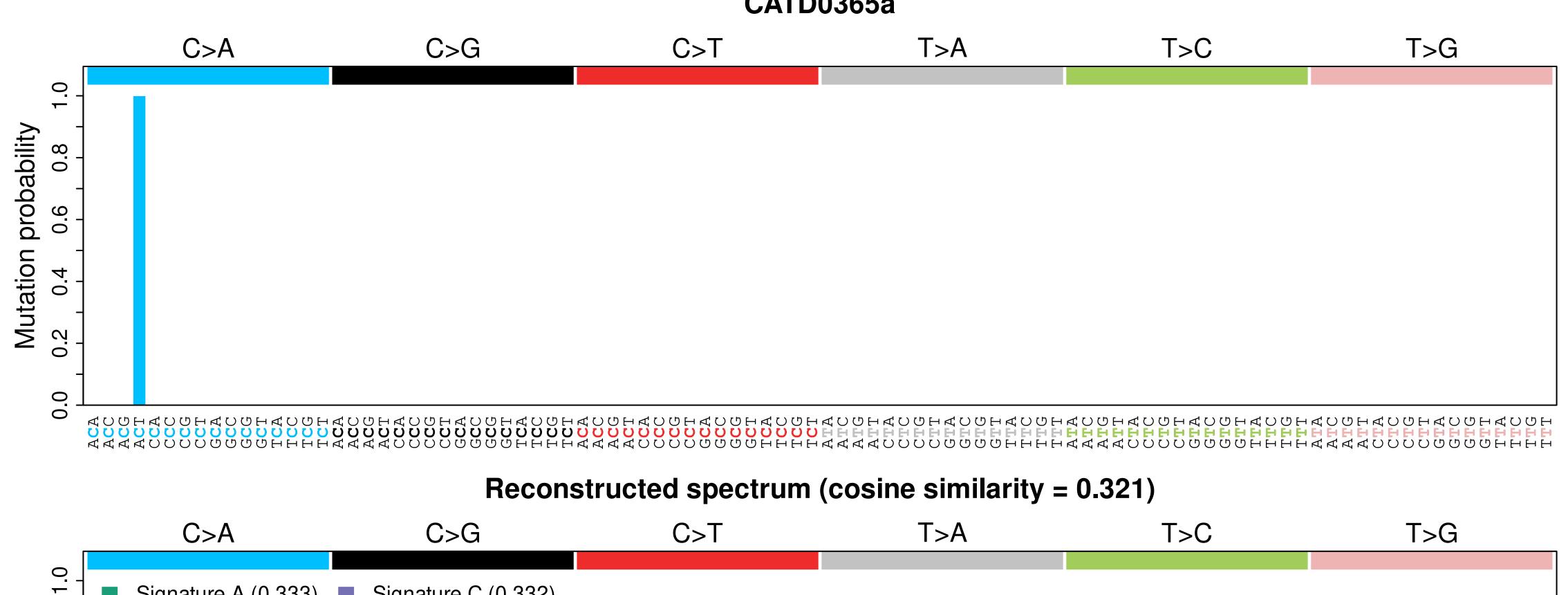
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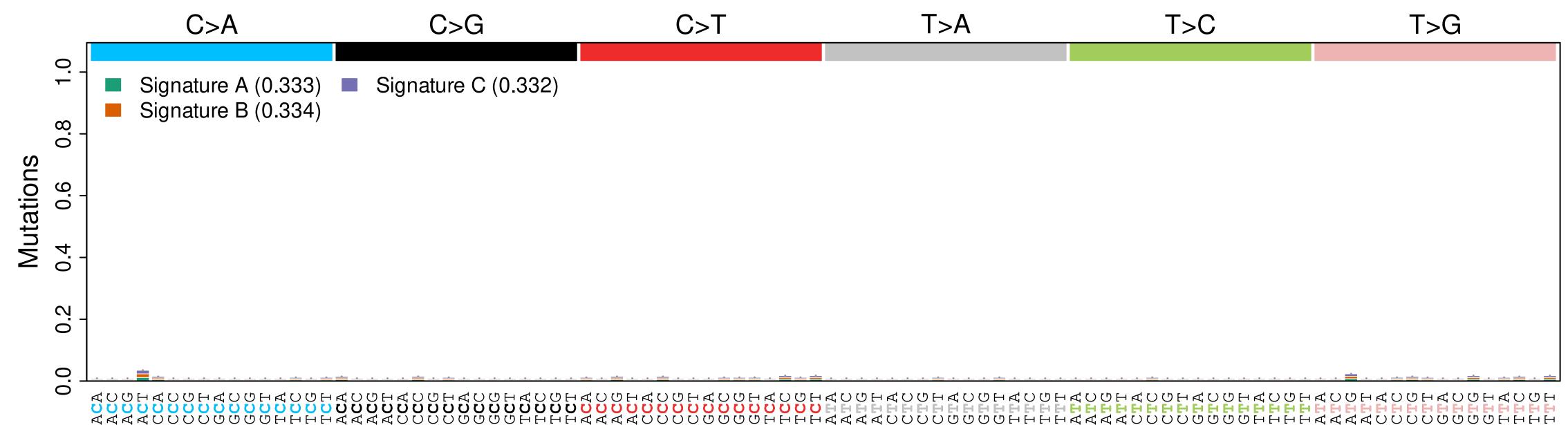




