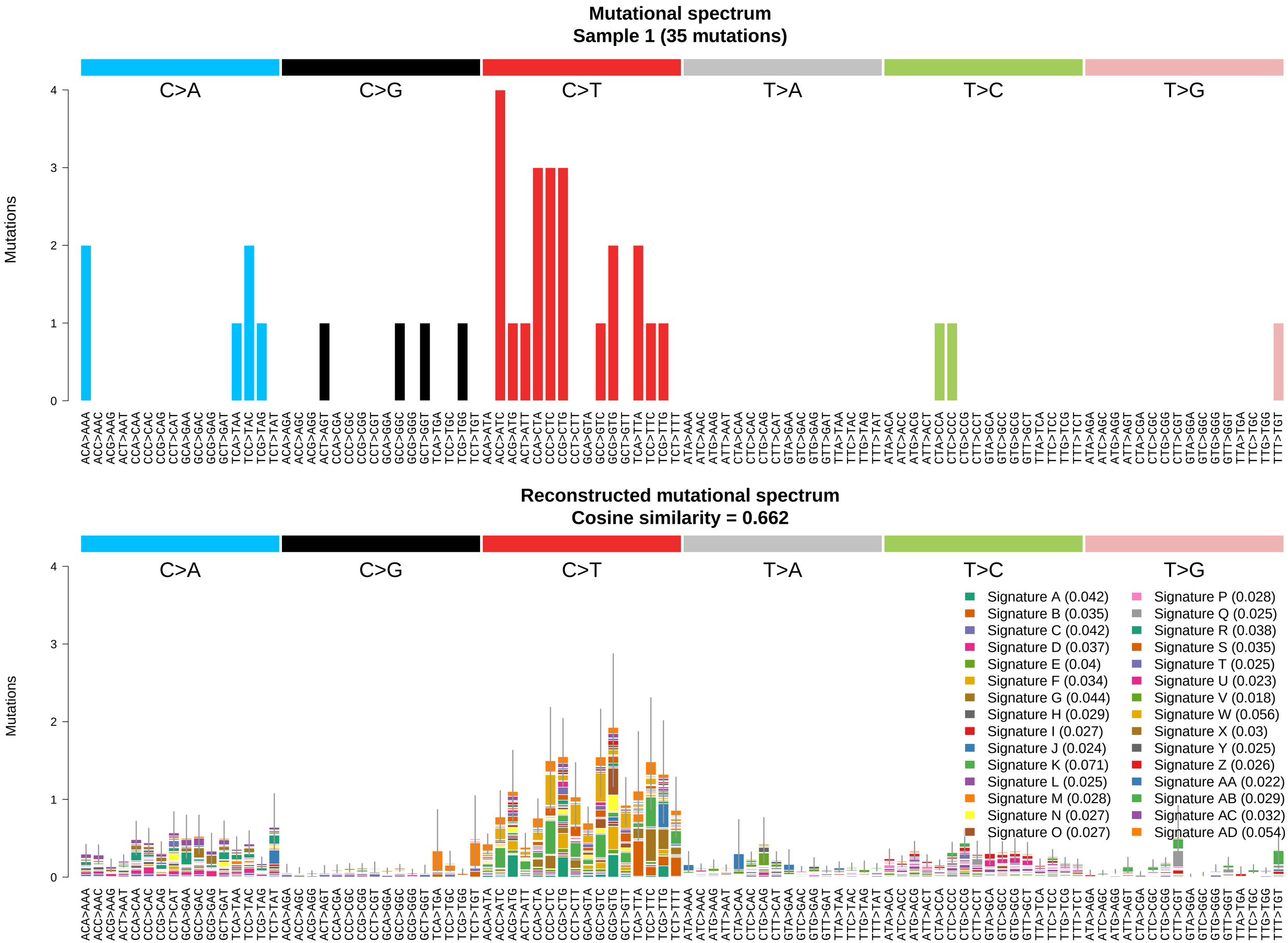
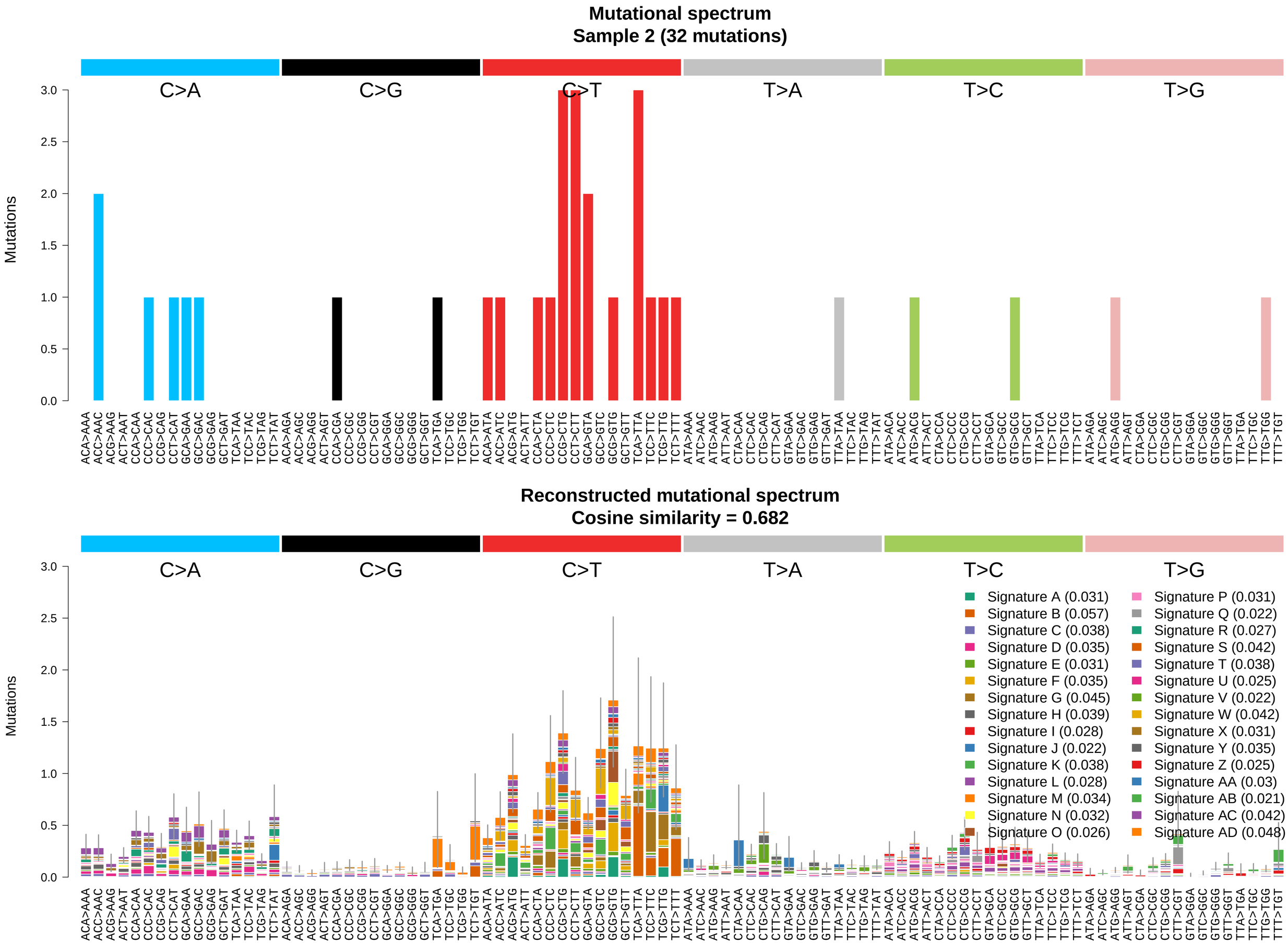
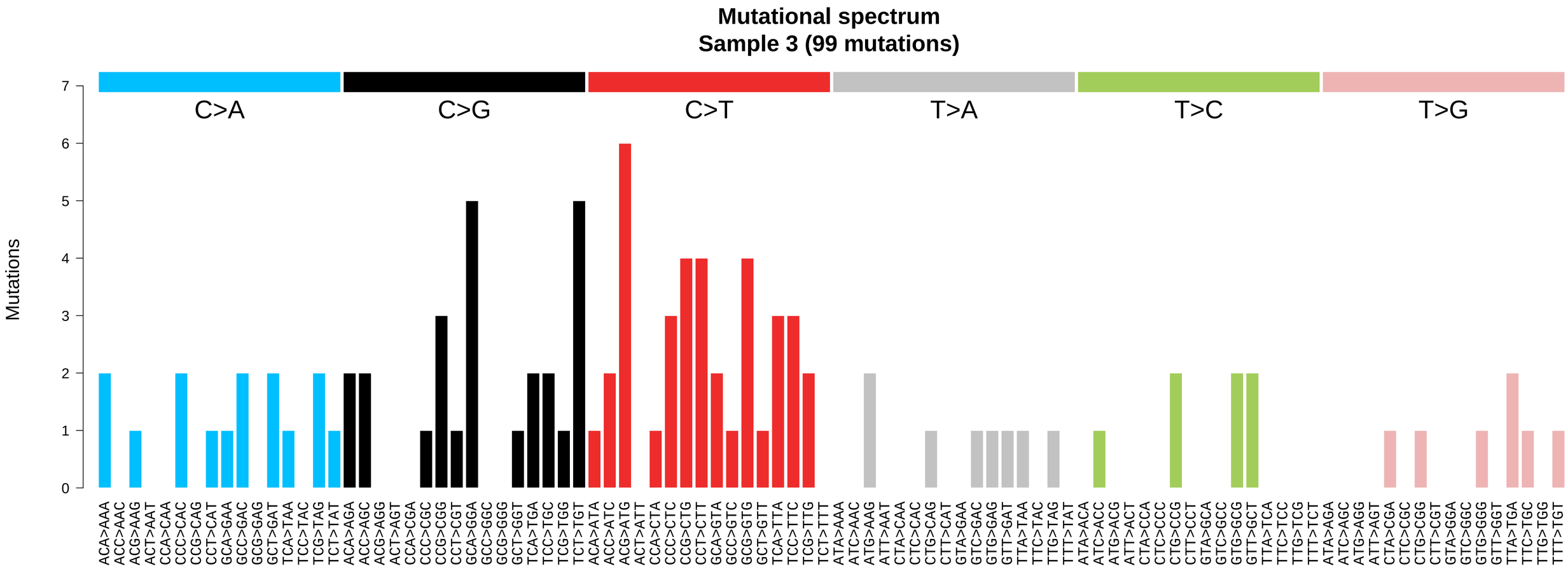
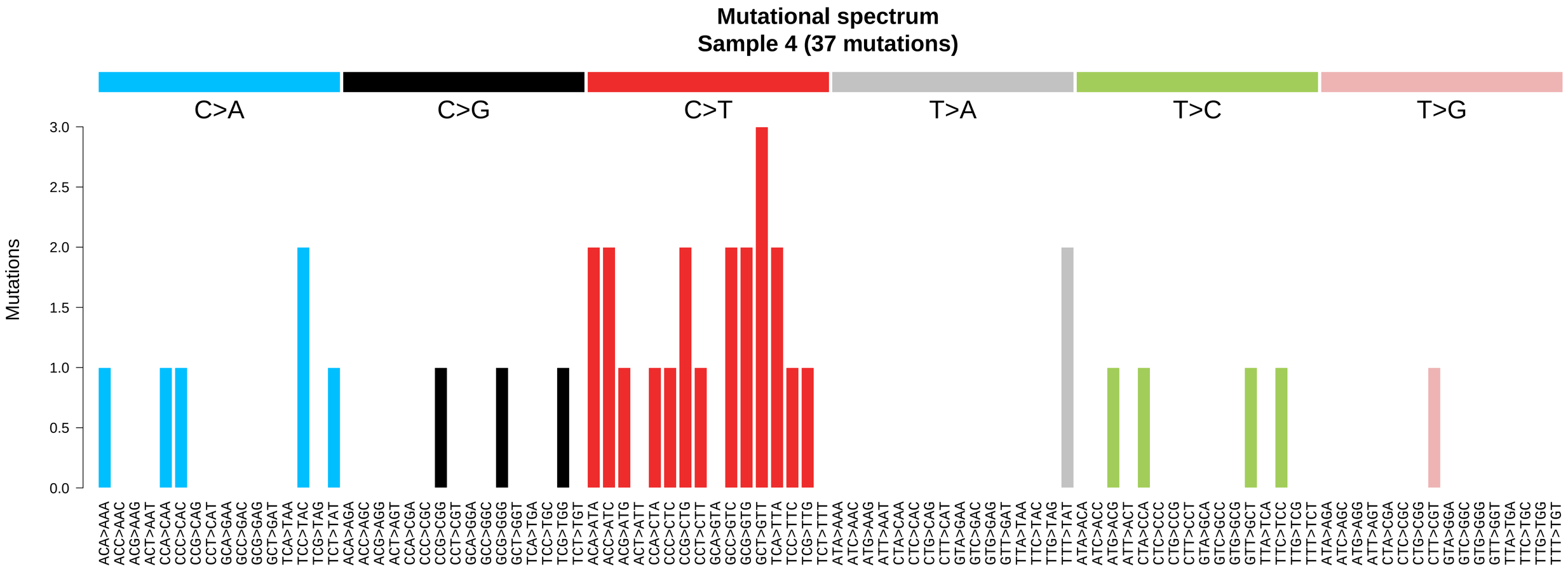
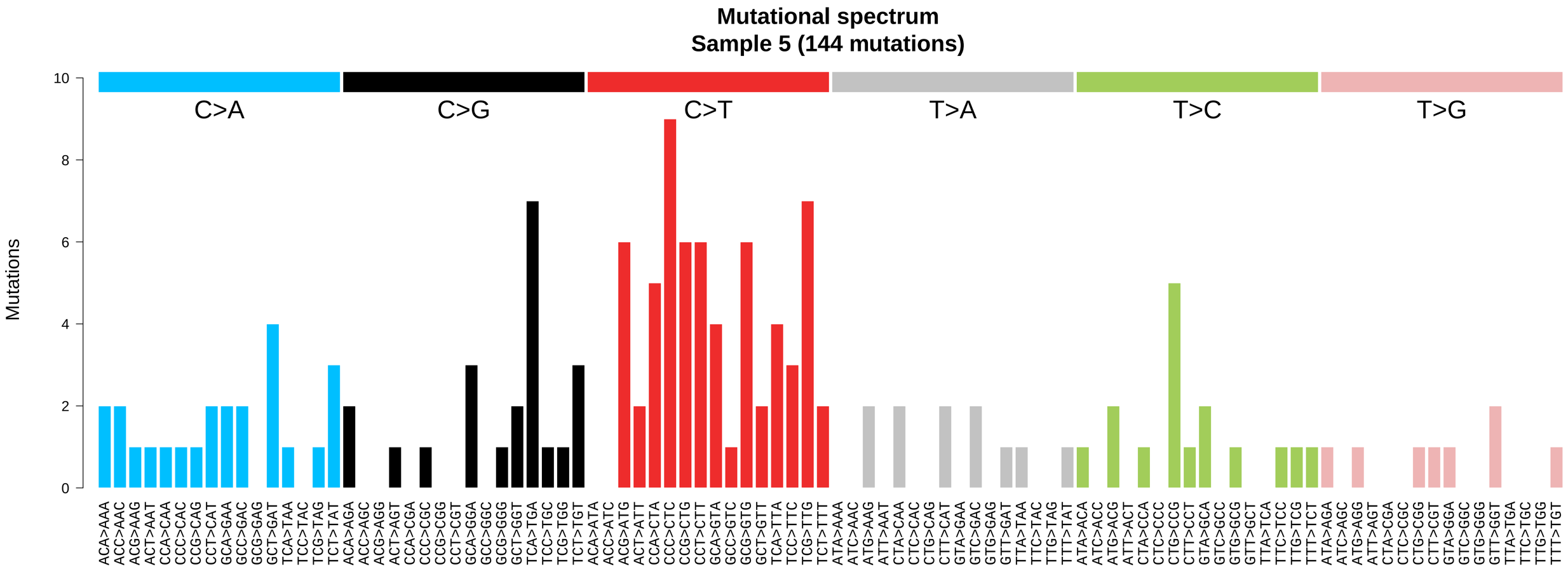
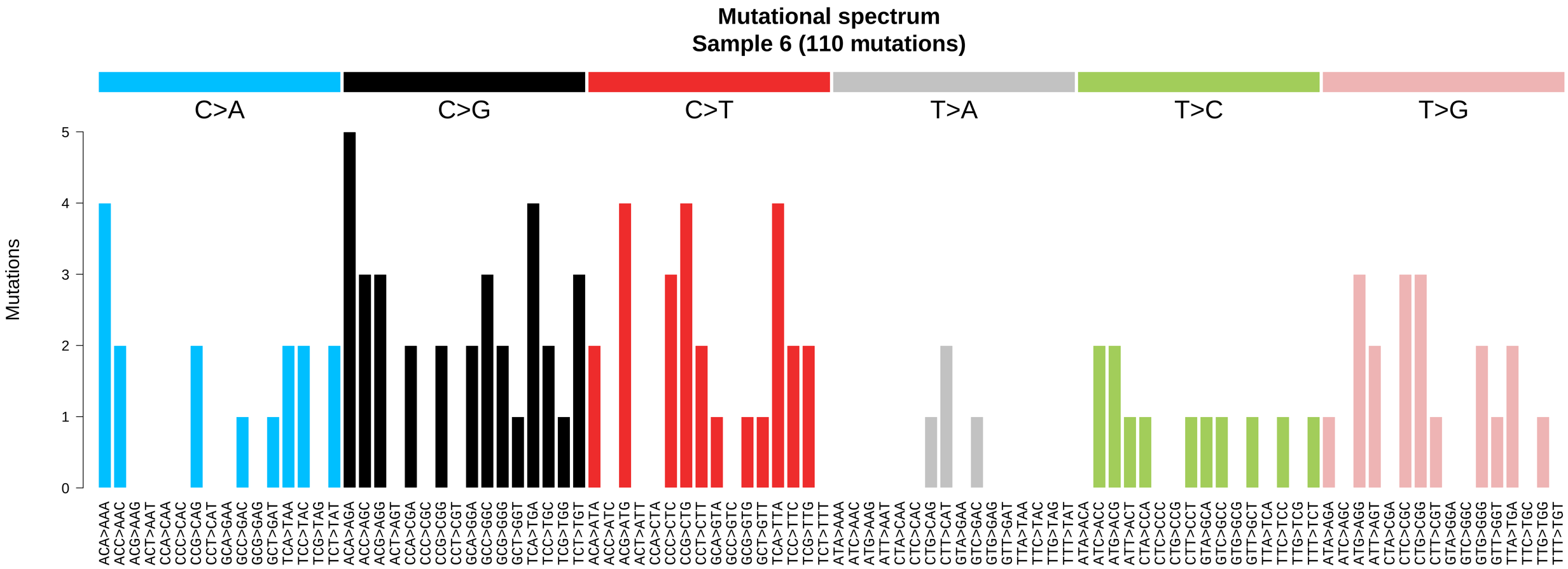

Mutational spectrum
Sample 1 (35 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.662
Signature A (0.042)
Signature B (0.035)
Signature C (0.042)
Signature D (0.037)
Signature E (0.04)
Signature F (0.034)
Signature G (0.044)
Signature H (0.029)
Signature I (0.027)
Signature J (0.024)
Signature K (0.071)
Signature L (0.025)
Signature M (0.028)
Signature N (0.027)
Signature O (0.027)
Signature P (0.028)
Signature Q (0.025)
Signature R (0.038)
Signature S (0.035)
Signature T (0.025)
Signature U (0.023)
Signature V (0.018)
Signature W (0.056)
Signature X (0.03)
Signature Y (0.025)
Signature Z (0.026)
Signature AA (0.022)
Signature AB (0.029)
Signature AC (0.032)
Signature AD (0.054)

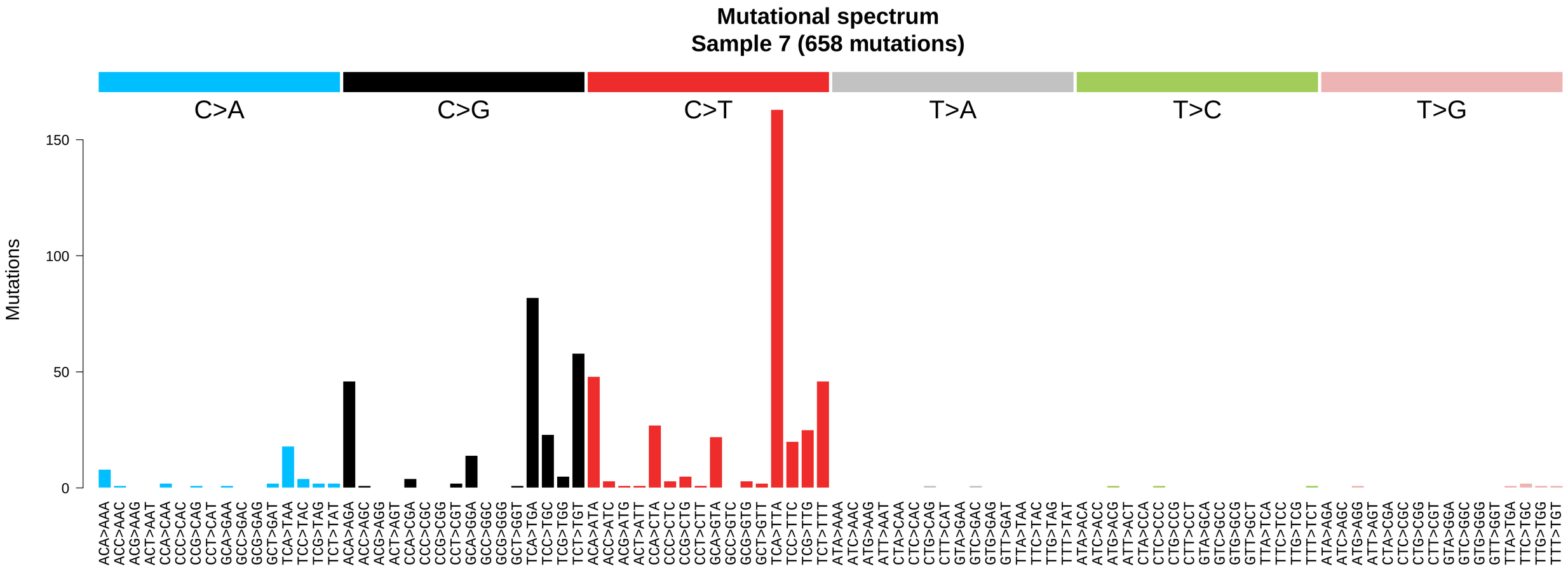

Mutational spectrum
Sample 2 (32 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.682
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Signature A (0.031)
Signature B (0.057)
Signature C (0.038)
Signature D (0.035)
Signature E (0.031)
Signature F (0.035)
Signature G (0.045)
Signature H (0.039)
Signature I (0.028)
Signature J (0.022)
Signature K (0.038)
Signature L (0.028)
Signature M (0.034)
Signature N (0.032)
Signature O (0.026)
Signature P (0.031)
Signature Q (0.022)
Signature R (0.027)
Signature S (0.042)
Signature T (0.038)
Signature U (0.025)
Signature V (0.022)
Signature W (0.042)
Signature X (0.031)
Signature Y (0.035)
Signature Z (0.025)
Signature AA (0.03)
Signature AB (0.021)
Signature AC (0.042)
Signature AD (0.048)
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT

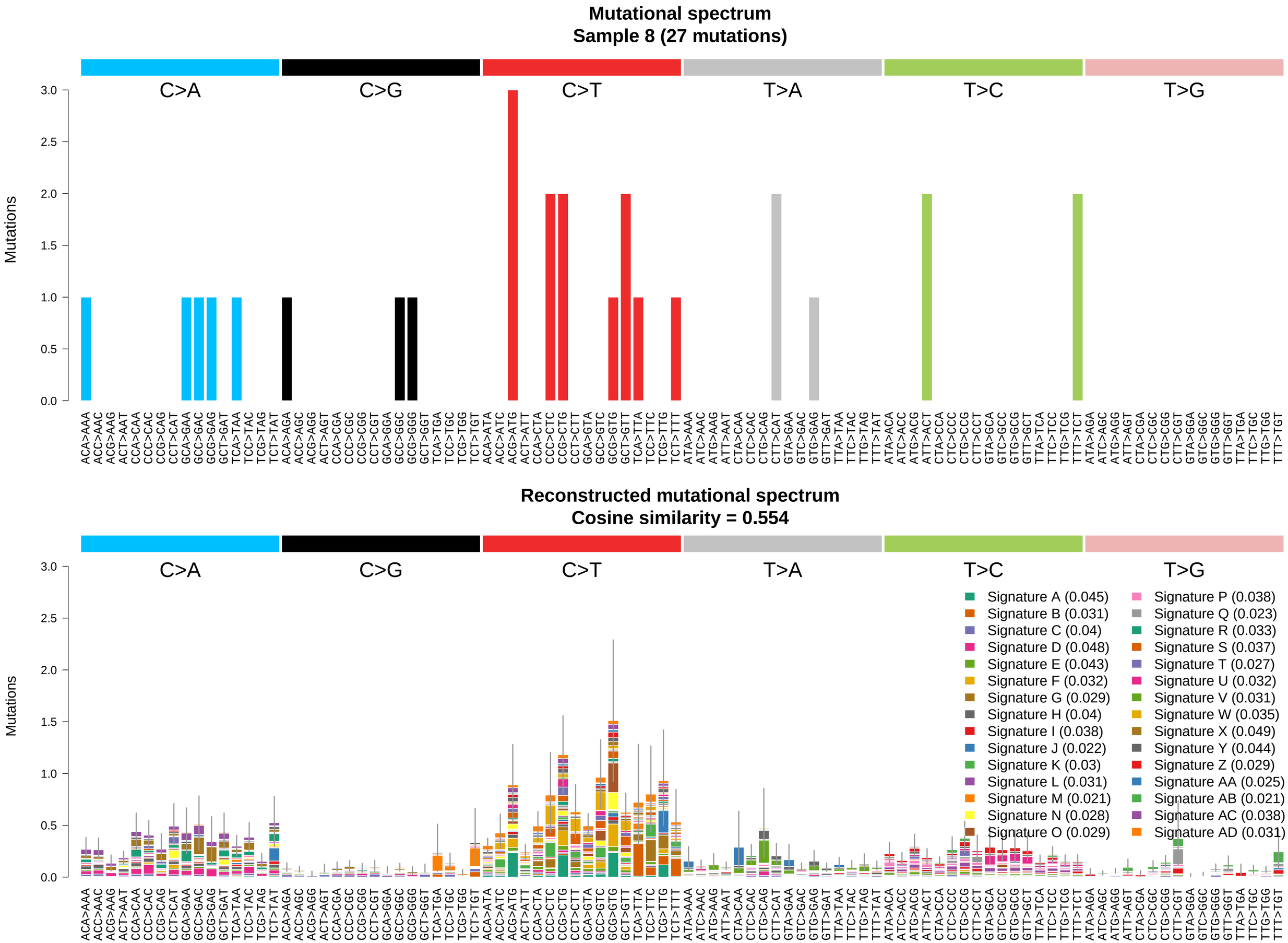

Mutational spectrum
Sample 3 (99 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
7
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.785
Signature A (0.04)
Signature B (0.021)
Signature C (0.143)
Signature D (0.048)
Signature E (0.046)
Signature F (0.027)
Signature G (0.025)
Signature H (0.031)
Signature I (0.046)
Signature J (0.017)
Signature K (0.024)
Signature L (0.019)
Signature M (0.08)
Signature N (0.023)
Signature O (0.021)
Signature P (0.025)
Signature Q (0.013)
Signature R (0.029)
Signature S (0.036)
Signature T (0.024)
Signature U (0.021)
Signature V (0.024)
Signature W (0.025)
Signature X (0.025)
Signature Y (0.032)
Signature Z (0.02)
Signature AA (0.013)
Signature AB (0.017)
Signature AC (0.031)
Signature AD (0.052)

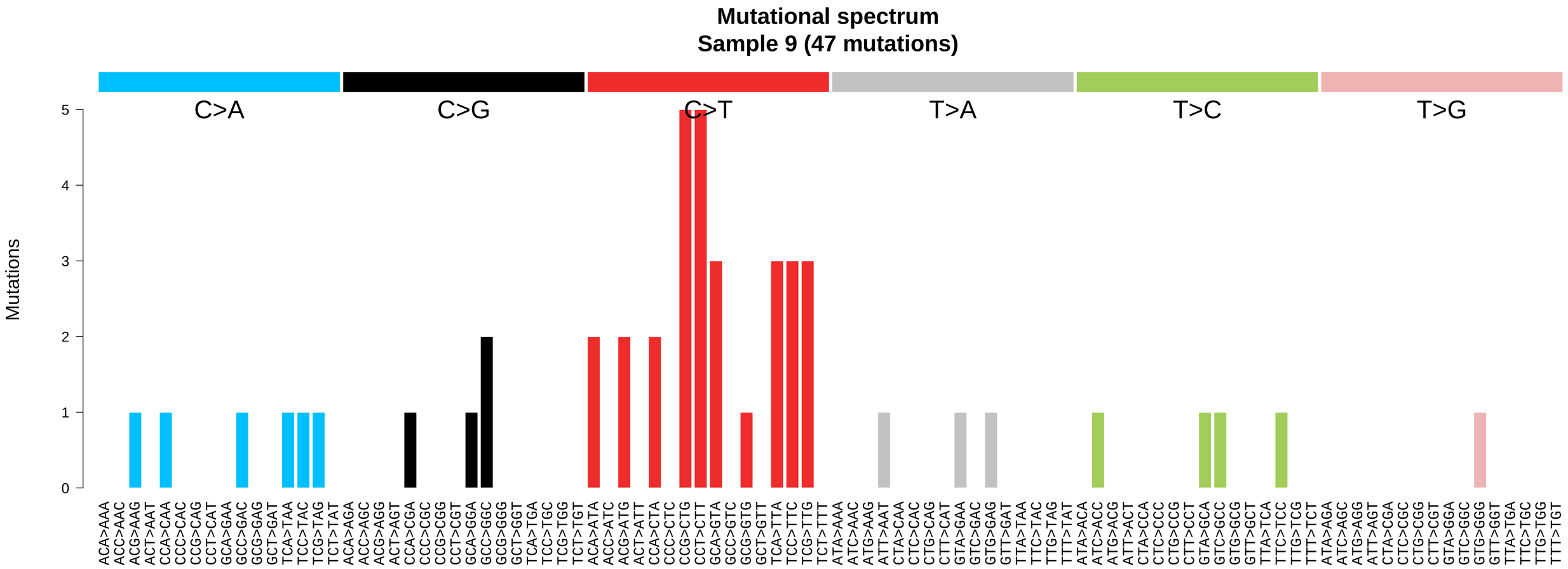

Mutational spectrum
Sample 4 (37 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.731
Signature A (0.034)
Signature B (0.032)
Signature C (0.036)
Signature D (0.047)
Signature E (0.039)
Signature F (0.035)
Signature G (0.035)
Signature H (0.034)
Signature I (0.027)
Signature J (0.028)
Signature K (0.044)
Signature L (0.031)
Signature M (0.025)
Signature N (0.032)
Signature O (0.033)
Signature P (0.031)
Signature Q (0.028)
Signature R (0.035)
Signature S (0.045)
Signature T (0.032)
Signature U (0.029)
Signature V (0.02)
Signature W (0.049)
Signature X (0.032)
Signature Y (0.031)
Signature Z (0.03)
Signature AA (0.021)
Signature AB (0.024)
Signature AC (0.028)
Signature AD (0.051)

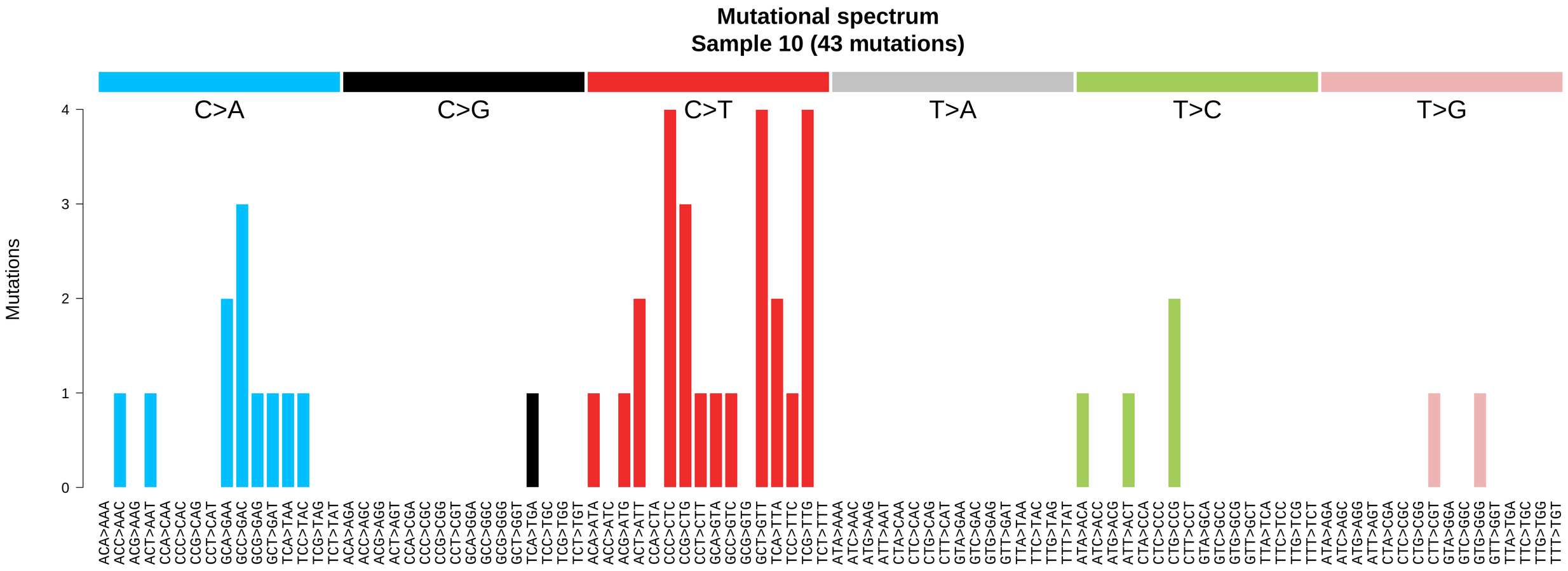

Mutational spectrum
Sample 5 (144 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.856
Signature A (0.037)
Signature B (0.022)
Signature C (0.07)
Signature D (0.03)
Signature E (0.049)
Signature F (0.027)
Signature G (0.043)
Signature H (0.047)
Signature I (0.041)
Signature J (0.03)
Signature K (0.026)
Signature L (0.023)
Signature M (0.079)
Signature N (0.024)
Signature O (0.019)
Signature P (0.027)
Signature Q (0.023)
Signature R (0.027)
Signature S (0.05)
Signature T (0.036)
Signature U (0.02)
Signature V (0.015)
Signature W (0.038)
Signature X (0.024)
Signature Y (0.034)
Signature Z (0.026)
Signature AA (0.022)
Signature AB (0.016)
Signature AC (0.036)
Signature AD (0.037)

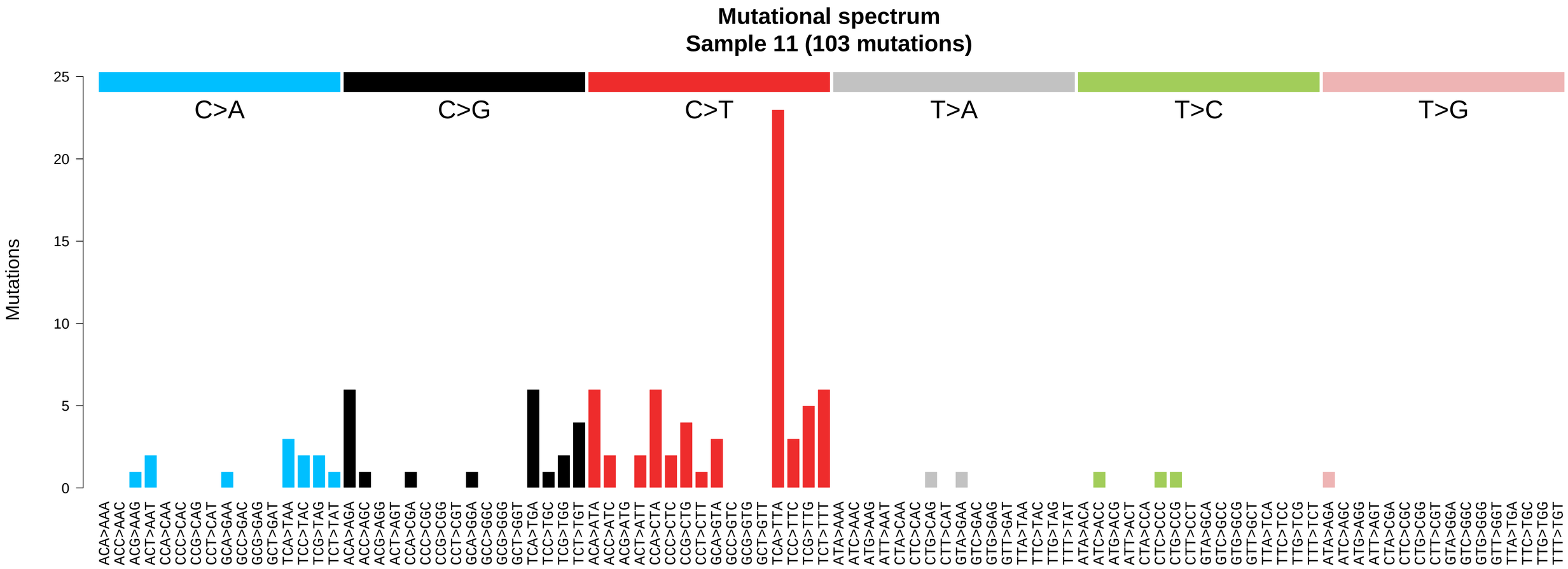

Mutational spectrum
Sample 6 (110 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.702
Signature A (0.023)
Signature B (0.022)
Signature C (0.332)
Signature D (0.027)
Signature E (0.035)
Signature F (0.017)
Signature G (0.018)
Signature H (0.026)
Signature I (0.051)
Signature J (0.017)
Signature K (0.015)
Signature L (0.019)
Signature M (0.065)
Signature N (0.013)
Signature O (0.012)
Signature P (0.025)
Signature Q (0.022)
Signature R (0.022)
Signature S (0.018)
Signature T (0.018)
Signature U (0.019)
Signature V (0.012)
Signature W (0.013)
Signature X (0.021)
Signature Y (0.025)
Signature Z (0.02)
Signature AA (0.011)
Signature AB (0.032)
Signature AC (0.023)
Signature AD (0.028)

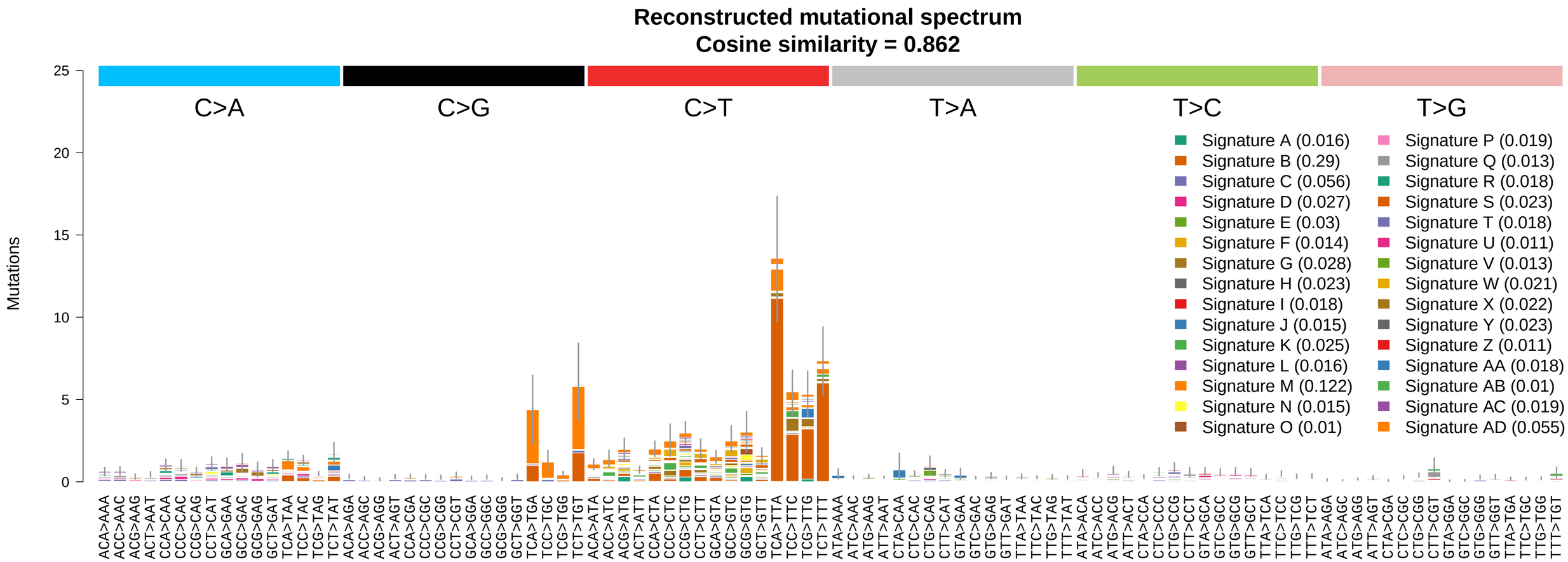

Mutational spectrum
Sample 7 (658 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
150
100
50
0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.914
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
150
100
50
0
Signature A (0.003)
Signature B (0.376)
Signature C (0.121)
Signature D (0.004)
Signature E (0.006)
Signature F (0.003)
Signature G (0.004)
Signature H (0.004)
Signature I (0.003)
Signature J (0.003)
Signature K (0.004)
Signature L (0.002)
Signature M (0.328)
Signature N (0.003)
Signature O (0.003)
Signature P (0.004)
Signature Q (0.002)
Signature R (0.003)
Signature S (0.004)
Signature T (0.003)
Signature U (0.002)
Signature V (0.002)
Signature W (0.004)
Signature X (0.004)
Signature Y (0.004)
Signature Z (0.002)
Signature AA (0.003)
Signature AB (0.002)
Signature AC (0.004)
Signature AD (0.092)

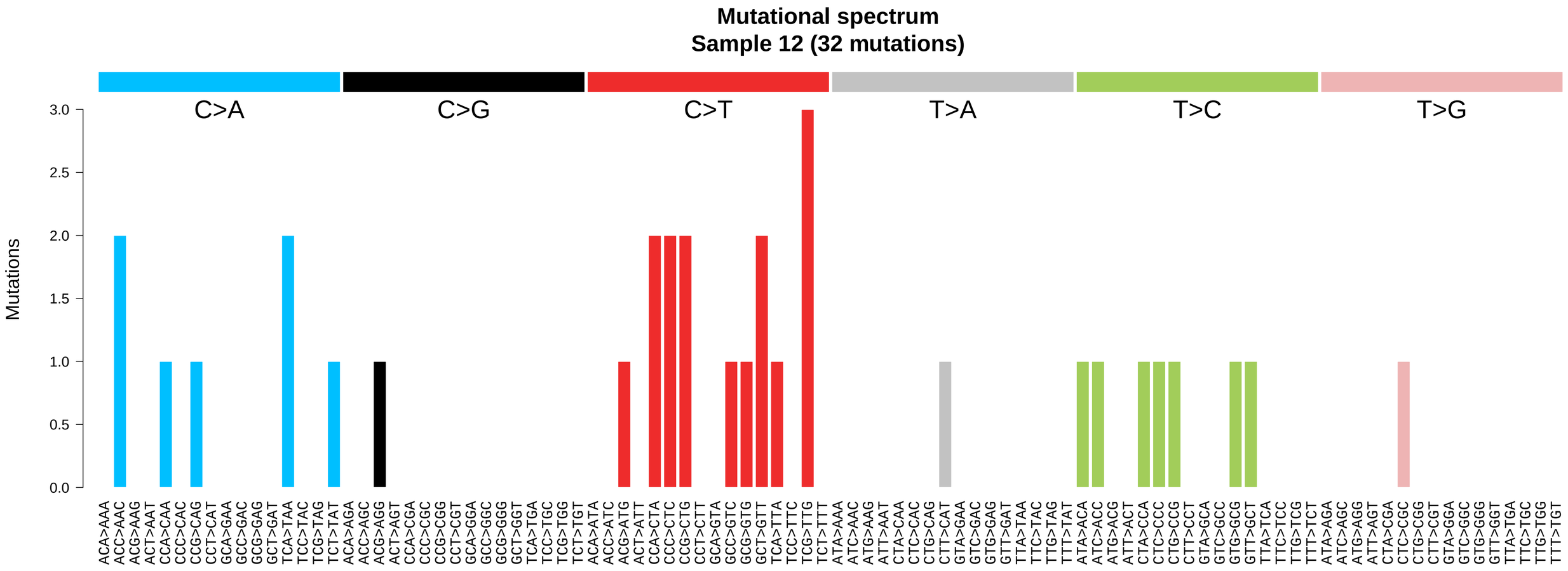

Mutational spectrum
Sample 8 (27 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.554
Signature A (0.045)
Signature B (0.031)
Signature C (0.04)
Signature D (0.048)
Signature E (0.043)
Signature F (0.032)
Signature G (0.029)
Signature H (0.04)
Signature I (0.038)
Signature J (0.022)
Signature K (0.03)
Signature L (0.031)
Signature M (0.021)
Signature N (0.028)
Signature O (0.029)
Signature P (0.038)
Signature Q (0.023)
Signature R (0.033)
Signature S (0.037)
Signature T (0.027)
Signature U (0.032)
Signature V (0.031)
Signature W (0.035)
Signature X (0.049)
Signature Y (0.044)
Signature Z (0.029)
Signature AA (0.025)
Signature AB (0.021)
Signature AC (0.038)
Signature AD (0.031)

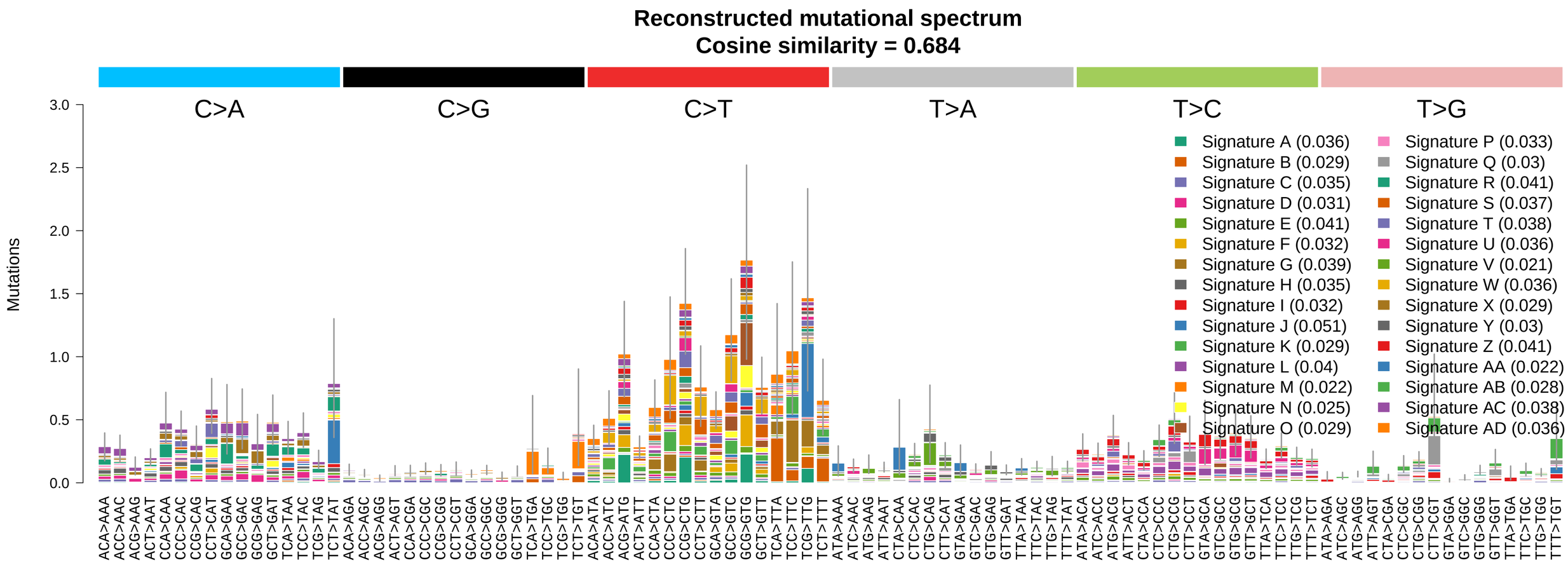

Mutational spectrum
Sample 9 (47 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.687
Signature A (0.05)
Signature B (0.042)
Signature C (0.04)
Signature D (0.039)
Signature E (0.038)
Signature F (0.036)
Signature G (0.067)
Signature H (0.031)
Signature I (0.024)
Signature J (0.026)
Signature K (0.03)
Signature L (0.027)
Signature M (0.02)
Signature N (0.023)
Signature O (0.022)
Signature P (0.028)
Signature Q (0.02)
Signature R (0.024)
Signature S (0.042)
Signature T (0.031)
Signature U (0.034)
Signature V (0.02)
Signature W (0.035)
Signature X (0.038)
Signature Y (0.037)
Signature Z (0.027)
Signature AA (0.031)
Signature AB (0.017)
Signature AC (0.03)
Signature AD (0.068)

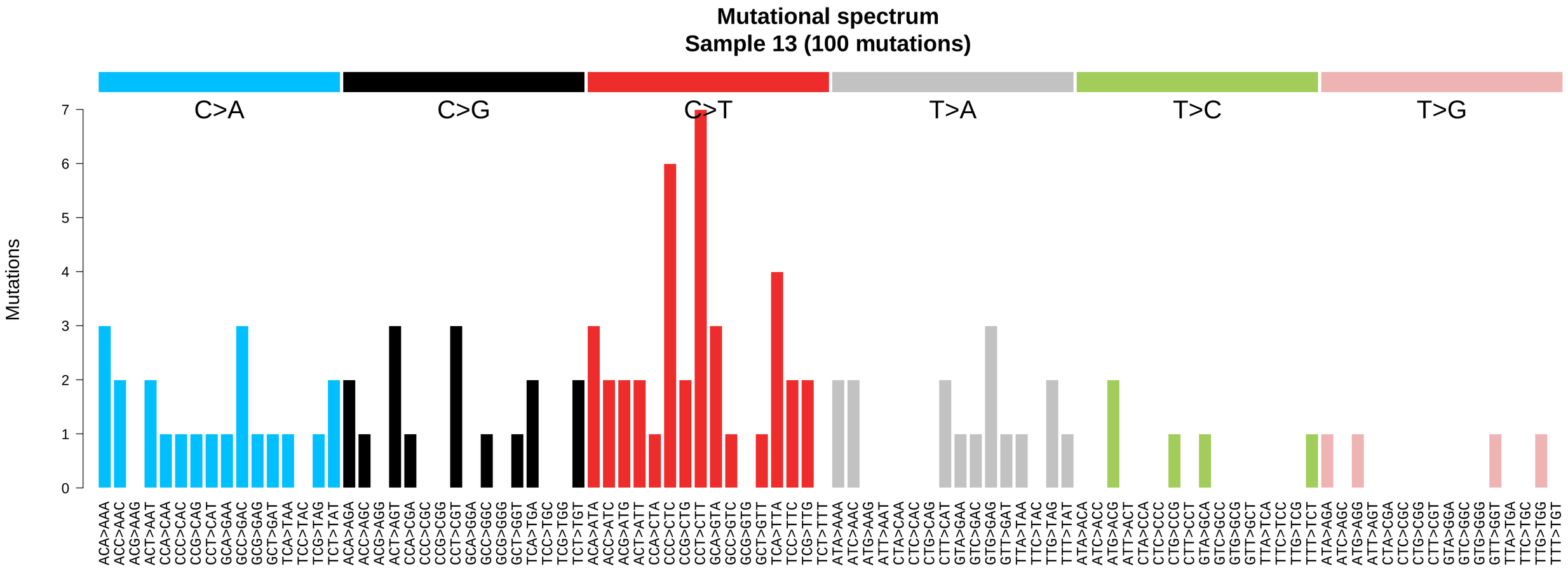

Mutational spectrum
Sample 10 (43 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.706
Signature A (0.033)
Signature B (0.035)
Signature C (0.027)
Signature D (0.032)
Signature E (0.031)
Signature F (0.031)
Signature G (0.046)
Signature H (0.03)
Signature I (0.026)
Signature J (0.037)
Signature K (0.045)
Signature L (0.025)
Signature M (0.03)
Signature N (0.031)
Signature O (0.026)
Signature P (0.029)
Signature Q (0.028)
Signature R (0.04)
Signature S (0.049)
Signature T (0.038)
Signature U (0.022)
Signature V (0.016)
Signature W (0.063)
Signature X (0.053)
Signature Y (0.025)
Signature Z (0.026)
Signature AA (0.02)
Signature AB (0.021)
Signature AC (0.054)
Signature AD (0.031)

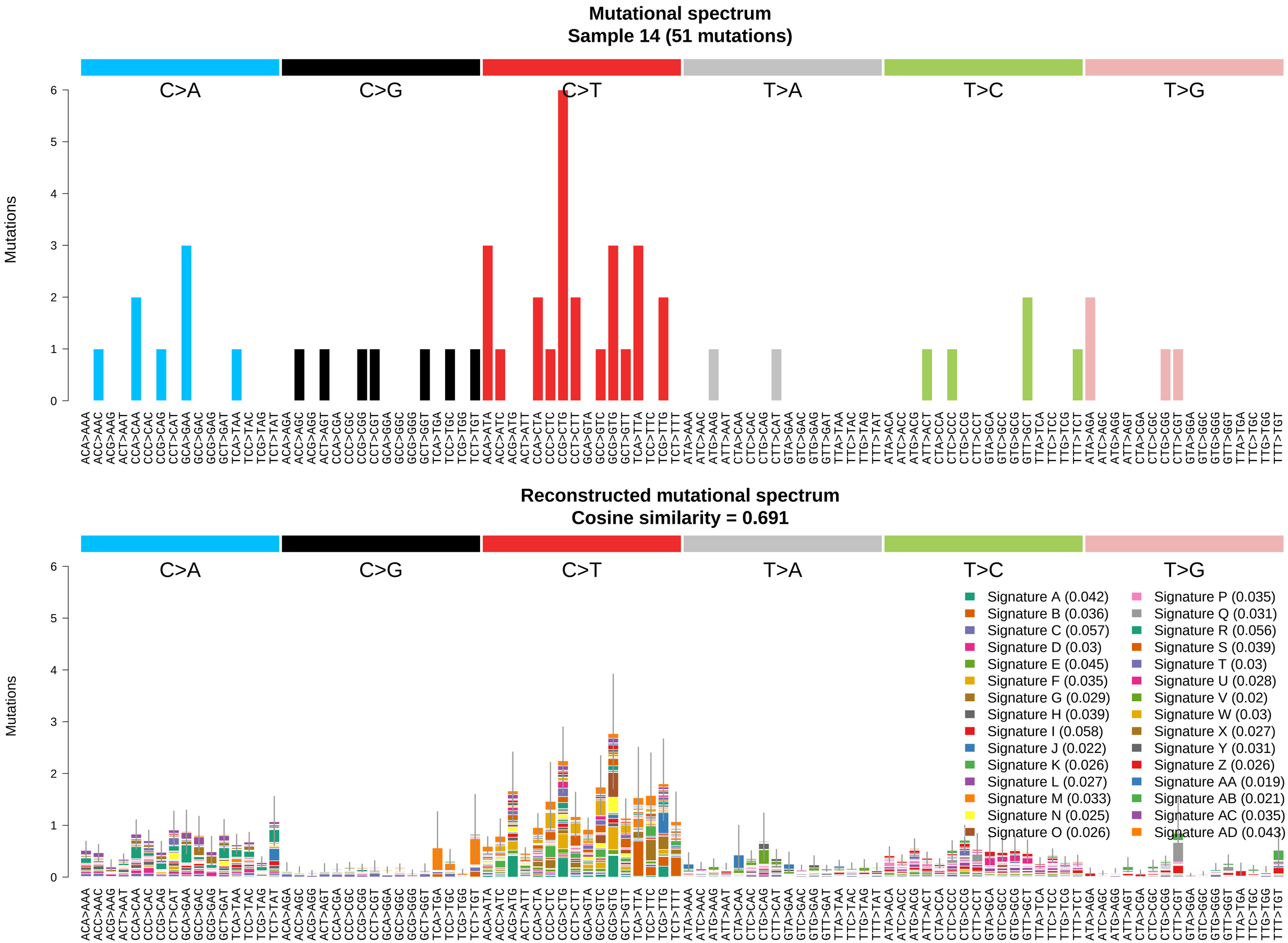

Mutational spectrum
Sample 11 (103 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
25
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

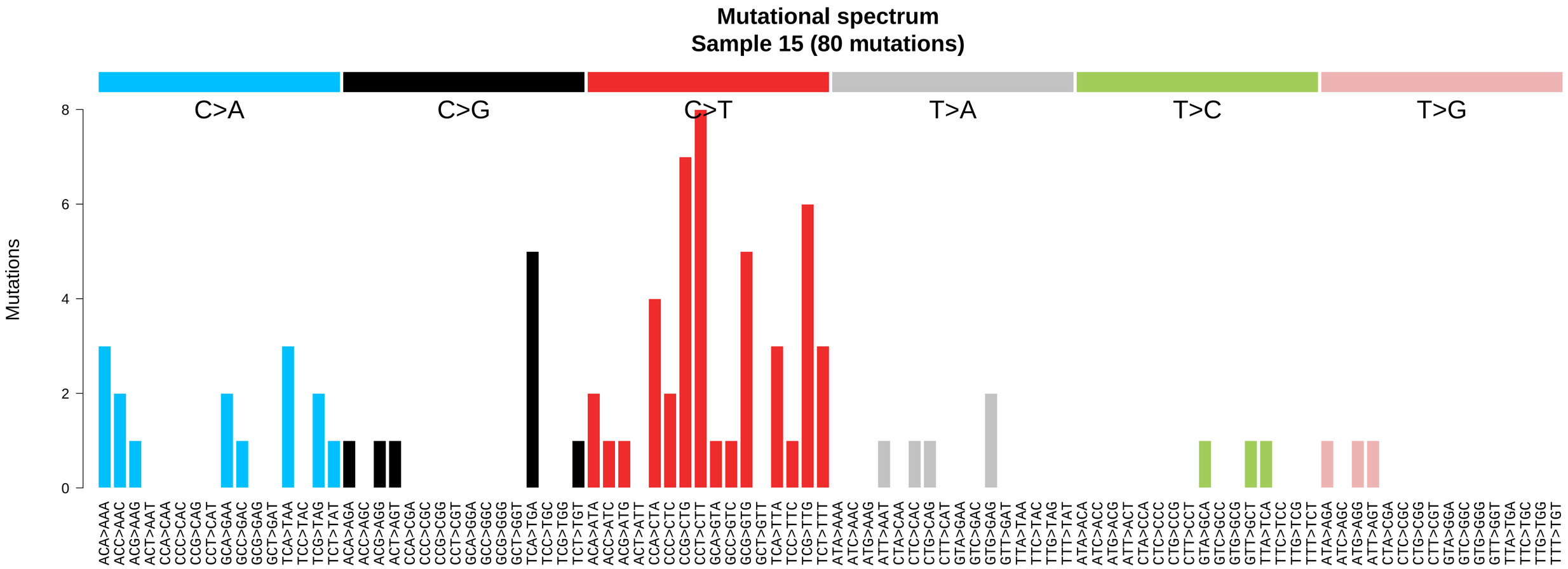

Reconstructed mutational spectrum
Cosine similarity = 0.862
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
25
Signature A (0.016)
Signature B (0.29)
Signature C (0.056)
Signature D (0.027)
Signature E (0.03)
Signature F (0.014)
Signature G (0.028)
Signature H (0.023)
Signature I (0.018)
Signature J (0.015)
Signature K (0.025)
Signature L (0.016)
Signature M (0.122)
Signature N (0.015)
Signature O (0.01)
Signature P (0.019)
Signature Q (0.013)
Signature R (0.018)
Signature S (0.023)
Signature T (0.018)
Signature U (0.011)
Signature V (0.013)
Signature W (0.021)
Signature X (0.022)
Signature Y (0.023)
Signature Z (0.011)
Signature AA (0.018)
Signature AB (0.01)
Signature AC (0.019)
Signature AD (0.055)

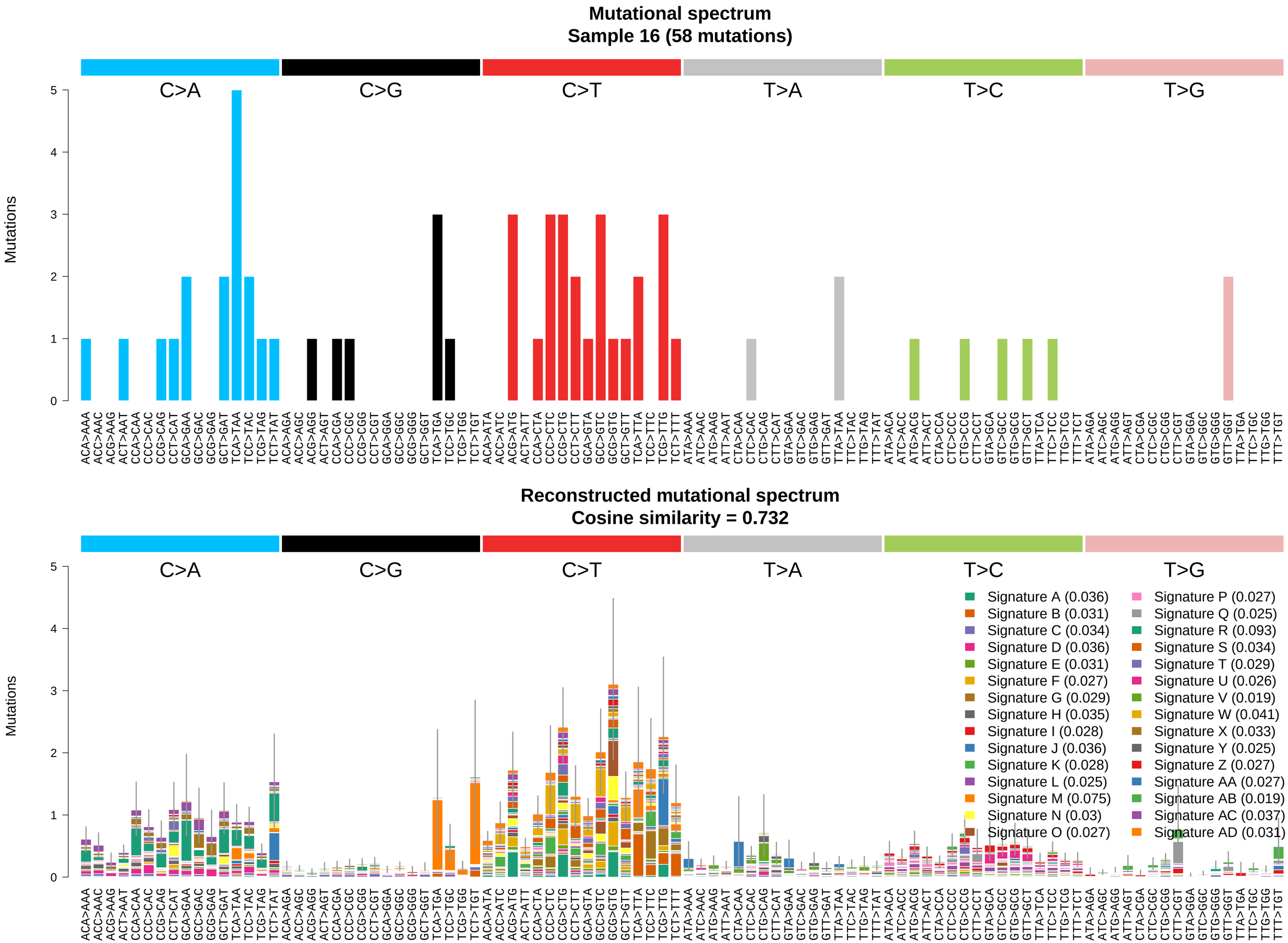

Mutational spectrum
Sample 12 (32 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

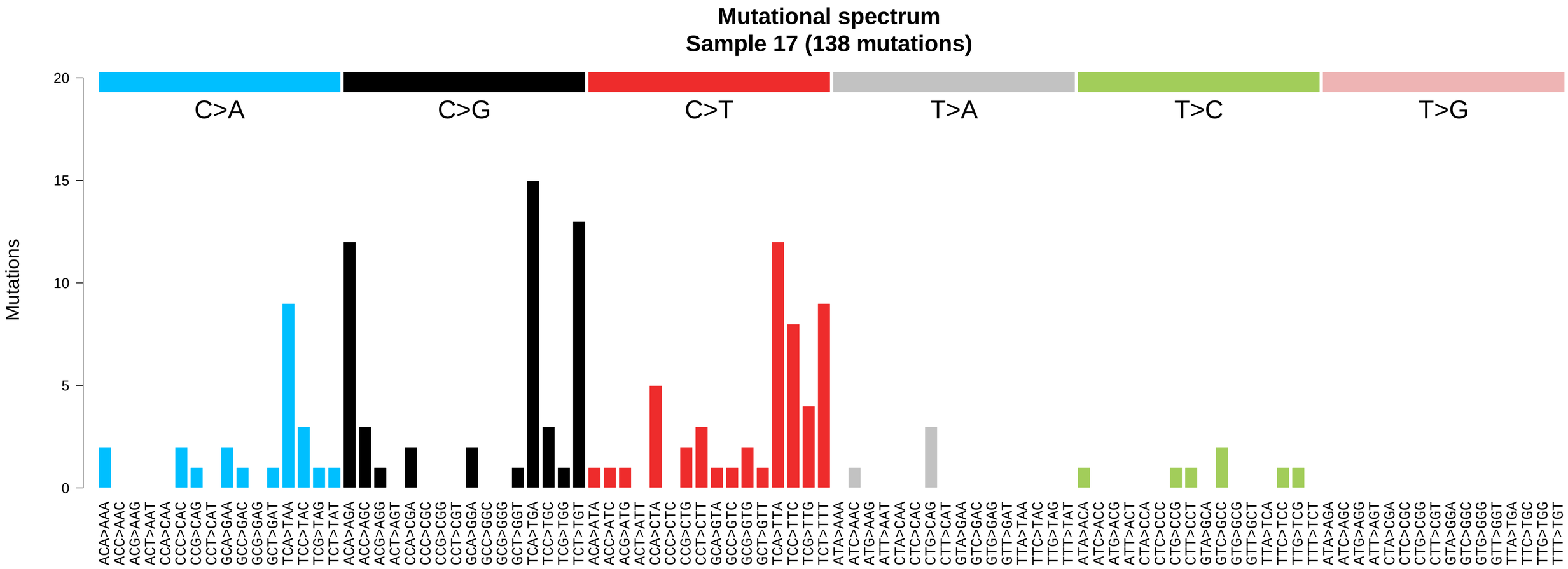

Reconstructed mutational spectrum
Cosine similarity = 0.684
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Signature A (0.036)
Signature B (0.029)
Signature C (0.035)
Signature D (0.031)
Signature E (0.041)
Signature F (0.032)
Signature G (0.039)
Signature H (0.035)
Signature I (0.032)
Signature J (0.051)
Signature K (0.029)
Signature L (0.04)
Signature M (0.022)
Signature N (0.025)
Signature O (0.029)
Signature P (0.033)
Signature Q (0.03)
Signature R (0.041)
Signature S (0.037)
Signature T (0.038)
Signature U (0.036)
Signature V (0.021)
Signature W (0.036)
Signature X (0.029)
Signature Y (0.03)
Signature Z (0.041)
Signature AA (0.022)
Signature AB (0.028)
Signature AC (0.038)
Signature AD (0.036)

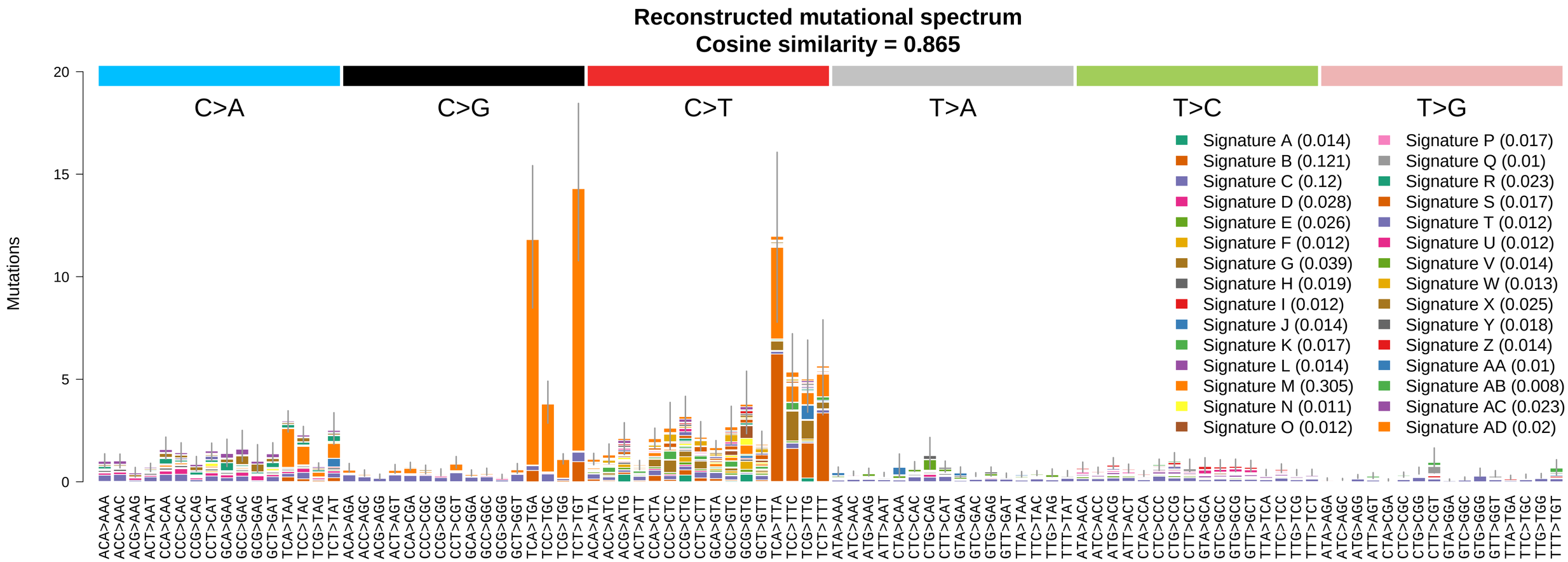

Mutational spectrum
Sample 13 (100 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
7
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.729
Signature A (0.017)
Signature B (0.026)
Signature C (0.152)
Signature D (0.038)
Signature E (0.037)
Signature F (0.015)
Signature G (0.029)
Signature H (0.08)
Signature I (0.028)
Signature J (0.015)
Signature K (0.038)
Signature L (0.018)
Signature M (0.036)
Signature N (0.016)
Signature O (0.012)
Signature P (0.029)
Signature Q (0.013)
Signature R (0.026)
Signature S (0.04)
Signature T (0.021)
Signature U (0.017)
Signature V (0.034)
Signature W (0.052)
Signature X (0.034)
Signature Y (0.052)
Signature Z (0.015)
Signature AA (0.027)
Signature AB (0.012)
Signature AC (0.036)
Signature AD (0.036)

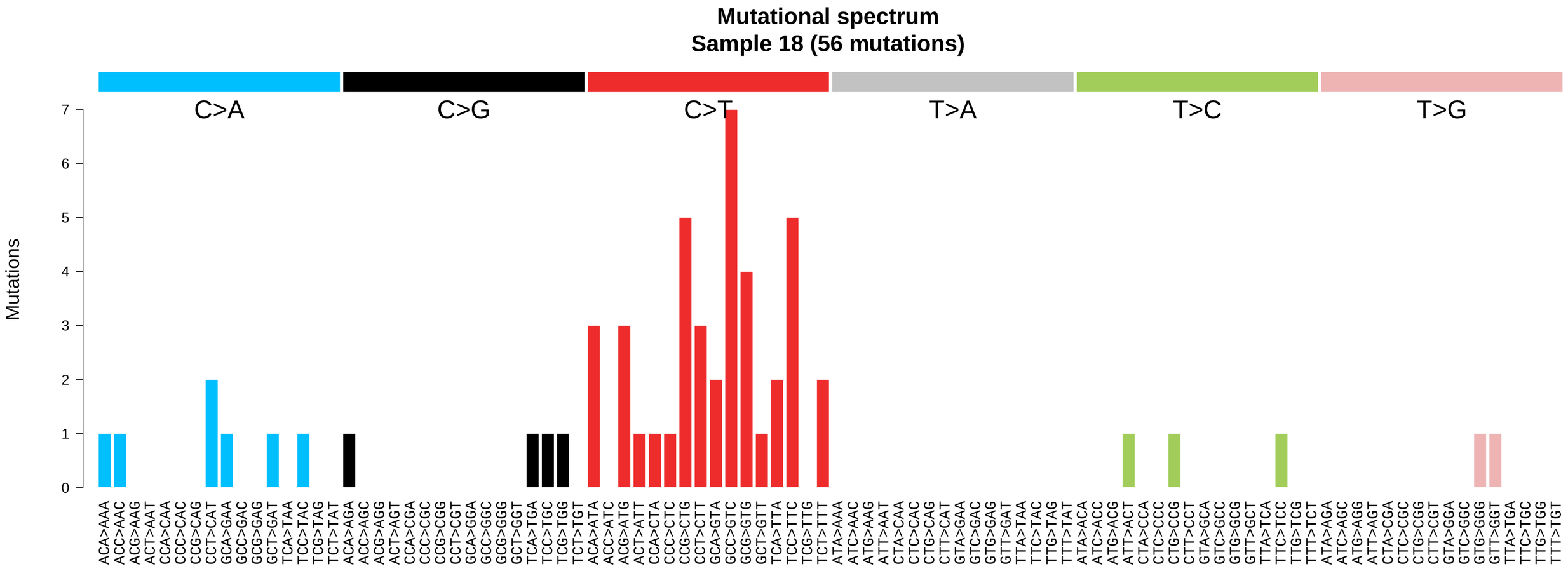

Mutational spectrum
Sample 14 (51 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.691
Signature A (0.042)
Signature B (0.036)
Signature C (0.057)
Signature D (0.03)
Signature E (0.045)
Signature F (0.035)
Signature G (0.029)
Signature H (0.039)
Signature I (0.058)
Signature J (0.022)
Signature K (0.026)
Signature L (0.027)
Signature M (0.033)
Signature N (0.025)
Signature O (0.026)
Signature P (0.035)
Signature Q (0.031)
Signature R (0.056)
Signature S (0.039)
Signature T (0.03)
Signature U (0.028)
Signature V (0.02)
Signature W (0.03)
Signature X (0.027)
Signature Y (0.031)
Signature Z (0.026)
Signature AA (0.019)
Signature AB (0.021)
Signature AC (0.035)
Signature AD (0.043)

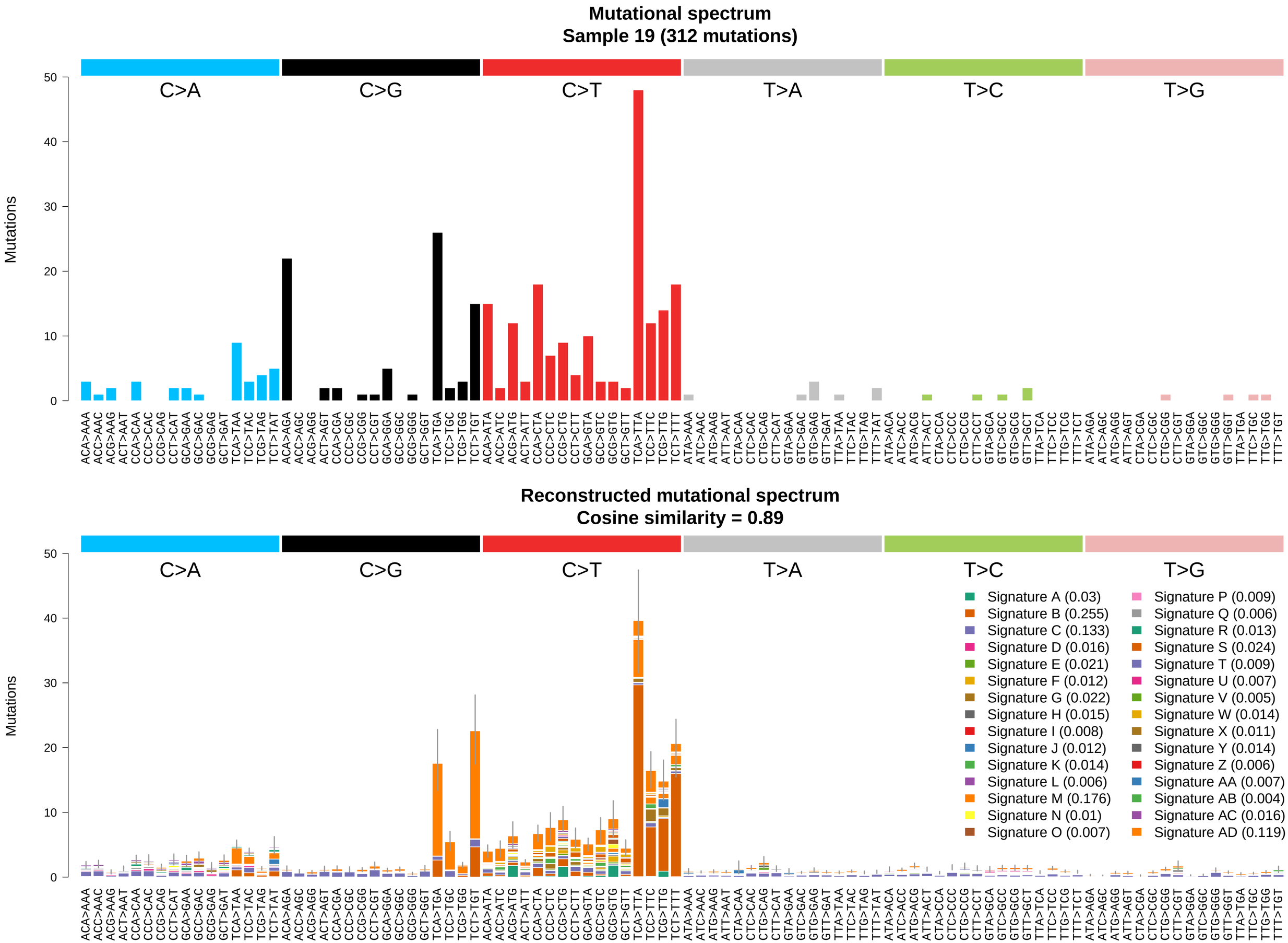

Mutational spectrum
Sample 15 (80 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.76
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
Signature A (0.055)
Signature B (0.047)
Signature C (0.034)
Signature D (0.035)
Signature E (0.03)
Signature F (0.028)
Signature G (0.061)
Signature H (0.038)
Signature I (0.026)
Signature J (0.036)
Signature K (0.029)
Signature L (0.02)
Signature M (0.078)
Signature N (0.019)
Signature O (0.023)
Signature P (0.025)
Signature Q (0.016)
Signature R (0.036)
Signature S (0.052)
Signature T (0.018)
Signature U (0.02)
Signature V (0.023)
Signature W (0.042)
Signature X (0.022)
Signature Y (0.035)
Signature Z (0.018)
Signature AA (0.015)
Signature AB (0.015)
Signature AC (0.05)
Signature AD (0.051)

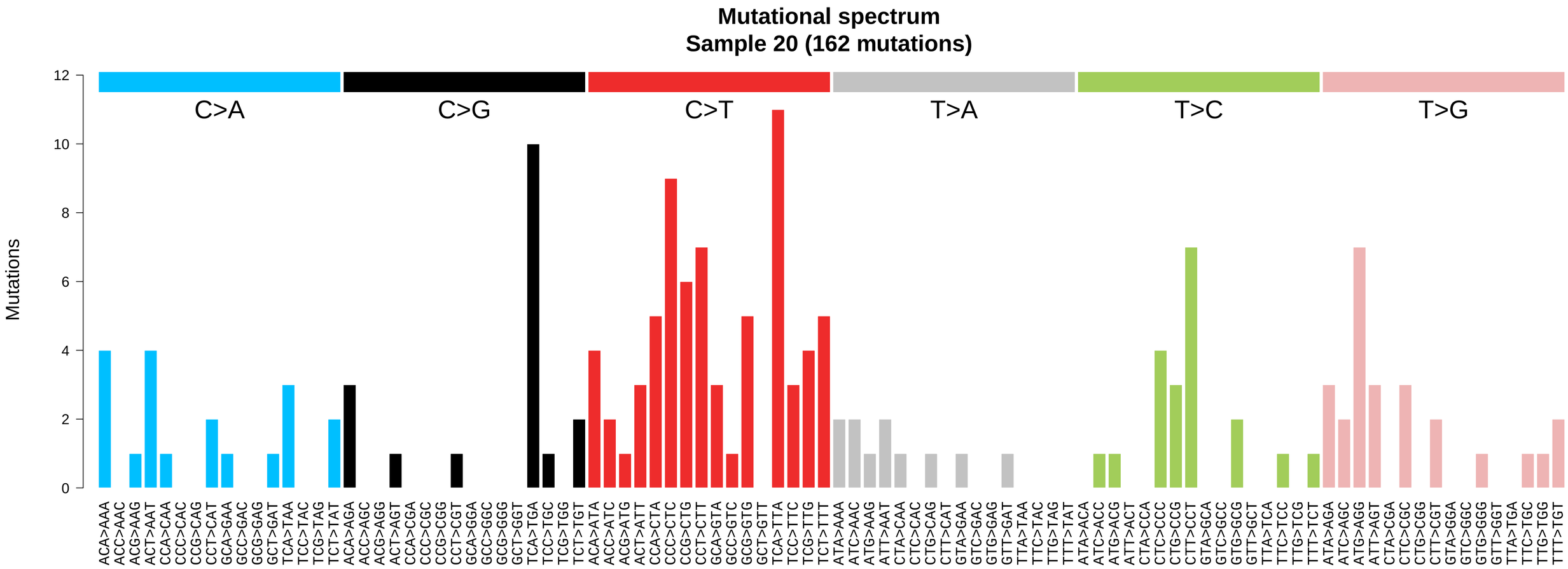

Mutational spectrum
Sample 16 (58 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.732
Signature A (0.036)
Signature B (0.031)
Signature C (0.034)
Signature D (0.036)
Signature E (0.031)
Signature F (0.027)
Signature G (0.029)
Signature H (0.035)
Signature I (0.028)
Signature J (0.036)
Signature K (0.028)
Signature L (0.025)
Signature M (0.075)
Signature N (0.03)
Signature O (0.027)
Signature P (0.027)
Signature Q (0.025)
Signature R (0.093)
Signature S (0.034)
Signature T (0.029)
Signature U (0.026)
Signature V (0.019)
Signature W (0.041)
Signature X (0.033)
Signature Y (0.025)
Signature Z (0.027)
Signature AA (0.027)
Signature AB (0.019)
Signature AC (0.037)
Signature AD (0.031)

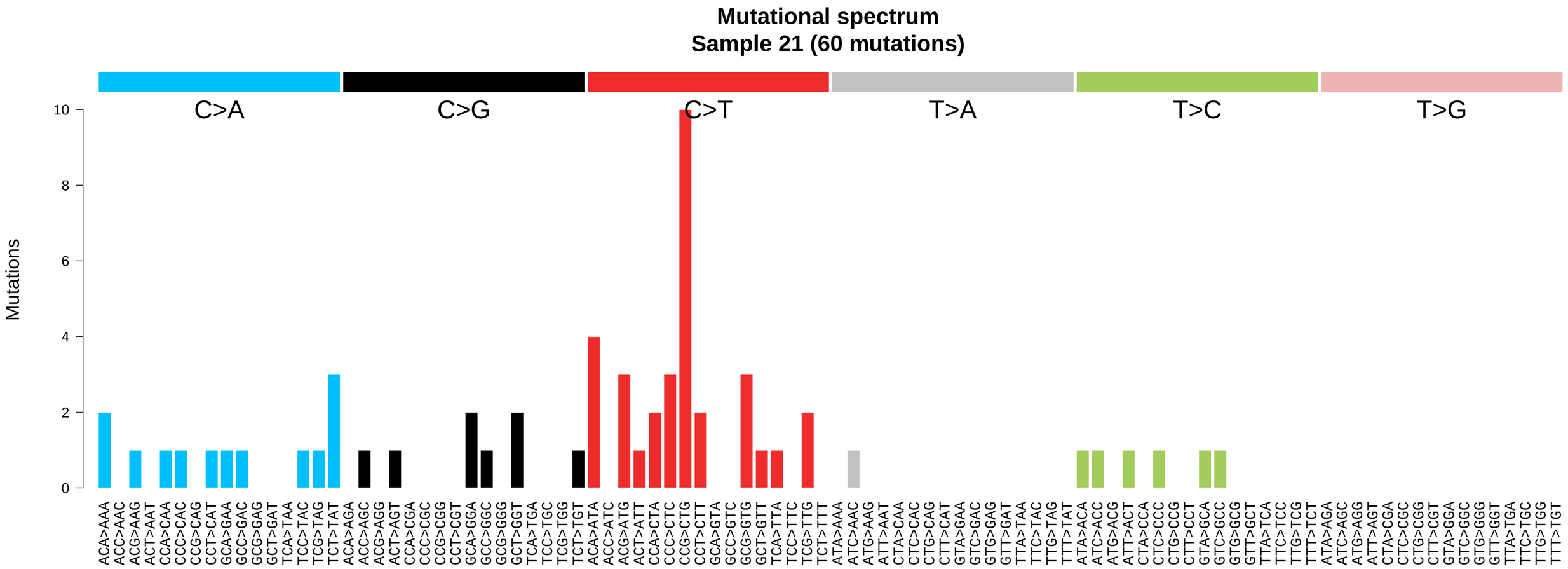

Mutational spectrum
Sample 17 (138 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

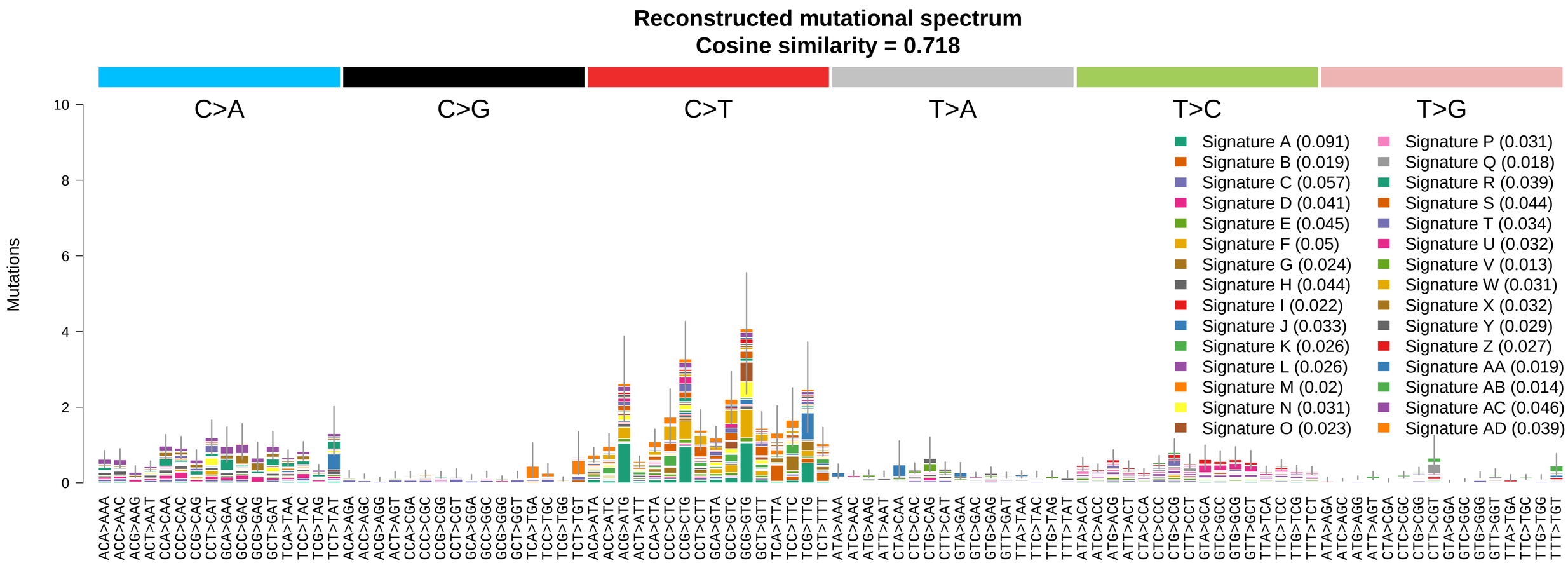

Reconstructed mutational spectrum
Cosine similarity = 0.865
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
Signature A (0.014)
Signature B (0.121)
Signature C (0.12)
Signature D (0.028)
Signature E (0.026)
Signature F (0.012)
Signature G (0.039)
Signature H (0.019)
Signature I (0.012)
Signature J (0.014)
Signature K (0.017)
Signature L (0.014)
Signature M (0.305)
Signature N (0.011)
Signature O (0.012)
Signature P (0.017)
Signature Q (0.01)
Signature R (0.023)
Signature S (0.017)
Signature T (0.012)
Signature U (0.012)
Signature V (0.014)
Signature W (0.013)
Signature X (0.025)
Signature Y (0.018)
Signature Z (0.014)
Signature AA (0.01)
Signature AB (0.008)
Signature AC (0.023)
Signature AD (0.02)

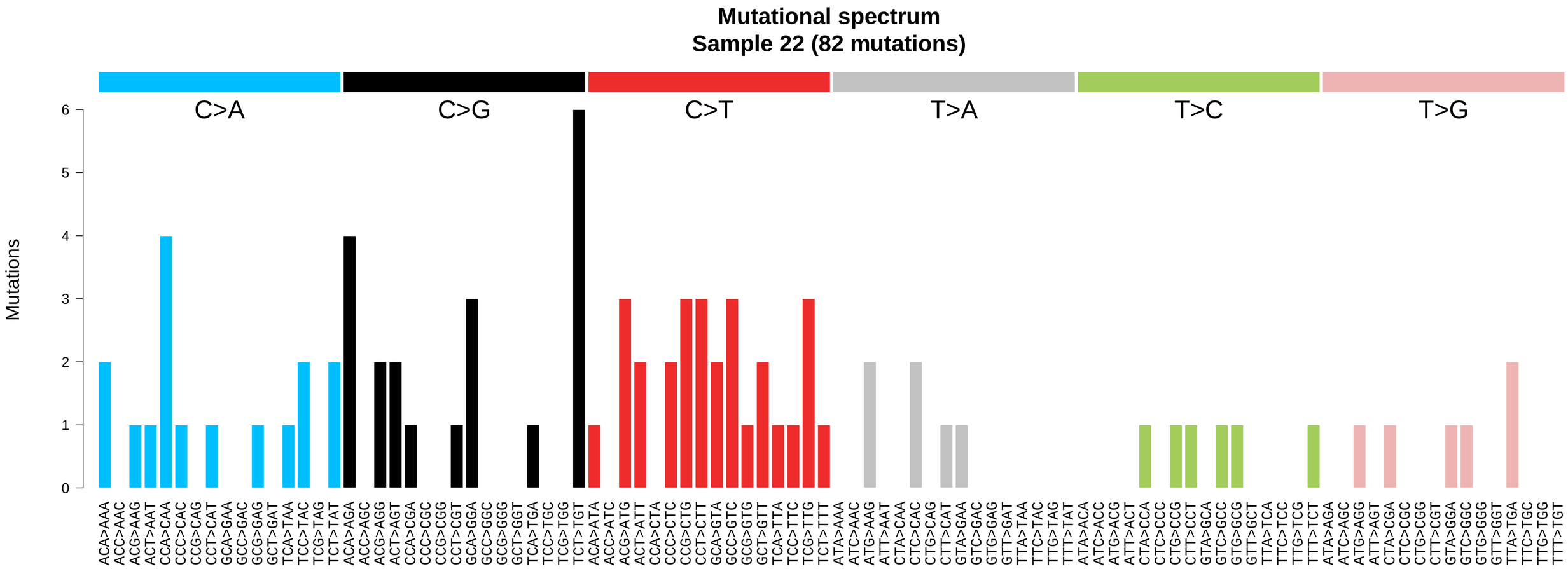

Mutational spectrum
Sample 18 (56 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
7
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.822
Signature A (0.047)
Signature B (0.038)
Signature C (0.033)
Signature D (0.024)
Signature E (0.03)
Signature F (0.054)
Signature G (0.045)
Signature H (0.026)
Signature I (0.022)
Signature J (0.017)
Signature K (0.064)
Signature L (0.021)
Signature M (0.035)
Signature N (0.054)
Signature O (0.044)
Signature P (0.022)
Signature Q (0.02)
Signature R (0.028)
Signature S (0.05)
Signature T (0.037)
Signature U (0.021)
Signature V (0.014)
Signature W (0.068)
Signature X (0.023)
Signature Y (0.023)
Signature Z (0.023)
Signature AA (0.019)
Signature AB (0.017)
Signature AC (0.028)
Signature AD (0.054)

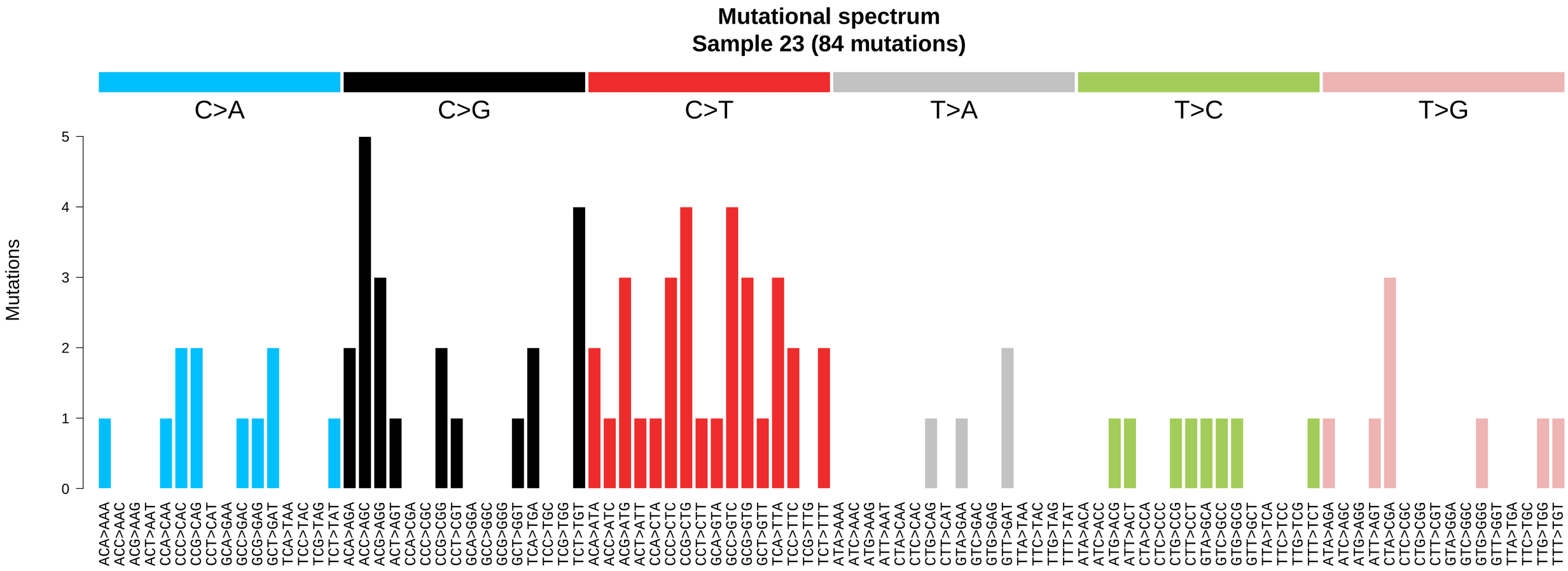

Mutational spectrum
Sample 19 (312 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.89
Signature A (0.03)
Signature B (0.255)
Signature C (0.133)
Signature D (0.016)
Signature E (0.021)
Signature F (0.012)
Signature G (0.022)
Signature H (0.015)
Signature I (0.008)
Signature J (0.012)
Signature K (0.014)
Signature L (0.006)
Signature M (0.176)
Signature N (0.01)
Signature O (0.007)
Signature P (0.009)
Signature Q (0.006)
Signature R (0.013)
Signature S (0.024)
Signature T (0.009)
Signature U (0.007)
Signature V (0.005)
Signature W (0.014)
Signature X (0.011)
Signature Y (0.014)
Signature Z (0.006)
Signature AA (0.007)
Signature AB (0.004)
Signature AC (0.016)
Signature AD (0.119)

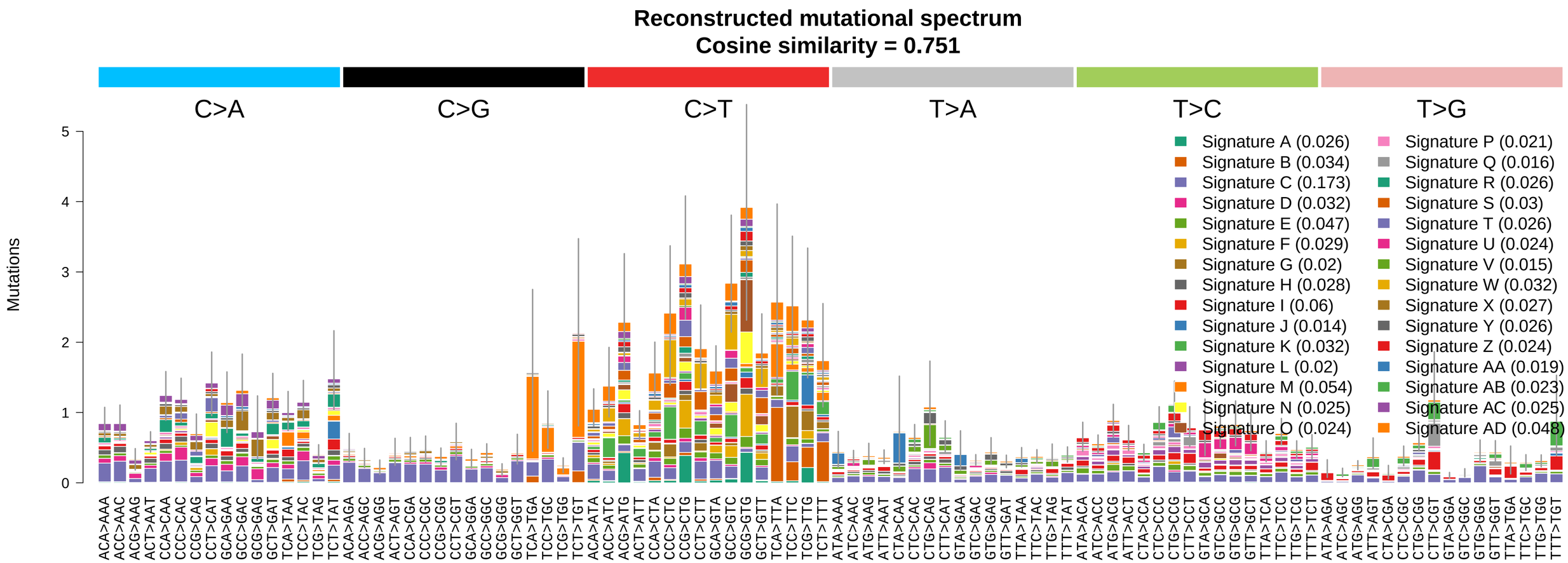

Mutational spectrum
Sample 20 (162 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.784
Signature A (0.017)
Signature B (0.063)
Signature C (0.053)
Signature D (0.015)
Signature E (0.036)
Signature F (0.016)
Signature G (0.035)
Signature H (0.058)
Signature I (0.074)
Signature J (0.015)
Signature K (0.036)
Signature L (0.022)
Signature M (0.087)
Signature N (0.018)
Signature O (0.012)
Signature P (0.037)
Signature Q (0.062)
Signature R (0.017)
Signature S (0.031)
Signature T (0.019)
Signature U (0.013)
Signature V (0.012)
Signature W (0.036)
Signature X (0.011)
Signature Y (0.027)
Signature Z (0.015)
Signature AA (0.023)
Signature AB (0.067)
Signature AC (0.017)
Signature AD (0.055)

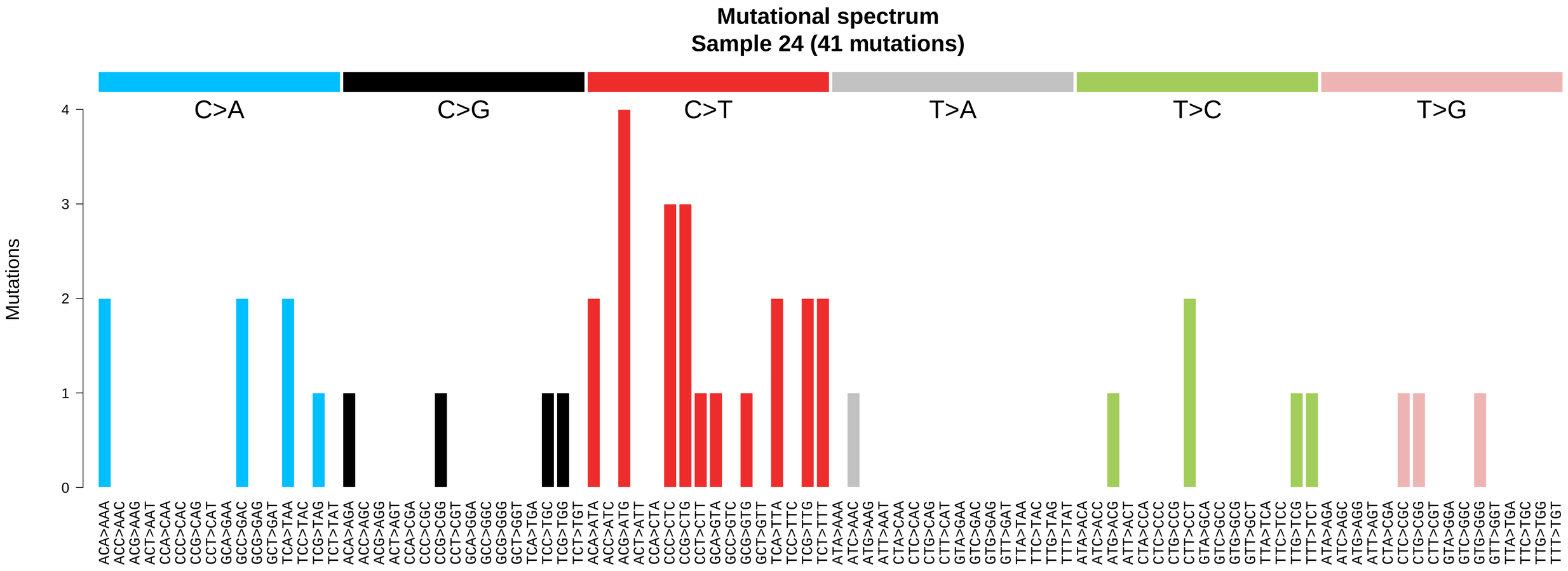

Mutational spectrum
Sample 21 (60 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

