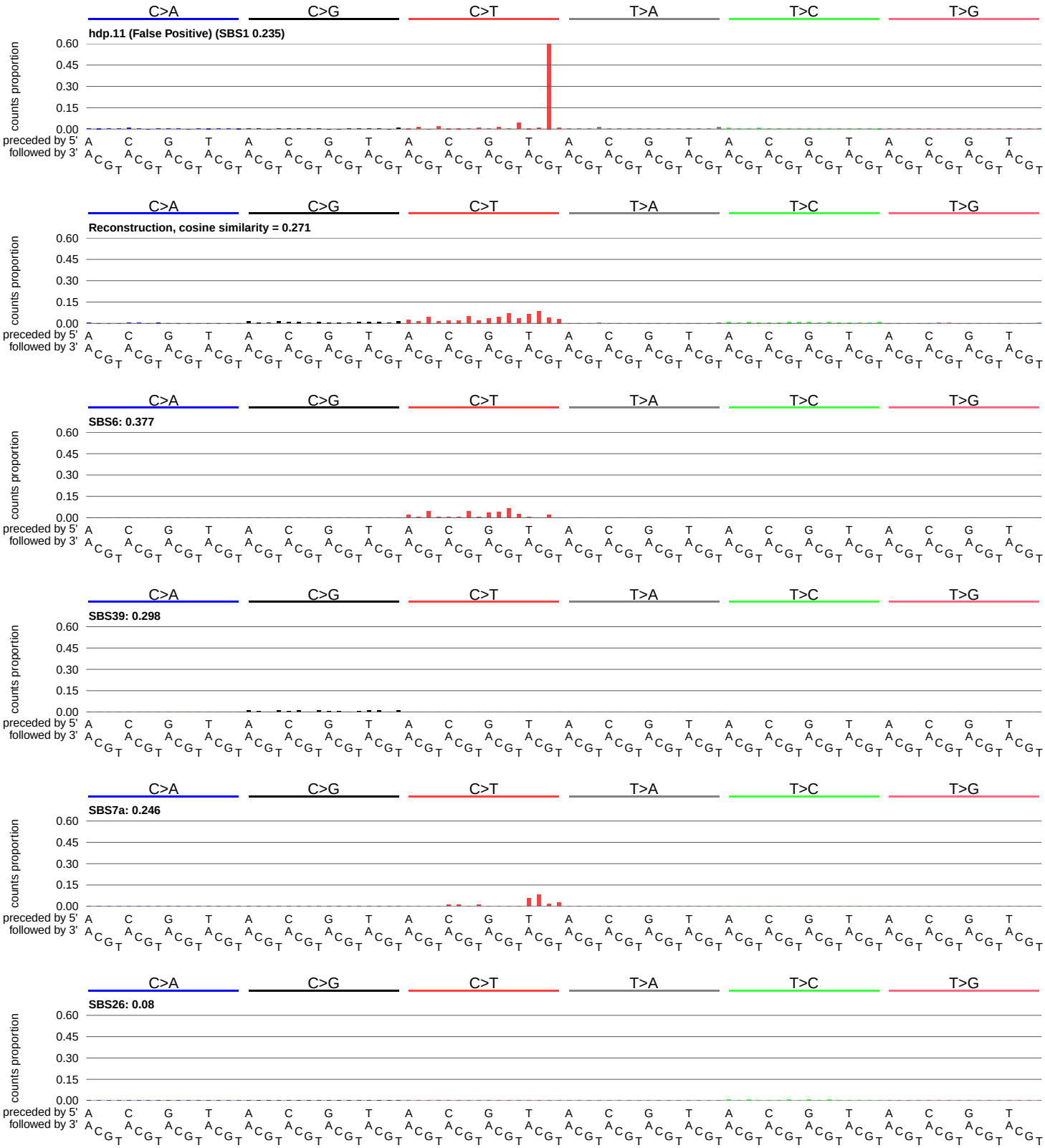
C>A
C>G
C>T
T>A
T>C
T>G
hdp.11 (False Positive) (SBS1 0.235)
Reconstruction, cosine similarity = 0.271
SBS6: 0.377
SBS39: 0.298
SBS7a: 0.246
SBS26: 0.08
counts proportion
0.60
0.45
0.30
0.15
0.00
preceded by 5'
followed by 3'