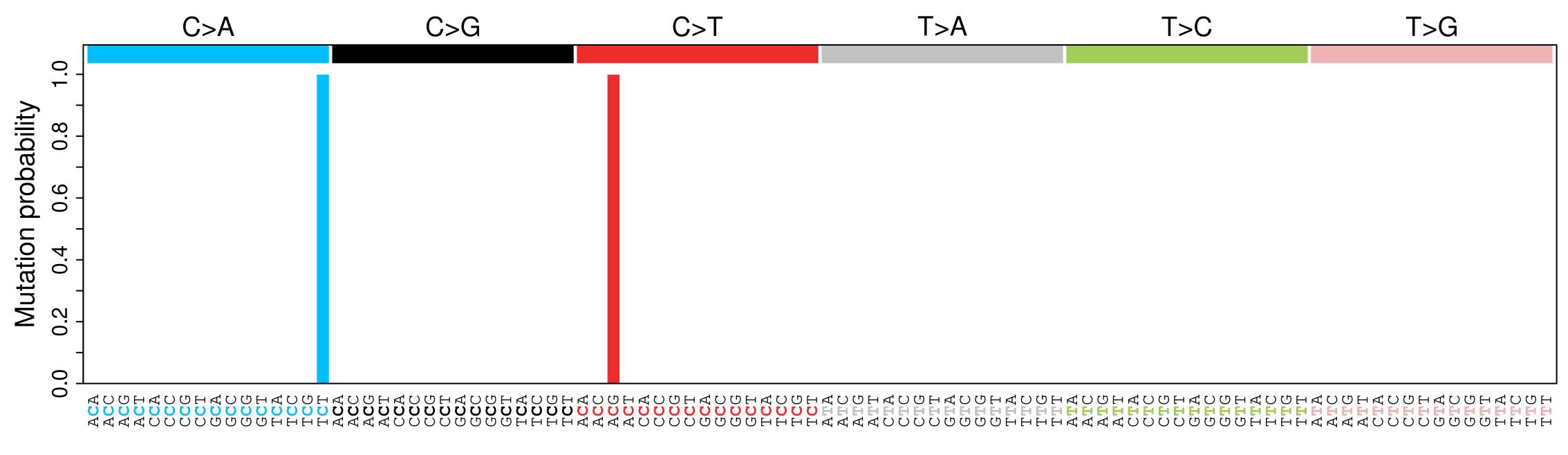




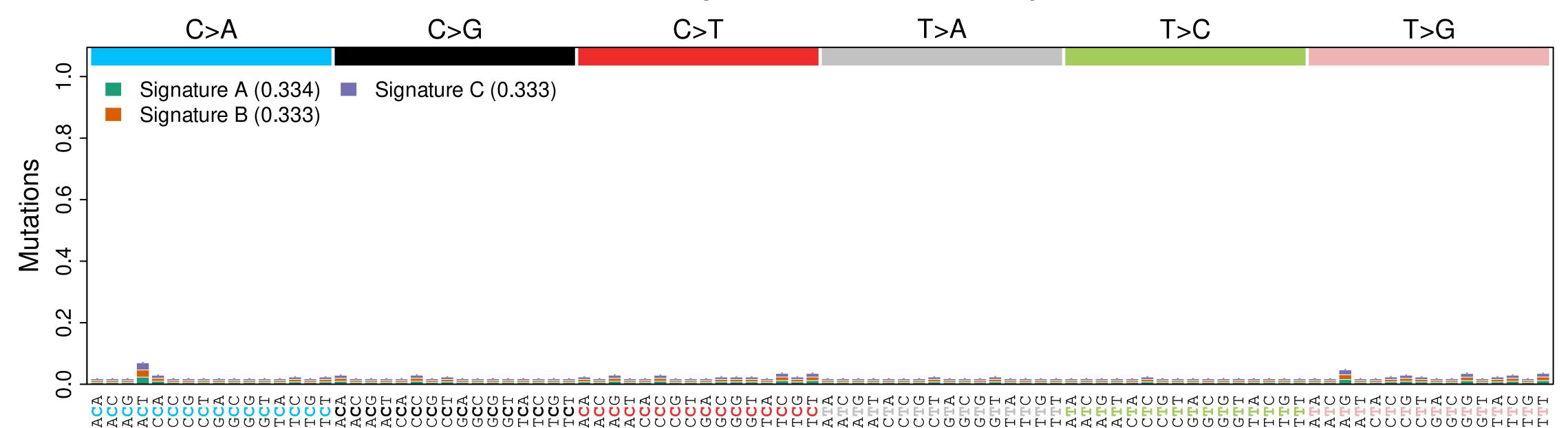