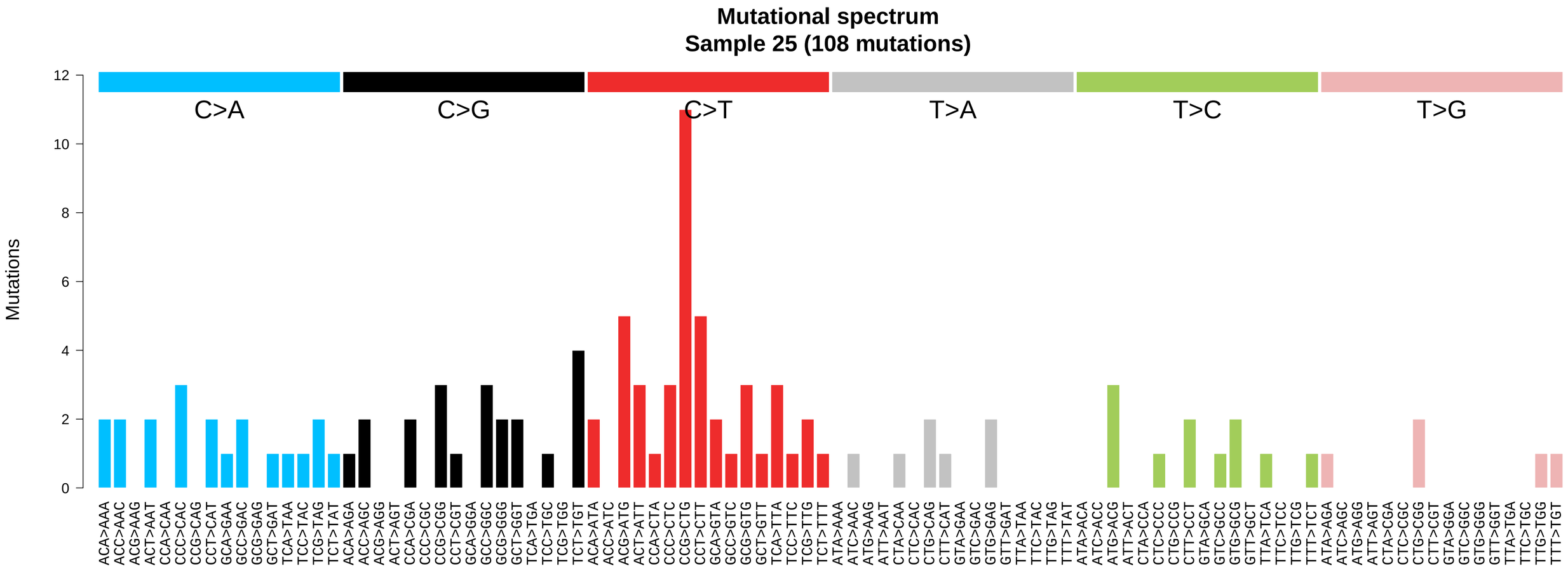

Reconstructed mutational spectrum
Cosine similarity = 0.718
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
Signature A (0.091)
Signature B (0.019)
Signature C (0.057)
Signature D (0.041)
Signature E (0.045)
Signature F (0.05)
Signature G (0.024)
Signature H (0.044)
Signature I (0.022)
Signature J (0.033)
Signature K (0.026)
Signature L (0.026)
Signature M (0.02)
Signature N (0.031)
Signature O (0.023)
Signature P (0.031)
Signature Q (0.018)
Signature R (0.039)
Signature S (0.044)
Signature T (0.034)
Signature U (0.032)
Signature V (0.013)
Signature W (0.031)
Signature X (0.032)
Signature Y (0.029)
Signature Z (0.027)
Signature AA (0.019)
Signature AB (0.014)
Signature AC (0.046)
Signature AD (0.039)

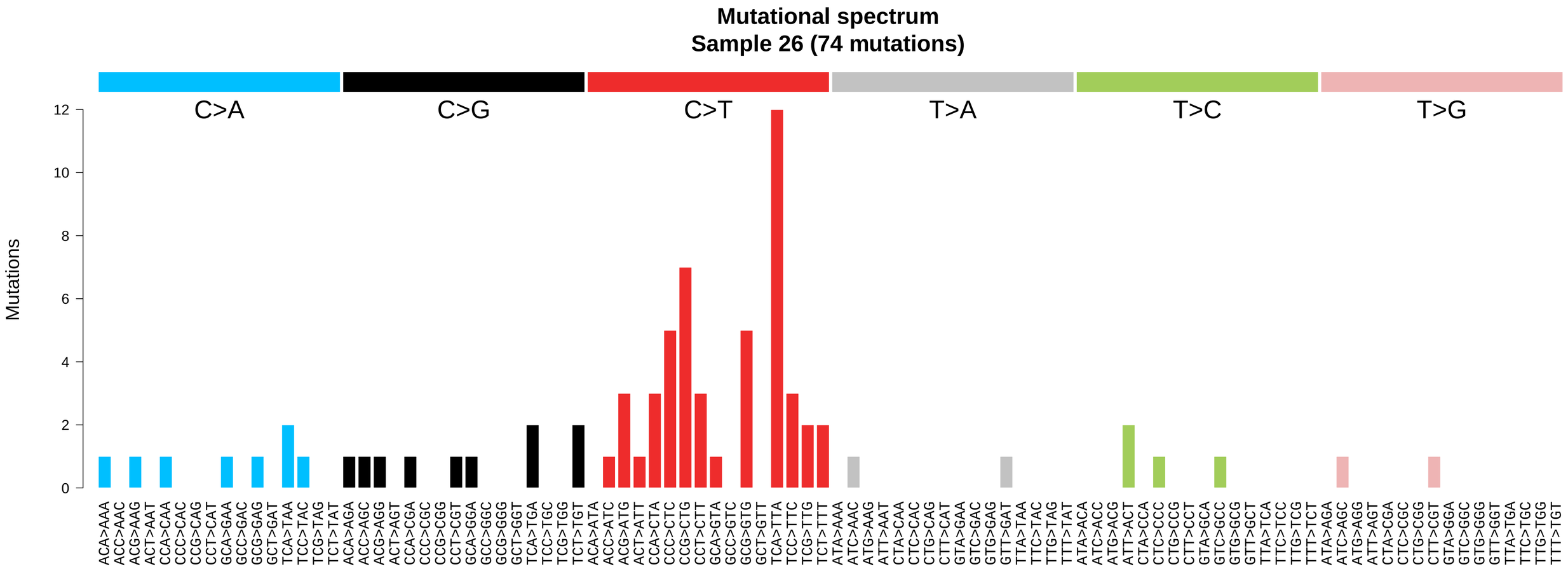

Mutational spectrum
Sample 22 (82 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.716
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
Signature A (0.028)
Signature B (0.021)
Signature C (0.2)
Signature D (0.04)
Signature E (0.036)
Signature F (0.022)
Signature G (0.019)
Signature H (0.04)
Signature I (0.046)
Signature J (0.028)
Signature K (0.024)
Signature L (0.021)
Signature M (0.065)
Signature N (0.022)
Signature O (0.019)
Signature P (0.027)
Signature Q (0.017)
Signature R (0.029)
Signature S (0.038)
Signature T (0.024)
Signature U (0.019)
Signature V (0.022)
Signature W (0.03)
Signature X (0.028)
Signature Y (0.028)
Signature Z (0.019)
Signature AA (0.017)
Signature AB (0.014)
Signature AC (0.027)
Signature AD (0.029)
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

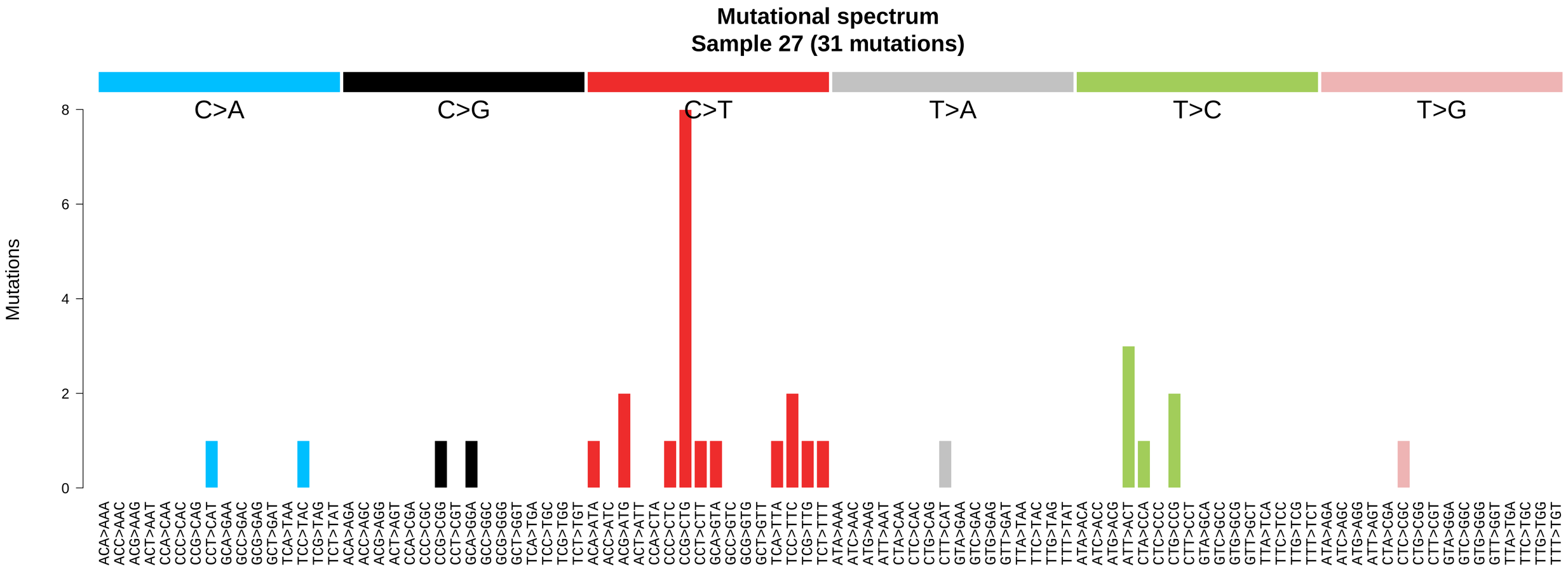

Mutational spectrum
Sample 23 (84 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

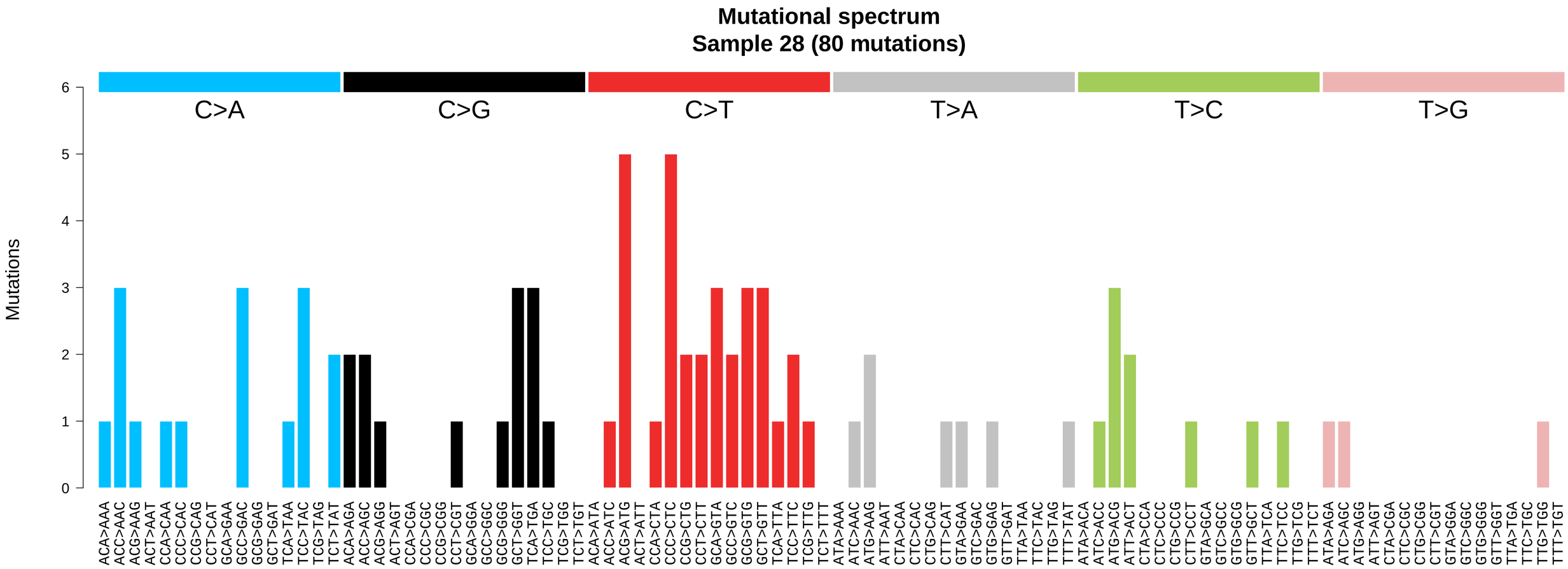

Reconstructed mutational spectrum
Cosine similarity = 0.751
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
Signature A (0.026)
Signature B (0.034)
Signature C (0.173)
Signature D (0.032)
Signature E (0.047)
Signature F (0.029)
Signature G (0.02)
Signature H (0.028)
Signature I (0.06)
Signature J (0.014)
Signature K (0.032)
Signature L (0.02)
Signature M (0.054)
Signature N (0.025)
Signature O (0.024)
Signature P (0.021)
Signature Q (0.016)
Signature R (0.026)
Signature S (0.03)
Signature T (0.026)
Signature U (0.024)
Signature V (0.015)
Signature W (0.032)
Signature X (0.027)
Signature Y (0.026)
Signature Z (0.024)
Signature AA (0.019)
Signature AB (0.023)
Signature AC (0.025)
Signature AD (0.048)

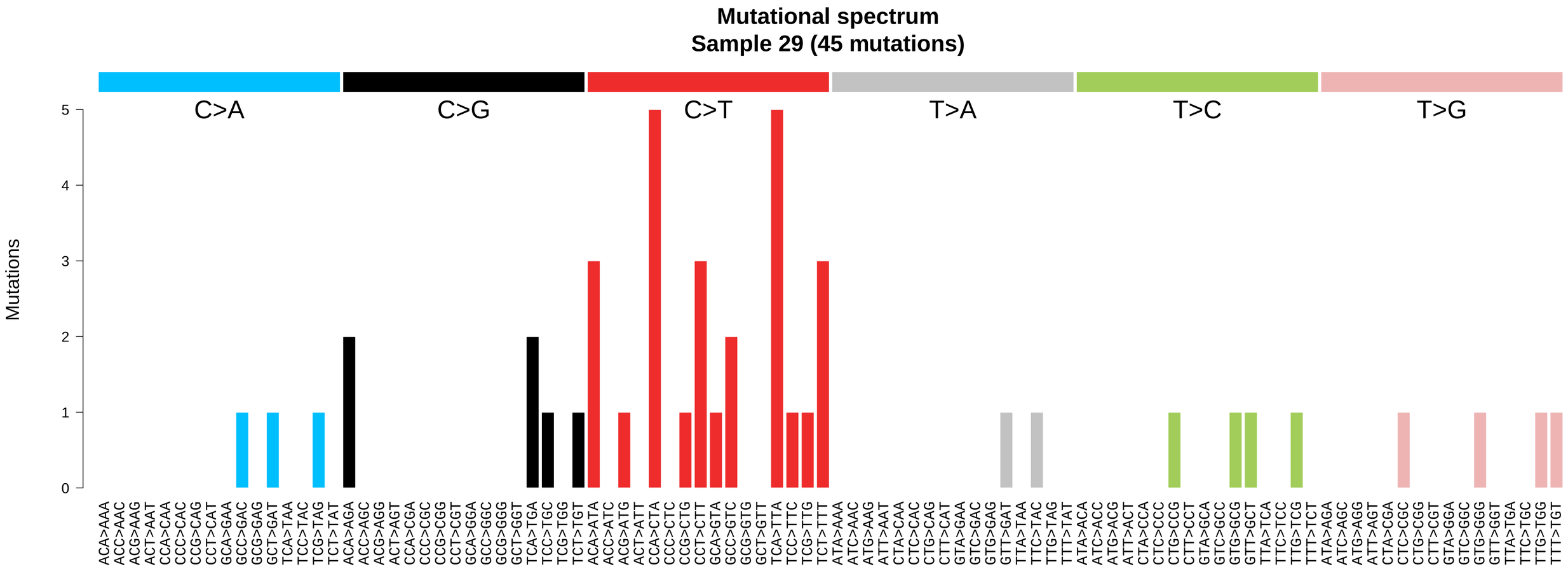

Mutational spectrum
Sample 24 (41 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.649
Signature A (0.059)
Signature B (0.045)
Signature C (0.045)
Signature D (0.036)
Signature E (0.042)
Signature F (0.036)
Signature G (0.03)
Signature H (0.032)
Signature I (0.032)
Signature J (0.026)
Signature K (0.031)
Signature L (0.031)
Signature M (0.035)
Signature N (0.024)
Signature O (0.022)
Signature P (0.037)
Signature Q (0.034)
Signature R (0.036)
Signature S (0.038)
Signature T (0.034)
Signature U (0.028)
Signature V (0.018)
Signature W (0.031)
Signature X (0.03)
Signature Y (0.031)
Signature Z (0.027)
Signature AA (0.02)
Signature AB (0.024)
Signature AC (0.042)
Signature AD (0.044)

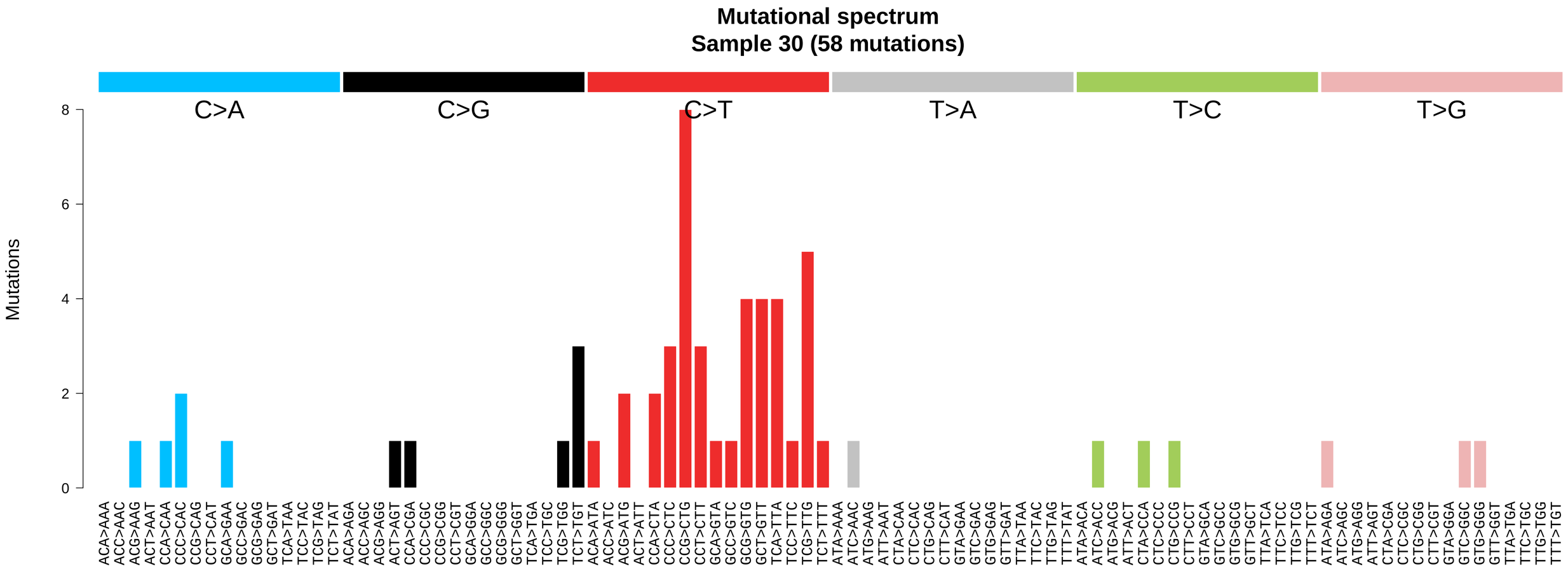

Mutational spectrum
Sample 25 (108 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.775
Signature A (0.059)
Signature B (0.024)
Signature C (0.135)
Signature D (0.086)
Signature E (0.047)
Signature F (0.038)
Signature G (0.02)
Signature H (0.042)
Signature I (0.028)
Signature J (0.014)
Signature K (0.022)
Signature L (0.021)
Signature M (0.032)
Signature N (0.023)
Signature O (0.016)
Signature P (0.032)
Signature Q (0.017)
Signature R (0.025)
Signature S (0.037)
Signature T (0.036)
Signature U (0.022)
Signature V (0.019)
Signature W (0.026)
Signature X (0.025)
Signature Y (0.038)
Signature Z (0.021)
Signature AA (0.018)
Signature AB (0.015)
Signature AC (0.03)
Signature AD (0.03)

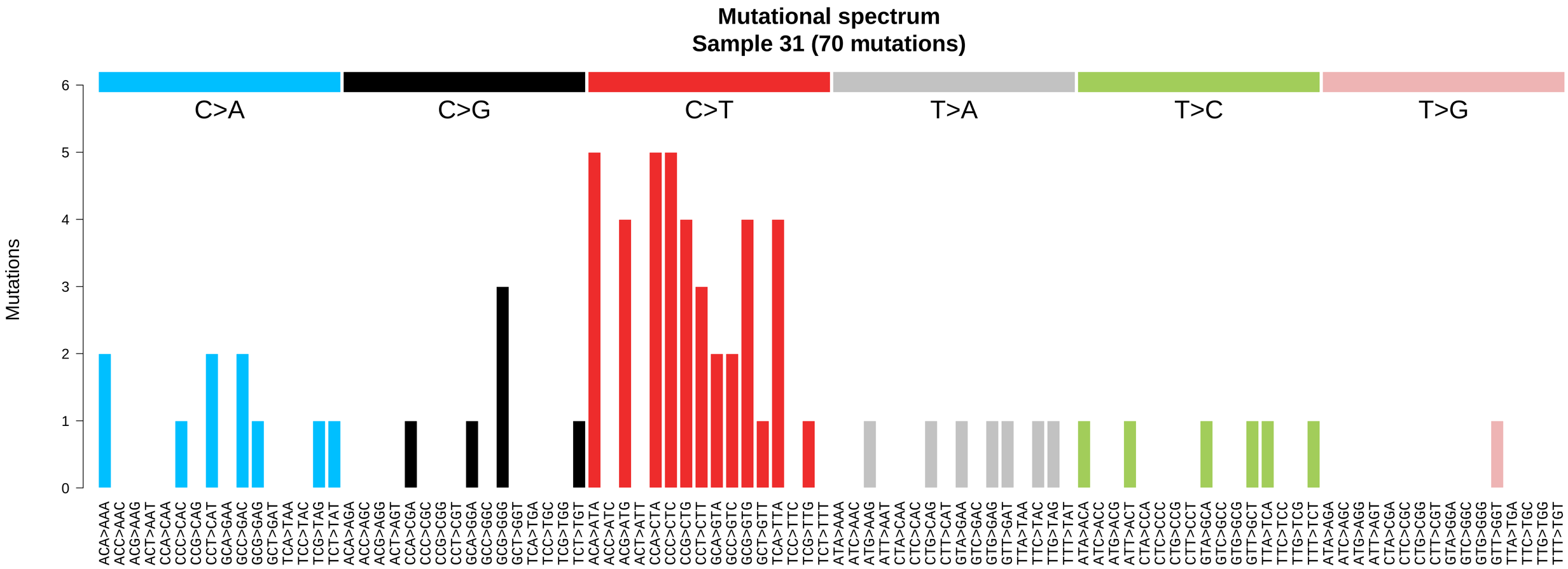

Mutational spectrum
Sample 26 (74 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.84
Signature A (0.06)
Signature B (0.154)
Signature C (0.042)
Signature D (0.029)
Signature E (0.032)
Signature F (0.033)
Signature G (0.055)
Signature H (0.028)
Signature I (0.021)
Signature J (0.016)
Signature K (0.036)
Signature L (0.018)
Signature M (0.05)
Signature N (0.022)
Signature O (0.026)
Signature P (0.027)
Signature Q (0.024)
Signature R (0.027)
Signature S (0.039)
Signature T (0.019)
Signature U (0.019)
Signature V (0.012)
Signature W (0.037)
Signature X (0.027)
Signature Y (0.021)
Signature Z (0.021)
Signature AA (0.015)
Signature AB (0.017)
Signature AC (0.027)
Signature AD (0.045)

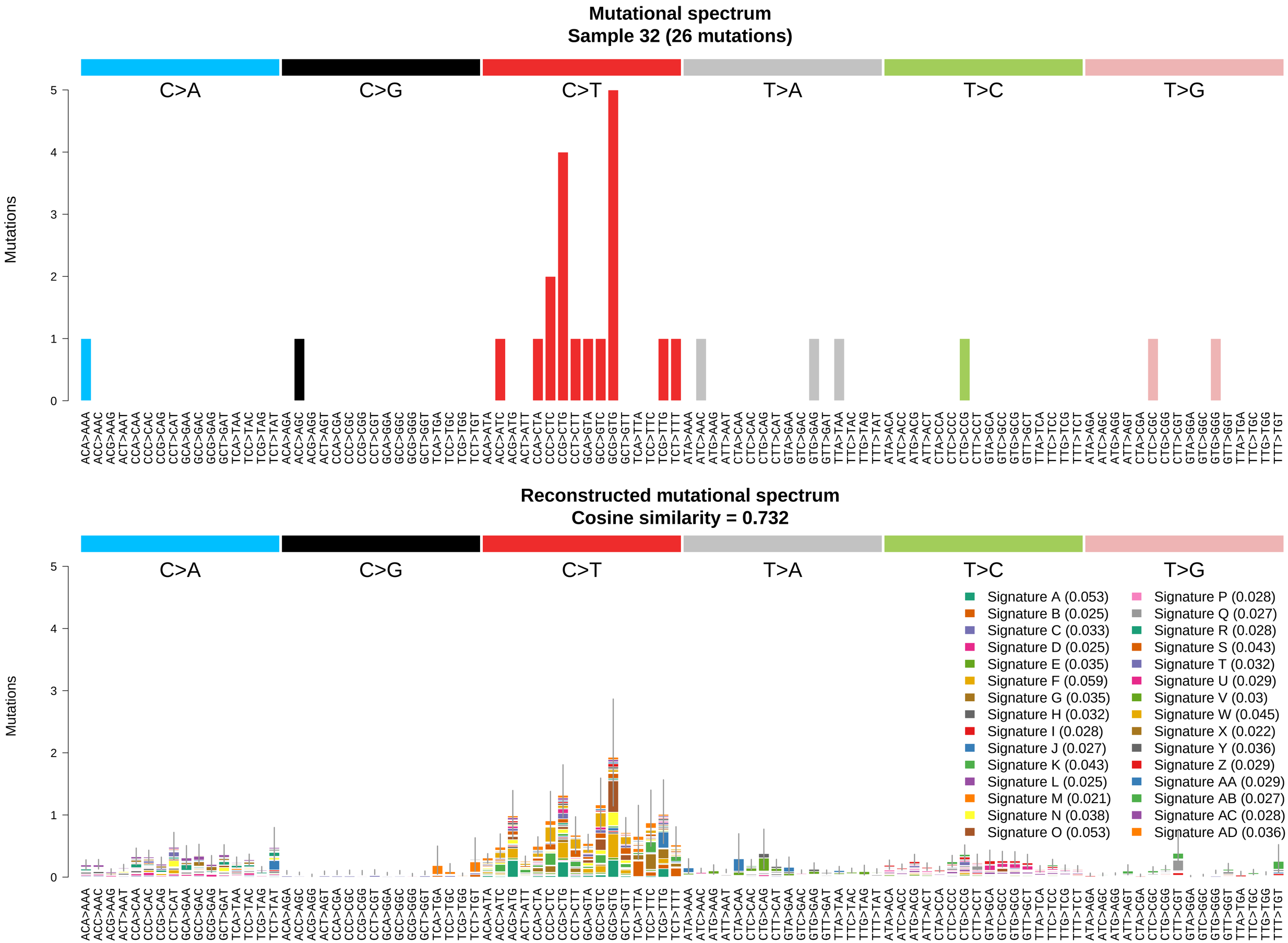

Mutational spectrum
Sample 27 (31 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.58
Signature A (0.061)
Signature B (0.036)
Signature C (0.032)
Signature D (0.029)
Signature E (0.04)
Signature F (0.05)
Signature G (0.046)
Signature H (0.029)
Signature I (0.028)
Signature J (0.024)
Signature K (0.032)
Signature L (0.034)
Signature M (0.019)
Signature N (0.031)
Signature O (0.022)
Signature P (0.041)
Signature Q (0.03)
Signature R (0.027)
Signature S (0.035)
Signature T (0.064)
Signature U (0.033)
Signature V (0.023)
Signature W (0.029)
Signature X (0.022)
Signature Y (0.032)
Signature Z (0.037)
Signature AA (0.022)
Signature AB (0.028)
Signature AC (0.024)
Signature AD (0.039)

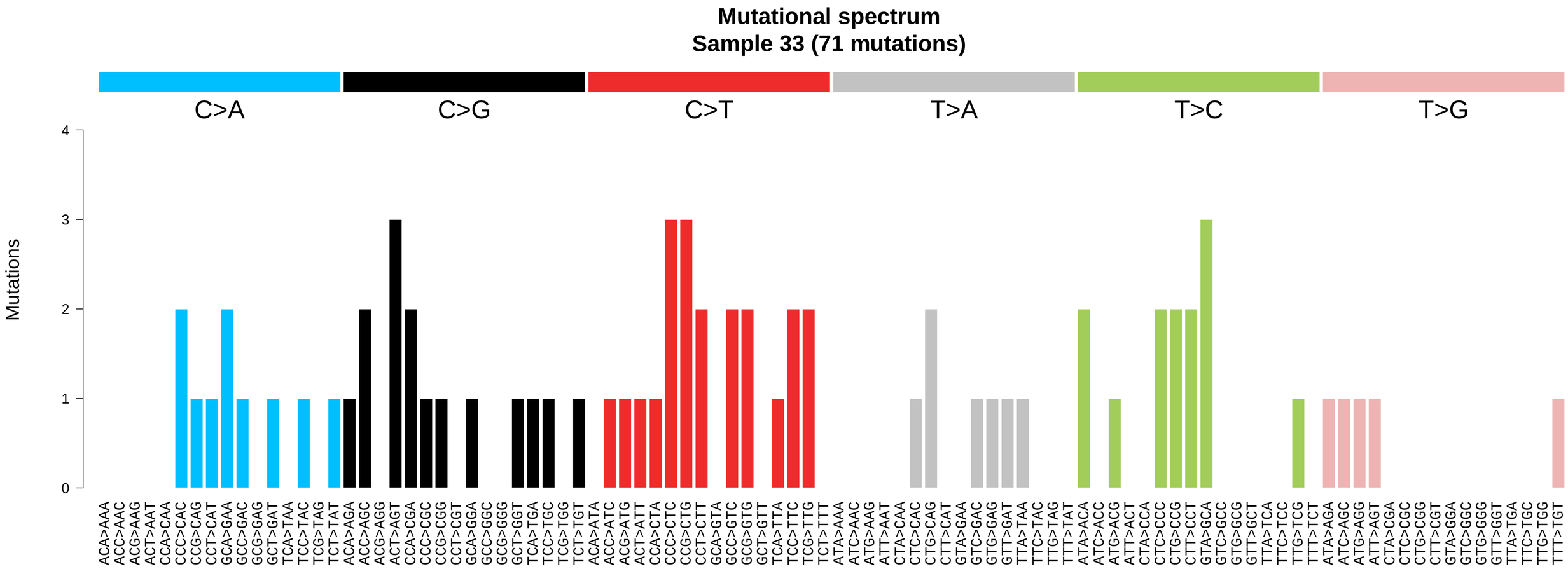

Mutational spectrum
Sample 28 (80 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.739
Signature A (0.036)
Signature B (0.016)
Signature C (0.12)
Signature D (0.046)
Signature E (0.054)
Signature F (0.028)
Signature G (0.023)
Signature H (0.049)
Signature I (0.036)
Signature J (0.019)
Signature K (0.029)
Signature L (0.025)
Signature M (0.041)
Signature N (0.023)
Signature O (0.023)
Signature P (0.035)
Signature Q (0.015)
Signature R (0.022)
Signature S (0.044)
Signature T (0.024)
Signature U (0.021)
Signature V (0.023)
Signature W (0.046)
Signature X (0.041)
Signature Y (0.032)
Signature Z (0.024)
Signature AA (0.021)
Signature AB (0.015)
Signature AC (0.039)
Signature AD (0.03)

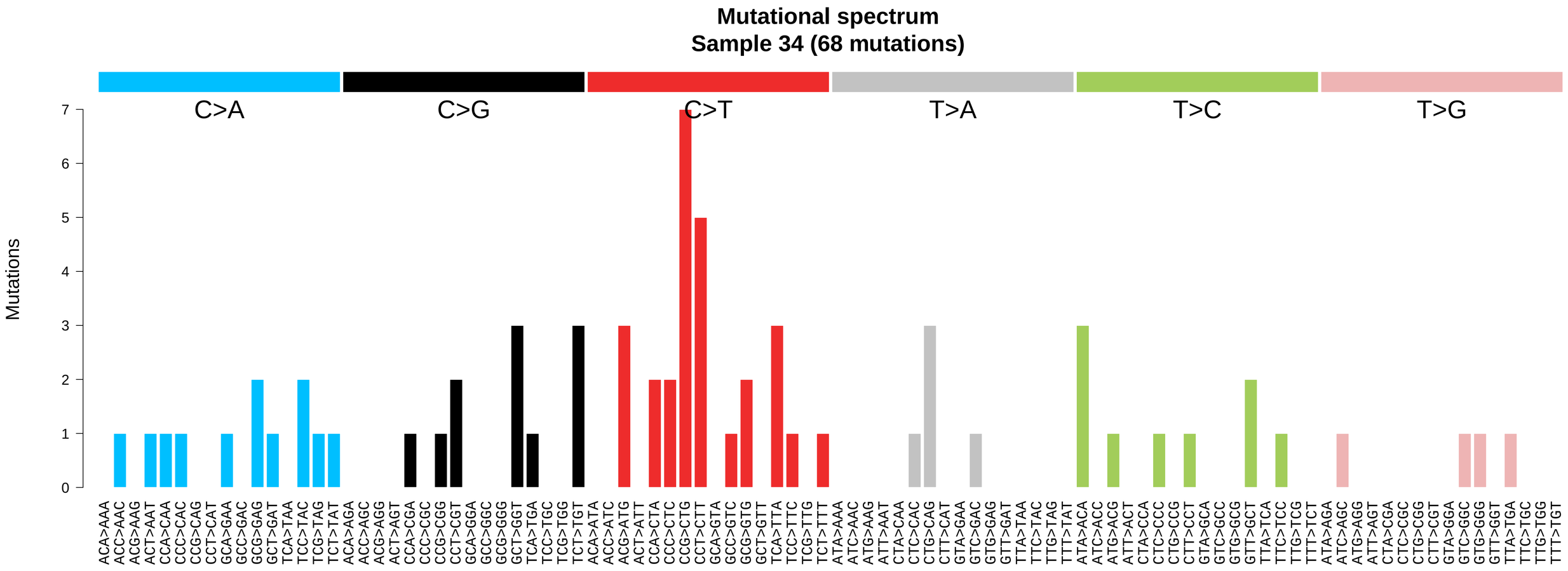

Mutational spectrum
Sample 29 (45 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.669
Signature A (0.023)
Signature B (0.101)
Signature C (0.047)
Signature D (0.023)
Signature E (0.035)
Signature F (0.023)
Signature G (0.044)
Signature H (0.026)
Signature I (0.026)
Signature J (0.02)
Signature K (0.03)
Signature L (0.031)
Signature M (0.065)
Signature N (0.022)
Signature O (0.02)
Signature P (0.031)
Signature Q (0.026)
Signature R (0.021)
Signature S (0.042)
Signature T (0.028)
Signature U (0.026)
Signature V (0.018)
Signature W (0.039)
Signature X (0.025)
Signature Y (0.032)
Signature Z (0.023)
Signature AA (0.021)
Signature AB (0.036)
Signature AC (0.023)
Signature AD (0.073)

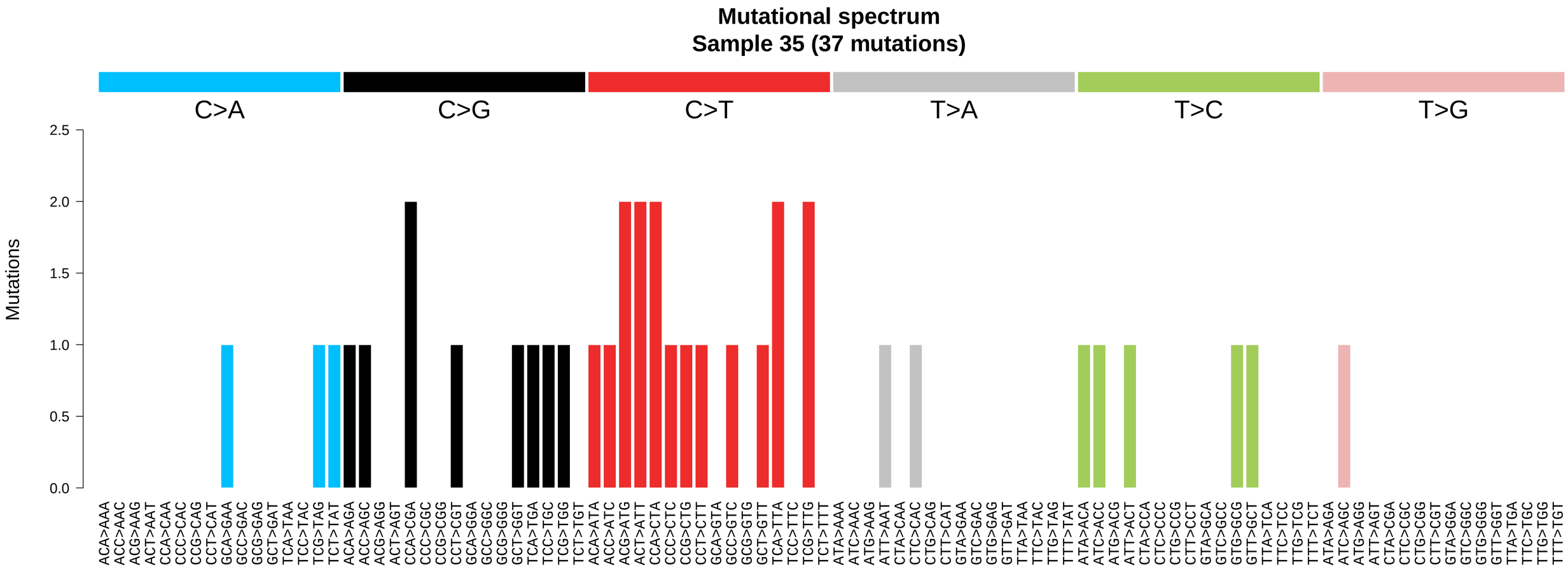

Mutational spectrum
Sample 30 (58 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.817
Signature A (0.066)
Signature B (0.062)
Signature C (0.033)
Signature D (0.028)
Signature E (0.027)
Signature F (0.062)
Signature G (0.056)
Signature H (0.023)
Signature I (0.025)
Signature J (0.029)
Signature K (0.03)
Signature L (0.023)
Signature M (0.051)
Signature N (0.026)
Signature O (0.03)
Signature P (0.023)
Signature Q (0.02)
Signature R (0.022)
Signature S (0.068)
Signature T (0.041)
Signature U (0.024)
Signature V (0.013)
Signature W (0.047)
Signature X (0.023)
Signature Y (0.026)
Signature Z (0.024)
Signature AA (0.018)
Signature AB (0.016)
Signature AC (0.026)
Signature AD (0.038)

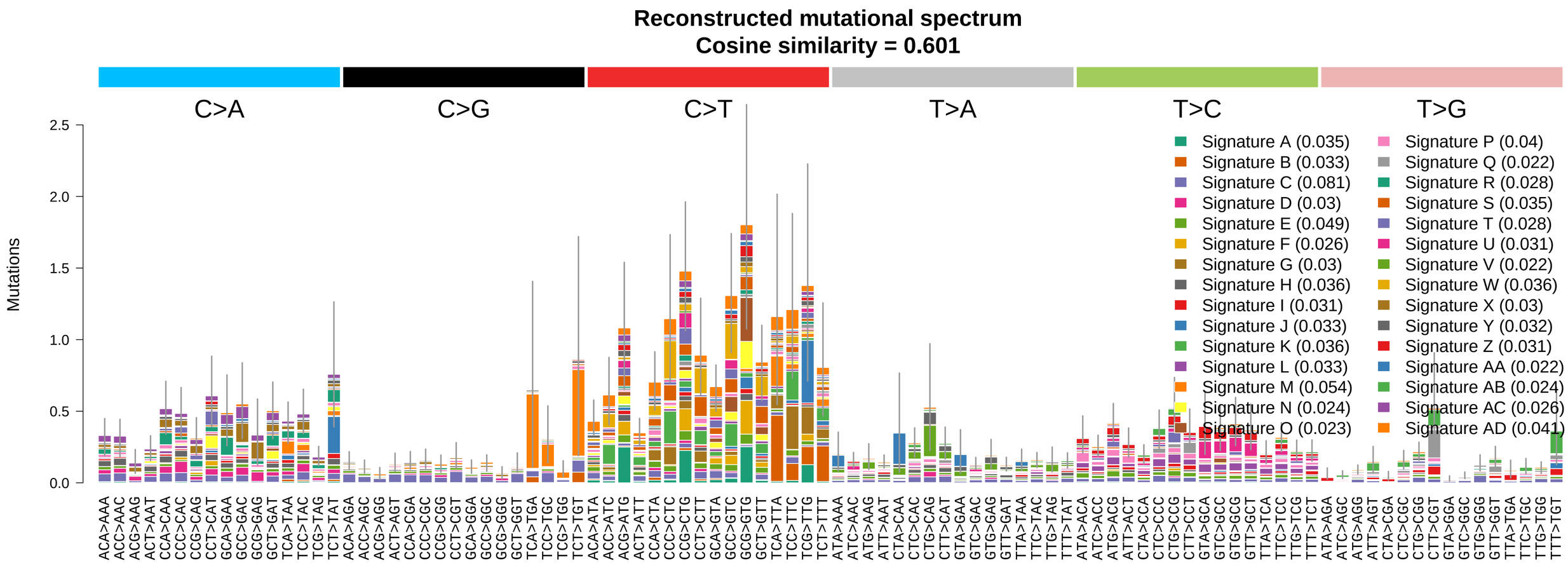

Mutational spectrum
Sample 31 (70 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.756
Signature A (0.045)
Signature B (0.031)
Signature C (0.031)
Signature D (0.058)
Signature E (0.041)
Signature F (0.035)
Signature G (0.028)
Signature H (0.03)
Signature I (0.022)
Signature J (0.017)
Signature K (0.027)
Signature L (0.027)
Signature M (0.019)
Signature N (0.032)
Signature O (0.028)
Signature P (0.029)
Signature Q (0.017)
Signature R (0.02)
Signature S (0.054)
Signature T (0.027)
Signature U (0.026)
Signature V (0.036)
Signature W (0.052)
Signature X (0.042)
Signature Y (0.04)
Signature Z (0.027)
Signature AA (0.021)
Signature AB (0.014)
Signature AC (0.028)
Signature AD (0.095)

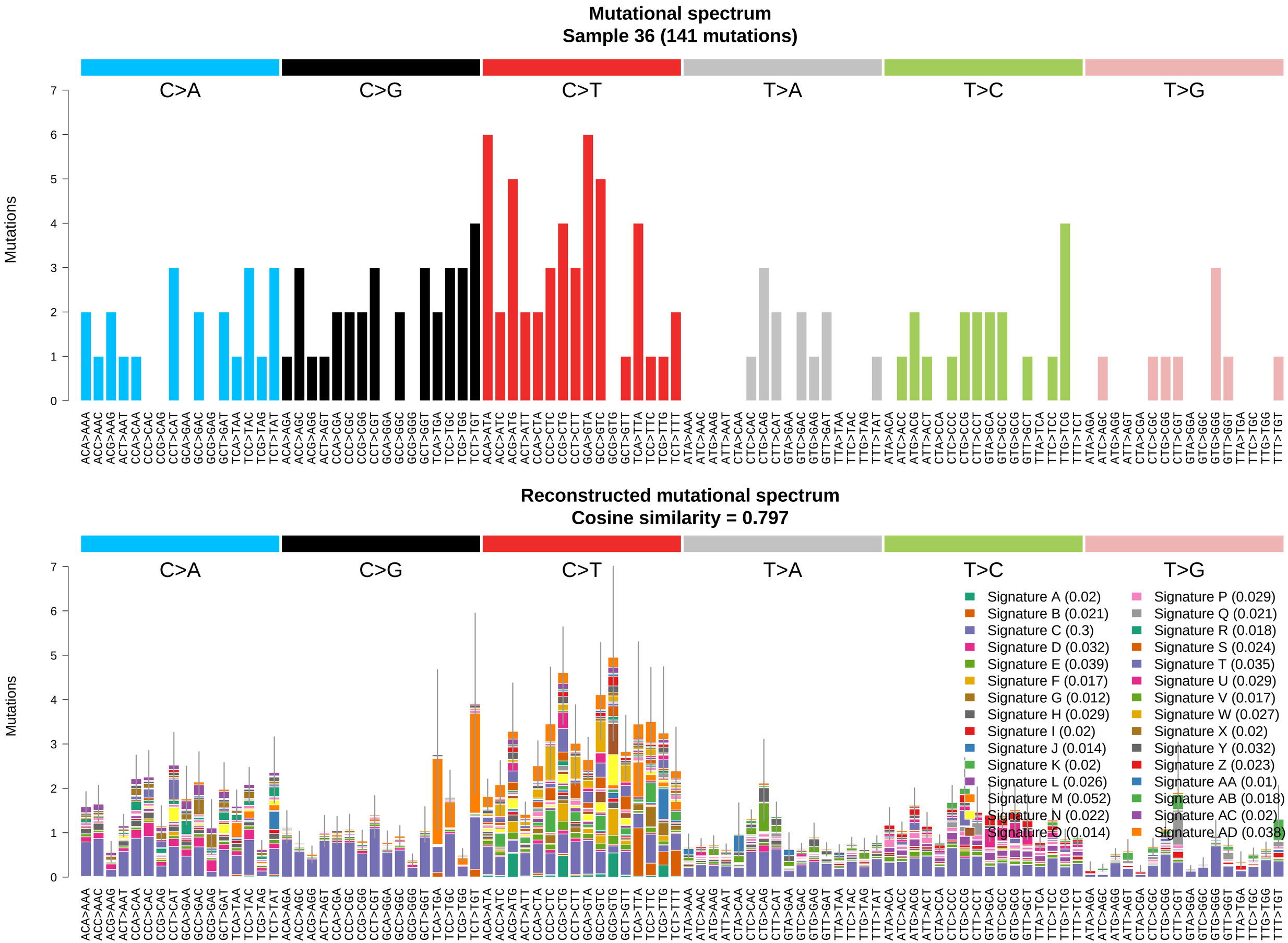

Mutational spectrum
Sample 32 (26 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.732
Signature A (0.053)
Signature B (0.025)
Signature C (0.033)
Signature D (0.025)
Signature E (0.035)
Signature F (0.059)
Signature G (0.035)
Signature H (0.032)
Signature I (0.028)
Signature J (0.027)
Signature K (0.043)
Signature L (0.025)
Signature M (0.021)
Signature N (0.038)
Signature O (0.053)
Signature P (0.028)
Signature Q (0.027)
Signature R (0.028)
Signature S (0.043)
Signature T (0.032)
Signature U (0.029)
Signature V (0.03)
Signature W (0.045)
Signature X (0.022)
Signature Y (0.036)
Signature Z (0.029)
Signature AA (0.029)
Signature AB (0.027)
Signature AC (0.028)
Signature AD (0.036)

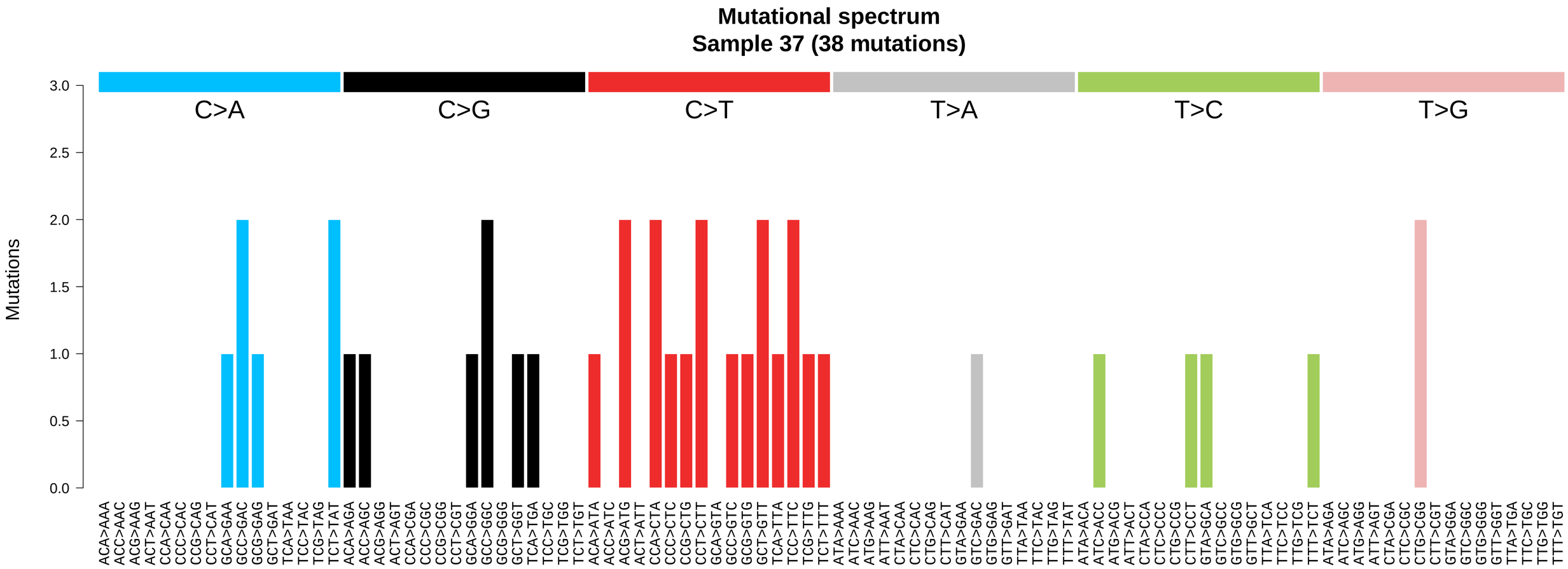

Mutational spectrum
Sample 33 (71 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.75
Signature A (0.025)
Signature B (0.017)
Signature C (0.137)
Signature D (0.037)
Signature E (0.05)
Signature F (0.023)
Signature G (0.029)
Signature H (0.035)
Signature I (0.038)
Signature J (0.023)
Signature K (0.03)
Signature L (0.036)
Signature M (0.029)
Signature N (0.022)
Signature O (0.019)
Signature P (0.048)
Signature Q (0.026)
Signature R (0.028)
Signature S (0.029)
Signature T (0.029)
Signature U (0.032)
Signature V (0.029)
Signature W (0.026)
Signature X (0.026)
Signature Y (0.041)
Signature Z (0.035)
Signature AA (0.019)
Signature AB (0.032)
Signature AC (0.024)
Signature AD (0.026)

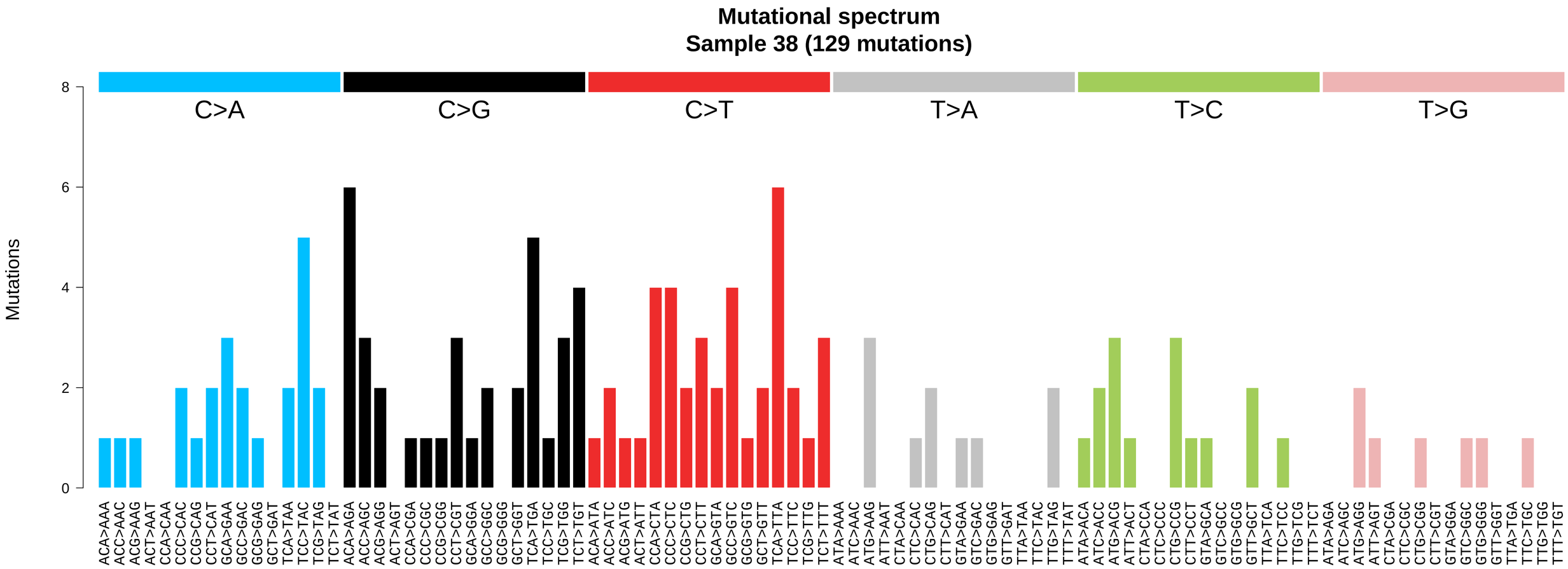

Mutational spectrum
Sample 34 (68 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
7
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.707
Signature A (0.042)
Signature B (0.031)
Signature C (0.081)
Signature D (0.05)
Signature E (0.037)
Signature F (0.028)
Signature G (0.031)
Signature H (0.038)
Signature I (0.033)
Signature J (0.017)
Signature K (0.025)
Signature L (0.03)
Signature M (0.053)
Signature N (0.024)
Signature O (0.019)
Signature P (0.056)
Signature Q (0.024)
Signature R (0.036)
Signature S (0.04)
Signature T (0.024)
Signature U (0.028)
Signature V (0.034)
Signature W (0.032)
Signature X (0.036)
Signature Y (0.029)
Signature Z (0.028)
Signature AA (0.017)
Signature AB (0.017)
Signature AC (0.032)
Signature AD (0.031)

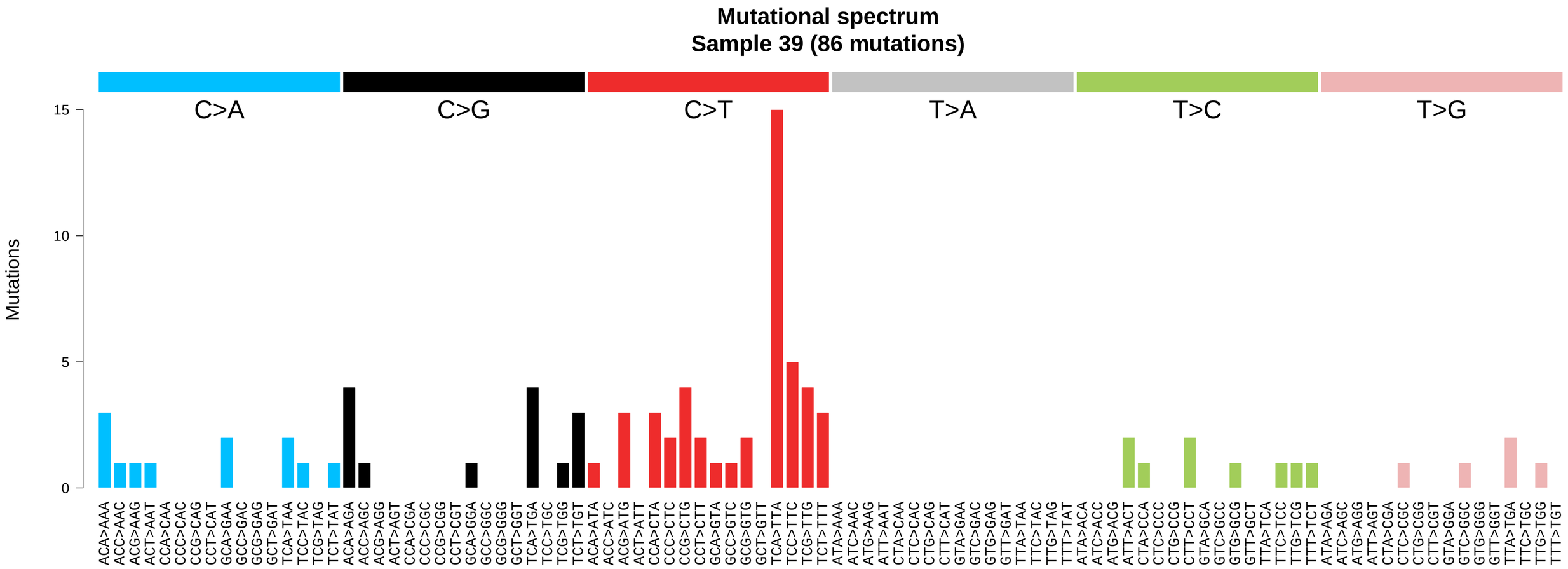

Mutational spectrum
Sample 35 (37 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

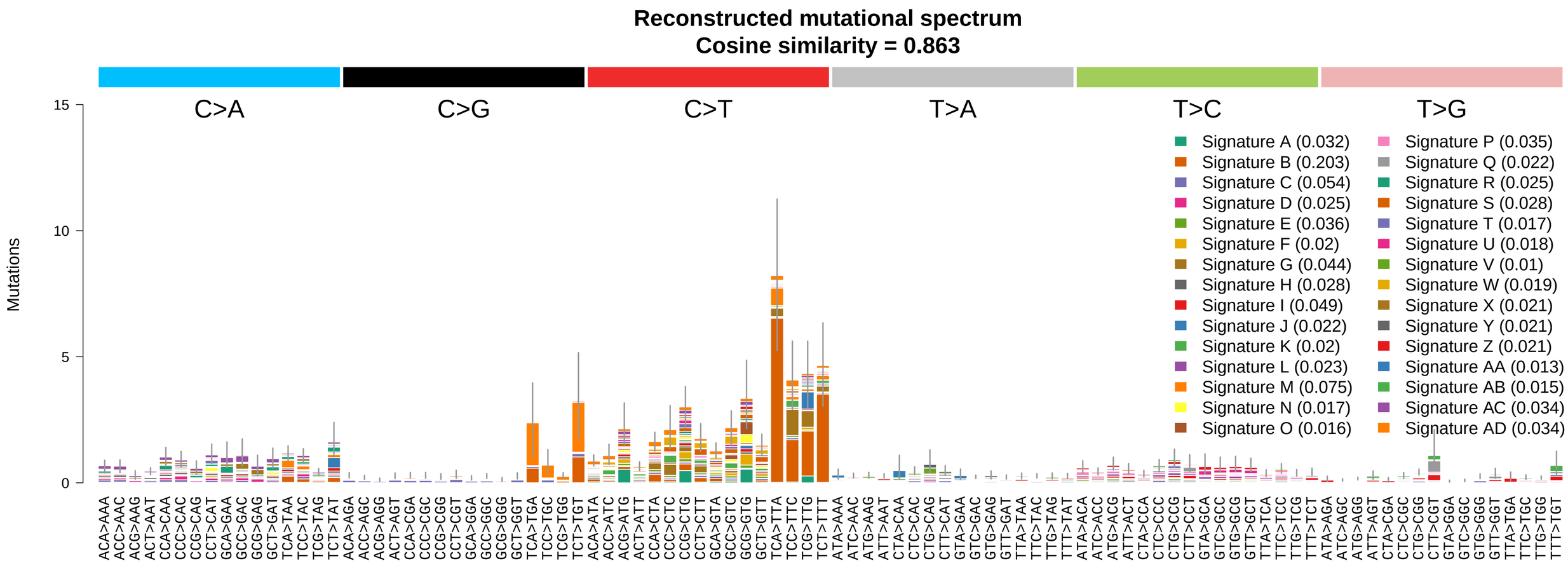

Reconstructed mutational spectrum
Cosine similarity = 0.601
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
2.5
2.0
1.5
1.0
0.5
0.0
Signature A (0.035)
Signature B (0.033)
Signature C (0.081)
Signature D (0.03)
Signature E (0.049)
Signature F (0.026)
Signature G (0.03)
Signature H (0.036)
Signature I (0.031)
Signature J (0.033)
Signature K (0.036)
Signature L (0.033)
Signature M (0.054)
Signature N (0.024)
Signature O (0.023)
Signature P (0.04)
Signature Q (0.022)
Signature R (0.028)
Signature S (0.035)
Signature T (0.028)
Signature U (0.031)
Signature V (0.022)
Signature W (0.036)
Signature X (0.03)
Signature Y (0.032)
Signature Z (0.031)
Signature AA (0.022)
Signature AB (0.024)
Signature AC (0.026)
Signature AD (0.041)

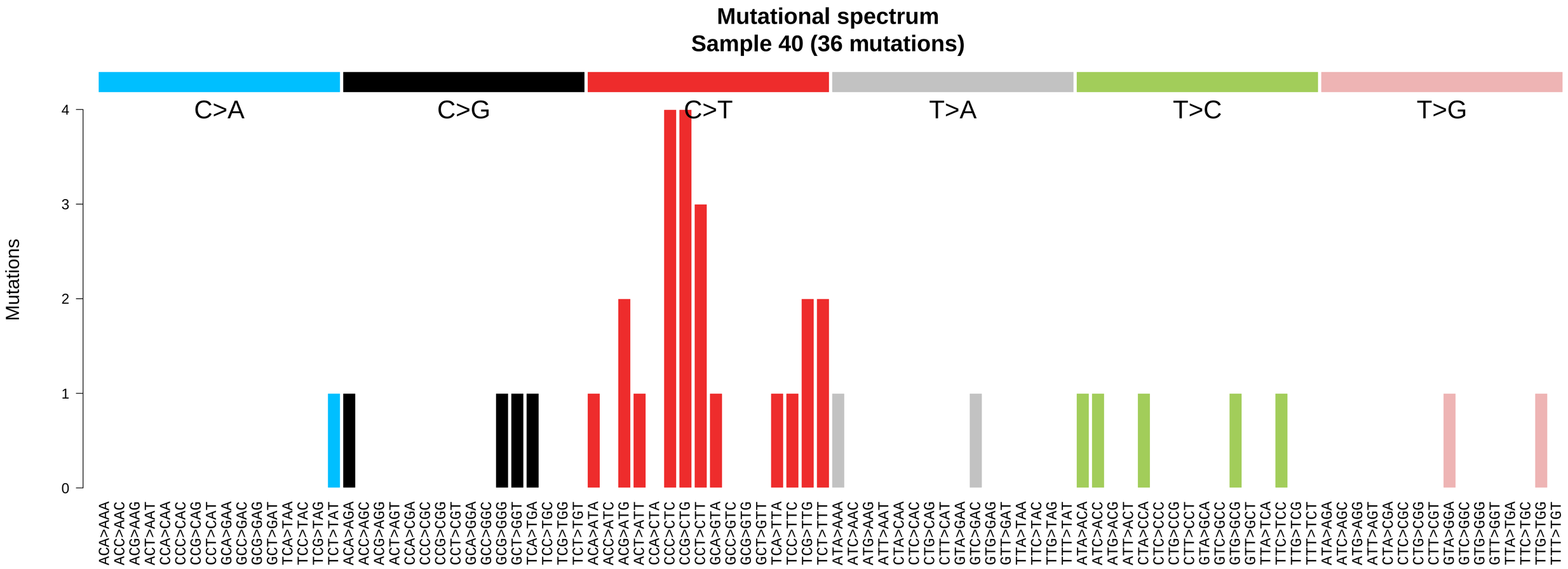

Mutational spectrum
Sample 36 (141 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.797
Signature A (0.02)
Signature B (0.021)
Signature C (0.3)
Signature D (0.032)
Signature E (0.039)
Signature F (0.017)
Signature G (0.012)
Signature H (0.029)
Signature I (0.02)
Signature J (0.014)
Signature K (0.02)
Signature L (0.026)
Signature M (0.052)
Signature N (0.022)
Signature O (0.014)
Signature P (0.029)
Signature Q (0.021)
Signature R (0.018)
Signature S (0.024)
Signature T (0.035)
Signature U (0.029)
Signature V (0.017)
Signature W (0.027)
Signature X (0.02)
Signature Y (0.032)
Signature Z (0.023)
Signature AA (0.01)
Signature AB (0.018)
Signature AC (0.02)
Signature AD (0.038)

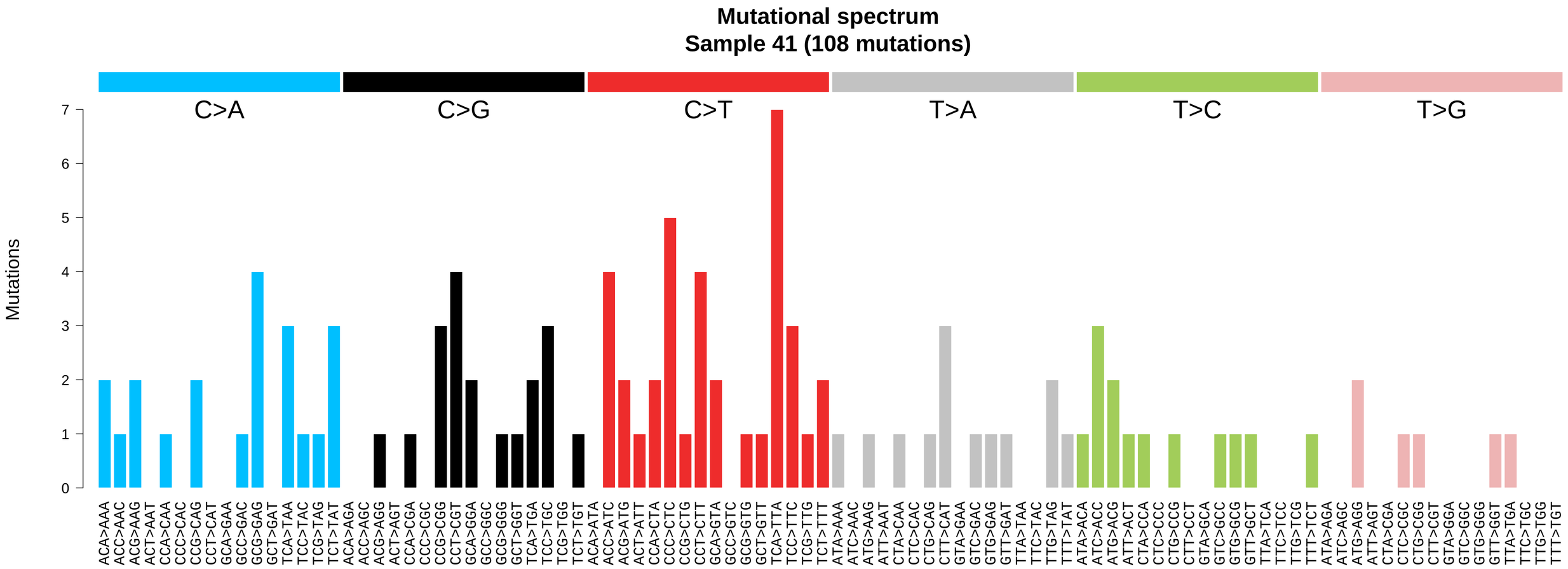

Mutational spectrum
Sample 37 (38 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.678
Signature A (0.031)
Signature B (0.034)
Signature C (0.057)
Signature D (0.037)
Signature E (0.047)
Signature F (0.03)
Signature G (0.042)
Signature H (0.032)
Signature I (0.034)
Signature J (0.034)
Signature K (0.036)
Signature L (0.03)
Signature M (0.028)
Signature N (0.028)
Signature O (0.026)
Signature P (0.032)
Signature Q (0.026)
Signature R (0.027)
Signature S (0.038)
Signature T (0.029)
Signature U (0.034)
Signature V (0.018)
Signature W (0.038)
Signature X (0.049)
Signature Y (0.03)
Signature Z (0.03)
Signature AA (0.023)
Signature AB (0.02)
Signature AC (0.034)
Signature AD (0.046)

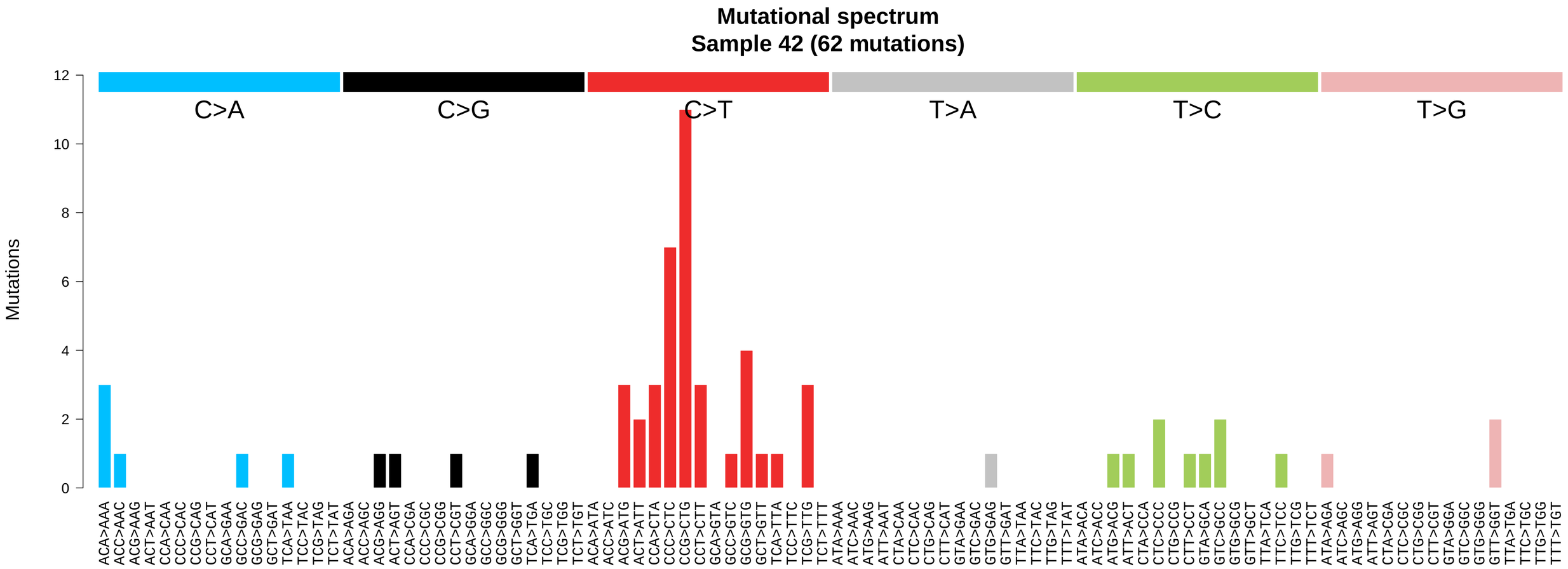

Mutational spectrum
Sample 38 (129 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.798
Signature A (0.012)
Signature B (0.036)
Signature C (0.25)
Signature D (0.055)
Signature E (0.041)
Signature F (0.013)
Signature G (0.02)
Signature H (0.023)
Signature I (0.017)
Signature J (0.01)
Signature K (0.026)
Signature L (0.025)
Signature M (0.09)
Signature N (0.012)
Signature O (0.012)
Signature P (0.035)
Signature Q (0.013)
Signature R (0.024)
Signature S (0.024)
Signature T (0.023)
Signature U (0.016)
Signature V (0.027)
Signature W (0.03)
Signature X (0.037)
Signature Y (0.021)
Signature Z (0.02)
Signature AA (0.013)
Signature AB (0.012)
Signature AC (0.023)
Signature AD (0.036)

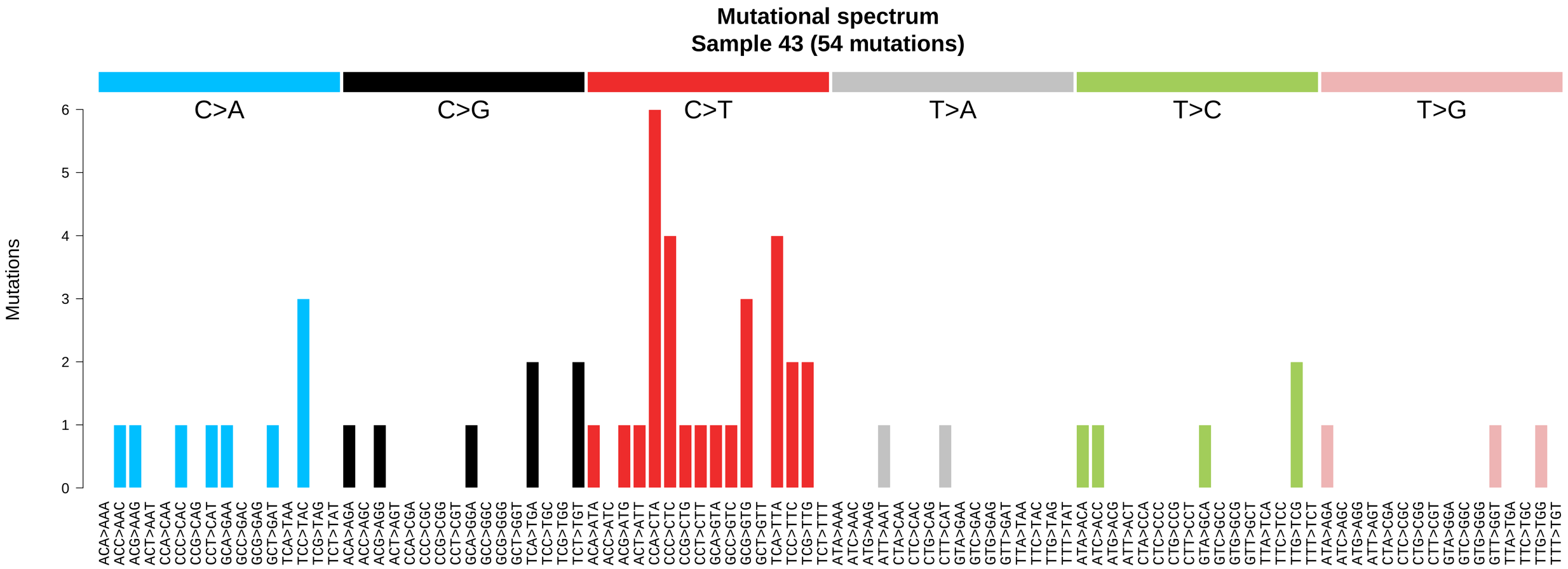

Mutational spectrum
Sample 39 (86 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

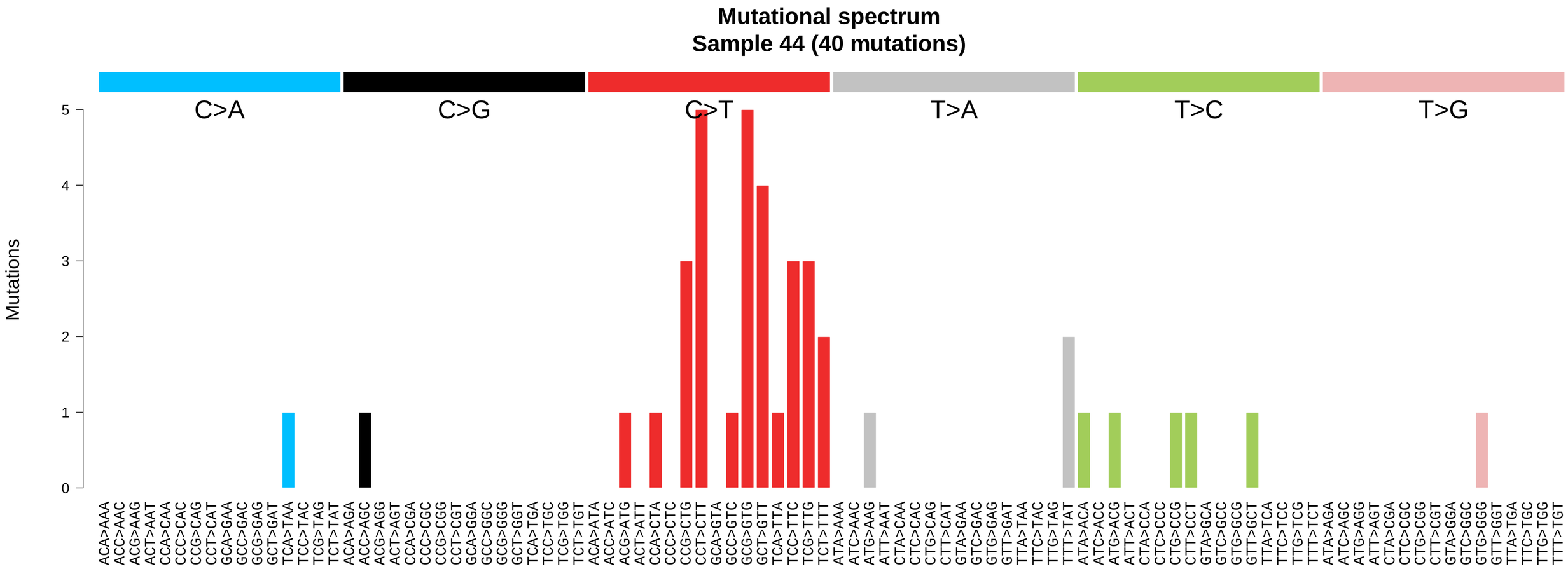

Reconstructed mutational spectrum
Cosine similarity = 0.863
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
Signature A (0.032)
Signature B (0.203)
Signature C (0.054)
Signature D (0.025)
Signature E (0.036)
Signature F (0.02)
Signature G (0.044)
Signature H (0.028)
Signature I (0.049)
Signature J (0.022)
Signature K (0.02)
Signature L (0.023)
Signature M (0.075)
Signature N (0.017)
Signature O (0.016)
Signature P (0.035)
Signature Q (0.022)
Signature R (0.025)
Signature S (0.028)
Signature T (0.017)
Signature U (0.018)
Signature V (0.01)
Signature W (0.019)
Signature X (0.021)
Signature Y (0.021)
Signature Z (0.021)
Signature AA (0.013)
Signature AB (0.015)
Signature AC (0.034)
Signature AD (0.034)

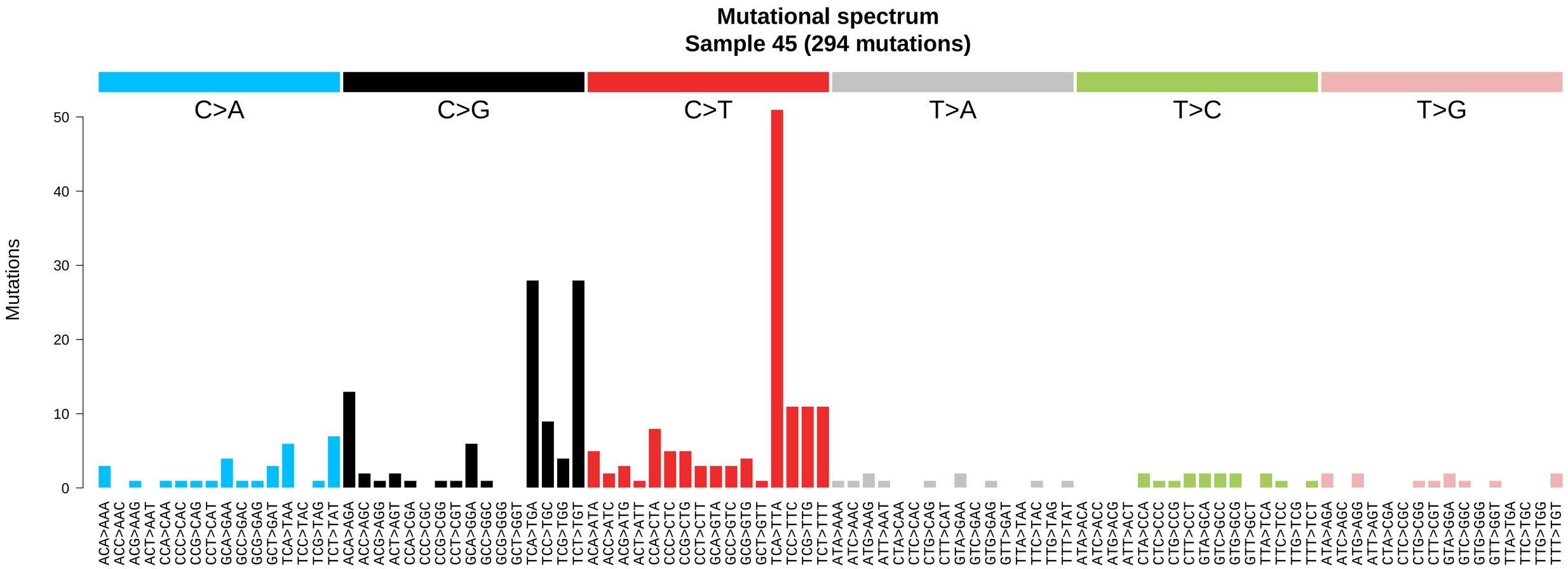

Mutational spectrum
Sample 40 (36 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.659
Signature A (0.036)
Signature B (0.041)
Signature C (0.046)
Signature D (0.027)
Signature E (0.041)
Signature F (0.029)
Signature G (0.051)
Signature H (0.028)
Signature I (0.036)
Signature J (0.034)
Signature K (0.054)
Signature L (0.034)
Signature M (0.03)
Signature N (0.026)
Signature O (0.022)
Signature P (0.029)
Signature Q (0.021)
Signature R (0.022)
Signature S (0.041)
Signature T (0.031)
Signature U (0.038)
Signature V (0.02)
Signature W (0.051)
Signature X (0.022)
Signature Y (0.038)
Signature Z (0.033)
Signature AA (0.029)
Signature AB (0.022)
Signature AC (0.022)
Signature AD (0.049)

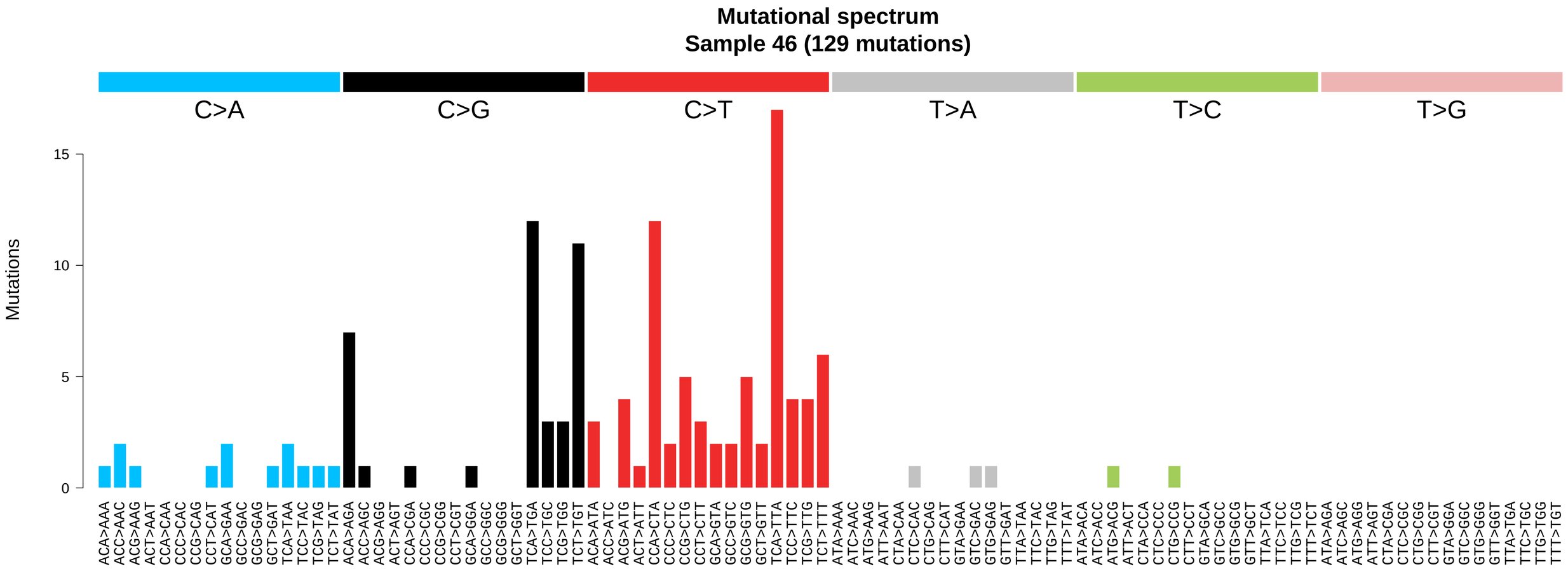

Mutational spectrum
Sample 41 (108 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
7
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.73
Signature A (0.014)
Signature B (0.053)
Signature C (0.136)
Signature D (0.079)
Signature E (0.046)
Signature F (0.014)
Signature G (0.027)
Signature H (0.031)
Signature I (0.029)
Signature J (0.015)
Signature K (0.036)
Signature L (0.029)
Signature M (0.043)
Signature N (0.012)
Signature O (0.013)
Signature P (0.052)
Signature Q (0.015)
Signature R (0.028)
Signature S (0.024)
Signature T (0.018)
Signature U (0.017)
Signature V (0.033)
Signature W (0.03)
Signature X (0.049)
Signature Y (0.032)
Signature Z (0.021)
Signature AA (0.019)
Signature AB (0.014)
Signature AC (0.024)
Signature AD (0.045)

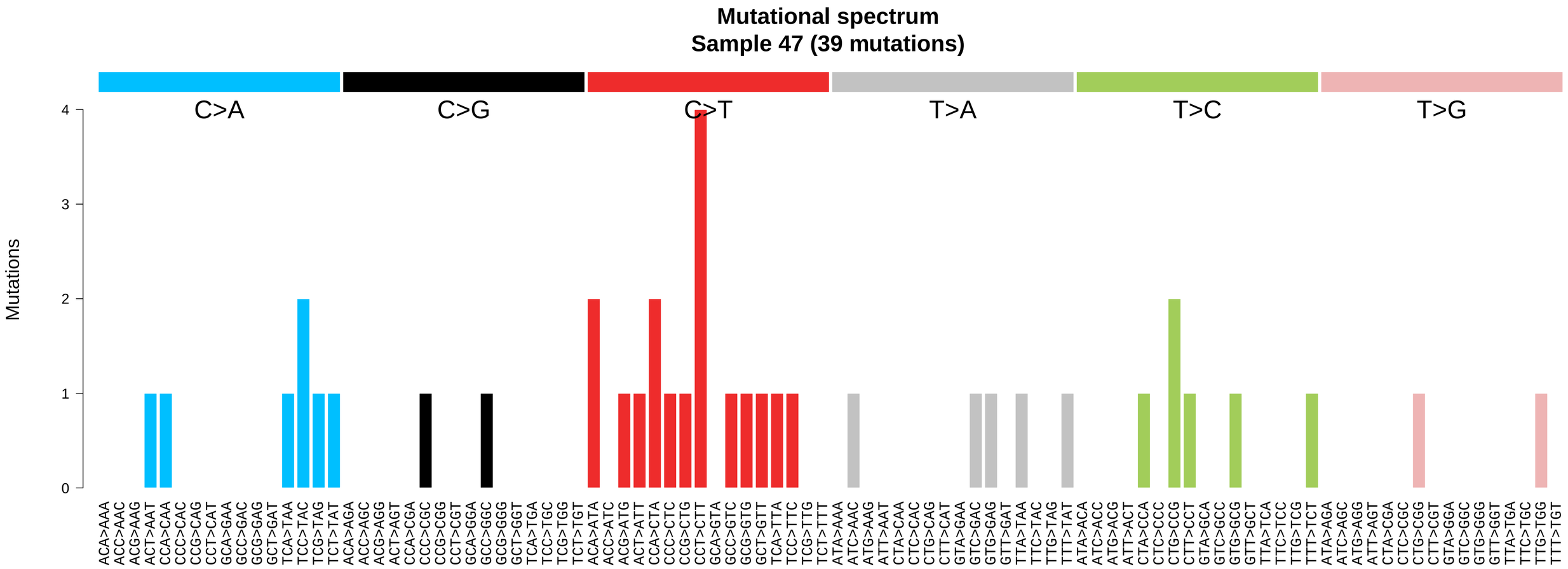

Mutational spectrum
Sample 42 (62 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.733
Signature A (0.102)
Signature B (0.019)
Signature C (0.037)
Signature D (0.023)
Signature E (0.039)
Signature F (0.045)
Signature G (0.037)
Signature H (0.033)
Signature I (0.036)
Signature J (0.023)
Signature K (0.04)
Signature L (0.031)
Signature M (0.022)
Signature N (0.023)
Signature O (0.029)
Signature P (0.029)
Signature Q (0.033)
Signature R (0.022)
Signature S (0.058)
Signature T (0.028)
Signature U (0.035)
Signature V (0.016)
Signature W (0.066)
Signature X (0.018)
Signature Y (0.023)
Signature Z (0.035)
Signature AA (0.017)
Signature AB (0.019)
Signature AC (0.03)
Signature AD (0.036)

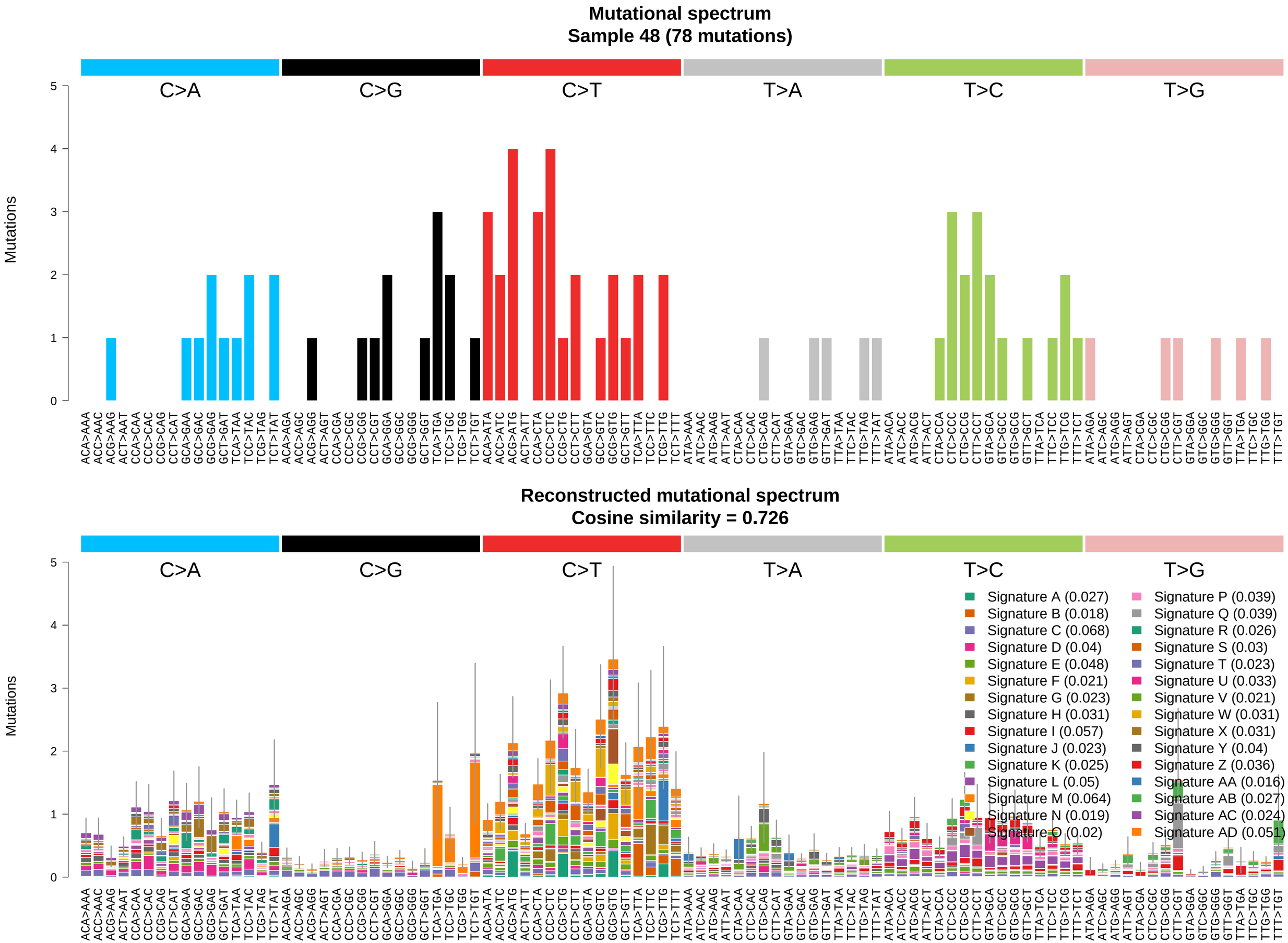

Mutational spectrum
Sample 43 (54 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.714
Signature A (0.029)
Signature B (0.046)
Signature C (0.044)
Signature D (0.04)
Signature E (0.035)
Signature F (0.025)
Signature G (0.057)
Signature H (0.032)
Signature I (0.033)
Signature J (0.021)
Signature K (0.032)
Signature L (0.031)
Signature M (0.065)
Signature N (0.029)
Signature O (0.028)
Signature P (0.033)
Signature Q (0.023)
Signature R (0.027)
Signature S (0.036)
Signature T (0.026)
Signature U (0.02)
Signature V (0.018)
Signature W (0.039)
Signature X (0.028)
Signature Y (0.03)
Signature Z (0.026)
Signature AA (0.018)
Signature AB (0.019)
Signature AC (0.031)
Signature AD (0.08)

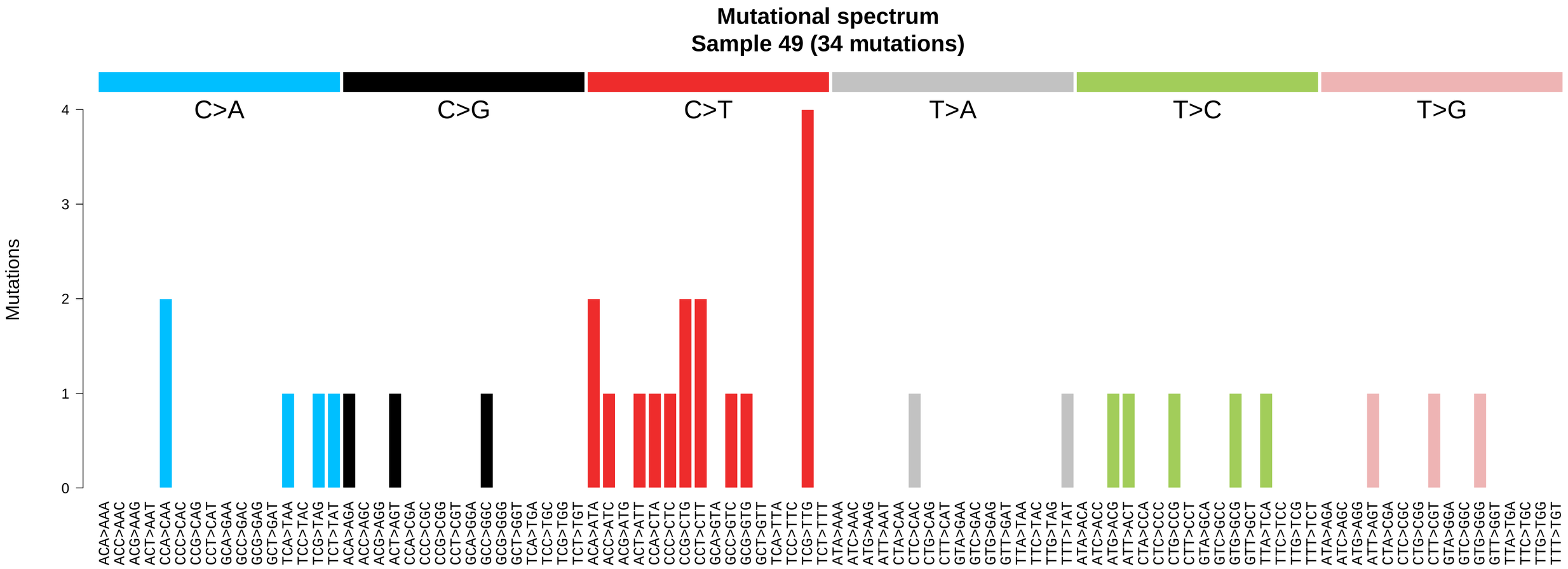

Mutational spectrum
Sample 44 (40 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.764
Signature A (0.045)
Signature B (0.039)
Signature C (0.029)
Signature D (0.02)
Signature E (0.036)
Signature F (0.044)
Signature G (0.078)
Signature H (0.03)
Signature I (0.028)
Signature J (0.035)
Signature K (0.041)
Signature L (0.031)
Signature M (0.02)
Signature N (0.034)
Signature O (0.043)
Signature P (0.028)
Signature Q (0.025)
Signature R (0.021)
Signature S (0.072)
Signature T (0.029)
Signature U (0.026)
Signature V (0.026)
Signature W (0.05)
Signature X (0.02)
Signature Y (0.028)
Signature Z (0.033)
Signature AA (0.021)
Signature AB (0.019)
Signature AC (0.02)
Signature AD (0.029)

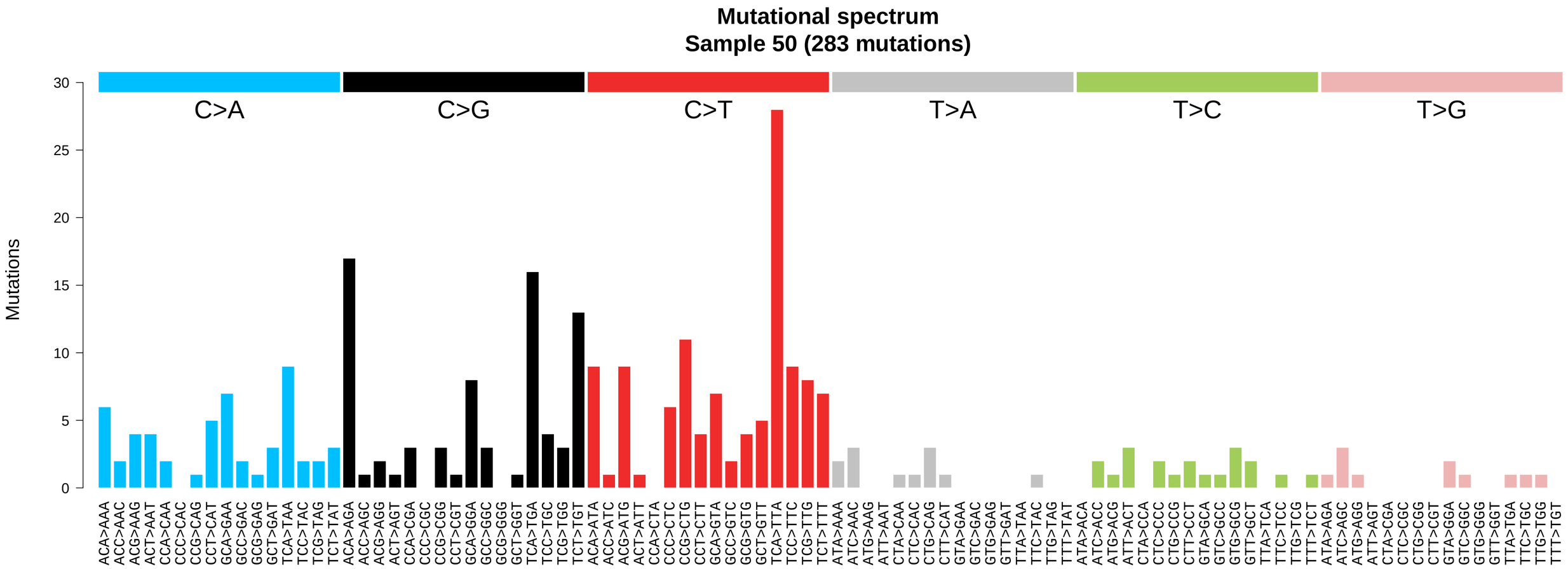

Mutational spectrum
Sample 45 (294 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
10
20
30
40
50
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.943
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
10
20
30
40
50
Signature A (0.011)
Signature B (0.215)
Signature C (0.129)
Signature D (0.013)
Signature E (0.025)
Signature F (0.009)
Signature G (0.019)
Signature H (0.013)
Signature I (0.023)
Signature J (0.015)
Signature K (0.013)
Signature L (0.012)
Signature M (0.281)
Signature N (0.009)
Signature O (0.008)
Signature P (0.014)
Signature Q (0.01)
Signature R (0.018)
Signature S (0.012)
Signature T (0.008)
Signature U (0.013)
Signature V (0.008)
Signature W (0.011)
Signature X (0.011)
Signature Y (0.019)
Signature Z (0.011)
Signature AA (0.009)
Signature AB (0.009)
Signature AC (0.015)
Signature AD (0.036)

