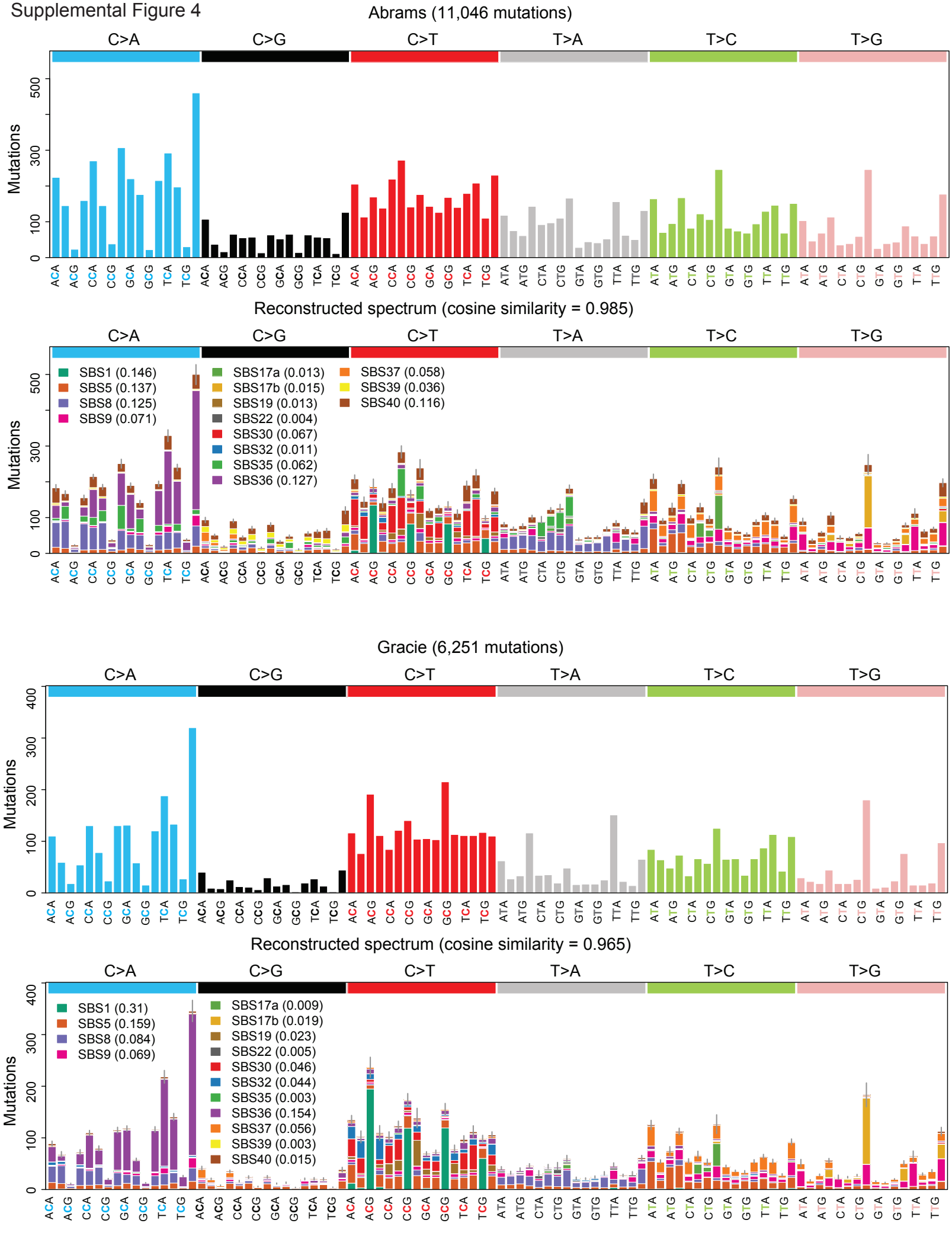
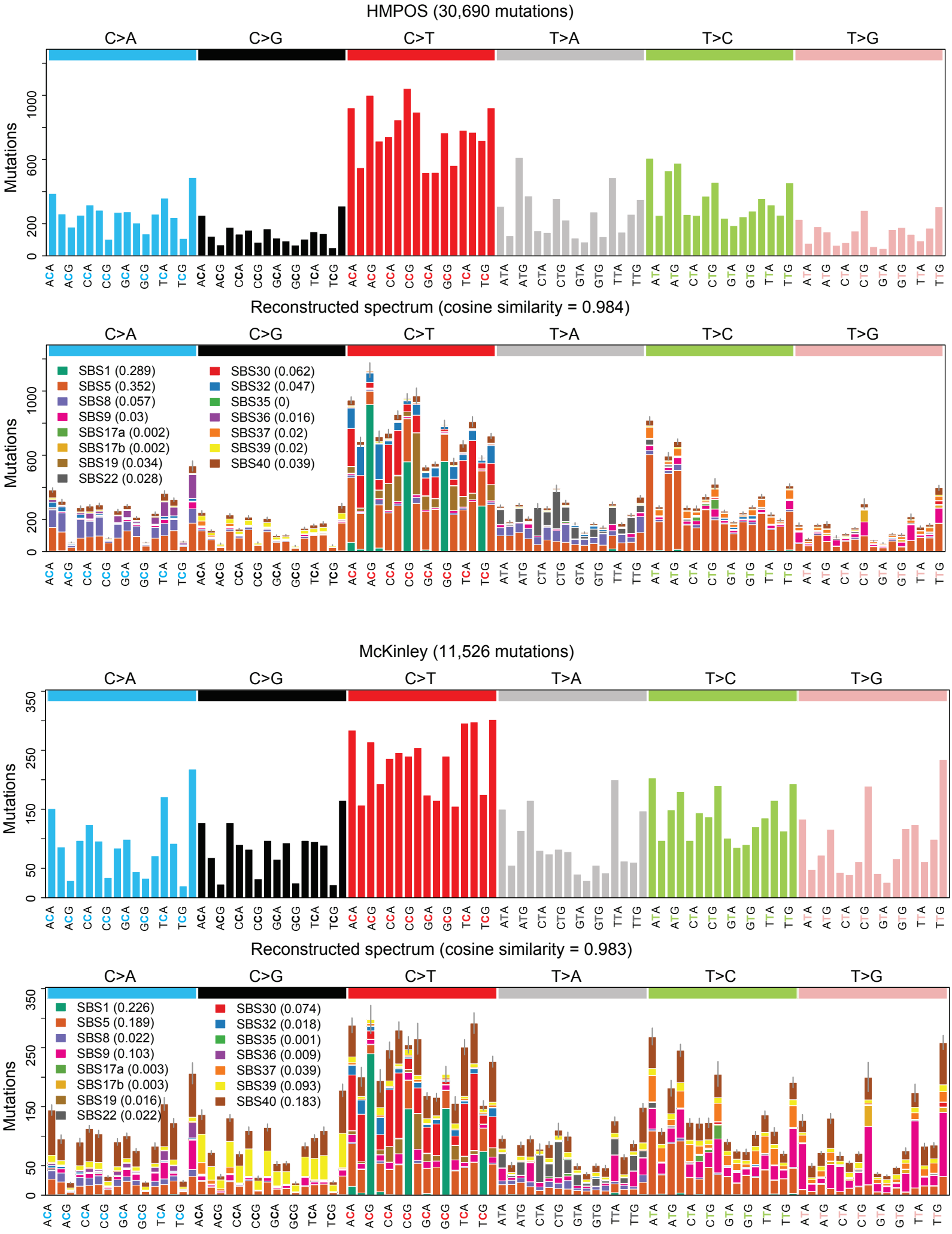
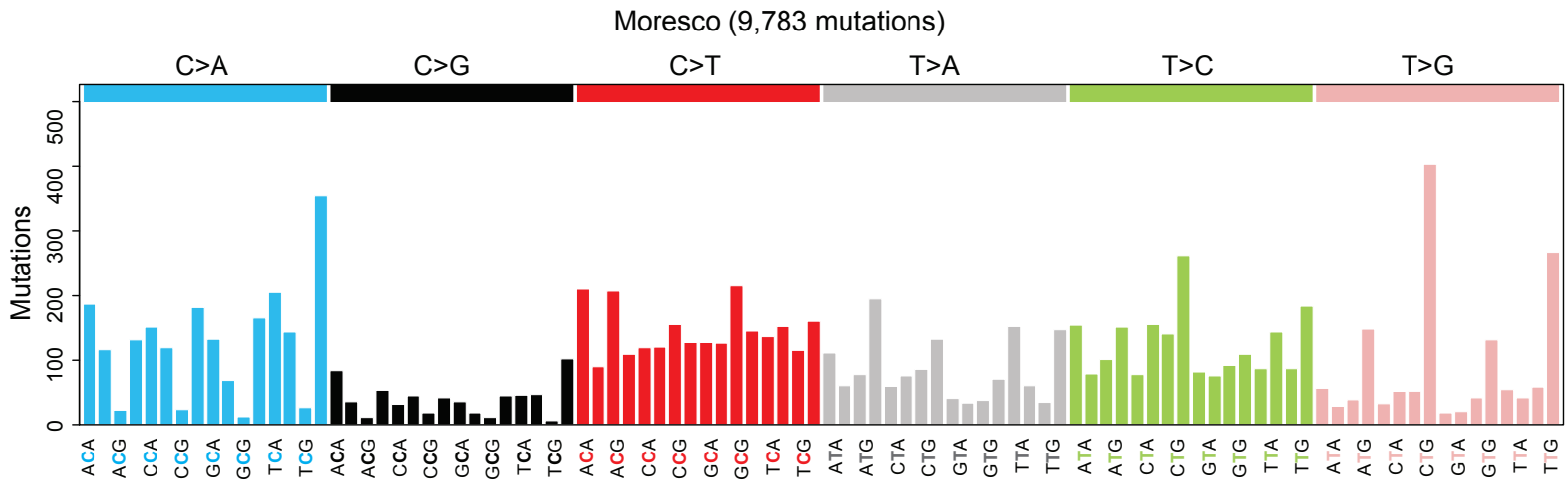
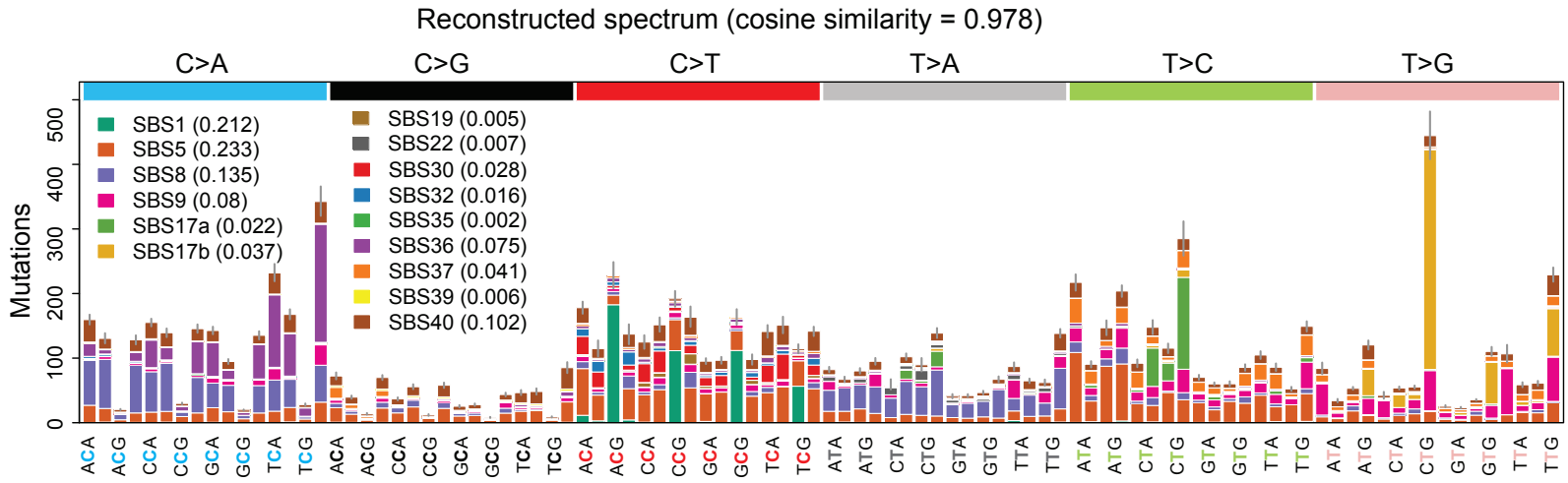
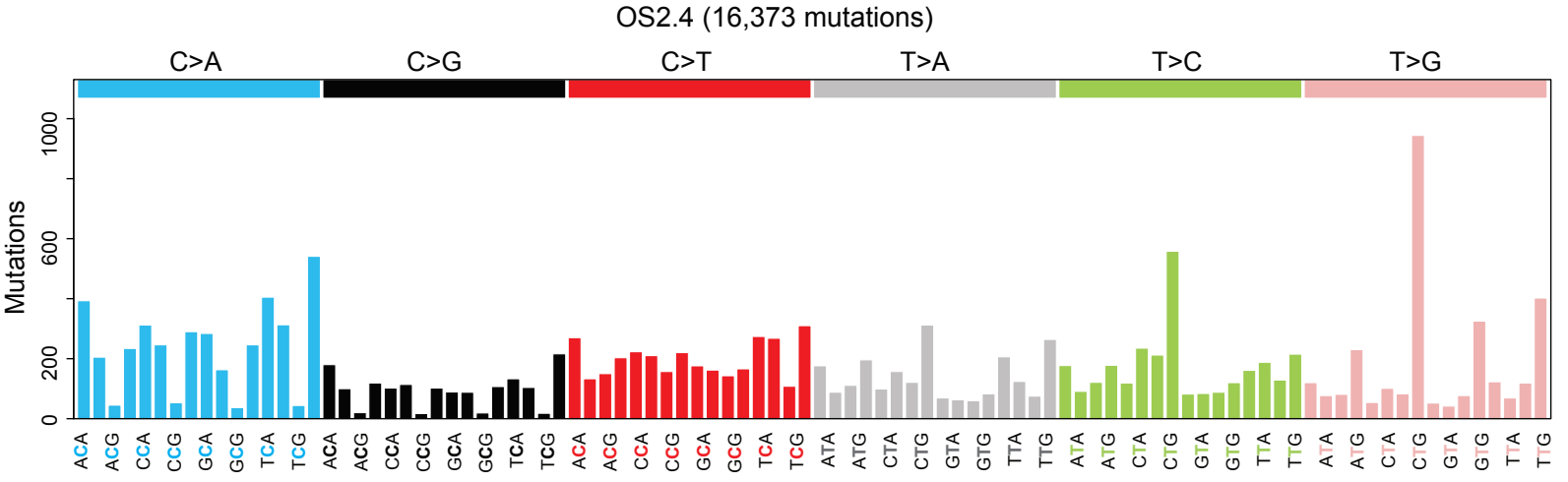
Supplemental Figure 4

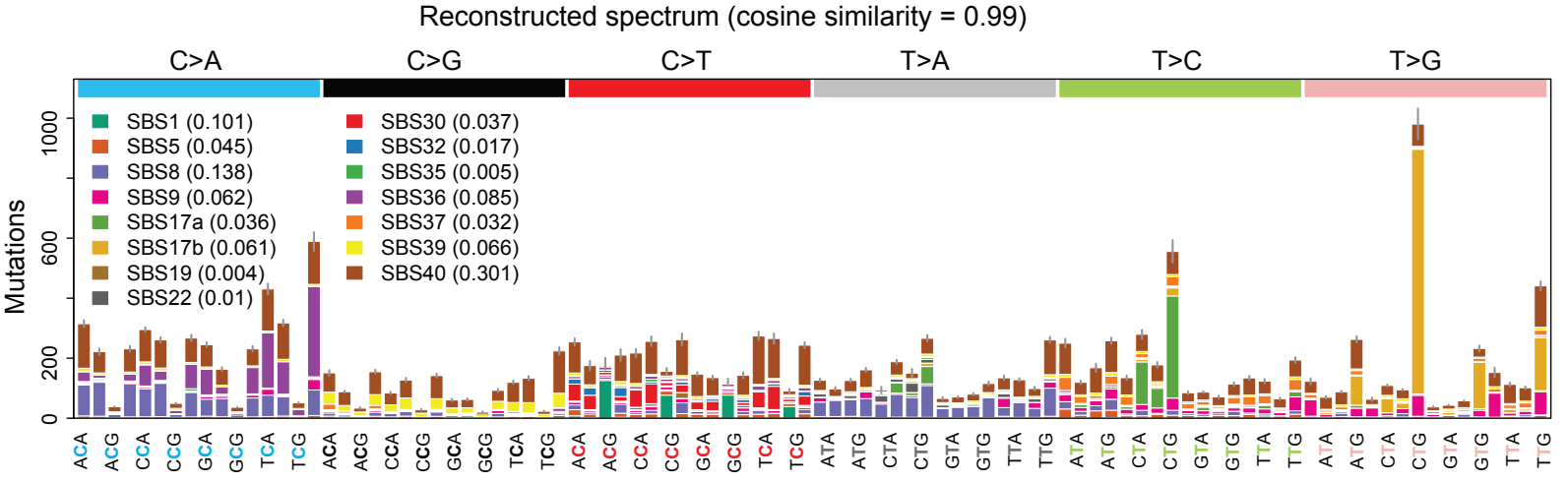


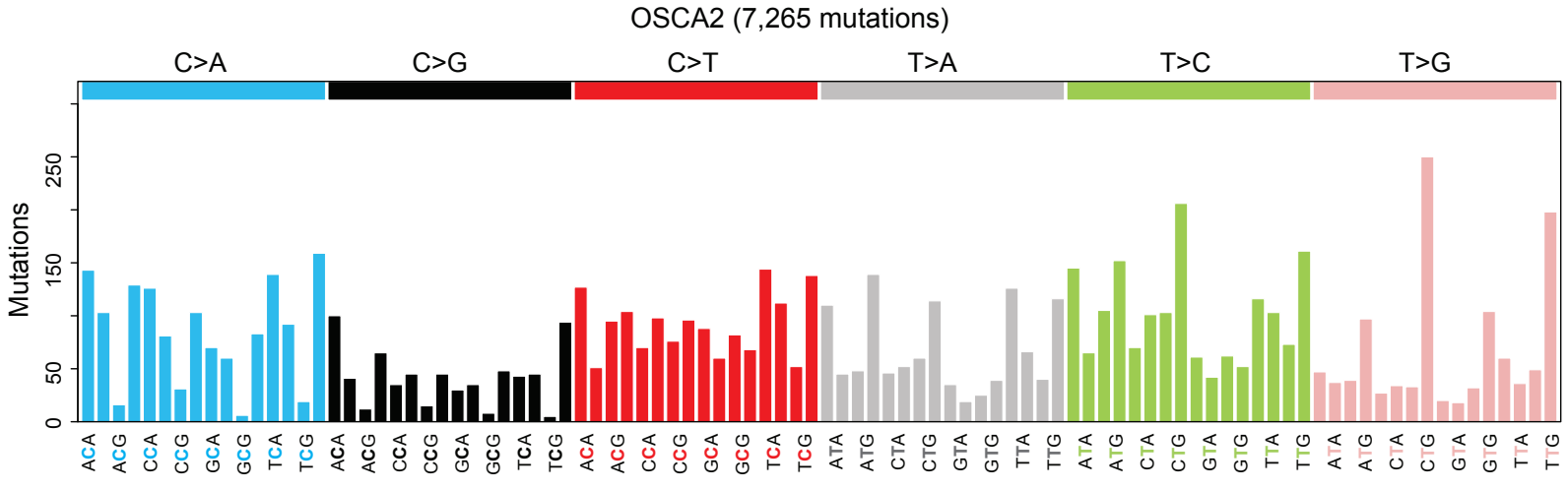

HMPOS (30,690 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed spectrum (cosine similarity = 0.984)
SBS1 (0.289)