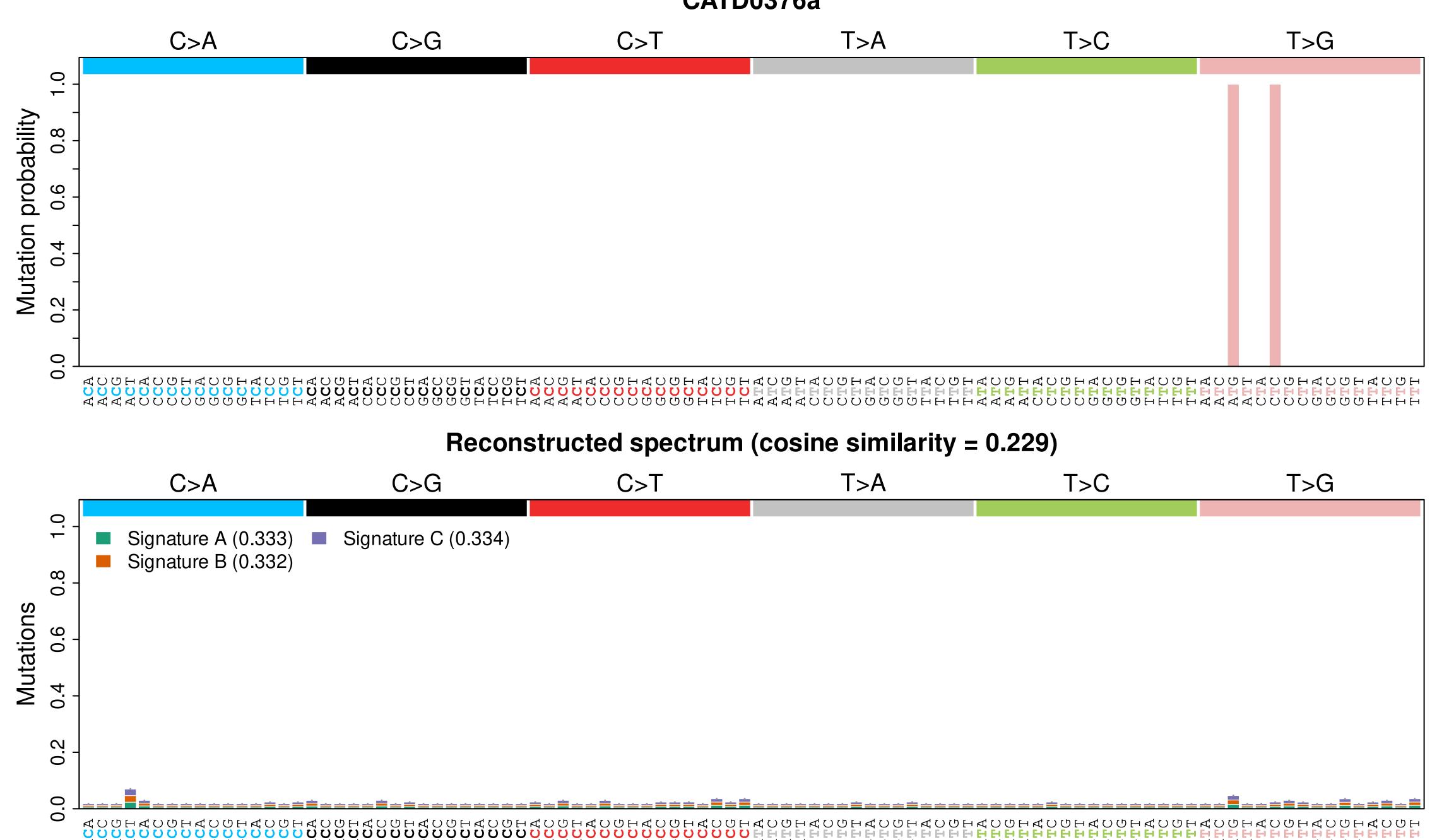




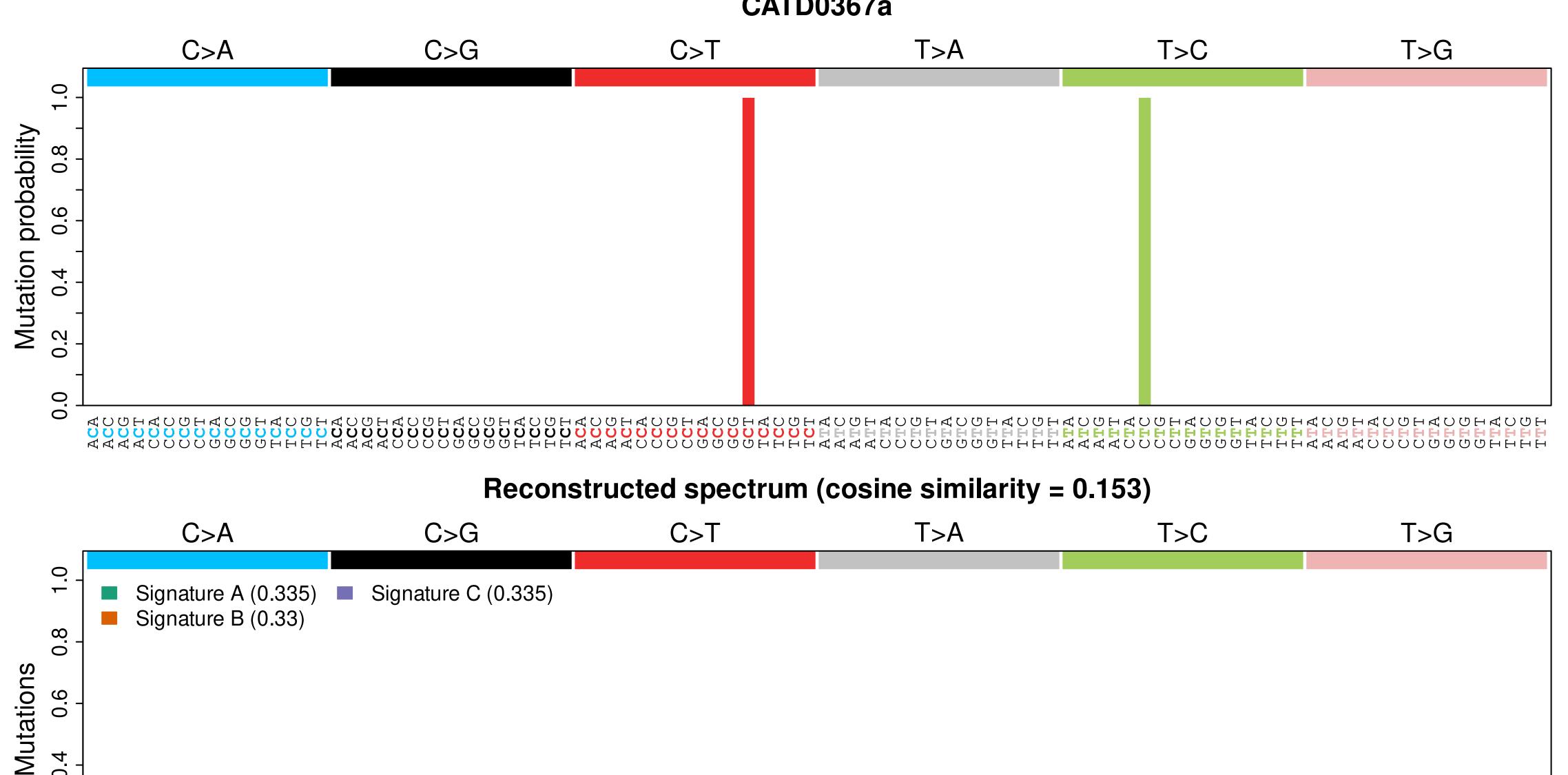
Reconstructed spectrum (cosine similarity = 0.172)