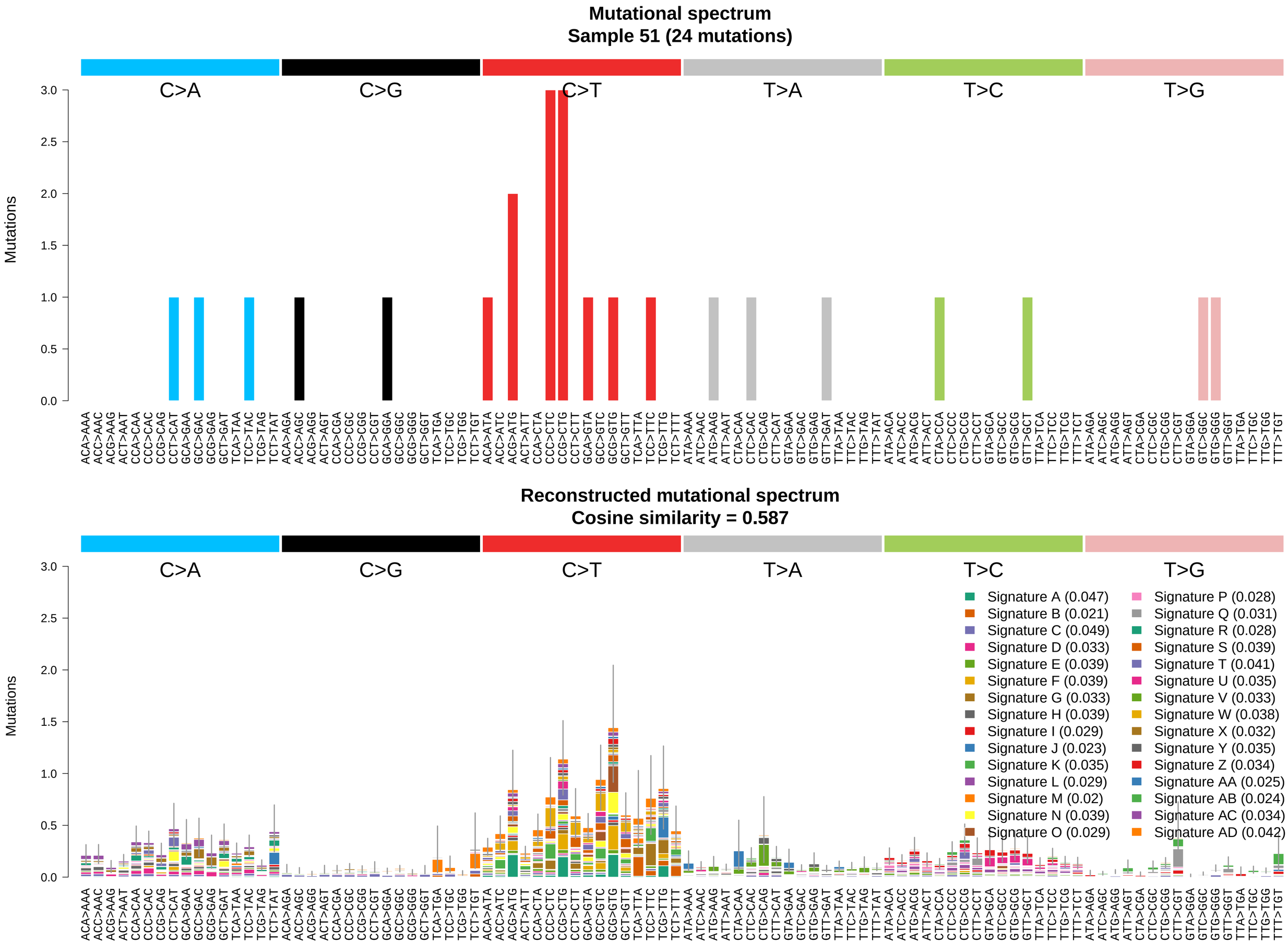

Mutational spectrum
Sample 46 (129 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.884
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
Signature A (0.035)
Signature B (0.139)
Signature C (0.039)
Signature D (0.025)
Signature E (0.026)
Signature F (0.026)
Signature G (0.044)
Signature H (0.02)
Signature I (0.012)
Signature J (0.013)
Signature K (0.021)
Signature L (0.012)
Signature M (0.256)
Signature N (0.019)
Signature O (0.017)
Signature P (0.016)
Signature Q (0.011)
Signature R (0.017)
Signature S (0.041)
Signature T (0.016)
Signature U (0.01)
Signature V (0.01)
Signature W (0.028)
Signature X (0.018)
Signature Y (0.02)
Signature Z (0.011)
Signature AA (0.013)
Signature AB (0.008)
Signature AC (0.027)
Signature AD (0.053)

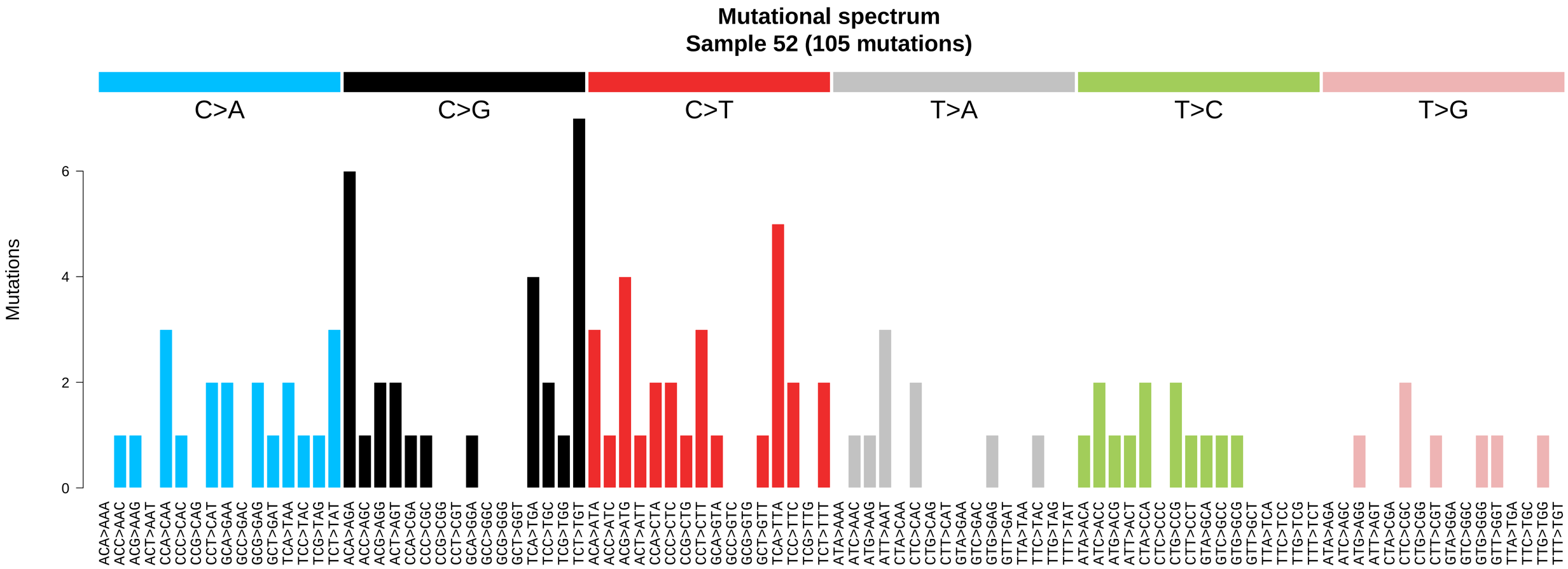

Mutational spectrum
Sample 47 (39 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.605
Signature A (0.027)
Signature B (0.024)
Signature C (0.042)
Signature D (0.042)
Signature E (0.044)
Signature F (0.026)
Signature G (0.032)
Signature H (0.047)
Signature I (0.039)
Signature J (0.022)
Signature K (0.032)
Signature L (0.042)
Signature M (0.02)
Signature N (0.027)
Signature O (0.024)
Signature P (0.041)
Signature Q (0.029)
Signature R (0.034)
Signature S (0.049)
Signature T (0.032)
Signature U (0.033)
Signature V (0.026)
Signature W (0.044)
Signature X (0.03)
Signature Y (0.045)
Signature Z (0.033)
Signature AA (0.024)
Signature AB (0.026)
Signature AC (0.023)
Signature AD (0.041)

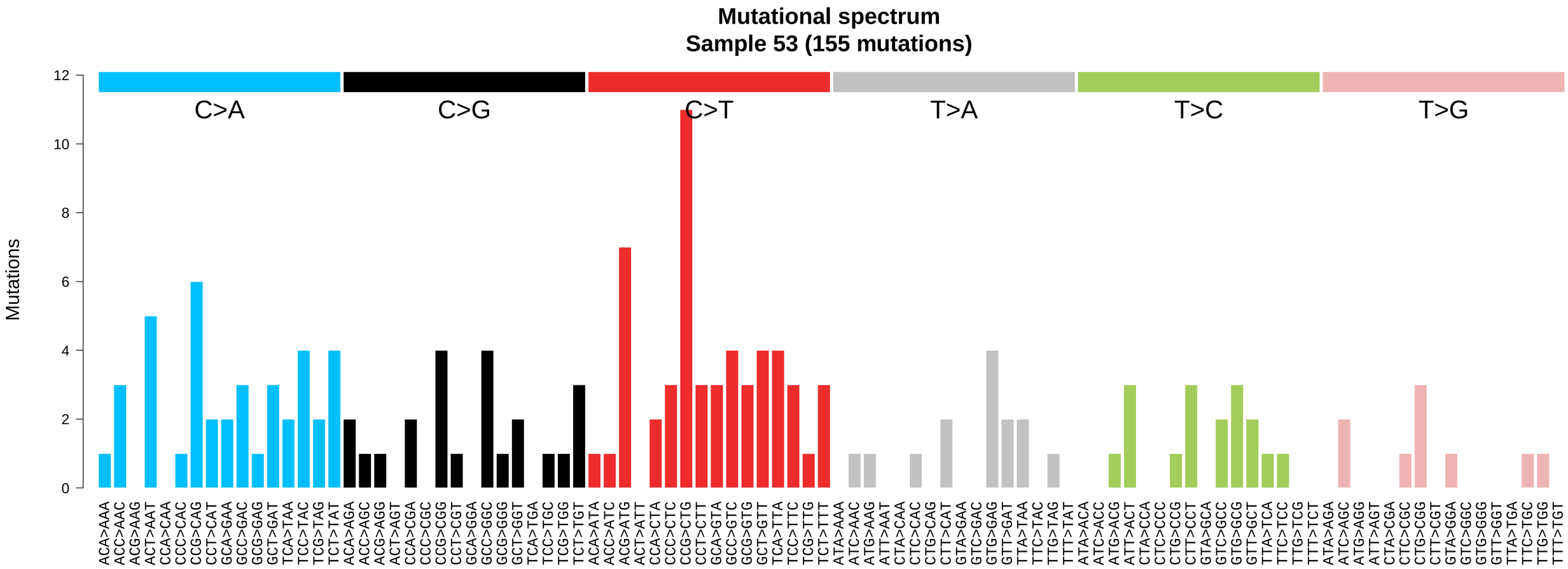

Mutational spectrum
Sample 48 (78 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.726
Signature A (0.027)
Signature B (0.018)
Signature C (0.068)
Signature D (0.04)
Signature E (0.048)
Signature F (0.021)
Signature G (0.023)
Signature H (0.031)
Signature I (0.057)
Signature J (0.023)
Signature K (0.025)
Signature L (0.05)
Signature M (0.064)
Signature N (0.019)
Signature O (0.02)
Signature P (0.039)
Signature Q (0.039)
Signature R (0.026)
Signature S (0.03)
Signature T (0.023)
Signature U (0.033)
Signature V (0.021)
Signature W (0.031)
Signature X (0.031)
Signature Y (0.04)
Signature Z (0.036)
Signature AA (0.016)
Signature AB (0.027)
Signature AC (0.024)
Signature AD (0.051)

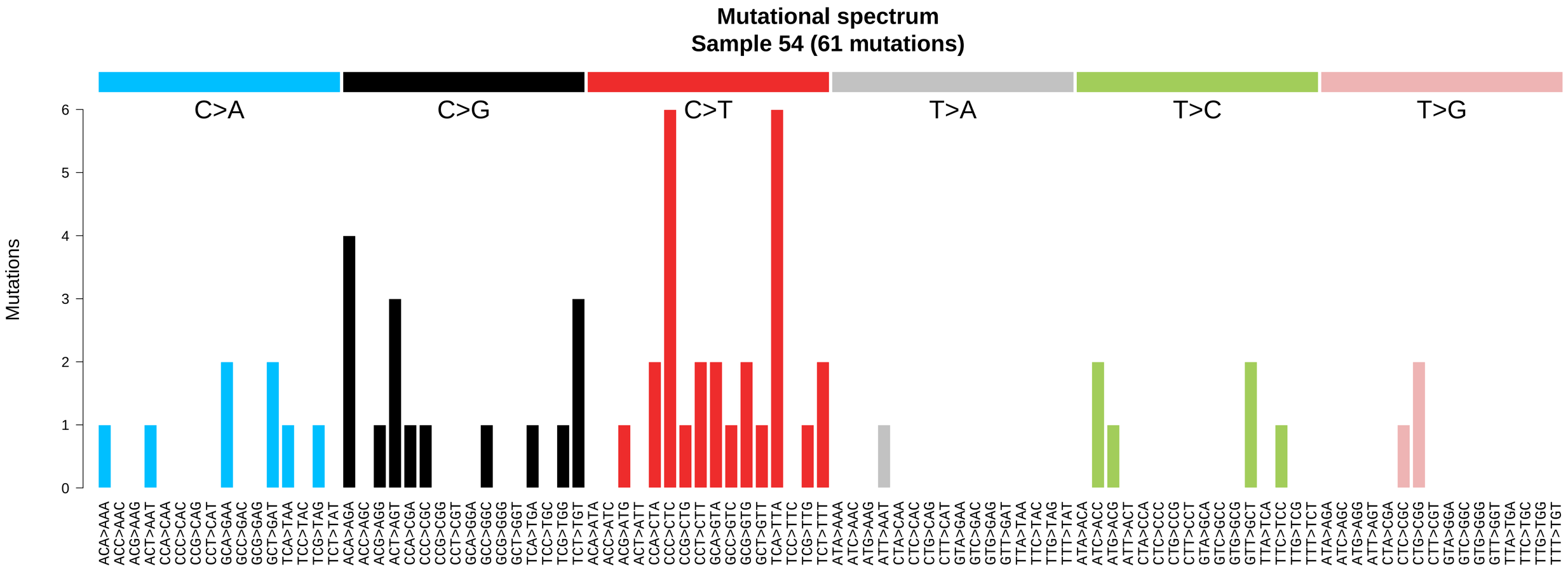

Mutational spectrum
Sample 49 (34 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.655
Signature A (0.034)
Signature B (0.021)
Signature C (0.051)
Signature D (0.03)
Signature E (0.043)
Signature F (0.031)
Signature G (0.032)
Signature H (0.039)
Signature I (0.036)
Signature J (0.062)
Signature K (0.032)
Signature L (0.039)
Signature M (0.019)
Signature N (0.026)
Signature O (0.023)
Signature P (0.039)
Signature Q (0.035)
Signature R (0.034)
Signature S (0.041)
Signature T (0.034)
Signature U (0.03)
Signature V (0.022)
Signature W (0.037)
Signature X (0.026)
Signature Y (0.035)
Signature Z (0.031)
Signature AA (0.021)
Signature AB (0.033)
Signature AC (0.026)
Signature AD (0.038)

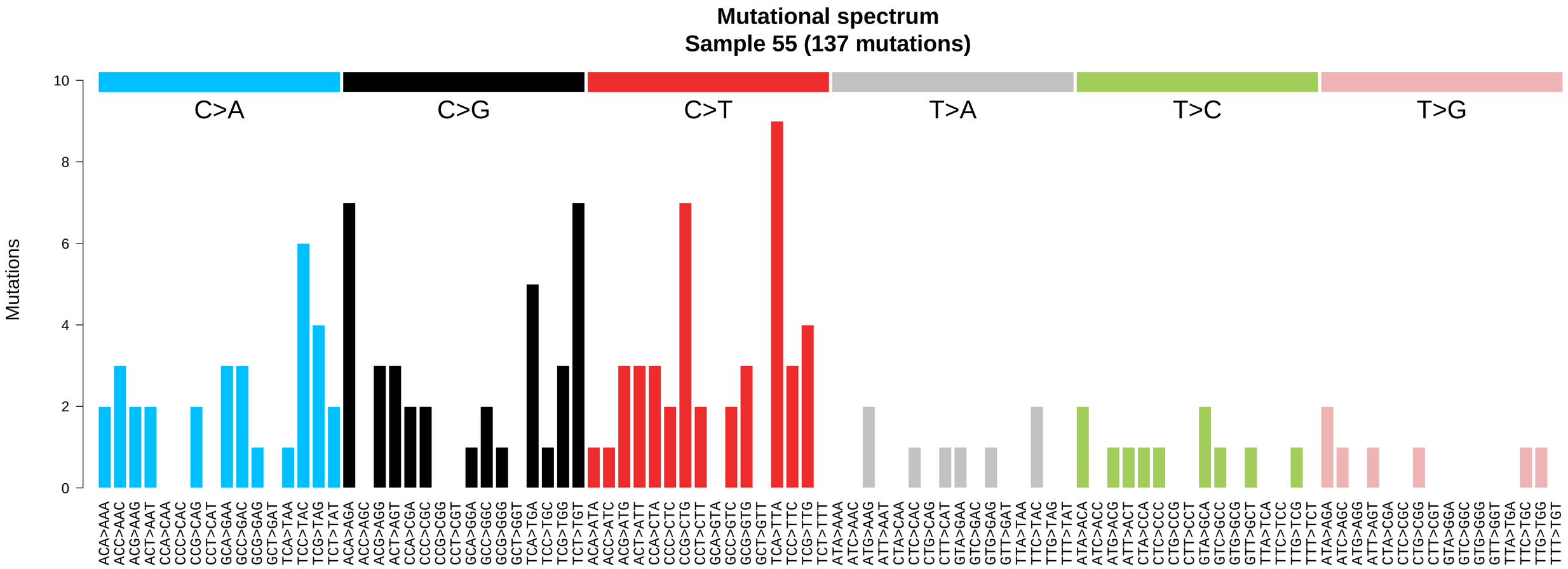

Mutational spectrum
Sample 50 (283 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
25
30
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.861
Signature A (0.028)
Signature B (0.12)
Signature C (0.25)
Signature D (0.027)
Signature E (0.032)
Signature F (0.016)
Signature G (0.016)
Signature H (0.024)
Signature I (0.017)
Signature J (0.011)
Signature K (0.012)
Signature L (0.011)
Signature M (0.142)
Signature N (0.016)
Signature O (0.008)
Signature P (0.017)
Signature Q (0.007)
Signature R (0.03)
Signature S (0.019)
Signature T (0.016)
Signature U (0.017)
Signature V (0.007)
Signature W (0.012)
Signature X (0.019)
Signature Y (0.016)
Signature Z (0.011)
Signature AA (0.011)
Signature AB (0.006)
Signature AC (0.041)
Signature AD (0.041)

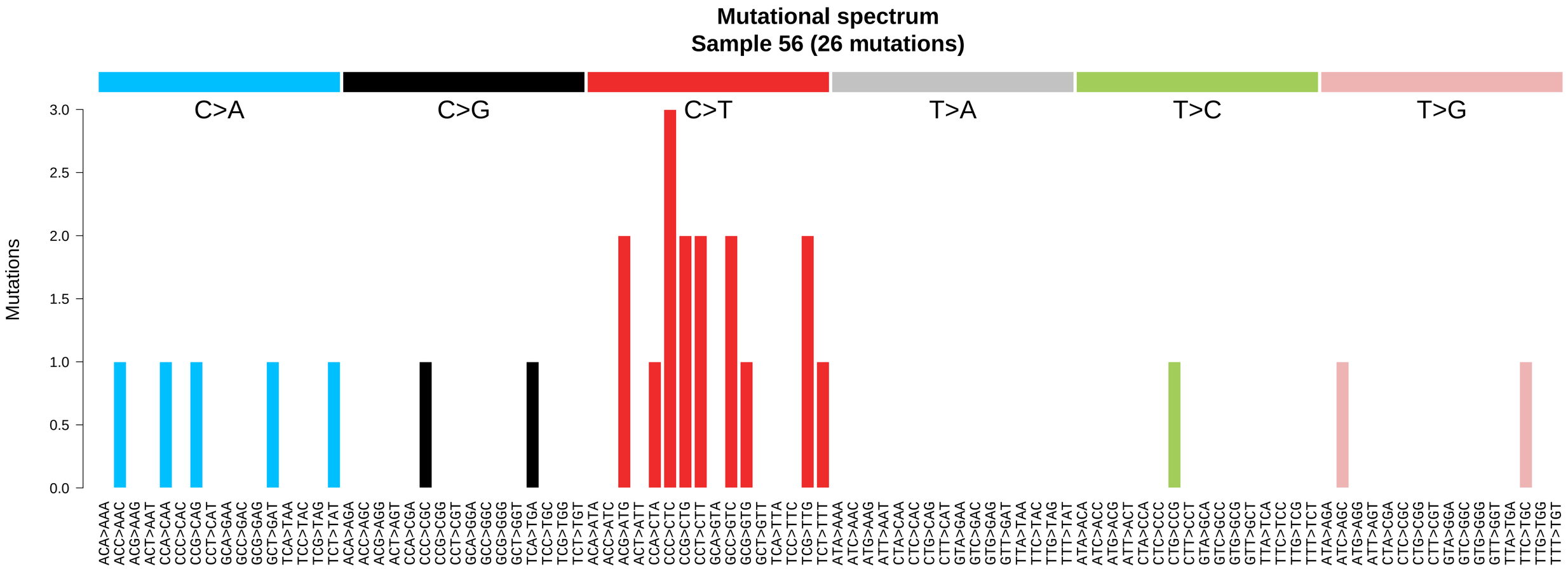

Mutational spectrum
Sample 51 (24 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.587
Signature A (0.047)
Signature B (0.021)
Signature C (0.049)
Signature D (0.033)
Signature E (0.039)
Signature F (0.039)
Signature G (0.033)
Signature H (0.039)
Signature I (0.029)
Signature J (0.023)
Signature K (0.035)
Signature L (0.029)
Signature M (0.02)
Signature N (0.039)
Signature O (0.029)
Signature P (0.028)
Signature Q (0.031)
Signature R (0.028)
Signature S (0.039)
Signature T (0.041)
Signature U (0.035)
Signature V (0.033)
Signature W (0.038)
Signature X (0.032)
Signature Y (0.035)
Signature Z (0.034)
Signature AA (0.025)
Signature AB (0.024)
Signature AC (0.034)
Signature AD (0.042)

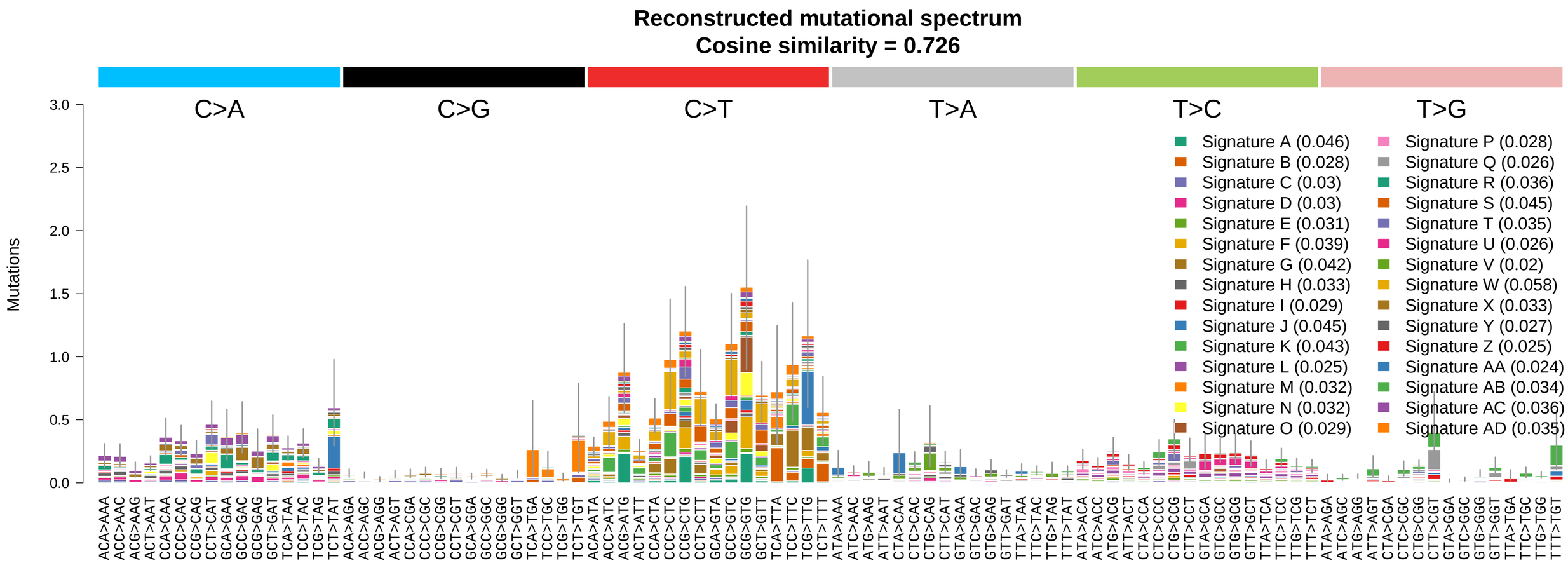

Mutational spectrum
Sample 52 (105 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.761
Signature A (0.018)
Signature B (0.032)
Signature C (0.186)
Signature D (0.04)
Signature E (0.046)
Signature F (0.013)
Signature G (0.016)
Signature H (0.041)
Signature I (0.027)
Signature J (0.014)
Signature K (0.018)
Signature L (0.031)
Signature M (0.125)
Signature N (0.016)
Signature O (0.012)
Signature P (0.04)
Signature Q (0.023)
Signature R (0.031)
Signature S (0.023)
Signature T (0.025)
Signature U (0.018)
Signature V (0.015)
Signature W (0.016)
Signature X (0.031)
Signature Y (0.028)
Signature Z (0.026)
Signature AA (0.013)
Signature AB (0.019)
Signature AC (0.027)
Signature AD (0.032)

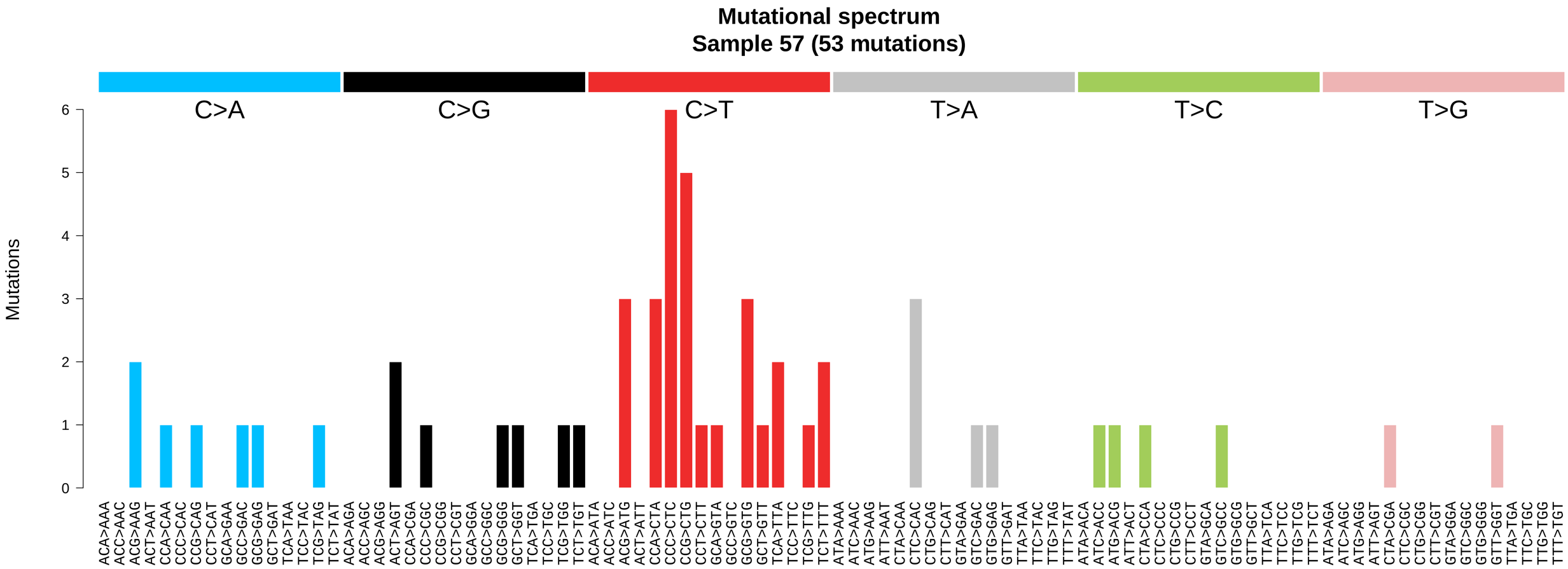

Mutational spectrum
Sample 53 (155 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.8
Signature A (0.037)
Signature B (0.025)
Signature C (0.144)
Signature D (0.071)
Signature E (0.052)
Signature F (0.027)
Signature G (0.018)
Signature H (0.045)
Signature I (0.026)
Signature J (0.014)
Signature K (0.018)
Signature L (0.018)
Signature M (0.019)
Signature N (0.025)
Signature O (0.016)
Signature P (0.035)
Signature Q (0.015)
Signature R (0.053)
Signature S (0.027)
Signature T (0.031)
Signature U (0.037)
Signature V (0.018)
Signature W (0.021)
Signature X (0.044)
Signature Y (0.044)
Signature Z (0.018)
Signature AA (0.012)
Signature AB (0.013)
Signature AC (0.04)
Signature AD (0.037)

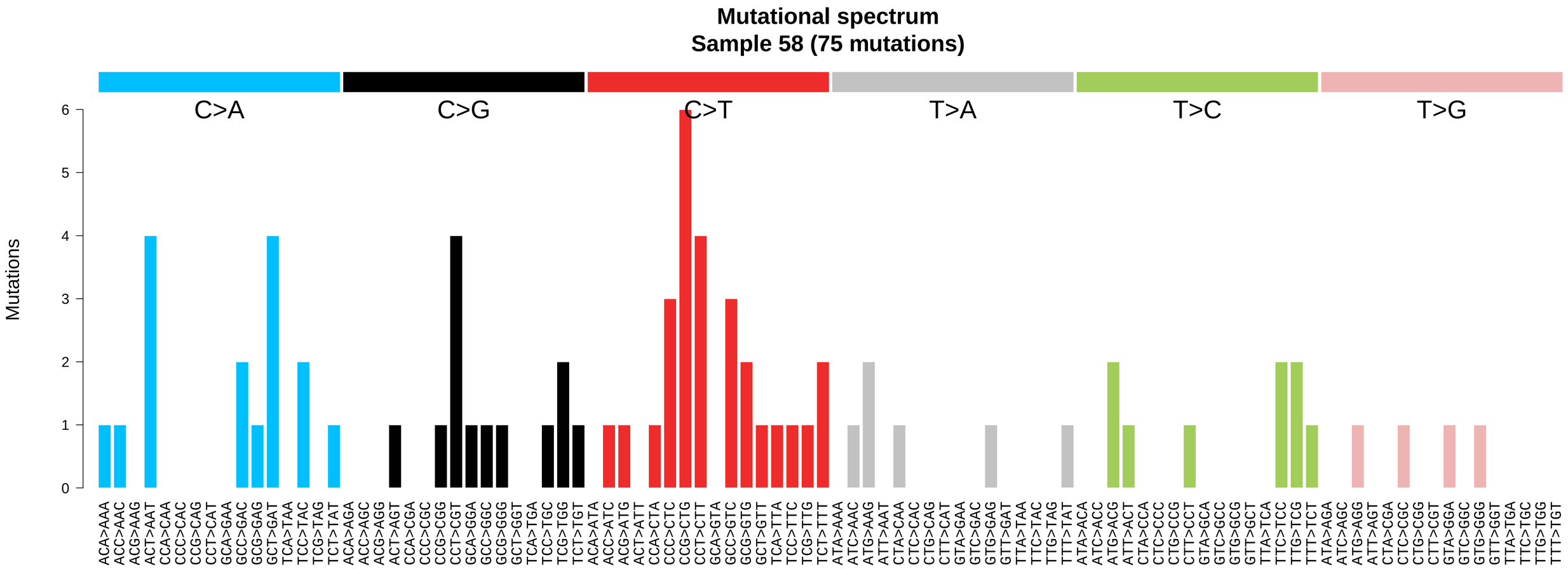

Mutational spectrum
Sample 54 (61 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.676
Signature A (0.023)
Signature B (0.075)
Signature C (0.12)
Signature D (0.028)
Signature E (0.046)
Signature F (0.021)
Signature G (0.032)
Signature H (0.032)
Signature I (0.025)
Signature J (0.017)
Signature K (0.033)
Signature L (0.027)
Signature M (0.067)
Signature N (0.021)
Signature O (0.021)
Signature P (0.029)
Signature Q (0.02)
Signature R (0.035)
Signature S (0.039)
Signature T (0.022)
Signature U (0.022)
Signature V (0.013)
Signature W (0.048)
Signature X (0.028)
Signature Y (0.026)
Signature Z (0.026)
Signature AA (0.016)
Signature AB (0.018)
Signature AC (0.029)
Signature AD (0.043)

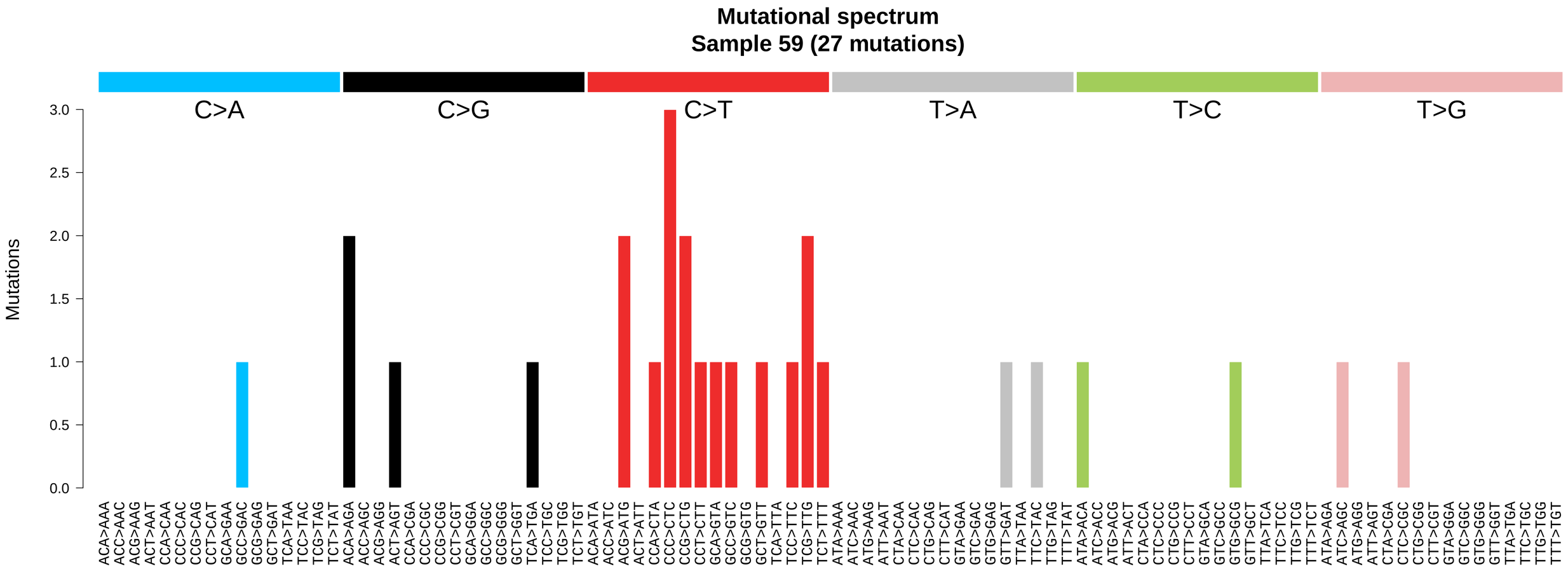

Mutational spectrum
Sample 55 (137 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.786
Signature A (0.029)
Signature B (0.041)
Signature C (0.161)
Signature D (0.064)
Signature E (0.051)
Signature F (0.018)
Signature G (0.023)
Signature H (0.032)
Signature I (0.025)
Signature J (0.018)
Signature K (0.016)
Signature L (0.019)
Signature M (0.123)
Signature N (0.013)
Signature O (0.012)
Signature P (0.03)
Signature Q (0.011)
Signature R (0.031)
Signature S (0.02)
Signature T (0.013)
Signature U (0.019)
Signature V (0.015)
Signature W (0.015)
Signature X (0.061)
Signature Y (0.022)
Signature Z (0.019)
Signature AA (0.012)
Signature AB (0.015)
Signature AC (0.041)
Signature AD (0.032)

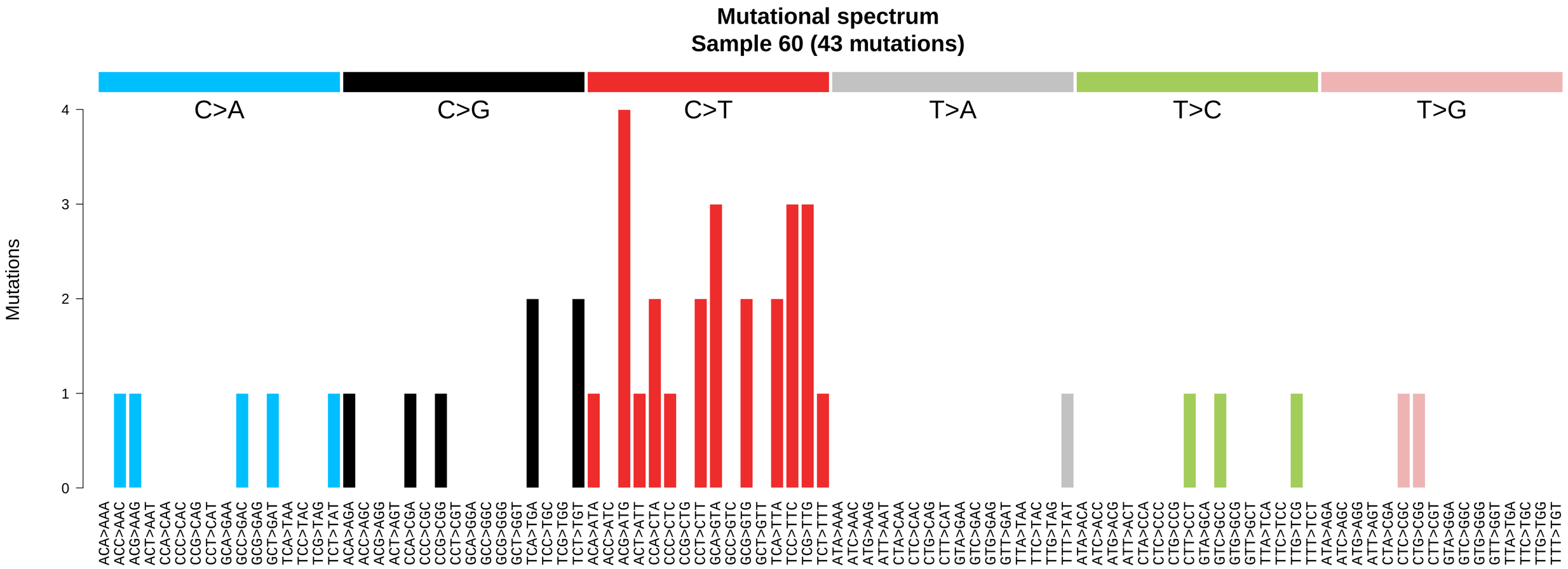

Mutational spectrum
Sample 56 (26 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

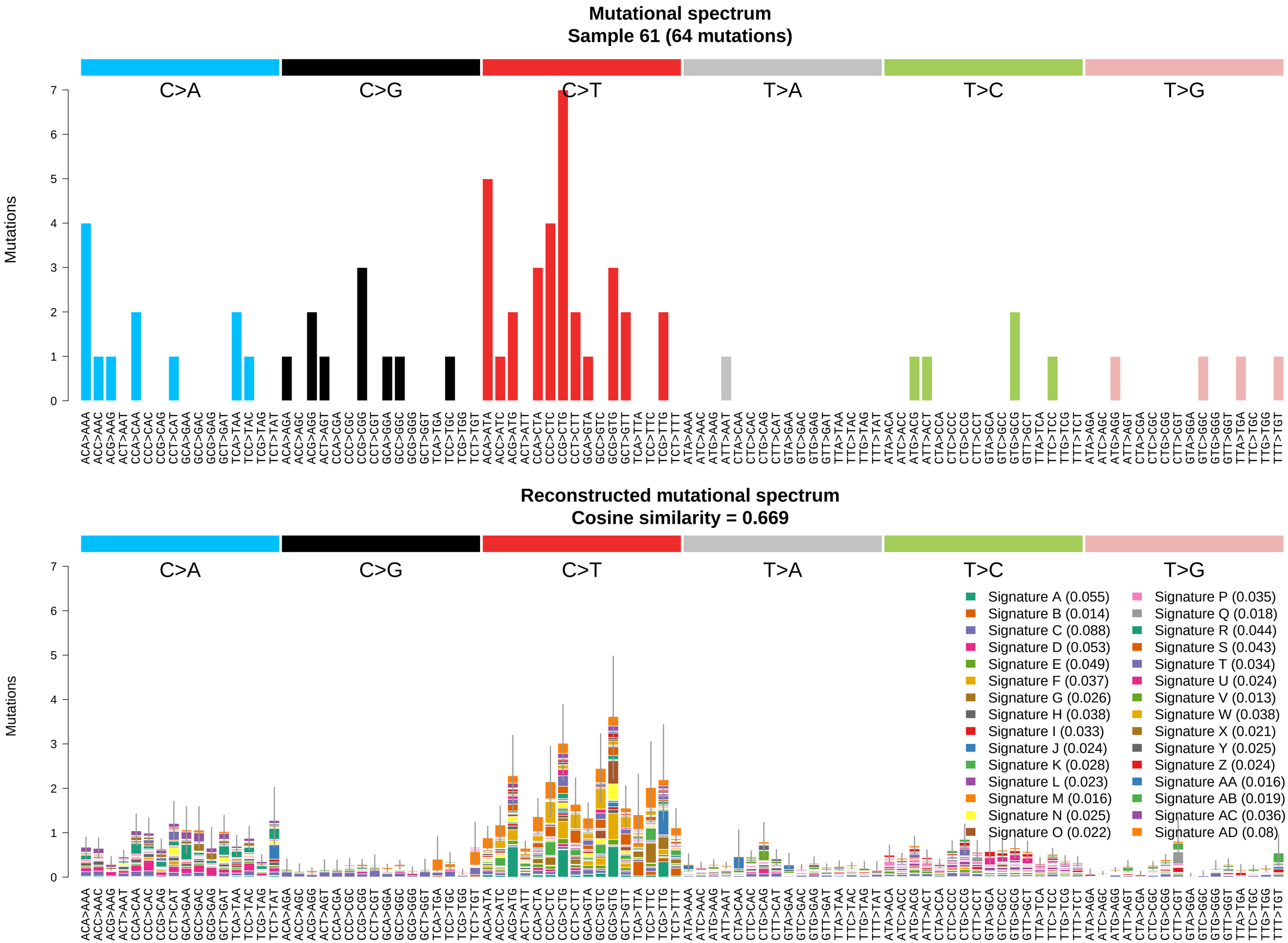

Reconstructed mutational spectrum
Cosine similarity = 0.726
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Signature A (0.046)
Signature B (0.028)
Signature C (0.03)
Signature D (0.03)
Signature E (0.031)
Signature F (0.039)
Signature G (0.042)
Signature H (0.033)
Signature I (0.029)
Signature J (0.045)
Signature K (0.043)
Signature L (0.025)
Signature M (0.032)
Signature N (0.032)
Signature O (0.029)
Signature P (0.028)
Signature Q (0.026)
Signature R (0.036)
Signature S (0.045)
Signature T (0.035)
Signature U (0.026)
Signature V (0.02)
Signature W (0.058)
Signature X (0.033)
Signature Y (0.027)
Signature Z (0.025)
Signature AA (0.024)
Signature AB (0.034)
Signature AC (0.036)
Signature AD (0.035)
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

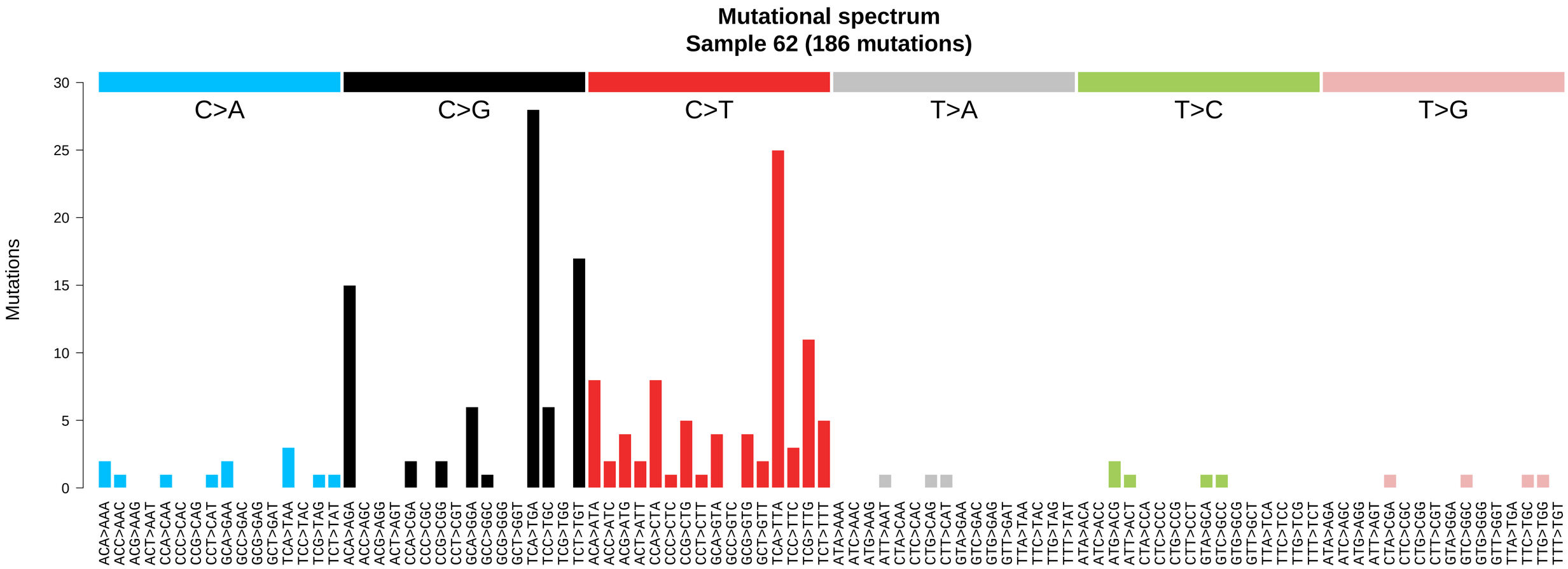

Mutational spectrum
Sample 57 (53 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.683
Signature A (0.048)
Signature B (0.037)
Signature C (0.045)
Signature D (0.052)
Signature E (0.041)
Signature F (0.038)
Signature G (0.037)
Signature H (0.029)
Signature I (0.031)
Signature J (0.017)
Signature K (0.037)
Signature L (0.026)
Signature M (0.027)
Signature N (0.024)
Signature O (0.027)
Signature P (0.03)
Signature Q (0.023)
Signature R (0.024)
Signature S (0.044)
Signature T (0.028)
Signature U (0.027)
Signature V (0.029)
Signature W (0.045)
Signature X (0.05)
Signature Y (0.03)
Signature Z (0.027)
Signature AA (0.019)
Signature AB (0.023)
Signature AC (0.035)
Signature AD (0.05)

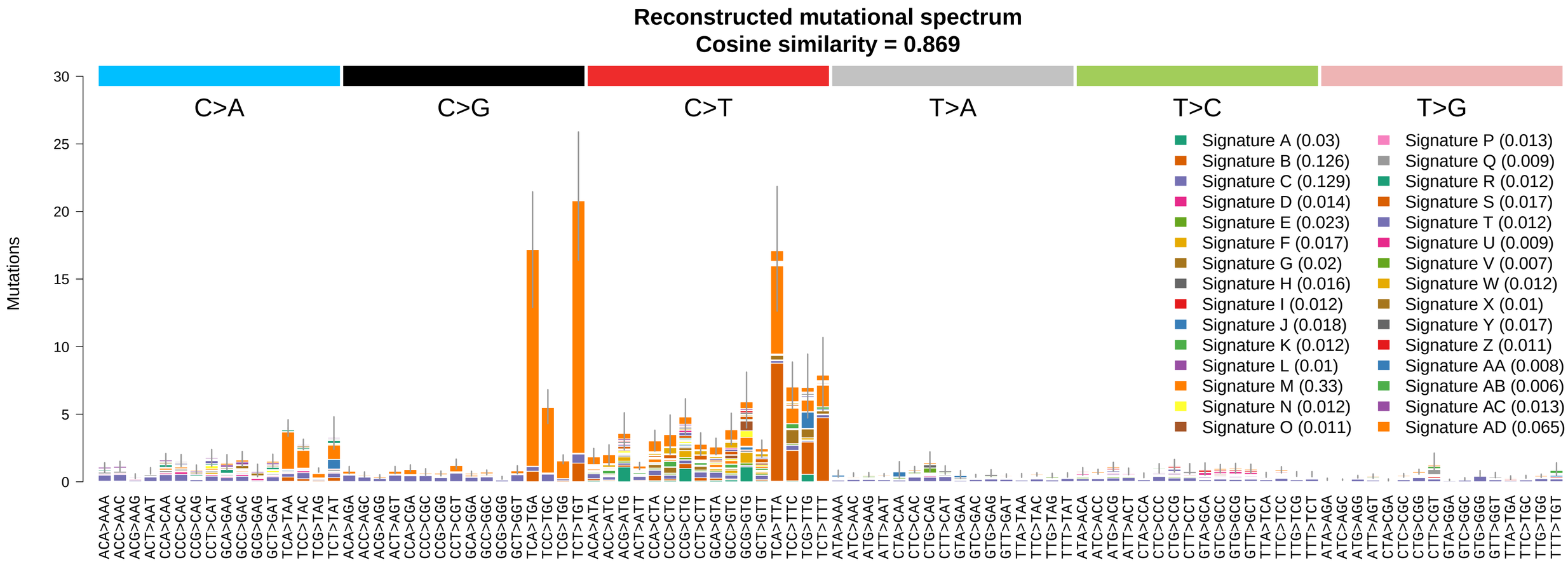

Mutational spectrum
Sample 58 (75 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.687
Signature A (0.028)
Signature B (0.021)
Signature C (0.142)
Signature D (0.053)
Signature E (0.048)
Signature F (0.024)
Signature G (0.027)
Signature H (0.041)
Signature I (0.027)
Signature J (0.018)
Signature K (0.031)
Signature L (0.026)
Signature M (0.026)
Signature N (0.031)
Signature O (0.022)
Signature P (0.037)
Signature Q (0.017)
Signature R (0.033)
Signature S (0.037)
Signature T (0.025)
Signature U (0.023)
Signature V (0.023)
Signature W (0.038)
Signature X (0.045)
Signature Y (0.03)
Signature Z (0.022)
Signature AA (0.022)
Signature AB (0.016)
Signature AC (0.033)
Signature AD (0.034)

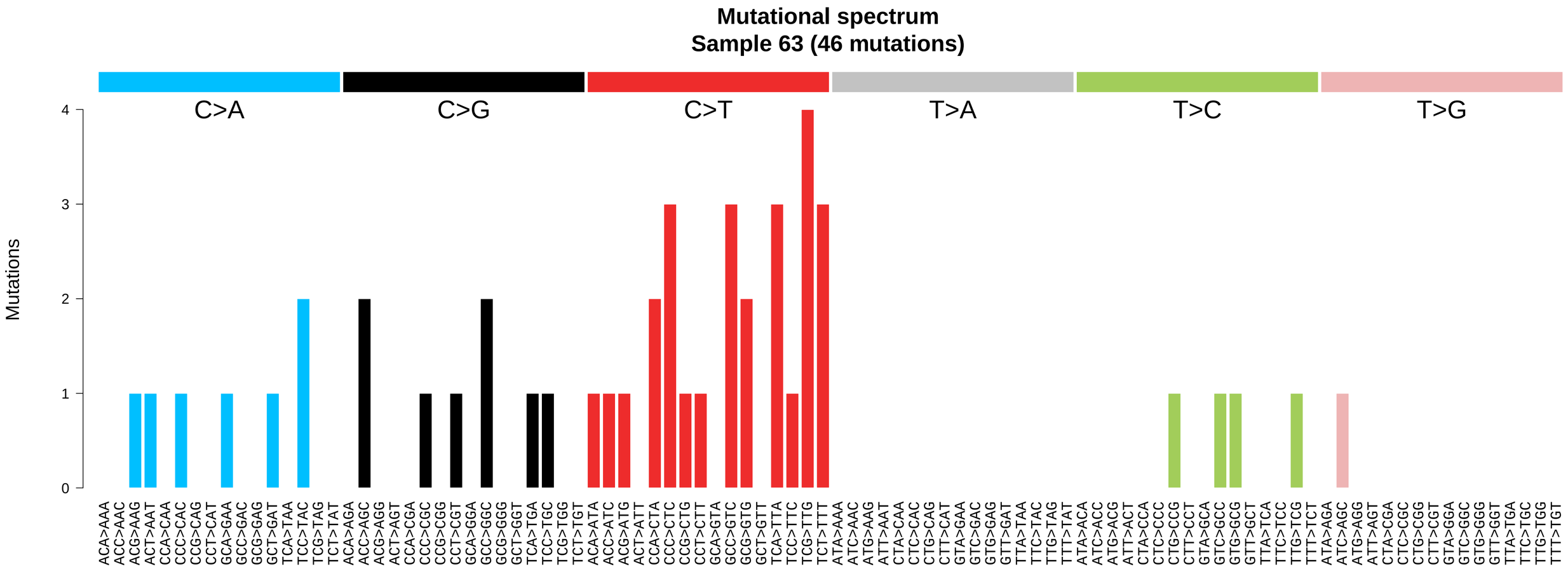

Mutational spectrum
Sample 59 (27 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.652
Signature A (0.041)
Signature B (0.03)
Signature C (0.044)
Signature D (0.027)
Signature E (0.04)
Signature F (0.033)
Signature G (0.048)
Signature H (0.031)
Signature I (0.03)
Signature J (0.03)
Signature K (0.043)
Signature L (0.033)
Signature M (0.033)
Signature N (0.028)
Signature O (0.026)
Signature P (0.036)
Signature Q (0.028)
Signature R (0.023)
Signature S (0.048)
Signature T (0.032)
Signature U (0.035)
Signature V (0.024)
Signature W (0.048)
Signature X (0.027)
Signature Y (0.031)
Signature Z (0.029)
Signature AA (0.022)
Signature AB (0.03)
Signature AC (0.028)
Signature AD (0.041)

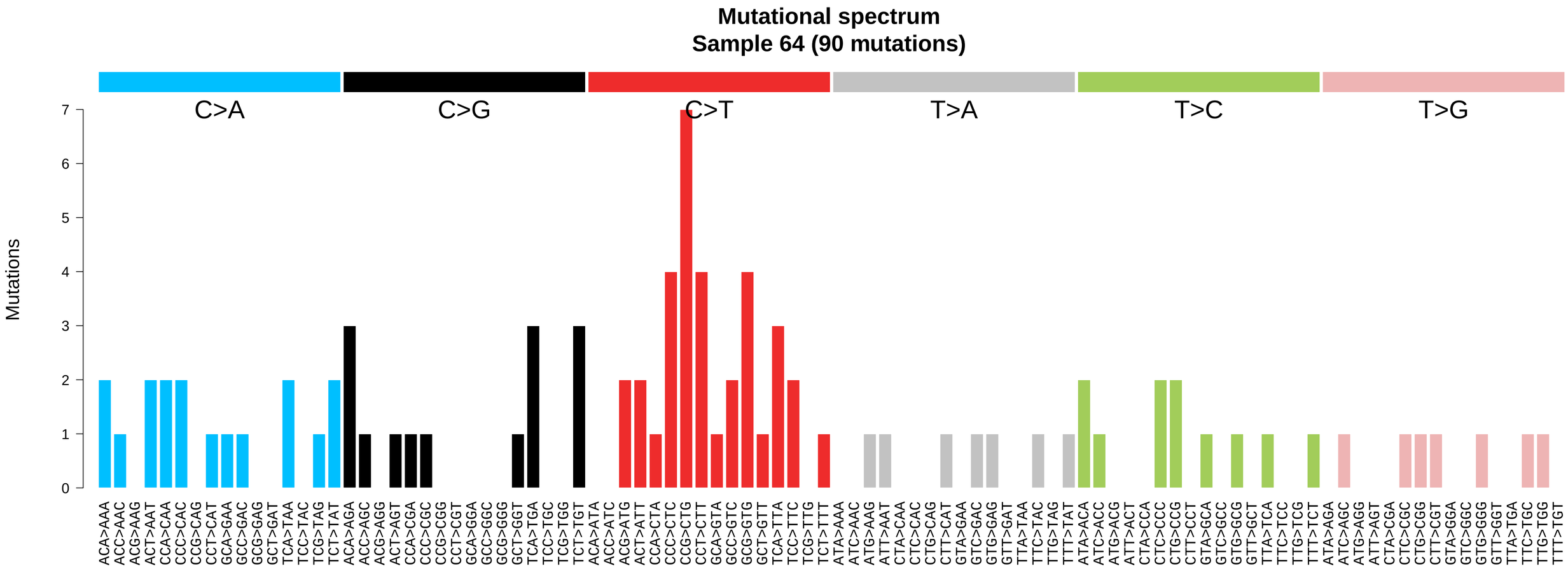

Mutational spectrum
Sample 60 (43 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.732
Signature A (0.049)
Signature B (0.051)
Signature C (0.04)
Signature D (0.031)
Signature E (0.033)
Signature F (0.032)
Signature G (0.055)
Signature H (0.031)
Signature I (0.027)
Signature J (0.035)
Signature K (0.036)
Signature L (0.026)
Signature M (0.068)
Signature N (0.034)
Signature O (0.025)
Signature P (0.03)
Signature Q (0.029)
Signature R (0.023)
Signature S (0.039)
Signature T (0.029)
Signature U (0.022)
Signature V (0.017)
Signature W (0.031)
Signature X (0.03)
Signature Y (0.025)
Signature Z (0.024)
Signature AA (0.02)
Signature AB (0.023)
Signature AC (0.034)
Signature AD (0.052)

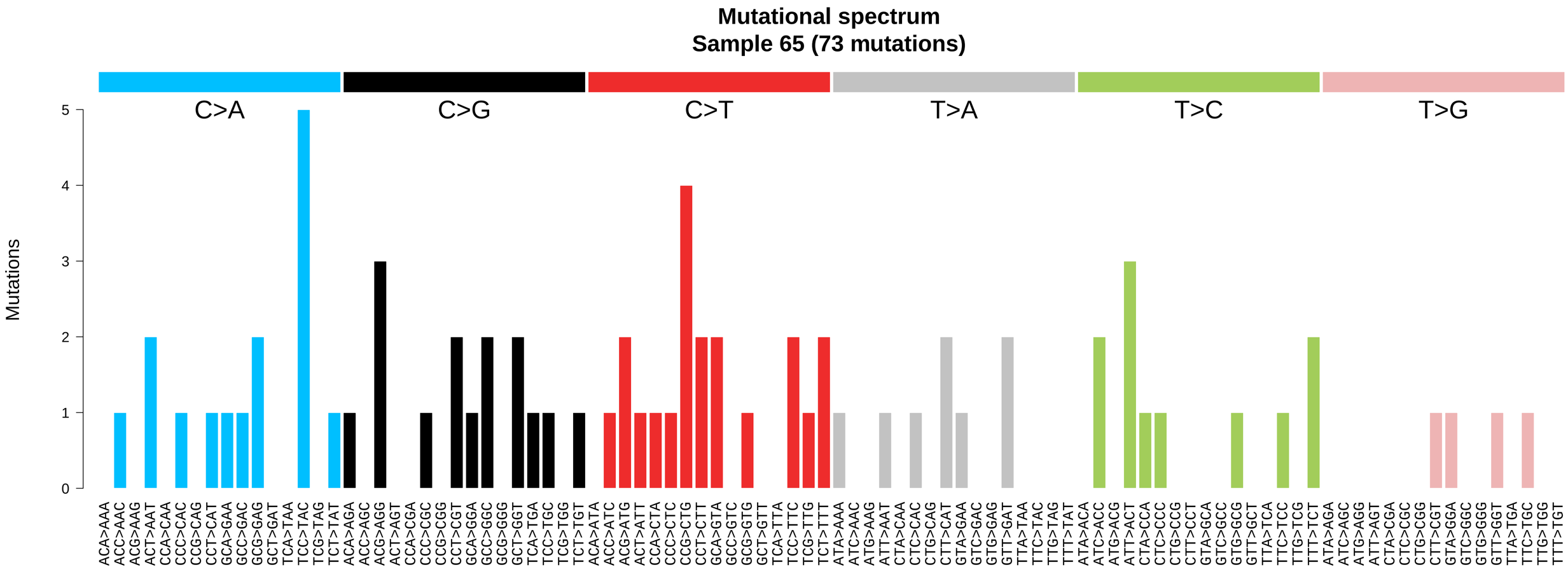

Mutational spectrum
Sample 61 (64 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.669
Signature A (0.055)
Signature B (0.014)
Signature C (0.088)
Signature D (0.053)
Signature E (0.049)
Signature F (0.037)
Signature G (0.026)
Signature H (0.038)
Signature I (0.033)
Signature J (0.024)
Signature K (0.028)
Signature L (0.023)
Signature M (0.016)
Signature N (0.025)
Signature O (0.022)
Signature P (0.035)
Signature Q (0.018)
Signature R (0.044)
Signature S (0.043)
Signature T (0.034)
Signature U (0.024)
Signature V (0.013)
Signature W (0.038)
Signature X (0.021)
Signature Y (0.025)
Signature Z (0.024)
Signature AA (0.016)
Signature AB (0.019)
Signature AC (0.036)
Signature AD (0.08)

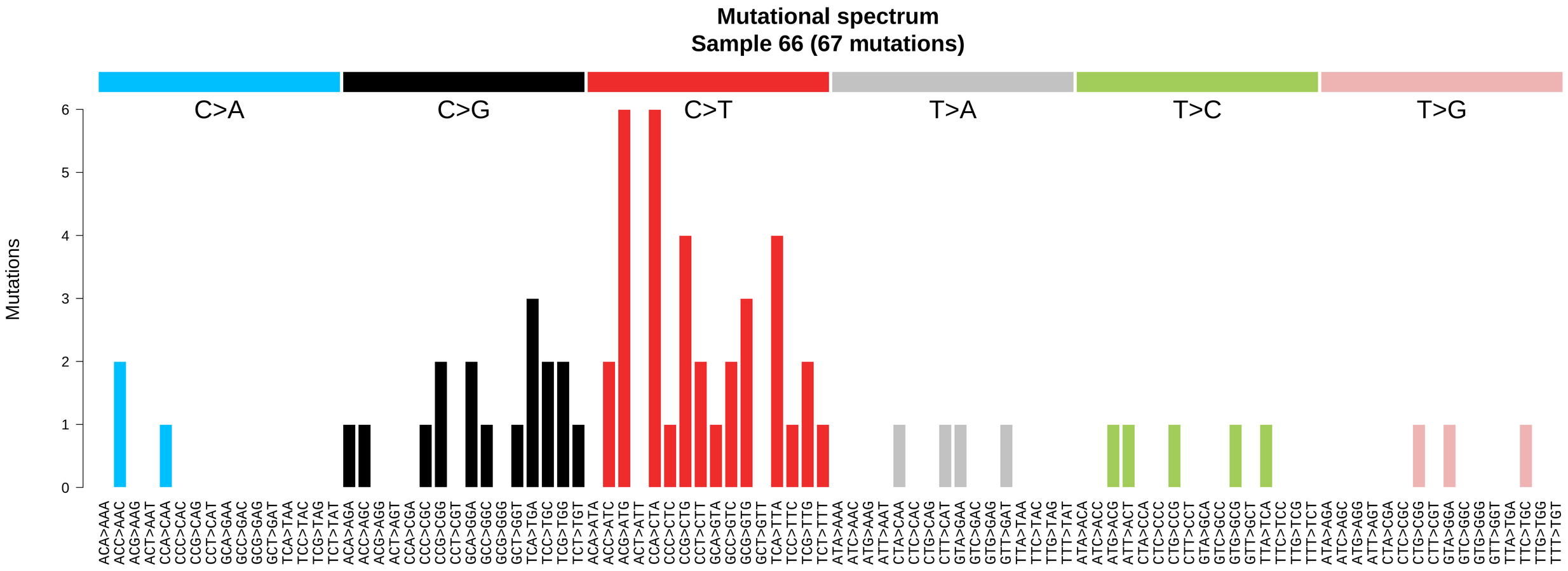

Mutational spectrum
Sample 62 (186 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
25
30
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

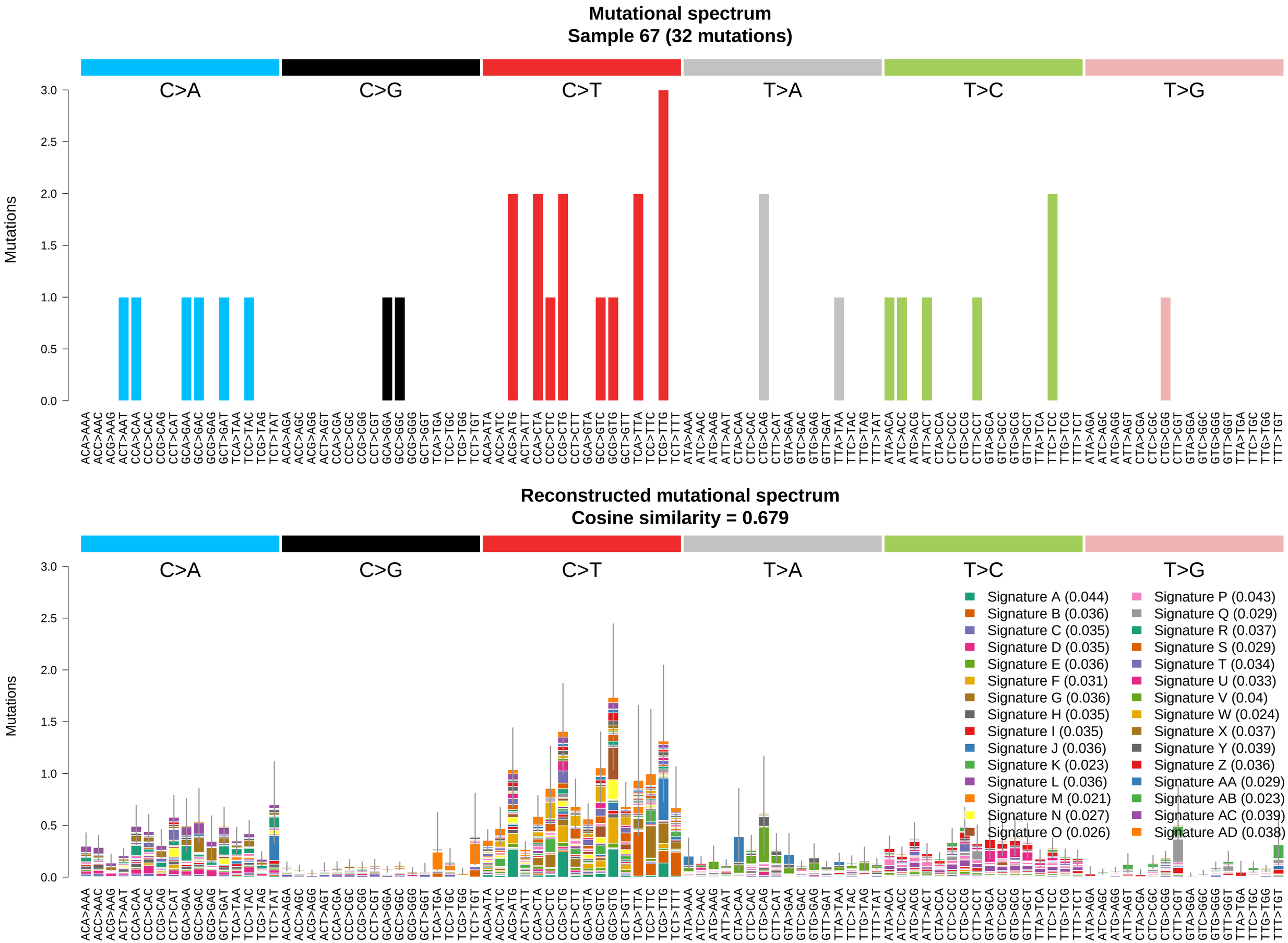

Reconstructed mutational spectrum
Cosine similarity = 0.869
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
25
30
Signature A (0.03)
Signature B (0.126)
Signature C (0.129)
Signature D (0.014)
Signature E (0.023)
Signature F (0.017)
Signature G (0.02)
Signature H (0.016)
Signature I (0.012)
Signature J (0.018)
Signature K (0.012)
Signature L (0.01)
Signature M (0.33)
Signature N (0.012)
Signature O (0.011)
Signature P (0.013)
Signature Q (0.009)
Signature R (0.012)
Signature S (0.017)
Signature T (0.012)
Signature U (0.009)
Signature V (0.007)
Signature W (0.012)
Signature X (0.01)
Signature Y (0.017)
Signature Z (0.011)
Signature AA (0.008)
Signature AB (0.006)
Signature AC (0.013)
Signature AD (0.065)

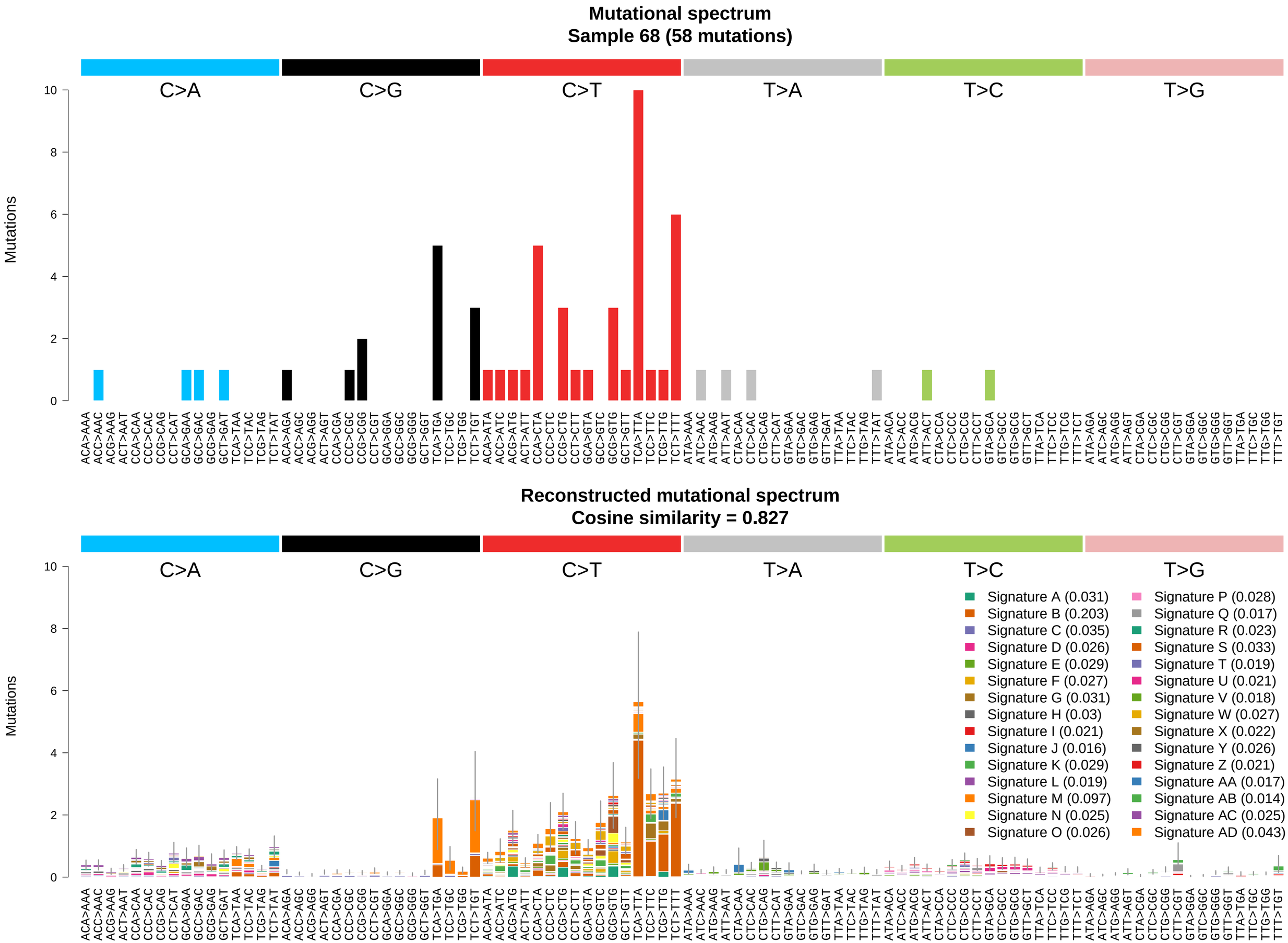

Mutational spectrum
Sample 63 (46 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.767
Signature A (0.031)
Signature B (0.07)
Signature C (0.05)
Signature D (0.045)
Signature E (0.037)
Signature F (0.028)
Signature G (0.051)
Signature H (0.028)
Signature I (0.023)
Signature J (0.037)
Signature K (0.044)
Signature L (0.028)
Signature M (0.037)
Signature N (0.028)
Signature O (0.03)
Signature P (0.032)
Signature Q (0.02)
Signature R (0.027)
Signature S (0.033)
Signature T (0.028)
Signature U (0.029)
Signature V (0.015)
Signature W (0.042)
Signature X (0.044)
Signature Y (0.023)
Signature Z (0.025)
Signature AA (0.02)
Signature AB (0.021)
Signature AC (0.029)
Signature AD (0.044)

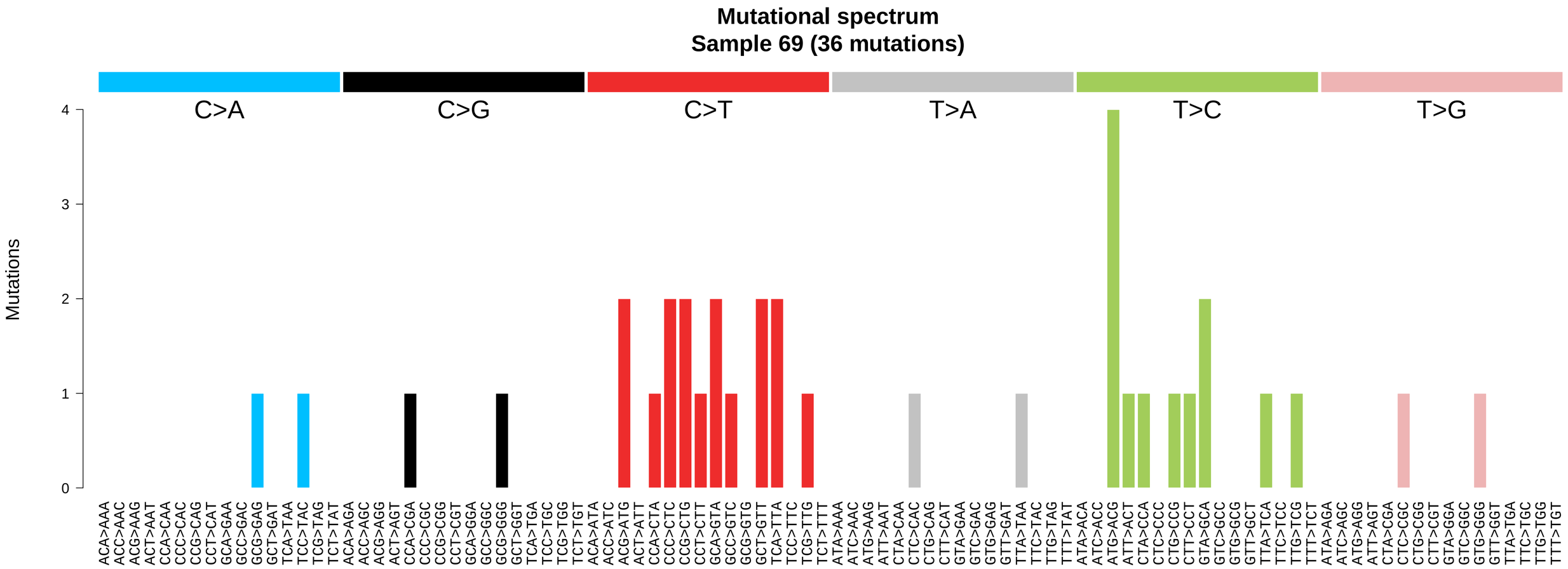

Mutational spectrum
Sample 64 (90 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
7
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.816
Signature A (0.03)
Signature B (0.025)
Signature C (0.099)
Signature D (0.029)
Signature E (0.049)
Signature F (0.029)
Signature G (0.023)
Signature H (0.072)
Signature I (0.033)
Signature J (0.016)
Signature K (0.029)
Signature L (0.036)
Signature M (0.063)
Signature N (0.024)
Signature O (0.022)
Signature P (0.041)
Signature Q (0.024)
Signature R (0.032)
Signature S (0.047)
Signature T (0.029)
Signature U (0.023)
Signature V (0.016)
Signature W (0.033)
Signature X (0.023)
Signature Y (0.029)
Signature Z (0.028)
Signature AA (0.013)
Signature AB (0.03)
Signature AC (0.03)
Signature AD (0.022)

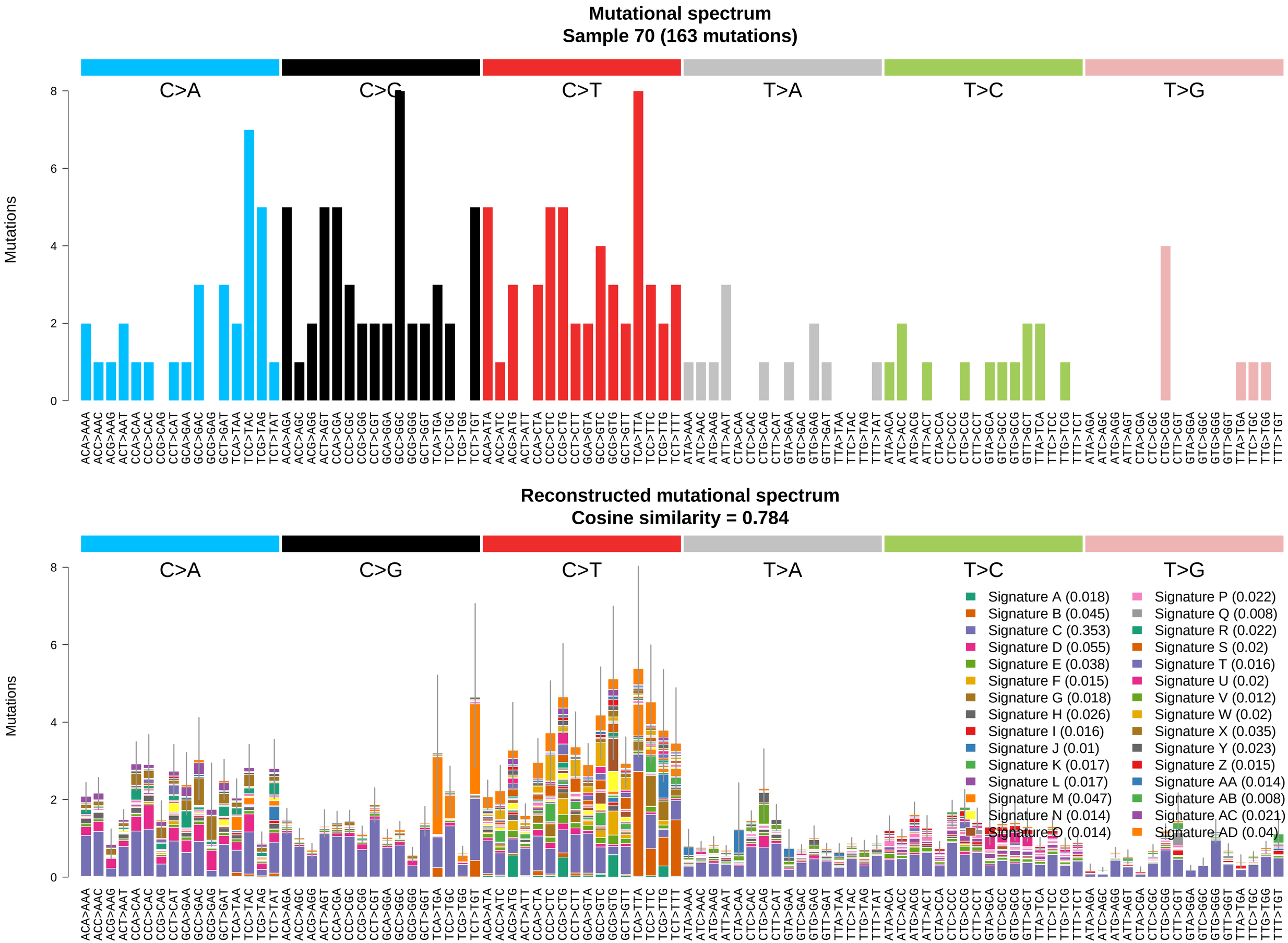

Mutational spectrum
Sample 65 (73 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.646
Signature A (0.025)
Signature B (0.019)
Signature C (0.206)
Signature D (0.049)
Signature E (0.044)
Signature F (0.021)
Signature G (0.022)
Signature H (0.051)
Signature I (0.034)
Signature J (0.019)
Signature K (0.024)
Signature L (0.028)
Signature M (0.025)
Signature N (0.021)
Signature O (0.016)
Signature P (0.036)
Signature Q (0.027)
Signature R (0.025)
Signature S (0.024)
Signature T (0.024)
Signature U (0.023)
Signature V (0.019)
Signature W (0.019)
Signature X (0.038)
Signature Y (0.036)
Signature Z (0.025)
Signature AA (0.024)
Signature AB (0.022)
Signature AC (0.026)
Signature AD (0.029)

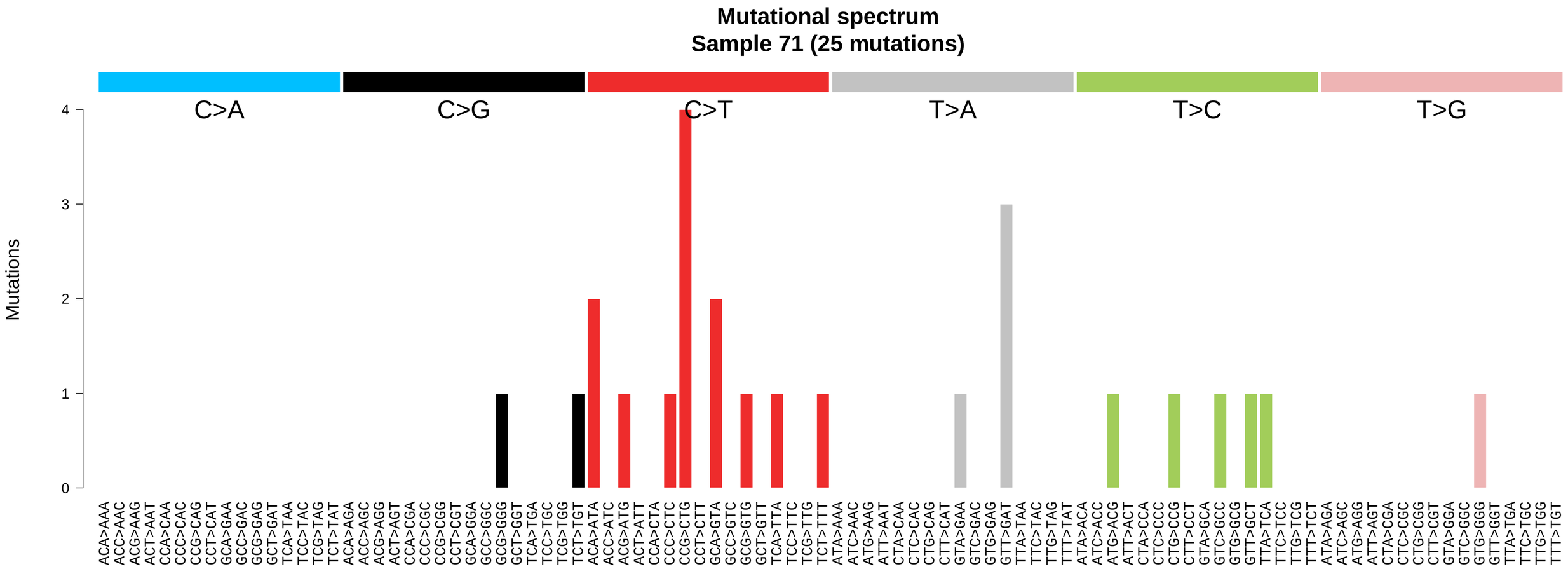

Mutational spectrum
Sample 66 (67 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.737
Signature A (0.067)
Signature B (0.038)
Signature C (0.093)
Signature D (0.026)
Signature E (0.043)
Signature F (0.032)
Signature G (0.035)
Signature H (0.026)
Signature I (0.024)
Signature J (0.017)
Signature K (0.026)
Signature L (0.021)
Signature M (0.083)
Signature N (0.021)
Signature O (0.023)
Signature P (0.03)
Signature Q (0.017)
Signature R (0.019)
Signature S (0.036)
Signature T (0.025)
Signature U (0.021)
Signature V (0.017)
Signature W (0.03)
Signature X (0.018)
Signature Y (0.044)
Signature Z (0.023)
Signature AA (0.034)
Signature AB (0.016)
Signature AC (0.021)
Signature AD (0.073)

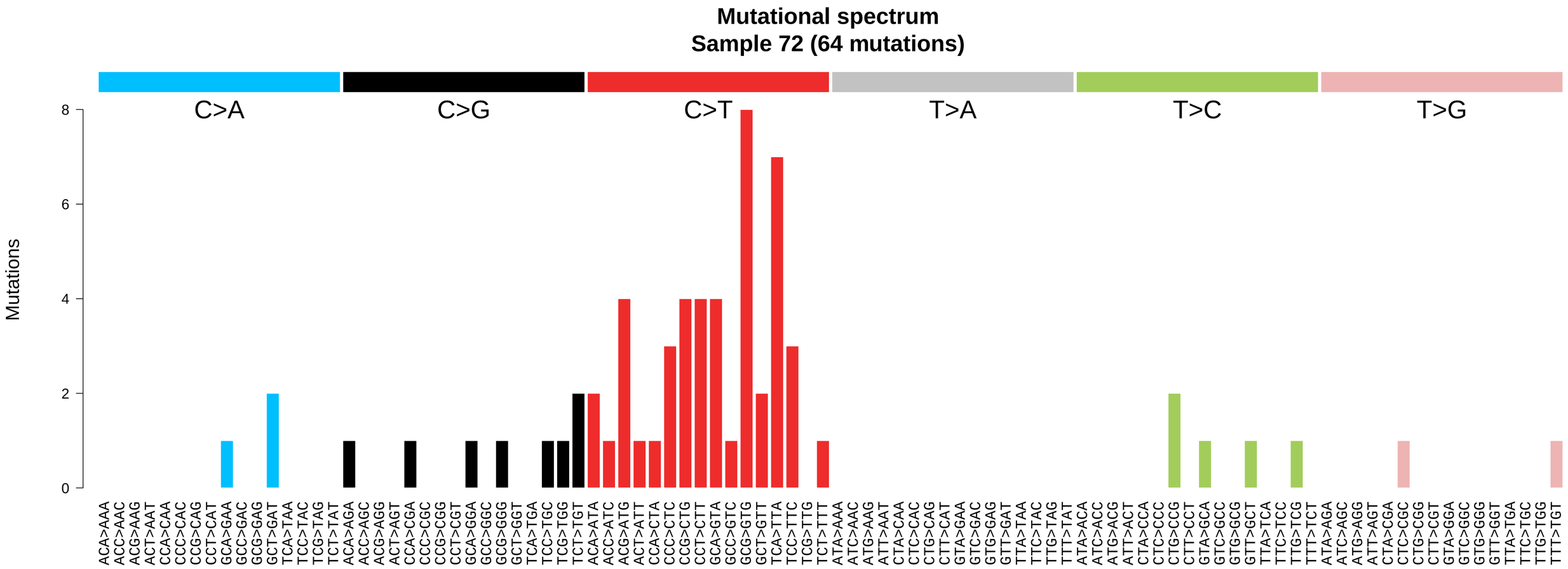

Mutational spectrum
Sample 67 (32 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.679
Signature A (0.044)
Signature B (0.036)
Signature C (0.035)
Signature D (0.035)
Signature E (0.036)
Signature F (0.031)
Signature G (0.036)
Signature H (0.035)
Signature I (0.035)
Signature J (0.036)
Signature K (0.023)
Signature L (0.036)
Signature M (0.021)
Signature N (0.027)
Signature O (0.026)
Signature P (0.043)
Signature Q (0.029)
Signature R (0.037)
Signature S (0.029)
Signature T (0.034)
Signature U (0.033)
Signature V (0.04)
Signature W (0.024)
Signature X (0.037)
Signature Y (0.039)
Signature Z (0.036)
Signature AA (0.029)
Signature AB (0.023)
Signature AC (0.039)
Signature AD (0.038)

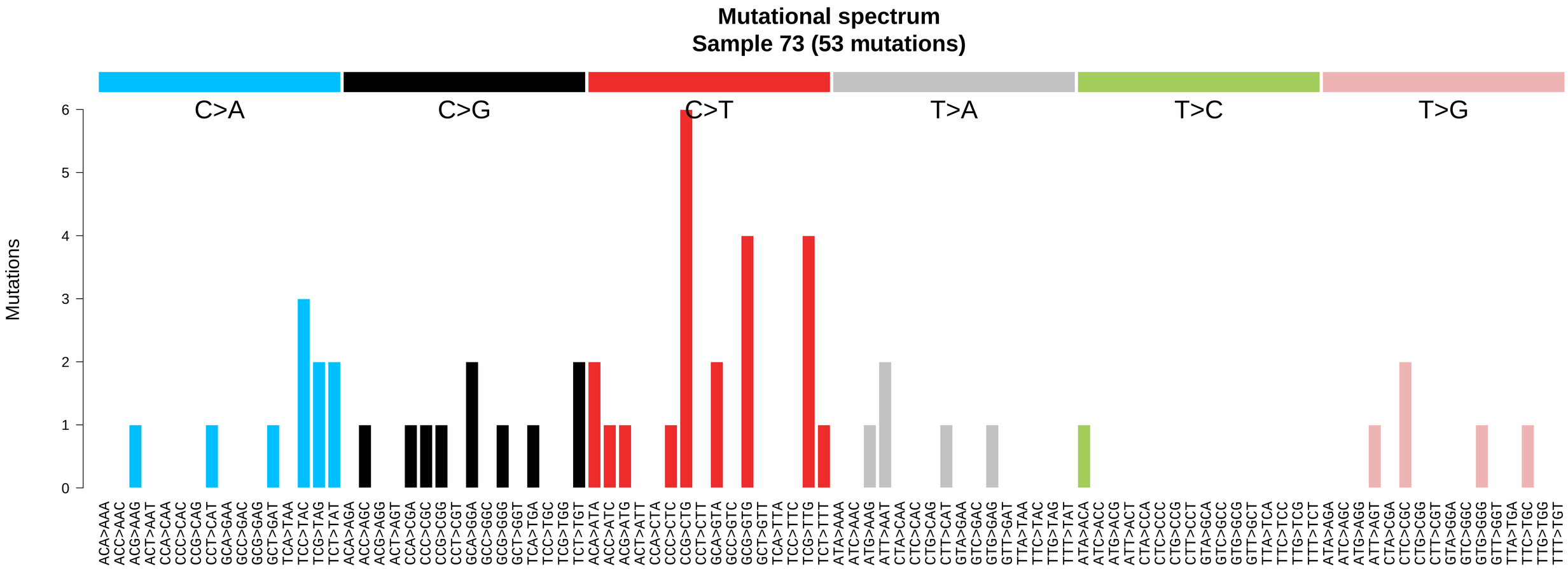

Mutational spectrum
Sample 68 (58 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.827
Signature A (0.031)
Signature B (0.203)
Signature C (0.035)
Signature D (0.026)
Signature E (0.029)
Signature F (0.027)
Signature G (0.031)
Signature H (0.03)
Signature I (0.021)
Signature J (0.016)
Signature K (0.029)
Signature L (0.019)
Signature M (0.097)
Signature N (0.025)
Signature O (0.026)
Signature P (0.028)
Signature Q (0.017)
Signature R (0.023)
Signature S (0.033)
Signature T (0.019)
Signature U (0.021)
Signature V (0.018)
Signature W (0.027)
Signature X (0.022)
Signature Y (0.026)
Signature Z (0.021)
Signature AA (0.017)
Signature AB (0.014)
Signature AC (0.025)
Signature AD (0.043)

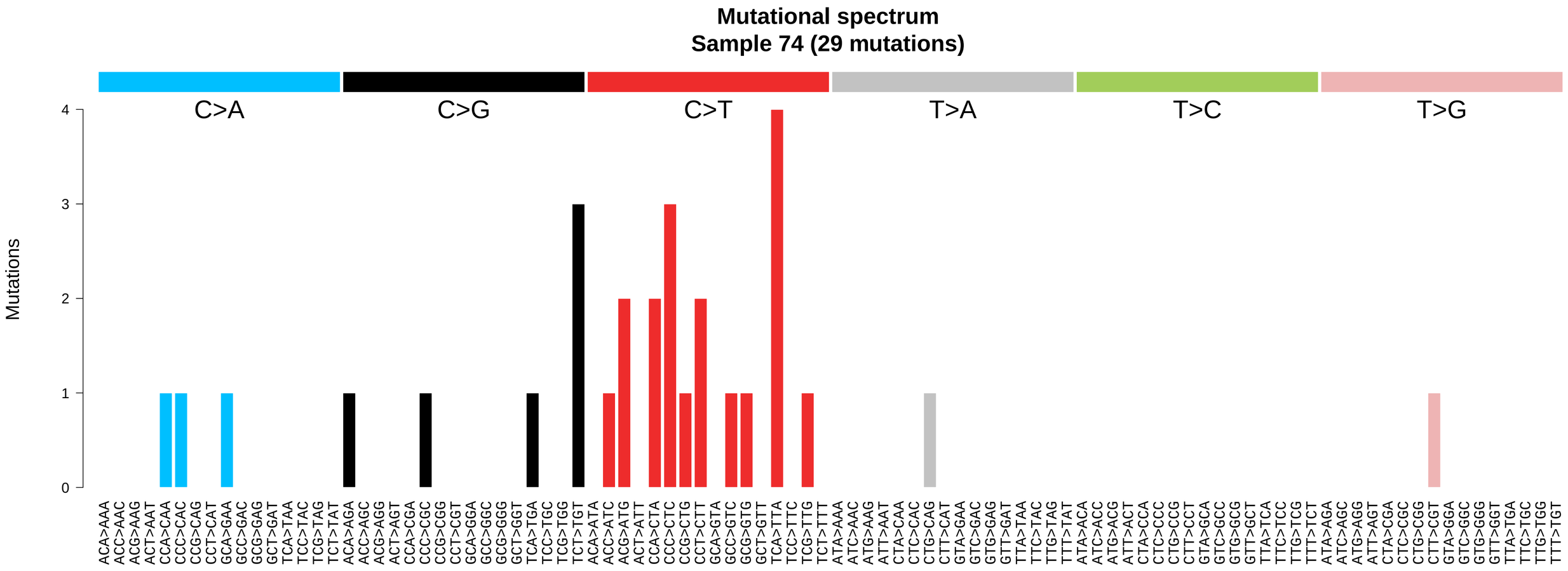

Mutational spectrum
Sample 69 (36 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.609
Signature A (0.033)
Signature B (0.03)
Signature C (0.032)
Signature D (0.034)
Signature E (0.041)
Signature F (0.031)
Signature G (0.028)
Signature H (0.026)
Signature I (0.031)
Signature J (0.021)
Signature K (0.029)
Signature L (0.066)
Signature M (0.02)
Signature N (0.024)
Signature O (0.025)
Signature P (0.042)
Signature Q (0.025)
Signature R (0.022)
Signature S (0.039)
Signature T (0.052)
Signature U (0.051)
Signature V (0.023)
Signature W (0.04)
Signature X (0.036)
Signature Y (0.033)
Signature Z (0.056)
Signature AA (0.025)
Signature AB (0.026)
Signature AC (0.024)
Signature AD (0.036)

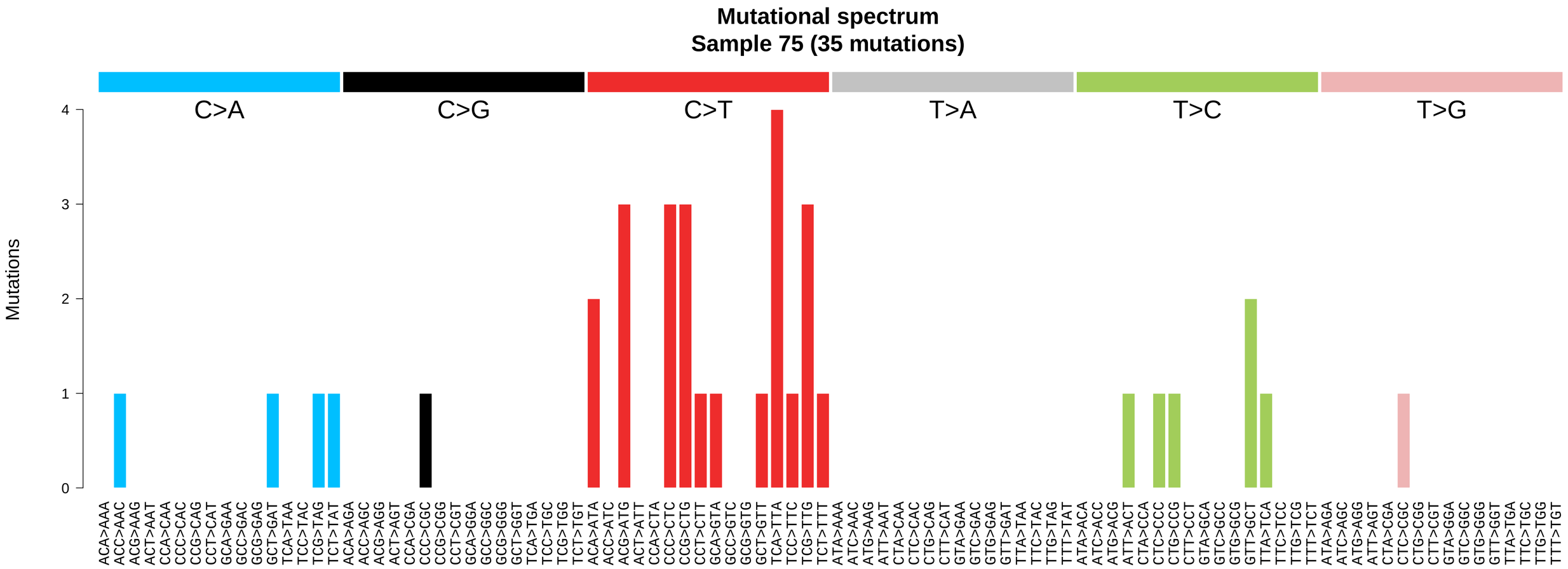

Mutational spectrum
Sample 70 (163 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.784
Signature A (0.018)
Signature B (0.045)
Signature C (0.353)
Signature D (0.055)
Signature E (0.038)
Signature F (0.015)
Signature G (0.018)
Signature H (0.026)
Signature I (0.016)
Signature J (0.01)
Signature K (0.017)
Signature L (0.017)
Signature M (0.047)
Signature N (0.014)
Signature O (0.014)
Signature P (0.022)
Signature Q (0.008)
Signature R (0.022)
Signature S (0.02)
Signature T (0.016)
Signature U (0.02)
Signature V (0.012)
Signature W (0.02)
Signature X (0.035)
Signature Y (0.023)
Signature Z (0.015)
Signature AA (0.014)
Signature AB (0.008)
Signature AC (0.021)
Signature AD (0.04)

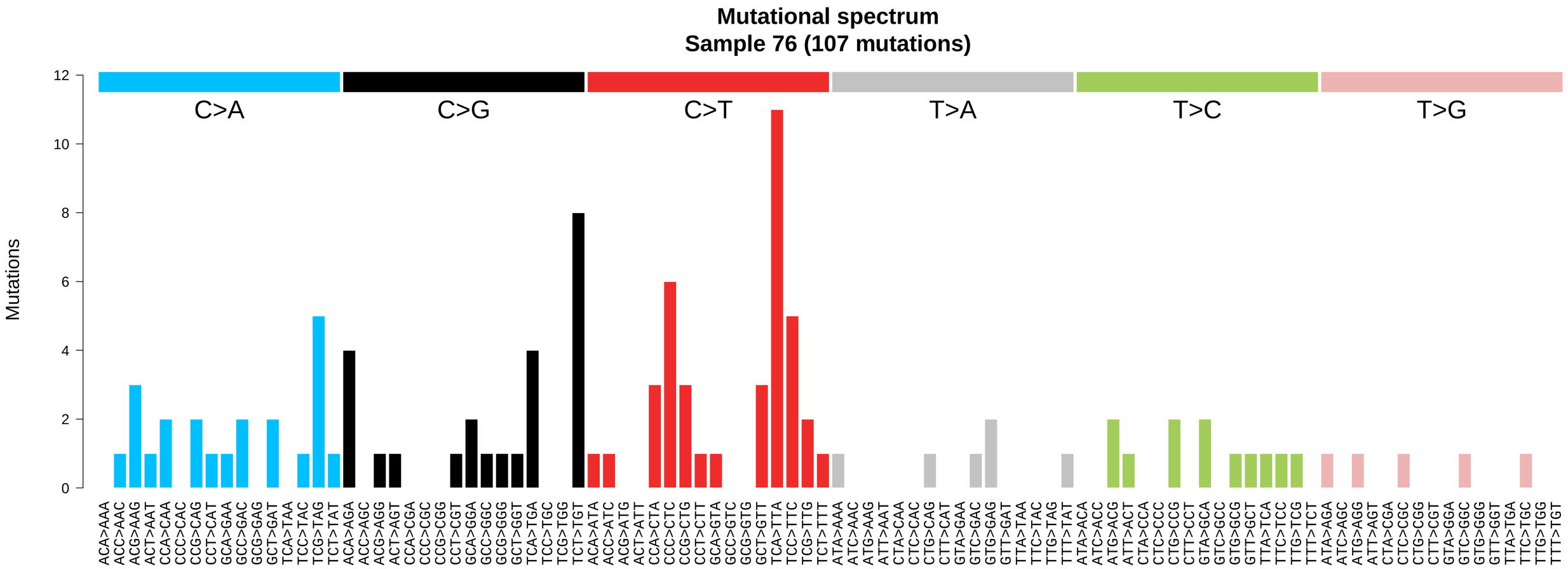

Mutational spectrum
Sample 71 (25 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.533
Signature A (0.042)
Signature B (0.037)
Signature C (0.038)
Signature D (0.029)
Signature E (0.038)
Signature F (0.043)
Signature G (0.024)
Signature H (0.034)
Signature I (0.028)
Signature J (0.021)
Signature K (0.031)
Signature L (0.035)
Signature M (0.032)
Signature N (0.03)
Signature O (0.032)
Signature P (0.027)
Signature Q (0.025)
Signature R (0.024)
Signature S (0.034)
Signature T (0.041)
Signature U (0.048)
Signature V (0.026)
Signature W (0.028)
Signature X (0.025)
Signature Y (0.06)
Signature Z (0.038)
Signature AA (0.034)
Signature AB (0.023)
Signature AC (0.023)
Signature AD (0.048)