SBS5 (0.352)
SBS8 (0.057)
SBS9 (0.03)
SBS17a (0.002)
SBS17b (0.002)
SBS19 (0.034)
SBS22 (0.028)
SBS30 (0.062)
SBS32 (0.047)
SBS35 (0)
SBS36 (0.016)
SBS37 (0.02)
SBS39 (0.02)
SBS40 (0.039)
McKinley (11,526 mutations)
Reconstructed spectrum (cosine similarity = 0.983)
SBS1 (0.226)
SBS5 (0.189)
SBS8 (0.022)
SBS9 (0.103)
SBS17a (0.003)
SBS17b (0.003)
SBS19 (0.016)
SBS22 (0.022)
SBS30 (0.074)
SBS32 (0.018)
SBS35 (0.001)
SBS36 (0.009)
SBS37 (0.039)
SBS39 (0.093)
SBS40 (0.183)

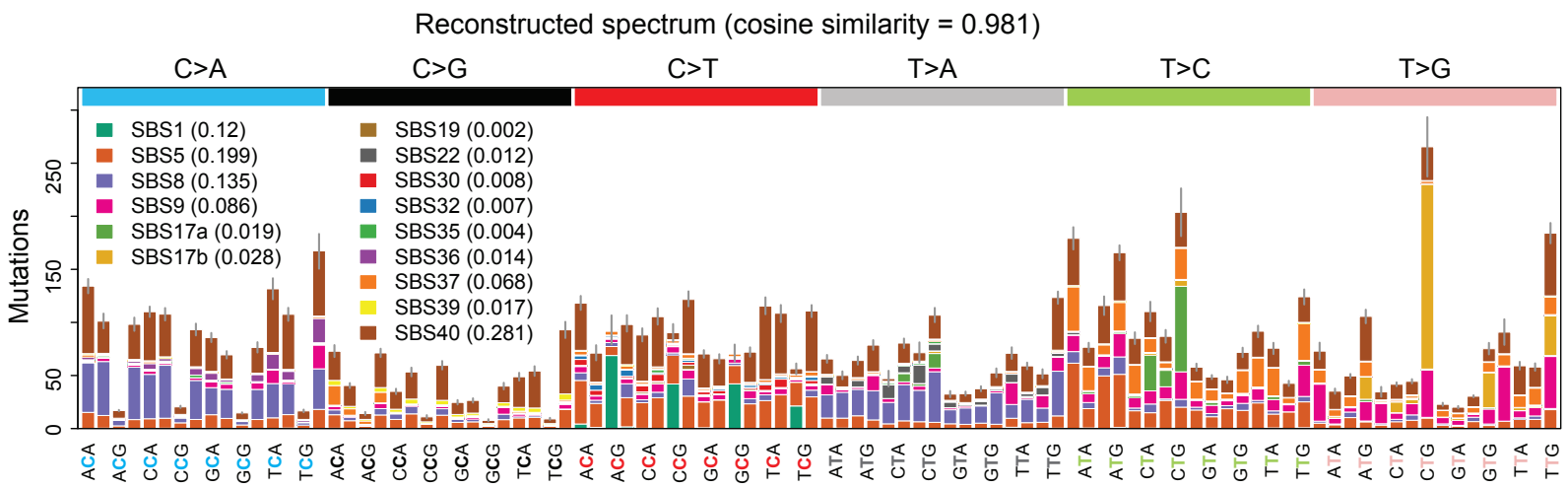

Moresco (9,783 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
100
200
300
400
500
ACA ACG CCA CCG GCA GCG TCA TCG ACA ACG CCA CCG GCA GCG TCA TCG ACA ACG CCA CCG GCA GCG TCA TCG ATA ATG CTA CTG GTA GTG TTA TTG ATA ATG CTA CTG GTA GTG TTA TTG ATA ATG CTA CTG GTA GTG TTA TTG

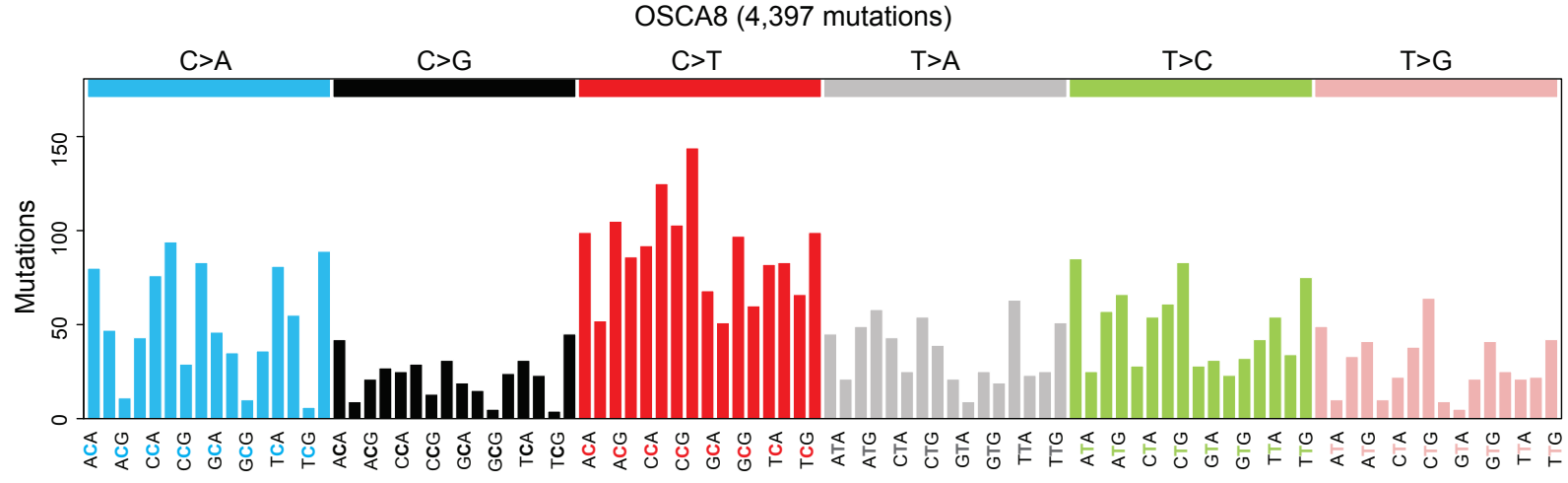