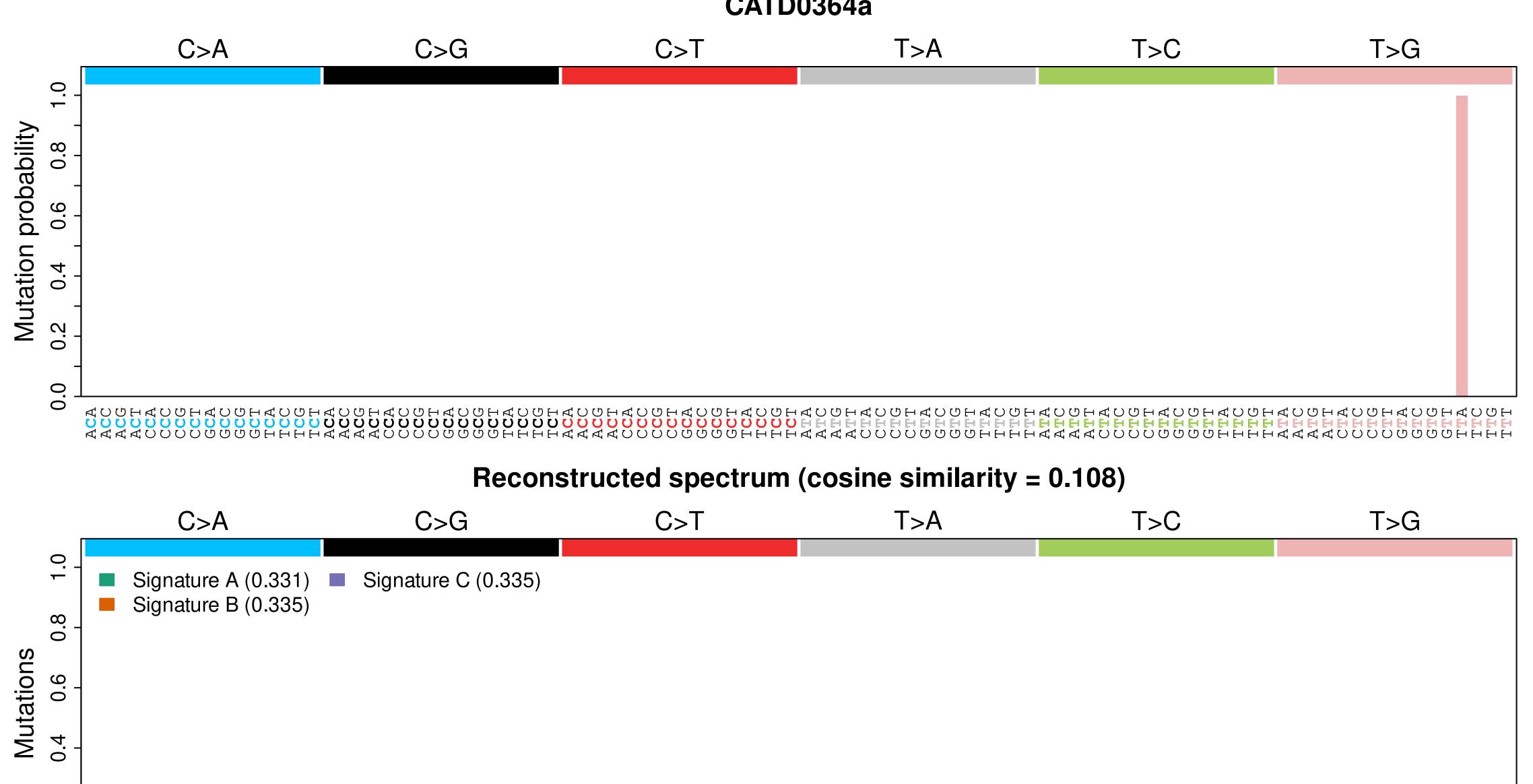






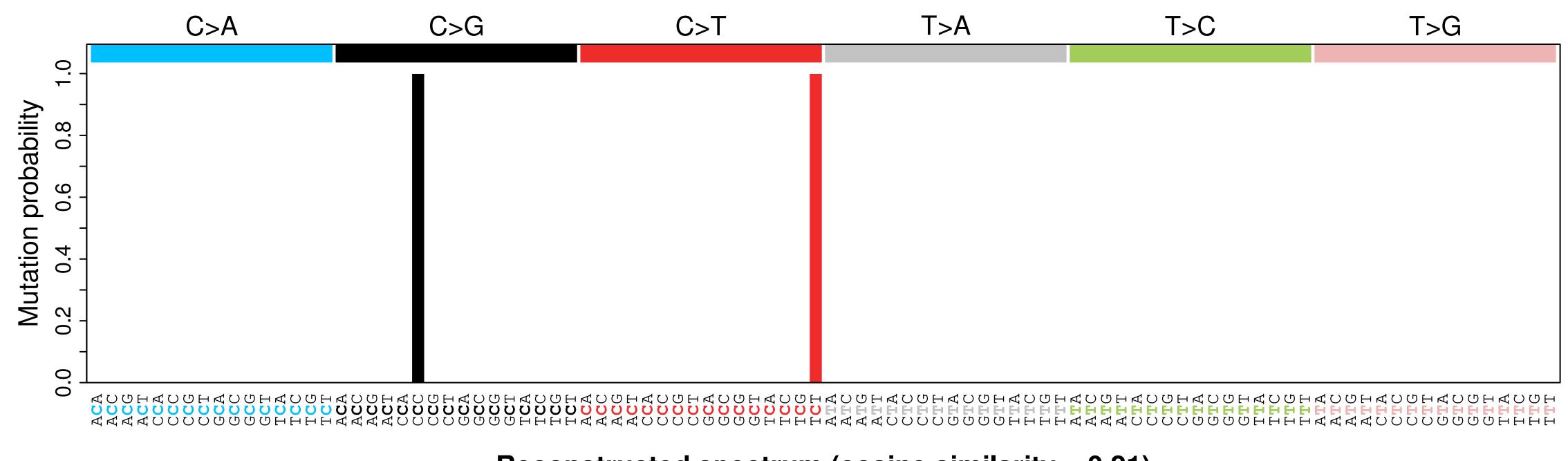
 \mathcal{O}