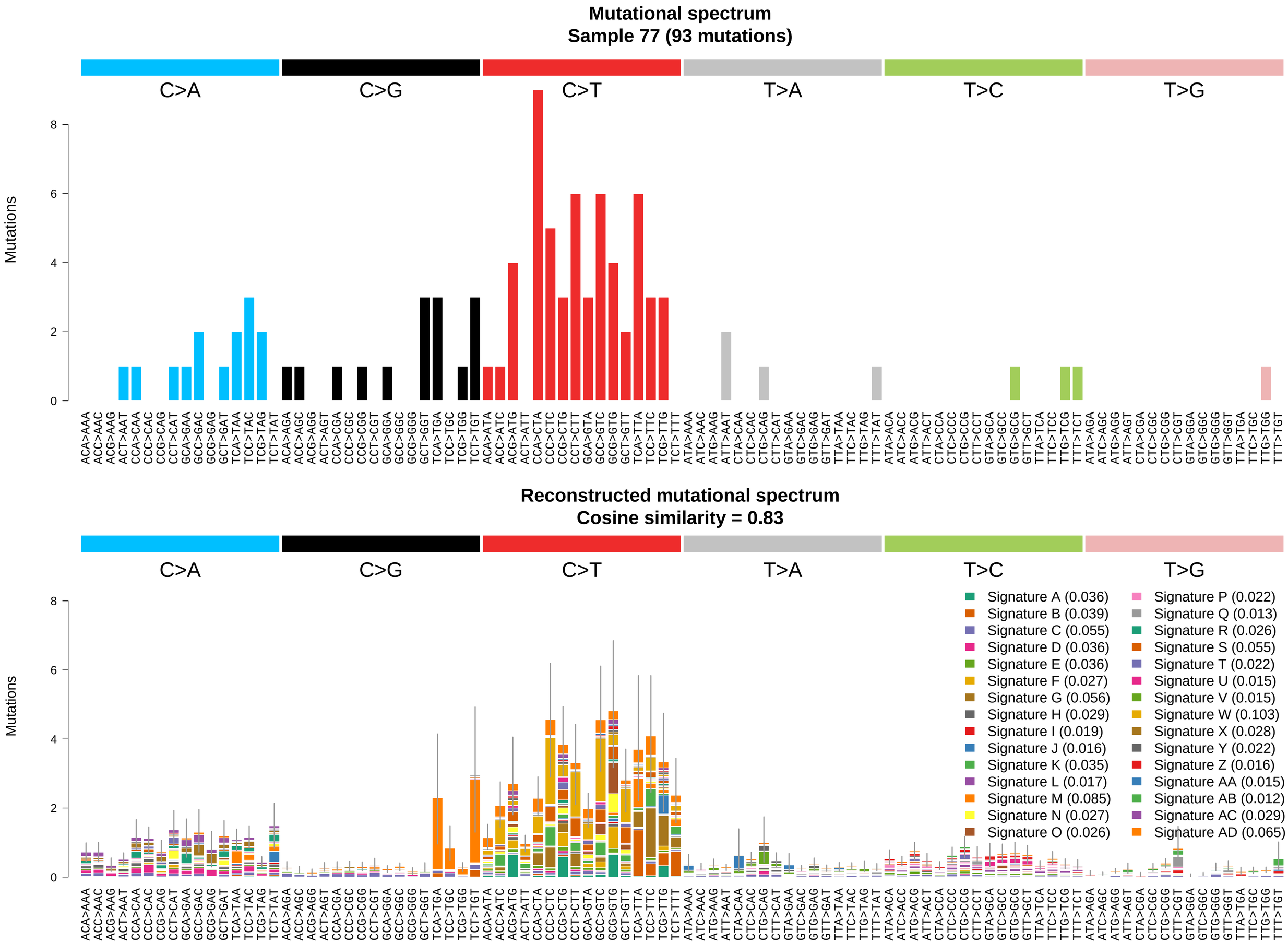

Mutational spectrum
Sample 72 (64 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.837
Signature A (0.051)
Signature B (0.074)
Signature C (0.029)
Signature D (0.023)
Signature E (0.032)
Signature F (0.055)
Signature G (0.033)
Signature H (0.02)
Signature I (0.02)
Signature J (0.014)
Signature K (0.046)
Signature L (0.023)
Signature M (0.048)
Signature N (0.048)
Signature O (0.054)
Signature P (0.02)
Signature Q (0.019)
Signature R (0.019)
Signature S (0.054)
Signature T (0.029)
Signature U (0.024)
Signature V (0.012)
Signature W (0.055)
Signature X (0.024)
Signature Y (0.022)
Signature Z (0.027)
Signature AA (0.016)
Signature AB (0.026)
Signature AC (0.02)
Signature AD (0.065)

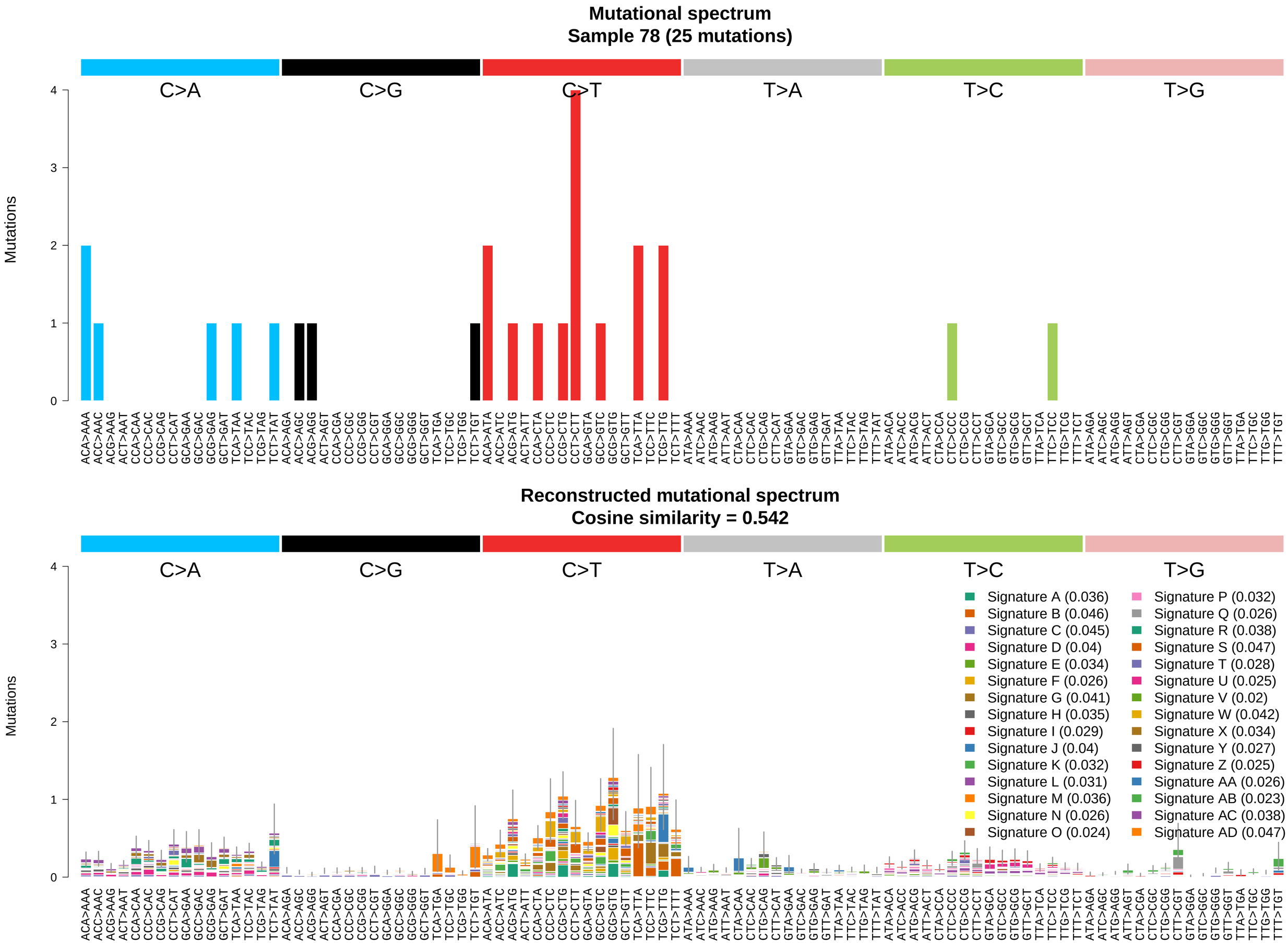

Mutational spectrum
Sample 73 (53 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.694
Signature A (0.054)
Signature B (0.022)
Signature C (0.065)
Signature D (0.055)
Signature E (0.043)
Signature F (0.046)
Signature G (0.021)
Signature H (0.039)
Signature I (0.025)
Signature J (0.055)
Signature K (0.02)
Signature L (0.019)
Signature M (0.045)
Signature N (0.035)
Signature O (0.028)
Signature P (0.031)
Signature Q (0.025)
Signature R (0.036)
Signature S (0.024)
Signature T (0.03)
Signature U (0.018)
Signature V (0.026)
Signature W (0.02)
Signature X (0.041)
Signature Y (0.036)
Signature Z (0.02)
Signature AA (0.019)
Signature AB (0.032)
Signature AC (0.032)
Signature AD (0.038)

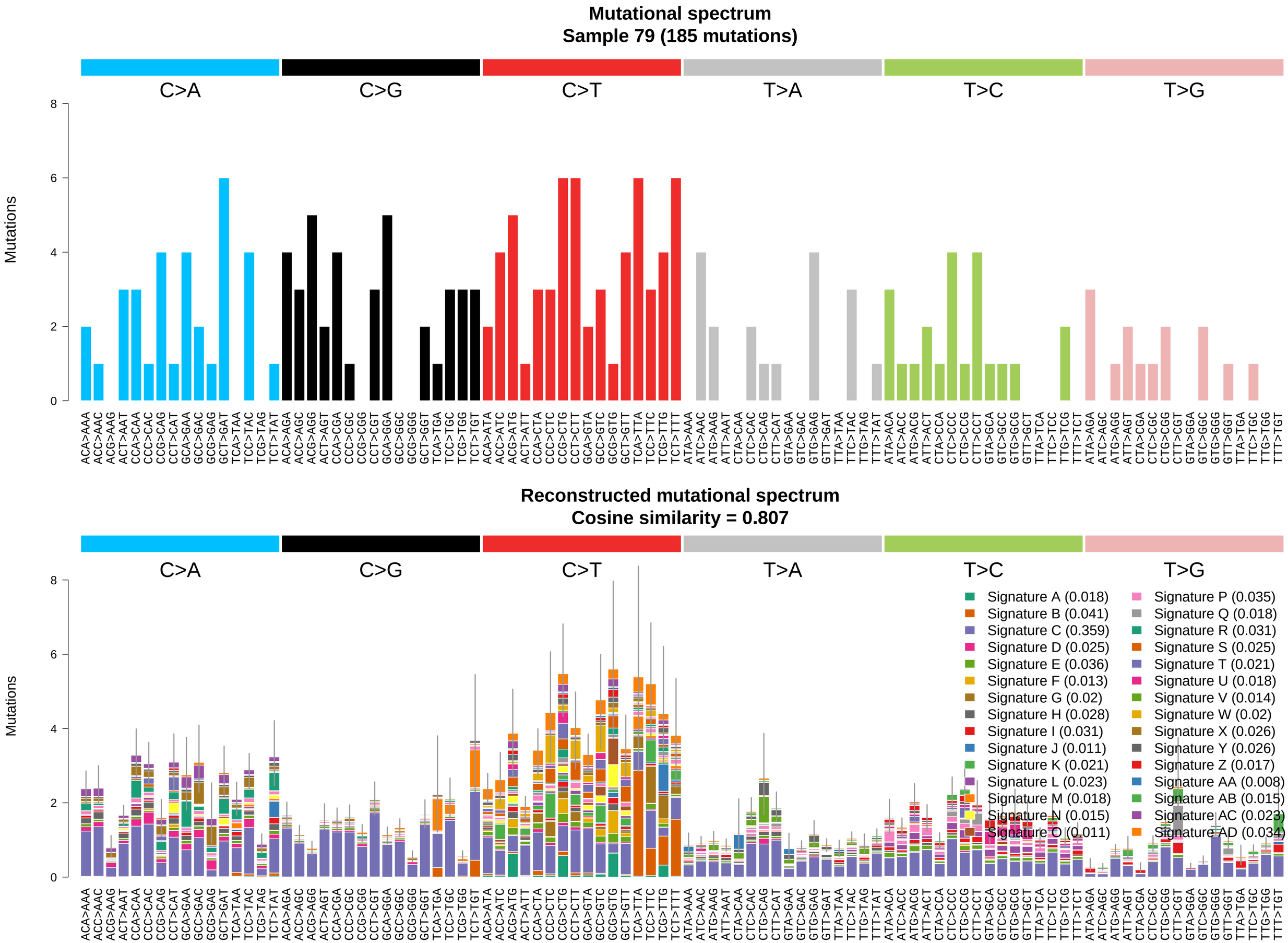

Mutational spectrum
Sample 74 (29 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.728
Signature A (0.035)
Signature B (0.063)
Signature C (0.034)
Signature D (0.033)
Signature E (0.029)
Signature F (0.029)
Signature G (0.046)
Signature H (0.028)
Signature I (0.025)
Signature J (0.022)
Signature K (0.043)
Signature L (0.022)
Signature M (0.088)
Signature N (0.024)
Signature O (0.024)
Signature P (0.027)
Signature Q (0.031)
Signature R (0.031)
Signature S (0.046)
Signature T (0.026)
Signature U (0.021)
Signature V (0.026)
Signature W (0.057)
Signature X (0.027)
Signature Y (0.029)
Signature Z (0.022)
Signature AA (0.021)
Signature AB (0.022)
Signature AC (0.028)
Signature AD (0.04)

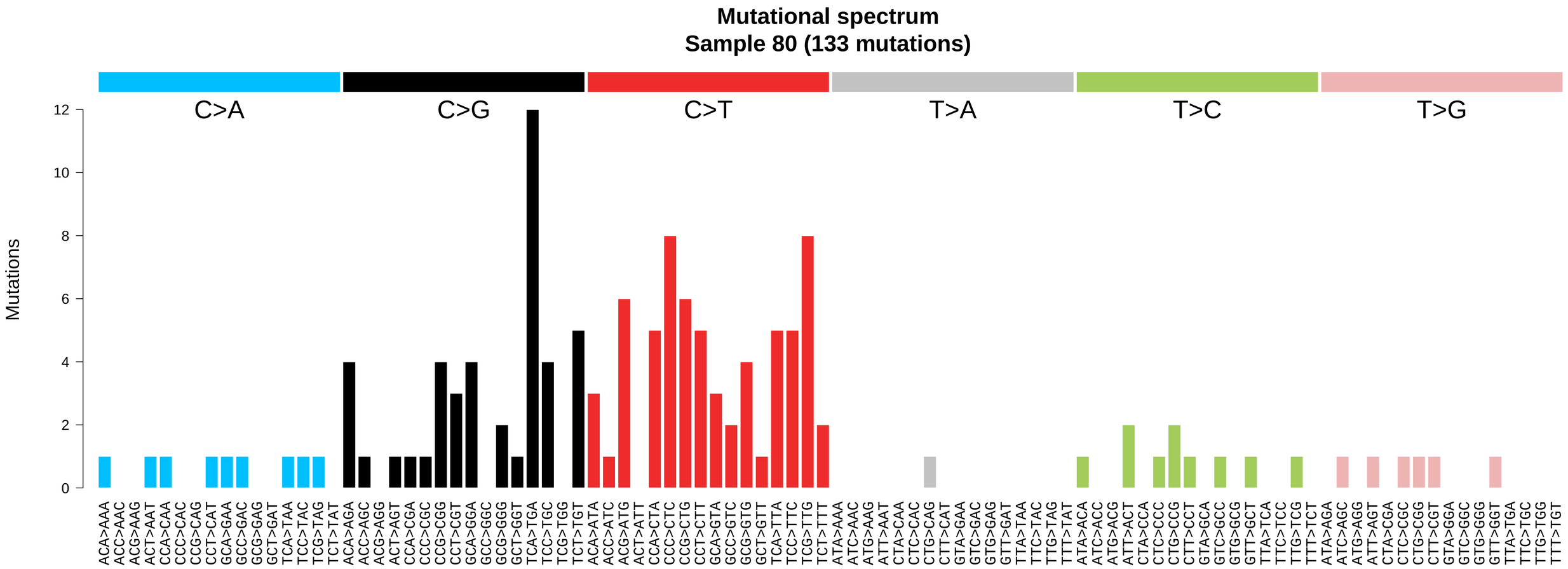

Mutational spectrum
Sample 75 (35 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.717
Signature A (0.051)
Signature B (0.076)
Signature C (0.027)
Signature D (0.026)
Signature E (0.034)
Signature F (0.033)
Signature G (0.048)
Signature H (0.028)
Signature I (0.026)
Signature J (0.04)
Signature K (0.034)
Signature L (0.036)
Signature M (0.02)
Signature N (0.03)
Signature O (0.022)
Signature P (0.035)
Signature Q (0.026)
Signature R (0.029)
Signature S (0.045)
Signature T (0.038)
Signature U (0.04)
Signature V (0.018)
Signature W (0.036)
Signature X (0.026)
Signature Y (0.028)
Signature Z (0.033)
Signature AA (0.019)
Signature AB (0.026)
Signature AC (0.032)
Signature AD (0.039)

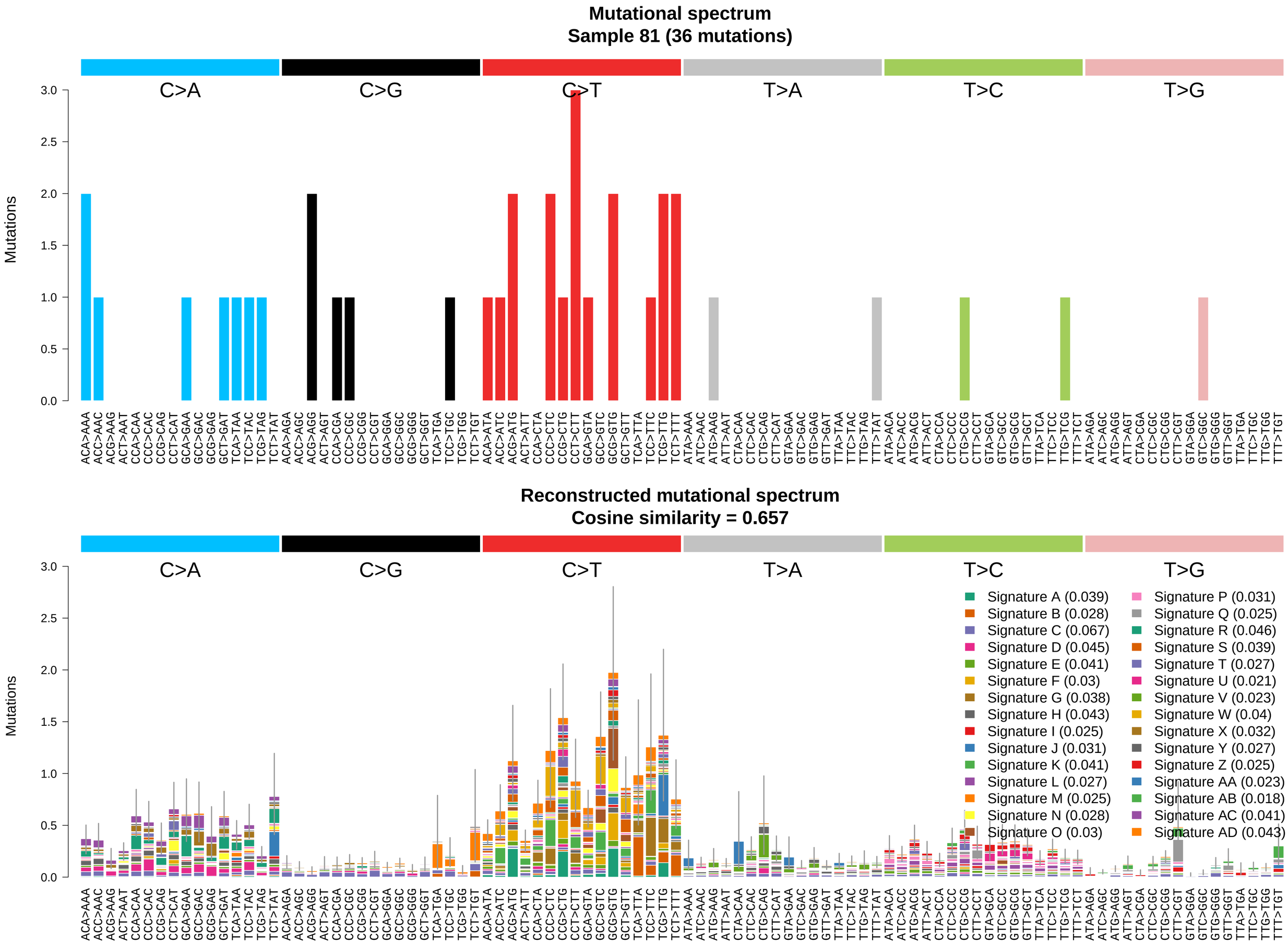

Mutational spectrum
Sample 76 (107 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.781
Signature A (0.012)
Signature B (0.079)
Signature C (0.095)
Signature D (0.064)
Signature E (0.037)
Signature F (0.013)
Signature G (0.044)
Signature H (0.023)
Signature I (0.02)
Signature J (0.014)
Signature K (0.026)
Signature L (0.031)
Signature M (0.115)
Signature N (0.013)
Signature O (0.012)
Signature P (0.039)
Signature Q (0.013)
Signature R (0.028)
Signature S (0.023)
Signature T (0.022)
Signature U (0.025)
Signature V (0.016)
Signature W (0.024)
Signature X (0.048)
Signature Y (0.028)
Signature Z (0.026)
Signature AA (0.015)
Signature AB (0.015)
Signature AC (0.035)
Signature AD (0.042)

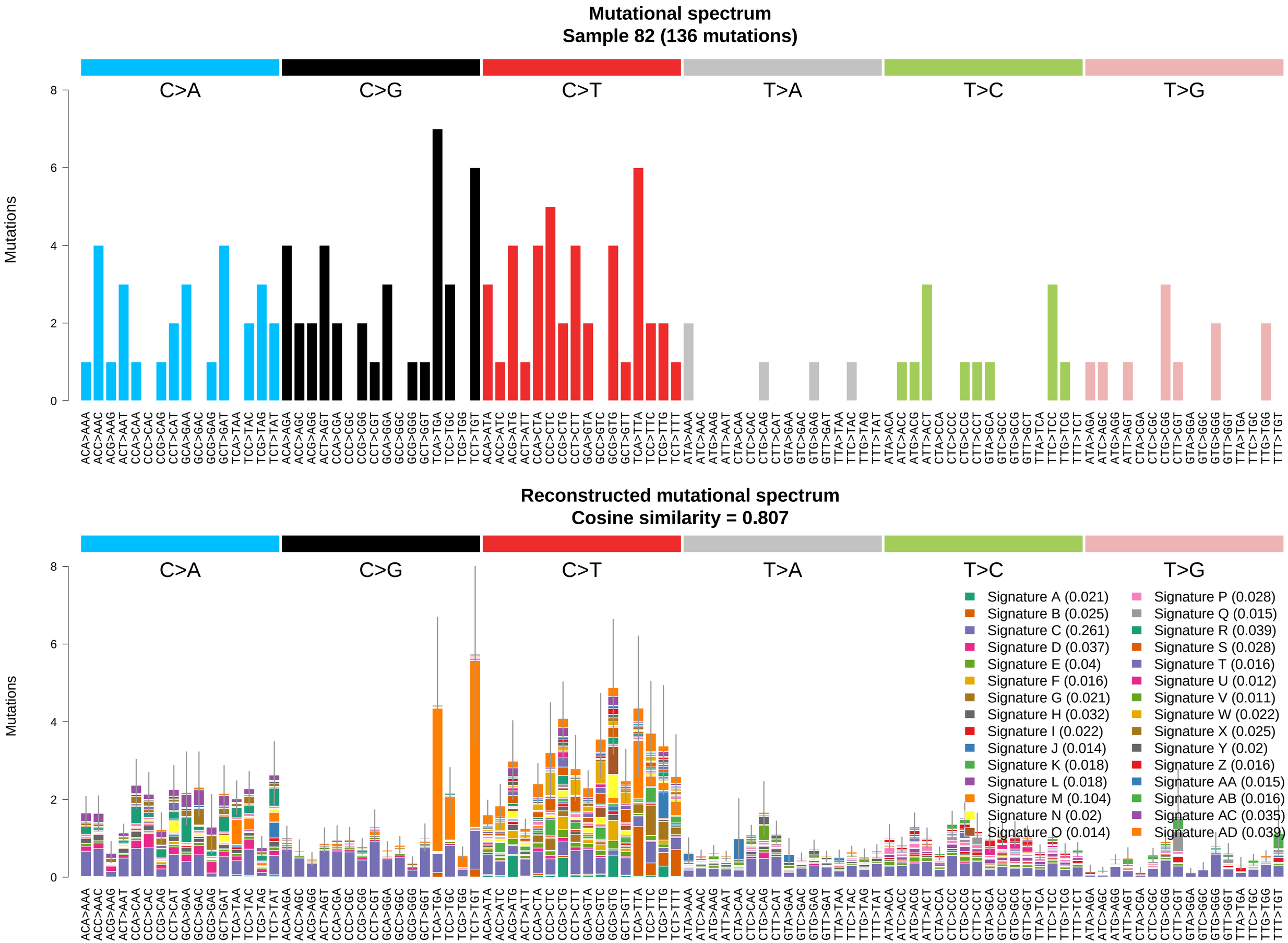

Mutational spectrum
Sample 77 (93 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.83
Signature A (0.036)
Signature B (0.039)
Signature C (0.055)
Signature D (0.036)
Signature E (0.036)
Signature F (0.027)
Signature G (0.056)
Signature H (0.029)
Signature I (0.019)
Signature J (0.016)
Signature K (0.035)
Signature L (0.017)
Signature M (0.085)
Signature N (0.027)
Signature O (0.026)
Signature P (0.022)
Signature Q (0.013)
Signature R (0.026)
Signature S (0.055)
Signature T (0.022)
Signature U (0.015)
Signature V (0.015)
Signature W (0.103)
Signature X (0.028)
Signature Y (0.022)
Signature Z (0.016)
Signature AA (0.015)
Signature AB (0.012)
Signature AC (0.029)
Signature AD (0.065)

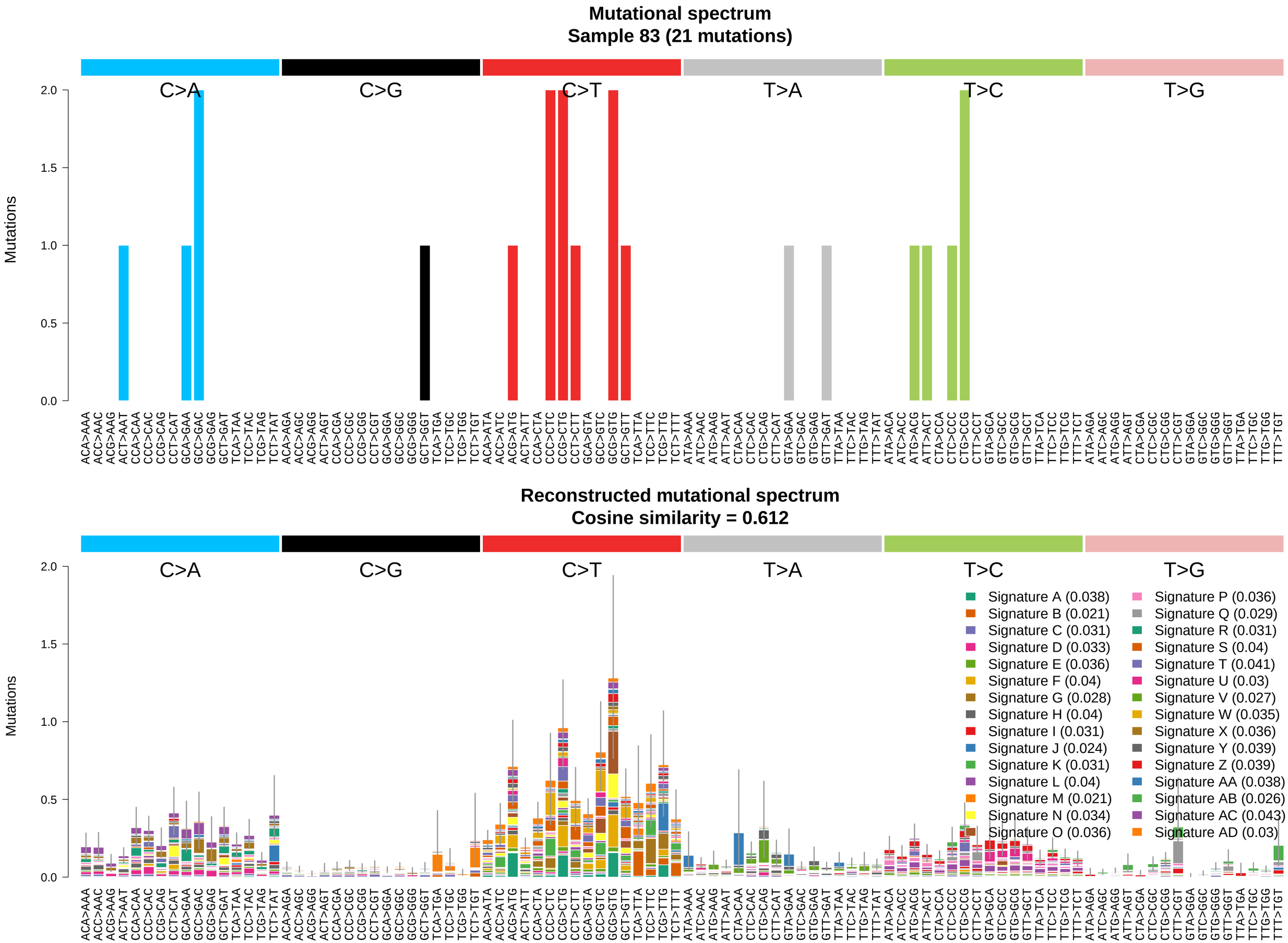

Mutational spectrum
Sample 78 (25 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.542
Signature A (0.036)
Signature B (0.046)
Signature C (0.045)
Signature D (0.04)
Signature E (0.034)
Signature F (0.026)
Signature G (0.041)
Signature H (0.035)
Signature I (0.029)
Signature J (0.04)
Signature K (0.032)
Signature L (0.031)
Signature M (0.036)
Signature N (0.026)
Signature O (0.024)
Signature P (0.032)
Signature Q (0.026)
Signature R (0.038)
Signature S (0.047)
Signature T (0.028)
Signature U (0.025)
Signature V (0.02)
Signature W (0.042)
Signature X (0.034)
Signature Y (0.027)
Signature Z (0.025)
Signature AA (0.026)
Signature AB (0.023)
Signature AC (0.038)
Signature AD (0.047)

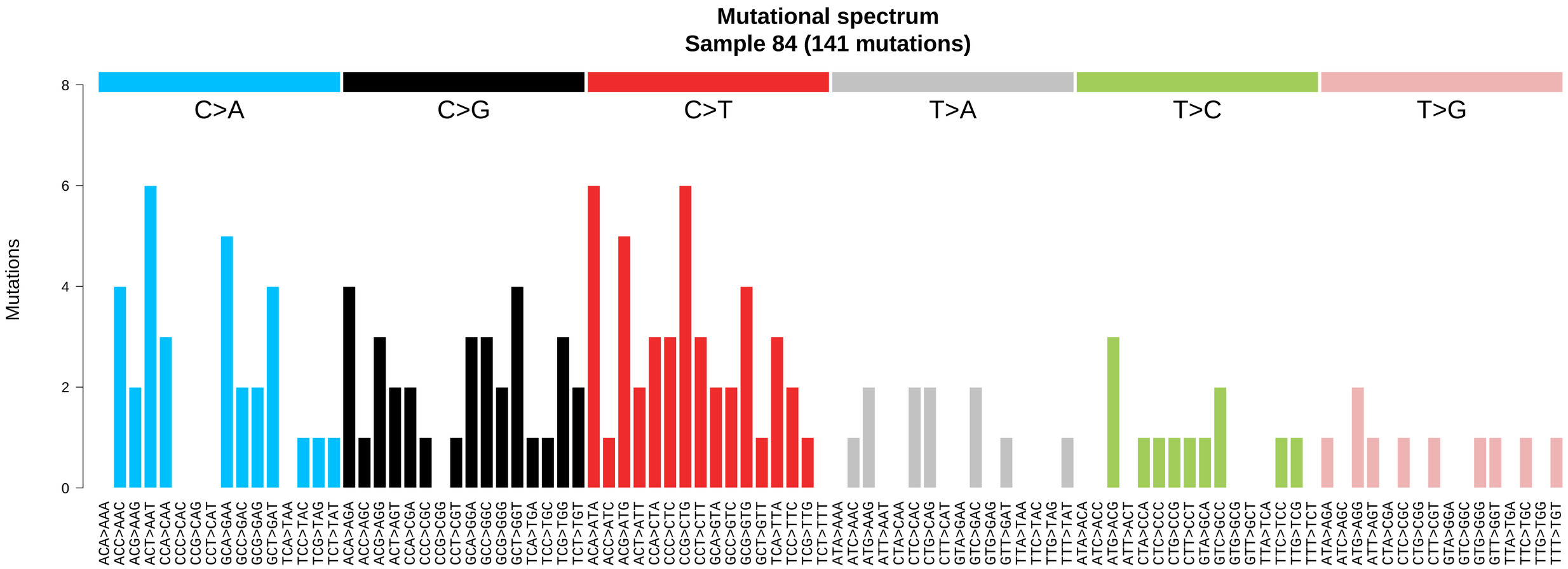

Mutational spectrum
Sample 79 (185 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.807
Signature A (0.018)
Signature B (0.041)
Signature C (0.359)
Signature D (0.025)
Signature E (0.036)
Signature F (0.013)
Signature G (0.02)
Signature H (0.028)
Signature I (0.031)
Signature J (0.011)
Signature K (0.021)
Signature L (0.023)
Signature M (0.018)
Signature N (0.015)
Signature O (0.011)
Signature P (0.035)
Signature Q (0.018)
Signature R (0.031)
Signature S (0.025)
Signature T (0.021)
Signature U (0.018)
Signature V (0.014)
Signature W (0.02)
Signature X (0.026)
Signature Y (0.026)
Signature Z (0.017)
Signature AA (0.008)
Signature AB (0.015)
Signature AC (0.023)
Signature AD (0.034)

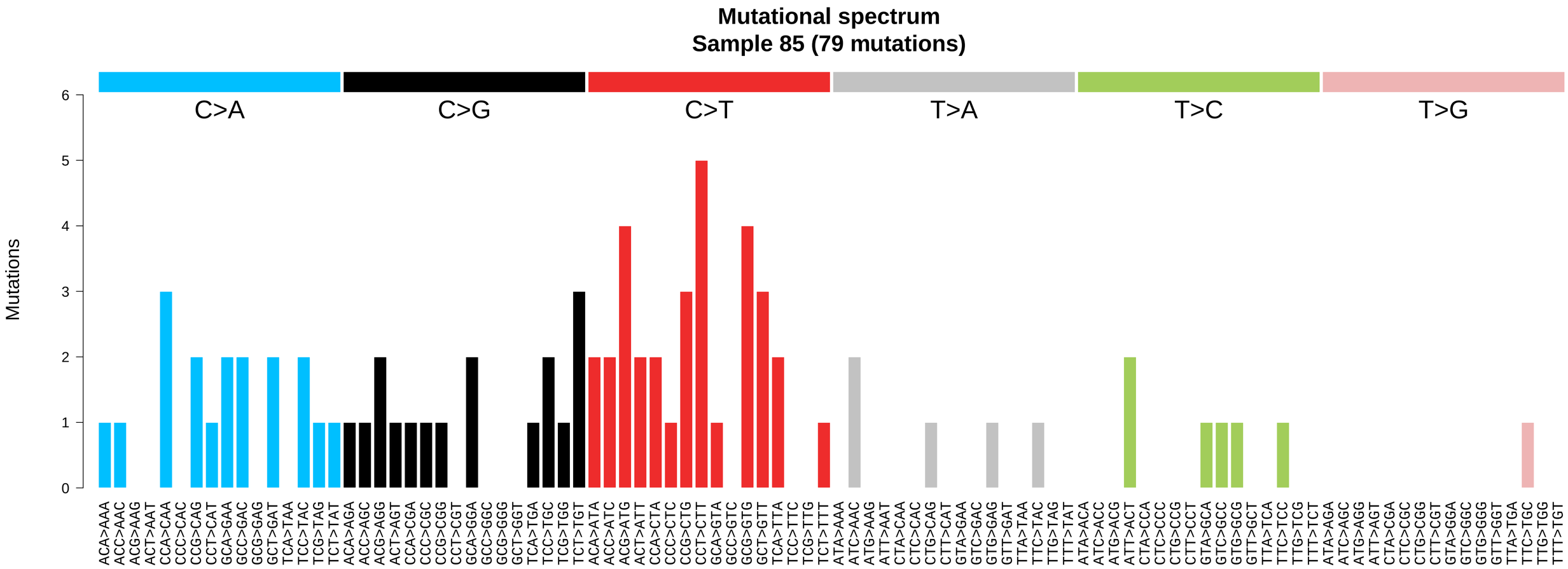

Mutational spectrum
Sample 80 (133 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.852
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
Signature A (0.049)
Signature B (0.024)
Signature C (0.137)
Signature D (0.027)
Signature E (0.038)
Signature F (0.025)
Signature G (0.068)
Signature H (0.017)
Signature I (0.016)
Signature J (0.021)
Signature K (0.03)
Signature L (0.016)
Signature M (0.163)
Signature N (0.017)
Signature O (0.016)
Signature P (0.027)
Signature Q (0.023)
Signature R (0.016)
Signature S (0.036)
Signature T (0.02)
Signature U (0.015)
Signature V (0.009)
Signature W (0.036)
Signature X (0.018)
Signature Y (0.017)
Signature Z (0.017)
Signature AA (0.01)
Signature AB (0.017)
Signature AC (0.015)
Signature AD (0.059)
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

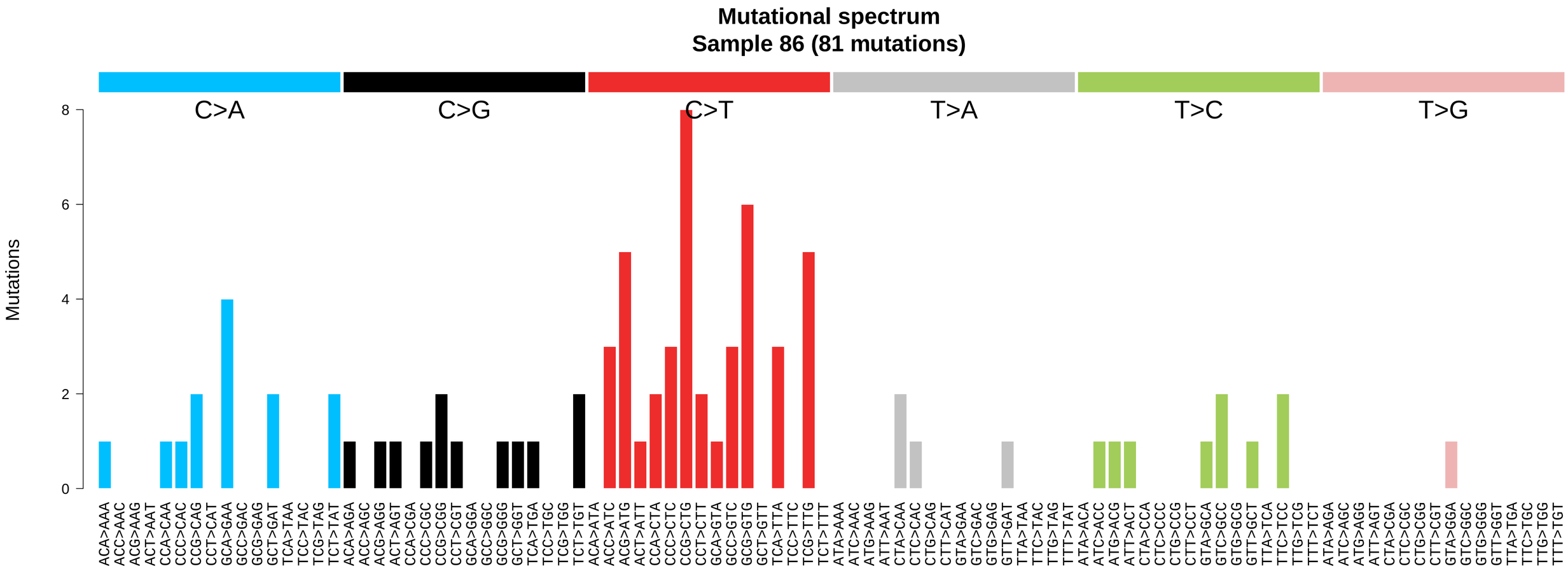

Mutational spectrum
Sample 81 (36 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.657
Signature A (0.039)
Signature B (0.028)
Signature C (0.067)
Signature D (0.045)
Signature E (0.041)
Signature F (0.03)
Signature G (0.038)
Signature H (0.043)
Signature I (0.025)
Signature J (0.031)
Signature K (0.041)
Signature L (0.027)
Signature M (0.025)
Signature N (0.028)
Signature O (0.03)
Signature P (0.031)
Signature Q (0.025)
Signature R (0.046)
Signature S (0.039)
Signature T (0.027)
Signature U (0.021)
Signature V (0.023)
Signature W (0.04)
Signature X (0.032)
Signature Y (0.027)
Signature Z (0.025)
Signature AA (0.023)
Signature AB (0.018)
Signature AC (0.041)
Signature AD (0.043)

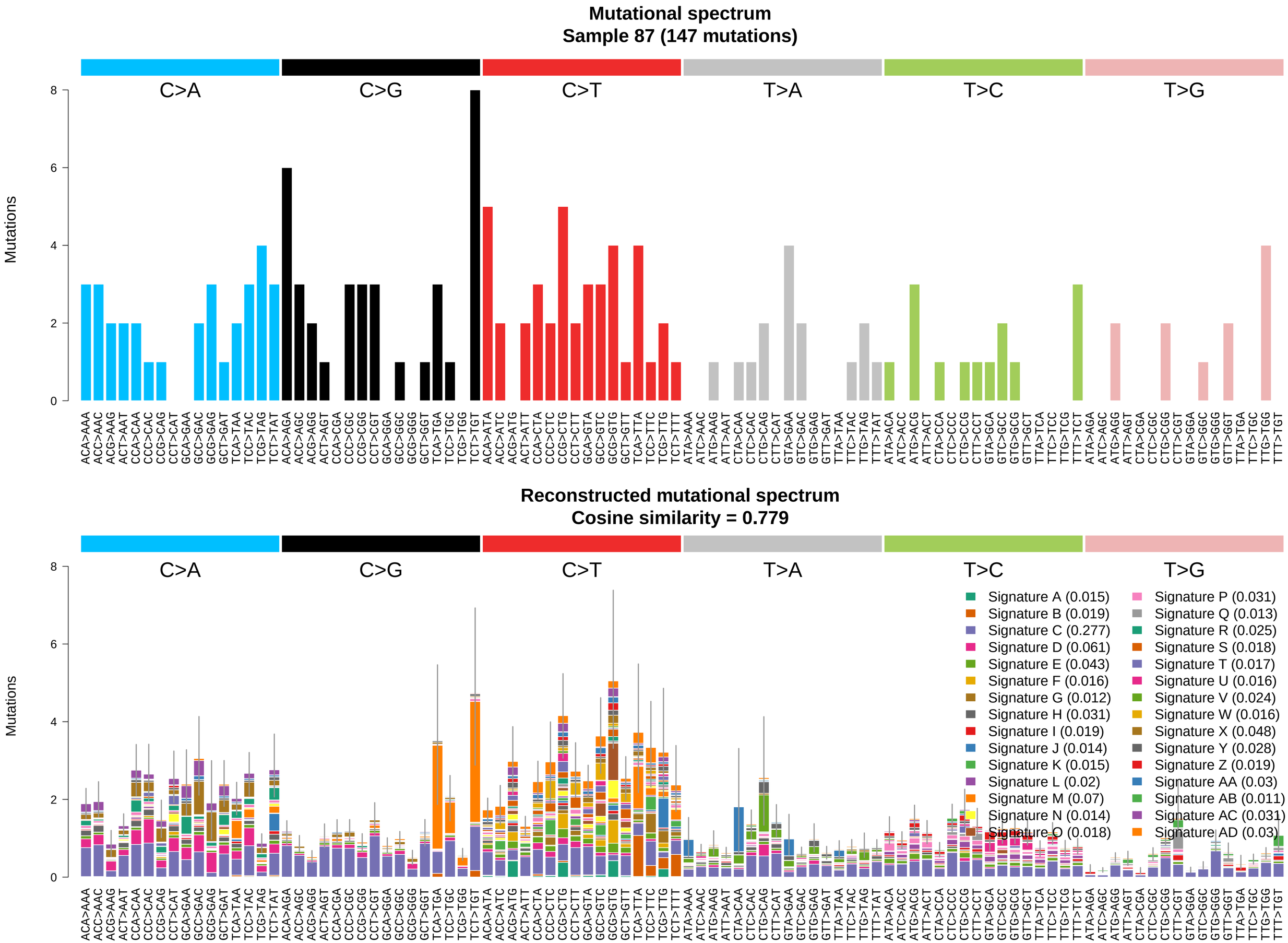

Mutational spectrum
Sample 82 (136 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.807
Signature A (0.021)
Signature B (0.025)
Signature C (0.261)
Signature D (0.037)
Signature E (0.04)
Signature F (0.016)
Signature G (0.021)
Signature H (0.032)
Signature I (0.022)
Signature J (0.014)
Signature K (0.018)
Signature L (0.018)
Signature M (0.104)
Signature N (0.02)
Signature O (0.014)
Signature P (0.028)
Signature Q (0.015)
Signature R (0.039)
Signature S (0.028)
Signature T (0.016)
Signature U (0.012)
Signature V (0.011)
Signature W (0.022)
Signature X (0.025)
Signature Y (0.02)
Signature Z (0.016)
Signature AA (0.015)
Signature AB (0.016)
Signature AC (0.035)
Signature AD (0.039)

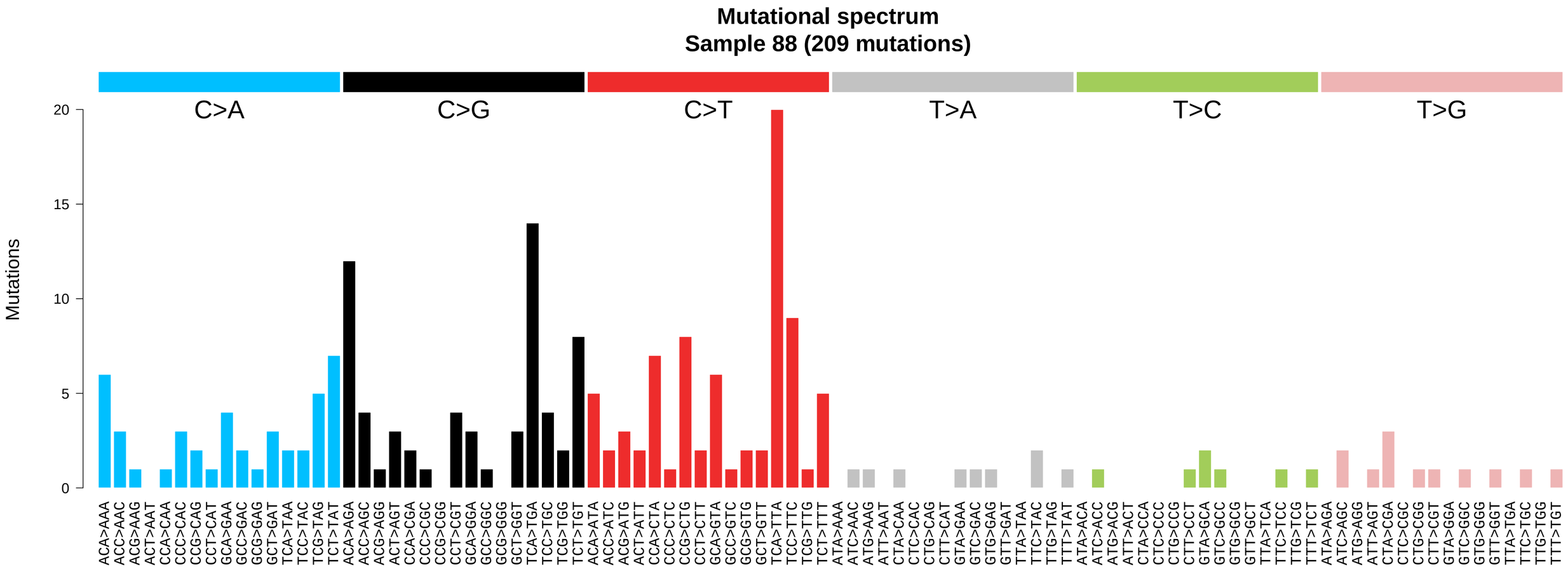

Mutational spectrum
Sample 83 (21 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
2.0
1.5
1.0
0.5
0.0
Reconstructed mutational spectrum
Cosine similarity = 0.612
Signature A (0.038)
Signature B (0.021)
Signature C (0.031)
Signature D (0.033)
Signature E (0.036)
Signature F (0.04)
Signature G (0.028)
Signature H (0.04)
Signature I (0.031)
Signature J (0.024)
Signature K (0.031)
Signature L (0.04)
Signature M (0.021)
Signature N (0.034)
Signature O (0.036)
Signature P (0.036)
Signature Q (0.029)
Signature R (0.031)
Signature S (0.04)
Signature T (0.041)
Signature U (0.03)
Signature V (0.027)
Signature W (0.035)
Signature X (0.036)
Signature Y (0.039)
Signature Z (0.039)
Signature AA (0.038)
Signature AB (0.026)
Signature AC (0.043)
Signature AD (0.03)

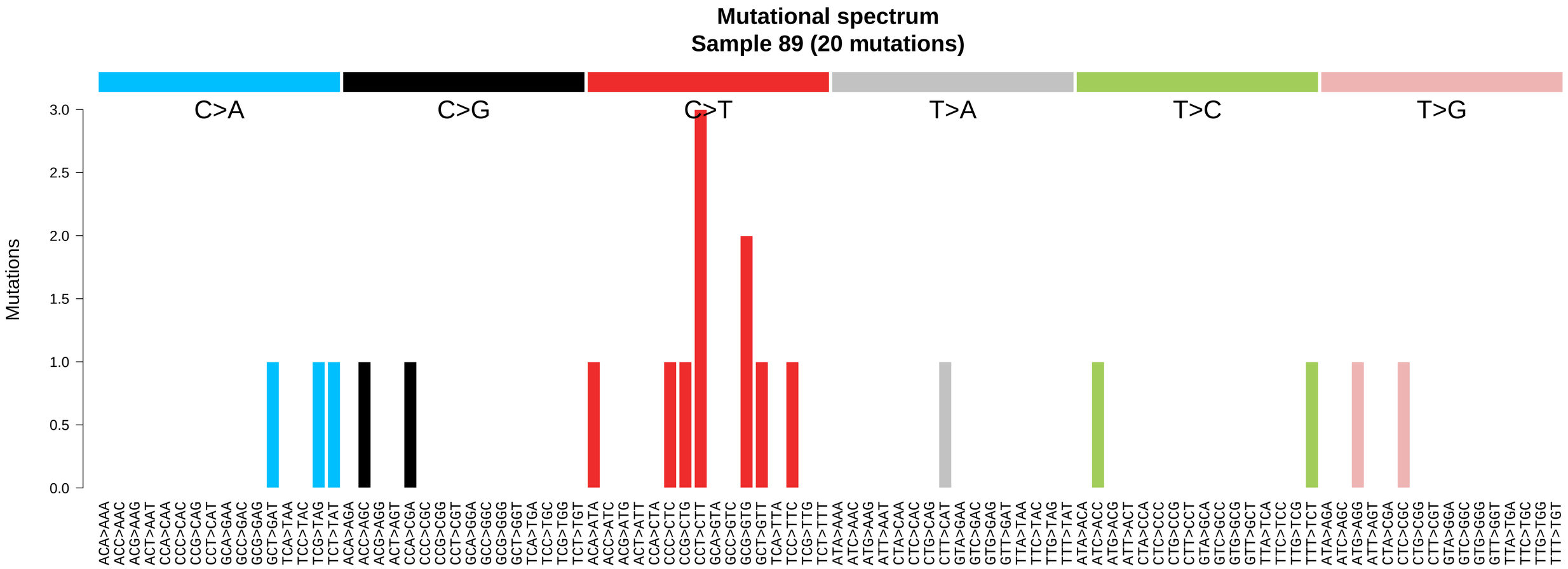

Mutational spectrum
Sample 84 (141 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.769
Signature A (0.027)
Signature B (0.013)
Signature C (0.306)
Signature D (0.055)
Signature E (0.039)
Signature F (0.021)
Signature G (0.013)
Signature H (0.043)
Signature I (0.022)
Signature J (0.01)
Signature K (0.016)
Signature L (0.018)
Signature M (0.02)
Signature N (0.022)
Signature O (0.017)
Signature P (0.023)
Signature Q (0.018)
Signature R (0.029)
Signature S (0.021)
Signature T (0.017)
Signature U (0.017)
Signature V (0.014)
Signature W (0.017)
Signature X (0.042)
Signature Y (0.023)
Signature Z (0.017)
Signature AA (0.01)
Signature AB (0.019)
Signature AC (0.042)
Signature AD (0.049)

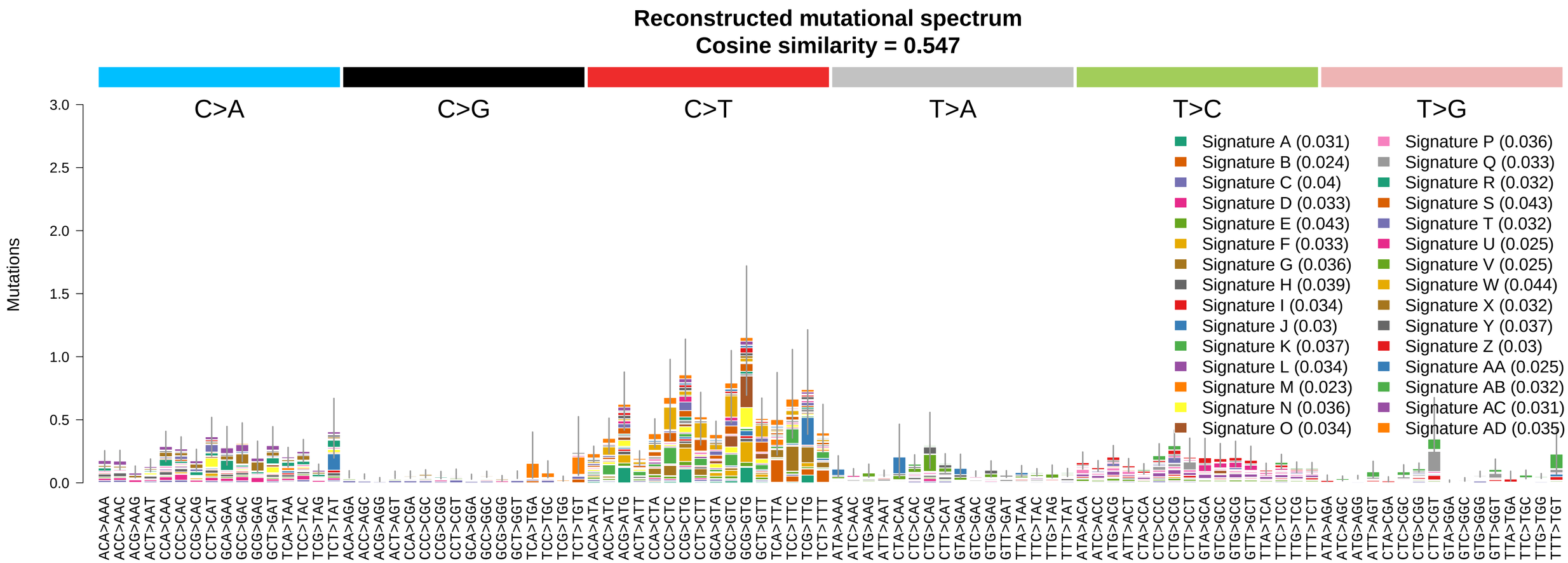

Mutational spectrum
Sample 85 (79 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.767
Signature A (0.032)
Signature B (0.021)
Signature C (0.11)
Signature D (0.048)
Signature E (0.046)
Signature F (0.027)
Signature G (0.017)
Signature H (0.039)
Signature I (0.018)
Signature J (0.014)
Signature K (0.027)
Signature L (0.023)
Signature M (0.058)
Signature N (0.03)
Signature O (0.027)
Signature P (0.03)
Signature Q (0.013)
Signature R (0.056)
Signature S (0.056)
Signature T (0.022)
Signature U (0.027)
Signature V (0.018)
Signature W (0.033)
Signature X (0.043)
Signature Y (0.03)
Signature Z (0.025)
Signature AA (0.015)
Signature AB (0.013)
Signature AC (0.041)
Signature AD (0.04)

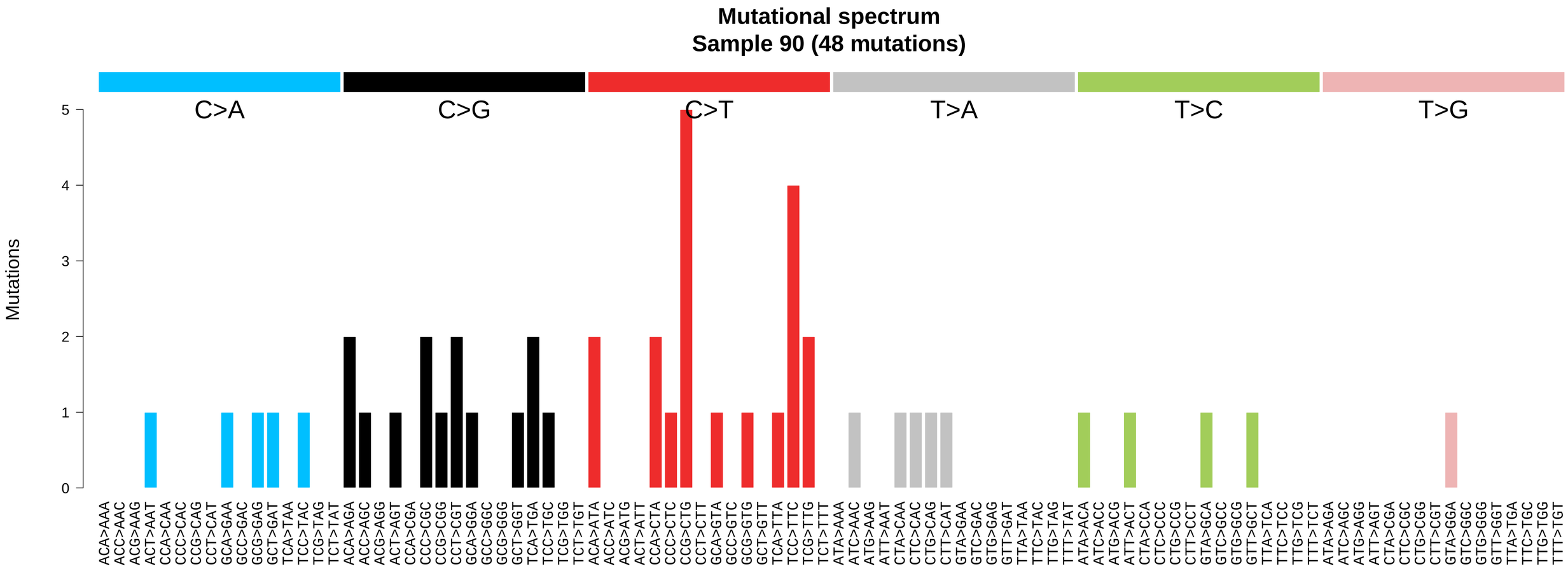

Mutational spectrum
Sample 86 (81 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.851
Signature A (0.083)
Signature B (0.027)
Signature C (0.058)
Signature D (0.033)
Signature E (0.037)
Signature F (0.051)
Signature G (0.026)
Signature H (0.027)
Signature I (0.021)
Signature J (0.033)
Signature K (0.029)
Signature L (0.021)
Signature M (0.032)
Signature N (0.029)
Signature O (0.033)
Signature P (0.023)
Signature Q (0.015)
Signature R (0.072)
Signature S (0.033)
Signature T (0.025)
Signature U (0.034)
Signature V (0.014)
Signature W (0.032)
Signature X (0.025)
Signature Y (0.028)
Signature Z (0.032)
Signature AA (0.033)
Signature AB (0.012)
Signature AC (0.032)
Signature AD (0.048)

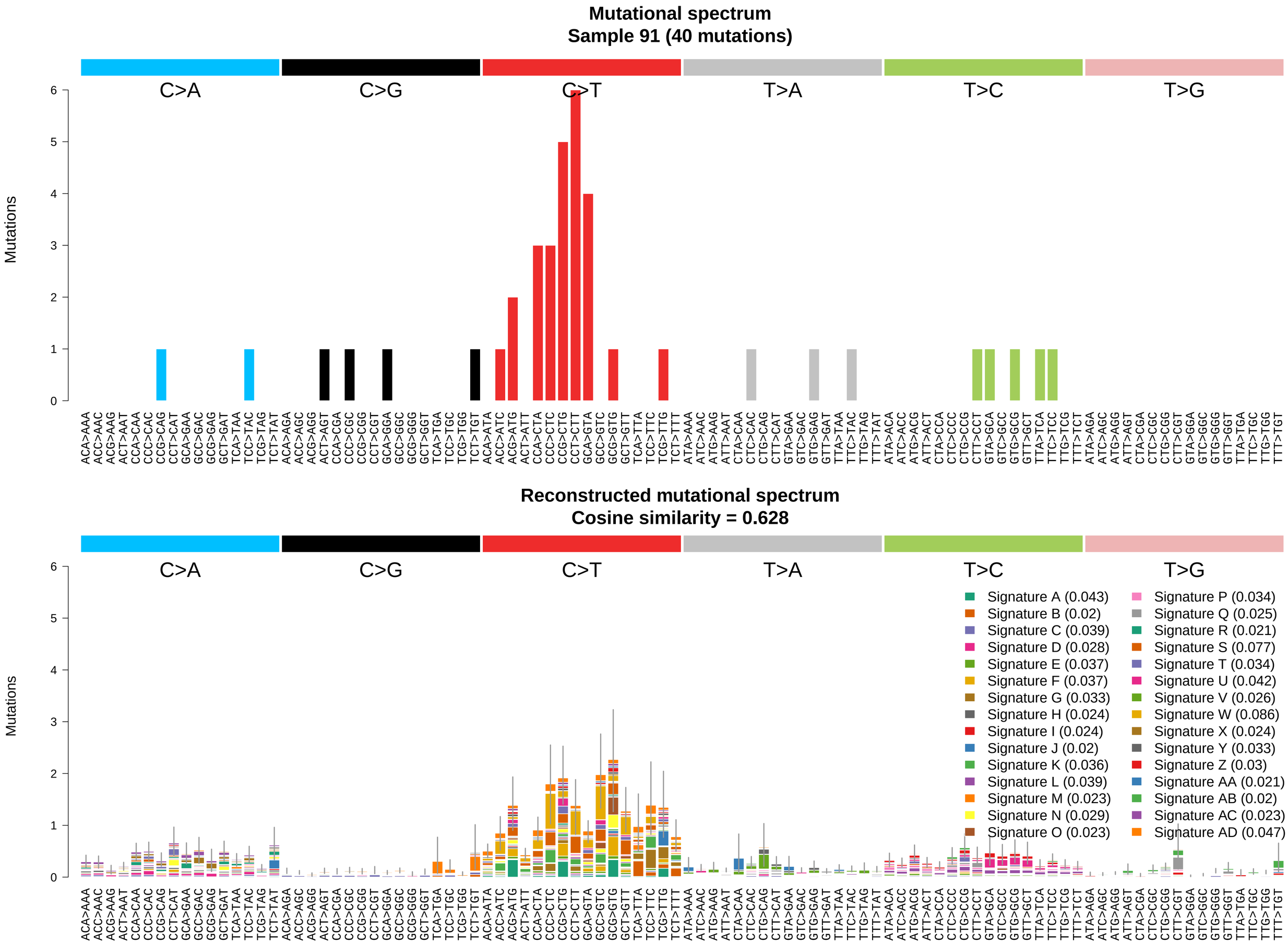

Mutational spectrum
Sample 87 (147 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.779
Signature A (0.015)
Signature B (0.019)
Signature C (0.277)
Signature D (0.061)
Signature E (0.043)
Signature F (0.016)
Signature G (0.012)
Signature H (0.031)
Signature I (0.019)
Signature J (0.014)
Signature K (0.015)
Signature L (0.02)
Signature M (0.07)
Signature N (0.014)
Signature O (0.018)
Signature P (0.031)
Signature Q (0.013)
Signature R (0.025)
Signature S (0.018)
Signature T (0.017)
Signature U (0.016)
Signature V (0.024)
Signature W (0.016)
Signature X (0.048)
Signature Y (0.028)
Signature Z (0.019)
Signature AA (0.03)
Signature AB (0.011)
Signature AC (0.031)
Signature AD (0.03)

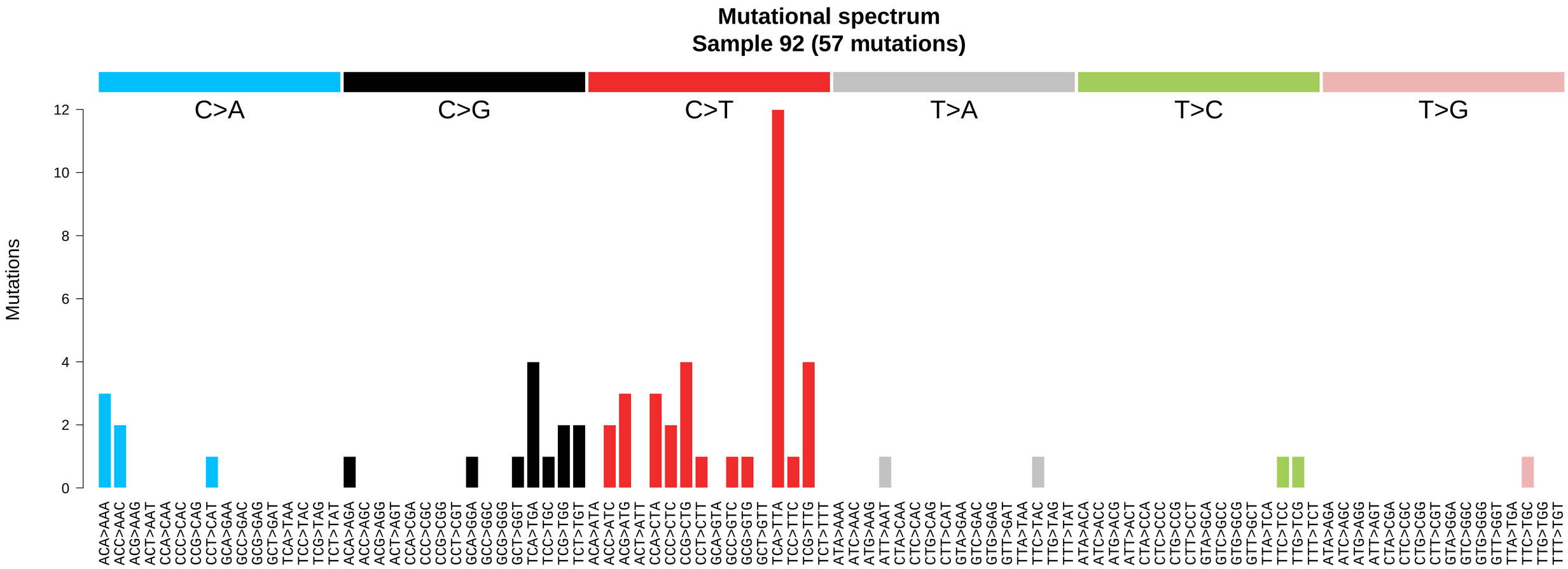

Mutational spectrum
Sample 88 (209 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.833
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
Signature A (0.014)
Signature B (0.098)
Signature C (0.268)
Signature D (0.029)
Signature E (0.026)
Signature F (0.013)
Signature G (0.019)
Signature H (0.022)
Signature I (0.023)
Signature J (0.012)
Signature K (0.014)
Signature L (0.011)
Signature M (0.148)
Signature N (0.012)
Signature O (0.009)
Signature P (0.015)
Signature Q (0.012)
Signature R (0.039)
Signature S (0.015)
Signature T (0.012)
Signature U (0.011)
Signature V (0.008)
Signature W (0.011)
Signature X (0.03)
Signature Y (0.012)
Signature Z (0.009)
Signature AA (0.013)
Signature AB (0.014)
Signature AC (0.038)
Signature AD (0.041)

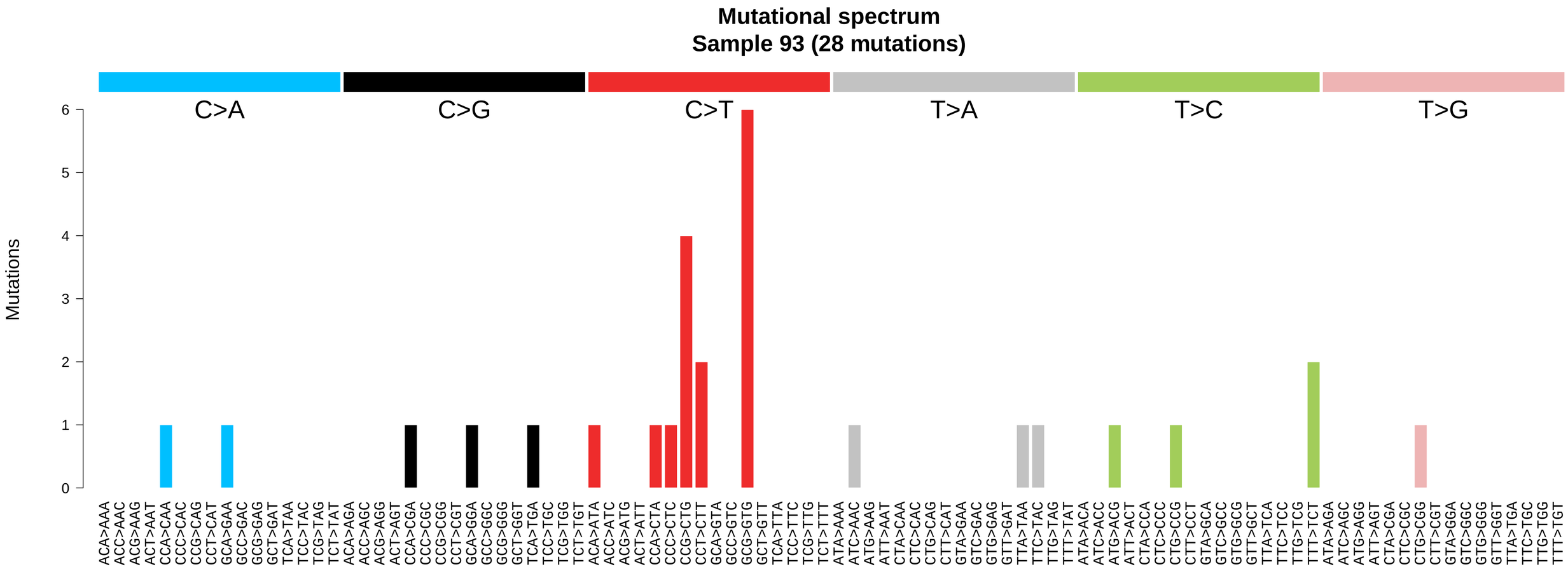

Mutational spectrum
Sample 89 (20 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

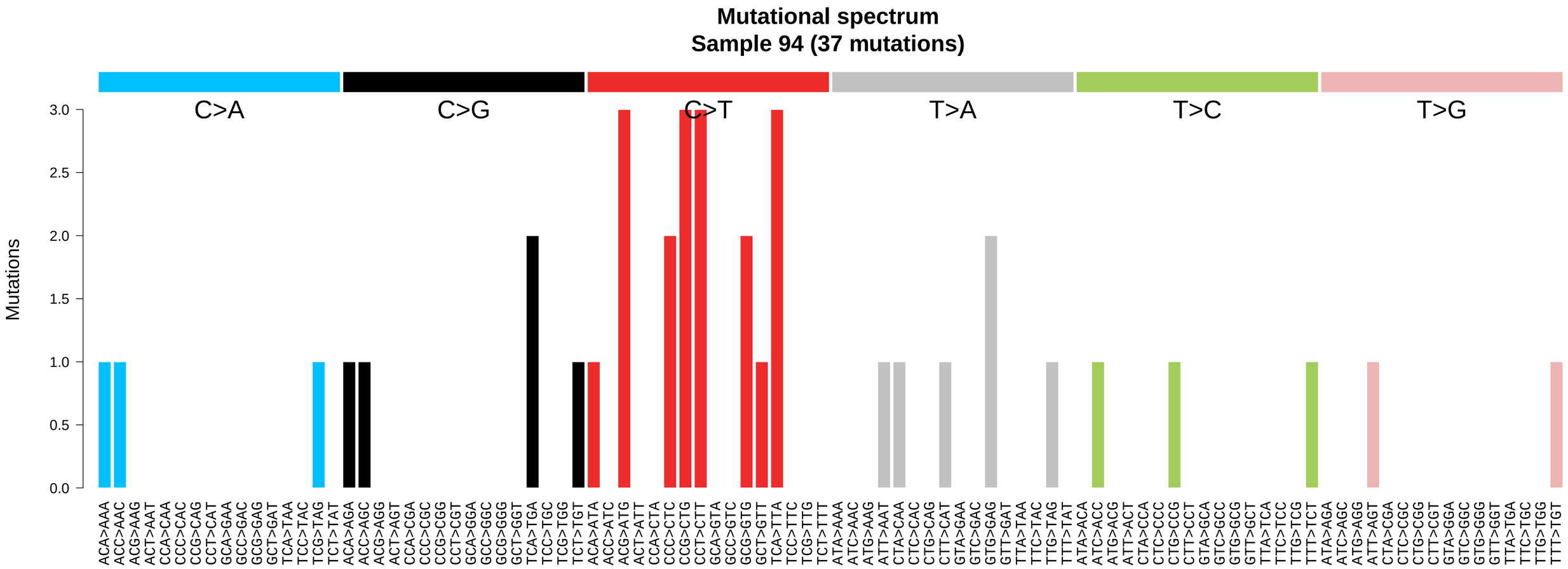

Reconstructed mutational spectrum
Cosine similarity = 0.547
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Signature A (0.031)
Signature B (0.024)
Signature C (0.04)
Signature D (0.033)
Signature E (0.043)
Signature F (0.033)
Signature G (0.036)
Signature H (0.039)
Signature I (0.034)
Signature J (0.03)
Signature K (0.037)
Signature L (0.034)
Signature M (0.023)
Signature N (0.036)
Signature O (0.034)
Signature P (0.036)
Signature Q (0.033)
Signature R (0.032)
Signature S (0.043)
Signature T (0.032)
Signature U (0.025)
Signature V (0.025)
Signature W (0.044)
Signature X (0.032)
Signature Y (0.037)
Signature Z (0.03)
Signature AA (0.025)
Signature AB (0.032)
Signature AC (0.031)
Signature AD (0.035)

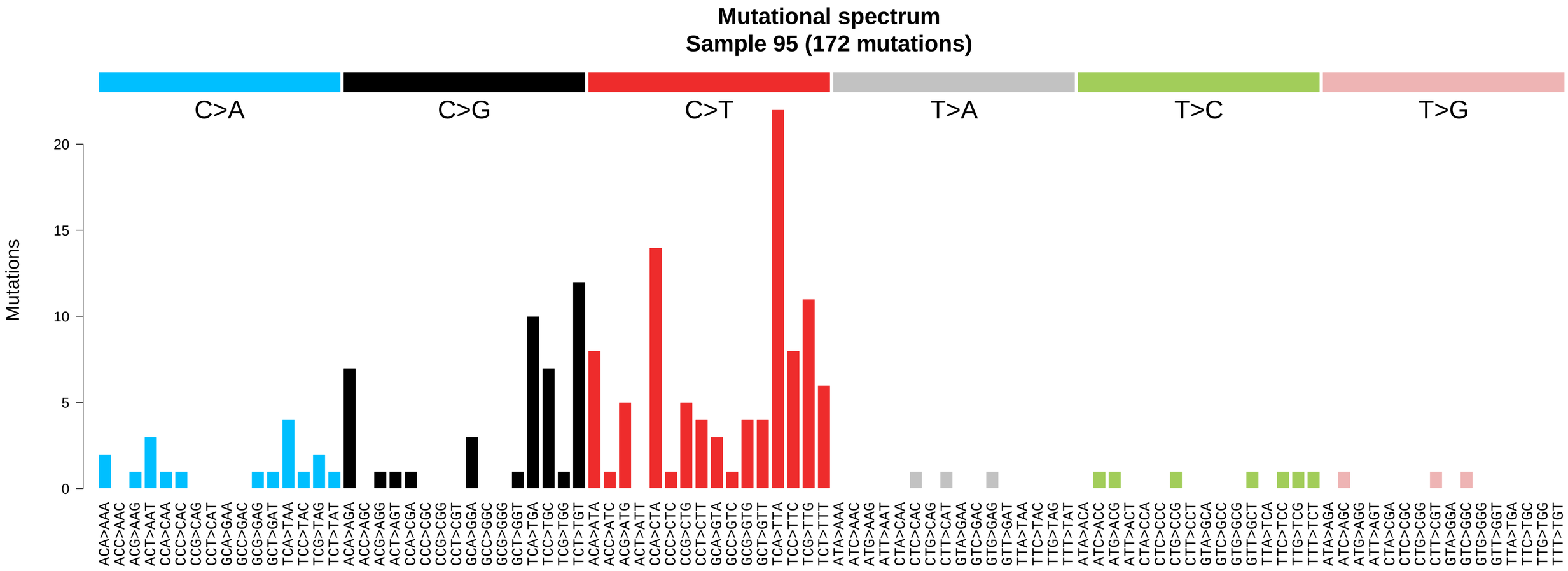

Mutational spectrum
Sample 90 (48 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.643
Signature A (0.029)
Signature B (0.026)
Signature C (0.15)
Signature D (0.035)
Signature E (0.043)
Signature F (0.026)
Signature G (0.054)
Signature H (0.035)
Signature I (0.025)
Signature J (0.021)
Signature K (0.026)
Signature L (0.025)
Signature M (0.042)
Signature N (0.021)
Signature O (0.02)
Signature P (0.036)
Signature Q (0.019)
Signature R (0.029)
Signature S (0.024)
Signature T (0.024)
Signature U (0.03)
Signature V (0.031)
Signature W (0.02)
Signature X (0.037)
Signature Y (0.039)
Signature Z (0.026)
Signature AA (0.028)
Signature AB (0.015)
Signature AC (0.027)
Signature AD (0.036)

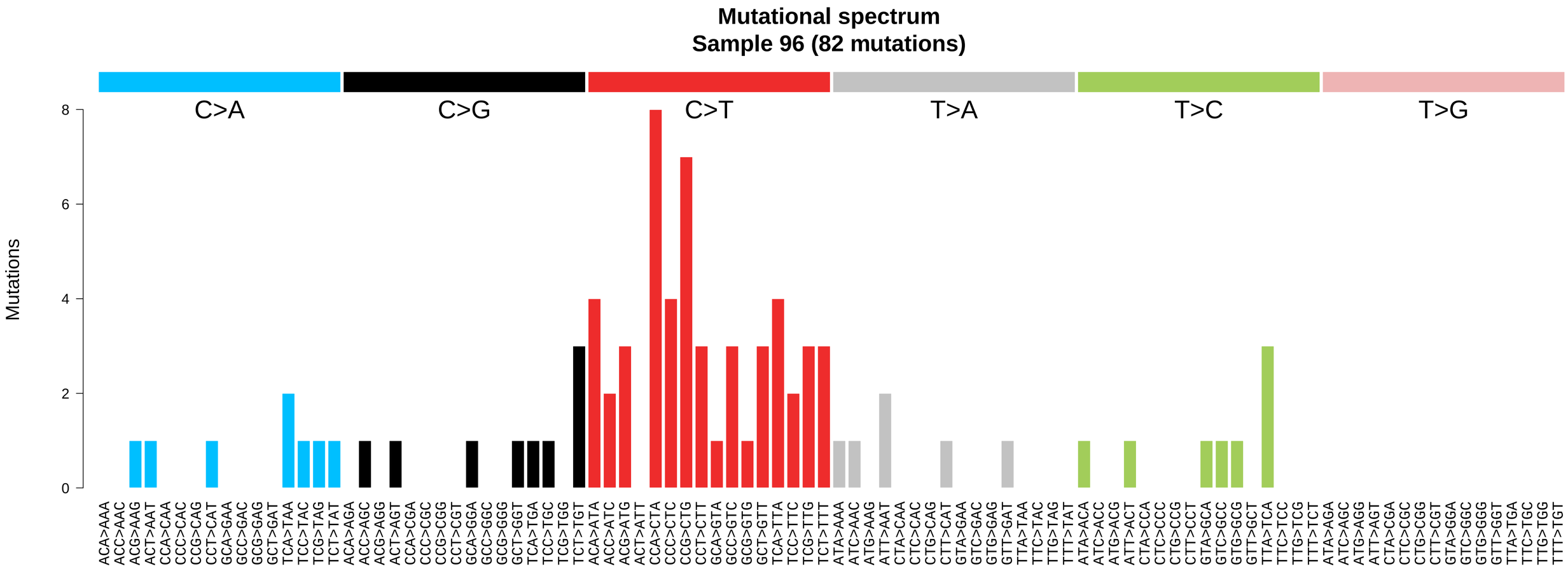

Mutational spectrum
Sample 91 (40 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.628
Signature A (0.043)
Signature B (0.02)
Signature C (0.039)
Signature D (0.028)
Signature E (0.037)
Signature F (0.037)
Signature G (0.033)
Signature H (0.024)
Signature I (0.024)
Signature J (0.02)
Signature K (0.036)
Signature L (0.039)
Signature M (0.023)
Signature N (0.029)
Signature O (0.023)
Signature P (0.034)
Signature Q (0.025)
Signature R (0.021)
Signature S (0.077)
Signature T (0.034)
Signature U (0.042)
Signature V (0.026)
Signature W (0.086)
Signature X (0.024)
Signature Y (0.033)
Signature Z (0.03)
Signature AA (0.021)
Signature AB (0.02)
Signature AC (0.023)
Signature AD (0.047)

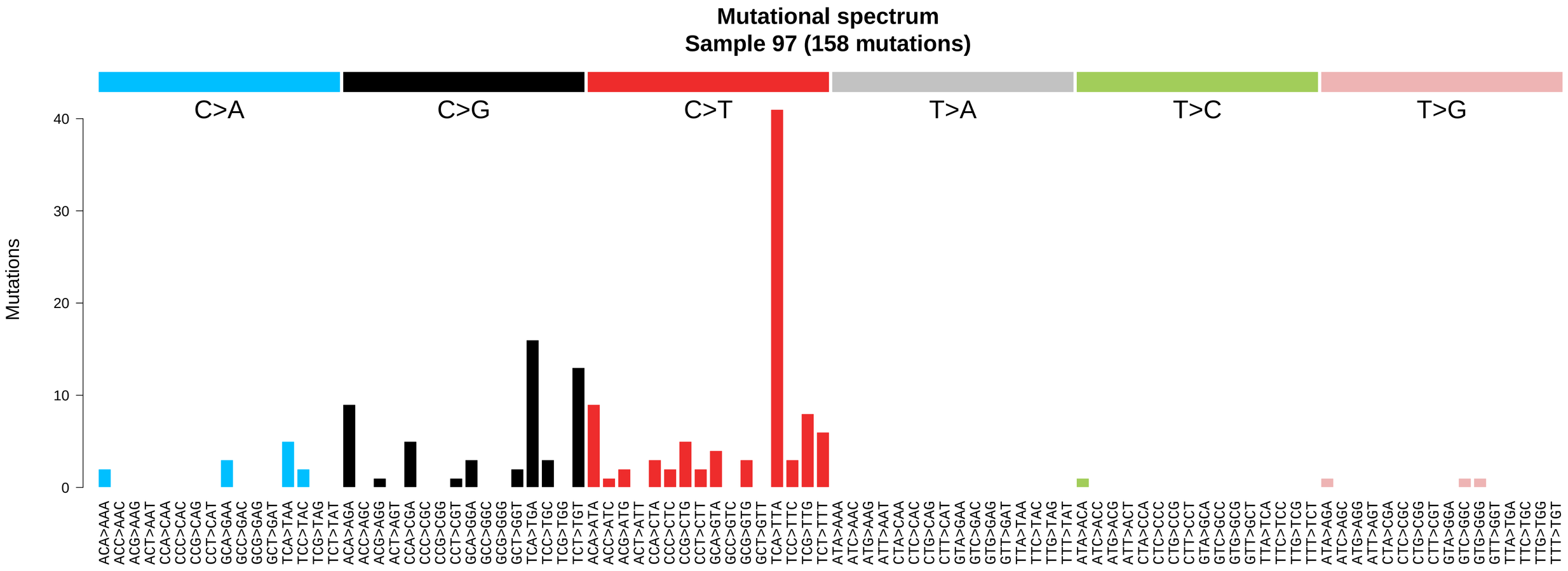

Mutational spectrum
Sample 92 (57 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.765
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
Signature A (0.044)
Signature B (0.148)
Signature C (0.037)
Signature D (0.024)
Signature E (0.029)
Signature F (0.028)
Signature G (0.047)
Signature H (0.032)
Signature I (0.021)
Signature J (0.024)
Signature K (0.028)
Signature L (0.021)
Signature M (0.122)
Signature N (0.023)
Signature O (0.019)
Signature P (0.023)
Signature Q (0.018)
Signature R (0.022)
Signature S (0.029)
Signature T (0.024)
Signature U (0.02)
Signature V (0.016)
Signature W (0.029)
Signature X (0.018)
Signature Y (0.021)
Signature Z (0.019)
Signature AA (0.017)
Signature AB (0.02)
Signature AC (0.035)
Signature AD (0.042)

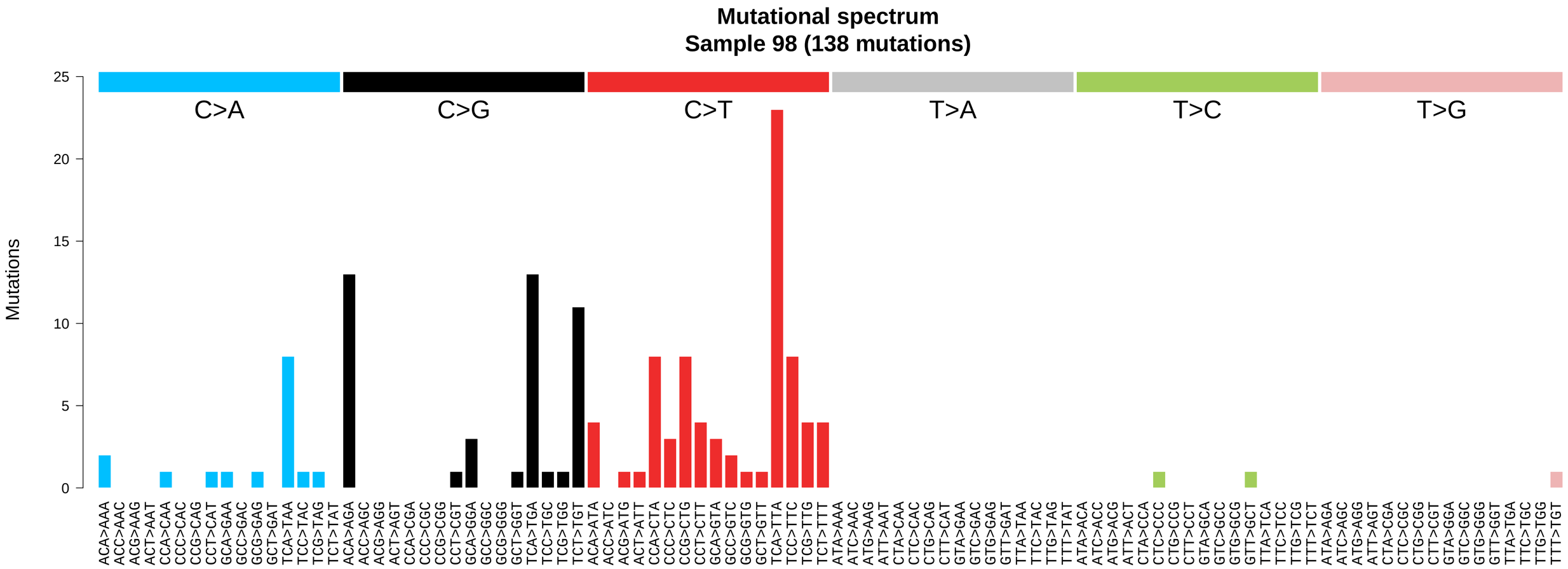

Mutational spectrum
Sample 93 (28 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.65
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
Signature A (0.05)
Signature B (0.02)
Signature C (0.039)
Signature D (0.029)
Signature E (0.039)
Signature F (0.056)
Signature G (0.026)
Signature H (0.034)
Signature I (0.036)
Signature J (0.021)
Signature K (0.027)
Signature L (0.038)
Signature M (0.031)
Signature N (0.035)
Signature O (0.05)
Signature P (0.032)
Signature Q (0.025)
Signature R (0.03)
Signature S (0.041)
Signature T (0.033)
Signature U (0.033)
Signature V (0.025)
Signature W (0.034)
Signature X (0.026)
Signature Y (0.039)
Signature Z (0.035)
Signature AA (0.03)
Signature AB (0.026)
Signature AC (0.027)
Signature AD (0.033)

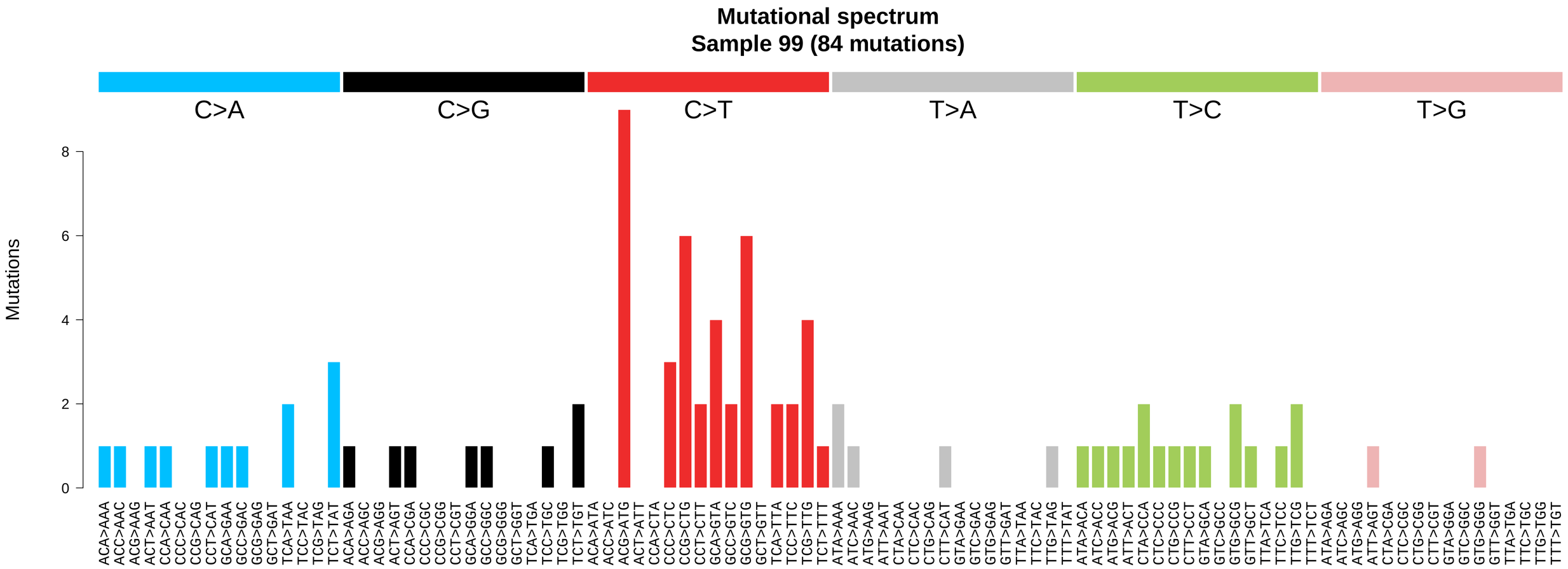

Mutational spectrum
Sample 94 (37 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.667
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Signature A (0.053)
Signature B (0.04)
Signature C (0.036)
Signature D (0.029)
Signature E (0.036)
Signature F (0.036)
Signature G (0.028)
Signature H (0.04)
Signature I (0.033)
Signature J (0.02)
Signature K (0.029)
Signature L (0.028)
Signature M (0.061)
Signature N (0.026)
Signature O (0.025)
Signature P (0.028)
Signature Q (0.027)
Signature R (0.023)
Signature S (0.043)
Signature T (0.027)
Signature U (0.024)
Signature V (0.047)
Signature W (0.038)
Signature X (0.022)
Signature Y (0.045)
Signature Z (0.025)
Signature AA (0.031)
Signature AB (0.041)
Signature AC (0.029)
Signature AD (0.029)

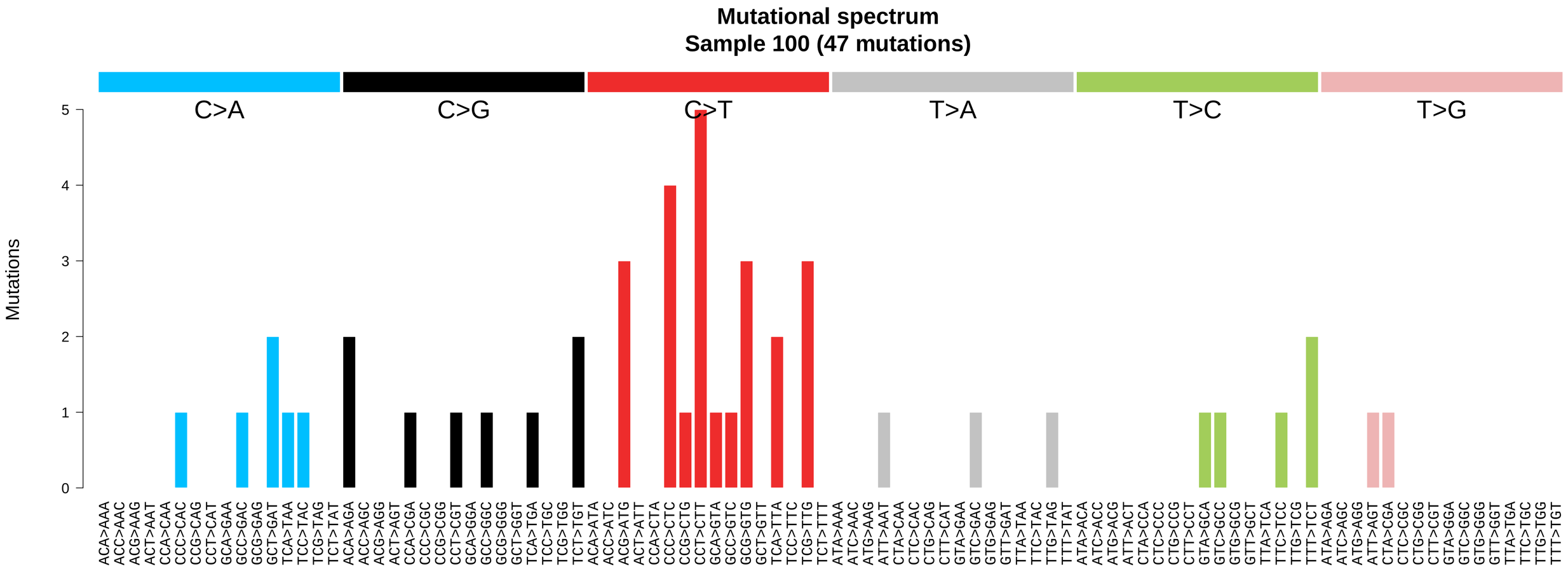

Mutational spectrum
Sample 95 (172 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.883
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
Signature A (0.031)
Signature B (0.166)
Signature C (0.076)
Signature D (0.023)
Signature E (0.032)
Signature F (0.019)
Signature G (0.055)
Signature H (0.019)
Signature I (0.012)
Signature J (0.018)
Signature K (0.016)
Signature L (0.013)
Signature M (0.196)
Signature N (0.015)
Signature O (0.013)
Signature P (0.018)
Signature Q (0.014)
Signature R (0.014)
Signature S (0.032)
Signature T (0.016)
Signature U (0.011)
Signature V (0.008)
Signature W (0.018)
Signature X (0.016)
Signature Y (0.017)
Signature Z (0.012)
Signature AA (0.009)
Signature AB (0.009)
Signature AC (0.017)
Signature AD (0.086)

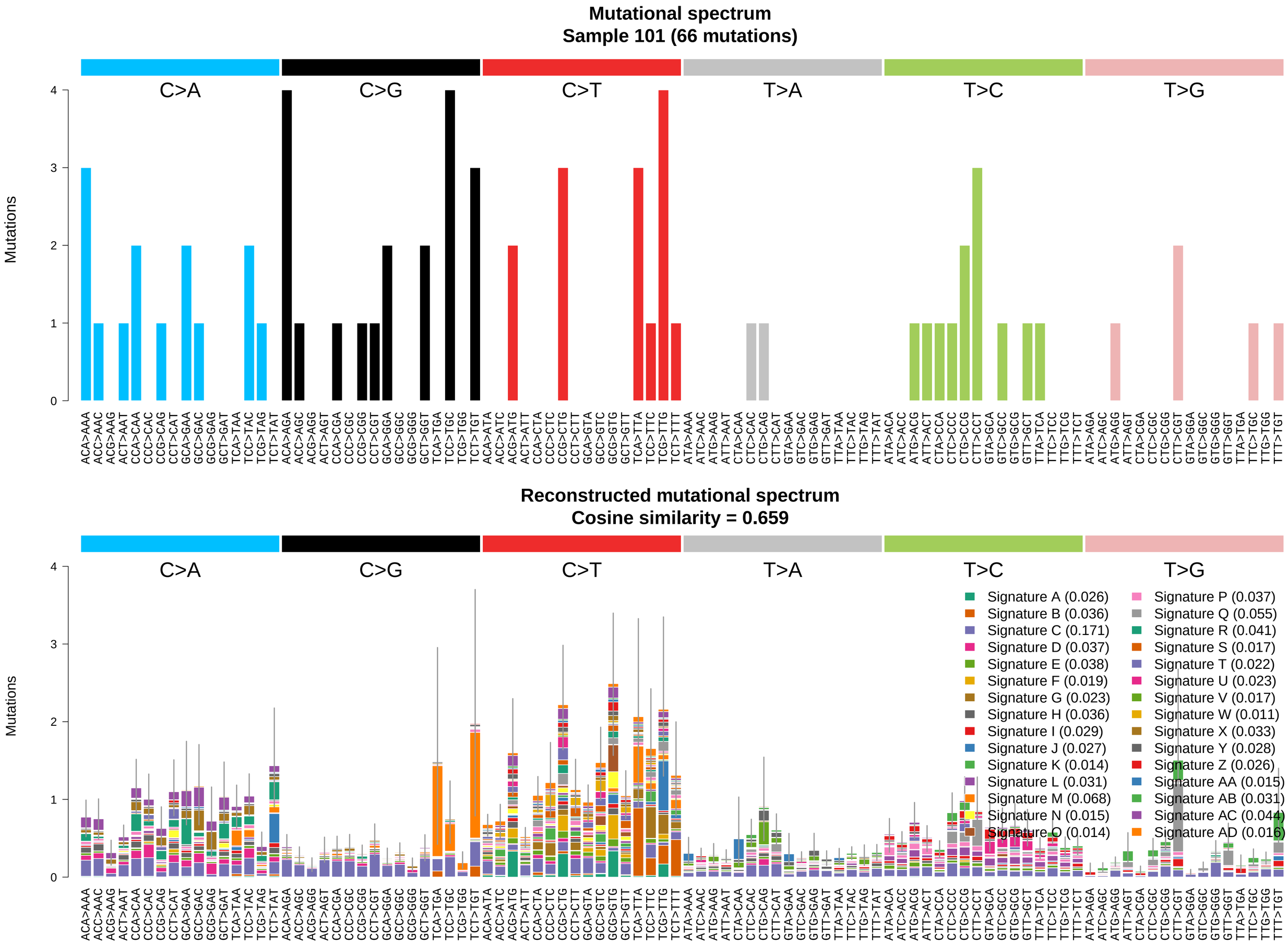

Mutational spectrum
Sample 96 (82 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.784
Signature A (0.043)
Signature B (0.054)
Signature C (0.037)
Signature D (0.023)
Signature E (0.041)
Signature F (0.028)
Signature G (0.054)
Signature H (0.032)
Signature I (0.021)
Signature J (0.022)
Signature K (0.04)
Signature L (0.031)
Signature M (0.059)
Signature N (0.023)
Signature O (0.02)
Signature P (0.034)
Signature Q (0.015)
Signature R (0.018)
Signature S (0.06)
Signature T (0.026)
Signature U (0.04)
Signature V (0.016)
Signature W (0.063)
Signature X (0.018)
Signature Y (0.031)
Signature Z (0.025)
Signature AA (0.021)
Signature AB (0.011)
Signature AC (0.021)
Signature AD (0.075)