Reconstructed spectrum (cosine similarity = 0.978)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
100
200
300
400
500
SBS1 (0.212)
SBS5 (0.233)
SBS8 (0.135)
SBS9 (0.08)
SBS17a (0.022)
SBS17b (0.037)
SBS19 (0.005)
SBS22 (0.007)
SBS30 (0.028)
SBS32 (0.016)
SBS35 (0.002)
SBS36 (0.075)
SBS37 (0.041)
SBS39 (0.006)
SBS40 (0.102)
ACA ACG CCA CCG GCA GCG TCA TCG ACA ACG CCA CCG GCA GCG TCA TCG ACA ACG CCA CCG GCA GCG TCA TCG ATA ATG CTA CTG GTA GTG TTA TTG ATA ATG CTA CTG GTA GTG TTA TTG ATA ATG CTA CTG GTA GTG TTA TTG

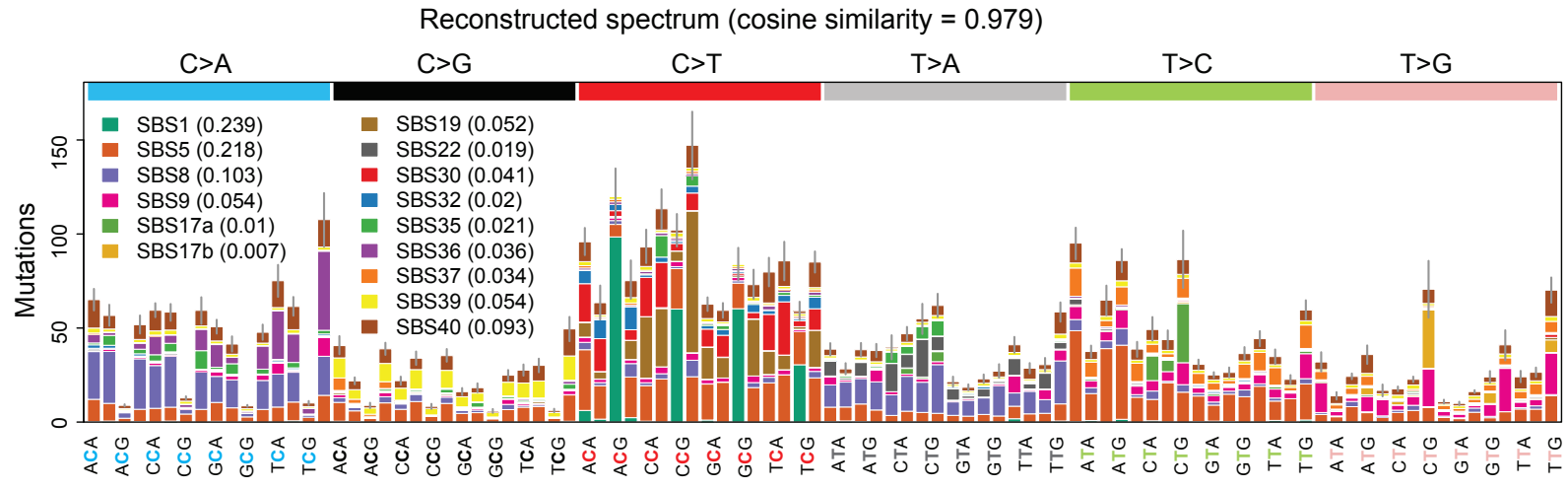

OS2.4 (16,373 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
200
600
1000
ACA ACG CCA CCG GCA GCG TCA TCG ACA ACG CCA CCG GCA GCG TCA TCG ACA ACG CCA CCG GCA GCG TCA TCG ATA ATG CTA CTG GTA GTG TTA TTG ATA ATG CTA CTG GTA GTG TTA TTG ATA ATG CTA CTG GTA GTG TTA TTG