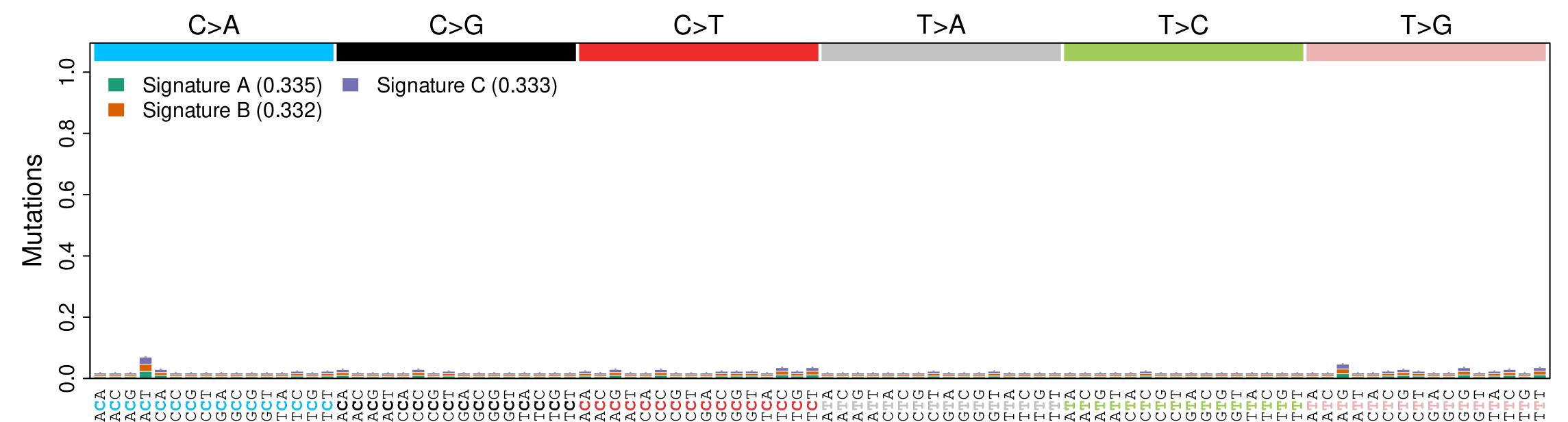


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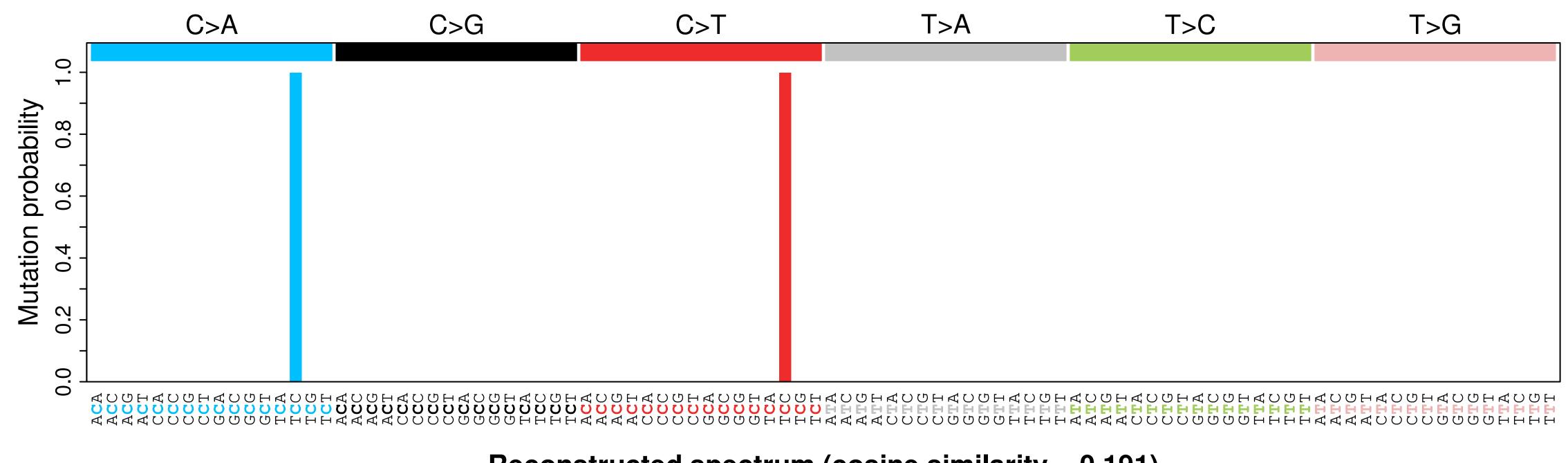