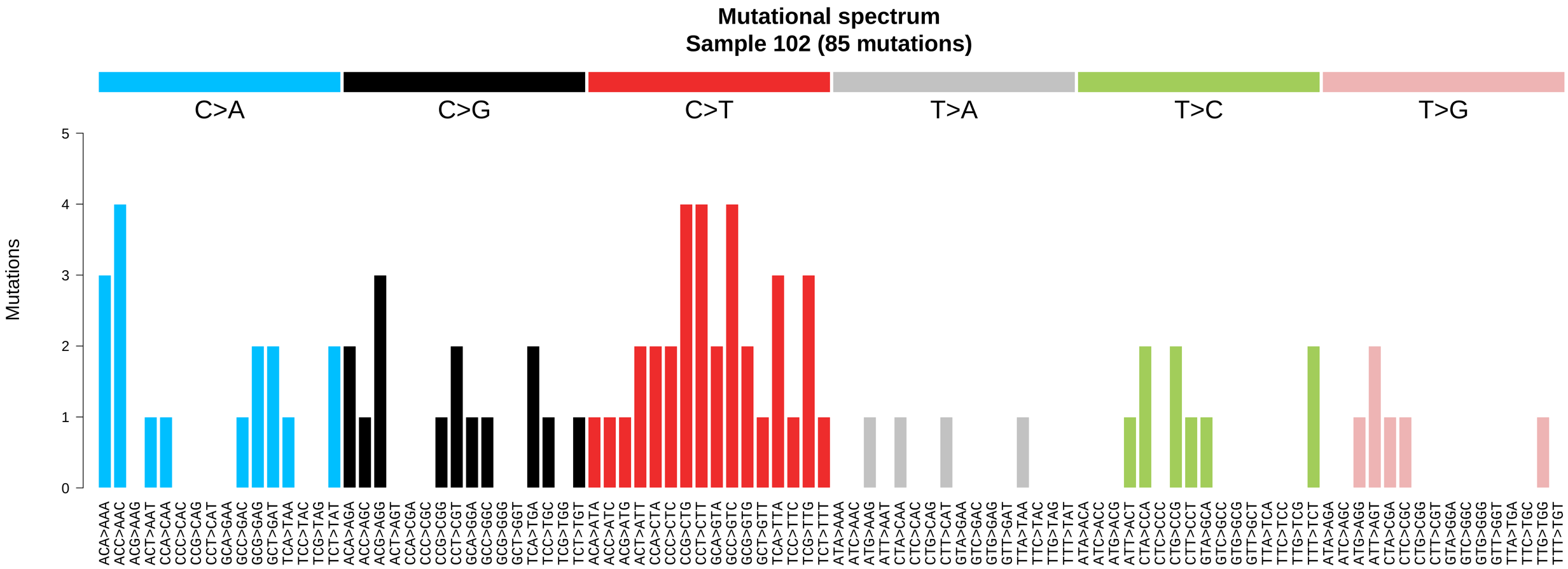

Mutational spectrum
Sample 97 (158 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
10
20
30
40
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.888
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
10
20
30
40
Signature A (0.022)
Signature B (0.303)
Signature C (0.106)
Signature D (0.013)
Signature E (0.018)
Signature F (0.015)
Signature G (0.016)
Signature H (0.016)
Signature I (0.012)
Signature J (0.01)
Signature K (0.012)
Signature L (0.008)
Signature M (0.241)
Signature N (0.011)
Signature O (0.01)
Signature P (0.012)
Signature Q (0.008)
Signature R (0.014)
Signature S (0.016)
Signature T (0.012)
Signature U (0.007)
Signature V (0.006)
Signature W (0.013)
Signature X (0.013)
Signature Y (0.013)
Signature Z (0.009)
Signature AA (0.009)
Signature AB (0.006)
Signature AC (0.013)
Signature AD (0.036)

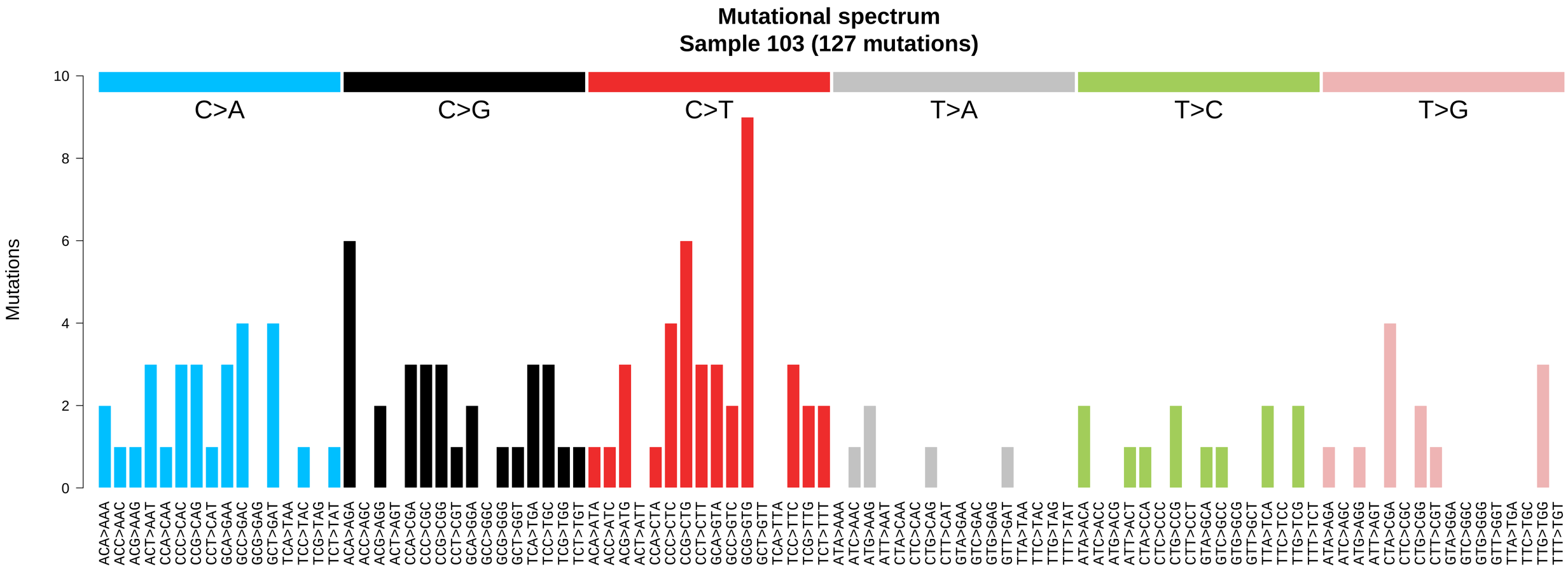

Mutational spectrum
Sample 98 (138 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
25
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.847
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
25
Signature A (0.019)
Signature B (0.177)
Signature C (0.087)
Signature D (0.02)
Signature E (0.025)
Signature F (0.017)
Signature G (0.06)
Signature H (0.016)
Signature I (0.012)
Signature J (0.011)
Signature K (0.024)
Signature L (0.012)
Signature M (0.247)
Signature N (0.013)
Signature O (0.01)
Signature P (0.013)
Signature Q (0.01)
Signature R (0.017)
Signature S (0.031)
Signature T (0.015)
Signature U (0.01)
Signature V (0.007)
Signature W (0.027)
Signature X (0.017)
Signature Y (0.014)
Signature Z (0.01)
Signature AA (0.01)
Signature AB (0.009)
Signature AC (0.018)
Signature AD (0.041)

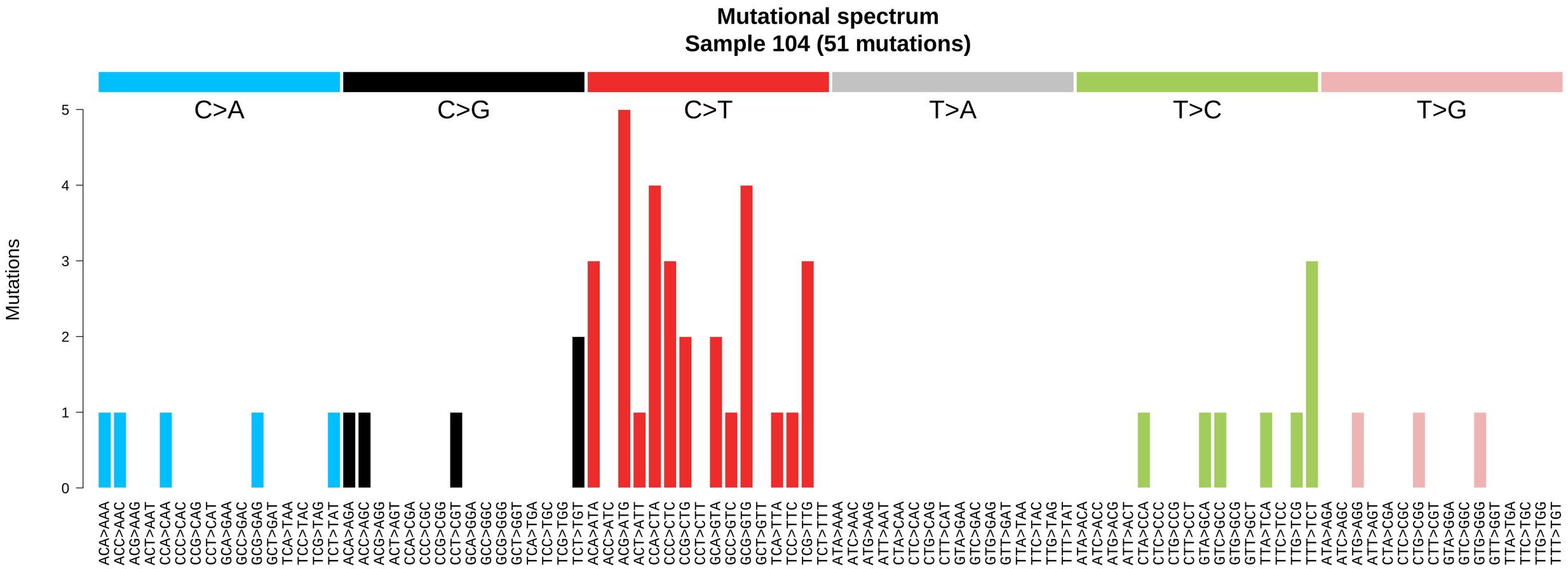

Mutational spectrum
Sample 99 (84 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.858
Signature A (0.112)
Signature B (0.025)
Signature C (0.045)
Signature D (0.022)
Signature E (0.04)
Signature F (0.045)
Signature G (0.026)
Signature H (0.036)
Signature I (0.029)
Signature J (0.04)
Signature K (0.022)
Signature L (0.035)
Signature M (0.031)
Signature N (0.029)
Signature O (0.028)
Signature P (0.032)
Signature Q (0.017)
Signature R (0.027)
Signature S (0.036)
Signature T (0.032)
Signature U (0.051)
Signature V (0.019)
Signature W (0.023)
Signature X (0.021)
Signature Y (0.028)
Signature Z (0.05)
Signature AA (0.027)
Signature AB (0.018)
Signature AC (0.029)
Signature AD (0.024)

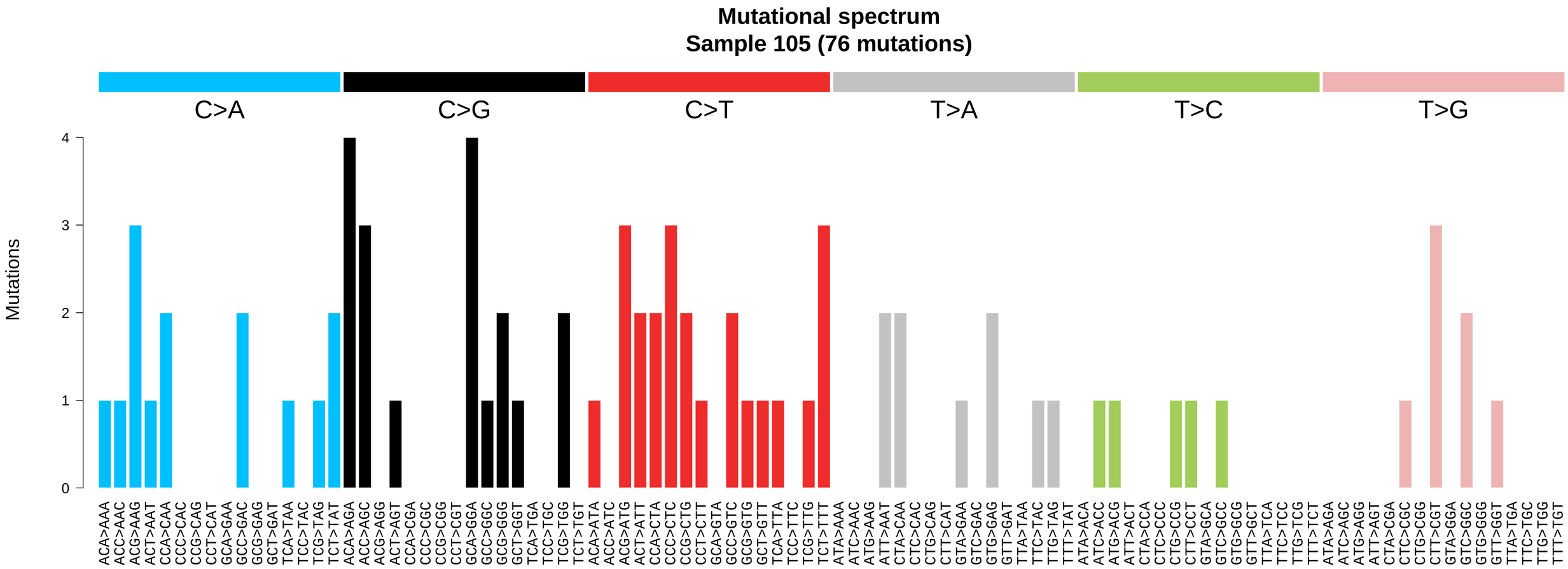

Mutational spectrum
Sample 100 (47 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.691
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
Signature A (0.042)
Signature B (0.032)
Signature C (0.049)
Signature D (0.029)
Signature E (0.036)
Signature F (0.031)
Signature G (0.038)
Signature H (0.035)
Signature I (0.047)
Signature J (0.033)
Signature K (0.033)
Signature L (0.031)
Signature M (0.055)
Signature N (0.031)
Signature O (0.031)
Signature P (0.029)
Signature Q (0.018)
Signature R (0.023)
Signature S (0.05)
Signature T (0.023)
Signature U (0.035)
Signature V (0.021)
Signature W (0.051)
Signature X (0.034)
Signature Y (0.028)
Signature Z (0.028)
Signature AA (0.018)
Signature AB (0.025)
Signature AC (0.028)
Signature AD (0.034)

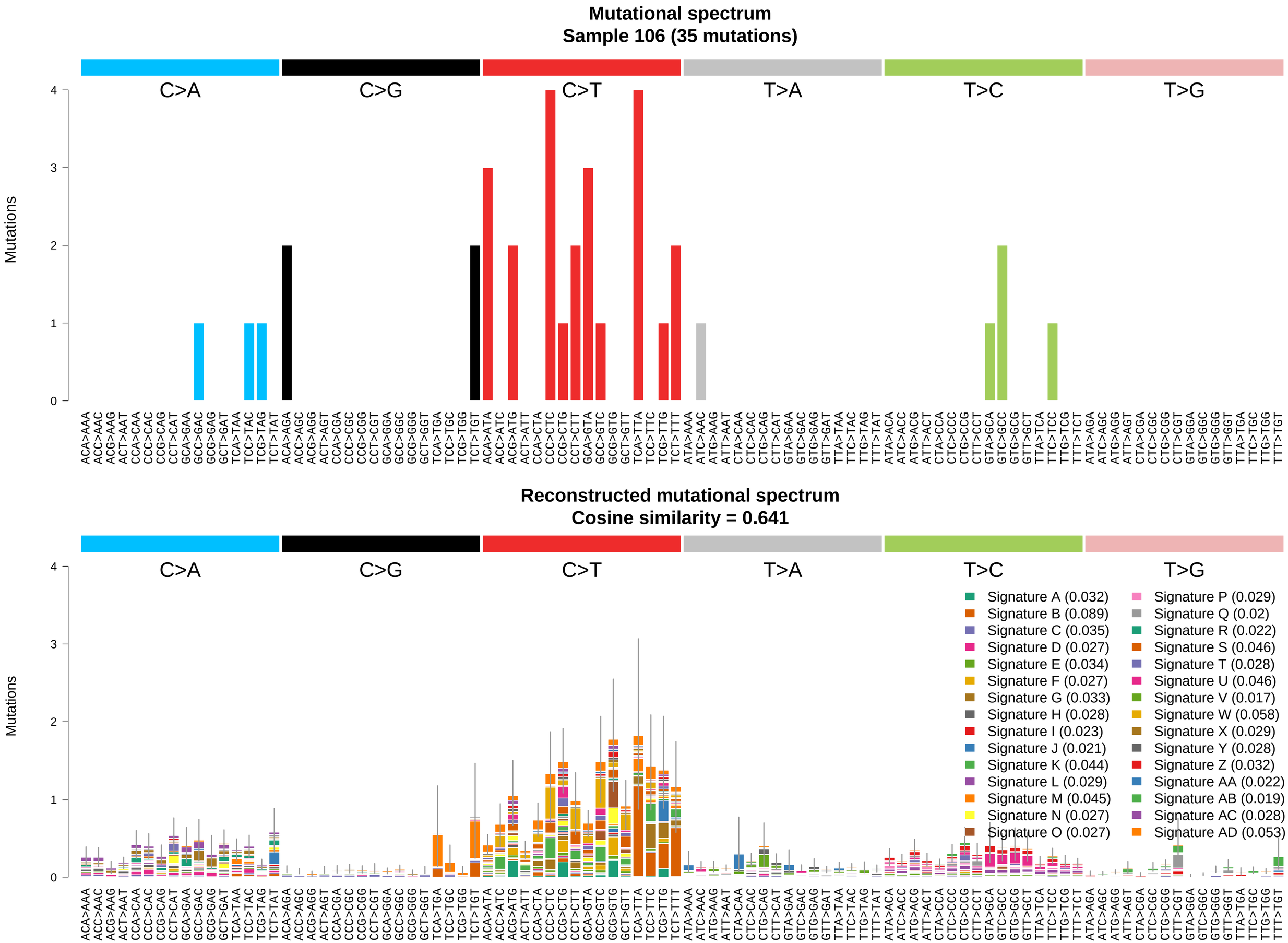

Mutational spectrum
Sample 101 (66 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.659
Signature A (0.026)
Signature B (0.036)
Signature C (0.171)
Signature D (0.037)
Signature E (0.038)
Signature F (0.019)
Signature G (0.023)
Signature H (0.036)
Signature I (0.029)
Signature J (0.027)
Signature K (0.014)
Signature L (0.031)
Signature M (0.068)
Signature N (0.015)
Signature O (0.014)
Signature P (0.037)
Signature Q (0.055)
Signature R (0.041)
Signature S (0.017)
Signature T (0.022)
Signature U (0.023)
Signature V (0.017)
Signature W (0.011)
Signature X (0.033)
Signature Y (0.028)
Signature Z (0.026)
Signature AA (0.015)
Signature AB (0.031)
Signature AC (0.044)
Signature AD (0.016)

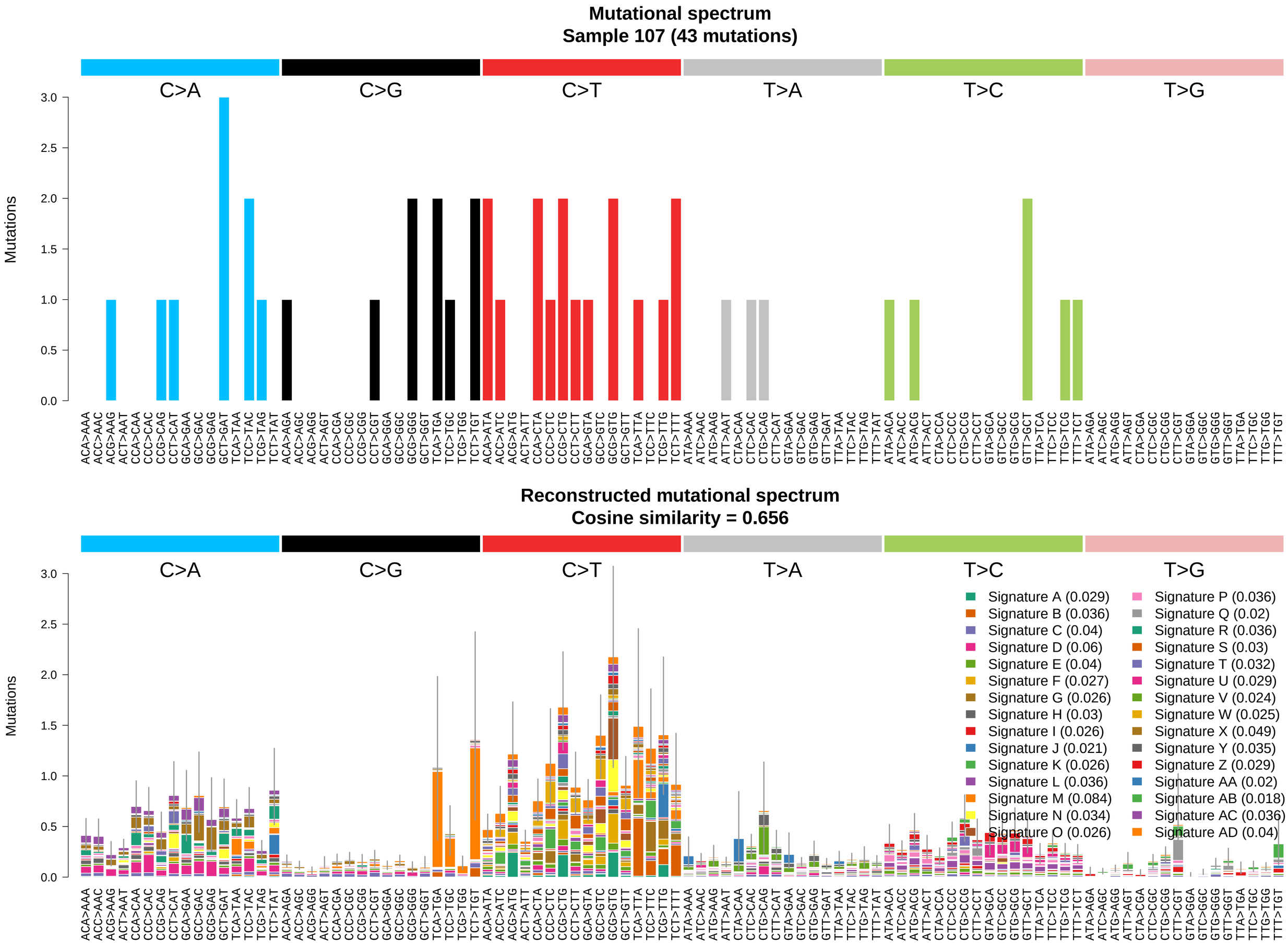

Mutational spectrum
Sample 102 (85 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.76
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
Signature A (0.026)
Signature B (0.029)
Signature C (0.148)
Signature D (0.039)
Signature E (0.049)
Signature F (0.024)
Signature G (0.026)
Signature H (0.042)
Signature I (0.039)
Signature J (0.027)
Signature K (0.028)
Signature L (0.025)
Signature M (0.036)
Signature N (0.021)
Signature O (0.02)
Signature P (0.034)
Signature Q (0.02)
Signature R (0.029)
Signature S (0.034)
Signature T (0.022)
Signature U (0.019)
Signature V (0.015)
Signature W (0.04)
Signature X (0.03)
Signature Y (0.022)
Signature Z (0.022)
Signature AA (0.026)
Signature AB (0.026)
Signature AC (0.038)
Signature AD (0.043)

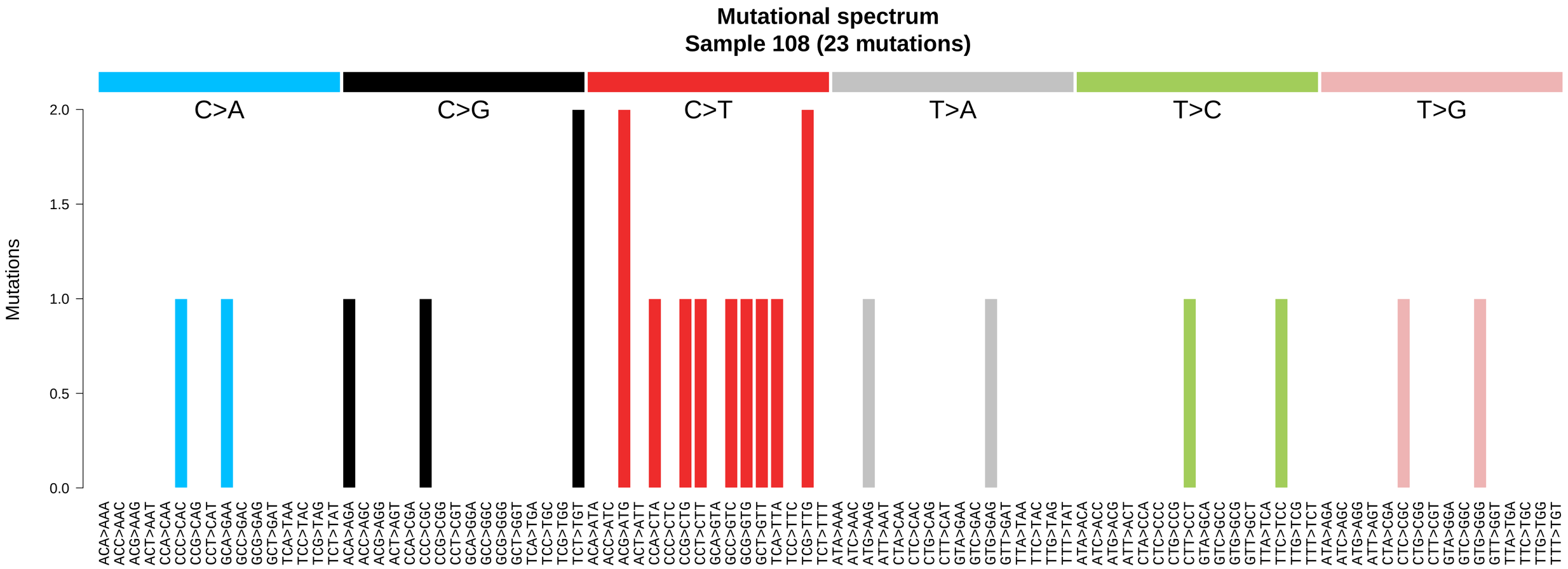

Mutational spectrum
Sample 103 (127 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.783
Signature A (0.032)
Signature B (0.012)
Signature C (0.228)
Signature D (0.056)
Signature E (0.039)
Signature F (0.035)
Signature G (0.019)
Signature H (0.034)
Signature I (0.059)
Signature J (0.014)
Signature K (0.02)
Signature L (0.019)
Signature M (0.029)
Signature N (0.028)
Signature O (0.03)
Signature P (0.025)
Signature Q (0.012)
Signature R (0.032)
Signature S (0.023)
Signature T (0.02)
Signature U (0.017)
Signature V (0.013)
Signature W (0.018)
Signature X (0.045)
Signature Y (0.023)
Signature Z (0.019)
Signature AA (0.01)
Signature AB (0.015)
Signature AC (0.043)
Signature AD (0.033)

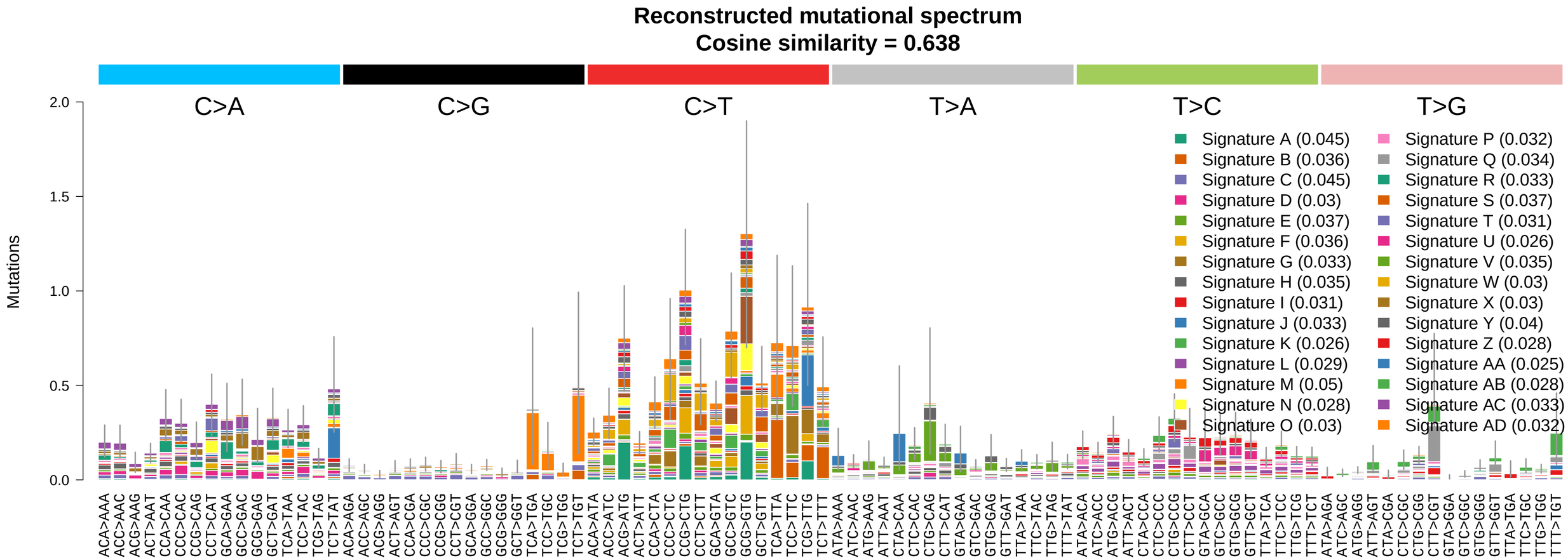

Mutational spectrum
Sample 104 (51 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.726
Signature A (0.078)
Signature B (0.025)
Signature C (0.052)
Signature D (0.025)
Signature E (0.047)
Signature F (0.044)
Signature G (0.035)
Signature H (0.031)
Signature I (0.031)
Signature J (0.032)
Signature K (0.03)
Signature L (0.039)
Signature M (0.031)
Signature N (0.031)
Signature O (0.031)
Signature P (0.033)
Signature Q (0.02)
Signature R (0.024)
Signature S (0.04)
Signature T (0.029)
Signature U (0.035)
Signature V (0.015)
Signature W (0.034)
Signature X (0.024)
Signature Y (0.031)
Signature Z (0.036)
Signature AA (0.019)
Signature AB (0.02)
Signature AC (0.03)
Signature AD (0.048)

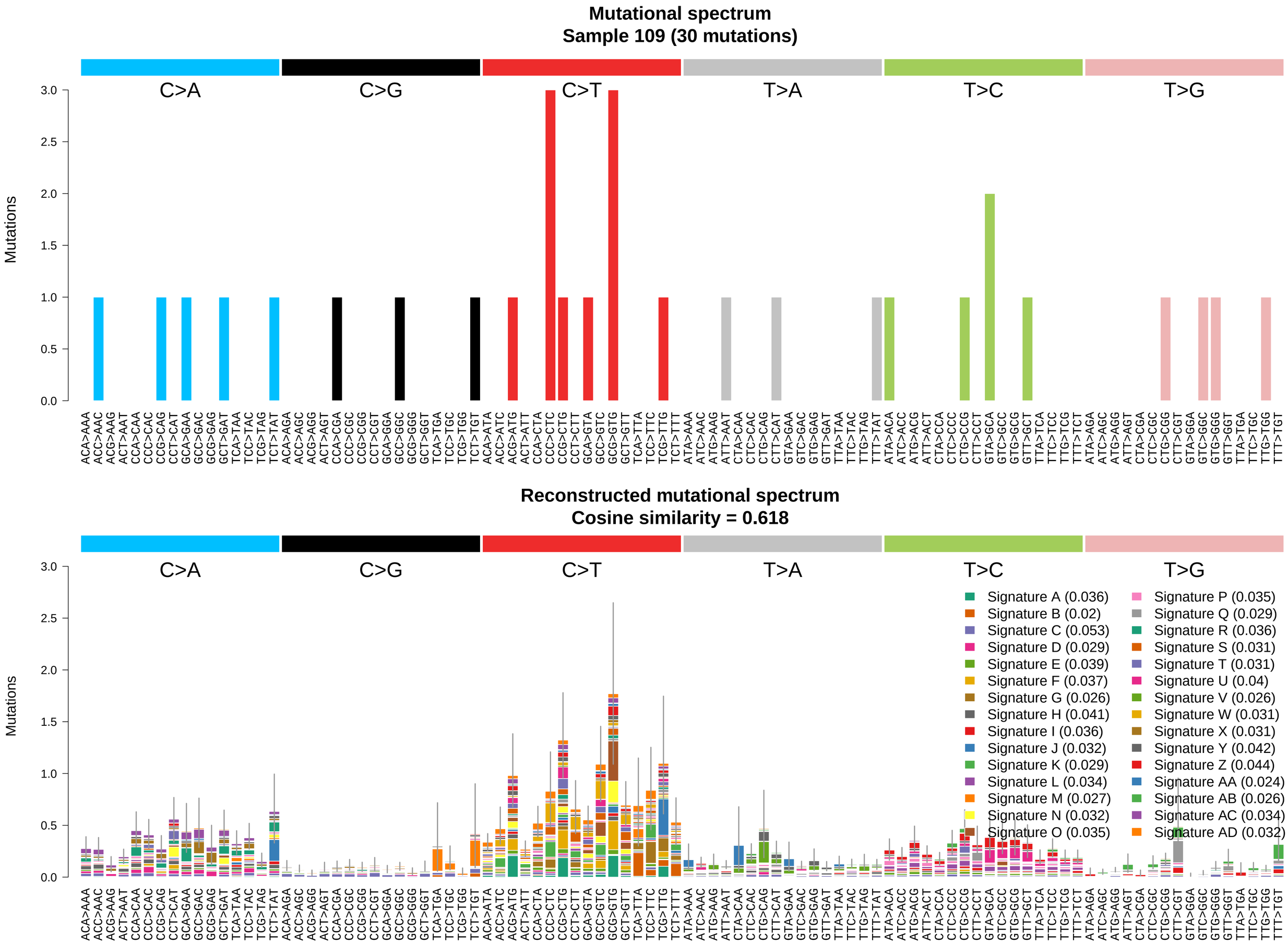

Mutational spectrum
Sample 105 (76 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.614
Signature A (0.023)
Signature B (0.022)
Signature C (0.17)
Signature D (0.073)
Signature E (0.041)
Signature F (0.019)
Signature G (0.02)
Signature H (0.039)
Signature I (0.027)
Signature J (0.021)
Signature K (0.025)
Signature L (0.02)
Signature M (0.016)
Signature N (0.018)
Signature O (0.019)
Signature P (0.029)
Signature Q (0.059)
Signature R (0.02)
Signature S (0.028)
Signature T (0.021)
Signature U (0.016)
Signature V (0.024)
Signature W (0.025)
Signature X (0.047)
Signature Y (0.034)
Signature Z (0.02)
Signature AA (0.038)
Signature AB (0.018)
Signature AC (0.034)
Signature AD (0.036)

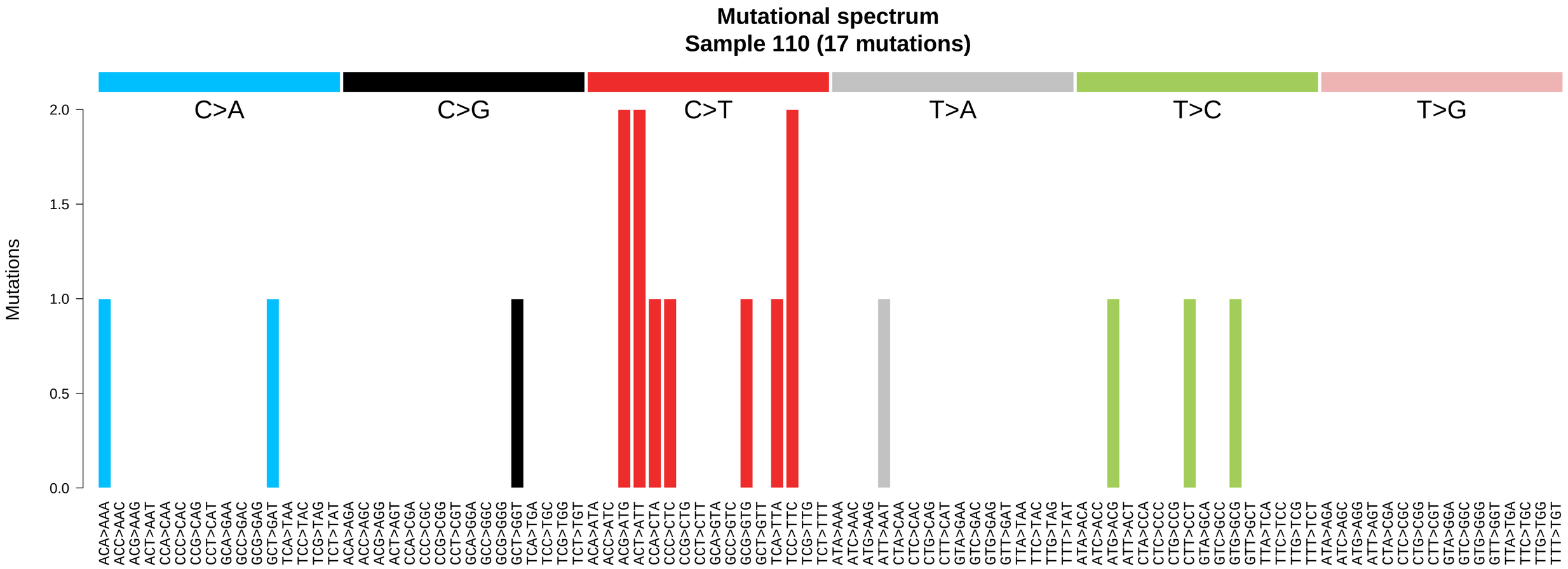

Mutational spectrum
Sample 106 (35 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.641
Signature A (0.032)
Signature B (0.089)
Signature C (0.035)
Signature D (0.027)
Signature E (0.034)
Signature F (0.027)
Signature G (0.033)
Signature H (0.028)
Signature I (0.023)
Signature J (0.021)
Signature K (0.044)
Signature L (0.029)
Signature M (0.045)
Signature N (0.027)
Signature O (0.027)
Signature P (0.029)
Signature Q (0.02)
Signature R (0.022)
Signature S (0.046)
Signature T (0.028)
Signature U (0.046)
Signature V (0.017)
Signature W (0.058)
Signature X (0.029)
Signature Y (0.028)
Signature Z (0.032)
Signature AA (0.022)
Signature AB (0.019)
Signature AC (0.028)
Signature AD (0.053)

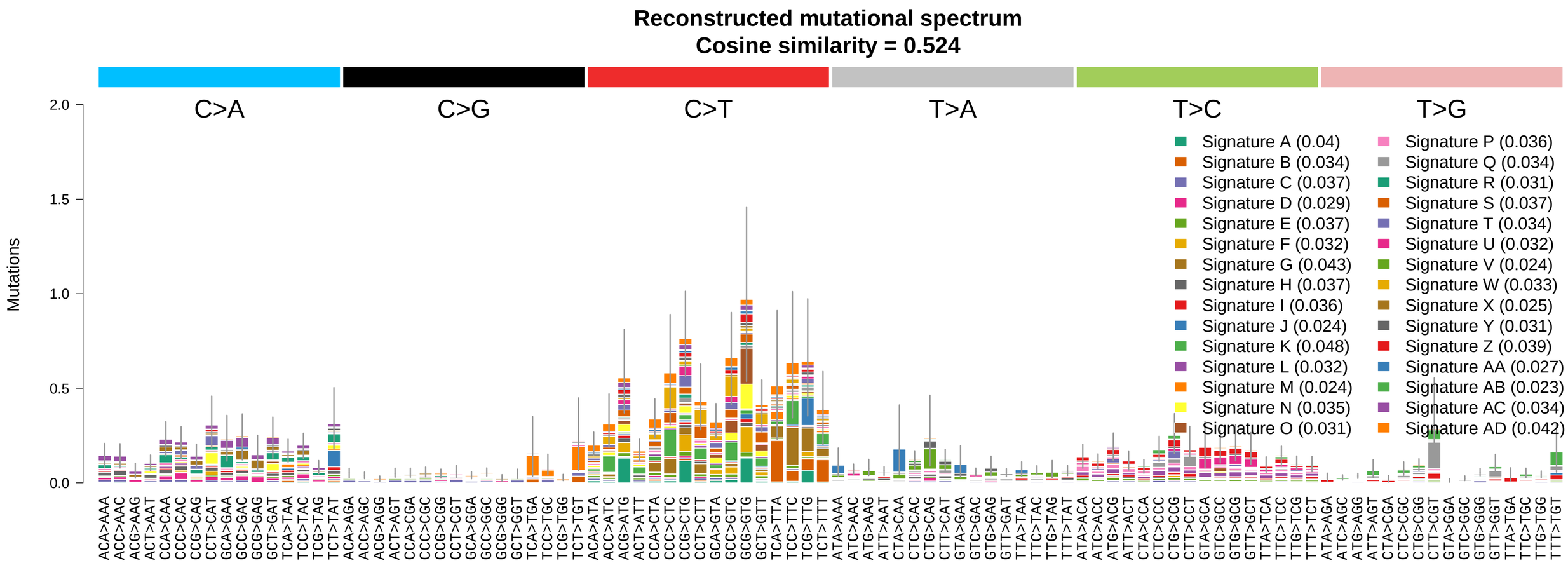

Mutational spectrum
Sample 107 (43 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.656
Signature A (0.029)
Signature B (0.036)
Signature C (0.04)
Signature D (0.06)
Signature E (0.04)
Signature F (0.027)
Signature G (0.026)
Signature H (0.03)
Signature I (0.026)
Signature J (0.021)
Signature K (0.026)
Signature L (0.036)
Signature M (0.084)
Signature N (0.034)
Signature O (0.026)
Signature P (0.036)
Signature Q (0.02)
Signature R (0.036)
Signature S (0.03)
Signature T (0.032)
Signature U (0.029)
Signature V (0.024)
Signature W (0.025)
Signature X (0.049)
Signature Y (0.035)
Signature Z (0.029)
Signature AA (0.02)
Signature AB (0.018)
Signature AC (0.036)
Signature AD (0.04)

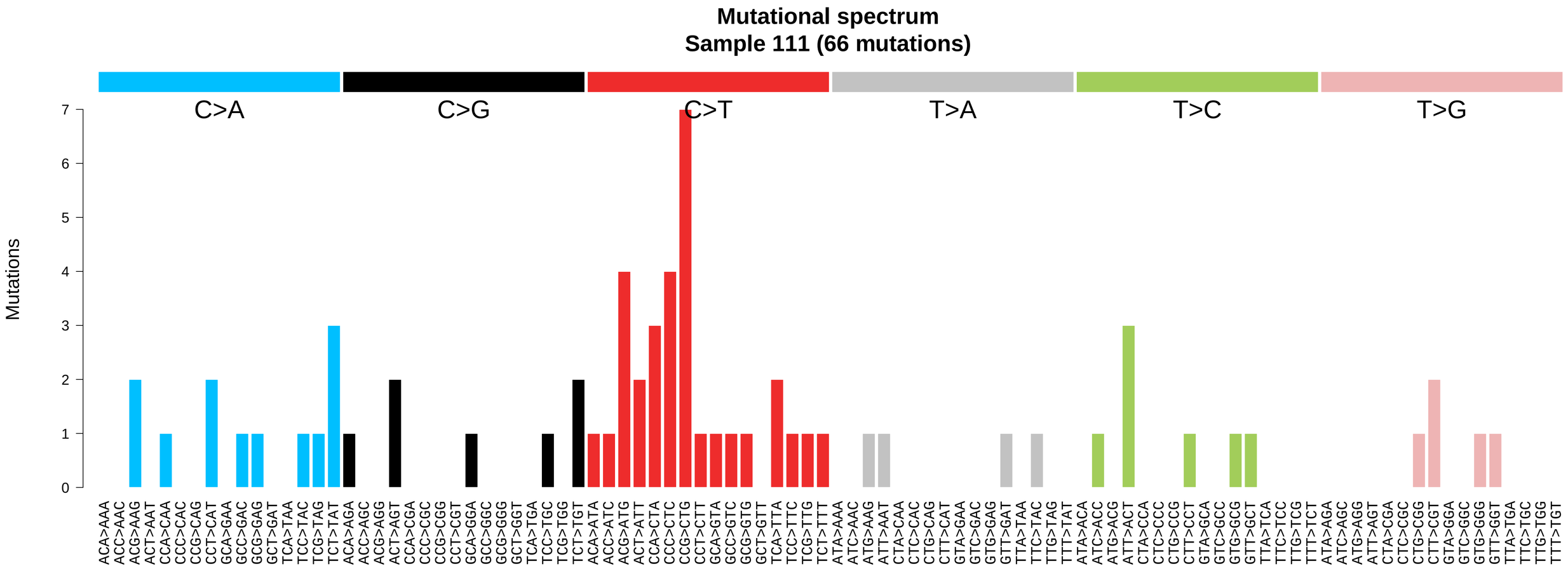

Mutational spectrum
Sample 108 (23 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

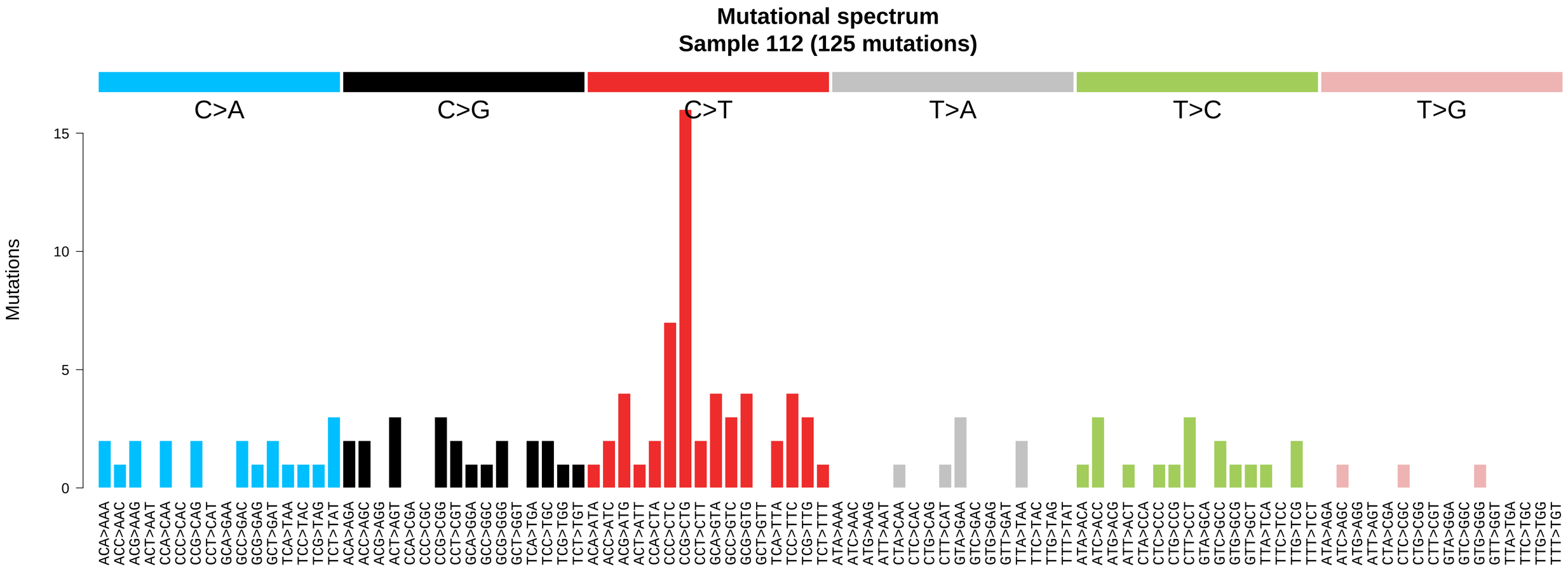

Reconstructed mutational spectrum
Cosine similarity = 0.638
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
2.0
1.5
1.0
0.5
0.0
Signature A (0.045)
Signature B (0.036)
Signature C (0.045)
Signature D (0.03)
Signature E (0.037)
Signature F (0.036)
Signature G (0.033)
Signature H (0.035)
Signature I (0.031)
Signature J (0.033)
Signature K (0.026)
Signature L (0.029)
Signature M (0.05)
Signature N (0.028)
Signature O (0.03)
Signature P (0.032)
Signature Q (0.034)
Signature R (0.033)
Signature S (0.037)
Signature T (0.031)
Signature U (0.026)
Signature V (0.035)
Signature W (0.03)
Signature X (0.03)
Signature Y (0.04)
Signature Z (0.028)
Signature AA (0.025)
Signature AB (0.028)
Signature AC (0.033)
Signature AD (0.032)

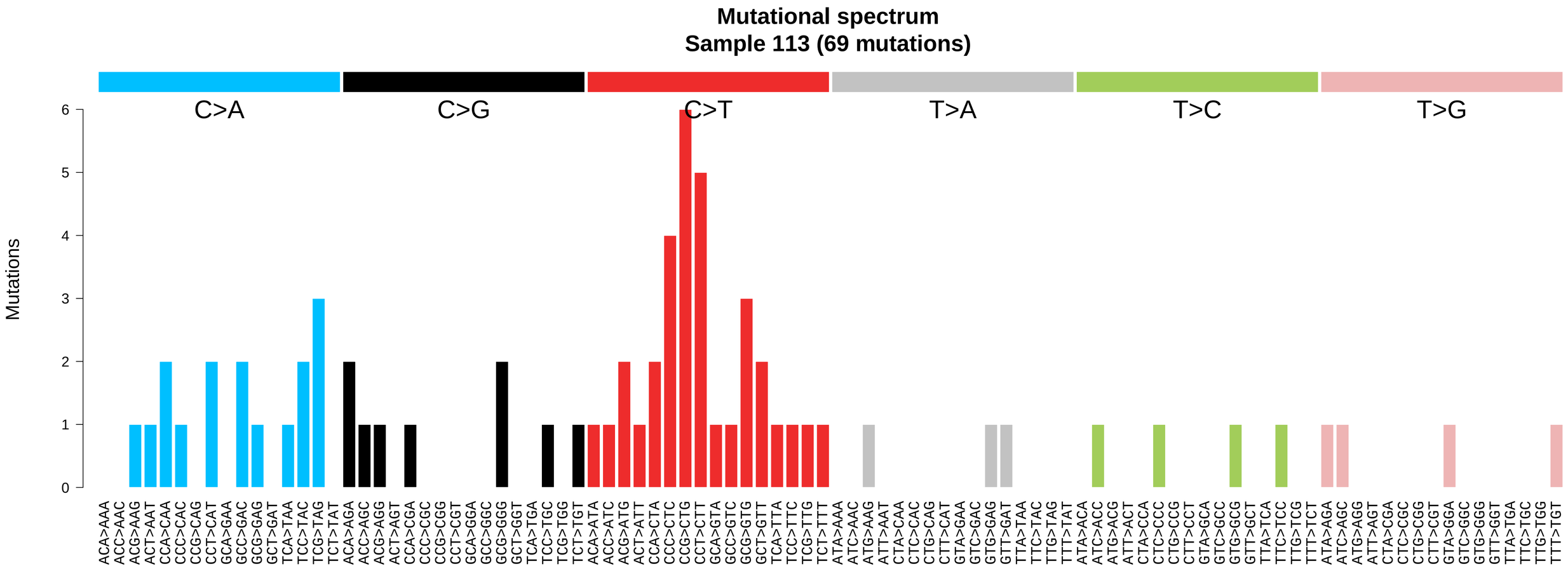

Mutational spectrum
Sample 109 (30 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.618
Signature A (0.036)
Signature B (0.02)
Signature C (0.053)
Signature D (0.029)
Signature E (0.039)
Signature F (0.037)
Signature G (0.026)
Signature H (0.041)
Signature I (0.036)
Signature J (0.032)
Signature K (0.029)
Signature L (0.034)
Signature M (0.027)
Signature N (0.032)
Signature O (0.035)
Signature P (0.035)
Signature Q (0.029)
Signature R (0.036)
Signature S (0.031)
Signature T (0.031)
Signature U (0.04)
Signature V (0.026)
Signature W (0.031)
Signature X (0.031)
Signature Y (0.042)
Signature Z (0.044)
Signature AA (0.024)
Signature AB (0.026)
Signature AC (0.034)
Signature AD (0.032)

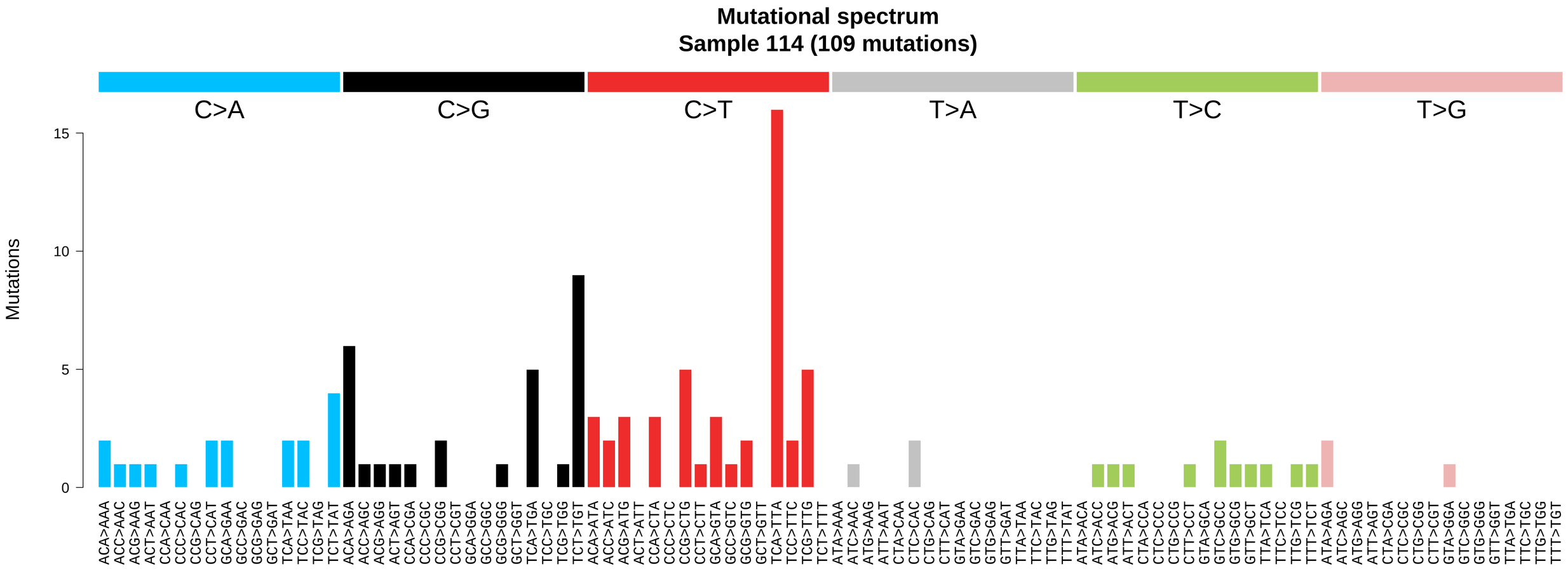

Mutational spectrum
Sample 110 (17 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

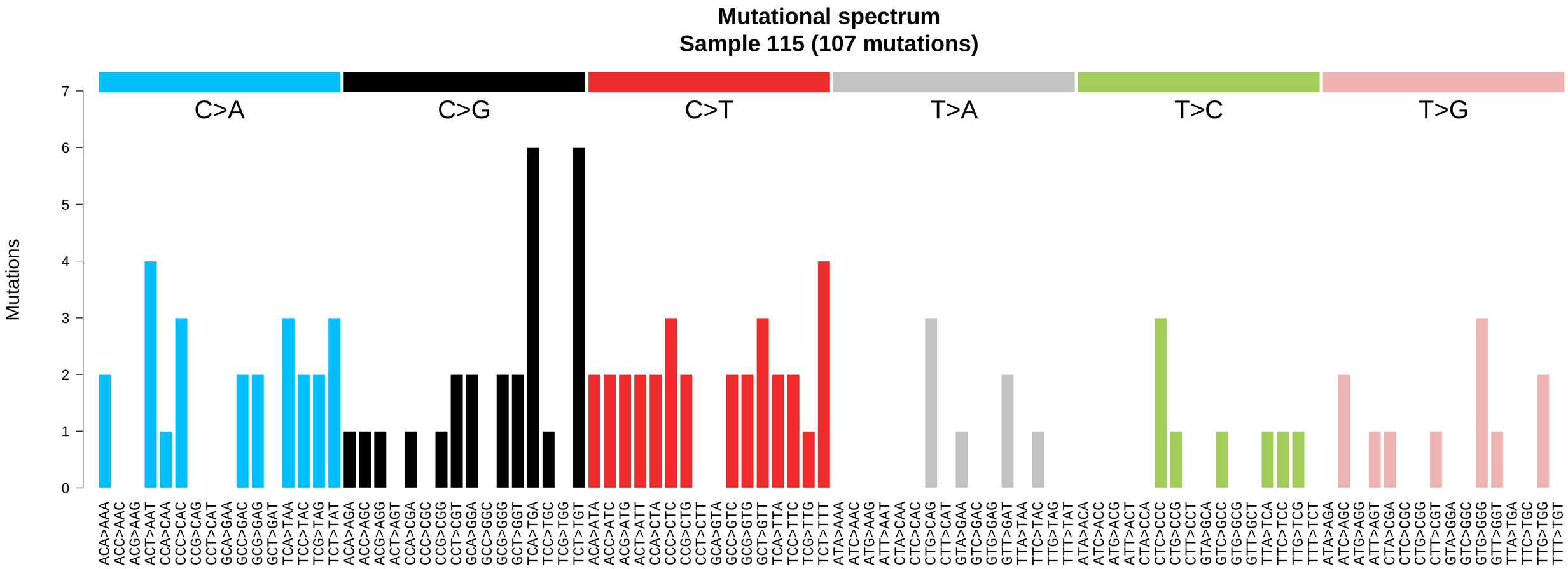

Reconstructed mutational spectrum
Cosine similarity = 0.524
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
2.0
1.5
1.0
0.5
0.0
Signature A (0.04)
Signature B (0.034)
Signature C (0.037)
Signature D (0.029)
Signature E (0.037)
Signature F (0.032)
Signature G (0.043)
Signature H (0.037)
Signature I (0.036)
Signature J (0.024)
Signature K (0.048)
Signature L (0.032)
Signature M (0.024)
Signature N (0.035)
Signature O (0.031)
Signature P (0.036)
Signature Q (0.034)
Signature R (0.031)
Signature S (0.037)
Signature T (0.034)
Signature U (0.032)
Signature V (0.024)
Signature W (0.033)
Signature X (0.025)
Signature Y (0.031)
Signature Z (0.039)
Signature AA (0.027)
Signature AB (0.023)
Signature AC (0.034)
Signature AD (0.042)

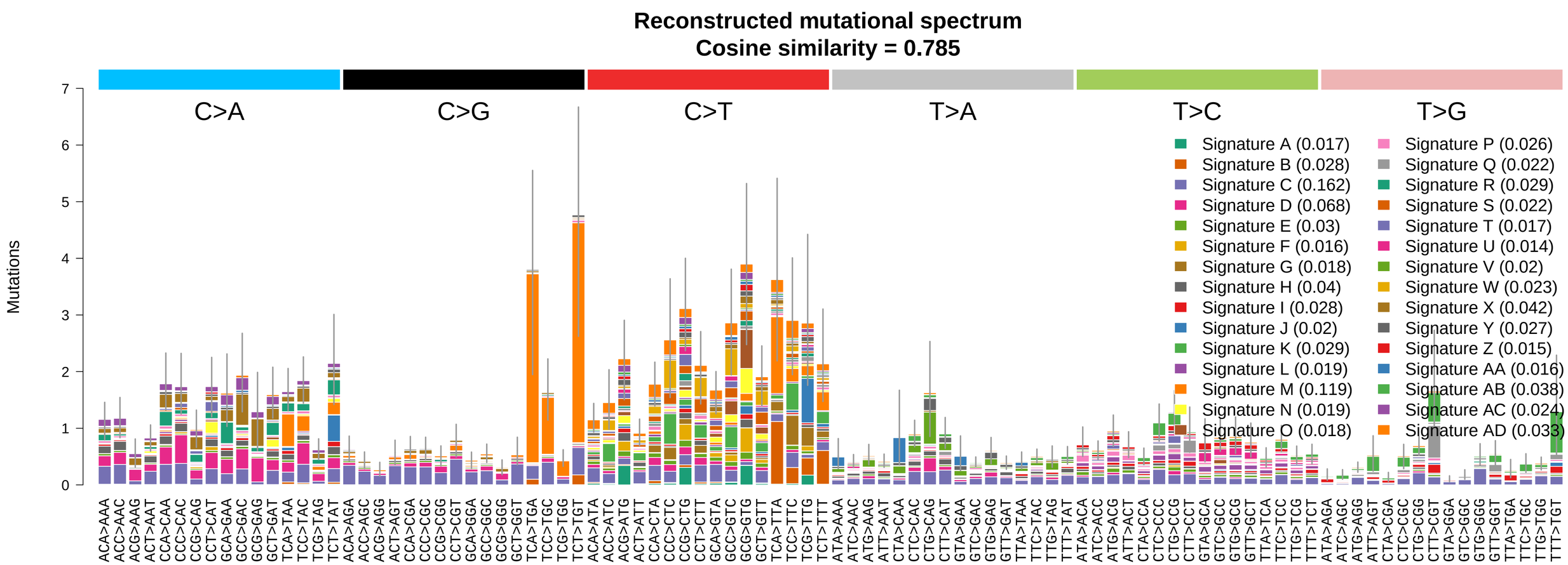

Mutational spectrum
Sample 111 (66 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
7
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.722
Signature A (0.048)
Signature B (0.027)
Signature C (0.053)
Signature D (0.036)
Signature E (0.048)
Signature F (0.032)
Signature G (0.029)
Signature H (0.043)
Signature I (0.031)
Signature J (0.028)
Signature K (0.037)
Signature L (0.027)
Signature M (0.033)
Signature N (0.028)
Signature O (0.019)
Signature P (0.04)
Signature Q (0.042)
Signature R (0.03)
Signature S (0.046)
Signature T (0.037)
Signature U (0.027)
Signature V (0.017)
Signature W (0.033)
Signature X (0.033)
Signature Y (0.032)
Signature Z (0.027)
Signature AA (0.017)
Signature AB (0.02)
Signature AC (0.036)
Signature AD (0.044)

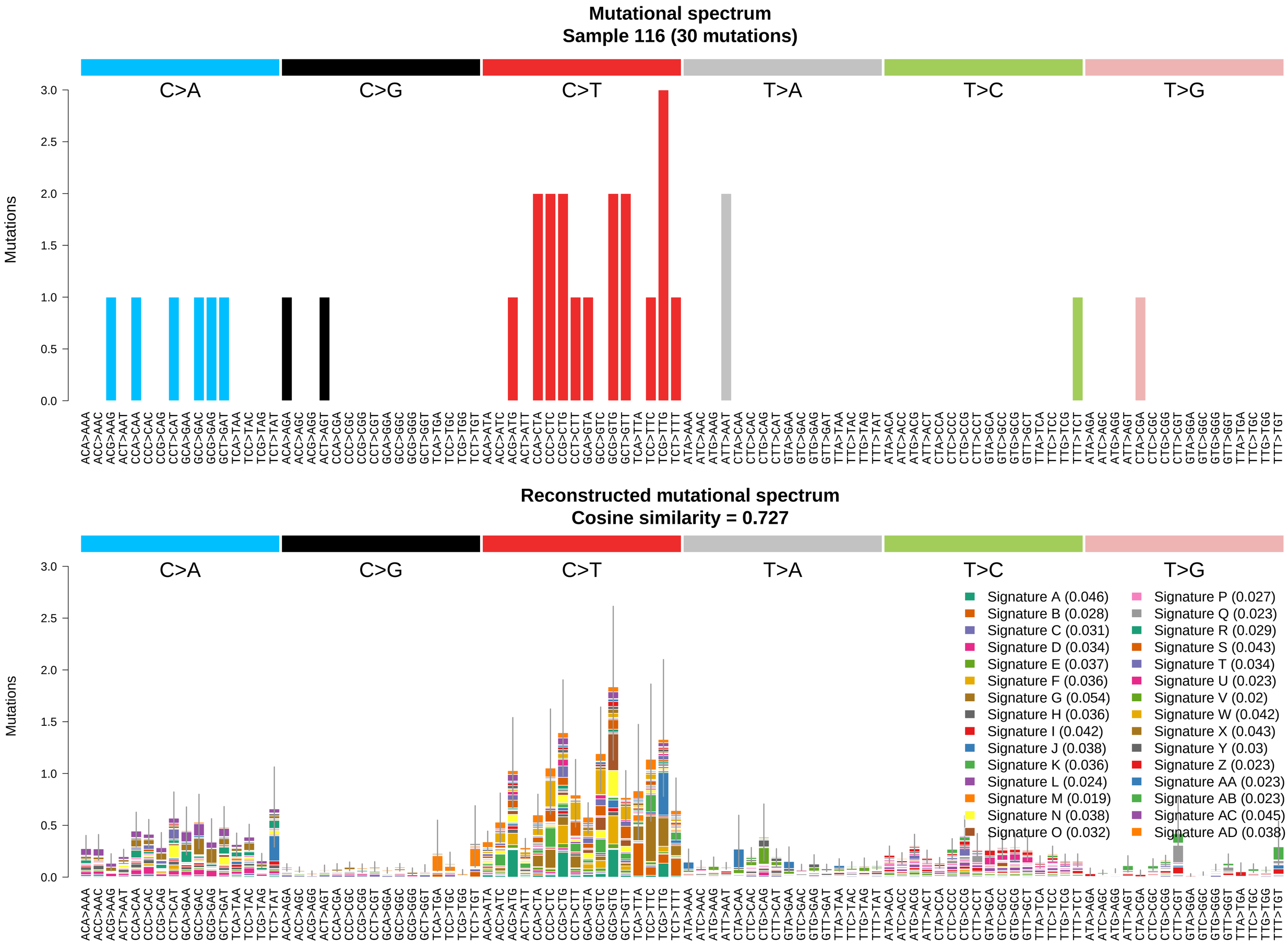

Mutational spectrum
Sample 112 (125 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.776
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
Signature A (0.072)
Signature B (0.016)
Signature C (0.099)
Signature D (0.05)
Signature E (0.064)
Signature F (0.04)
Signature G (0.031)
Signature H (0.022)
Signature I (0.019)
Signature J (0.02)
Signature K (0.037)
Signature L (0.027)
Signature M (0.033)
Signature N (0.021)
Signature O (0.016)
Signature P (0.032)
Signature Q (0.019)
Signature R (0.032)
Signature S (0.03)
Signature T (0.03)
Signature U (0.029)
Signature V (0.013)
Signature W (0.033)
Signature X (0.04)
Signature Y (0.023)
Signature Z (0.022)
Signature AA (0.045)
Signature AB (0.011)
Signature AC (0.032)
Signature AD (0.04)
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT

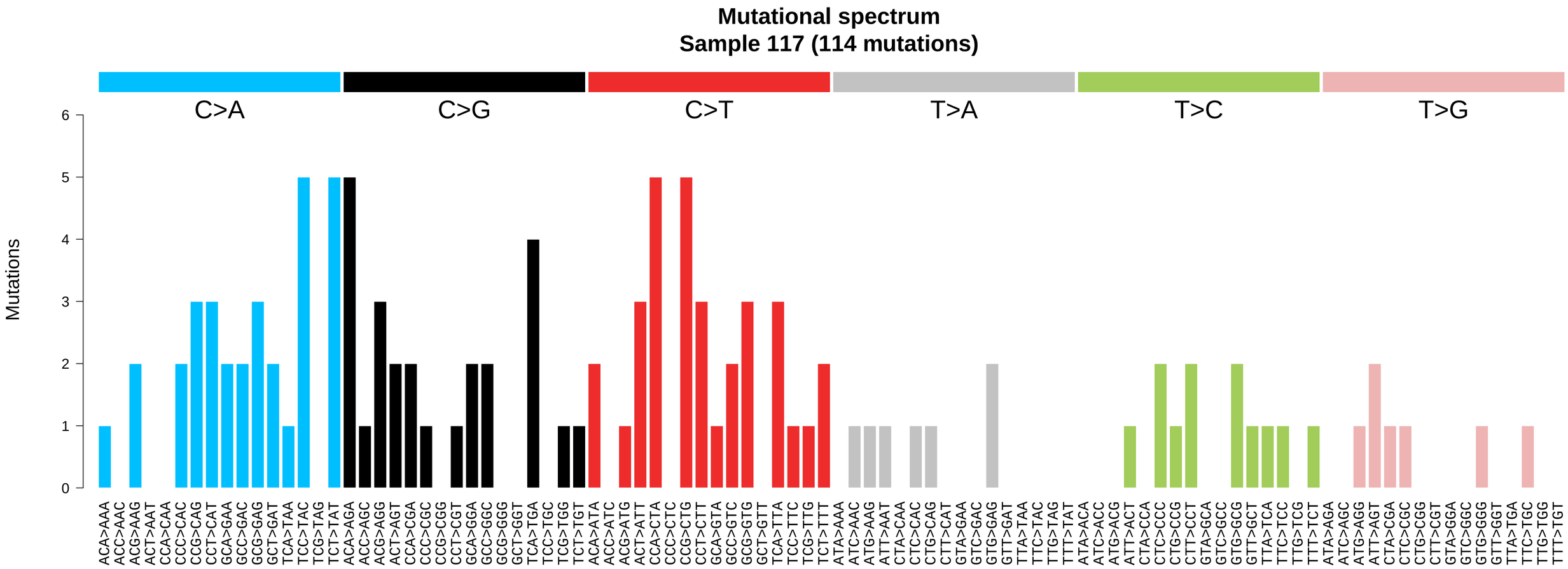

Mutational spectrum
Sample 113 (69 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.77
Signature A (0.039)
Signature B (0.02)
Signature C (0.054)
Signature D (0.084)
Signature E (0.041)
Signature F (0.031)
Signature G (0.028)
Signature H (0.032)
Signature I (0.034)
Signature J (0.018)
Signature K (0.039)
Signature L (0.023)
Signature M (0.022)
Signature N (0.029)
Signature O (0.024)
Signature P (0.025)
Signature Q (0.019)
Signature R (0.034)
Signature S (0.051)
Signature T (0.027)
Signature U (0.021)
Signature V (0.017)
Signature W (0.056)
Signature X (0.063)
Signature Y (0.031)
Signature Z (0.02)
Signature AA (0.017)
Signature AB (0.021)
Signature AC (0.034)
Signature AD (0.044)

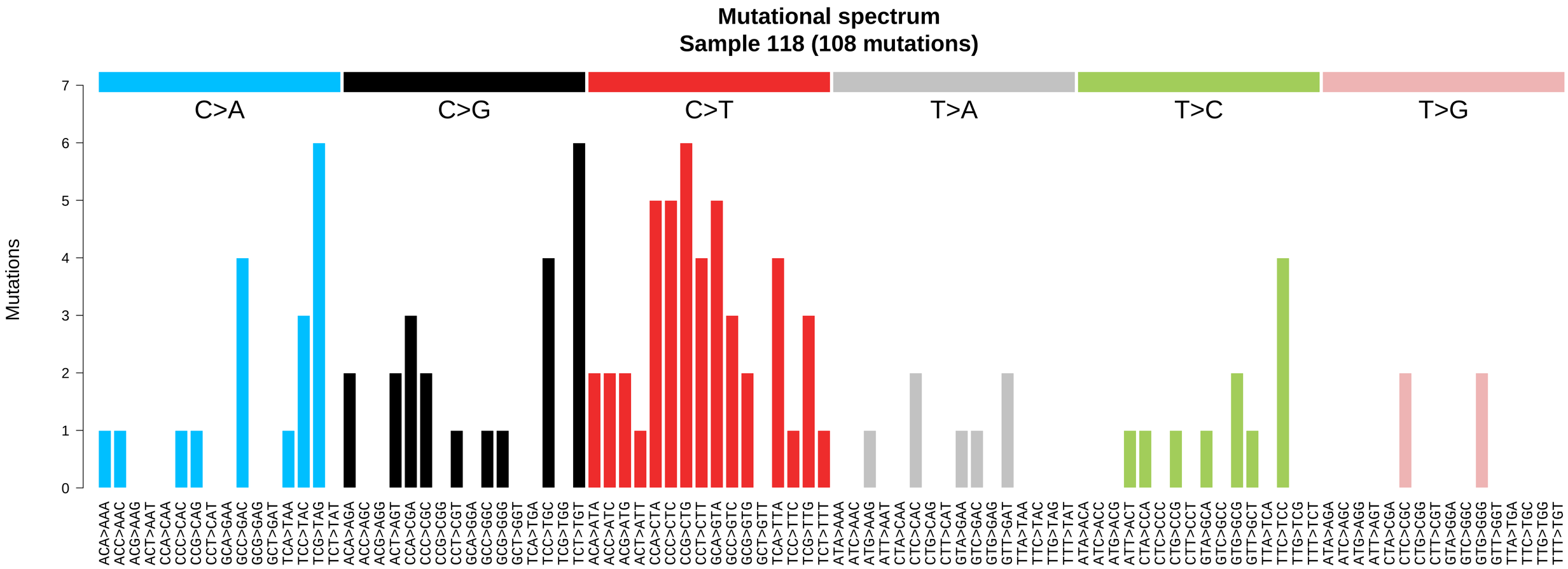

Mutational spectrum
Sample 114 (109 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.82
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
Signature A (0.031)
Signature B (0.125)
Signature C (0.097)
Signature D (0.035)
Signature E (0.04)
Signature F (0.022)
Signature G (0.019)
Signature H (0.03)
Signature I (0.035)
Signature J (0.031)
Signature K (0.014)
Signature L (0.024)
Signature M (0.148)
Signature N (0.019)
Signature O (0.015)
Signature P (0.027)
Signature Q (0.013)
Signature R (0.029)
Signature S (0.02)
Signature T (0.022)
Signature U (0.025)
Signature V (0.011)
Signature W (0.013)
Signature X (0.021)
Signature Y (0.024)
Signature Z (0.02)
Signature AA (0.011)
Signature AB (0.011)
Signature AC (0.029)
Signature AD (0.04)

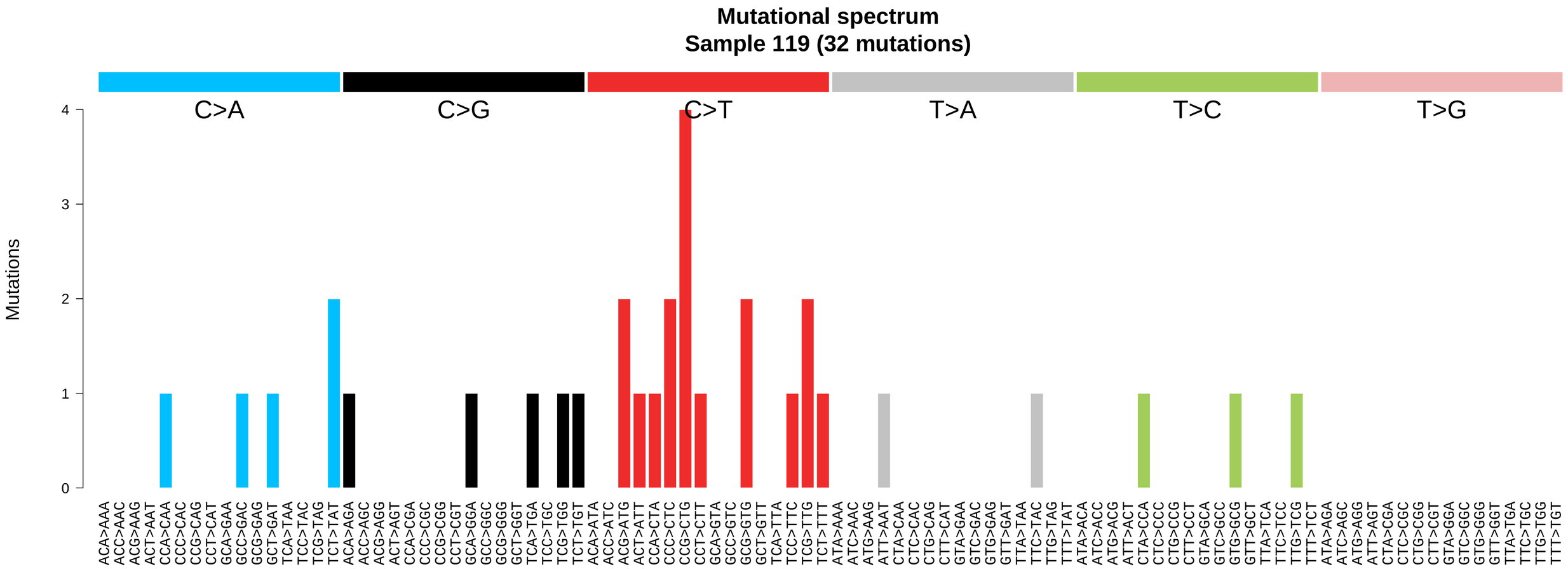

Mutational spectrum
Sample 115 (107 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations

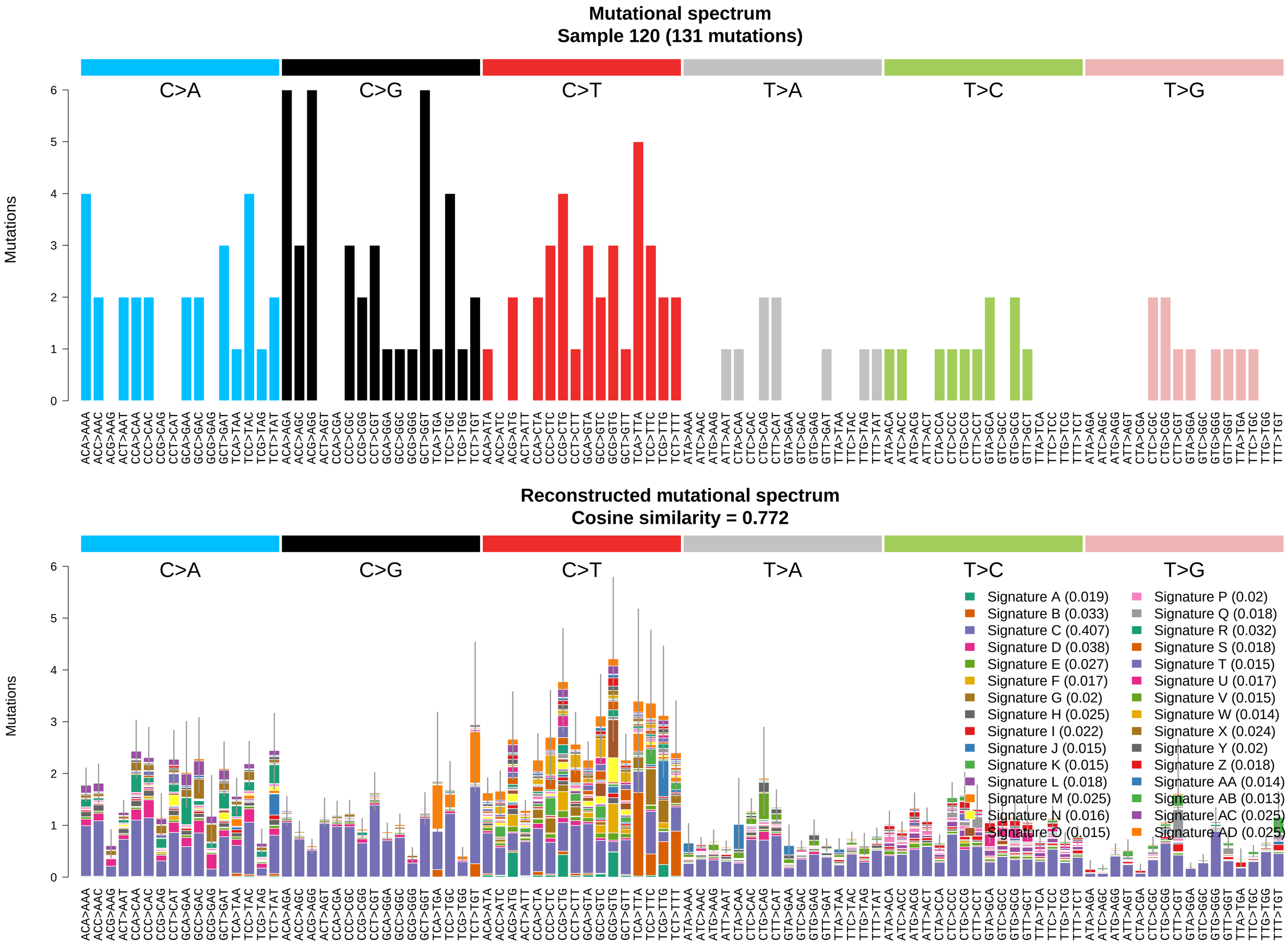

Reconstructed mutational spectrum
Cosine similarity = 0.785
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Signature A (0.017)
Signature B (0.028)
Signature C (0.162)
Signature D (0.068)
Signature E (0.03)
Signature F (0.016)
Signature G (0.018)
Signature H (0.04)
Signature I (0.028)
Signature J (0.02)
Signature K (0.029)
Signature L (0.019)
Signature M (0.119)
Signature N (0.019)
Signature O (0.018)
Signature P (0.026)
Signature Q (0.022)
Signature R (0.029)
Signature S (0.022)
Signature T (0.017)
Signature U (0.014)
Signature V (0.02)
Signature W (0.023)
Signature X (0.042)
Signature Y (0.027)
Signature Z (0.015)
Signature AA (0.016)
Signature AB (0.038)
Signature AC (0.024)
Signature AD (0.033)

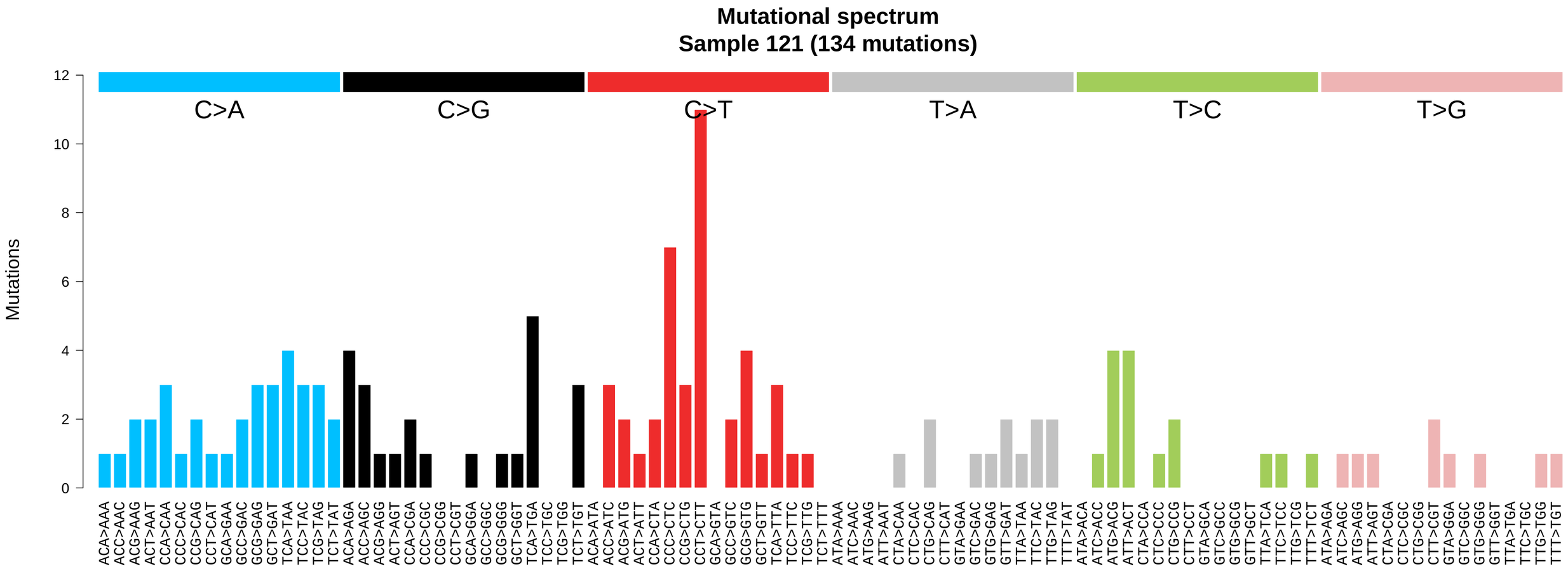

Mutational spectrum
Sample 116 (30 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.727
Signature A (0.046)
Signature B (0.028)
Signature C (0.031)
Signature D (0.034)
Signature E (0.037)
Signature F (0.036)
Signature G (0.054)
Signature H (0.036)
Signature I (0.042)
Signature J (0.038)
Signature K (0.036)
Signature L (0.024)
Signature M (0.019)
Signature N (0.038)
Signature O (0.032)
Signature P (0.027)
Signature Q (0.023)
Signature R (0.029)
Signature S (0.043)
Signature T (0.034)
Signature U (0.023)
Signature V (0.02)
Signature W (0.042)
Signature X (0.043)
Signature Y (0.03)
Signature Z (0.023)
Signature AA (0.023)
Signature AB (0.023)
Signature AC (0.045)
Signature AD (0.038)

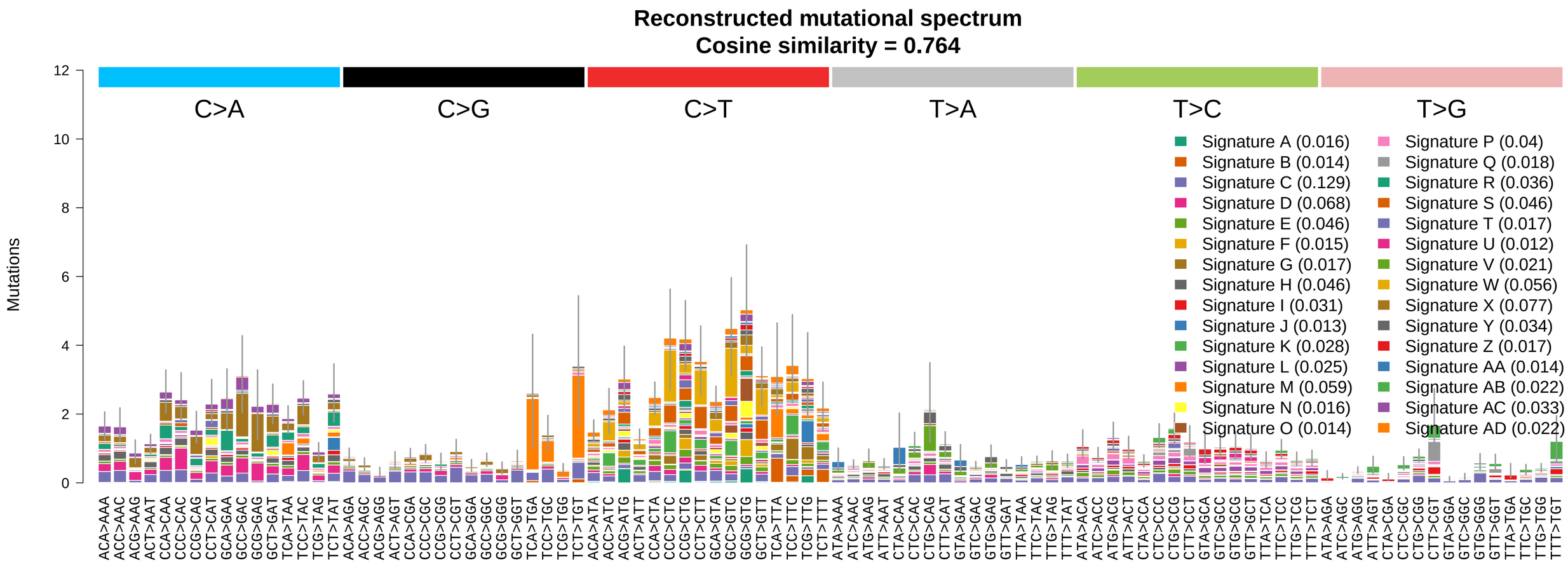

Mutational spectrum
Sample 117 (114 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.744
Signature A (0.019)
Signature B (0.024)
Signature C (0.205)
Signature D (0.082)
Signature E (0.043)
Signature F (0.02)
Signature G (0.016)
Signature H (0.032)
Signature I (0.028)
Signature J (0.022)
Signature K (0.017)
Signature L (0.024)
Signature M (0.045)
Signature N (0.022)
Signature O (0.015)
Signature P (0.029)
Signature Q (0.02)
Signature R (0.039)
Signature S (0.02)
Signature T (0.023)
Signature U (0.019)
Signature V (0.015)
Signature W (0.015)
Signature X (0.062)
Signature Y (0.027)
Signature Z (0.018)
Signature AA (0.011)
Signature AB (0.023)
Signature AC (0.033)
Signature AD (0.031)

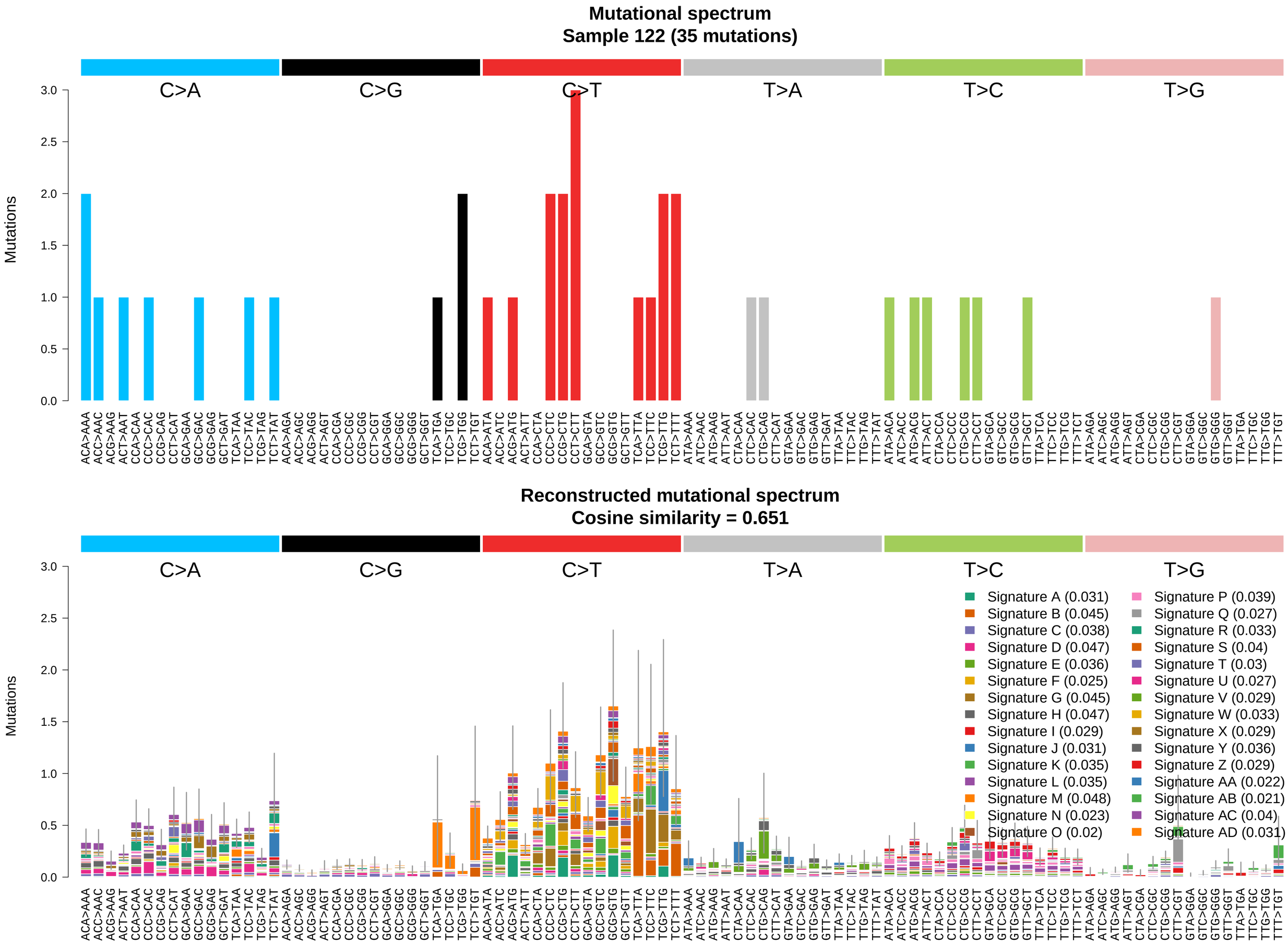

Mutational spectrum
Sample 118 (108 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
7
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.734
Signature A (0.025)
Signature B (0.026)
Signature C (0.127)
Signature D (0.046)
Signature E (0.047)
Signature F (0.022)
Signature G (0.027)
Signature H (0.026)
Signature I (0.016)
Signature J (0.014)
Signature K (0.029)
Signature L (0.028)
Signature M (0.08)
Signature N (0.017)
Signature O (0.018)
Signature P (0.033)
Signature Q (0.014)
Signature R (0.025)
Signature S (0.041)
Signature T (0.025)
Signature U (0.032)
Signature V (0.014)
Signature W (0.045)
Signature X (0.053)
Signature Y (0.027)
Signature Z (0.026)
Signature AA (0.018)
Signature AB (0.016)
Signature AC (0.028)
Signature AD (0.055)

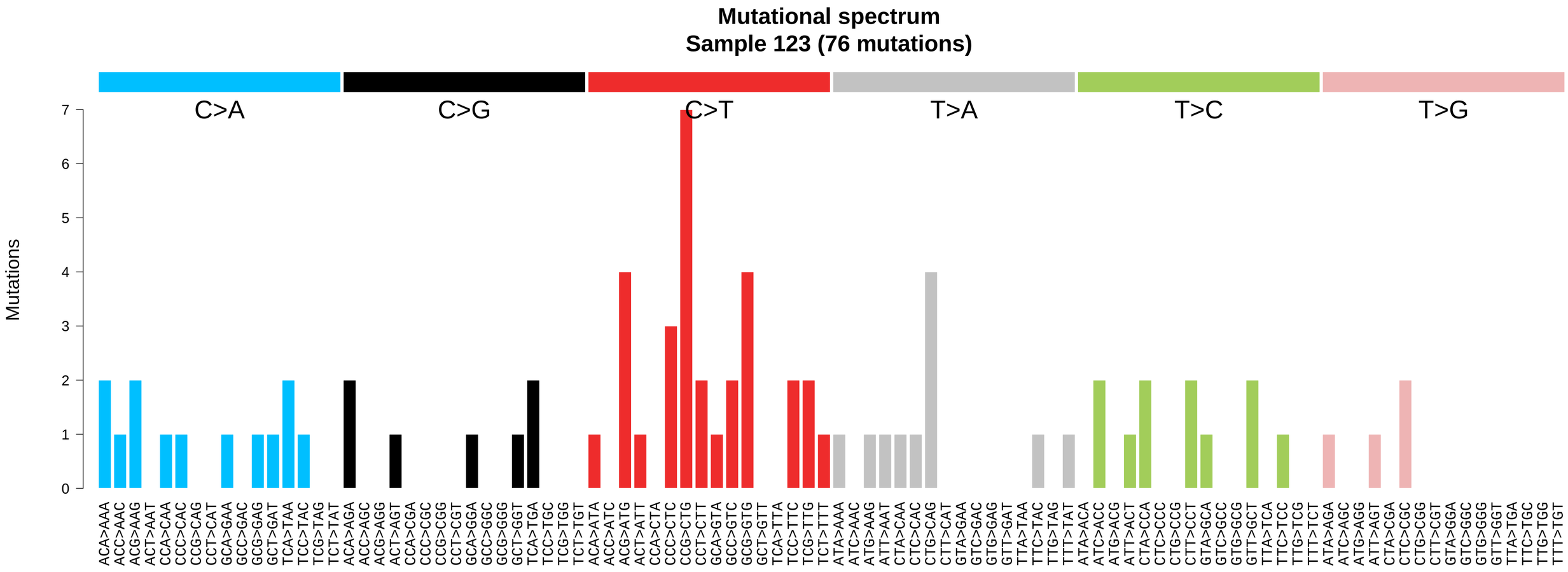

Mutational spectrum
Sample 119 (32 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.74
Signature A (0.054)
Signature B (0.029)
Signature C (0.038)
Signature D (0.03)
Signature E (0.035)
Signature F (0.04)
Signature G (0.04)
Signature H (0.032)
Signature I (0.028)
Signature J (0.049)
Signature K (0.035)
Signature L (0.031)
Signature M (0.054)
Signature N (0.035)
Signature O (0.03)
Signature P (0.029)
Signature Q (0.021)
Signature R (0.034)
Signature S (0.037)
Signature T (0.032)
Signature U (0.035)
Signature V (0.022)
Signature W (0.031)
Signature X (0.03)
Signature Y (0.031)
Signature Z (0.027)
Signature AA (0.023)
Signature AB (0.022)
Signature AC (0.03)
Signature AD (0.035)

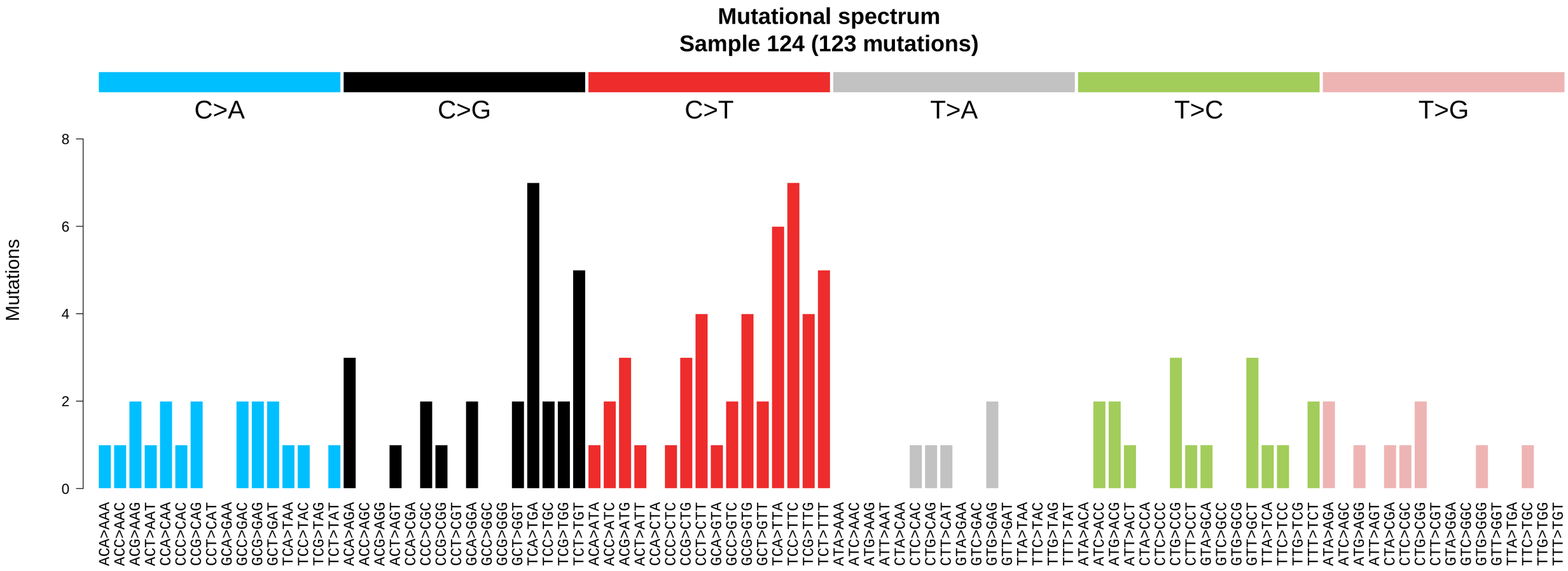

Mutational spectrum
Sample 120 (131 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.772
Signature A (0.019)
Signature B (0.033)
Signature C (0.407)
Signature D (0.038)
Signature E (0.027)
Signature F (0.017)
Signature G (0.02)
Signature H (0.025)
Signature I (0.022)
Signature J (0.015)
Signature K (0.015)
Signature L (0.018)
Signature M (0.025)
Signature N (0.016)
Signature O (0.015)
Signature P (0.02)
Signature Q (0.018)
Signature R (0.032)
Signature S (0.018)
Signature T (0.015)
Signature U (0.017)
Signature V (0.015)
Signature W (0.014)
Signature X (0.024)
Signature Y (0.02)
Signature Z (0.018)
Signature AA (0.014)
Signature AB (0.013)
Signature AC (0.025)
Signature AD (0.025)

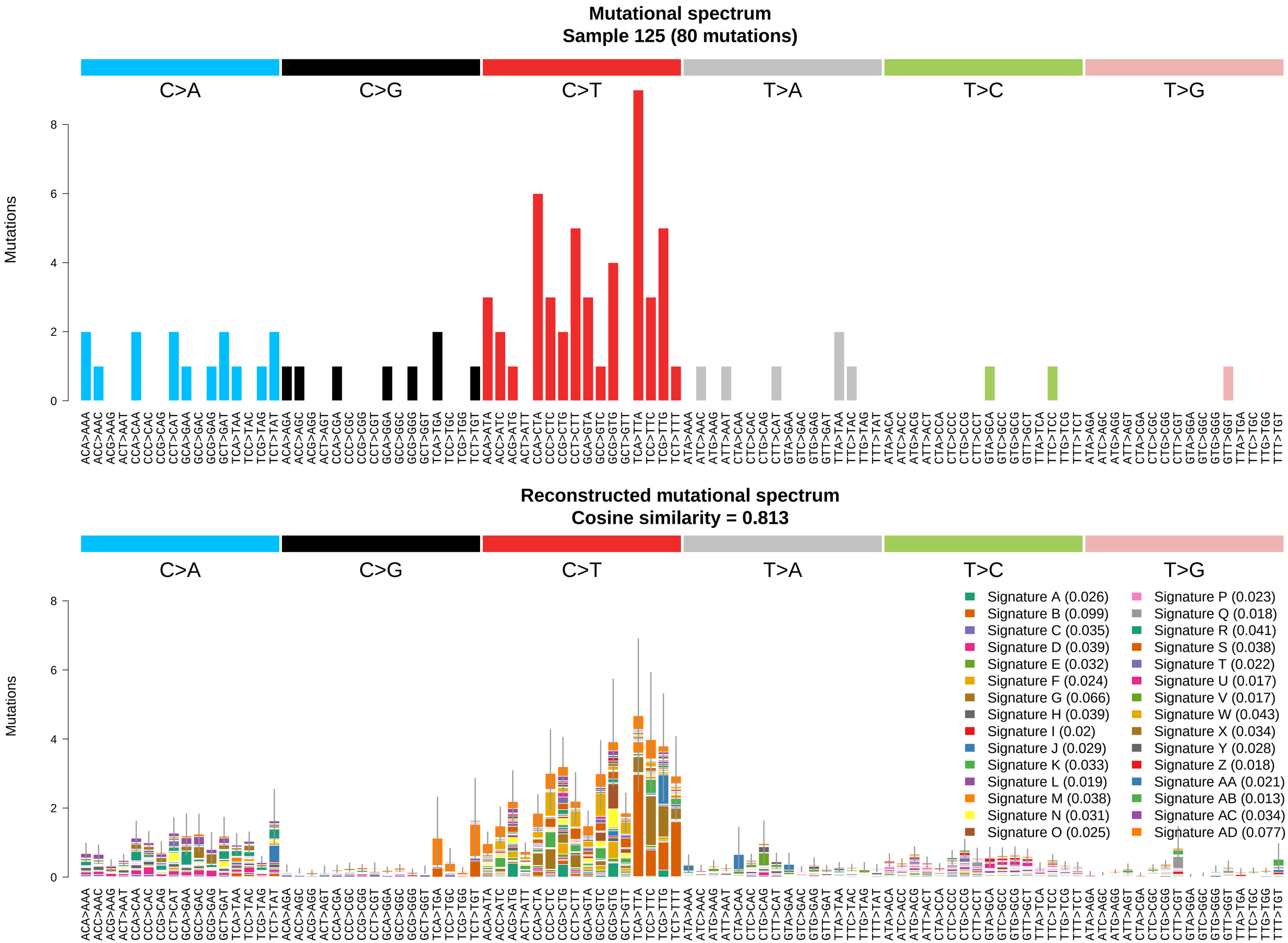

Mutational spectrum
Sample 121 (134 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT

