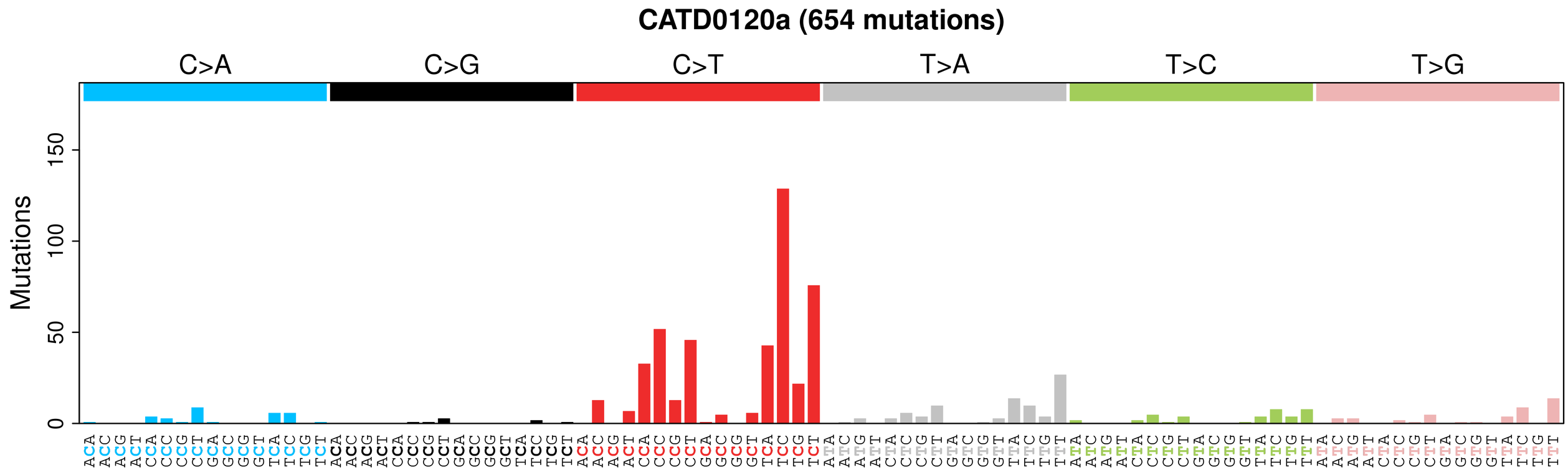
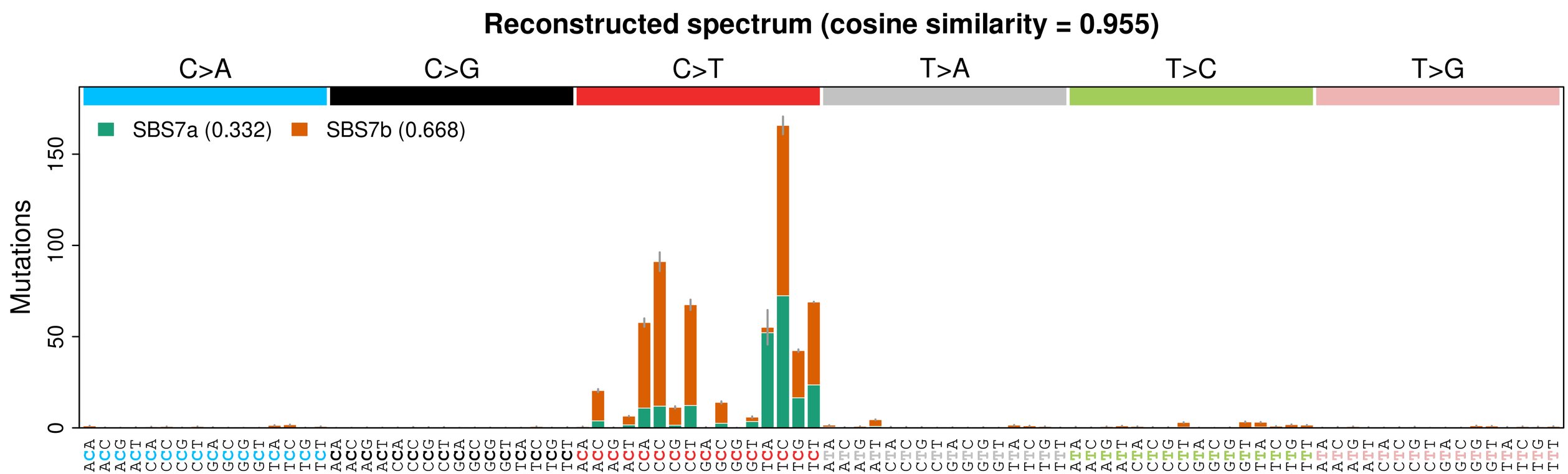

CATD0120a (654 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
50
100
150


Reconstructed spectrum (cosine similarity = 0.955)
C>A
C>G
C>T
T>A
T>C
T>G
SBS7a (0.332)
SBS7b (0.668)
Mutations
0
50
100
150