Reconstructed spectrum (cosine similarity = 0.99)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
200
600
1000
SBS1 (0.101)
SBS5 (0.045)
SBS8 (0.138)
SBS9 (0.062)
SBS17a (0.036)
SBS17b (0.061)
SBS19 (0.004)
SBS22 (0.01)
SBS30 (0.037)
SBS32 (0.017)
SBS35 (0.005)
SBS36 (0.085)
SBS37 (0.032)
SBS39 (0.066)
SBS40 (0.301)
ACA ACG CCA CCG GCA GCG TCA TCG ACA ACG CCA CCG GCA GCG TCA TCG ACA ACG CCA CCG GCA GCG TCA TCG ATA ATG CTA CTG GTA GTG TTA TTG ATA ATG CTA CTG GTA GTG TTA TTG ATA ATG CTA CTG GTA GTG TTA TTG


OSCA2 (7,265 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
50
150
250


Reconstructed spectrum (cosine similarity = 0.981)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
50
150
250
SBS1 (0.12)
SBS5 (0.199)
SBS8 (0.135)
SBS9 (0.086)
SBS17a (0.019)
SBS17b (0.028)
SBS19 (0.002)
SBS22 (0.012)
SBS30 (0.008)
SBS32 (0.007)
SBS35 (0.004)
SBS36 (0.014)
SBS37 (0.068)
SBS39 (0.017)
SBS40 (0.281)


OSCA8 (4,397 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
50
100
150


Reconstructed spectrum (cosine similarity = 0.979)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
50
100
150
SBS1 (0.239)
SBS5 (0.218)
SBS8 (0.103)
SBS9 (0.054)
SBS17a (0.01)
SBS17b (0.007)
SBS19 (0.052)
SBS22 (0.019)
SBS30 (0.041)
SBS32 (0.02)
SBS35 (0.021)
SBS36 (0.036)
SBS37 (0.034)
SBS39 (0.054)
SBS40 (0.093)