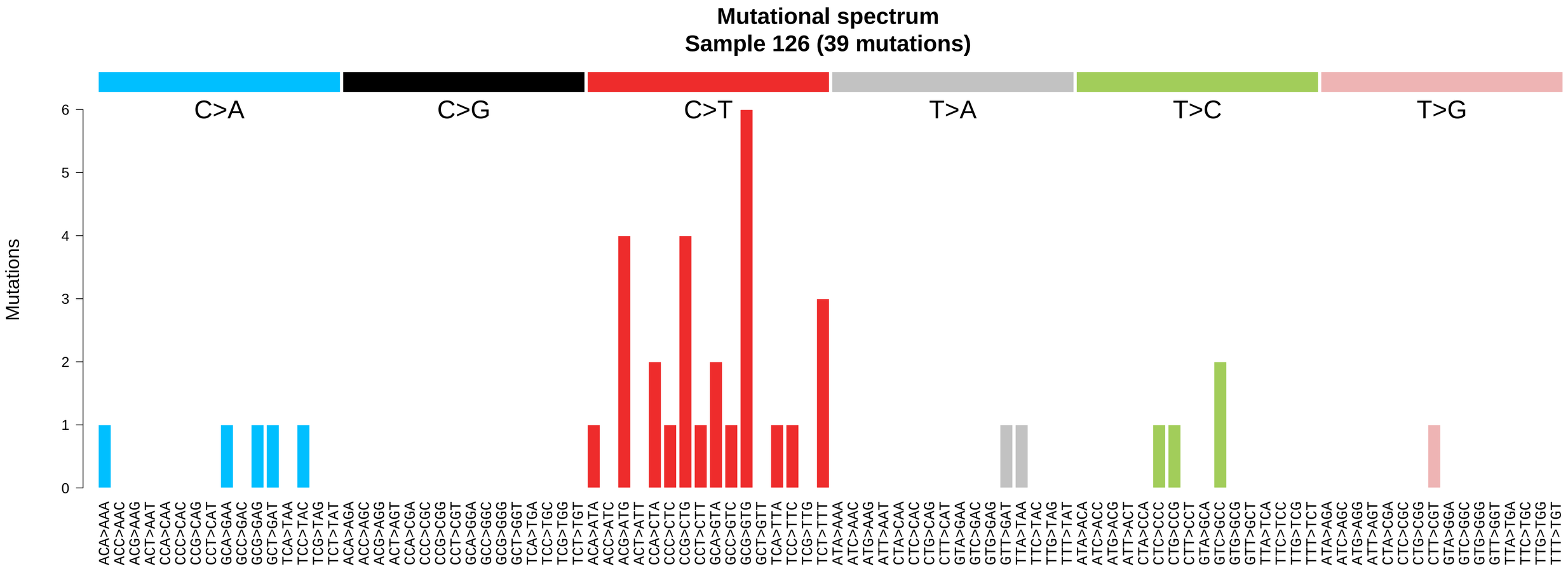

Reconstructed mutational spectrum
Cosine similarity = 0.764
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
Signature A (0.016)
Signature B (0.014)
Signature C (0.129)
Signature D (0.068)
Signature E (0.046)
Signature F (0.015)
Signature G (0.017)
Signature H (0.046)
Signature I (0.031)
Signature J (0.013)
Signature K (0.028)
Signature L (0.025)
Signature M (0.059)
Signature N (0.016)
Signature O (0.014)
Signature P (0.04)
Signature Q (0.018)
Signature R (0.036)
Signature S (0.046)
Signature T (0.017)
Signature U (0.012)
Signature V (0.021)
Signature W (0.056)
Signature X (0.077)
Signature Y (0.034)
Signature Z (0.017)
Signature AA (0.014)
Signature AB (0.022)
Signature AC (0.033)
Signature AD (0.022)

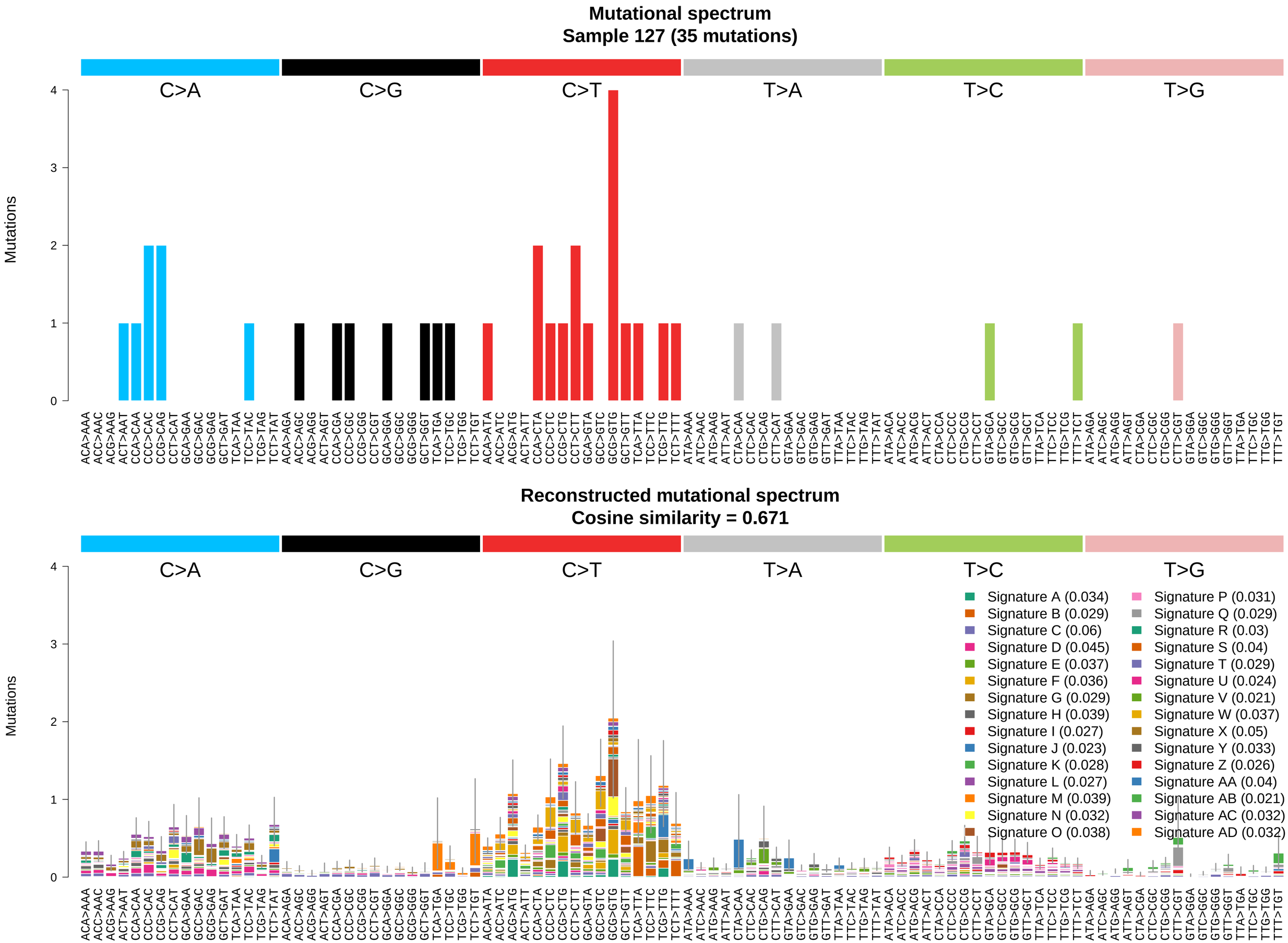

Mutational spectrum
Sample 122 (35 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.651
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Signature A (0.031)
Signature B (0.045)
Signature C (0.038)
Signature D (0.047)
Signature E (0.036)
Signature F (0.025)
Signature G (0.045)
Signature H (0.047)
Signature I (0.029)
Signature J (0.031)
Signature K (0.035)
Signature L (0.035)
Signature M (0.048)
Signature N (0.023)
Signature O (0.02)
Signature P (0.039)
Signature Q (0.027)
Signature R (0.033)
Signature S (0.04)
Signature T (0.03)
Signature U (0.027)
Signature V (0.029)
Signature W (0.033)
Signature X (0.029)
Signature Y (0.036)
Signature Z (0.029)
Signature AA (0.022)
Signature AB (0.021)
Signature AC (0.04)
Signature AD (0.031)
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT

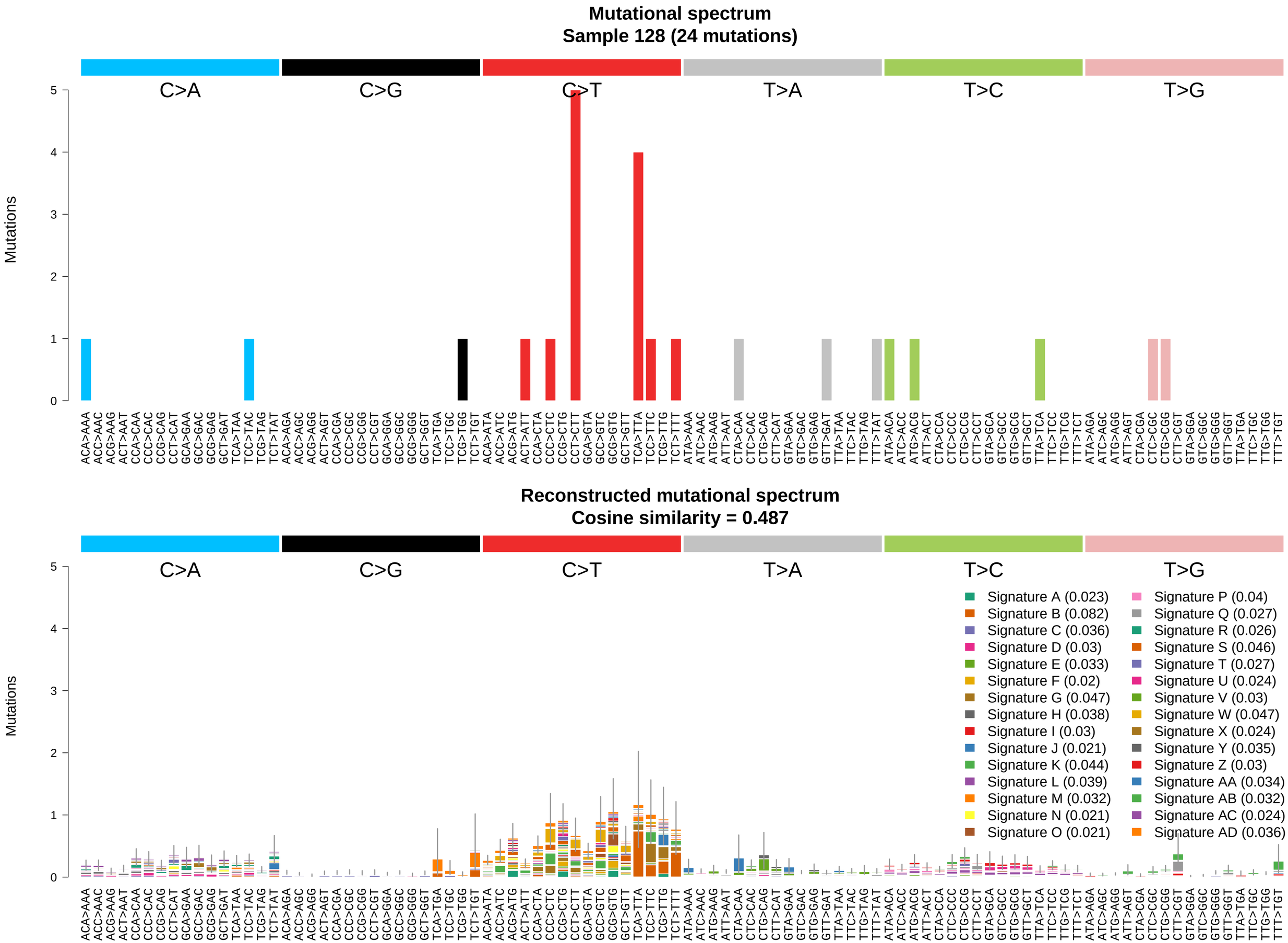

Mutational spectrum
Sample 123 (76 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
7
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.786
Signature A (0.061)
Signature B (0.016)
Signature C (0.049)
Signature D (0.041)
Signature E (0.041)
Signature F (0.037)
Signature G (0.025)
Signature H (0.054)
Signature I (0.042)
Signature J (0.018)
Signature K (0.026)
Signature L (0.033)
Signature M (0.026)
Signature N (0.024)
Signature O (0.023)
Signature P (0.035)
Signature Q (0.026)
Signature R (0.027)
Signature S (0.032)
Signature T (0.024)
Signature U (0.035)
Signature V (0.06)
Signature W (0.025)
Signature X (0.03)
Signature Y (0.036)
Signature Z (0.032)
Signature AA (0.028)
Signature AB (0.027)
Signature AC (0.04)
Signature AD (0.028)

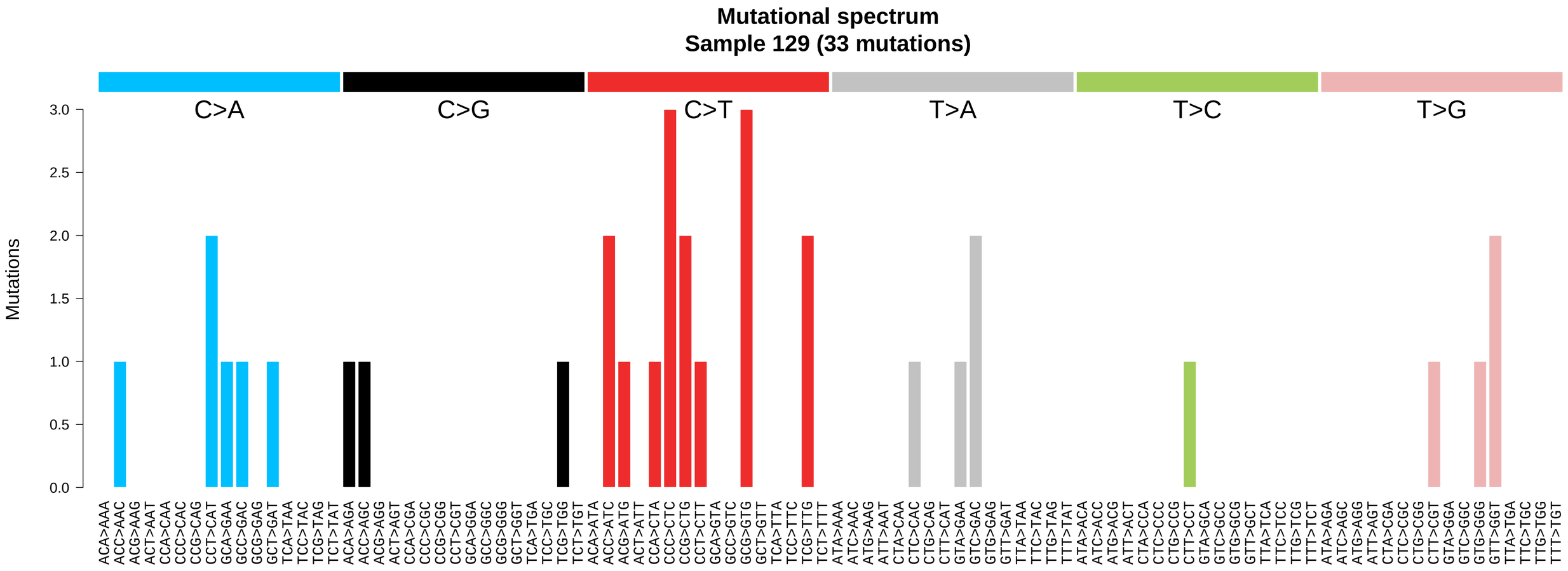

Mutational spectrum
Sample 124 (123 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.867
Signature A (0.022)
Signature B (0.063)
Signature C (0.092)
Signature D (0.038)
Signature E (0.042)
Signature F (0.021)
Signature G (0.038)
Signature H (0.029)
Signature I (0.045)
Signature J (0.018)
Signature K (0.03)
Signature L (0.031)
Signature M (0.122)
Signature N (0.019)
Signature O (0.018)
Signature P (0.034)
Signature Q (0.015)
Signature R (0.02)
Signature S (0.024)
Signature T (0.023)
Signature U (0.023)
Signature V (0.014)
Signature W (0.019)
Signature X (0.042)
Signature Y (0.041)
Signature Z (0.029)
Signature AA (0.011)
Signature AB (0.016)
Signature AC (0.032)
Signature AD (0.03)

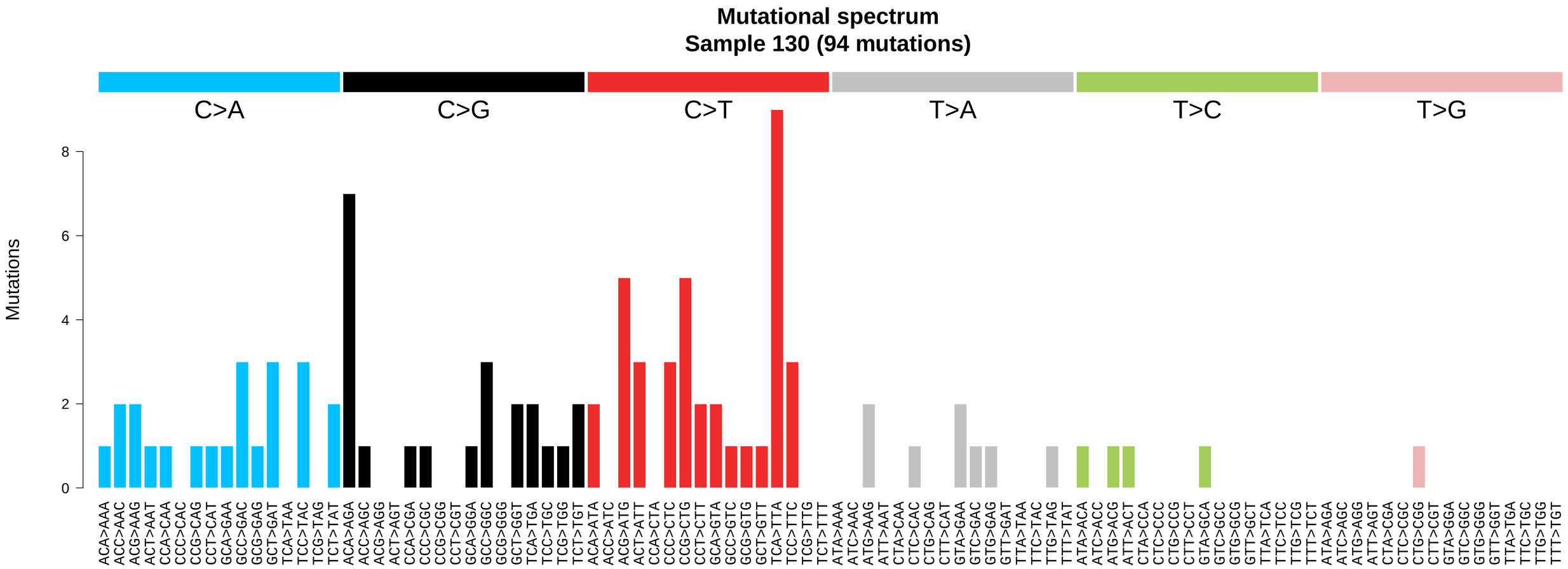

Mutational spectrum
Sample 125 (80 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.813
Signature A (0.026)
Signature B (0.099)
Signature C (0.035)
Signature D (0.039)
Signature E (0.032)
Signature F (0.024)
Signature G (0.066)
Signature H (0.039)
Signature I (0.02)
Signature J (0.029)
Signature K (0.033)
Signature L (0.019)
Signature M (0.038)
Signature N (0.031)
Signature O (0.025)
Signature P (0.023)
Signature Q (0.018)
Signature R (0.041)
Signature S (0.038)
Signature T (0.022)
Signature U (0.017)
Signature V (0.017)
Signature W (0.043)
Signature X (0.034)
Signature Y (0.028)
Signature Z (0.018)
Signature AA (0.021)
Signature AB (0.013)
Signature AC (0.034)
Signature AD (0.077)

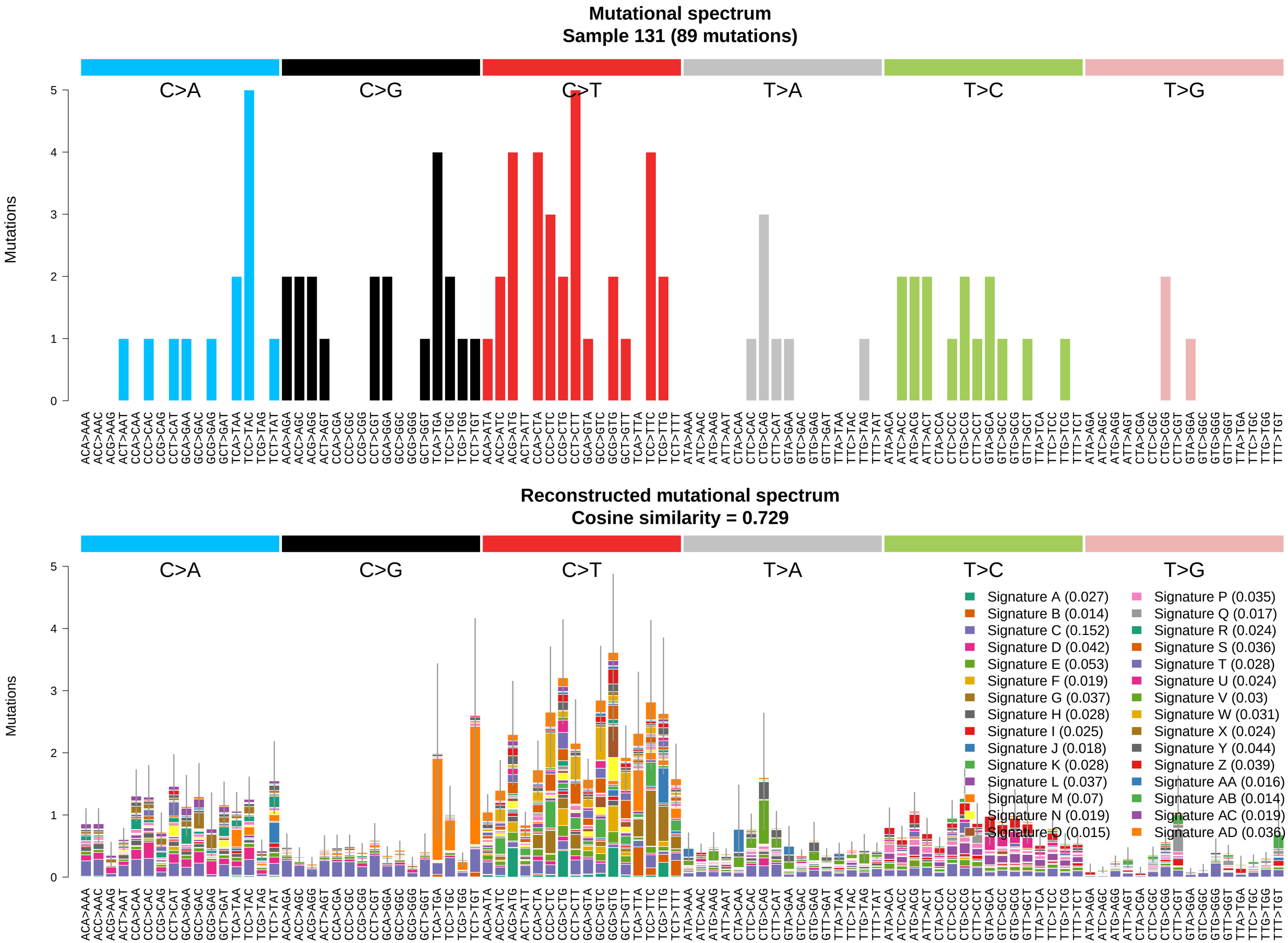

Mutational spectrum
Sample 126 (39 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.809
Signature A (0.077)
Signature B (0.042)
Signature C (0.022)
Signature D (0.027)
Signature E (0.029)
Signature F (0.064)
Signature G (0.032)
Signature H (0.028)
Signature I (0.027)
Signature J (0.021)
Signature K (0.032)
Signature L (0.026)
Signature M (0.017)
Signature N (0.05)
Signature O (0.057)
Signature P (0.024)
Signature Q (0.032)
Signature R (0.03)
Signature S (0.04)
Signature T (0.031)
Signature U (0.031)
Signature V (0.018)
Signature W (0.033)
Signature X (0.029)
Signature Y (0.029)
Signature Z (0.029)
Signature AA (0.026)
Signature AB (0.022)
Signature AC (0.033)
Signature AD (0.041)

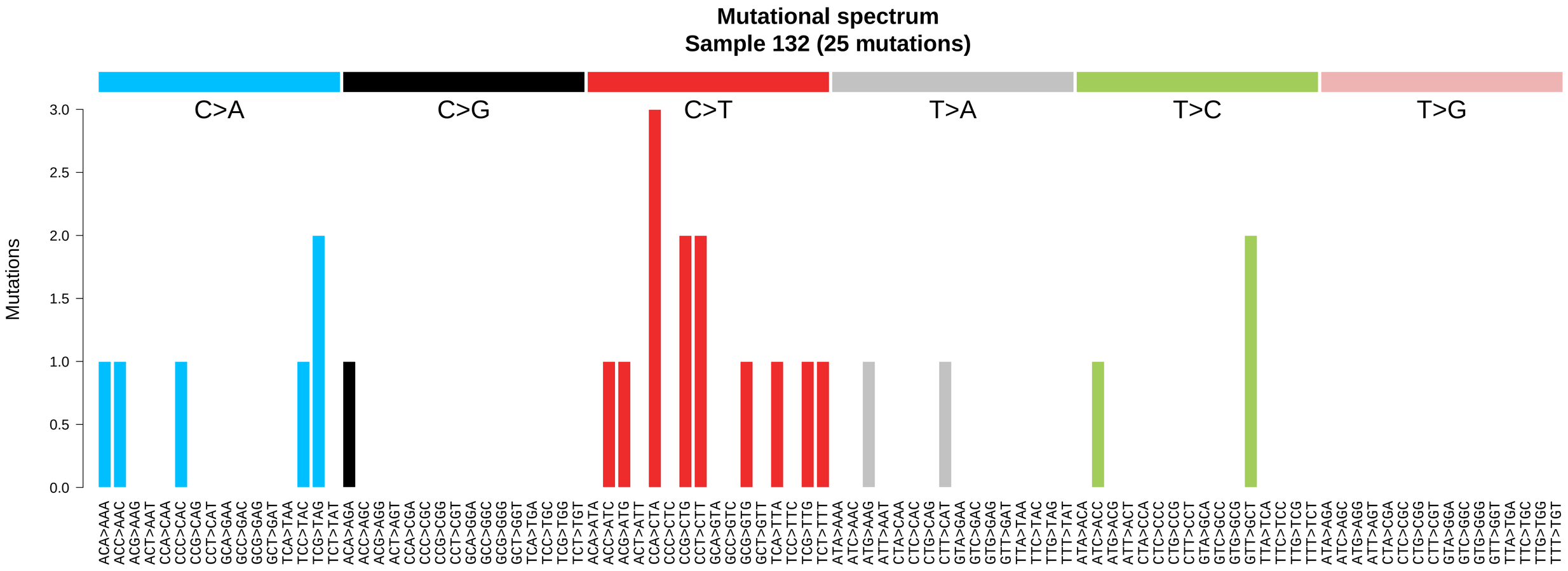

Mutational spectrum
Sample 127 (35 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.671
Signature A (0.034)
Signature B (0.029)
Signature C (0.06)
Signature D (0.045)
Signature E (0.037)
Signature F (0.036)
Signature G (0.029)
Signature H (0.039)
Signature I (0.027)
Signature J (0.023)
Signature K (0.028)
Signature L (0.027)
Signature M (0.039)
Signature N (0.032)
Signature O (0.038)
Signature P (0.031)
Signature Q (0.029)
Signature R (0.03)
Signature S (0.04)
Signature T (0.029)
Signature U (0.024)
Signature V (0.021)
Signature W (0.037)
Signature X (0.05)
Signature Y (0.033)
Signature Z (0.026)
Signature AA (0.04)
Signature AB (0.021)
Signature AC (0.032)
Signature AD (0.032)

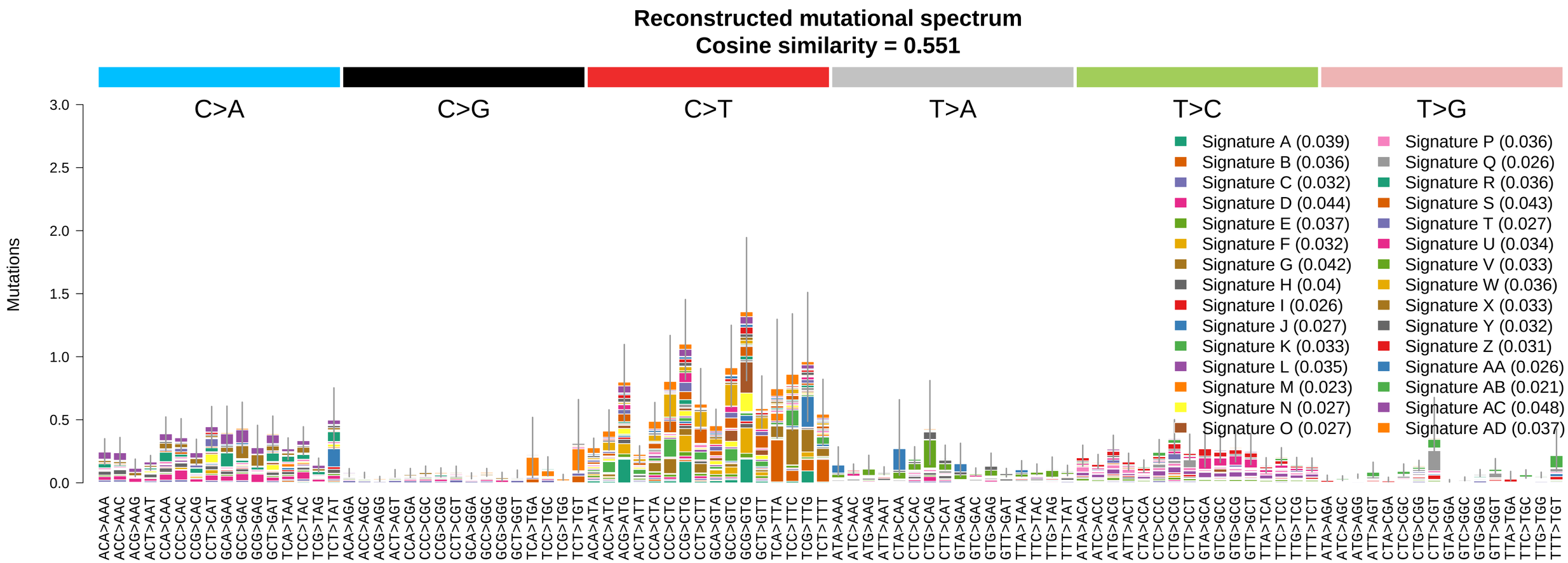

Mutational spectrum
Sample 128 (24 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.487
Signature A (0.023)
Signature B (0.082)
Signature C (0.036)
Signature D (0.03)
Signature E (0.033)
Signature F (0.02)
Signature G (0.047)
Signature H (0.038)
Signature I (0.03)
Signature J (0.021)
Signature K (0.044)
Signature L (0.039)
Signature M (0.032)
Signature N (0.021)
Signature O (0.021)
Signature P (0.04)
Signature Q (0.027)
Signature R (0.026)
Signature S (0.046)
Signature T (0.027)
Signature U (0.024)
Signature V (0.03)
Signature W (0.047)
Signature X (0.024)
Signature Y (0.035)
Signature Z (0.03)
Signature AA (0.034)
Signature AB (0.032)
Signature AC (0.024)
Signature AD (0.036)

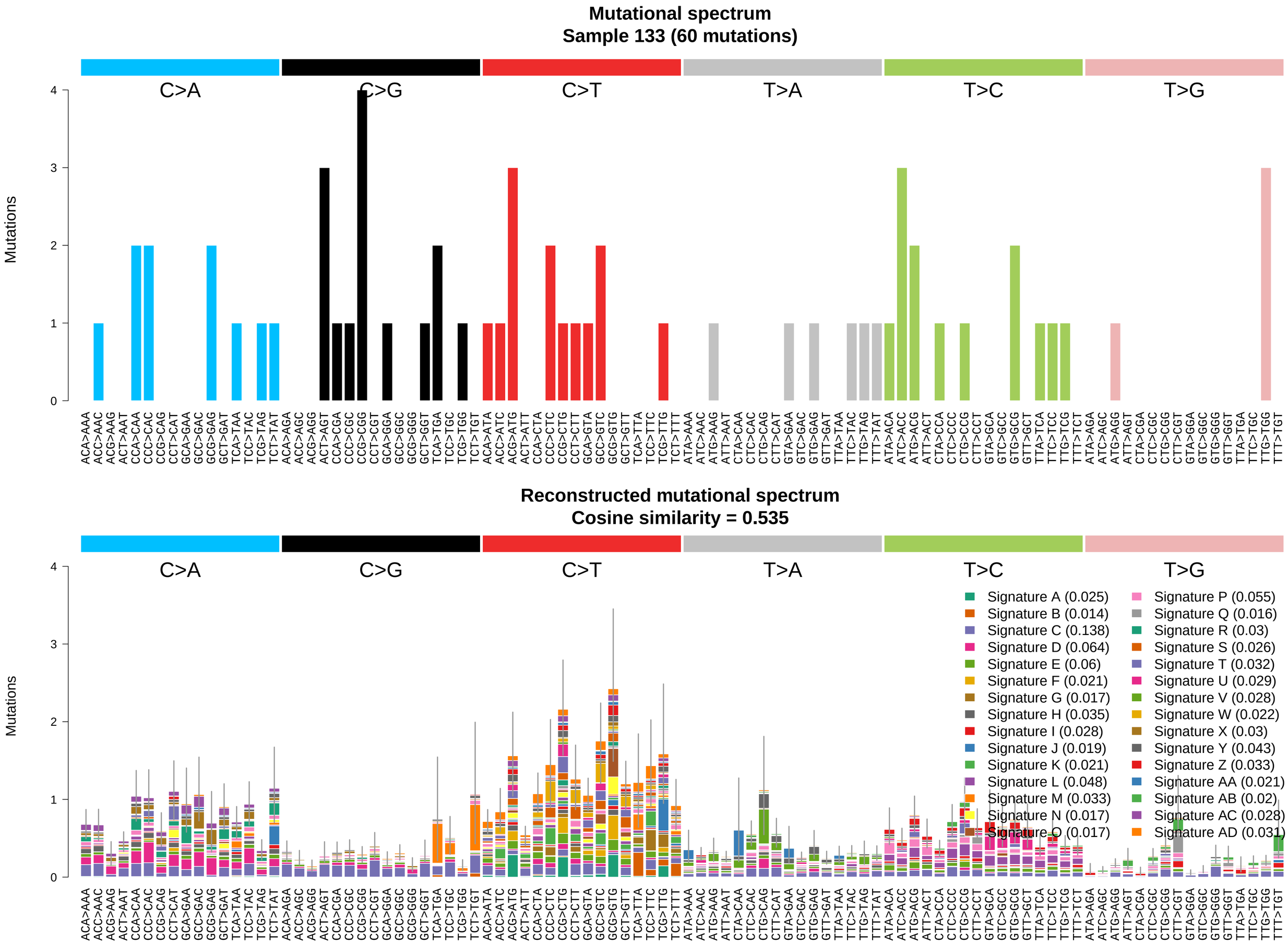

Mutational spectrum
Sample 129 (33 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.67
Signature A (0.036)
Signature B (0.02)
Signature C (0.04)
Signature D (0.037)
Signature E (0.034)
Signature F (0.037)
Signature G (0.034)
Signature H (0.038)
Signature I (0.03)
Signature J (0.03)
Signature K (0.038)
Signature L (0.021)
Signature M (0.021)
Signature N (0.044)
Signature O (0.034)
Signature P (0.026)
Signature Q (0.064)
Signature R (0.033)
Signature S (0.035)
Signature T (0.03)
Signature U (0.026)
Signature V (0.028)
Signature W (0.042)
Signature X (0.033)
Signature Y (0.039)
Signature Z (0.024)
Signature AA (0.029)
Signature AB (0.026)
Signature AC (0.039)
Signature AD (0.036)

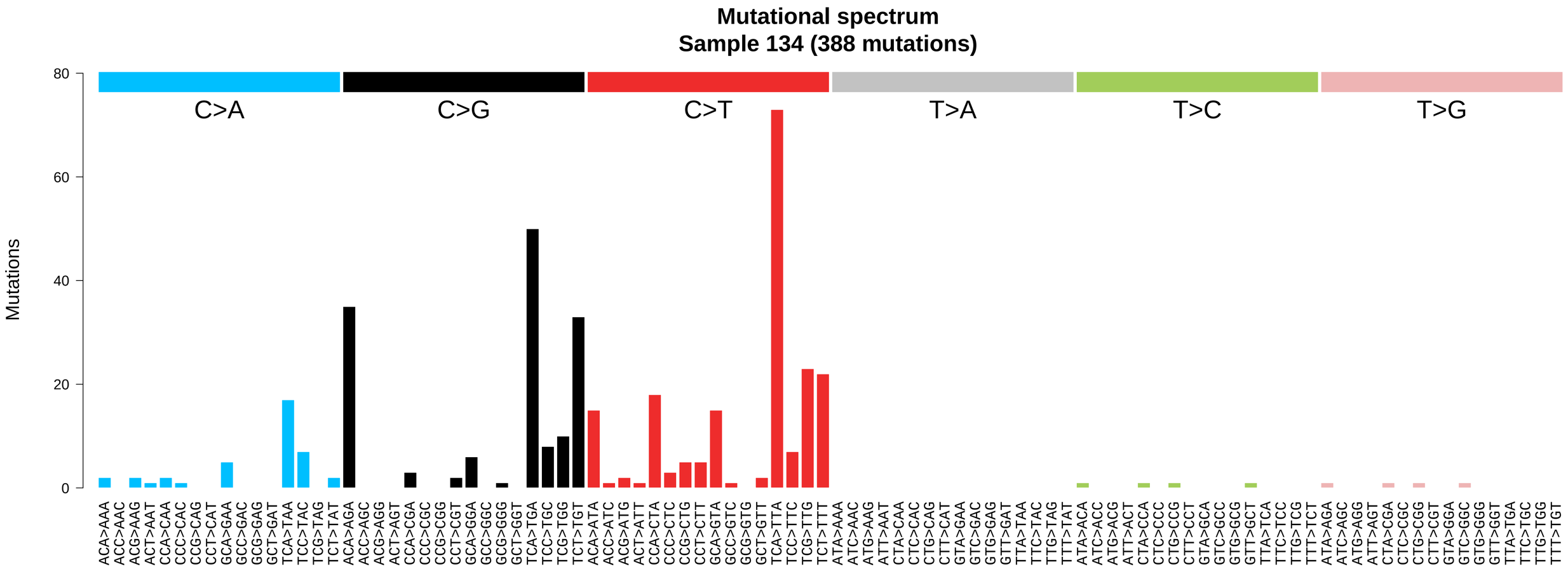

Mutational spectrum
Sample 130 (94 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.706
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
Signature A (0.032)
Signature B (0.066)
Signature C (0.135)
Signature D (0.059)
Signature E (0.039)
Signature F (0.023)
Signature G (0.021)
Signature H (0.044)
Signature I (0.018)
Signature J (0.013)
Signature K (0.027)
Signature L (0.016)
Signature M (0.05)
Signature N (0.025)
Signature O (0.015)
Signature P (0.024)
Signature Q (0.012)
Signature R (0.027)
Signature S (0.029)
Signature T (0.022)
Signature U (0.017)
Signature V (0.025)
Signature W (0.022)
Signature X (0.075)
Signature Y (0.032)
Signature Z (0.017)
Signature AA (0.022)
Signature AB (0.009)
Signature AC (0.054)
Signature AD (0.031)

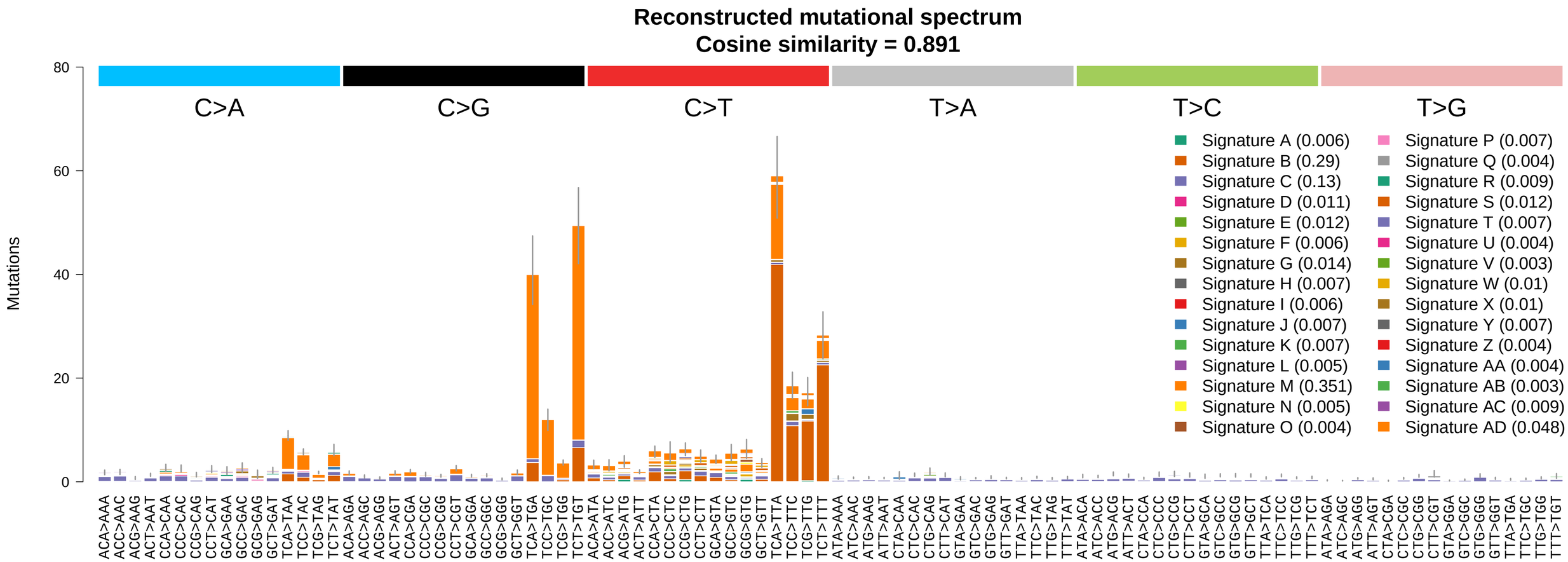

Mutational spectrum
Sample 131 (89 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.729
Signature A (0.027)
Signature B (0.014)
Signature C (0.152)
Signature D (0.042)
Signature E (0.053)
Signature F (0.019)
Signature G (0.037)
Signature H (0.028)
Signature I (0.025)
Signature J (0.018)
Signature K (0.028)
Signature L (0.037)
Signature M (0.07)
Signature N (0.019)
Signature O (0.015)
Signature P (0.035)
Signature Q (0.017)
Signature R (0.024)
Signature S (0.036)
Signature T (0.028)
Signature U (0.024)
Signature V (0.03)
Signature W (0.031)
Signature X (0.024)
Signature Y (0.044)
Signature Z (0.039)
Signature AA (0.016)
Signature AB (0.014)
Signature AC (0.019)
Signature AD (0.036)

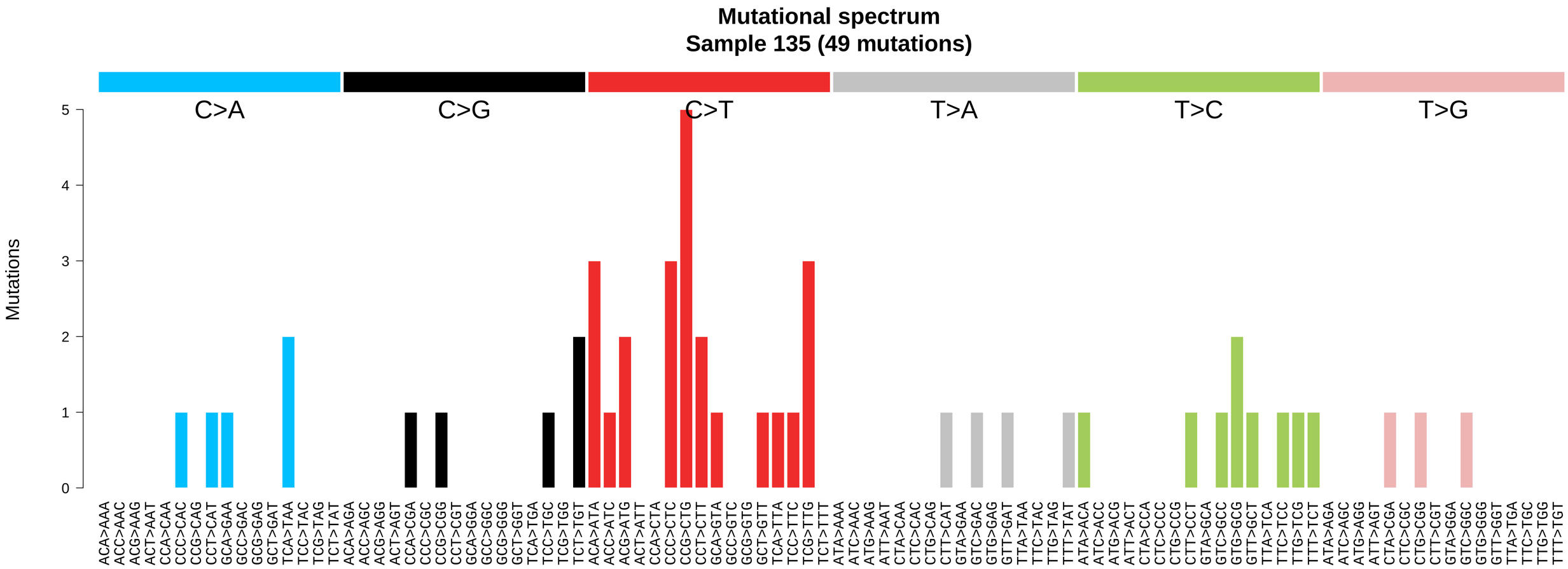

Mutational spectrum
Sample 132 (25 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

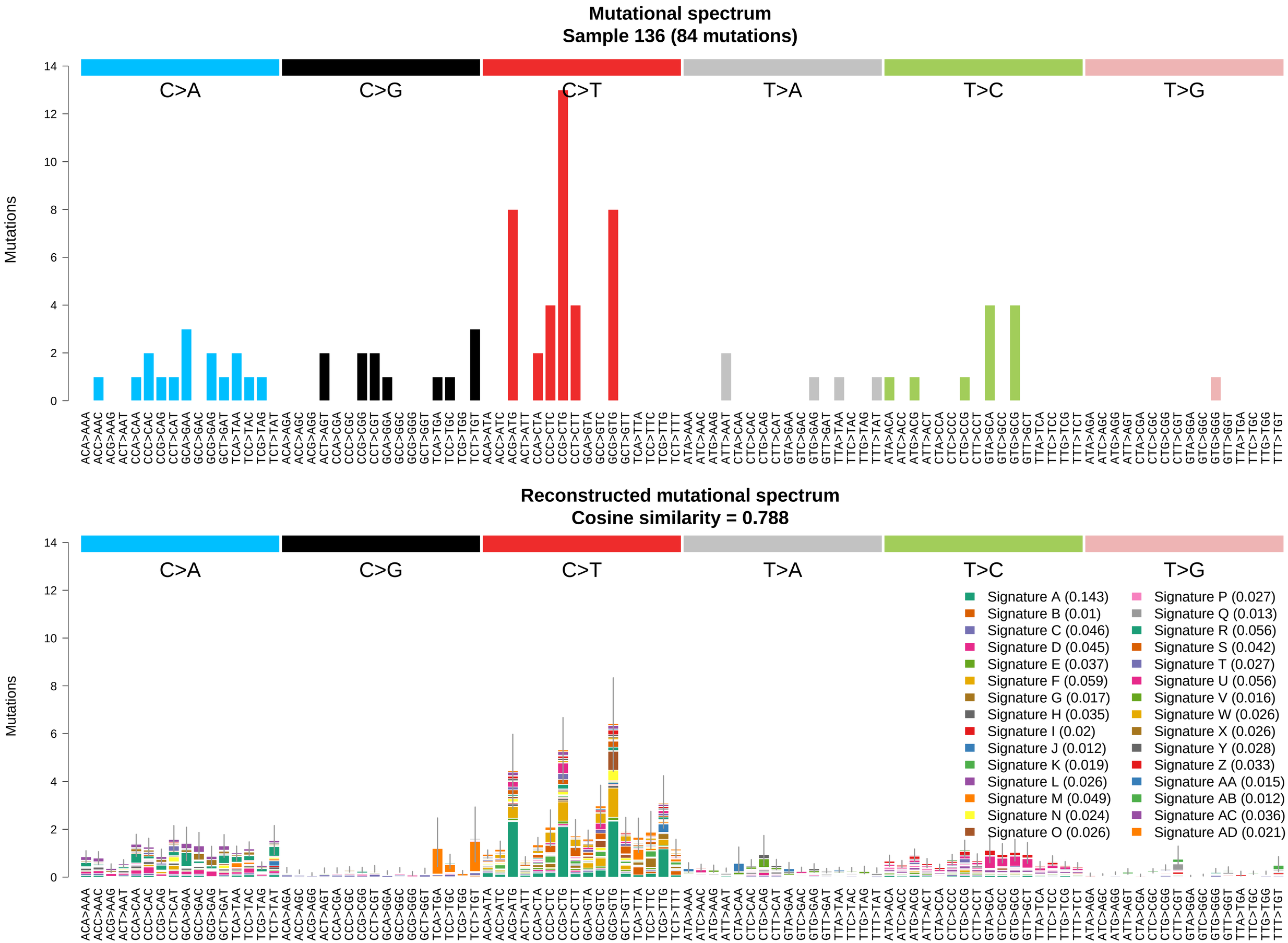

Reconstructed mutational spectrum
Cosine similarity = 0.551
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Signature A (0.039)
Signature B (0.036)
Signature C (0.032)
Signature D (0.044)
Signature E (0.037)
Signature F (0.032)
Signature G (0.042)
Signature H (0.04)
Signature I (0.026)
Signature J (0.027)
Signature K (0.033)
Signature L (0.035)
Signature M (0.023)
Signature N (0.027)
Signature O (0.027)
Signature P (0.036)
Signature Q (0.026)
Signature R (0.036)
Signature S (0.043)
Signature T (0.027)
Signature U (0.034)
Signature V (0.033)
Signature W (0.036)
Signature X (0.033)
Signature Y (0.032)
Signature Z (0.031)
Signature AA (0.026)
Signature AB (0.021)
Signature AC (0.048)
Signature AD (0.037)

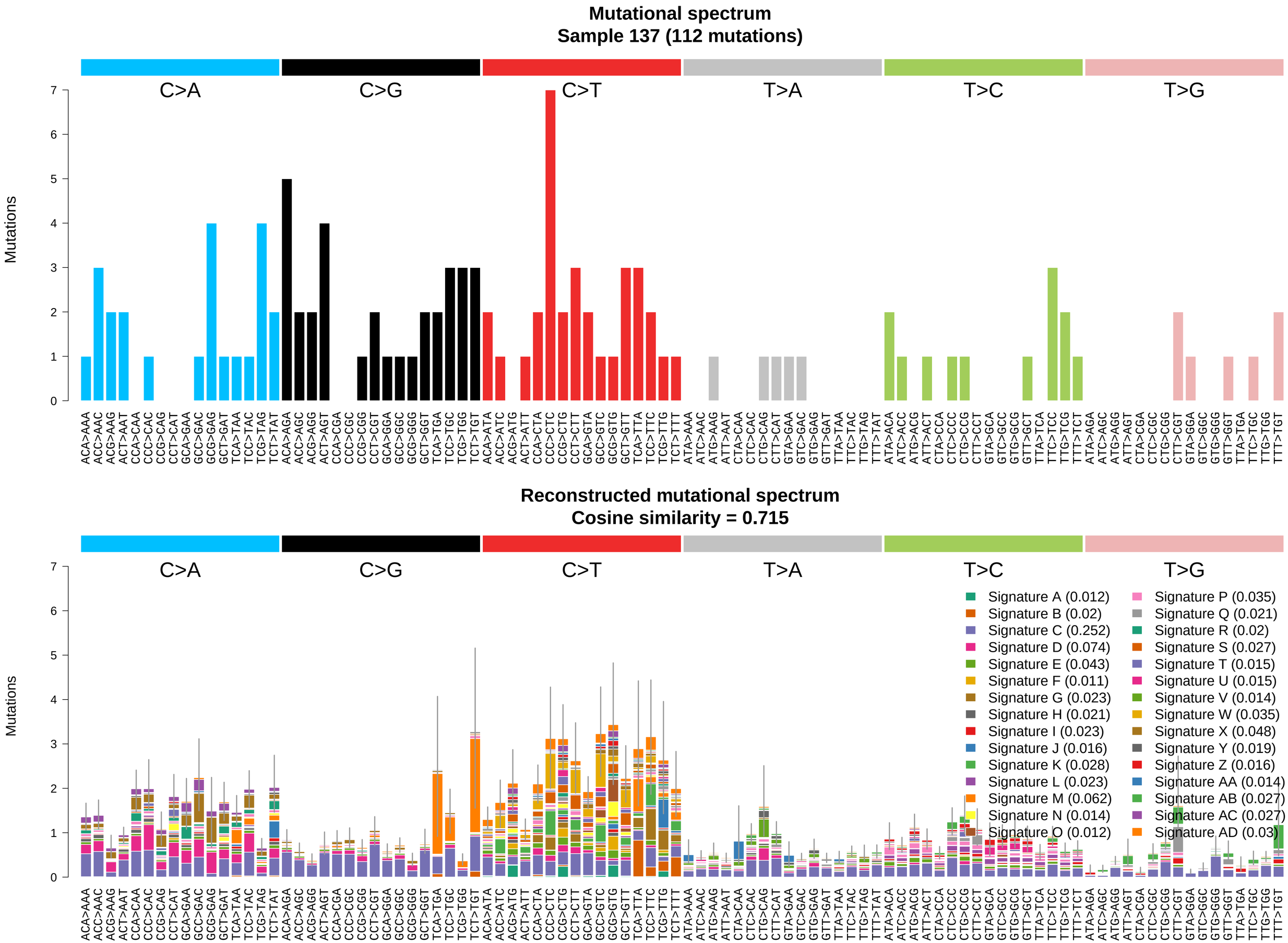

Mutational spectrum
Sample 133 (60 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.535
Signature A (0.025)
Signature B (0.014)
Signature C (0.138)
Signature D (0.064)
Signature E (0.06)
Signature F (0.021)
Signature G (0.017)
Signature H (0.035)
Signature I (0.028)
Signature J (0.019)
Signature K (0.021)
Signature L (0.048)
Signature M (0.033)
Signature N (0.017)
Signature O (0.017)
Signature P (0.055)
Signature Q (0.016)
Signature R (0.03)
Signature S (0.026)
Signature T (0.032)
Signature U (0.029)
Signature V (0.028)
Signature W (0.022)
Signature X (0.03)
Signature Y (0.043)
Signature Z (0.033)
Signature AA (0.021)
Signature AB (0.02)
Signature AC (0.028)
Signature AD (0.031)

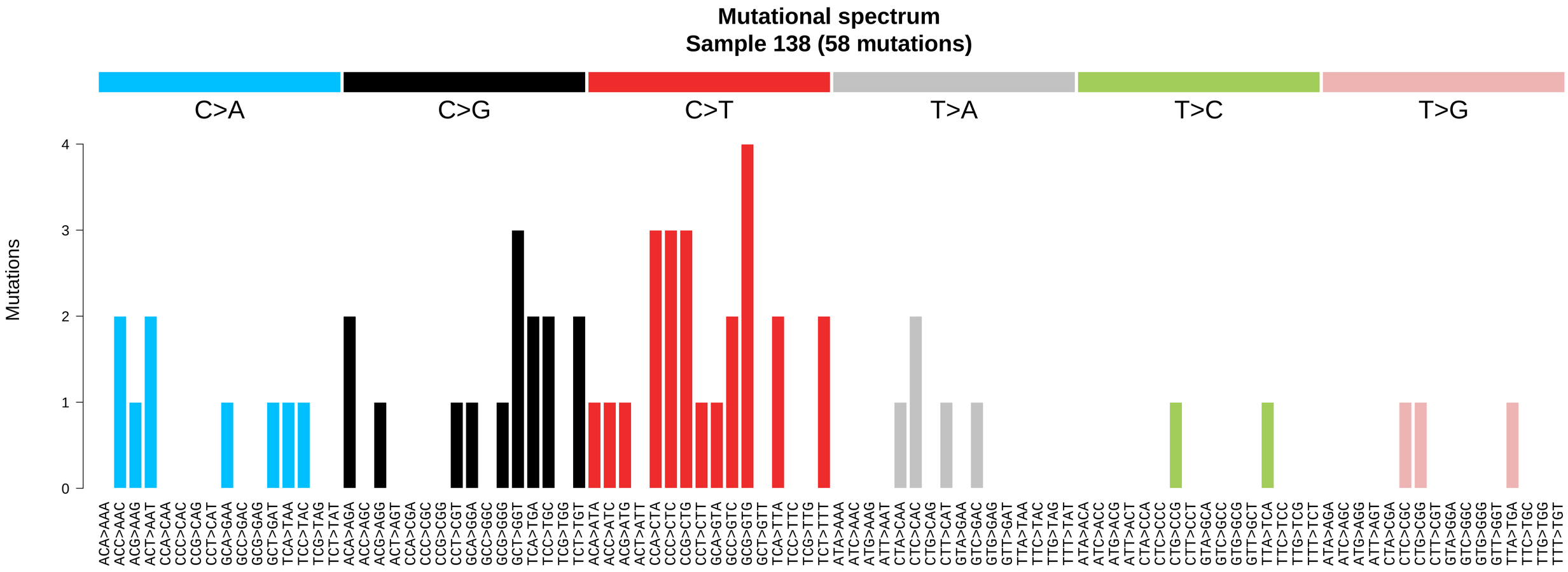

Mutational spectrum
Sample 134 (388 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
20
40
60
80
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

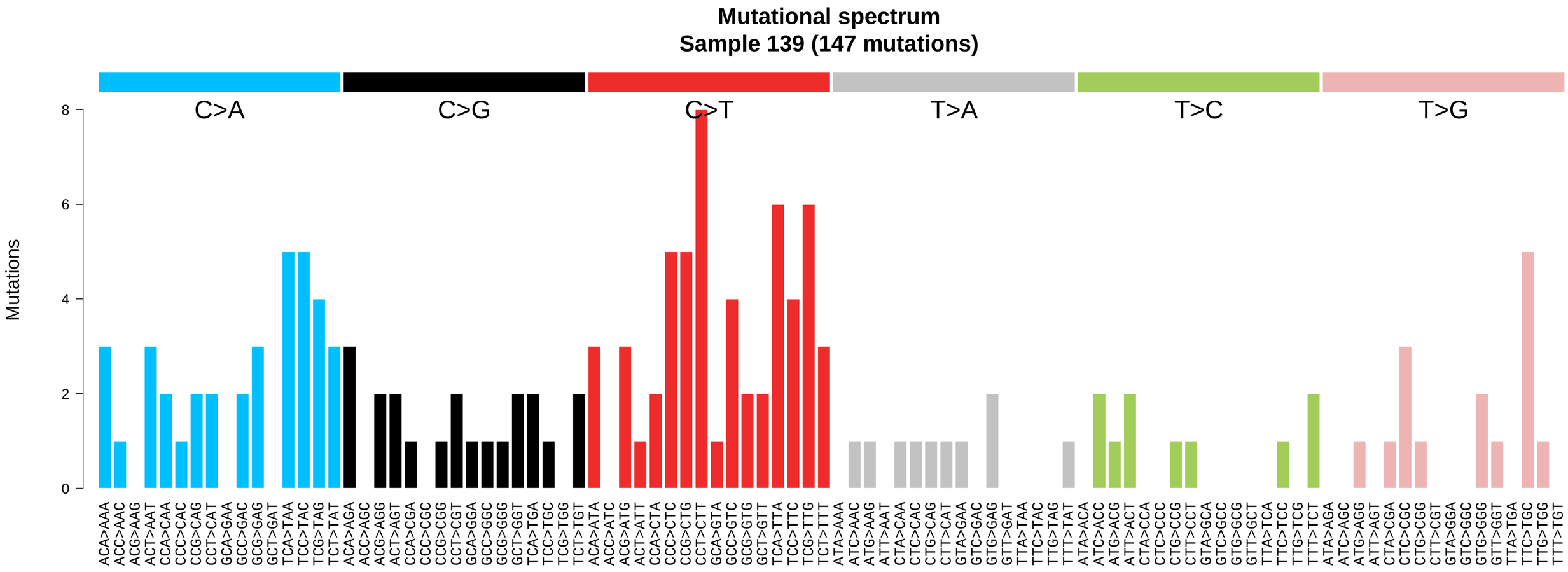

Reconstructed mutational spectrum
Cosine similarity = 0.891
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
20
40
60
80
Signature A (0.006)
Signature B (0.29)
Signature C (0.13)
Signature D (0.011)
Signature E (0.012)
Signature F (0.006)
Signature G (0.014)
Signature H (0.007)
Signature I (0.006)
Signature J (0.007)
Signature K (0.007)
Signature L (0.005)
Signature M (0.351)
Signature N (0.005)
Signature O (0.004)
Signature P (0.007)
Signature Q (0.004)
Signature R (0.009)
Signature S (0.012)
Signature T (0.007)
Signature U (0.004)
Signature V (0.003)
Signature W (0.01)
Signature X (0.01)
Signature Y (0.007)
Signature Z (0.004)
Signature AA (0.004)
Signature AB (0.003)
Signature AC (0.009)
Signature AD (0.048)

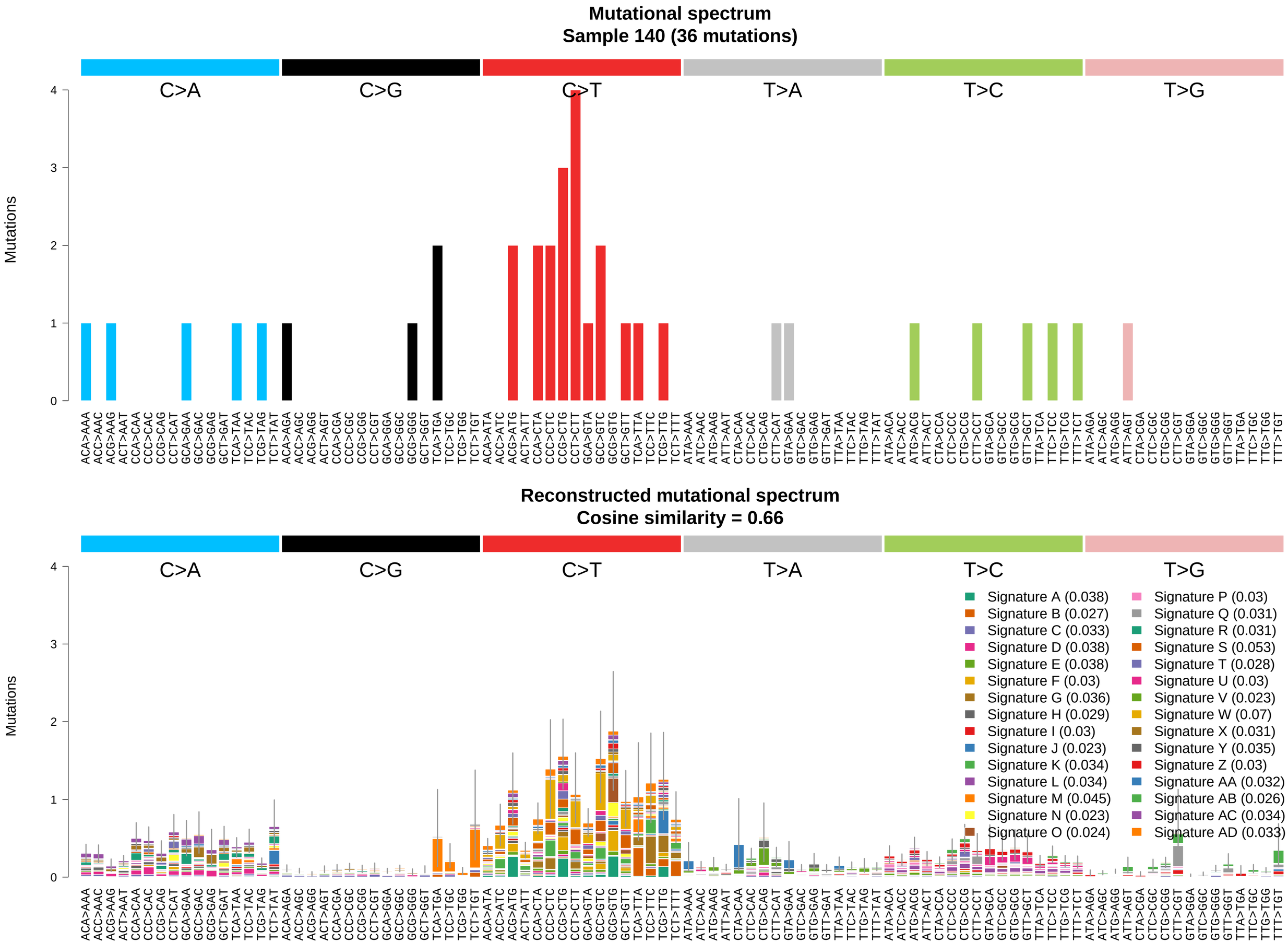

Mutational spectrum
Sample 135 (49 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.681
Signature A (0.04)
Signature B (0.025)
Signature C (0.041)
Signature D (0.027)
Signature E (0.036)
Signature F (0.032)
Signature G (0.033)
Signature H (0.036)
Signature I (0.042)
Signature J (0.03)
Signature K (0.035)
Signature L (0.04)
Signature M (0.044)
Signature N (0.026)
Signature O (0.02)
Signature P (0.037)
Signature Q (0.028)
Signature R (0.028)
Signature S (0.038)
Signature T (0.044)
Signature U (0.06)
Signature V (0.02)
Signature W (0.035)
Signature X (0.02)
Signature Y (0.036)
Signature Z (0.038)
Signature AA (0.019)
Signature AB (0.021)
Signature AC (0.024)
Signature AD (0.045)

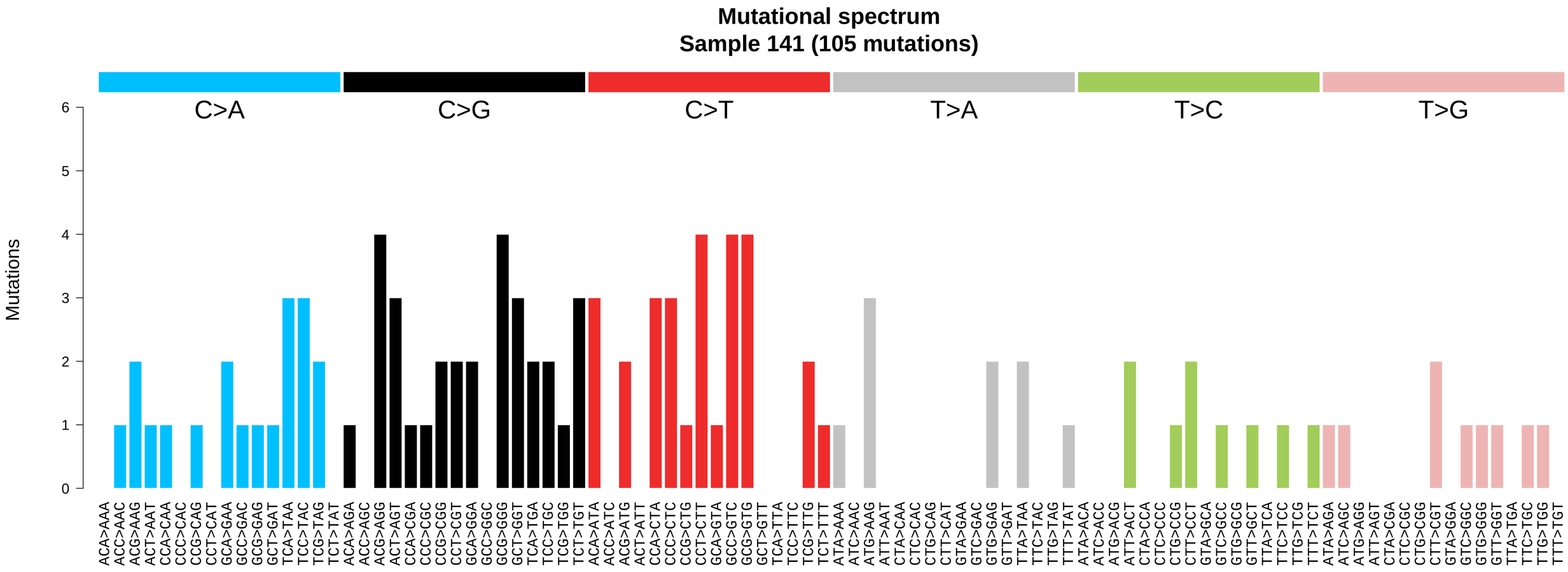

Mutational spectrum
Sample 136 (84 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.788
Signature A (0.143)
Signature B (0.01)
Signature C (0.046)
Signature D (0.045)
Signature E (0.037)
Signature F (0.059)
Signature G (0.017)
Signature H (0.035)
Signature I (0.02)
Signature J (0.012)
Signature K (0.019)
Signature L (0.026)
Signature M (0.049)
Signature N (0.024)
Signature O (0.026)
Signature P (0.027)
Signature Q (0.013)
Signature R (0.056)
Signature S (0.042)
Signature T (0.027)
Signature U (0.056)
Signature V (0.016)
Signature W (0.026)
Signature X (0.026)
Signature Y (0.028)
Signature Z (0.033)
Signature AA (0.015)
Signature AB (0.012)
Signature AC (0.036)
Signature AD (0.021)

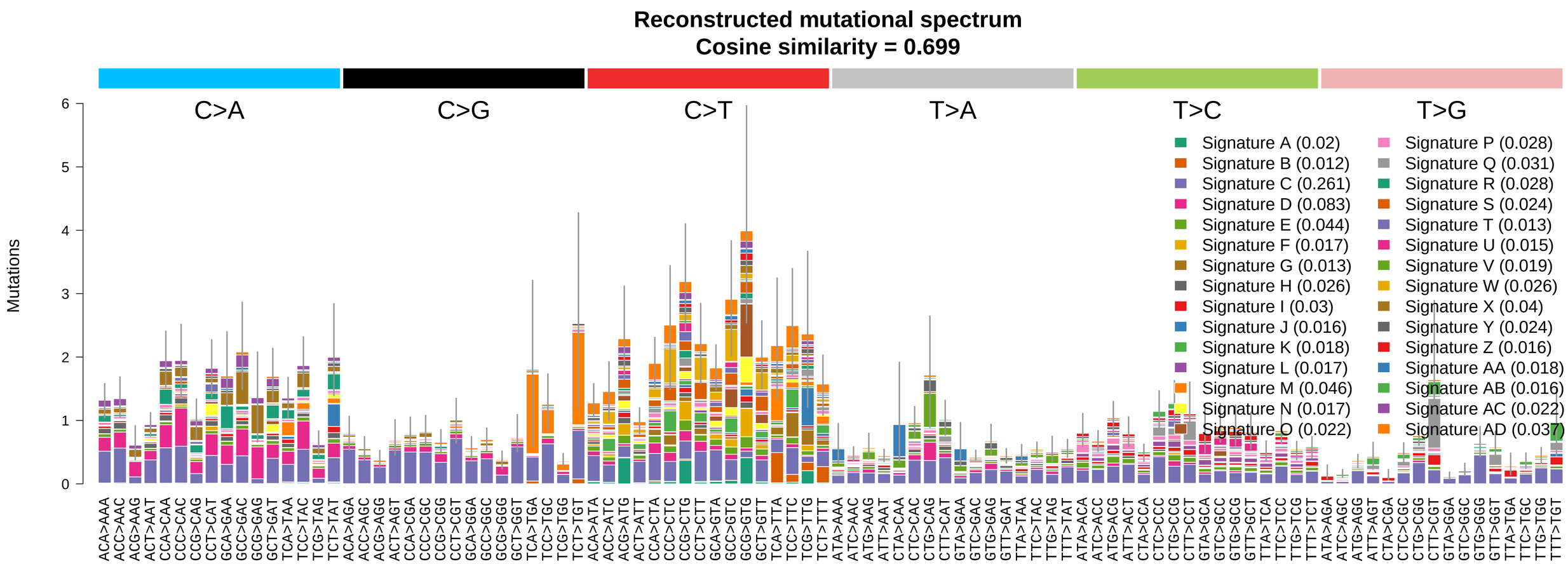

Mutational spectrum
Sample 137 (112 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.715
Signature A (0.012)
Signature B (0.02)
Signature C (0.252)
Signature D (0.074)
Signature E (0.043)
Signature F (0.011)
Signature G (0.023)
Signature H (0.021)
Signature I (0.023)
Signature J (0.016)
Signature K (0.028)
Signature L (0.023)
Signature M (0.062)
Signature N (0.014)
Signature O (0.012)
Signature P (0.035)
Signature Q (0.021)
Signature R (0.02)
Signature S (0.027)
Signature T (0.015)
Signature U (0.015)
Signature V (0.014)
Signature W (0.035)
Signature X (0.048)
Signature Y (0.019)
Signature Z (0.016)
Signature AA (0.014)
Signature AB (0.027)
Signature AC (0.027)
Signature AD (0.03)

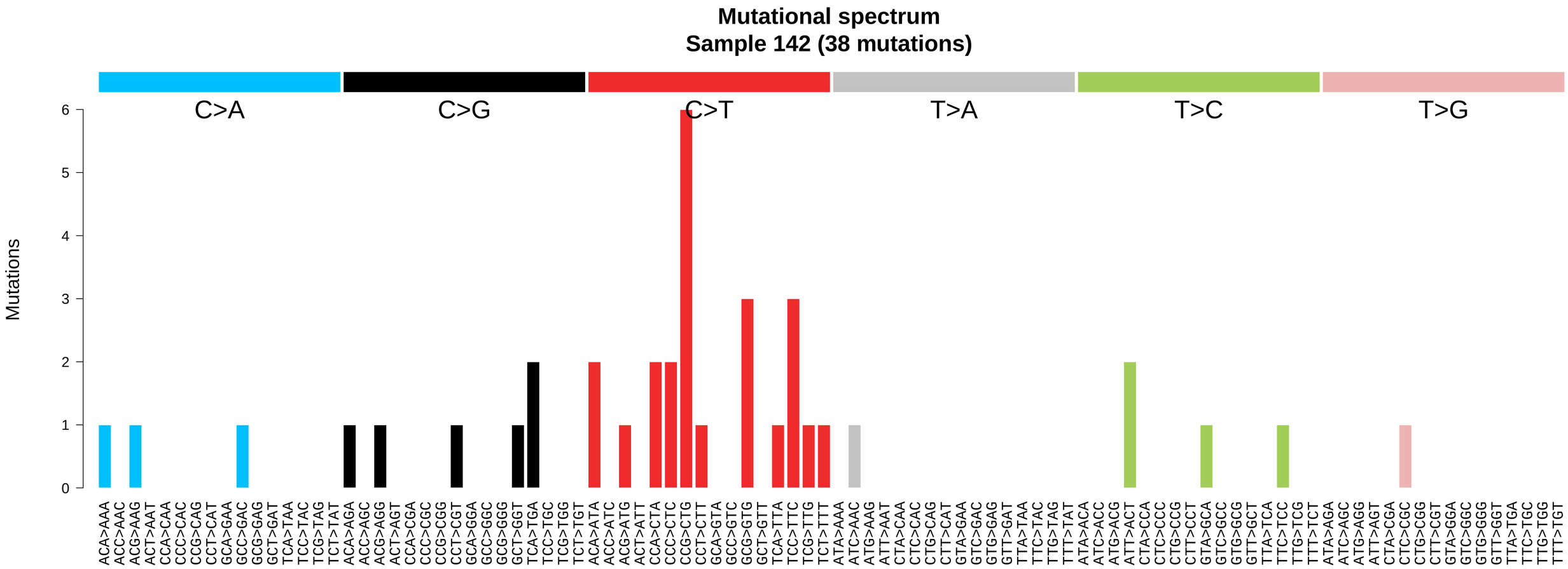

Mutational spectrum
Sample 138 (58 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.728
Signature A (0.032)
Signature B (0.03)
Signature C (0.127)
Signature D (0.046)
Signature E (0.038)
Signature F (0.029)
Signature G (0.024)
Signature H (0.038)
Signature I (0.029)
Signature J (0.016)
Signature K (0.03)
Signature L (0.023)
Signature M (0.079)
Signature N (0.029)
Signature O (0.029)
Signature P (0.027)
Signature Q (0.02)
Signature R (0.025)
Signature S (0.031)
Signature T (0.023)
Signature U (0.017)
Signature V (0.02)
Signature W (0.036)
Signature X (0.027)
Signature Y (0.029)
Signature Z (0.021)
Signature AA (0.029)
Signature AB (0.021)
Signature AC (0.032)
Signature AD (0.043)

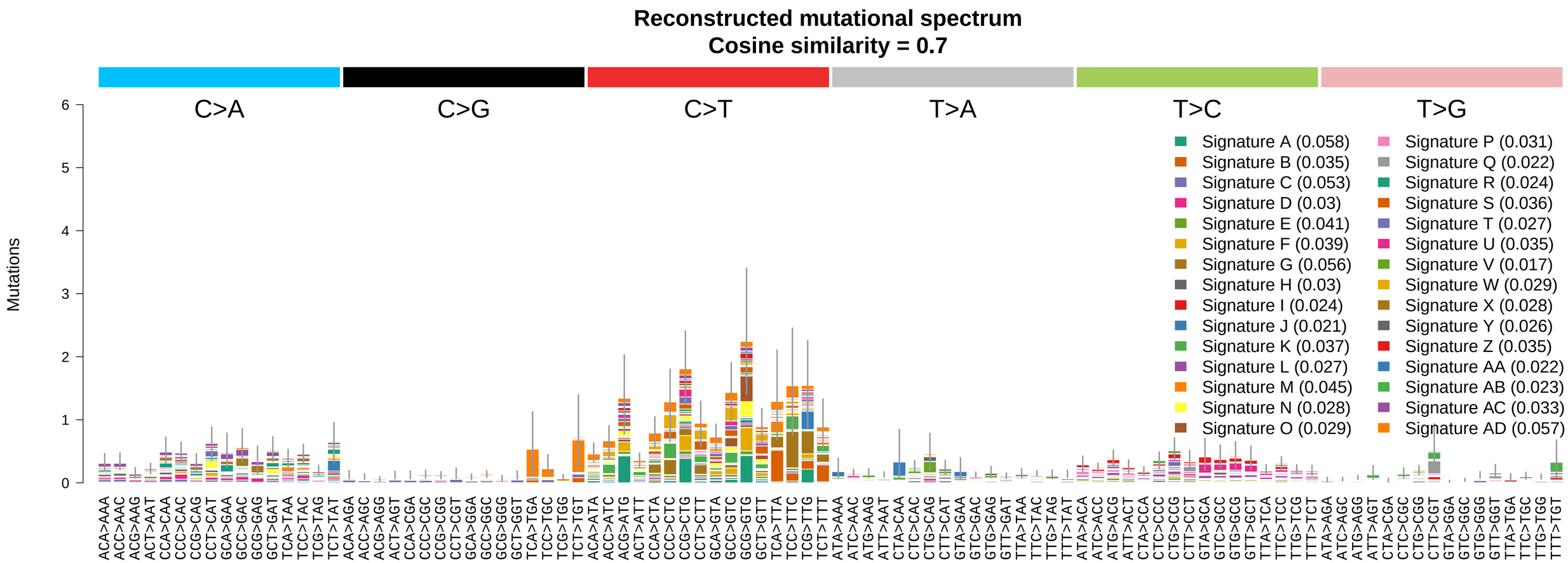

Mutational spectrum
Sample 139 (147 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.821
Signature A (0.02)
Signature B (0.047)
Signature C (0.188)
Signature D (0.066)
Signature E (0.043)
Signature F (0.016)
Signature G (0.039)
Signature H (0.037)
Signature I (0.027)
Signature J (0.032)
Signature K (0.026)
Signature L (0.015)
Signature M (0.029)
Signature N (0.014)
Signature O (0.012)
Signature P (0.033)
Signature Q (0.016)
Signature R (0.043)
Signature S (0.036)
Signature T (0.019)
Signature U (0.011)
Signature V (0.015)
Signature W (0.032)
Signature X (0.04)
Signature Y (0.022)
Signature Z (0.014)
Signature AA (0.017)
Signature AB (0.025)
Signature AC (0.028)
Signature AD (0.034)

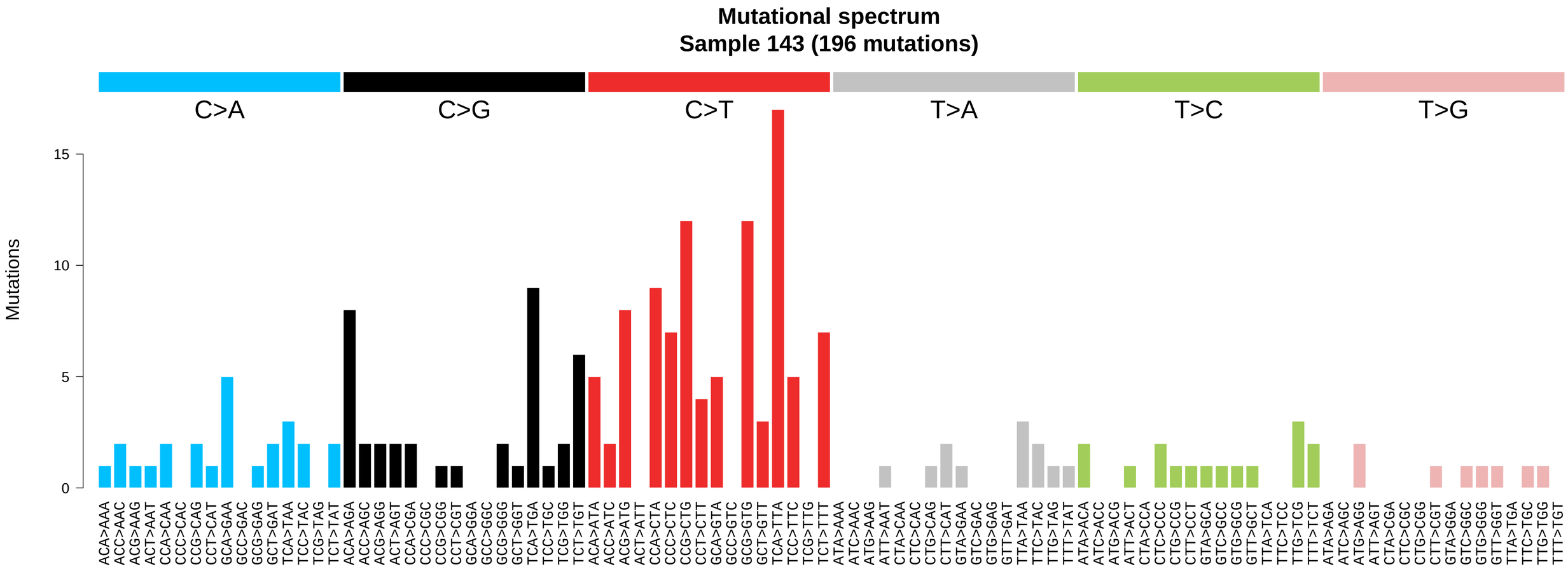

Mutational spectrum
Sample 140 (36 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.66
Signature A (0.038)
Signature B (0.027)
Signature C (0.033)
Signature D (0.038)
Signature E (0.038)
Signature F (0.03)
Signature G (0.036)
Signature H (0.029)
Signature I (0.03)
Signature J (0.023)
Signature K (0.034)
Signature L (0.034)
Signature M (0.045)
Signature N (0.023)
Signature O (0.024)
Signature P (0.03)
Signature Q (0.031)
Signature R (0.031)
Signature S (0.053)
Signature T (0.028)
Signature U (0.03)
Signature V (0.023)
Signature W (0.07)
Signature X (0.031)
Signature Y (0.035)
Signature Z (0.03)
Signature AA (0.032)
Signature AB (0.026)
Signature AC (0.034)
Signature AD (0.033)

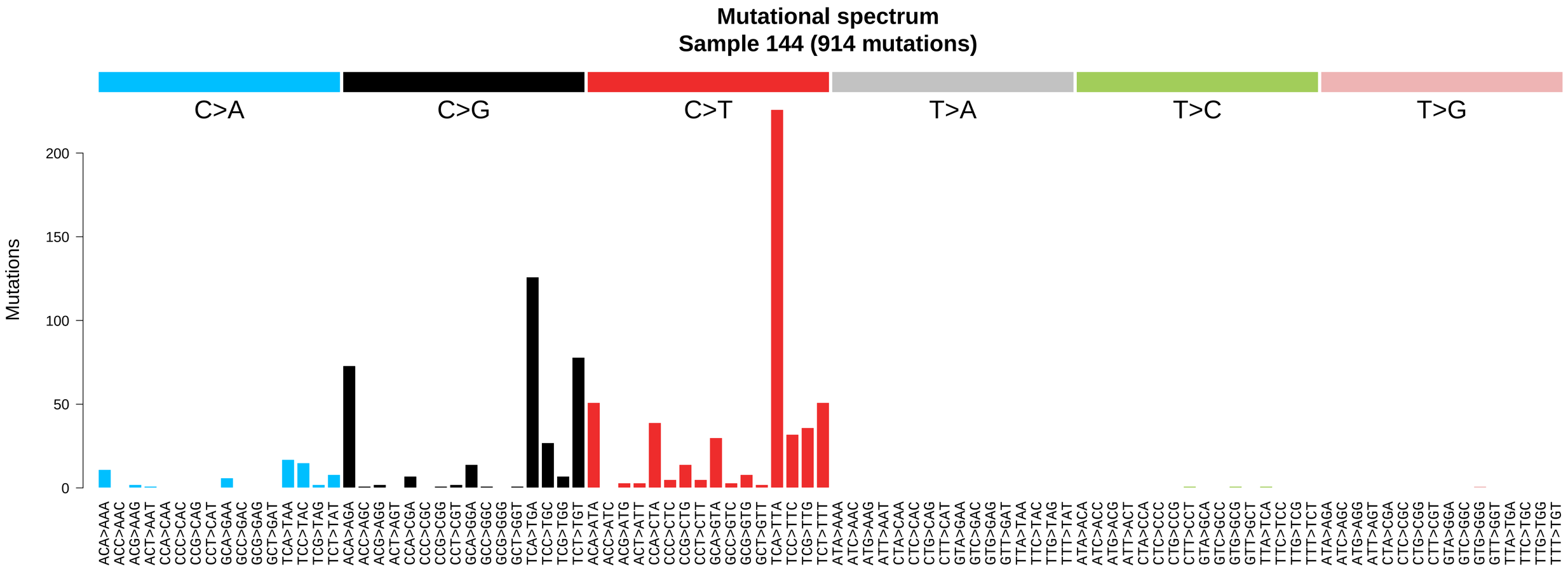

Mutational spectrum
Sample 141 (105 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations

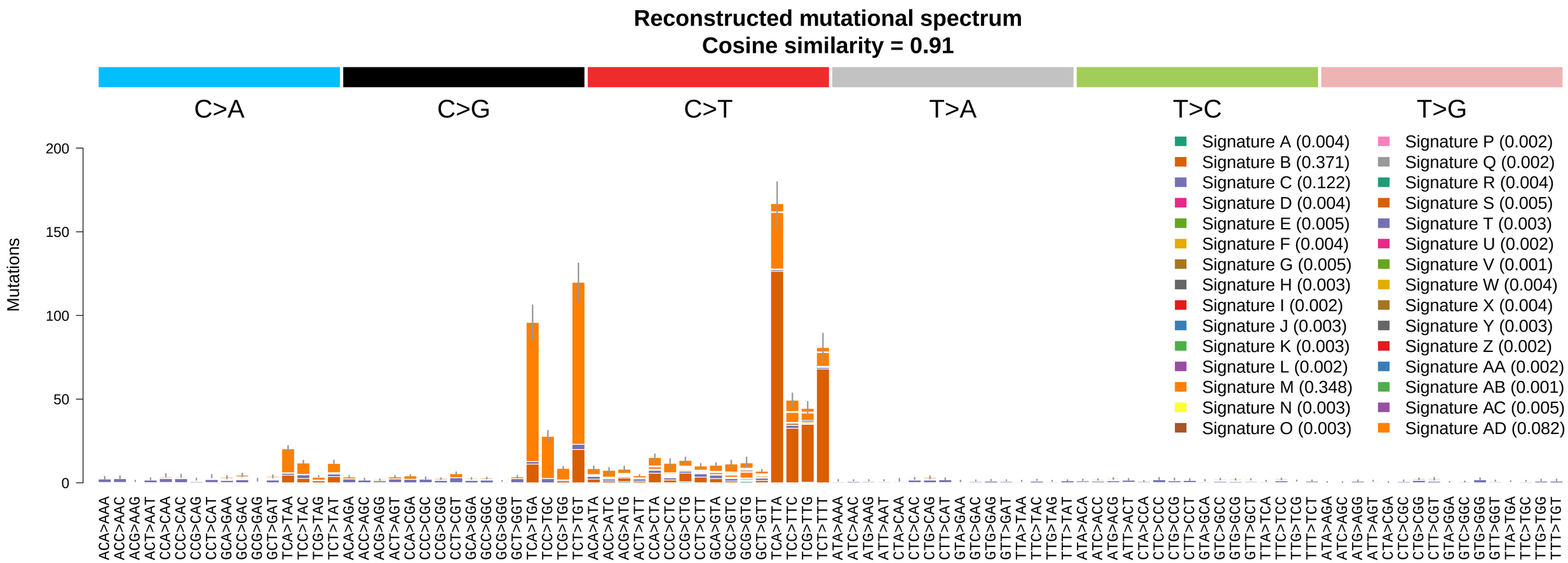

Reconstructed mutational spectrum
Cosine similarity = 0.699
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Signature A (0.02)
Signature B (0.012)
Signature C (0.261)
Signature D (0.083)
Signature E (0.044)
Signature F (0.017)
Signature G (0.013)
Signature H (0.026)
Signature I (0.03)
Signature J (0.016)
Signature K (0.018)
Signature L (0.017)
Signature M (0.046)
Signature N (0.017)
Signature O (0.022)
Signature P (0.028)
Signature Q (0.031)
Signature R (0.028)
Signature S (0.024)
Signature T (0.013)
Signature U (0.015)
Signature V (0.019)
Signature W (0.026)
Signature X (0.04)
Signature Y (0.024)
Signature Z (0.016)
Signature AA (0.018)
Signature AB (0.016)
Signature AC (0.022)
Signature AD (0.037)

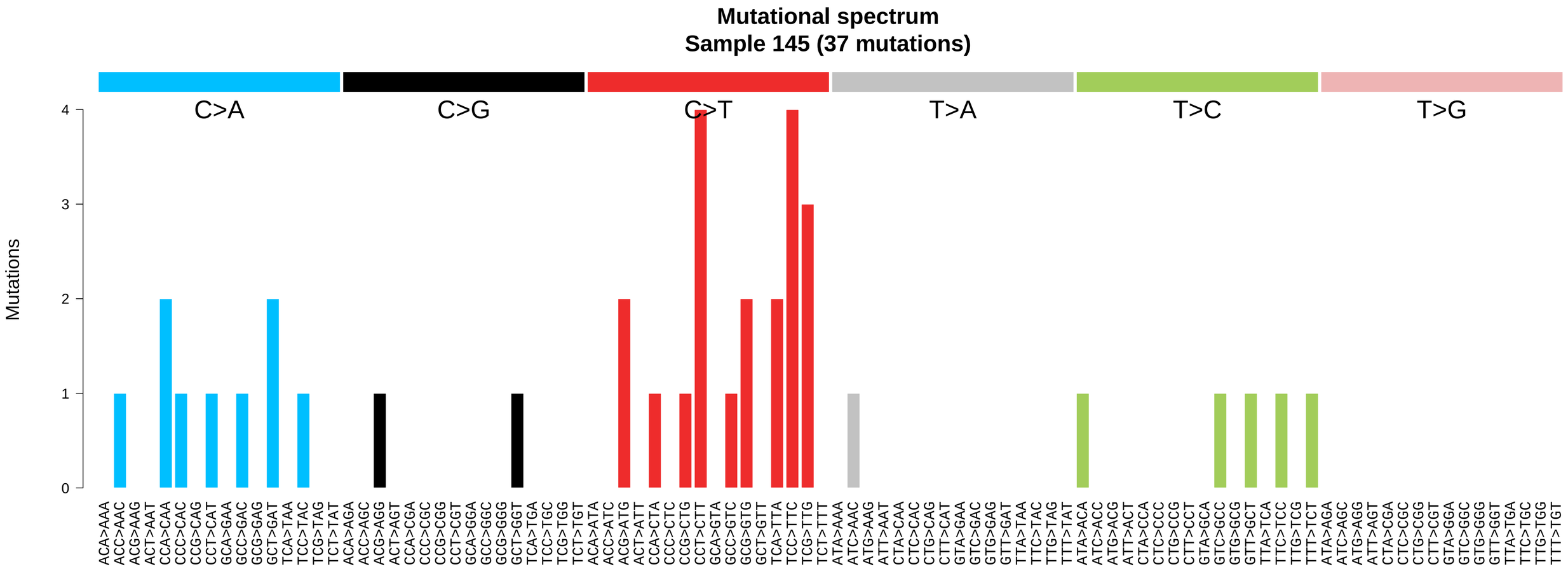

Mutational spectrum
Sample 142 (38 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

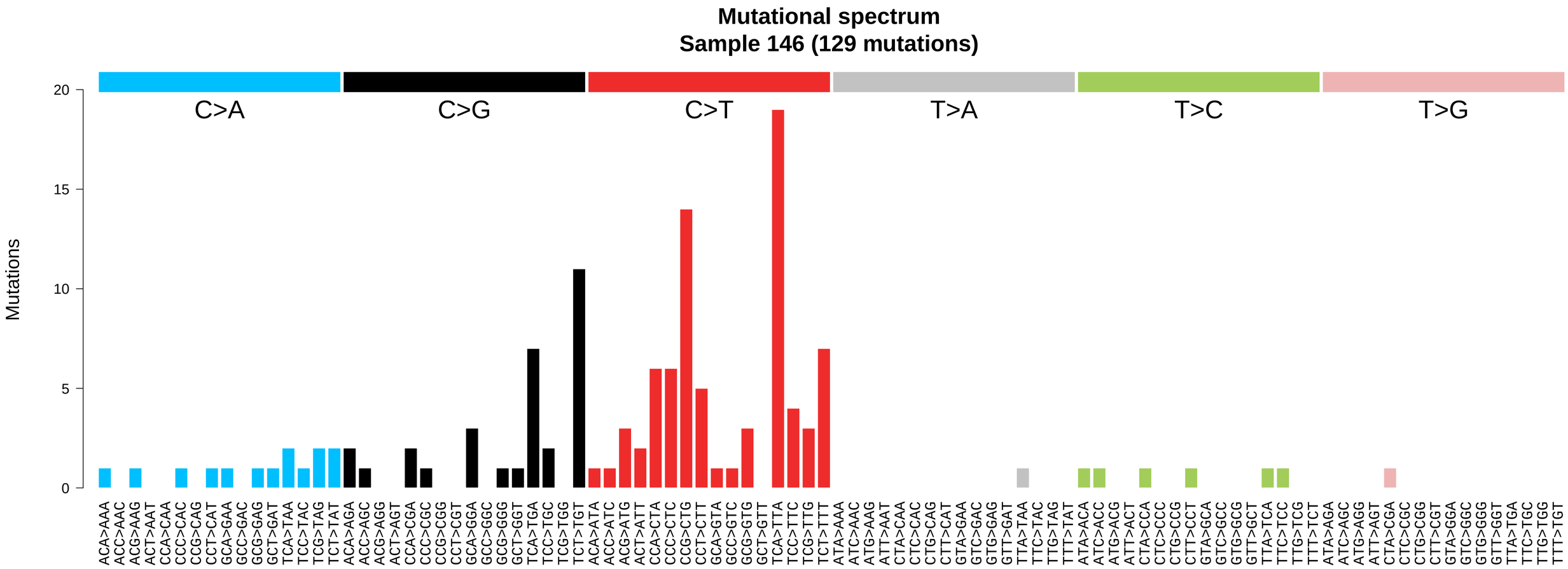

Reconstructed mutational spectrum
Cosine similarity = 0.7
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
Signature A (0.058)
Signature B (0.035)
Signature C (0.053)
Signature D (0.03)
Signature E (0.041)
Signature F (0.039)
Signature G (0.056)
Signature H (0.03)
Signature I (0.024)
Signature J (0.021)
Signature K (0.037)
Signature L (0.027)
Signature M (0.045)
Signature N (0.028)
Signature O (0.029)
Signature P (0.031)
Signature Q (0.022)
Signature R (0.024)
Signature S (0.036)
Signature T (0.027)
Signature U (0.035)
Signature V (0.017)
Signature W (0.029)
Signature X (0.028)
Signature Y (0.026)
Signature Z (0.035)
Signature AA (0.022)
Signature AB (0.023)
Signature AC (0.033)
Signature AD (0.057)

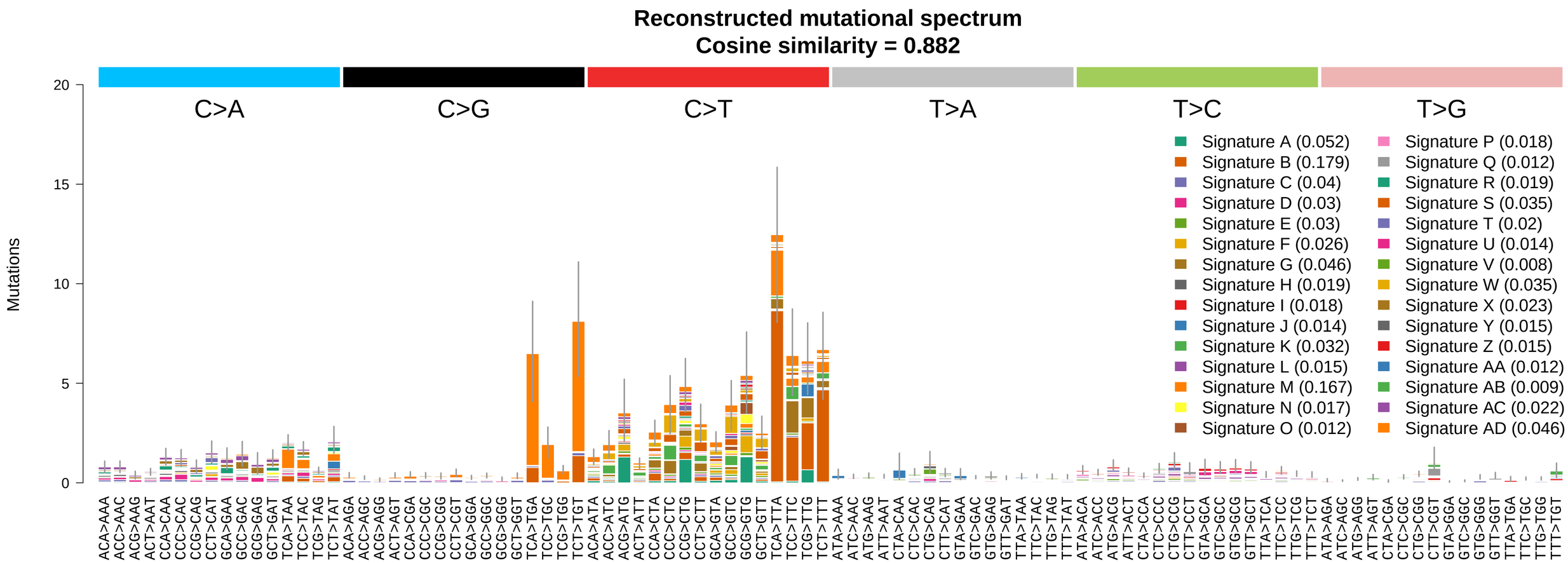

Mutational spectrum
Sample 143 (196 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.862
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
Signature A (0.059)
Signature B (0.095)
Signature C (0.151)
Signature D (0.023)
Signature E (0.051)
Signature F (0.032)
Signature G (0.021)
Signature H (0.025)
Signature I (0.019)
Signature J (0.008)
Signature K (0.019)
Signature L (0.019)
Signature M (0.093)
Signature N (0.021)
Signature O (0.02)
Signature P (0.022)
Signature Q (0.016)
Signature R (0.029)
Signature S (0.035)
Signature T (0.015)
Signature U (0.014)
Signature V (0.013)
Signature W (0.021)
Signature X (0.019)
Signature Y (0.026)
Signature Z (0.015)
Signature AA (0.014)
Signature AB (0.01)
Signature AC (0.024)
Signature AD (0.074)