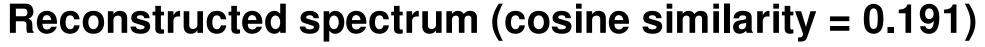


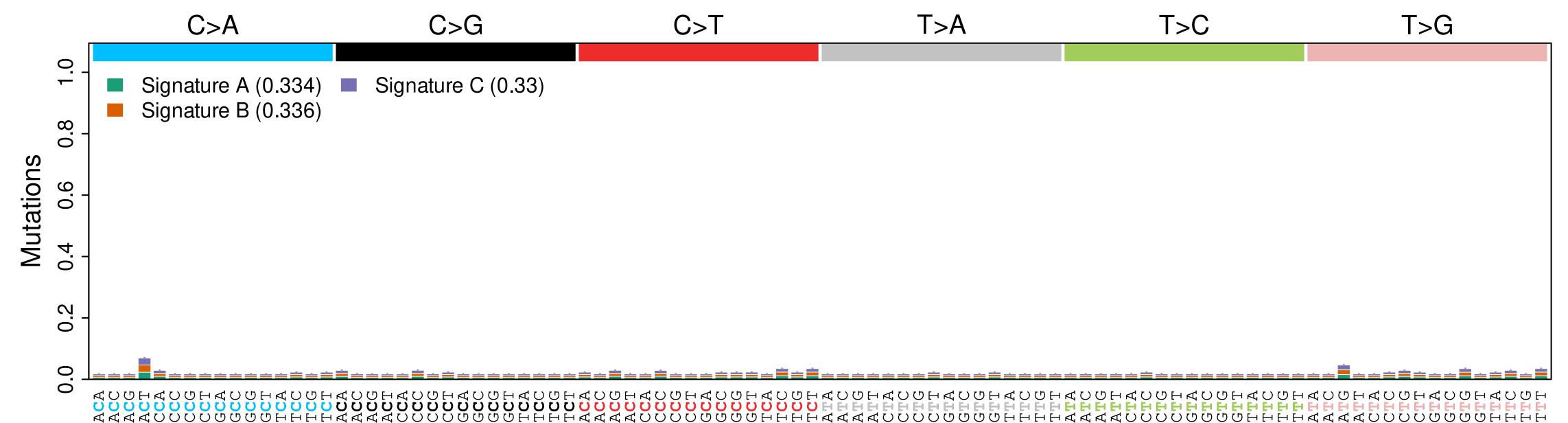
Reconstructed spectrum (cosine similarity = 0.21)











CATD0368a (3 mutations) T>G C>A C>G C>T T>A T>C 2.0 5 Mutations 0.5 0 **Reconstructed spectrum (cosine similarity = 0.253)** C>A C>G T>A T>C T>G C>T 2.0 Signature C (0.336) Signature A (0.33) Signature B (0.334) 5 Mutations 5 0