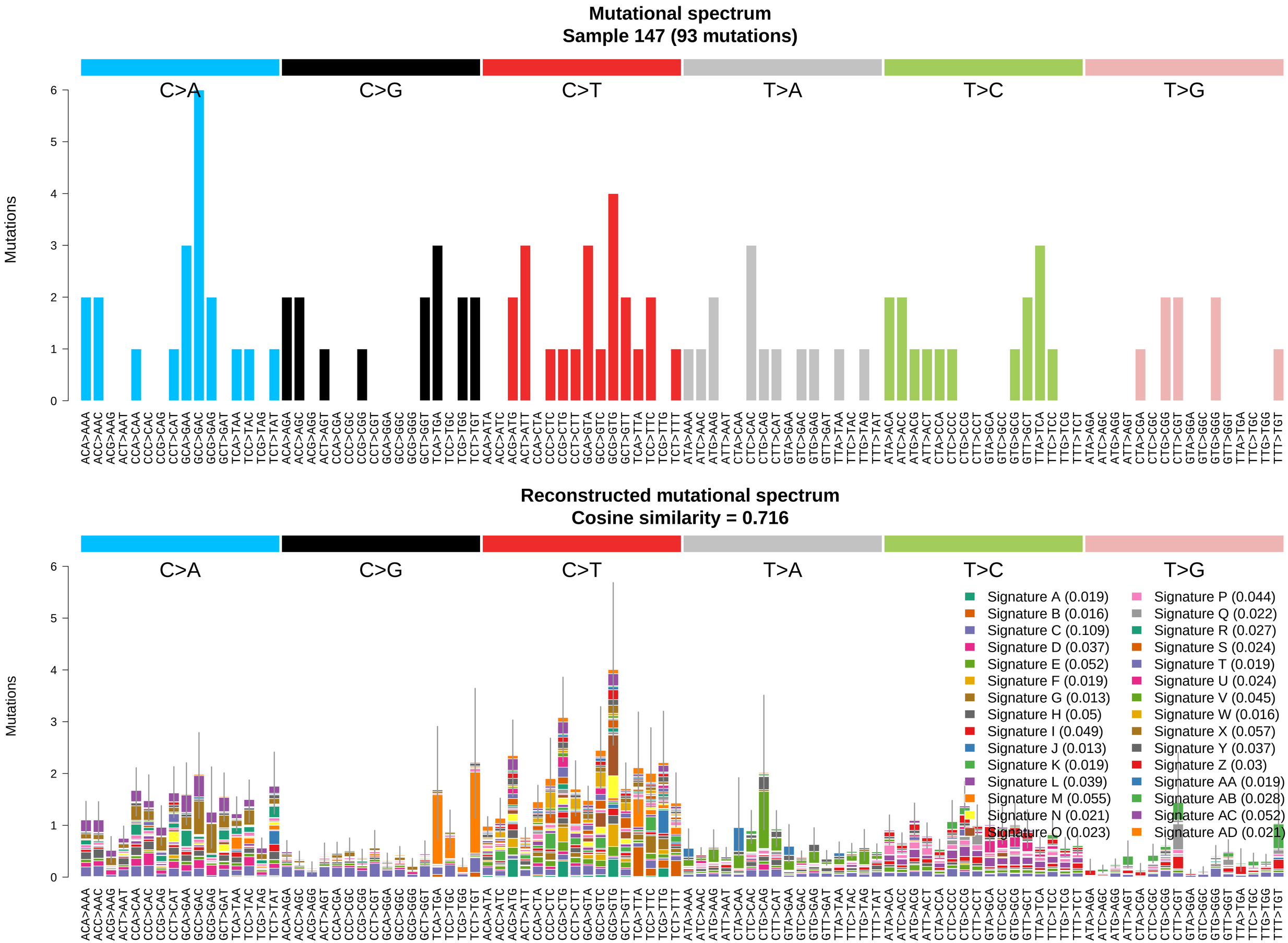

Mutational spectrum
Sample 144 (914 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
200
150
100
50
0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

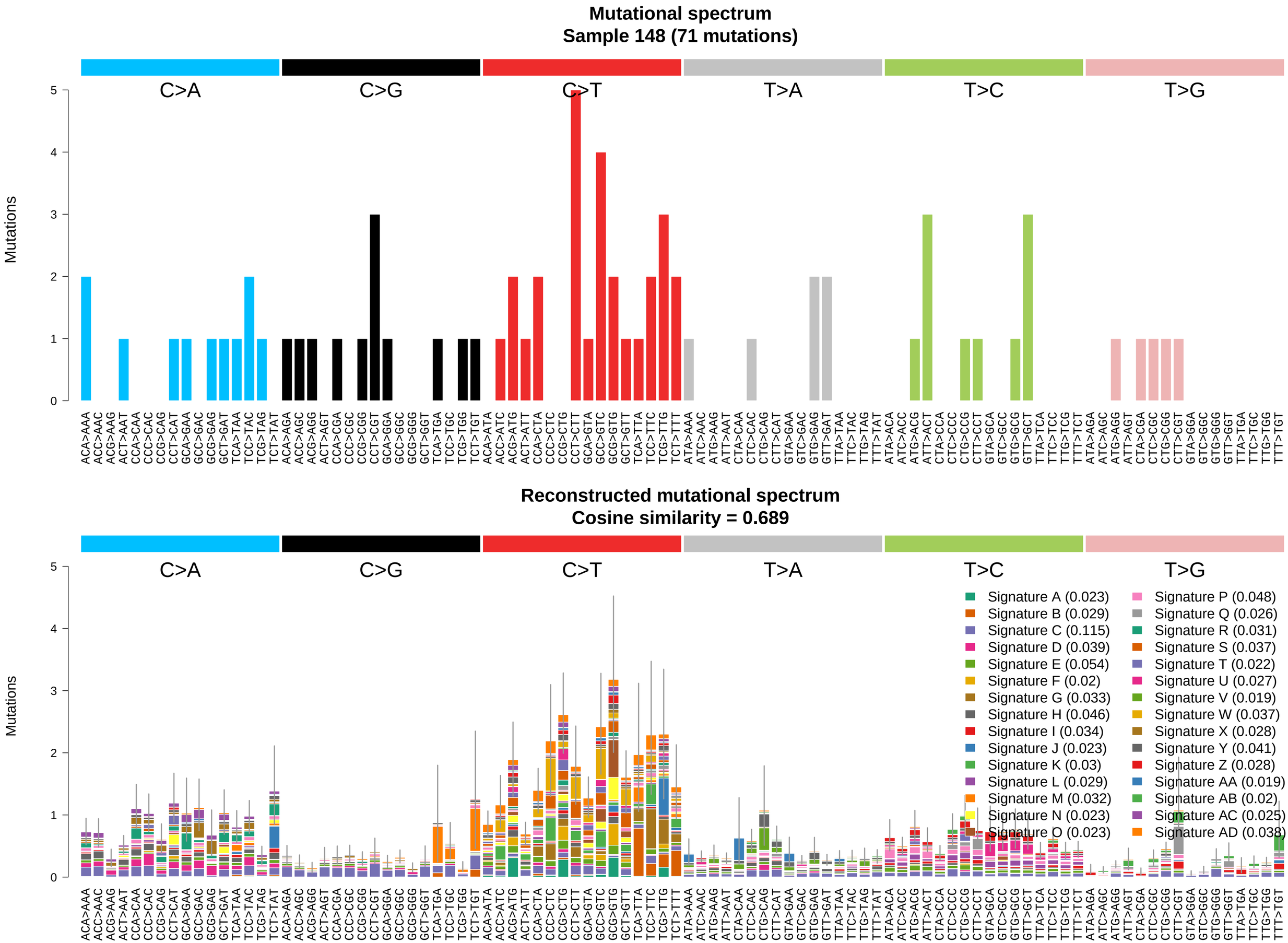

Reconstructed mutational spectrum
Cosine similarity = 0.91
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
200
150
100
50
0
Signature A (0.004)
Signature B (0.371)
Signature C (0.122)
Signature D (0.004)
Signature E (0.005)
Signature F (0.004)
Signature G (0.005)
Signature H (0.003)
Signature I (0.002)
Signature J (0.003)
Signature K (0.003)
Signature L (0.002)
Signature M (0.348)
Signature N (0.003)
Signature O (0.003)
Signature P (0.002)
Signature Q (0.002)
Signature R (0.004)
Signature S (0.005)
Signature T (0.003)
Signature U (0.002)
Signature V (0.001)
Signature W (0.004)
Signature X (0.004)
Signature Y (0.003)
Signature Z (0.002)
Signature AA (0.002)
Signature AB (0.001)
Signature AC (0.005)
Signature AD (0.082)

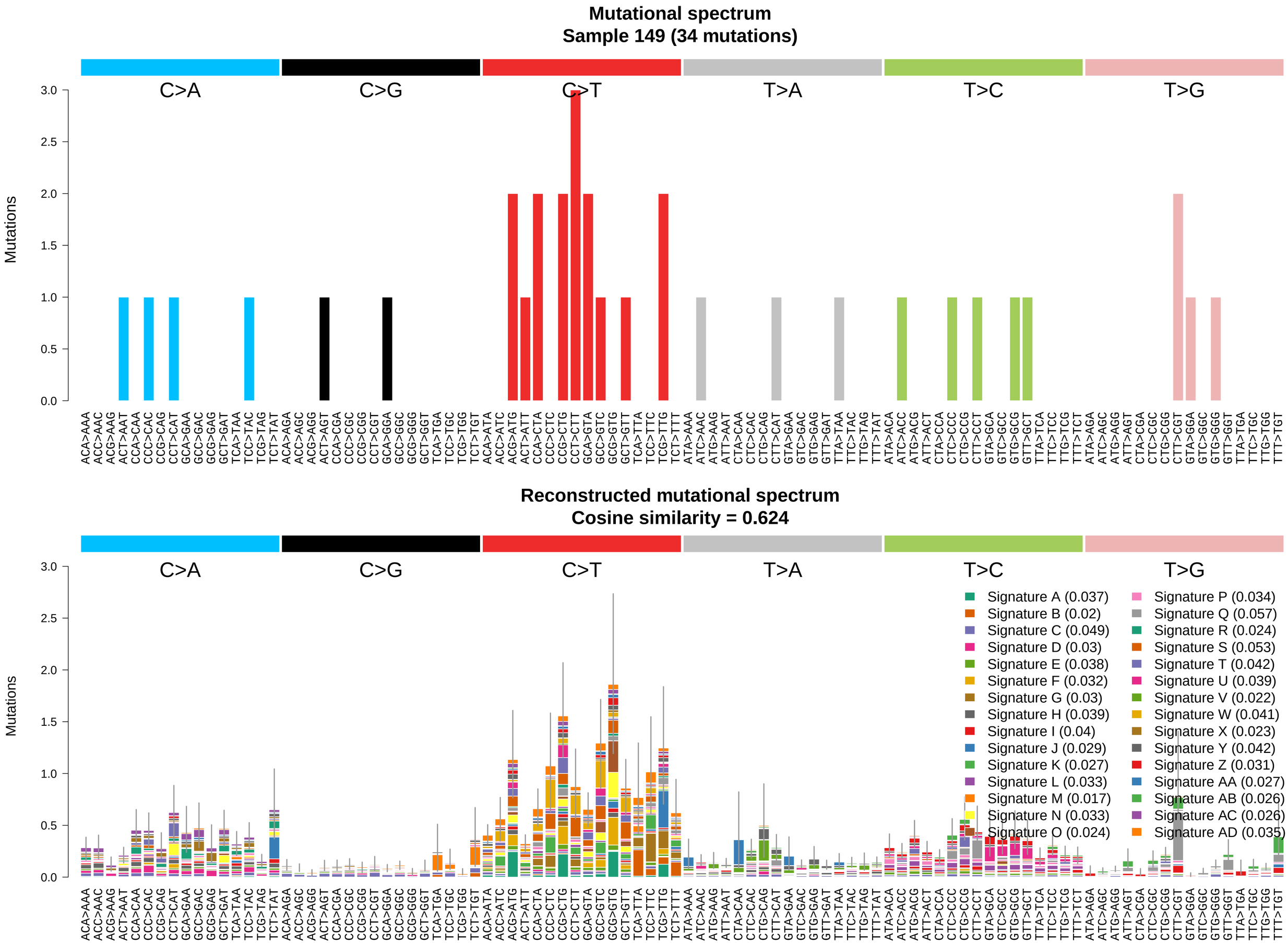

Mutational spectrum
Sample 145 (37 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.728
Signature A (0.038)
Signature B (0.037)
Signature C (0.036)
Signature D (0.038)
Signature E (0.033)
Signature F (0.029)
Signature G (0.082)
Signature H (0.037)
Signature I (0.028)
Signature J (0.032)
Signature K (0.032)
Signature L (0.033)
Signature M (0.019)
Signature N (0.037)
Signature O (0.031)
Signature P (0.031)
Signature Q (0.021)
Signature R (0.04)
Signature S (0.04)
Signature T (0.027)
Signature U (0.039)
Signature V (0.018)
Signature W (0.032)
Signature X (0.035)
Signature Y (0.025)
Signature Z (0.034)
Signature AA (0.022)
Signature AB (0.018)
Signature AC (0.04)
Signature AD (0.037)

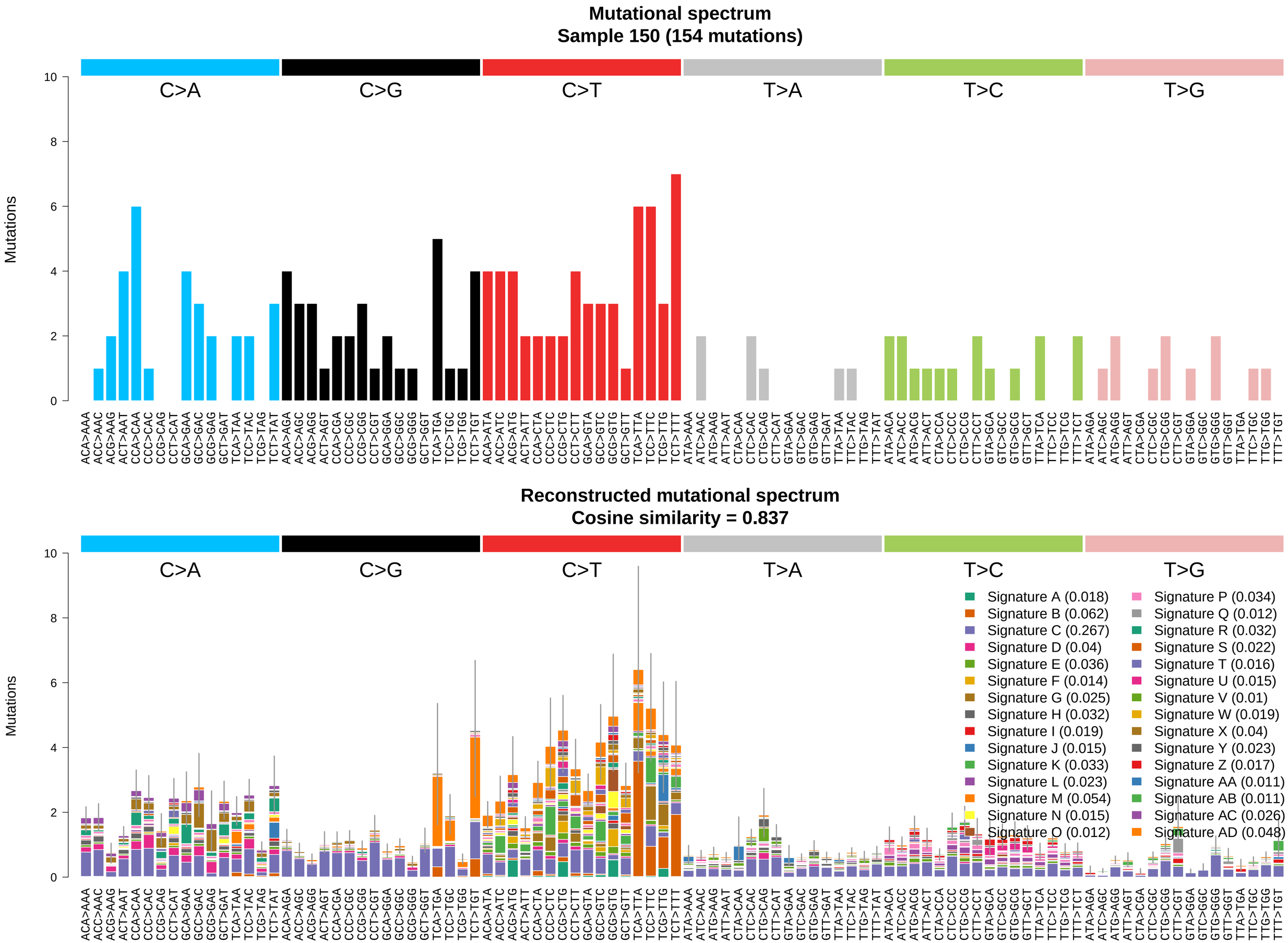

Mutational spectrum
Sample 146 (129 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

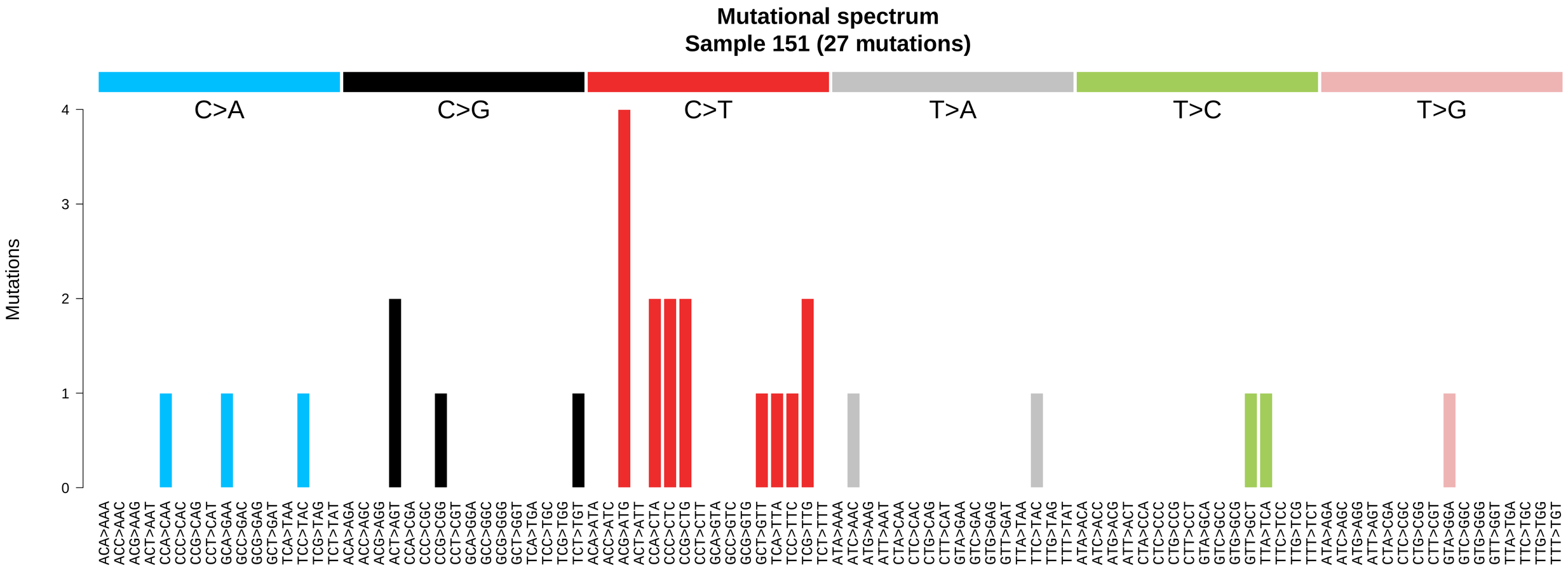

Reconstructed mutational spectrum
Cosine similarity = 0.882
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
20
Signature A (0.052)
Signature B (0.179)
Signature C (0.04)
Signature D (0.03)
Signature E (0.03)
Signature F (0.026)
Signature G (0.046)
Signature H (0.019)
Signature I (0.018)
Signature J (0.014)
Signature K (0.032)
Signature L (0.015)
Signature M (0.167)
Signature N (0.017)
Signature O (0.012)
Signature P (0.018)
Signature Q (0.012)
Signature R (0.019)
Signature S (0.035)
Signature T (0.02)
Signature U (0.014)
Signature V (0.008)
Signature W (0.035)
Signature X (0.023)
Signature Y (0.015)
Signature Z (0.015)
Signature AA (0.012)
Signature AB (0.009)
Signature AC (0.022)
Signature AD (0.046)

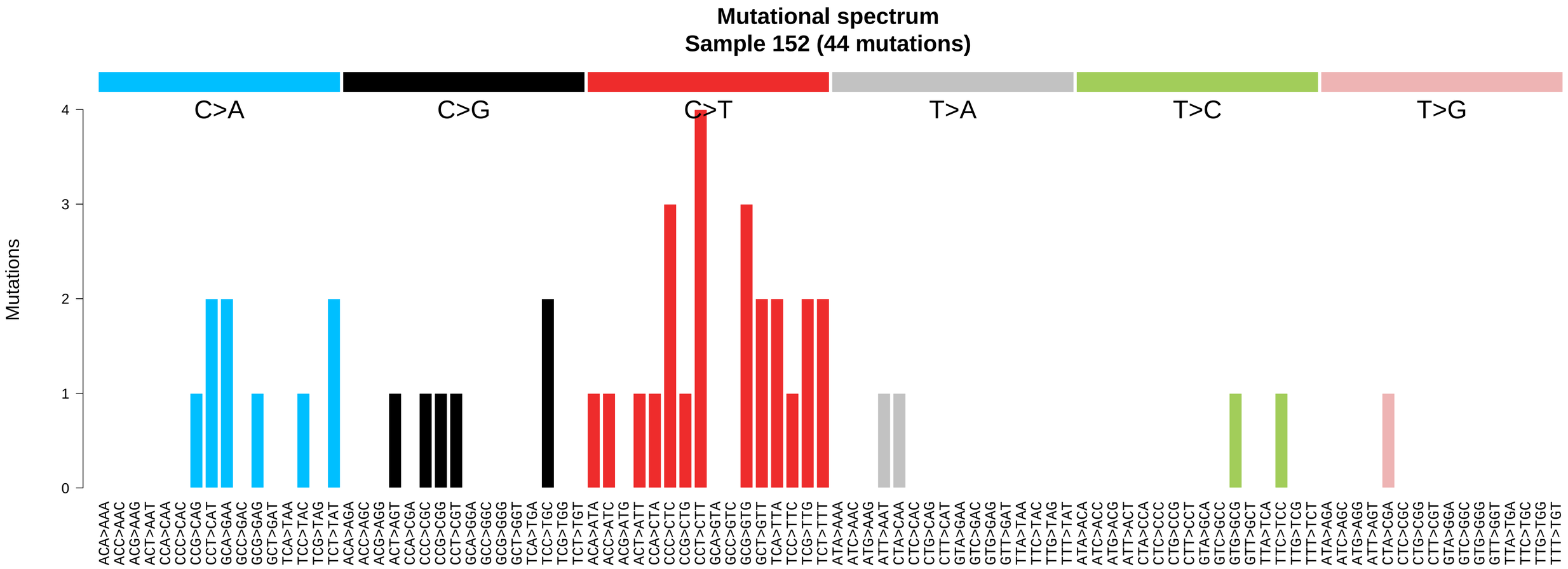

Mutational spectrum
Sample 147 (93 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.716
Signature A (0.019)
Signature B (0.016)
Signature C (0.109)
Signature D (0.037)
Signature E (0.052)
Signature F (0.019)
Signature G (0.013)
Signature H (0.05)
Signature I (0.049)
Signature J (0.013)
Signature K (0.019)
Signature L (0.039)
Signature M (0.055)
Signature N (0.021)
Signature O (0.023)
Signature P (0.044)
Signature Q (0.022)
Signature R (0.027)
Signature S (0.024)
Signature T (0.019)
Signature U (0.024)
Signature V (0.045)
Signature W (0.016)
Signature X (0.057)
Signature Y (0.037)
Signature Z (0.03)
Signature AA (0.019)
Signature AB (0.028)
Signature AC (0.052)
Signature AD (0.021)

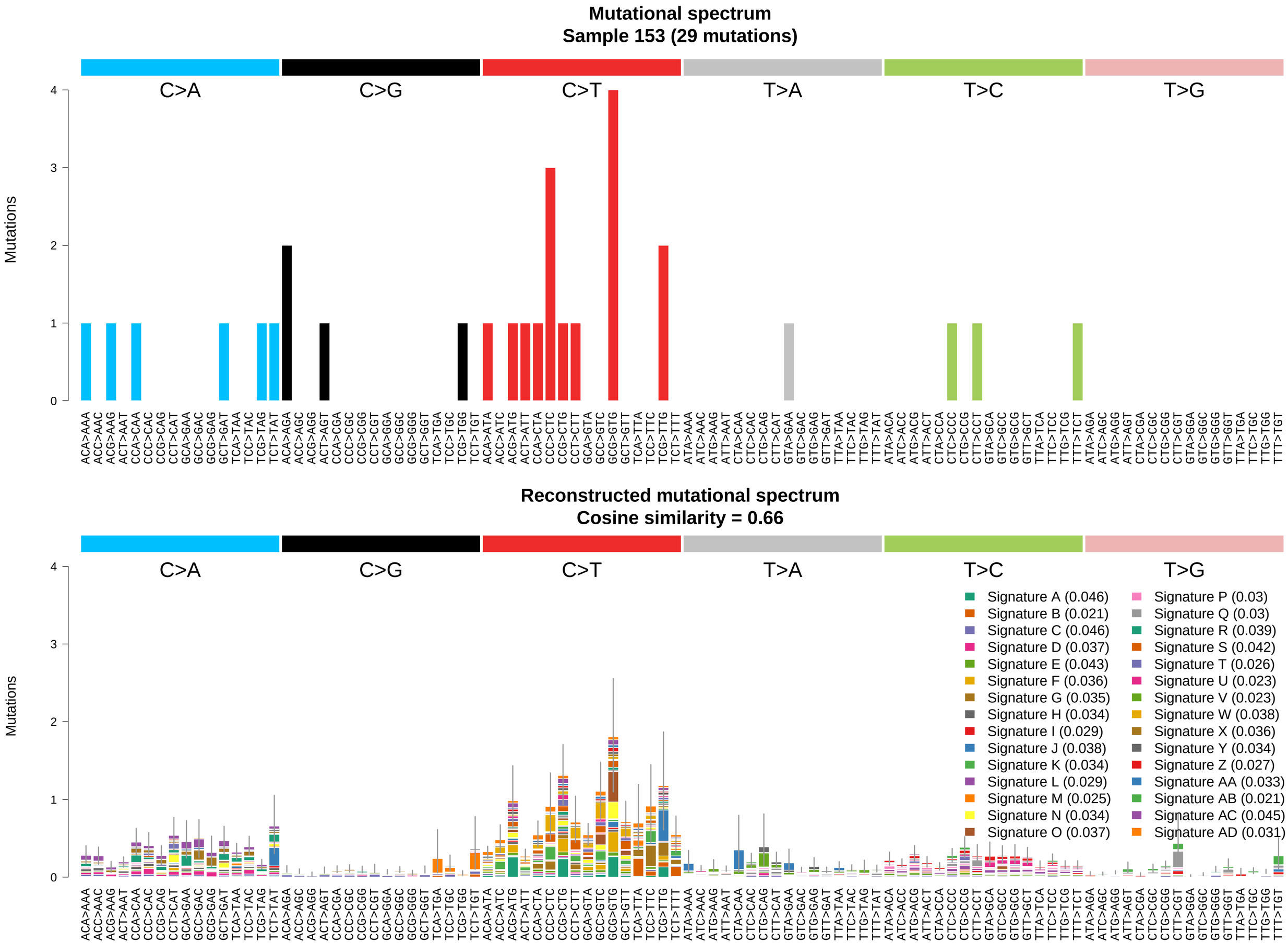

Mutational spectrum
Sample 148 (71 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.689
Signature A (0.023)
Signature B (0.029)
Signature C (0.115)
Signature D (0.039)
Signature E (0.054)
Signature F (0.02)
Signature G (0.033)
Signature H (0.046)
Signature I (0.034)
Signature J (0.023)
Signature K (0.03)
Signature L (0.029)
Signature M (0.032)
Signature N (0.023)
Signature O (0.023)
Signature P (0.048)
Signature Q (0.026)
Signature R (0.031)
Signature S (0.037)
Signature T (0.022)
Signature U (0.027)
Signature V (0.019)
Signature W (0.037)
Signature X (0.028)
Signature Y (0.041)
Signature Z (0.028)
Signature AA (0.019)
Signature AB (0.02)
Signature AC (0.025)
Signature AD (0.038)

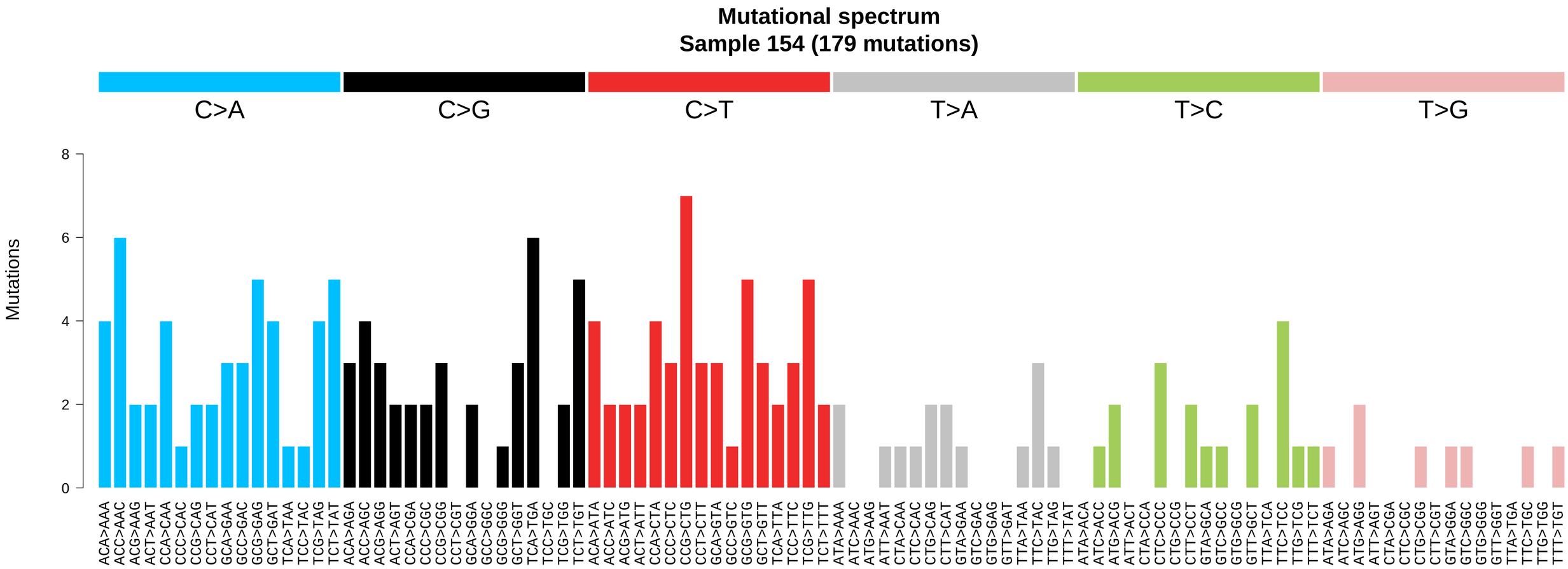

Mutational spectrum
Sample 149 (34 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.624
Signature A (0.037)
Signature B (0.02)
Signature C (0.049)
Signature D (0.03)
Signature E (0.038)
Signature F (0.032)
Signature G (0.03)
Signature H (0.039)
Signature I (0.04)
Signature J (0.029)
Signature K (0.027)
Signature L (0.033)
Signature M (0.017)
Signature N (0.033)
Signature O (0.024)
Signature P (0.034)
Signature Q (0.057)
Signature R (0.024)
Signature S (0.053)
Signature T (0.042)
Signature U (0.039)
Signature V (0.022)
Signature W (0.041)
Signature X (0.023)
Signature Y (0.042)
Signature Z (0.031)
Signature AA (0.027)
Signature AB (0.026)
Signature AC (0.026)
Signature AD (0.035)

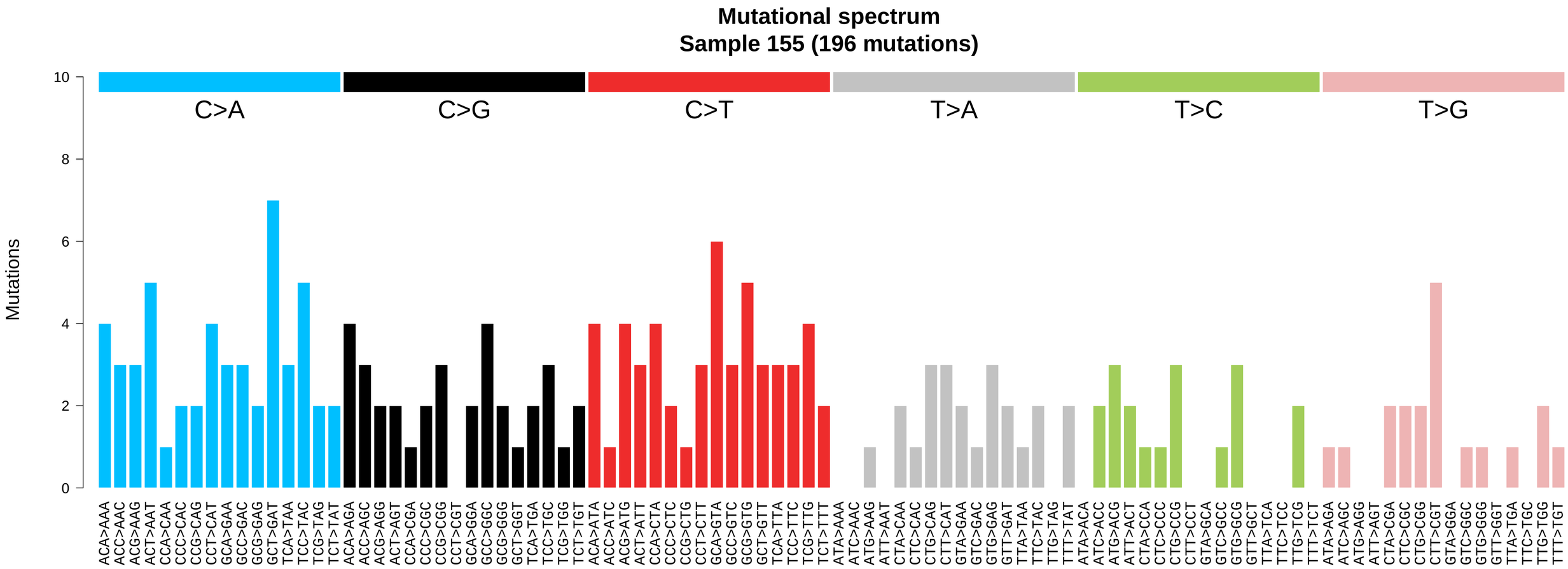

Mutational spectrum
Sample 150 (154 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.837
Signature A (0.018)
Signature B (0.062)
Signature C (0.267)
Signature D (0.04)
Signature E (0.036)
Signature F (0.014)
Signature G (0.025)
Signature H (0.032)
Signature I (0.019)
Signature J (0.015)
Signature K (0.033)
Signature L (0.023)
Signature M (0.054)
Signature N (0.015)
Signature O (0.012)
Signature P (0.034)
Signature Q (0.012)
Signature R (0.032)
Signature S (0.022)
Signature T (0.016)
Signature U (0.015)
Signature V (0.01)
Signature W (0.019)
Signature X (0.04)
Signature Y (0.023)
Signature Z (0.017)
Signature AA (0.011)
Signature AB (0.011)
Signature AC (0.026)
Signature AD (0.048)

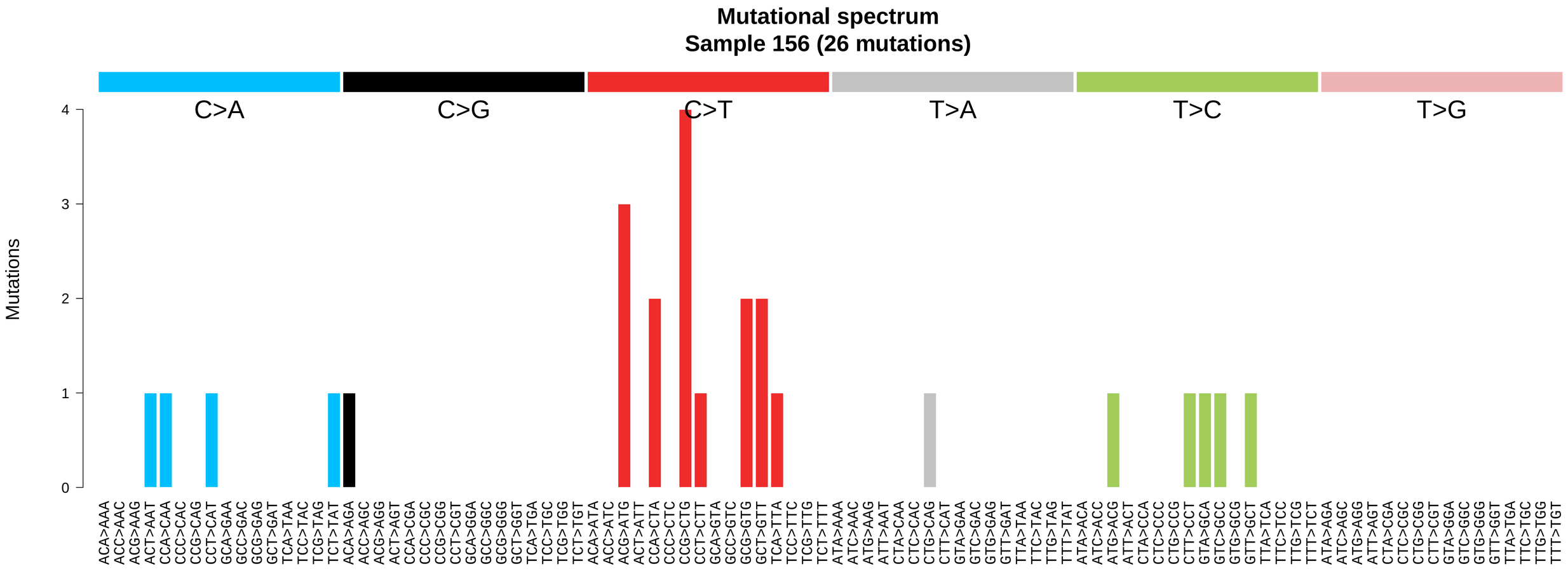

Mutational spectrum
Sample 151 (27 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.595
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
Signature A (0.06)
Signature B (0.035)
Signature C (0.048)
Signature D (0.029)
Signature E (0.039)
Signature F (0.034)
Signature G (0.045)
Signature H (0.035)
Signature I (0.033)
Signature J (0.029)
Signature K (0.03)
Signature L (0.031)
Signature M (0.034)
Signature N (0.027)
Signature O (0.024)
Signature P (0.031)
Signature Q (0.023)
Signature R (0.039)
Signature S (0.042)
Signature T (0.027)
Signature U (0.038)
Signature V (0.023)
Signature W (0.032)
Signature X (0.026)
Signature Y (0.035)
Signature Z (0.03)
Signature AA (0.024)
Signature AB (0.02)
Signature AC (0.034)
Signature AD (0.044)

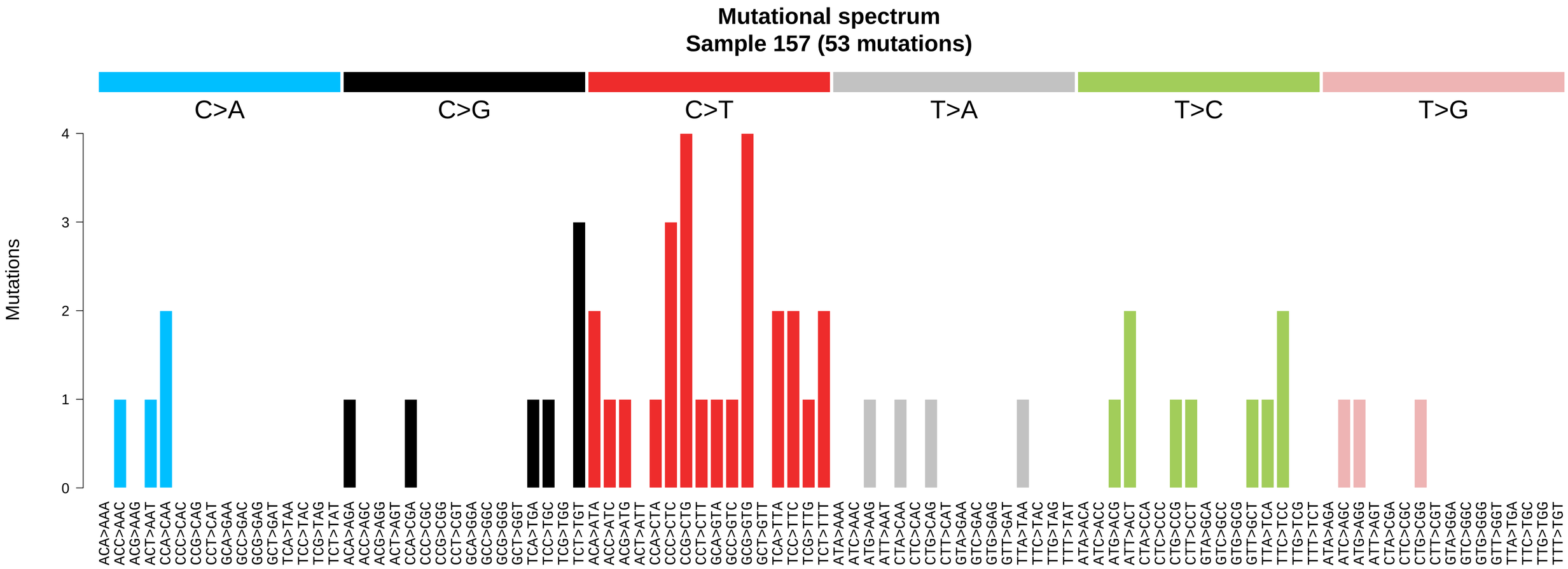

Mutational spectrum
Sample 152 (44 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.735
Signature A (0.027)
Signature B (0.042)
Signature C (0.043)
Signature D (0.037)
Signature E (0.036)
Signature F (0.029)
Signature G (0.047)
Signature H (0.029)
Signature I (0.033)
Signature J (0.036)
Signature K (0.053)
Signature L (0.022)
Signature M (0.032)
Signature N (0.034)
Signature O (0.029)
Signature P (0.028)
Signature Q (0.018)
Signature R (0.054)
Signature S (0.045)
Signature T (0.028)
Signature U (0.021)
Signature V (0.018)
Signature W (0.057)
Signature X (0.038)
Signature Y (0.025)
Signature Z (0.023)
Signature AA (0.032)
Signature AB (0.018)
Signature AC (0.03)
Signature AD (0.038)

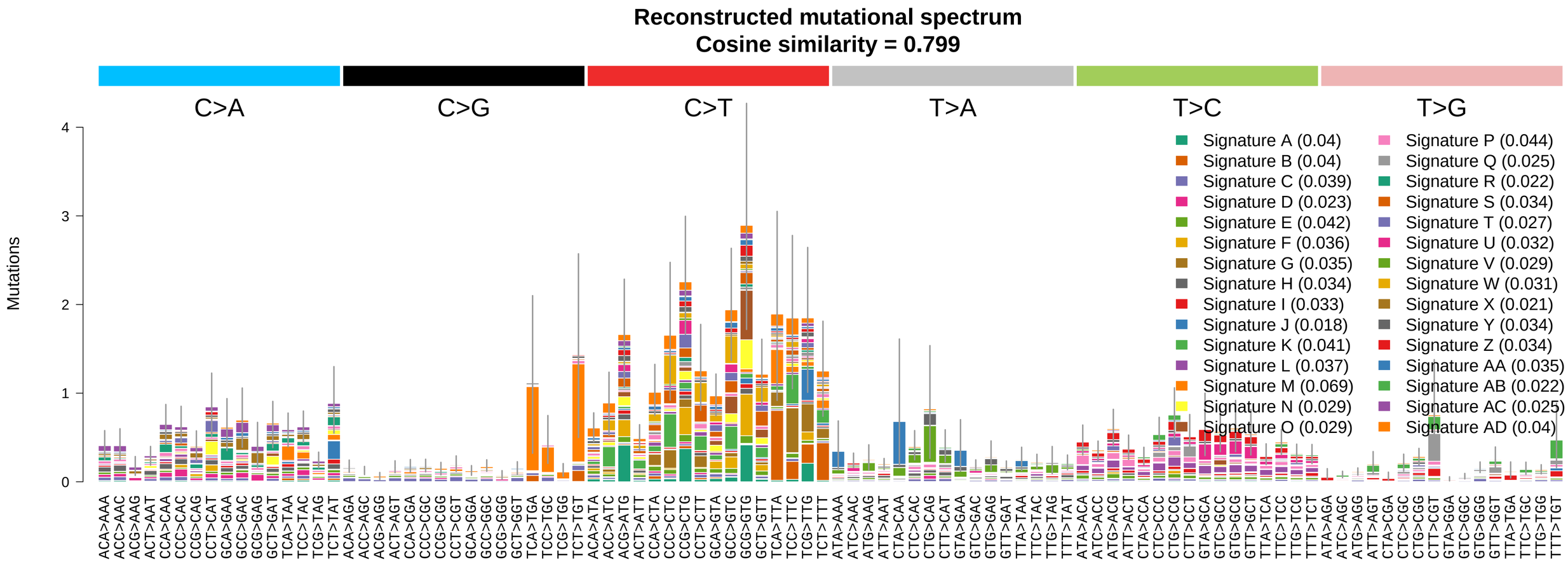

Mutational spectrum
Sample 153 (29 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.66
Signature A (0.046)
Signature B (0.021)
Signature C (0.046)
Signature D (0.037)
Signature E (0.043)
Signature F (0.036)
Signature G (0.035)
Signature H (0.034)
Signature I (0.029)
Signature J (0.038)
Signature K (0.034)
Signature L (0.029)
Signature M (0.025)
Signature N (0.034)
Signature O (0.037)
Signature P (0.03)
Signature Q (0.03)
Signature R (0.039)
Signature S (0.042)
Signature T (0.026)
Signature U (0.023)
Signature V (0.023)
Signature W (0.038)
Signature X (0.036)
Signature Y (0.034)
Signature Z (0.027)
Signature AA (0.033)
Signature AB (0.021)
Signature AC (0.045)
Signature AD (0.031)

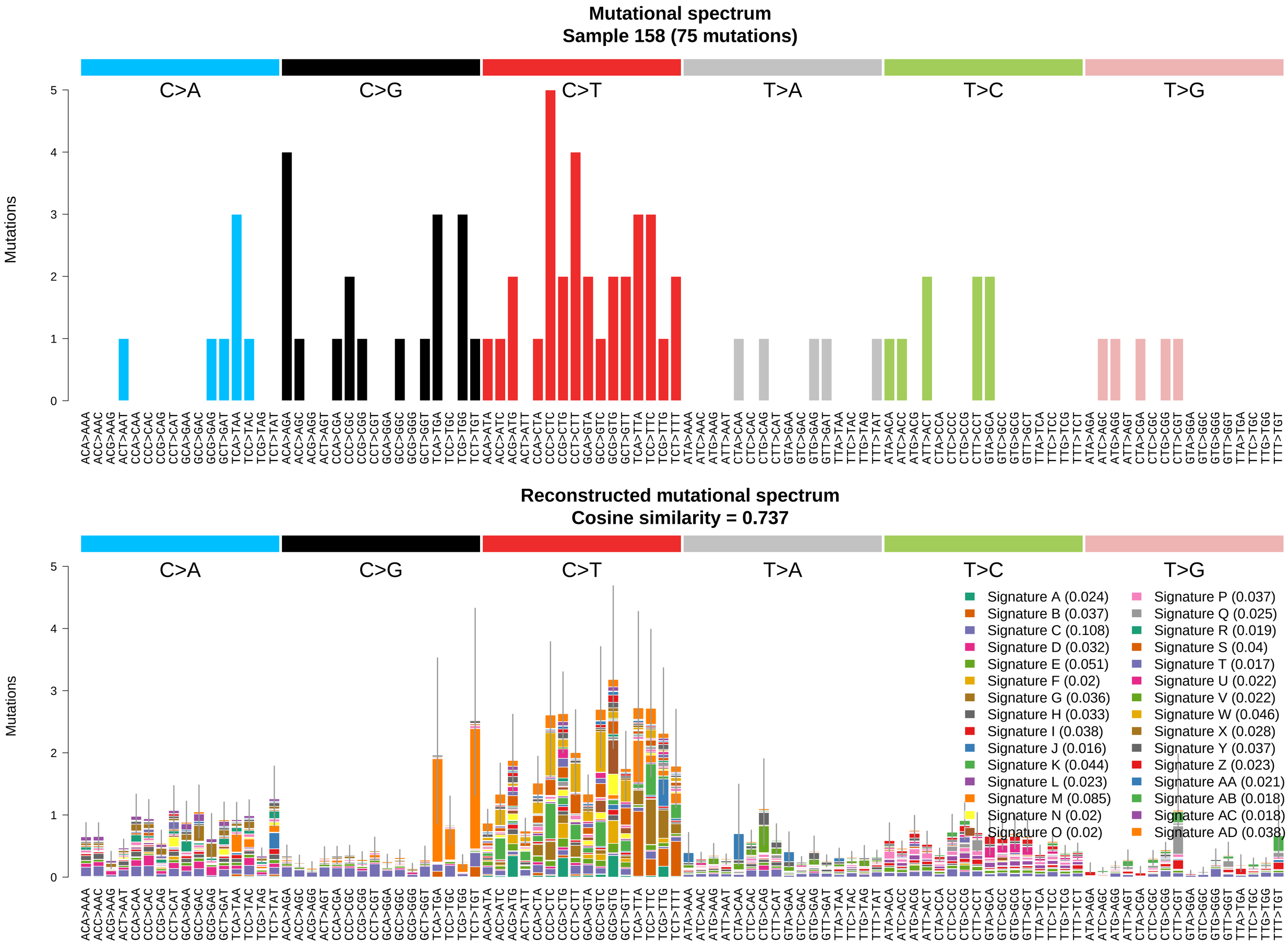

Mutational spectrum
Sample 154 (179 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.853
Signature A (0.021)
Signature B (0.013)
Signature C (0.235)
Signature D (0.059)
Signature E (0.041)
Signature F (0.017)
Signature G (0.017)
Signature H (0.035)
Signature I (0.022)
Signature J (0.024)
Signature K (0.016)
Signature L (0.021)
Signature M (0.057)
Signature N (0.018)
Signature O (0.013)
Signature P (0.024)
Signature Q (0.012)
Signature R (0.046)
Signature S (0.02)
Signature T (0.015)
Signature U (0.014)
Signature V (0.015)
Signature W (0.015)
Signature X (0.06)
Signature Y (0.024)
Signature Z (0.016)
Signature AA (0.023)
Signature AB (0.012)
Signature AC (0.064)
Signature AD (0.031)

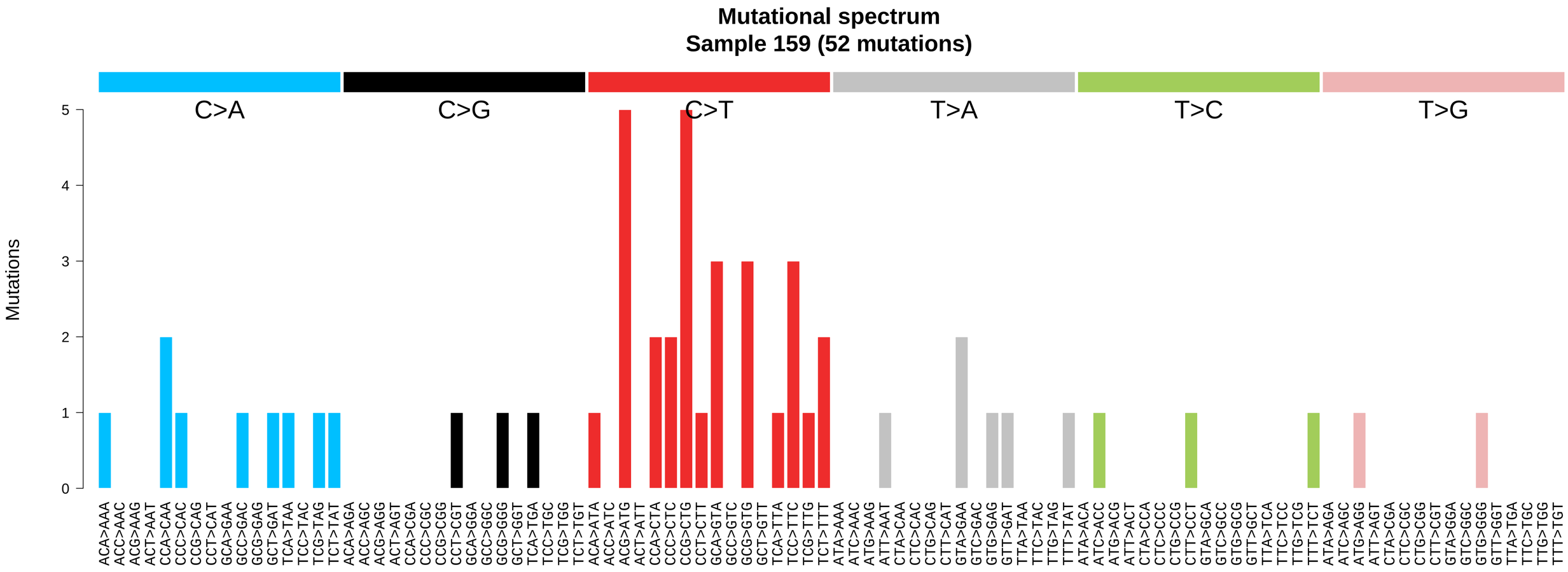

Mutational spectrum
Sample 155 (196 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.848
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
Signature A (0.015)
Signature B (0.015)
Signature C (0.257)
Signature D (0.093)
Signature E (0.037)
Signature F (0.014)
Signature G (0.013)
Signature H (0.043)
Signature I (0.039)
Signature J (0.014)
Signature K (0.013)
Signature L (0.017)
Signature M (0.018)
Signature N (0.023)
Signature O (0.014)
Signature P (0.029)
Signature Q (0.025)
Signature R (0.03)
Signature S (0.018)
Signature T (0.023)
Signature U (0.011)
Signature V (0.021)
Signature W (0.013)
Signature X (0.048)
Signature Y (0.036)
Signature Z (0.014)
Signature AA (0.021)
Signature AB (0.023)
Signature AC (0.032)
Signature AD (0.032)
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT

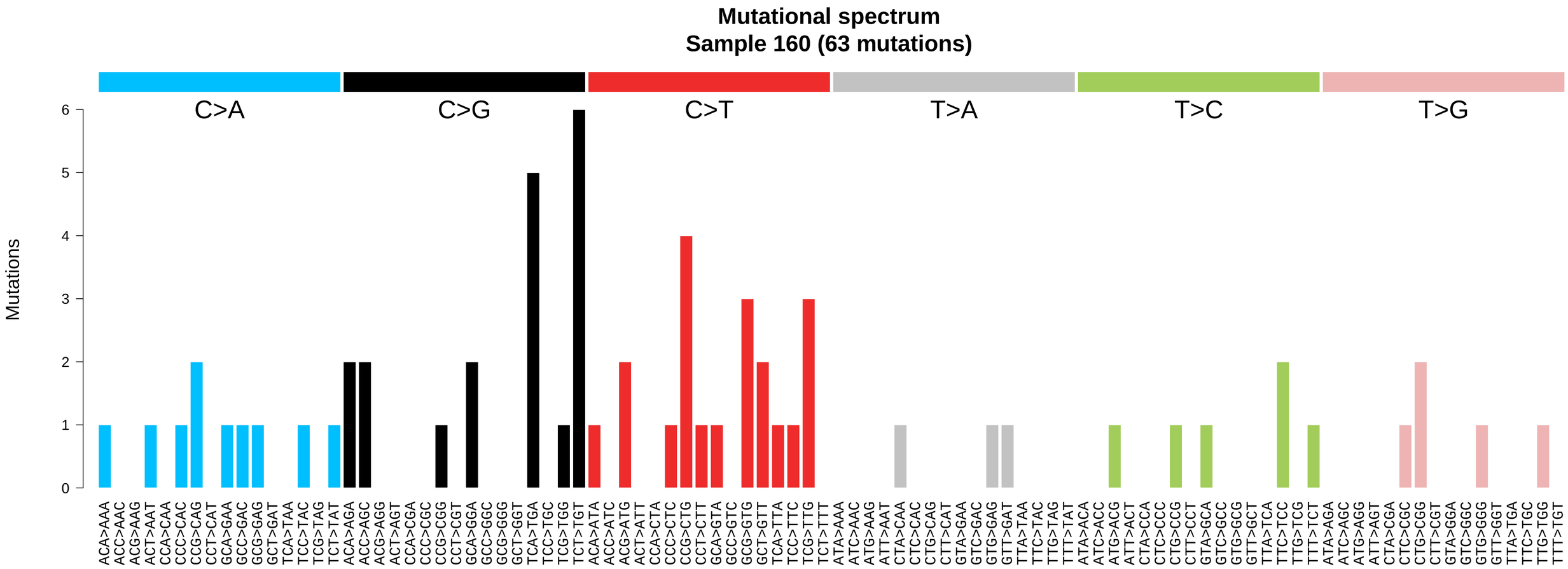

Mutational spectrum
Sample 156 (26 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.693
Signature A (0.058)
Signature B (0.026)
Signature C (0.028)
Signature D (0.03)
Signature E (0.034)
Signature F (0.049)
Signature G (0.029)
Signature H (0.034)
Signature I (0.029)
Signature J (0.03)
Signature K (0.027)
Signature L (0.035)
Signature M (0.019)
Signature N (0.043)
Signature O (0.036)
Signature P (0.032)
Signature Q (0.029)
Signature R (0.032)
Signature S (0.047)
Signature T (0.039)
Signature U (0.049)
Signature V (0.028)
Signature W (0.032)
Signature X (0.024)
Signature Y (0.033)
Signature Z (0.041)
Signature AA (0.025)
Signature AB (0.02)
Signature AC (0.034)
Signature AD (0.029)

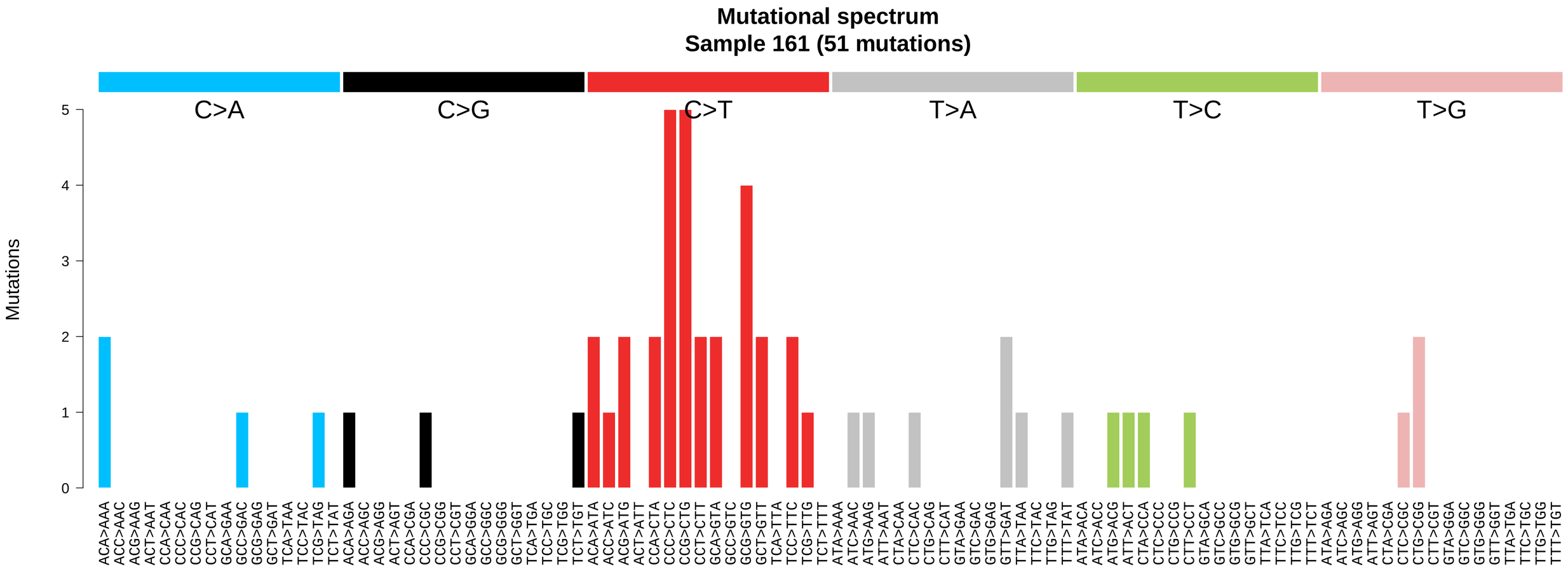

Mutational spectrum
Sample 157 (53 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

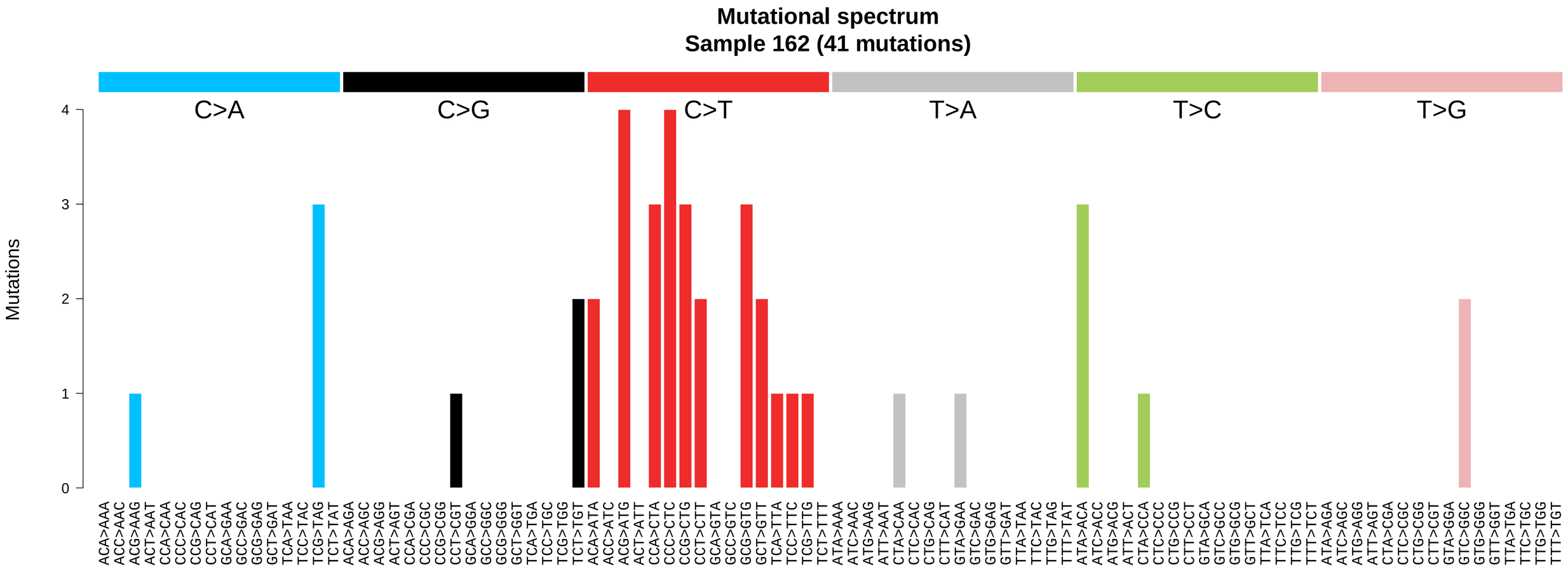

Reconstructed mutational spectrum
Cosine similarity = 0.799
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
Signature A (0.04)
Signature B (0.04)
Signature C (0.039)
Signature D (0.023)
Signature E (0.042)
Signature F (0.036)
Signature G (0.035)
Signature H (0.034)
Signature I (0.033)
Signature J (0.018)
Signature K (0.041)
Signature L (0.037)
Signature M (0.069)
Signature N (0.029)
Signature O (0.029)
Signature P (0.044)
Signature Q (0.025)
Signature R (0.022)
Signature S (0.034)
Signature T (0.027)
Signature U (0.032)
Signature V (0.029)
Signature W (0.031)
Signature X (0.021)
Signature Y (0.034)
Signature Z (0.034)
Signature AA (0.035)
Signature AB (0.022)
Signature AC (0.025)
Signature AD (0.04)

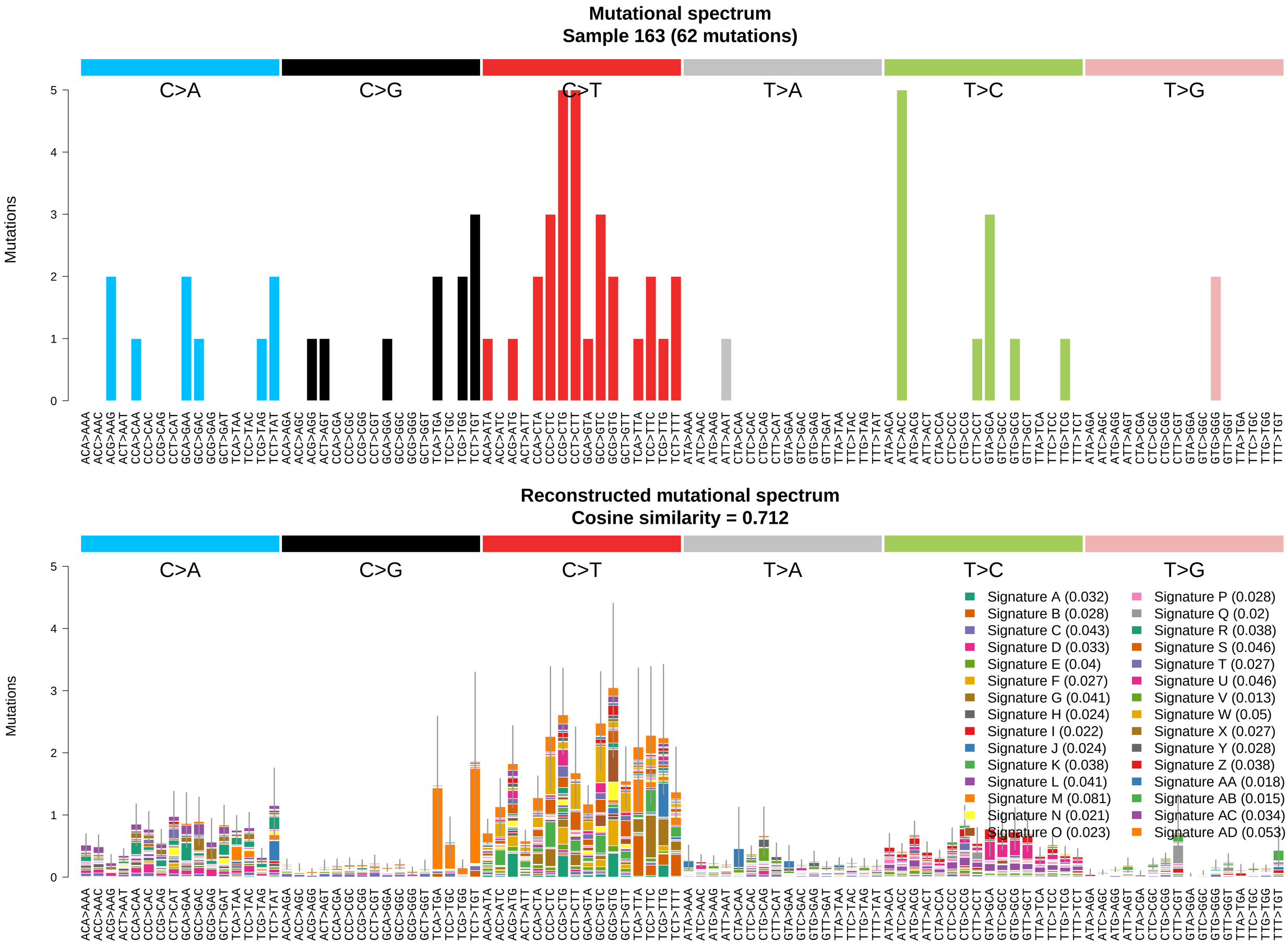

Mutational spectrum
Sample 158 (75 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.737
Signature A (0.024)
Signature B (0.037)
Signature C (0.108)
Signature D (0.032)
Signature E (0.051)
Signature F (0.02)
Signature G (0.036)
Signature H (0.033)
Signature I (0.038)
Signature J (0.016)
Signature K (0.044)
Signature L (0.023)
Signature M (0.085)
Signature N (0.02)
Signature O (0.02)
Signature P (0.037)
Signature Q (0.025)
Signature R (0.019)
Signature S (0.04)
Signature T (0.017)
Signature U (0.022)
Signature V (0.022)
Signature W (0.046)
Signature X (0.028)
Signature Y (0.037)
Signature Z (0.023)
Signature AA (0.021)
Signature AB (0.018)
Signature AC (0.018)
Signature AD (0.038)

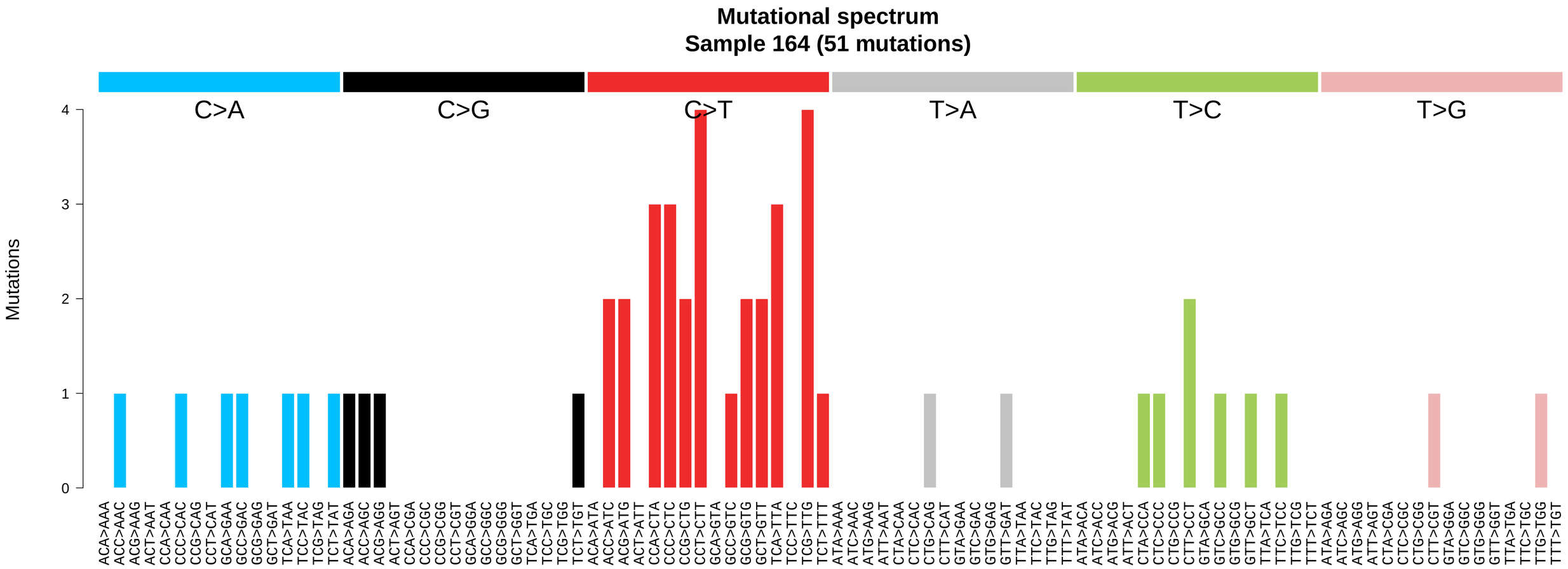

Mutational spectrum
Sample 159 (52 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.764
Signature A (0.075)
Signature B (0.034)
Signature C (0.039)
Signature D (0.035)
Signature E (0.036)
Signature F (0.043)
Signature G (0.043)
Signature H (0.044)
Signature I (0.028)
Signature J (0.023)
Signature K (0.031)
Signature L (0.023)
Signature M (0.026)
Signature N (0.031)
Signature O (0.028)
Signature P (0.025)
Signature Q (0.022)
Signature R (0.038)
Signature S (0.038)
Signature T (0.028)
Signature U (0.022)
Signature V (0.026)
Signature W (0.026)
Signature X (0.032)
Signature Y (0.049)
Signature Z (0.021)
Signature AA (0.034)
Signature AB (0.017)
Signature AC (0.035)
Signature AD (0.05)

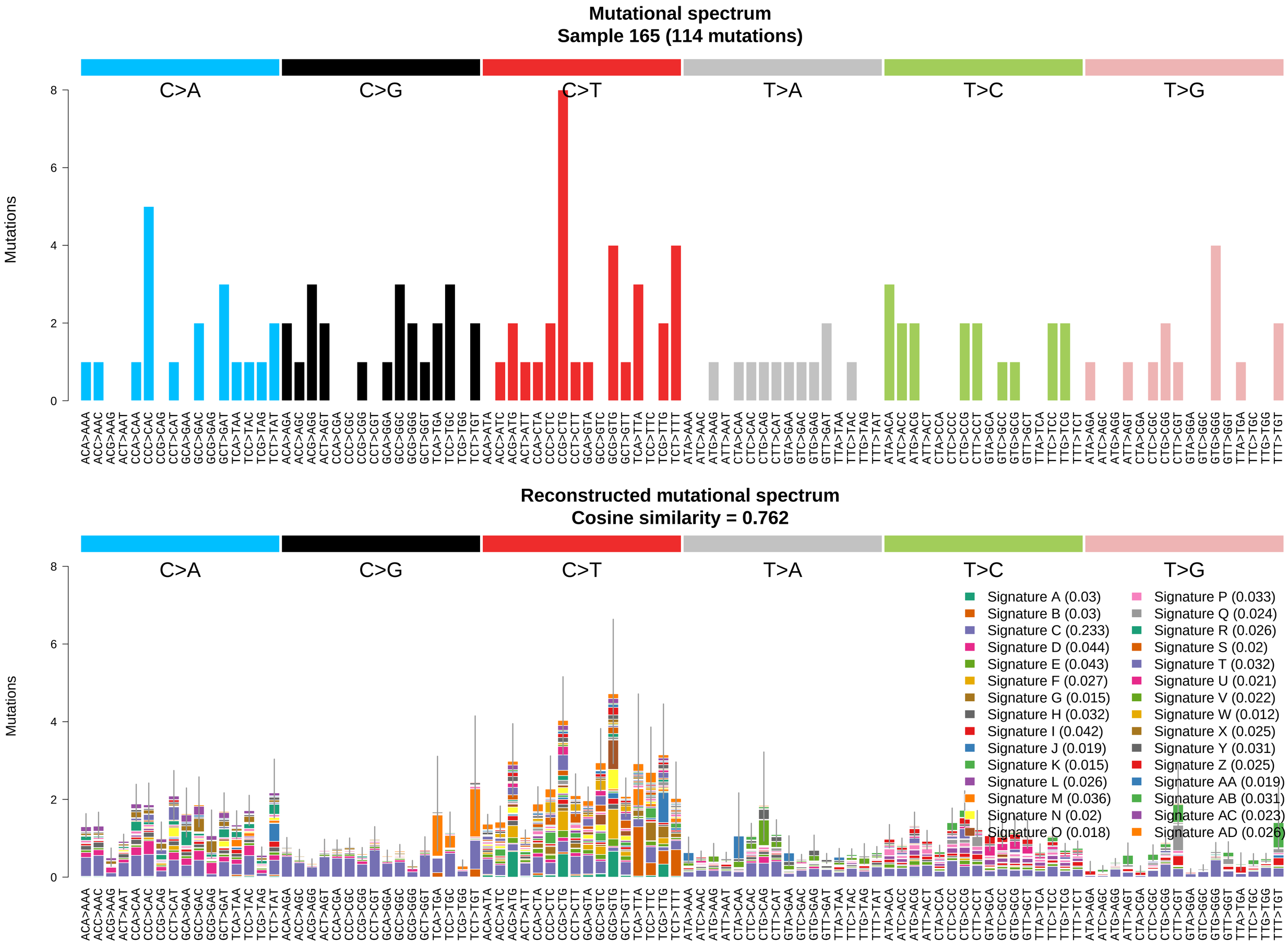

Mutational spectrum
Sample 160 (63 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.784
Signature A (0.04)
Signature B (0.02)
Signature C (0.072)
Signature D (0.037)
Signature E (0.038)
Signature F (0.037)
Signature G (0.021)
Signature H (0.031)
Signature I (0.025)
Signature J (0.028)
Signature K (0.018)
Signature L (0.026)
Signature M (0.146)
Signature N (0.022)
Signature O (0.023)
Signature P (0.026)
Signature Q (0.02)
Signature R (0.033)
Signature S (0.028)
Signature T (0.036)
Signature U (0.023)
Signature V (0.018)
Signature W (0.018)
Signature X (0.038)
Signature Y (0.042)
Signature Z (0.028)
Signature AA (0.025)
Signature AB (0.023)
Signature AC (0.032)
Signature AD (0.027)

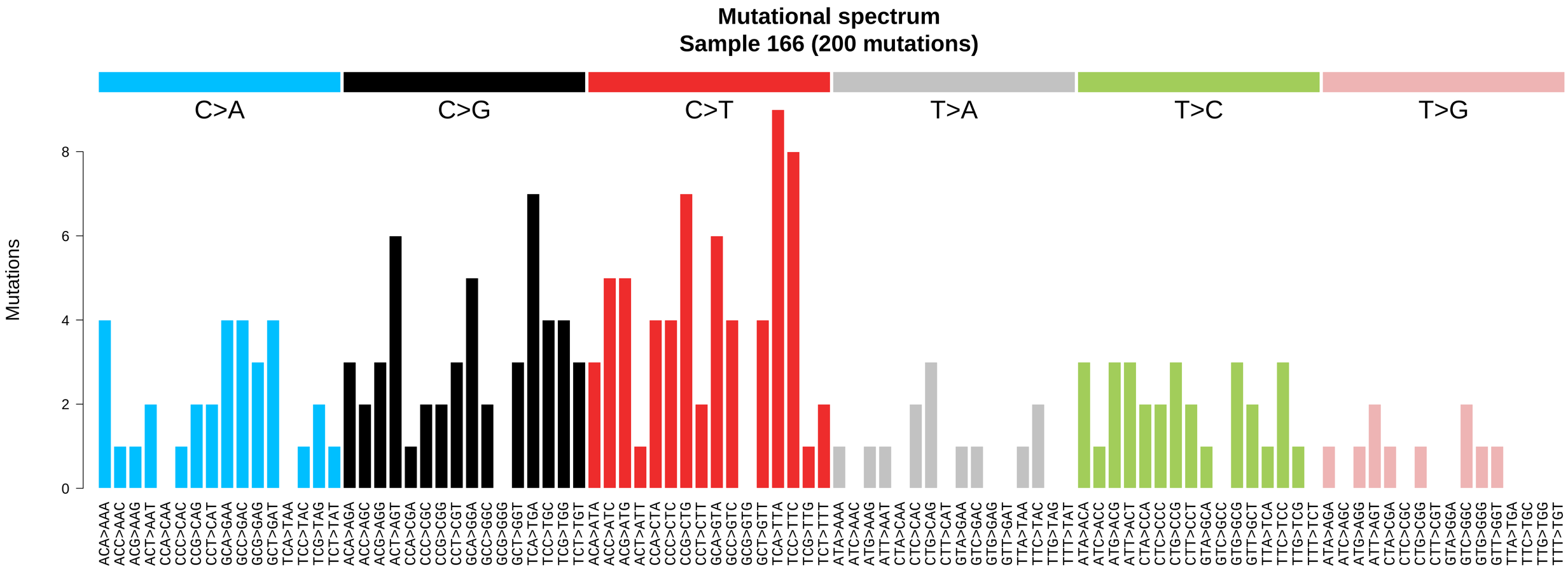

Mutational spectrum
Sample 161 (51 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.753
Signature A (0.05)
Signature B (0.019)
Signature C (0.039)
Signature D (0.025)
Signature E (0.043)
Signature F (0.043)
Signature G (0.036)
Signature H (0.044)
Signature I (0.03)
Signature J (0.018)
Signature K (0.047)
Signature L (0.026)
Signature M (0.018)
Signature N (0.027)
Signature O (0.032)
Signature P (0.037)
Signature Q (0.027)
Signature R (0.022)
Signature S (0.069)
Signature T (0.031)
Signature U (0.023)
Signature V (0.03)
Signature W (0.056)
Signature X (0.023)
Signature Y (0.04)
Signature Z (0.025)
Signature AA (0.021)
Signature AB (0.025)
Signature AC (0.027)
Signature AD (0.048)

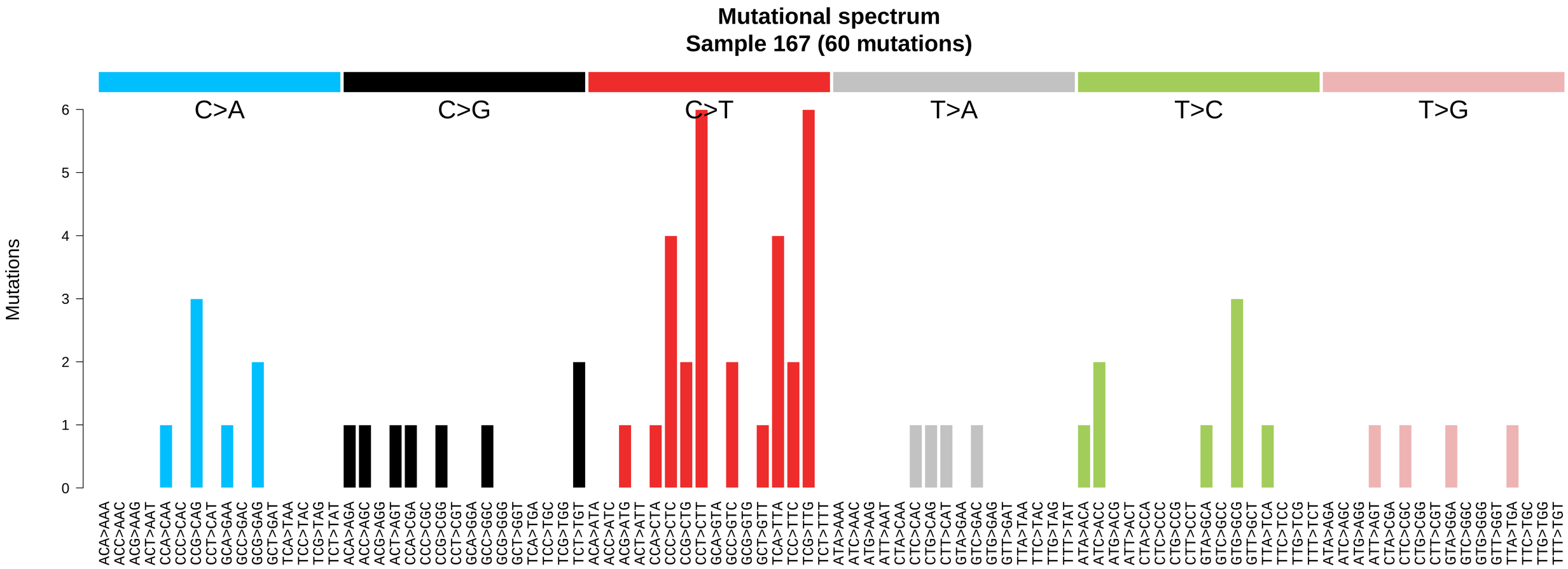

Mutational spectrum
Sample 162 (41 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.677
Signature A (0.063)
Signature B (0.027)
Signature C (0.03)
Signature D (0.03)
Signature E (0.036)
Signature F (0.042)
Signature G (0.038)
Signature H (0.022)
Signature I (0.023)
Signature J (0.022)
Signature K (0.04)
Signature L (0.028)
Signature M (0.04)
Signature N (0.029)
Signature O (0.031)
Signature P (0.043)
Signature Q (0.027)
Signature R (0.023)
Signature S (0.058)
Signature T (0.03)
Signature U (0.024)
Signature V (0.021)
Signature W (0.056)
Signature X (0.026)
Signature Y (0.024)
Signature Z (0.033)
Signature AA (0.046)
Signature AB (0.017)
Signature AC (0.028)
Signature AD (0.043)

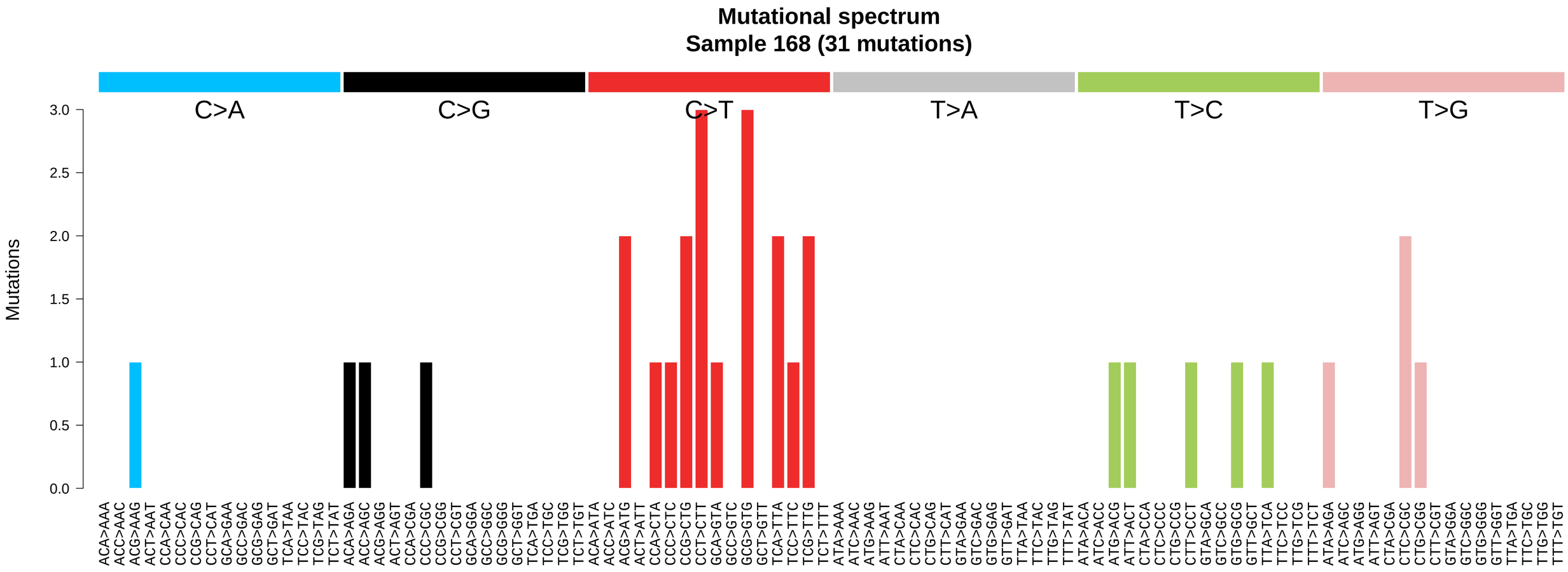

Mutational spectrum
Sample 163 (62 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.712
Signature A (0.032)
Signature B (0.028)
Signature C (0.043)
Signature D (0.033)
Signature E (0.04)
Signature F (0.027)
Signature G (0.041)
Signature H (0.024)
Signature I (0.022)
Signature J (0.024)
Signature K (0.038)
Signature L (0.041)
Signature M (0.081)
Signature N (0.021)
Signature O (0.023)
Signature P (0.028)
Signature Q (0.02)
Signature R (0.038)
Signature S (0.046)
Signature T (0.027)
Signature U (0.046)
Signature V (0.013)
Signature W (0.05)
Signature X (0.027)
Signature Y (0.028)
Signature Z (0.038)
Signature AA (0.018)
Signature AB (0.015)
Signature AC (0.034)
Signature AD (0.053)

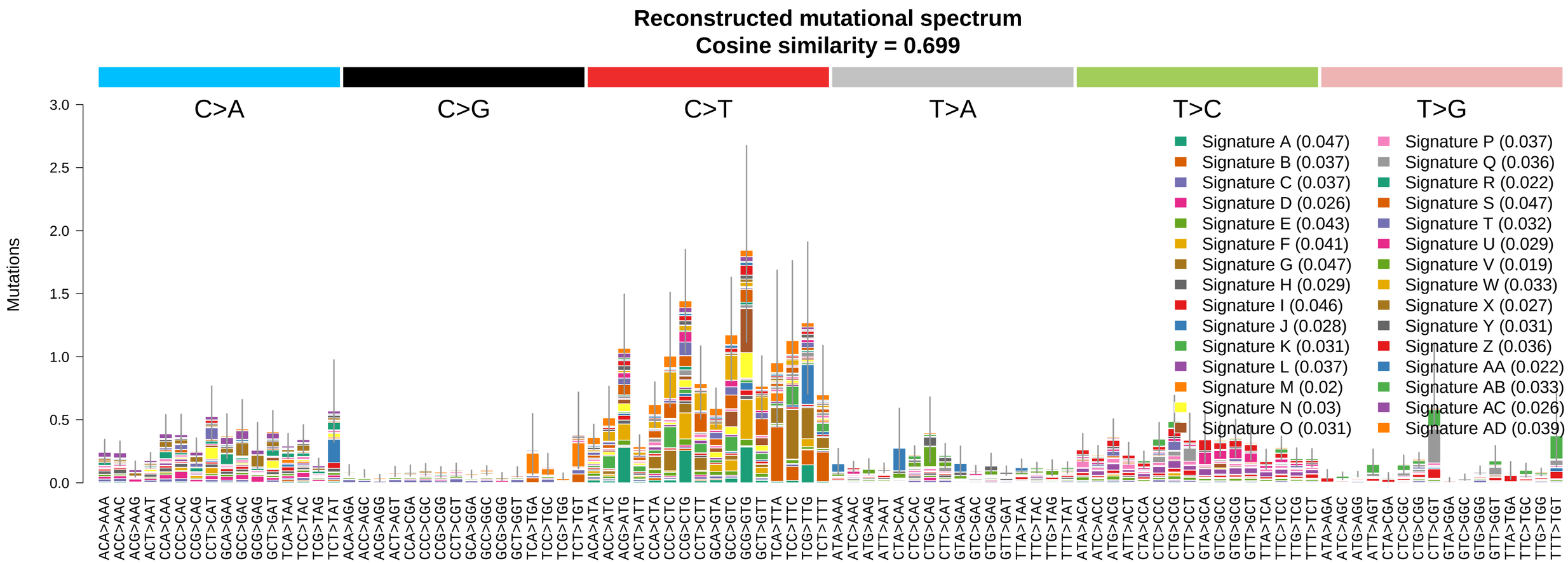

Mutational spectrum
Sample 164 (51 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.793
Signature A (0.038)
Signature B (0.047)
Signature C (0.041)
Signature D (0.031)
Signature E (0.039)
Signature F (0.025)
Signature G (0.051)
Signature H (0.031)
Signature I (0.029)
Signature J (0.038)
Signature K (0.039)
Signature L (0.032)
Signature M (0.025)
Signature N (0.024)
Signature O (0.026)
Signature P (0.03)
Signature Q (0.042)
Signature R (0.029)
Signature S (0.053)
Signature T (0.023)
Signature U (0.029)
Signature V (0.02)
Signature W (0.061)
Signature X (0.026)
Signature Y (0.033)
Signature Z (0.028)
Signature AA (0.019)
Signature AB (0.02)
Signature AC (0.028)
Signature AD (0.043)

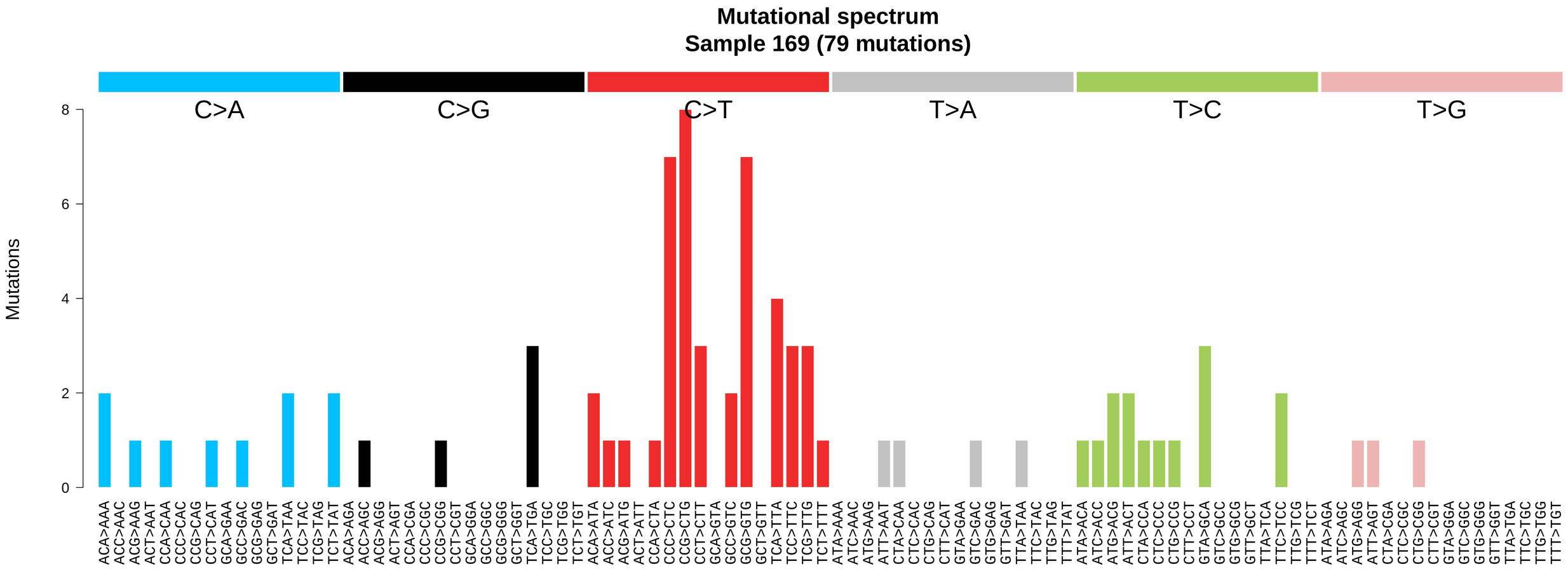

Mutational spectrum
Sample 165 (114 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.762
Signature A (0.03)
Signature B (0.03)
Signature C (0.233)
Signature D (0.044)
Signature E (0.043)
Signature F (0.027)
Signature G (0.015)
Signature H (0.032)
Signature I (0.042)
Signature J (0.019)
Signature K (0.015)
Signature L (0.026)
Signature M (0.036)
Signature N (0.02)
Signature O (0.018)
Signature P (0.033)
Signature Q (0.024)
Signature R (0.026)
Signature S (0.02)
Signature T (0.032)
Signature U (0.021)
Signature V (0.022)
Signature W (0.012)
Signature X (0.025)
Signature Y (0.031)
Signature Z (0.025)
Signature AA (0.019)
Signature AB (0.031)
Signature AC (0.023)
Signature AD (0.026)

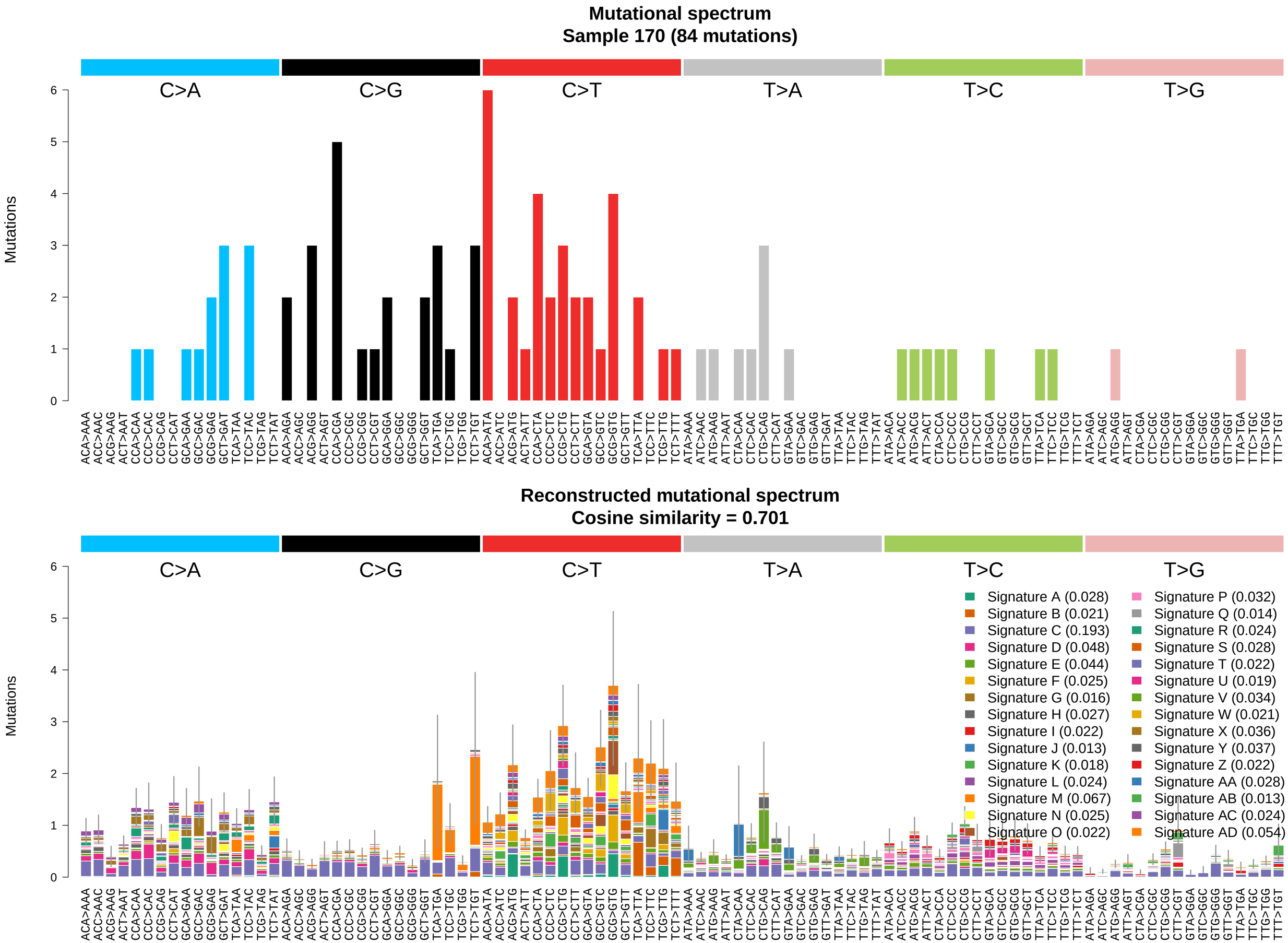

Mutational spectrum
Sample 166 (200 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.834
Signature A (0.015)
Signature B (0.028)
Signature C (0.306)
Signature D (0.029)
Signature E (0.045)
Signature F (0.012)
Signature G (0.021)
Signature H (0.018)
Signature I (0.02)
Signature J (0.007)
Signature K (0.024)
Signature L (0.029)
Signature M (0.062)
Signature N (0.012)
Signature O (0.009)
Signature P (0.039)
Signature Q (0.012)
Signature R (0.021)
Signature S (0.018)
Signature T (0.028)
Signature U (0.022)
Signature V (0.013)
Signature W (0.018)
Signature X (0.033)
Signature Y (0.02)
Signature Z (0.025)
Signature AA (0.012)
Signature AB (0.012)
Signature AC (0.027)
Signature AD (0.062)

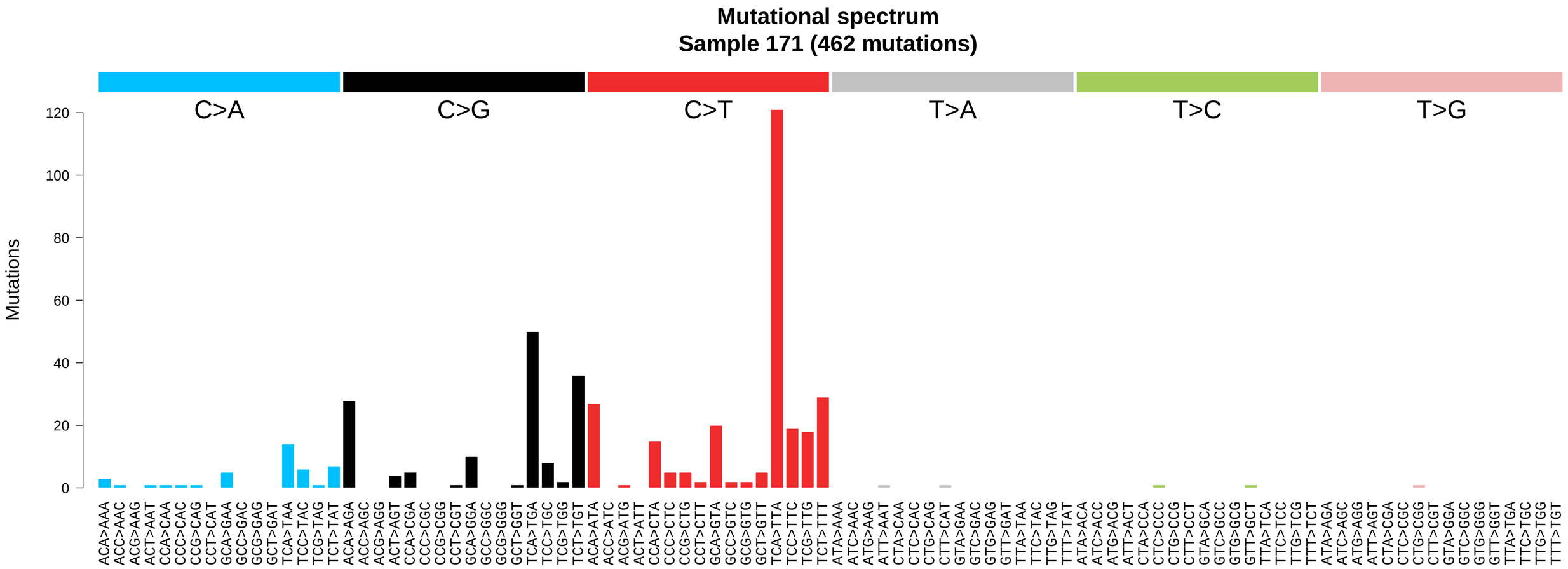

Mutational spectrum
Sample 167 (60 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.7
Signature A (0.023)
Signature B (0.044)
Signature C (0.055)
Signature D (0.033)
Signature E (0.037)
Signature F (0.02)
Signature G (0.084)
Signature H (0.022)
Signature I (0.034)
Signature J (0.032)
Signature K (0.033)
Signature L (0.032)
Signature M (0.031)
Signature N (0.015)
Signature O (0.018)
Signature P (0.038)
Signature Q (0.021)
Signature R (0.03)
Signature S (0.041)
Signature T (0.028)
Signature U (0.045)
Signature V (0.023)
Signature W (0.05)
Signature X (0.042)
Signature Y (0.035)
Signature Z (0.03)
Signature AA (0.015)
Signature AB (0.024)
Signature AC (0.027)
Signature AD (0.04)

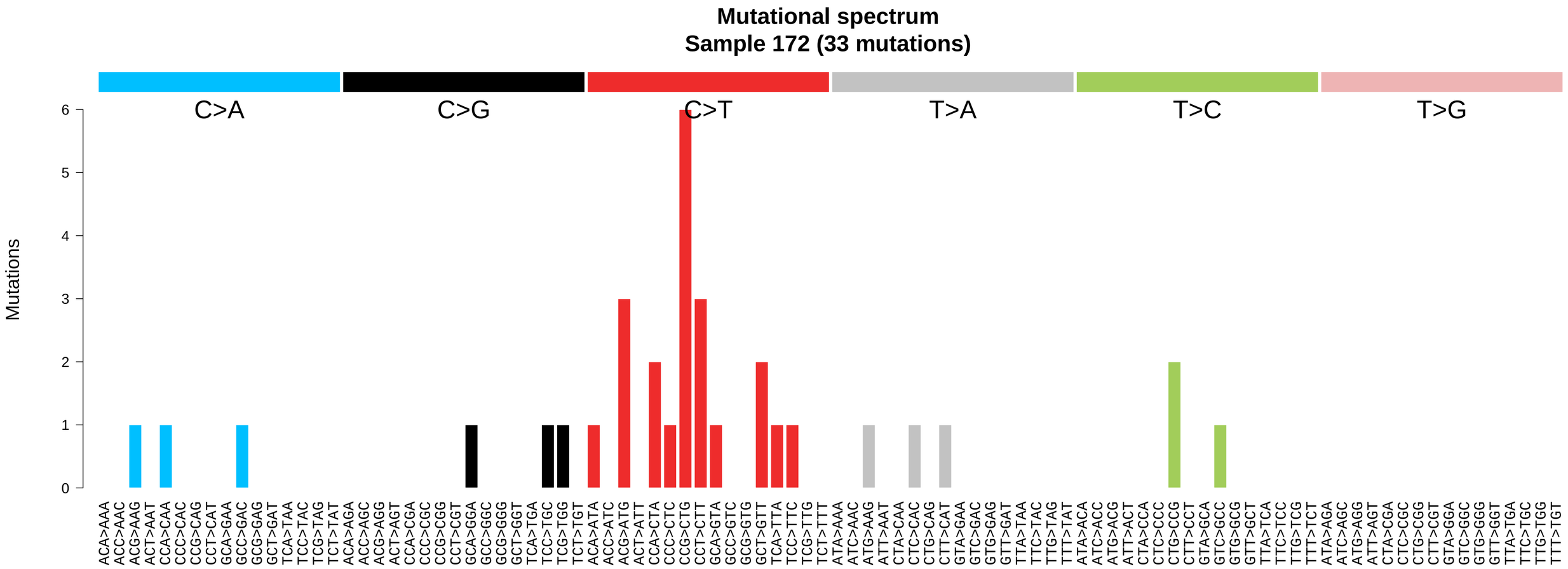

Mutational spectrum
Sample 168 (31 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

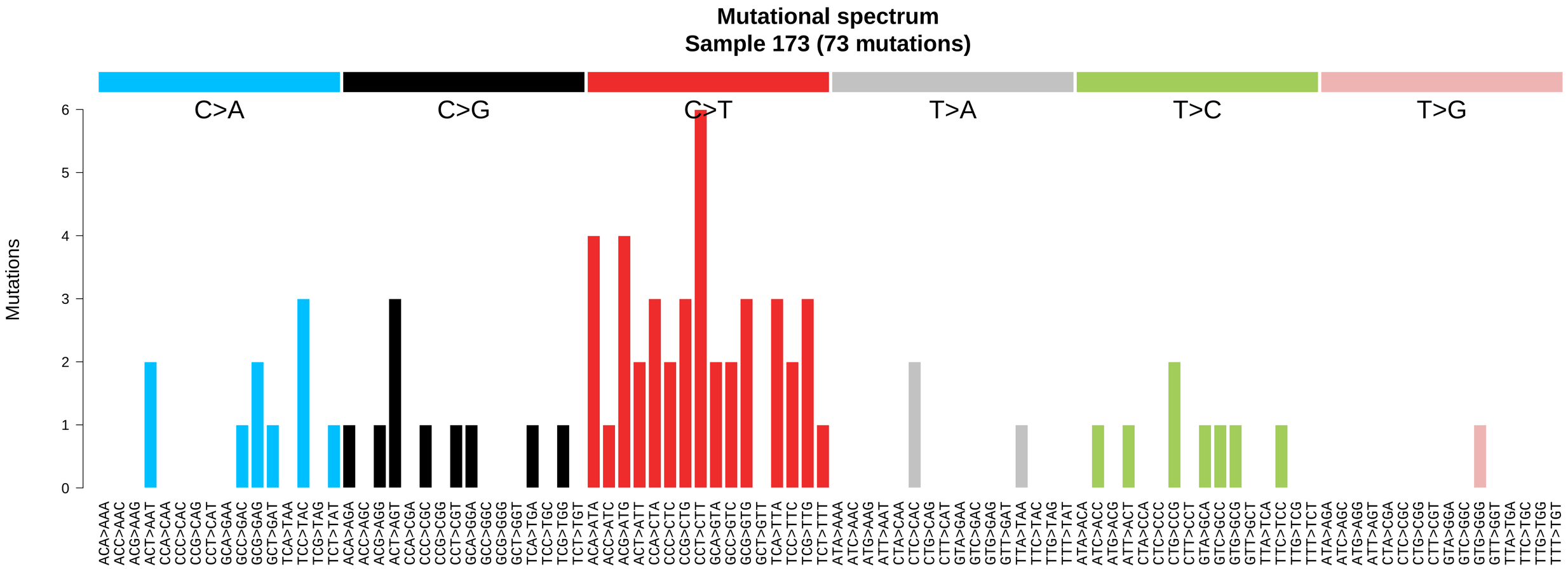

Reconstructed mutational spectrum
Cosine similarity = 0.699
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Signature A (0.047)
Signature B (0.037)
Signature C (0.037)
Signature D (0.026)
Signature E (0.043)
Signature F (0.041)
Signature G (0.047)
Signature H (0.029)
Signature I (0.046)
Signature J (0.028)
Signature K (0.031)
Signature L (0.037)
Signature M (0.02)
Signature N (0.03)
Signature O (0.031)
Signature P (0.037)
Signature Q (0.036)
Signature R (0.022)
Signature S (0.047)
Signature T (0.032)
Signature U (0.029)
Signature V (0.019)
Signature W (0.033)
Signature X (0.027)
Signature Y (0.031)
Signature Z (0.036)
Signature AA (0.022)
Signature AB (0.033)
Signature AC (0.026)
Signature AD (0.039)

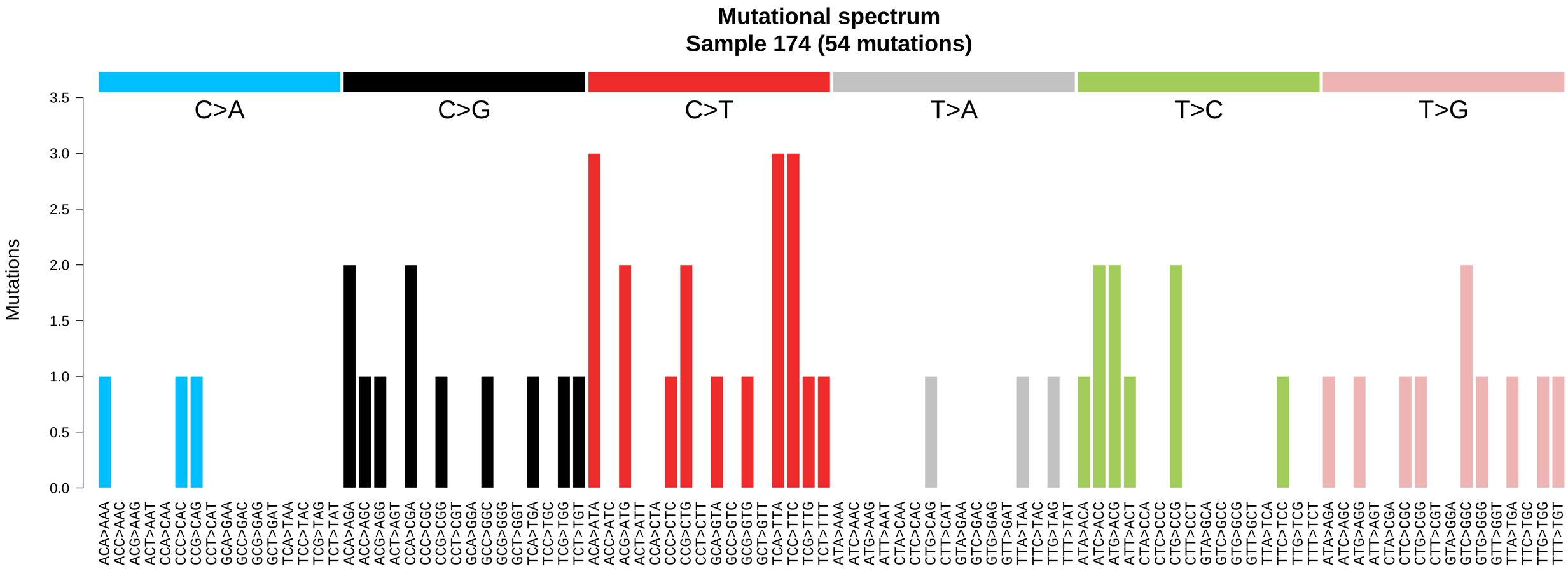

Mutational spectrum
Sample 169 (79 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.819
Signature A (0.051)
Signature B (0.038)
Signature C (0.025)
Signature D (0.023)
Signature E (0.036)
Signature F (0.043)
Signature G (0.054)
Signature H (0.029)
Signature I (0.03)
Signature J (0.032)
Signature K (0.039)
Signature L (0.039)
Signature M (0.042)
Signature N (0.029)
Signature O (0.028)
Signature P (0.036)
Signature Q (0.017)
Signature R (0.027)
Signature S (0.038)
Signature T (0.03)
Signature U (0.035)
Signature V (0.014)
Signature W (0.046)
Signature X (0.018)
Signature Y (0.027)
Signature Z (0.055)
Signature AA (0.027)
Signature AB (0.021)
Signature AC (0.027)
Signature AD (0.043)

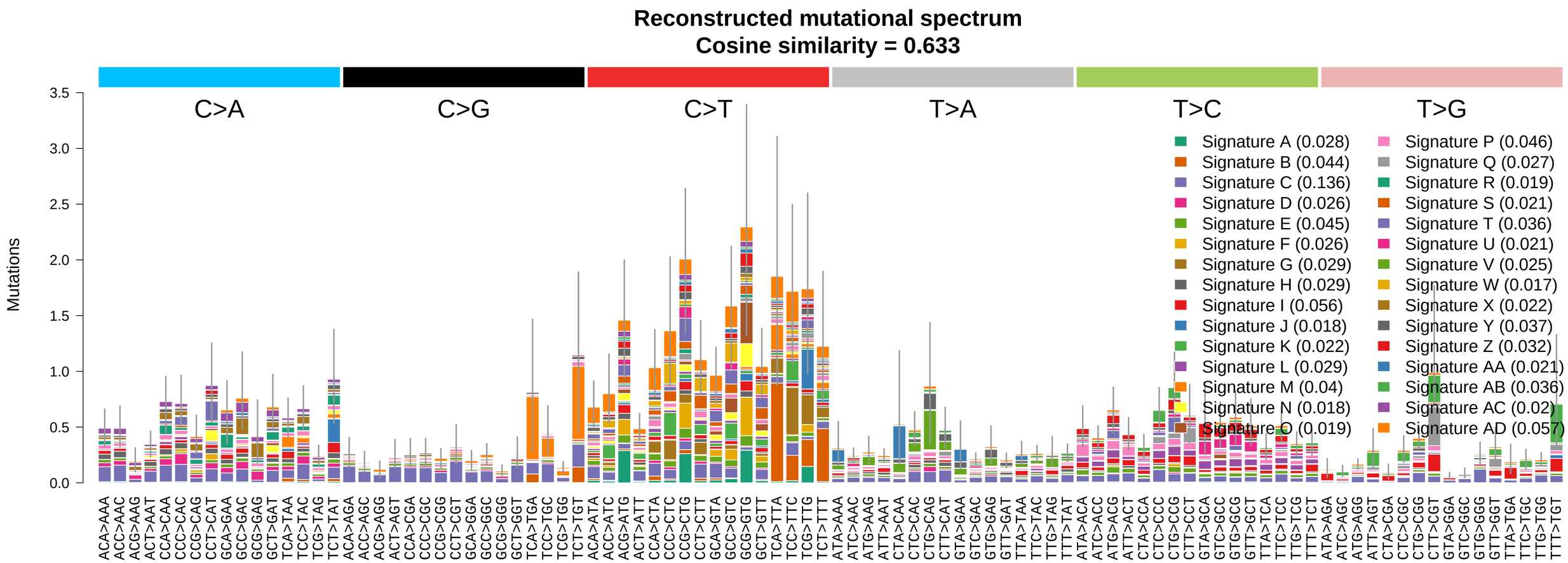

Mutational spectrum
Sample 170 (84 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.701
Signature A (0.028)
Signature B (0.021)
Signature C (0.193)
Signature D (0.048)
Signature E (0.044)
Signature F (0.025)
Signature G (0.016)
Signature H (0.027)
Signature I (0.022)
Signature J (0.013)
Signature K (0.018)
Signature L (0.024)
Signature M (0.067)
Signature N (0.025)
Signature O (0.022)
Signature P (0.032)
Signature Q (0.014)
Signature R (0.024)
Signature S (0.028)
Signature T (0.022)
Signature U (0.019)
Signature V (0.034)
Signature W (0.021)
Signature X (0.036)
Signature Y (0.037)
Signature Z (0.022)
Signature AA (0.028)
Signature AB (0.013)
Signature AC (0.024)
Signature AD (0.054)

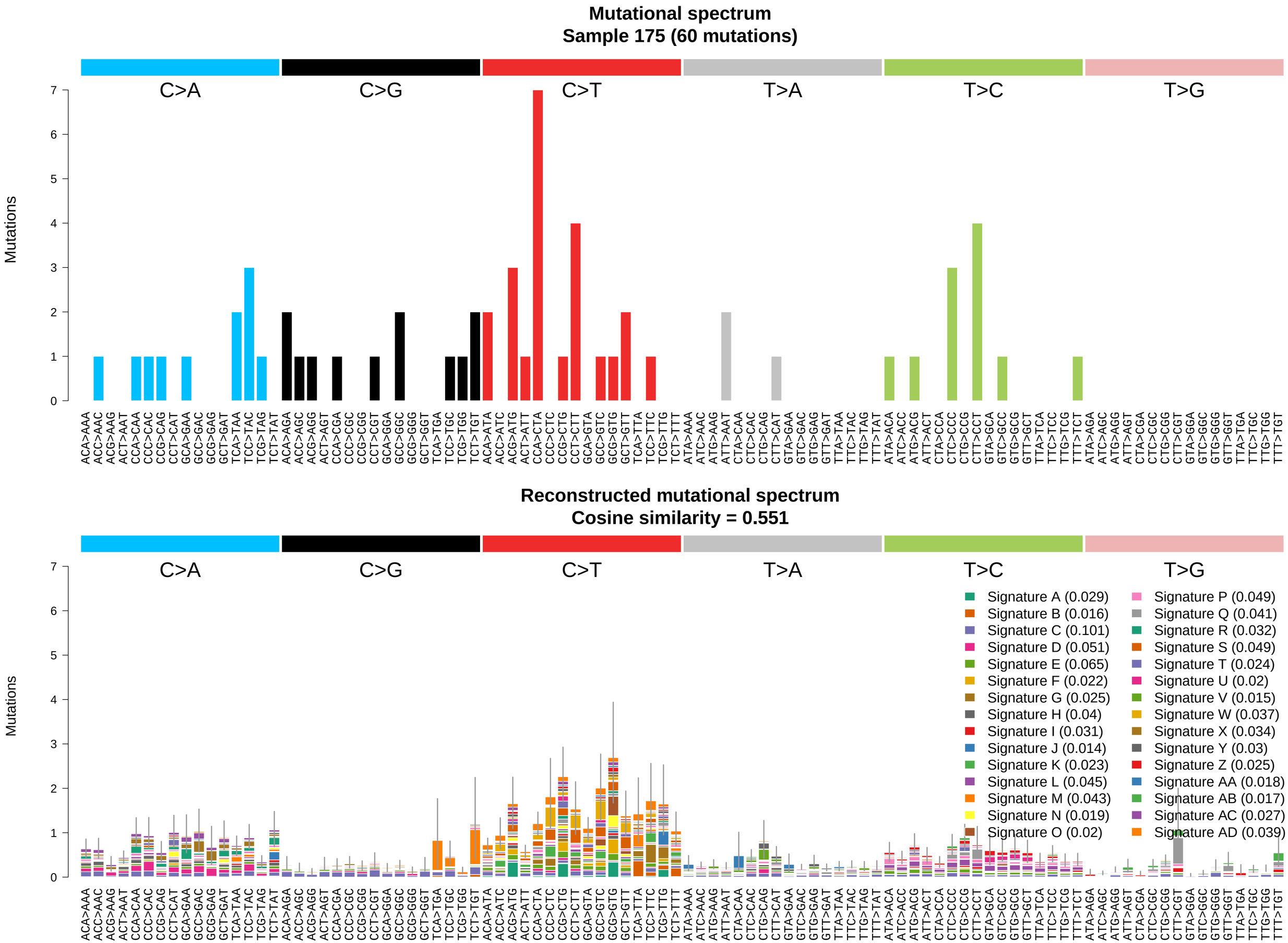

Mutational spectrum
Sample 171 (462 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
20
40
60
80
100
120
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.922
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
20
40
60
80
100
120
Signature A (0.005)
Signature B (0.408)
Signature C (0.116)
Signature D (0.007)
Signature E (0.008)
Signature F (0.005)
Signature G (0.008)
Signature H (0.007)
Signature I (0.004)
Signature J (0.005)
Signature K (0.007)
Signature L (0.004)
Signature M (0.268)
Signature N (0.005)
Signature O (0.004)
Signature P (0.005)
Signature Q (0.003)
Signature R (0.008)
Signature S (0.01)
Signature T (0.006)
Signature U (0.003)
Signature V (0.002)
Signature W (0.008)
Signature X (0.007)
Signature Y (0.006)
Signature Z (0.003)
Signature AA (0.004)
Signature AB (0.002)
Signature AC (0.007)
Signature AD (0.065)

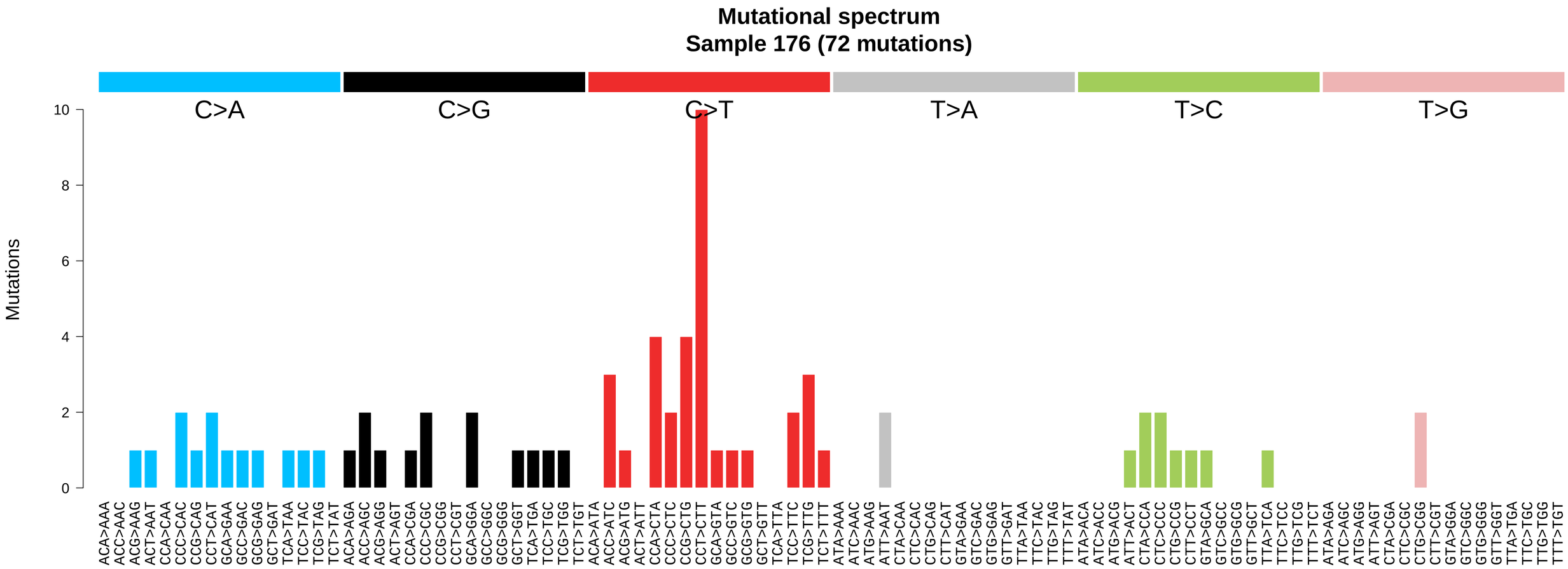

Mutational spectrum
Sample 172 (33 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.614
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
Signature A (0.056)
Signature B (0.025)
Signature C (0.031)
Signature D (0.038)
Signature E (0.036)
Signature F (0.046)
Signature G (0.039)
Signature H (0.03)
Signature I (0.025)
Signature J (0.02)
Signature K (0.034)
Signature L (0.029)
Signature M (0.03)
Signature N (0.028)
Signature O (0.025)
Signature P (0.028)
Signature Q (0.026)
Signature R (0.025)
Signature S (0.054)
Signature T (0.046)
Signature U (0.032)
Signature V (0.034)
Signature W (0.048)
Signature X (0.032)
Signature Y (0.031)
Signature Z (0.029)
Signature AA (0.023)
Signature AB (0.022)
Signature AC (0.032)
Signature AD (0.046)

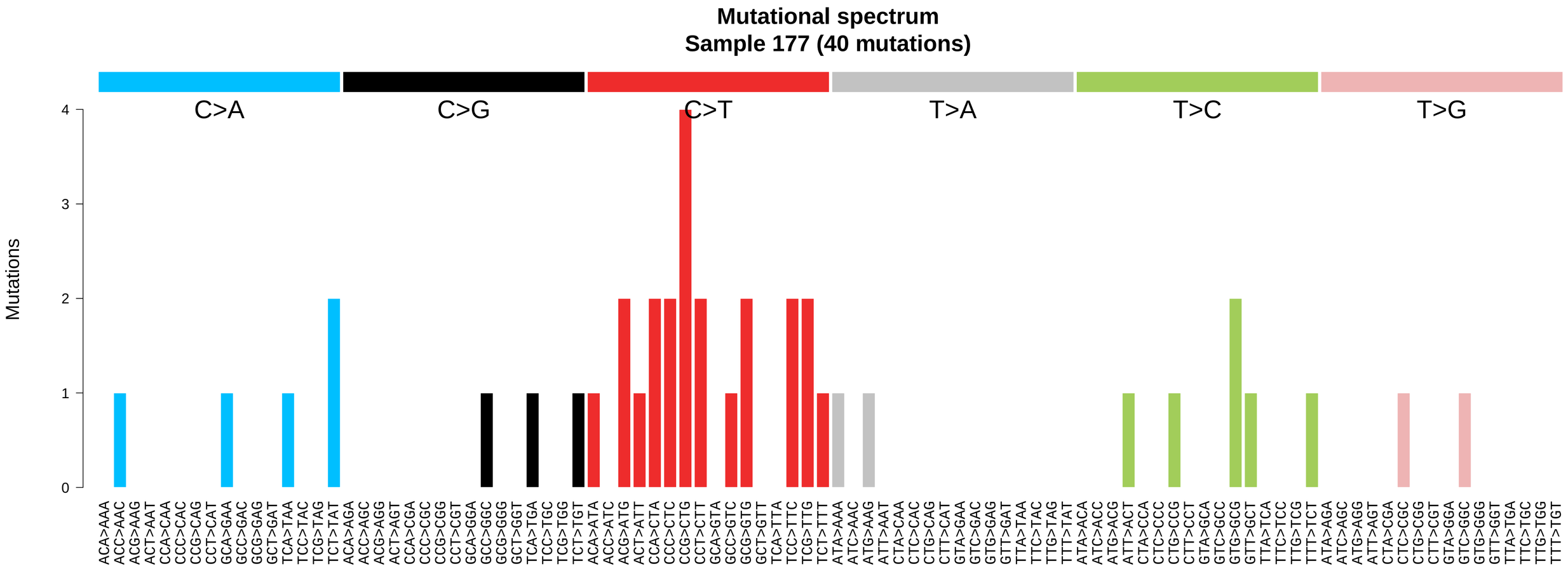

Mutational spectrum
Sample 173 (73 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.762
Signature A (0.044)
Signature B (0.034)
Signature C (0.083)
Signature D (0.035)
Signature E (0.046)
Signature F (0.028)
Signature G (0.039)
Signature H (0.035)
Signature I (0.02)
Signature J (0.024)
Signature K (0.038)
Signature L (0.026)
Signature M (0.024)
Signature N (0.031)
Signature O (0.026)
Signature P (0.031)
Signature Q (0.017)
Signature R (0.024)
Signature S (0.058)
Signature T (0.03)
Signature U (0.026)
Signature V (0.015)
Signature W (0.043)
Signature X (0.036)
Signature Y (0.028)
Signature Z (0.03)
Signature AA (0.02)
Signature AB (0.014)
Signature AC (0.027)
Signature AD (0.067)

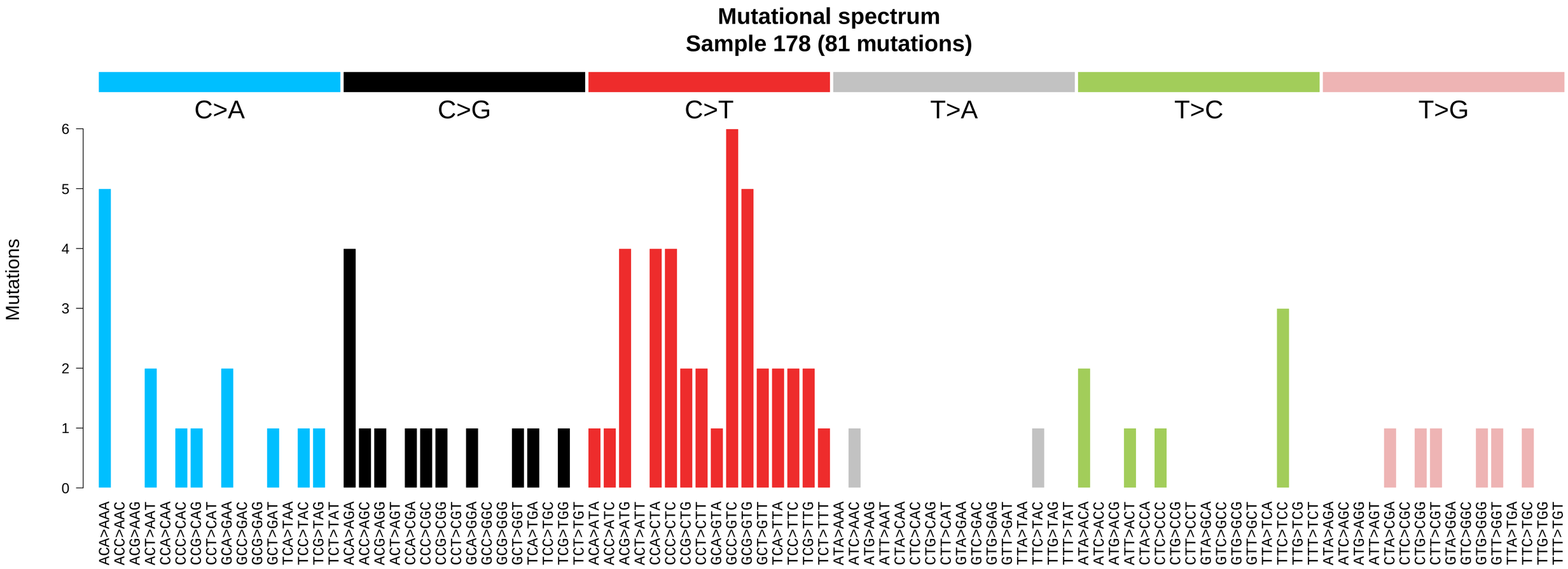

Mutational spectrum
Sample 174 (54 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT
ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT
ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT
ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT
ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT
ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT

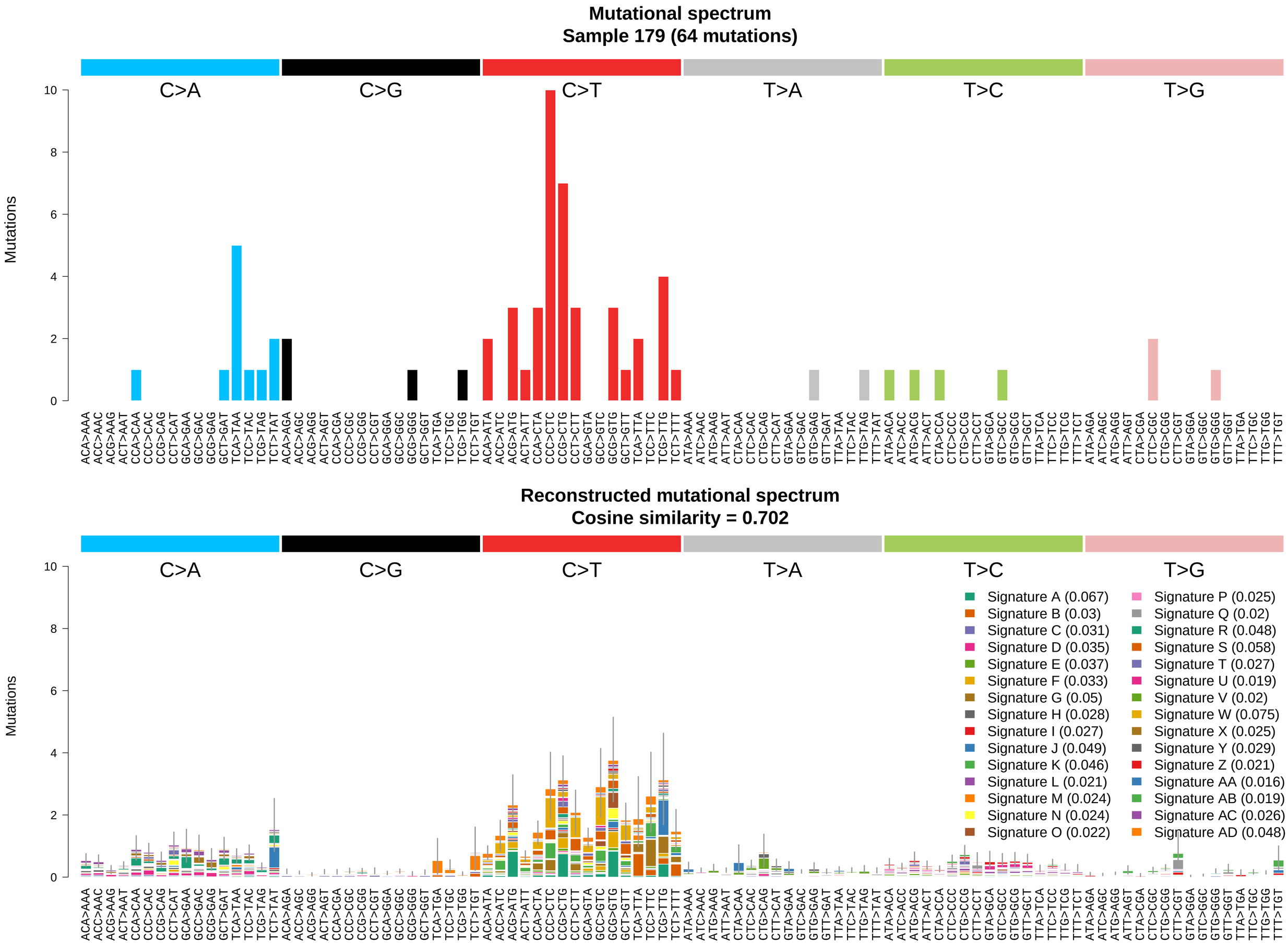

Reconstructed mutational spectrum
Cosine similarity = 0.633
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Signature A (0.028)
Signature B (0.044)
Signature C (0.136)
Signature D (0.026)
Signature E (0.045)
Signature F (0.026)
Signature G (0.029)
Signature H (0.029)
Signature I (0.056)
Signature J (0.018)
Signature K (0.022)
Signature L (0.029)
Signature M (0.04)
Signature N (0.018)
Signature O (0.019)
Signature P (0.046)
Signature Q (0.027)
Signature R (0.019)
Signature S (0.021)
Signature T (0.036)
Signature U (0.021)
Signature V (0.025)
Signature W (0.017)
Signature X (0.022)
Signature Y (0.037)
Signature Z (0.032)
Signature AA (0.021)
Signature AB (0.036)
Signature AC (0.02)
Signature AD (0.057)

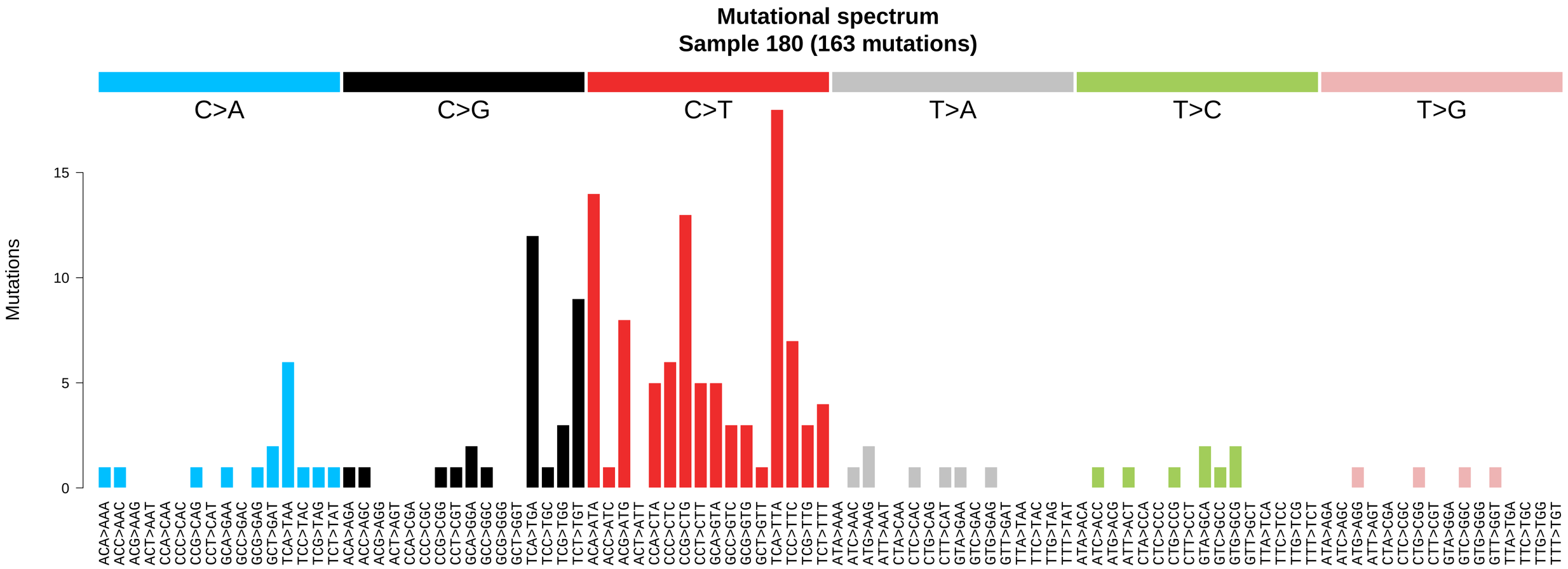

Mutational spectrum
Sample 175 (60 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.551
Signature A (0.029)
Signature B (0.016)
Signature C (0.101)
Signature D (0.051)
Signature E (0.065)
Signature F (0.022)
Signature G (0.025)
Signature H (0.04)
Signature I (0.031)
Signature J (0.014)
Signature K (0.023)
Signature L (0.045)
Signature M (0.043)
Signature N (0.019)
Signature O (0.02)
Signature P (0.049)
Signature Q (0.041)
Signature R (0.032)
Signature S (0.049)
Signature T (0.024)
Signature U (0.02)
Signature V (0.015)
Signature W (0.037)
Signature X (0.034)
Signature Y (0.03)
Signature Z (0.025)
Signature AA (0.018)
Signature AB (0.017)
Signature AC (0.027)
Signature AD (0.039)

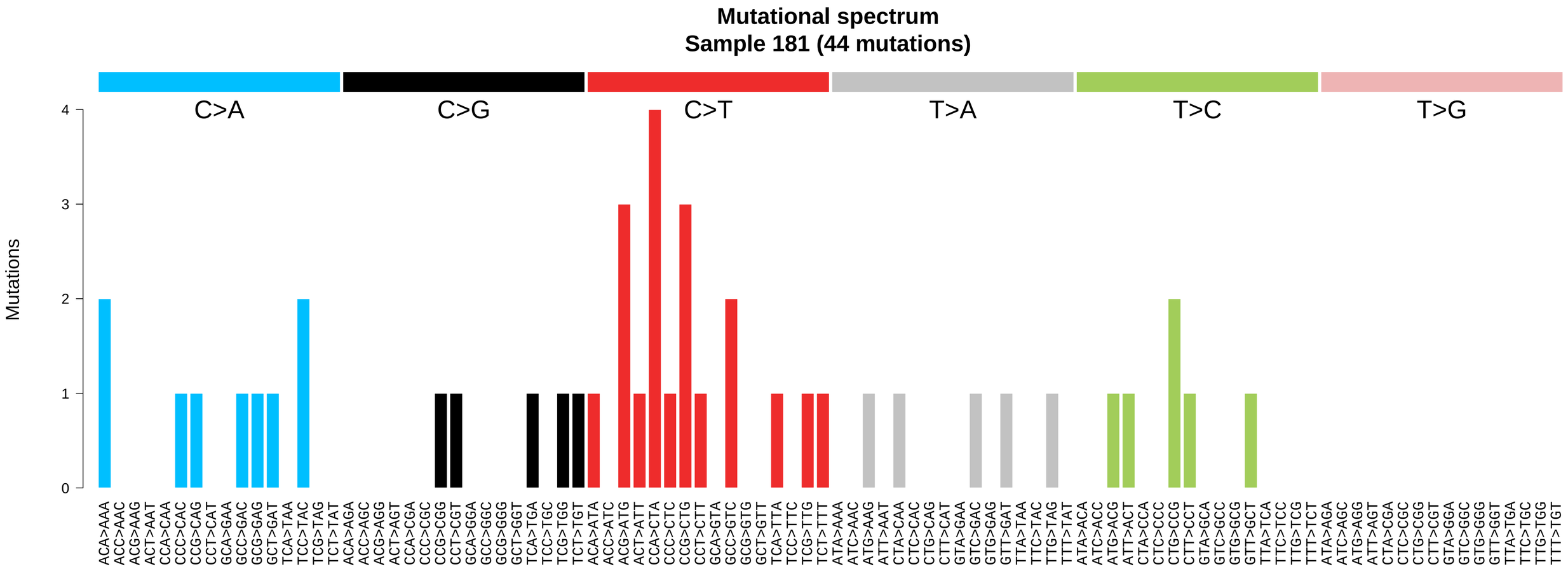

Mutational spectrum
Sample 176 (72 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.648
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
Signature A (0.027)
Signature B (0.017)
Signature C (0.1)
Signature D (0.066)
Signature E (0.049)
Signature F (0.024)
Signature G (0.051)
Signature H (0.032)
Signature I (0.023)
Signature J (0.019)
Signature K (0.039)
Signature L (0.036)
Signature M (0.024)
Signature N (0.02)
Signature O (0.015)
Signature P (0.034)
Signature Q (0.022)
Signature R (0.026)
Signature S (0.054)
Signature T (0.038)
Signature U (0.02)
Signature V (0.012)
Signature W (0.065)
Signature X (0.042)
Signature Y (0.025)
Signature Z (0.026)
Signature AA (0.016)
Signature AB (0.017)
Signature AC (0.026)
Signature AD (0.034)
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT

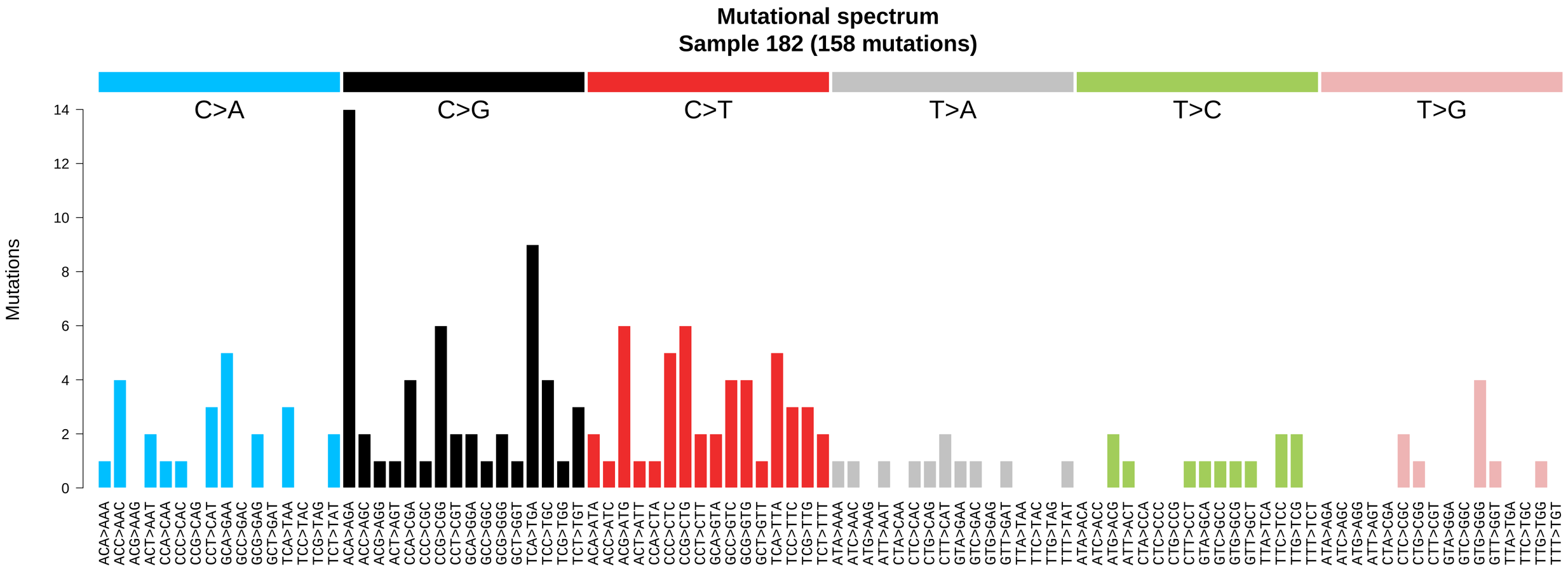

Mutational spectrum
Sample 177 (40 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.779
Signature A (0.049)
Signature B (0.028)
Signature C (0.032)
Signature D (0.024)
Signature E (0.033)
Signature F (0.036)
Signature G (0.046)
Signature H (0.031)
Signature I (0.032)
Signature J (0.047)
Signature K (0.038)
Signature L (0.033)
Signature M (0.04)
Signature N (0.03)
Signature O (0.026)
Signature P (0.034)
Signature Q (0.027)
Signature R (0.029)
Signature S (0.04)
Signature T (0.031)
Signature U (0.042)
Signature V (0.022)
Signature W (0.039)
Signature X (0.02)
Signature Y (0.027)
Signature Z (0.037)
Signature AA (0.029)
Signature AB (0.022)
Signature AC (0.029)
Signature AD (0.045)

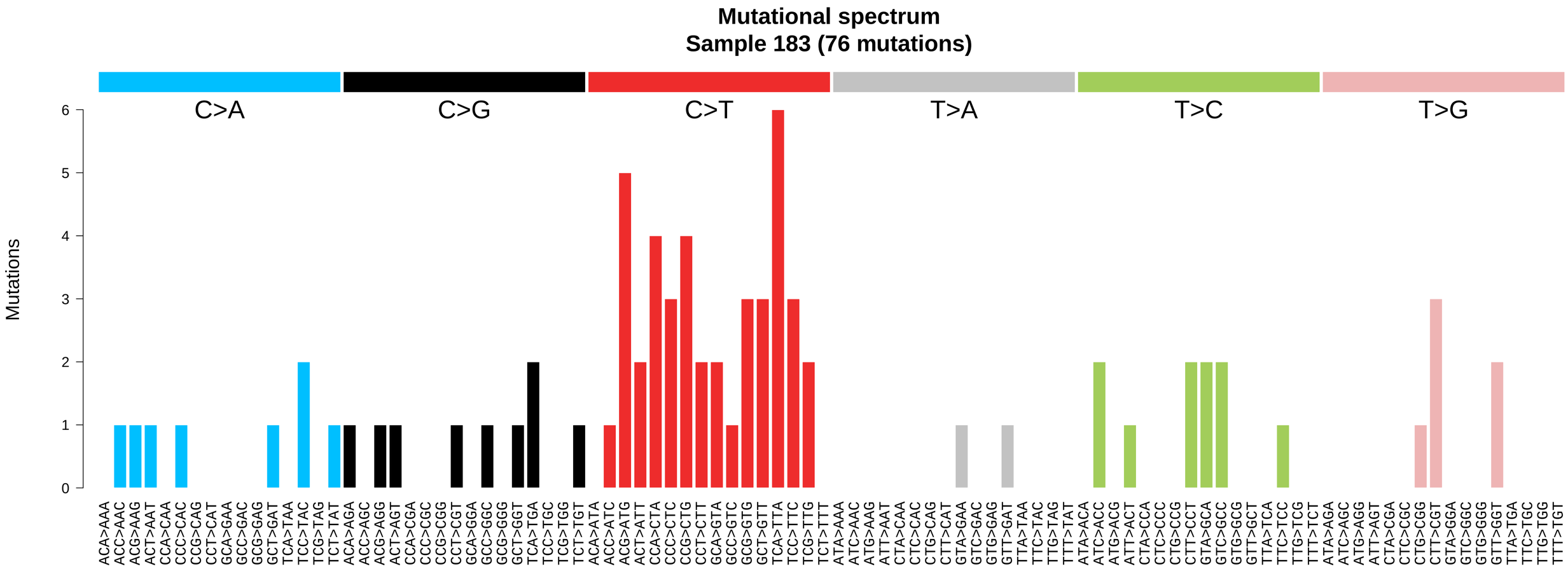

Mutational spectrum
Sample 178 (81 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.773
Signature A (0.037)
Signature B (0.022)
Signature C (0.121)
Signature D (0.035)
Signature E (0.052)
Signature F (0.028)
Signature G (0.032)
Signature H (0.034)
Signature I (0.03)
Signature J (0.017)
Signature K (0.034)
Signature L (0.023)
Signature M (0.02)
Signature N (0.027)
Signature O (0.037)
Signature P (0.034)
Signature Q (0.023)
Signature R (0.038)
Signature S (0.048)
Signature T (0.022)
Signature U (0.019)
Signature V (0.012)
Signature W (0.054)
Signature X (0.028)
Signature Y (0.022)
Signature Z (0.023)
Signature AA (0.015)
Signature AB (0.022)
Signature AC (0.038)
Signature AD (0.053)

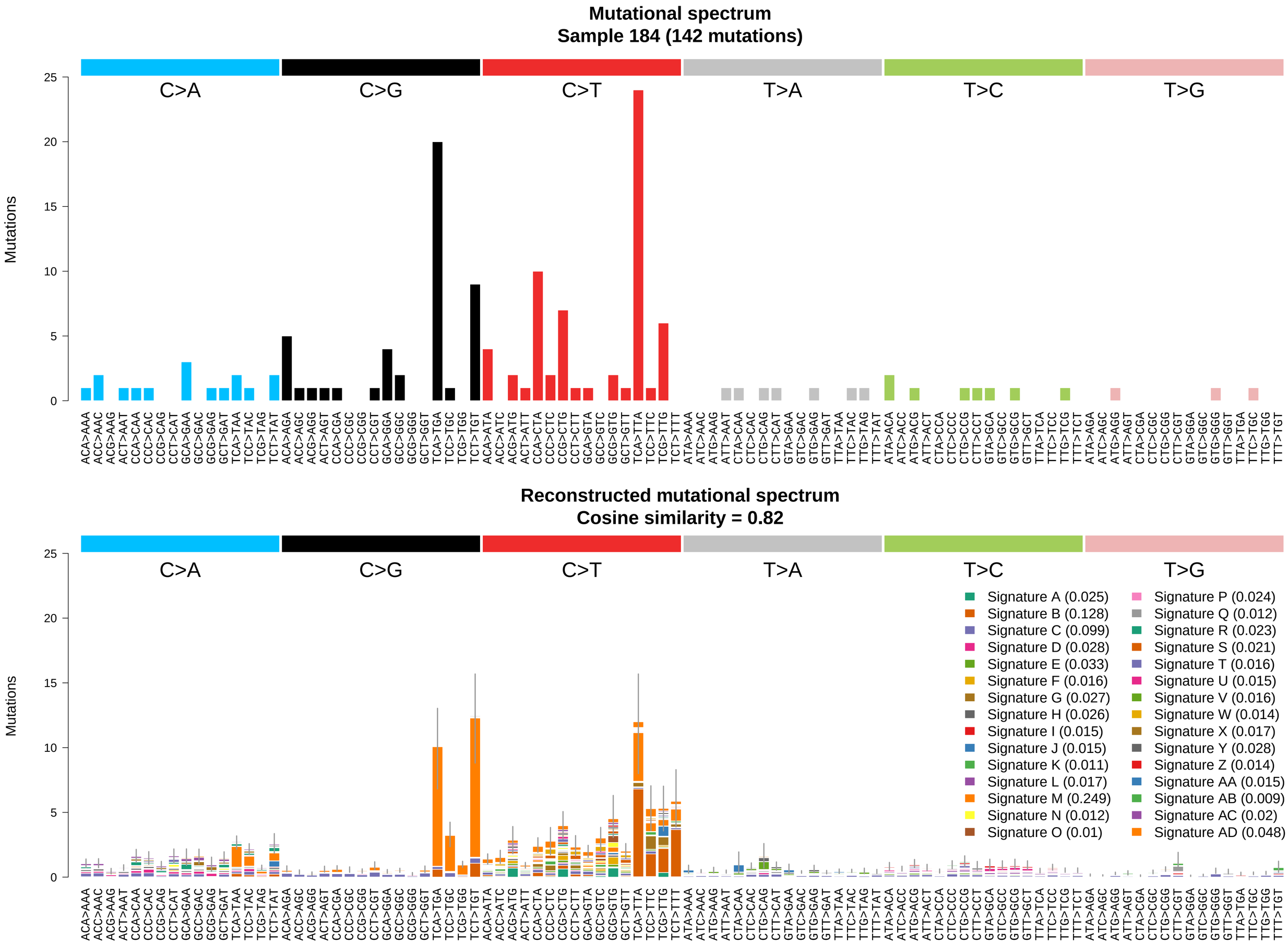

Mutational spectrum
Sample 179 (64 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.702
Signature A (0.067)
Signature B (0.03)
Signature C (0.031)
Signature D (0.035)
Signature E (0.037)
Signature F (0.033)
Signature G (0.05)
Signature H (0.028)
Signature I (0.027)
Signature J (0.049)
Signature K (0.046)
Signature L (0.021)
Signature M (0.024)
Signature N (0.024)
Signature O (0.022)
Signature P (0.025)
Signature Q (0.02)
Signature R (0.048)
Signature S (0.058)
Signature T (0.027)
Signature U (0.019)
Signature V (0.02)
Signature W (0.075)
Signature X (0.025)
Signature Y (0.029)
Signature Z (0.021)
Signature AA (0.016)
Signature AB (0.019)
Signature AC (0.026)
Signature AD (0.048)

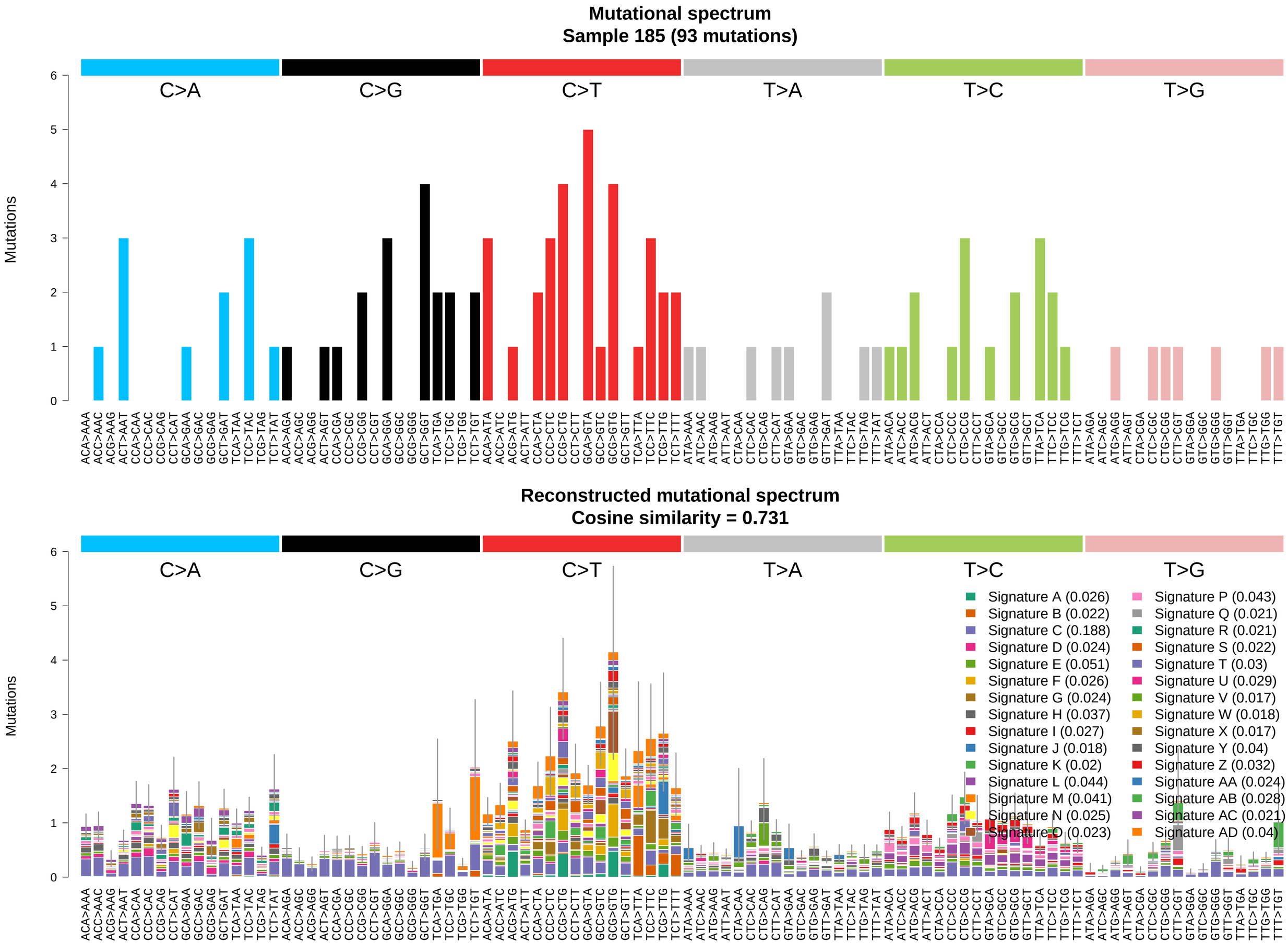

Mutational spectrum
Sample 180 (163 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.856
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
5
10
15
Signature A (0.053)
Signature B (0.086)
Signature C (0.024)
Signature D (0.018)
Signature E (0.025)
Signature F (0.026)
Signature G (0.025)
Signature H (0.018)
Signature I (0.011)
Signature J (0.01)
Signature K (0.021)
Signature L (0.012)
Signature M (0.189)
Signature N (0.017)
Signature O (0.013)
Signature P (0.016)
Signature Q (0.012)
Signature R (0.018)
Signature S (0.03)
Signature T (0.022)
Signature U (0.024)
Signature V (0.014)
Signature W (0.023)
Signature X (0.015)
Signature Y (0.021)
Signature Z (0.017)
Signature AA (0.011)
Signature AB (0.008)
Signature AC (0.016)
Signature AD (0.207)

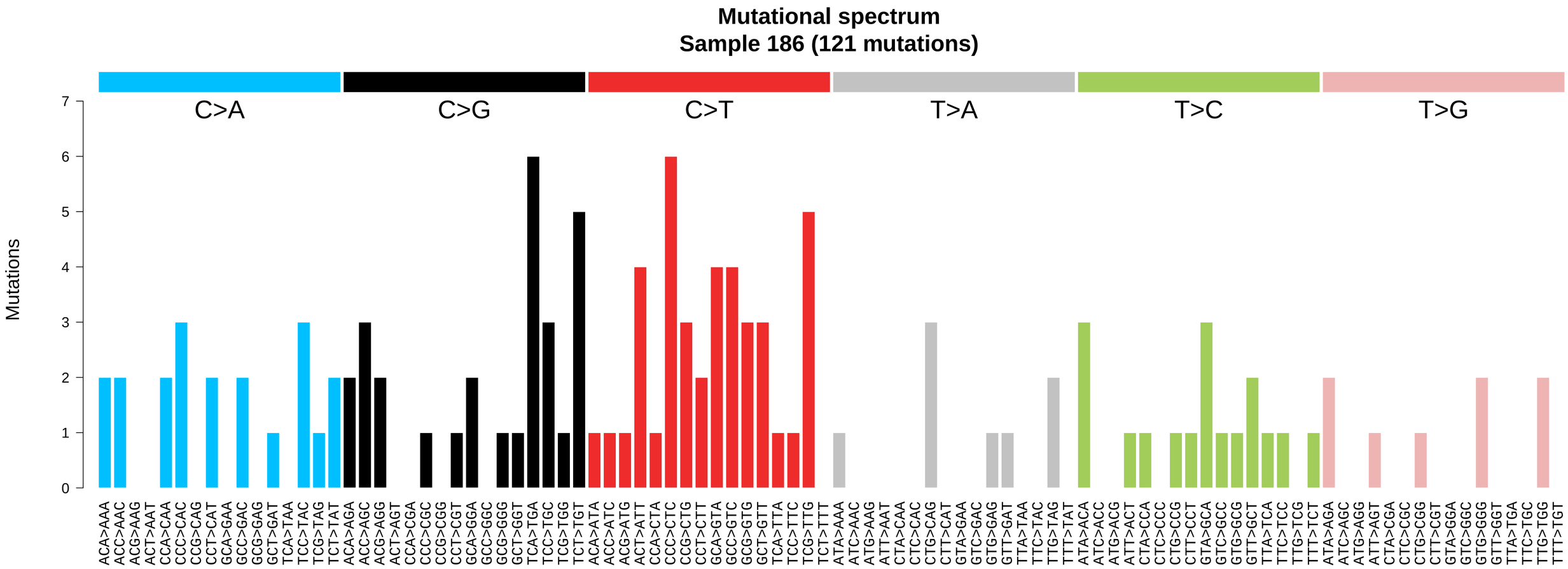

Mutational spectrum
Sample 181 (44 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.649
Signature A (0.039)
Signature B (0.031)
Signature C (0.039)
Signature D (0.05)
Signature E (0.042)
Signature F (0.032)
Signature G (0.03)
Signature H (0.035)
Signature I (0.025)
Signature J (0.019)
Signature K (0.029)
Signature L (0.033)
Signature M (0.045)
Signature N (0.023)
Signature O (0.021)
Signature P (0.041)
Signature Q (0.025)
Signature R (0.036)
Signature S (0.037)
Signature T (0.039)
Signature U (0.029)
Signature V (0.033)
Signature W (0.031)
Signature X (0.043)
Signature Y (0.034)
Signature Z (0.03)
Signature AA (0.031)
Signature AB (0.017)
Signature AC (0.039)
Signature AD (0.042)

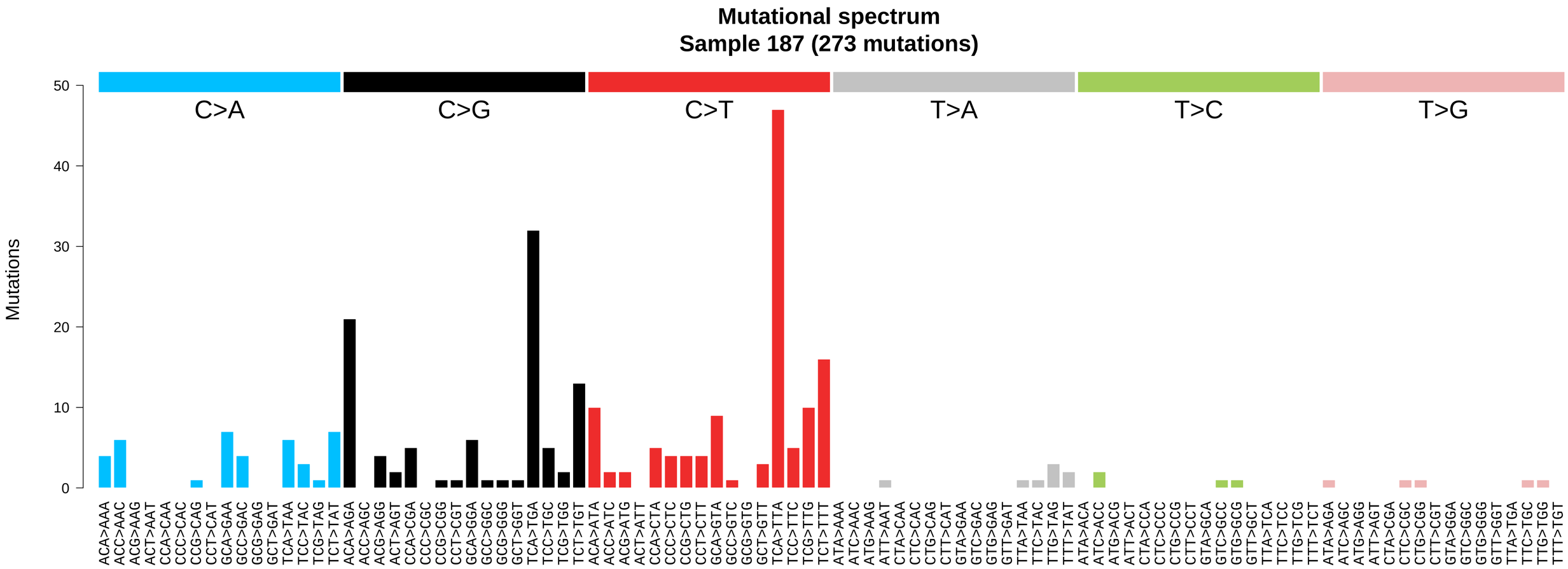

Mutational spectrum
Sample 182 (158 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
14
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.731
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
10
12
14
Signature A (0.034)
Signature B (0.021)
Signature C (0.362)
Signature D (0.032)
Signature E (0.03)
Signature F (0.02)
Signature G (0.018)
Signature H (0.028)
Signature I (0.014)
Signature J (0.014)
Signature K (0.021)
Signature L (0.014)
Signature M (0.091)
Signature N (0.017)
Signature O (0.015)
Signature P (0.017)
Signature Q (0.012)
Signature R (0.028)
Signature S (0.021)
Signature T (0.02)
Signature U (0.017)
Signature V (0.011)
Signature W (0.018)
Signature X (0.019)
Signature Y (0.022)
Signature Z (0.015)
Signature AA (0.013)
Signature AB (0.009)
Signature AC (0.022)
Signature AD (0.024)

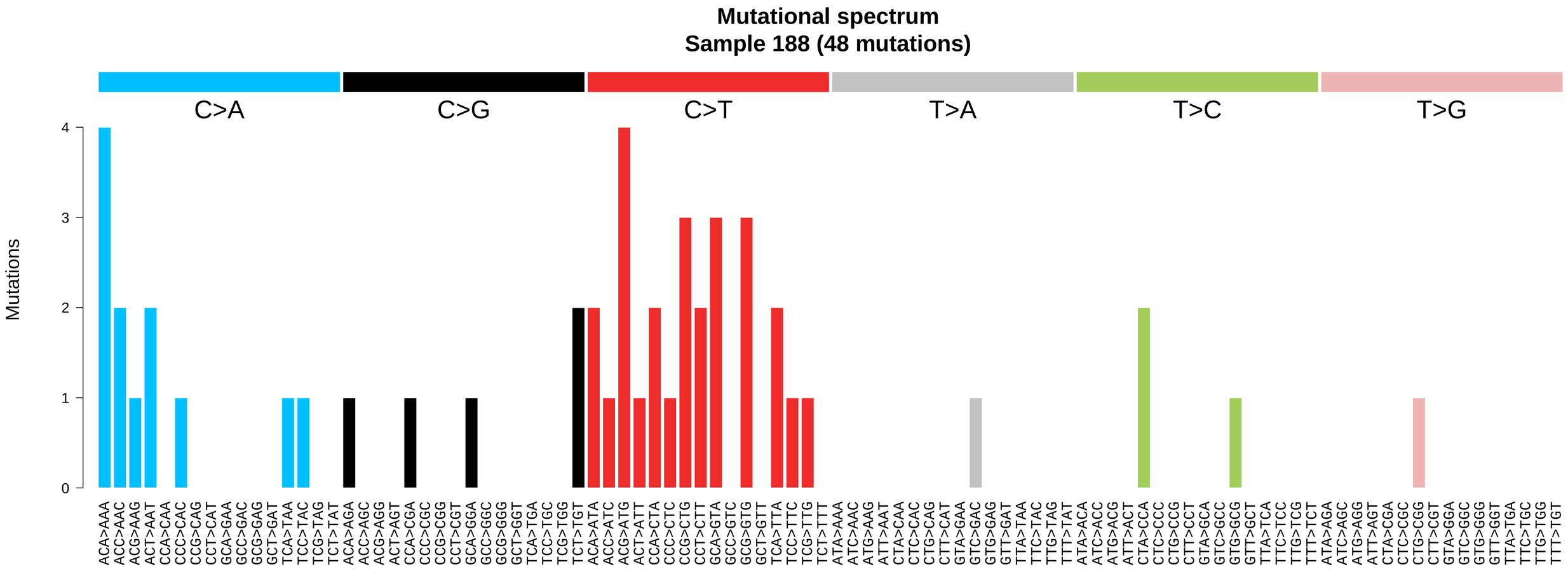

Mutational spectrum
Sample 183 (76 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.812
Signature A (0.046)
Signature B (0.052)
Signature C (0.055)
Signature D (0.026)
Signature E (0.038)
Signature F (0.032)
Signature G (0.041)
Signature H (0.03)
Signature I (0.028)
Signature J (0.021)
Signature K (0.035)
Signature L (0.027)
Signature M (0.043)
Signature N (0.031)
Signature O (0.029)
Signature P (0.029)
Signature Q (0.066)
Signature R (0.019)
Signature S (0.047)
Signature T (0.026)
Signature U (0.034)
Signature V (0.012)
Signature W (0.038)
Signature X (0.021)
Signature Y (0.024)
Signature Z (0.033)
Signature AA (0.021)
Signature AB (0.018)
Signature AC (0.026)
Signature AD (0.052)

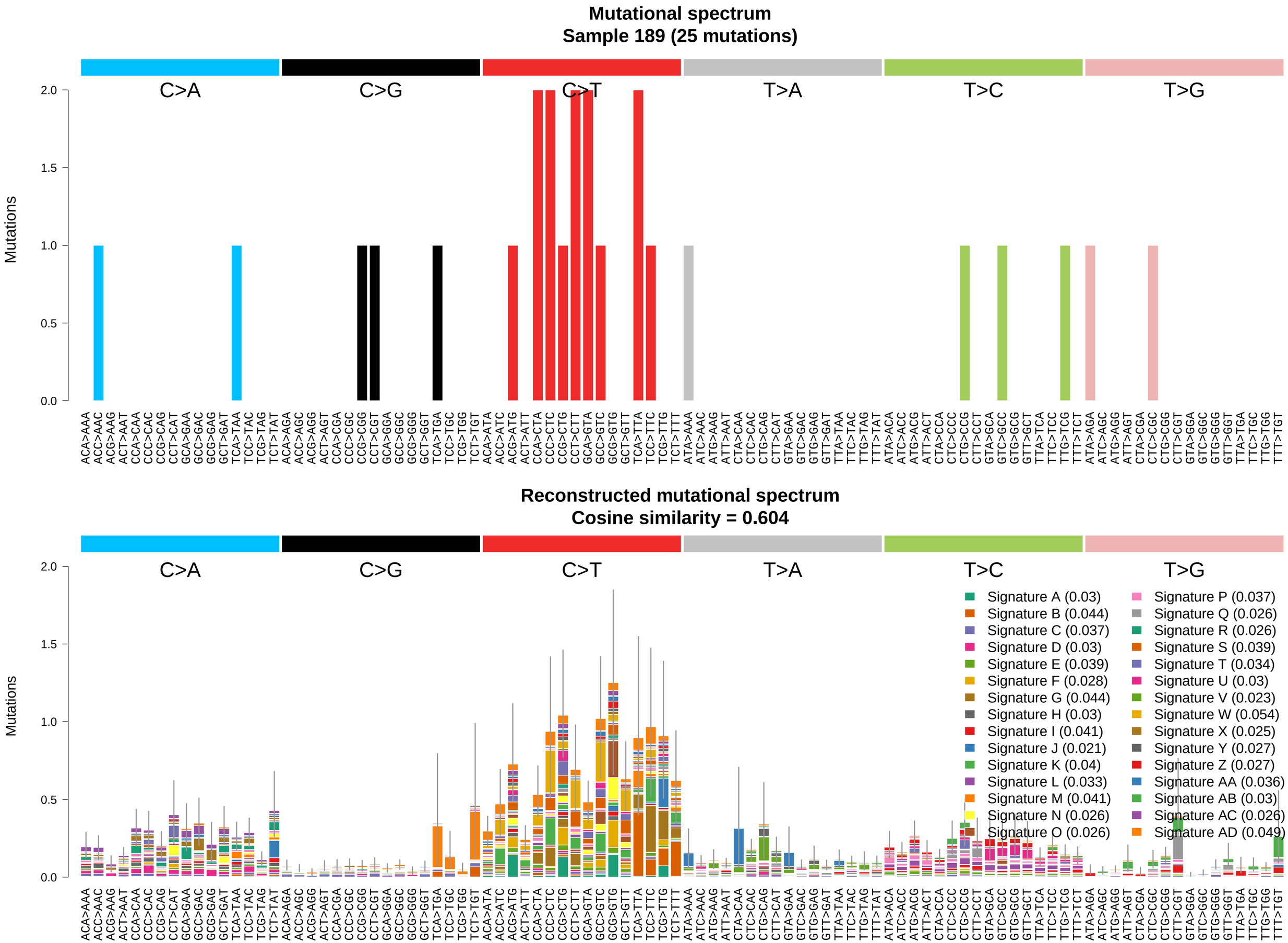

Mutational spectrum
Sample 184 (142 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.82
Signature A (0.025)
Signature B (0.128)
Signature C (0.099)
Signature D (0.028)
Signature E (0.033)
Signature F (0.016)
Signature G (0.027)
Signature H (0.026)
Signature I (0.015)
Signature J (0.015)
Signature K (0.011)
Signature L (0.017)
Signature M (0.249)
Signature N (0.012)
Signature O (0.01)
Signature P (0.024)
Signature Q (0.012)
Signature R (0.023)
Signature S (0.021)
Signature T (0.016)
Signature U (0.015)
Signature V (0.016)
Signature W (0.014)
Signature X (0.017)
Signature Y (0.028)
Signature Z (0.014)
Signature AA (0.015)
Signature AB (0.009)
Signature AC (0.02)
Signature AD (0.048)

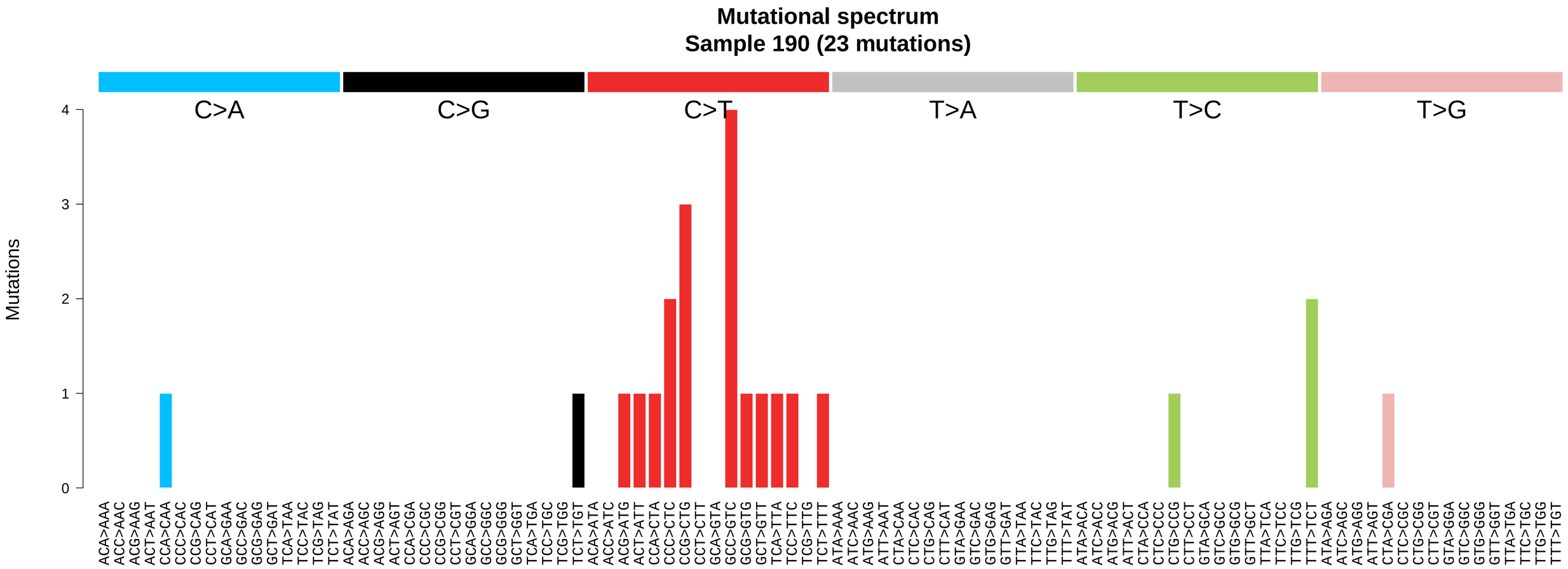

Mutational spectrum
Sample 185 (93 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.731
Signature A (0.026)
Signature B (0.022)
Signature C (0.188)
Signature D (0.024)
Signature E (0.051)
Signature F (0.026)
Signature G (0.024)
Signature H (0.037)
Signature I (0.027)
Signature J (0.018)
Signature K (0.02)
Signature L (0.044)
Signature M (0.041)
Signature N (0.025)
Signature O (0.023)
Signature P (0.043)
Signature Q (0.021)
Signature R (0.021)
Signature S (0.022)
Signature T (0.03)
Signature U (0.029)
Signature V (0.017)
Signature W (0.018)
Signature X (0.017)
Signature Y (0.04)
Signature Z (0.032)
Signature AA (0.024)
Signature AB (0.028)
Signature AC (0.021)
Signature AD (0.04)

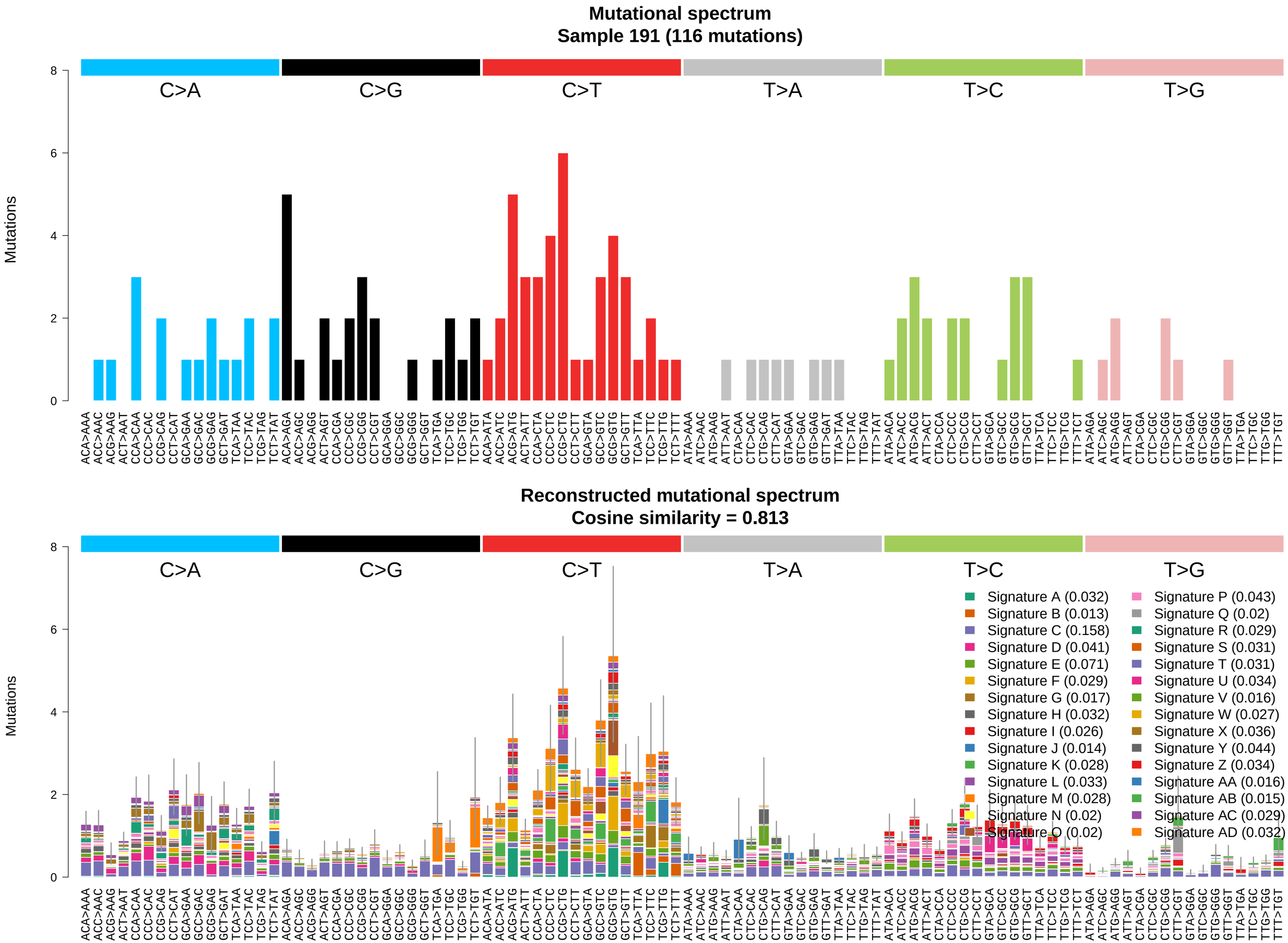

Mutational spectrum
Sample 186 (121 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
7
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.818
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
5
6
7
Signature A (0.018)
Signature B (0.012)
Signature C (0.175)
Signature D (0.038)
Signature E (0.043)
Signature F (0.019)
Signature G (0.018)
Signature H (0.033)
Signature I (0.034)
Signature J (0.024)
Signature K (0.028)
Signature L (0.026)
Signature M (0.097)
Signature N (0.022)
Signature O (0.021)
Signature P (0.031)
Signature Q (0.011)
Signature R (0.019)
Signature S (0.034)
Signature T (0.023)
Signature U (0.035)
Signature V (0.026)
Signature W (0.042)
Signature X (0.025)
Signature Y (0.038)
Signature Z (0.032)
Signature AA (0.013)
Signature AB (0.013)
Signature AC (0.022)
Signature AD (0.026)
ACA>AAA ACC>AAC ACG>AAG ACT>AAT CCA>CAA CCC>CAC CCG>CAG CCT>CAT GCA>GAA GCC>GAC GCG>GAG GCT>GAT TCA>TAA TCC>TAC TCG>TAG TCT>TAT ACA>AGA ACC>AGC ACG>AGG ACT>AGT CCA>CGA CCC>CGC CCG>CGG CCT>CGT GCA>GGA GCC>GGC GCG>GGG GCT>GGT TCA>TGA TCC>TGC TCG>TGG TCT>TGT ACA>ATA ACC>ATC ACG>ATG ACT>ATT CCA>CTA CCC>CTC CCG>CTG CCT>CTT GCA>GTA GCC>GTC GCG>GTG GCT>GTT TCA>TTA TCC>TTC TCG>TTG TCT>TTT ATA>AAA ATC>AAC ATG>AAG ATT>AAT CTA>CAA CTC>CAC CTG>CAG CTT>CAT GTA>GAA GTC>GAC GTG>GAG GTT>GAT TTA>TAA TTC>TAC TTG>TAG TTT>TAT ATA>ACA ATC>ACC ATG>ACG ATT>ACT CTA>CCA CTC>CCC CTG>CCG CTT>CCT GTA>GCA GTC>GCC GTG>GCG GTT>GCT TTA>TCA TTC>TCC TTG>TCG TTT>TCT ATA>AGA ATC>AGC ATG>AGG ATT>AGT CTA>CGA CTC>CGC CTG>CGG CTT>CGT GTA>GGA GTC>GGC GTG>GGG GTT>GGT TTA>TGA TTC>TGC TTG>TGG TTT>TGT

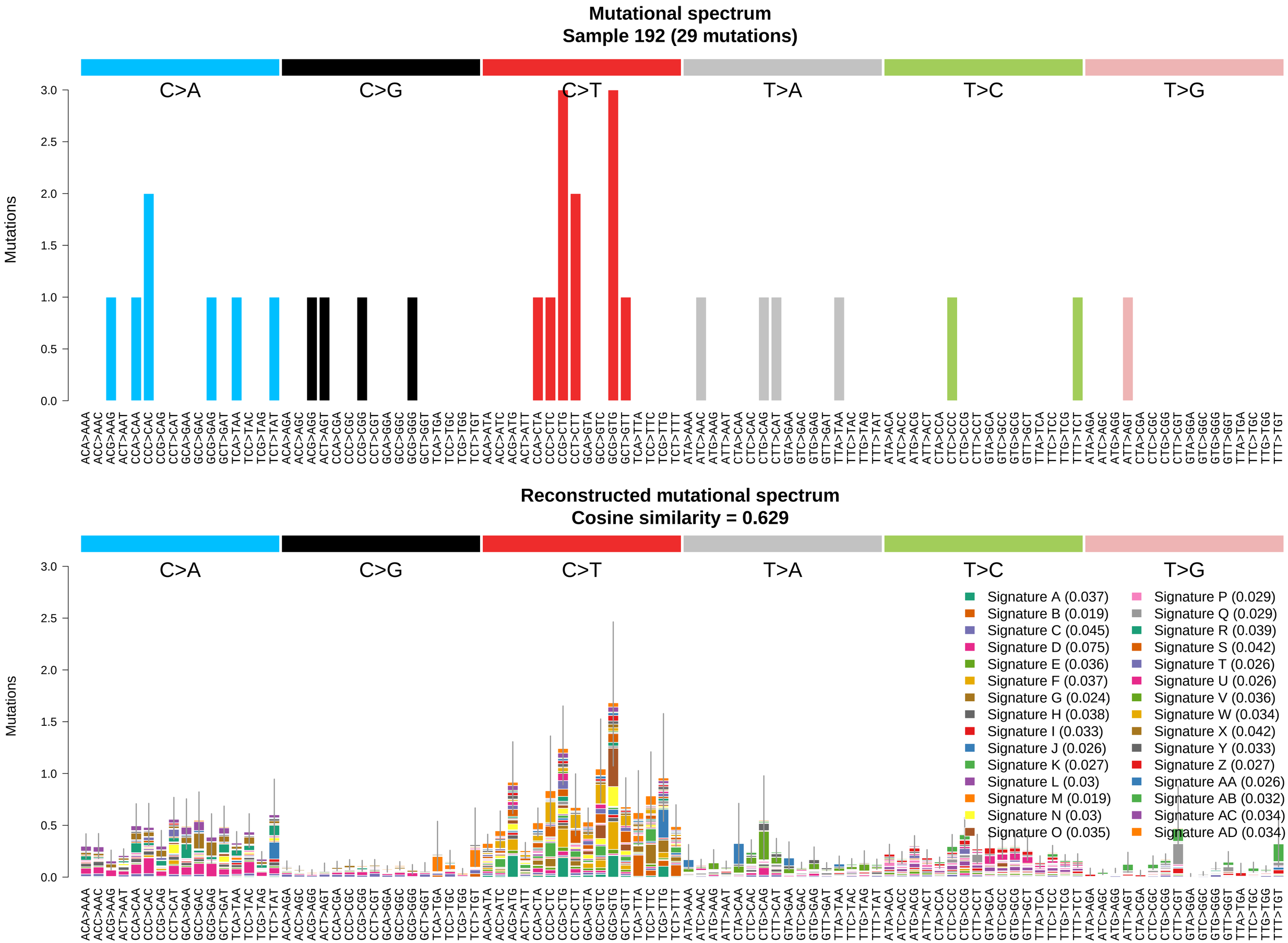

Mutational spectrum
Sample 187 (273 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
10
20
30
40
50
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.869
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
10
20
30
40
50
Signature A (0.008)
Signature B (0.244)
Signature C (0.229)
Signature D (0.016)
Signature E (0.015)
Signature F (0.007)
Signature G (0.011)
Signature H (0.015)
Signature I (0.009)
Signature J (0.011)
Signature K (0.012)
Signature L (0.007)
Signature M (0.222)
Signature N (0.006)
Signature O (0.006)
Signature P (0.009)
Signature Q (0.005)
Signature R (0.02)
Signature S (0.013)
Signature T (0.008)
Signature U (0.005)
Signature V (0.006)
Signature W (0.012)
Signature X (0.017)
Signature Y (0.01)
Signature Z (0.005)
Signature AA (0.006)
Signature AB (0.005)
Signature AC (0.021)
Signature AD (0.037)

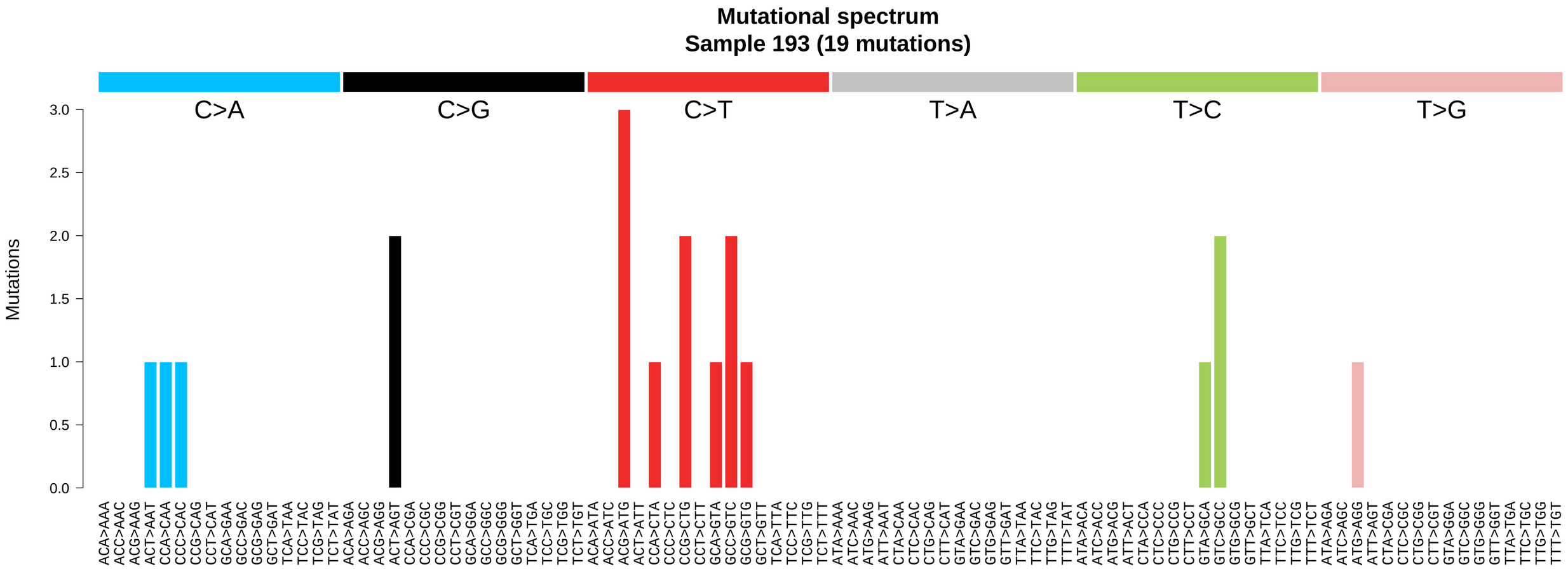

Mutational spectrum
Sample 188 (48 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.684
Signature A (0.059)
Signature B (0.033)
Signature C (0.049)
Signature D (0.05)
Signature E (0.038)
Signature F (0.041)
Signature G (0.028)
Signature H (0.06)
Signature I (0.024)
Signature J (0.019)
Signature K (0.03)
Signature L (0.027)
Signature M (0.038)
Signature N (0.035)
Signature O (0.026)
Signature P (0.029)
Signature Q (0.019)
Signature R (0.026)
Signature S (0.044)
Signature T (0.032)
Signature U (0.024)
Signature V (0.017)
Signature W (0.032)
Signature X (0.031)
Signature Y (0.03)
Signature Z (0.024)
Signature AA (0.022)
Signature AB (0.018)
Signature AC (0.054)
Signature AD (0.042)

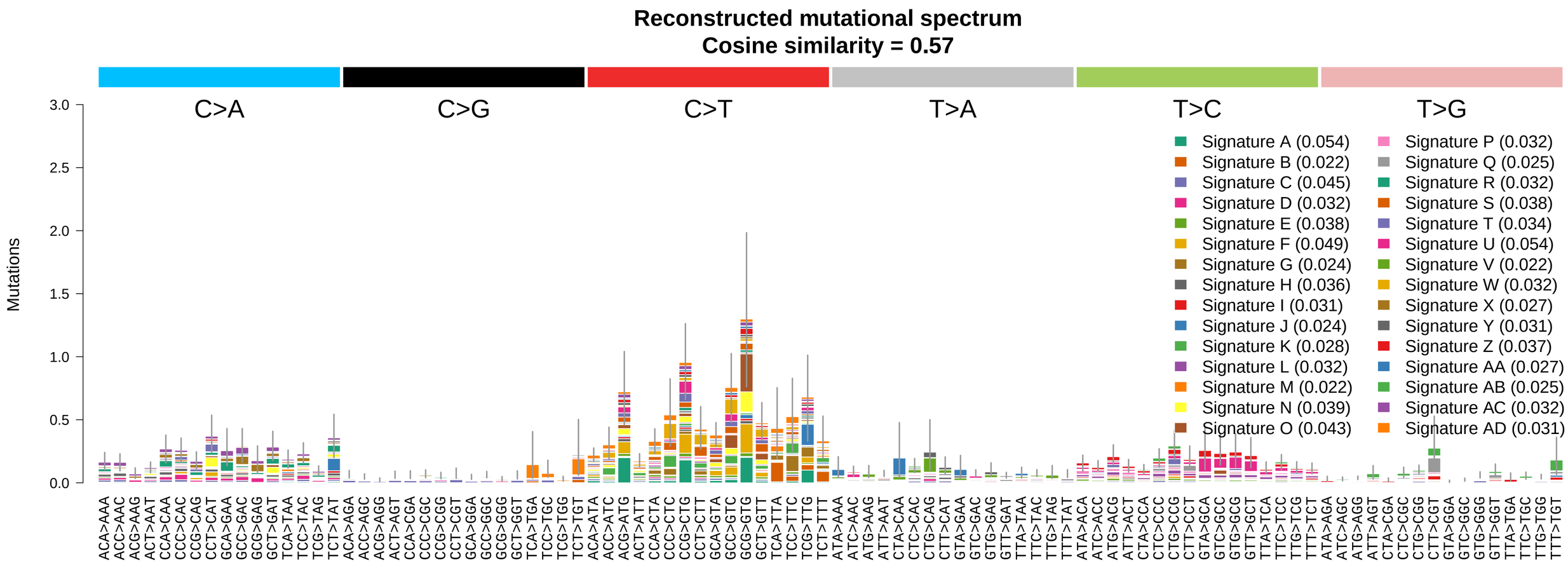

Mutational spectrum
Sample 189 (25 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
2.0
1.5
1.0
0.5
0.0
Reconstructed mutational spectrum
Cosine similarity = 0.604
Signature A (0.03)
Signature B (0.044)
Signature C (0.037)
Signature D (0.03)
Signature E (0.039)
Signature F (0.028)
Signature G (0.044)
Signature H (0.03)
Signature I (0.041)
Signature J (0.021)
Signature K (0.04)
Signature L (0.033)
Signature M (0.041)
Signature N (0.026)
Signature O (0.026)
Signature P (0.037)
Signature Q (0.026)
Signature R (0.026)
Signature S (0.039)
Signature T (0.034)
Signature U (0.03)
Signature V (0.023)
Signature W (0.054)
Signature X (0.025)
Signature Y (0.027)
Signature Z (0.027)
Signature AA (0.036)
Signature AB (0.03)
Signature AC (0.026)
Signature AD (0.049)

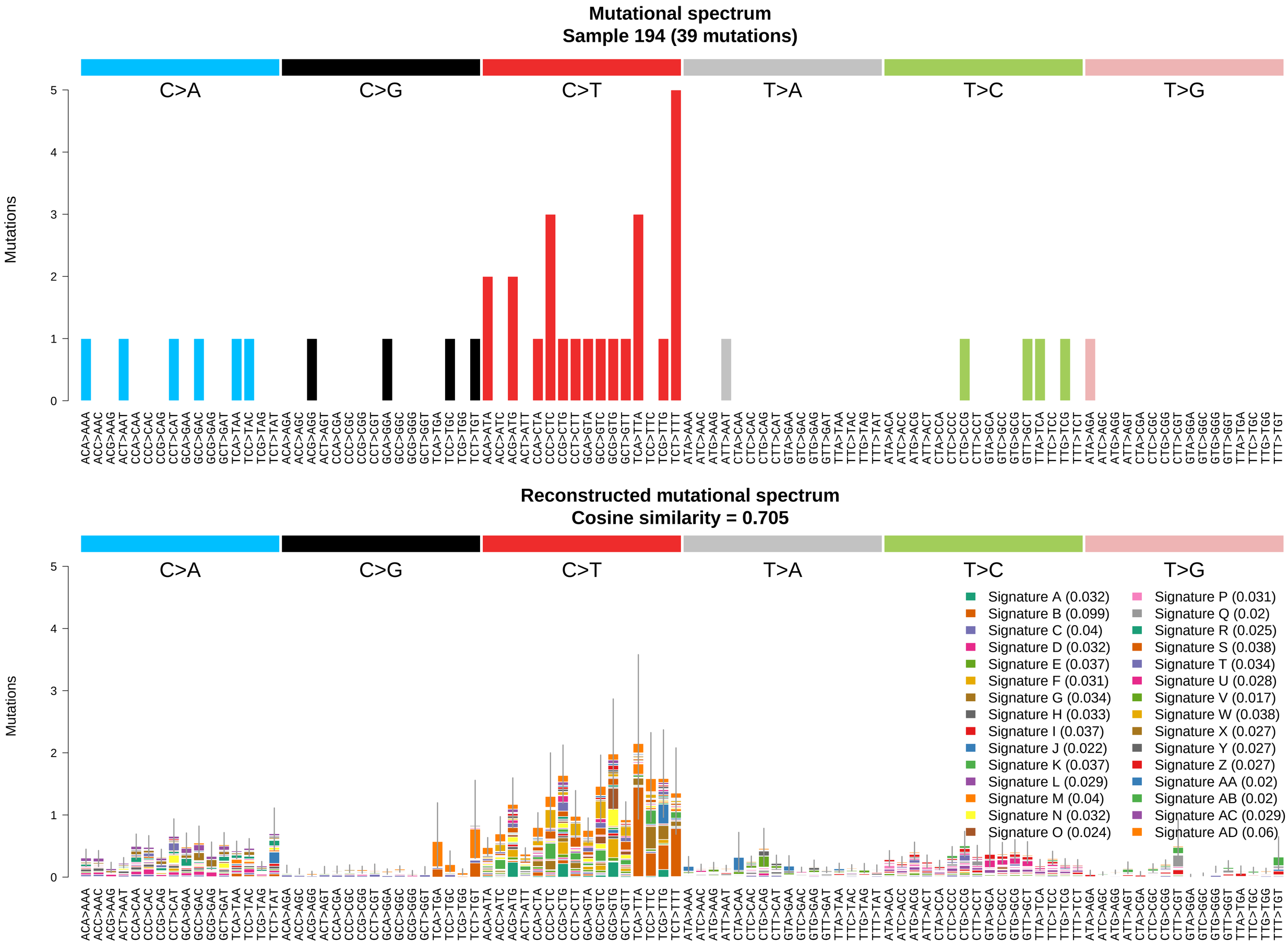

Mutational spectrum
Sample 190 (23 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
1
2
3
4
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.7
Signature A (0.041)
Signature B (0.041)
Signature C (0.026)
Signature D (0.023)
Signature E (0.031)
Signature F (0.041)
Signature G (0.04)
Signature H (0.025)
Signature I (0.043)
Signature J (0.024)
Signature K (0.055)
Signature L (0.032)
Signature M (0.034)
Signature N (0.033)
Signature O (0.035)
Signature P (0.028)
Signature Q (0.025)
Signature R (0.024)
Signature S (0.043)
Signature T (0.035)
Signature U (0.034)
Signature V (0.02)
Signature W (0.07)
Signature X (0.022)
Signature Y (0.029)
Signature Z (0.031)
Signature AA (0.023)
Signature AB (0.028)
Signature AC (0.027)
Signature AD (0.039)

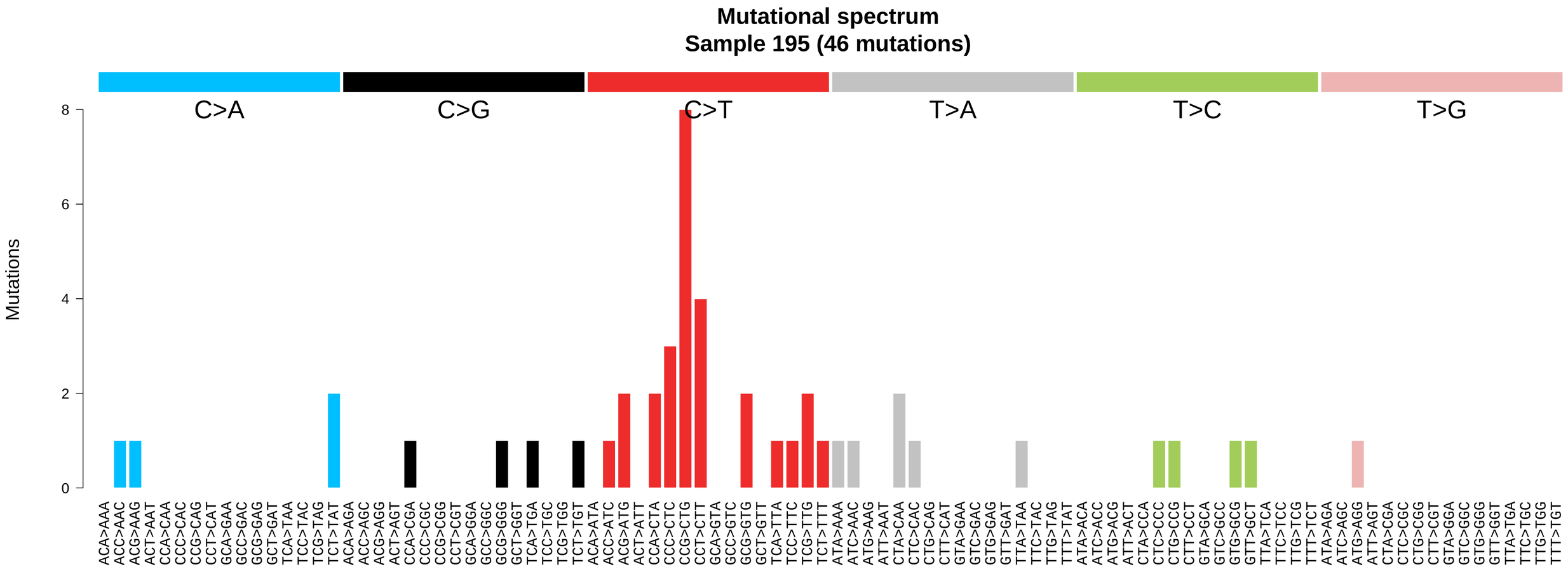

Mutational spectrum
Sample 191 (116 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.813
Signature A (0.032)
Signature B (0.013)
Signature C (0.158)
Signature D (0.041)
Signature E (0.071)
Signature F (0.029)
Signature G (0.017)
Signature H (0.032)
Signature I (0.026)
Signature J (0.014)
Signature K (0.028)
Signature L (0.033)
Signature M (0.028)
Signature N (0.02)
Signature O (0.02)
Signature P (0.043)
Signature Q (0.02)
Signature R (0.029)
Signature S (0.031)
Signature T (0.031)
Signature U (0.034)
Signature V (0.016)
Signature W (0.027)
Signature X (0.036)
Signature Y (0.044)
Signature Z (0.034)
Signature AA (0.016)
Signature AB (0.015)
Signature AC (0.029)
Signature AD (0.032)


Mutational spectrum
Sample 192 (29 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.629
Signature A (0.037)
Signature B (0.019)
Signature C (0.045)
Signature D (0.075)
Signature E (0.036)
Signature F (0.037)
Signature G (0.024)
Signature H (0.038)
Signature I (0.033)
Signature J (0.026)
Signature K (0.027)
Signature L (0.03)
Signature M (0.019)
Signature N (0.03)
Signature O (0.035)
Signature P (0.029)
Signature Q (0.029)
Signature R (0.039)
Signature S (0.042)
Signature T (0.026)
Signature U (0.026)
Signature V (0.036)
Signature W (0.034)
Signature X (0.042)
Signature Y (0.033)
Signature Z (0.027)
Signature AA (0.026)
Signature AB (0.032)
Signature AC (0.034)
Signature AD (0.034)


Mutational spectrum
Sample 193 (19 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT


Reconstructed mutational spectrum
Cosine similarity = 0.57
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Signature A (0.054)
Signature B (0.022)
Signature C (0.045)
Signature D (0.032)
Signature E (0.038)
Signature F (0.049)
Signature G (0.024)
Signature H (0.036)
Signature I (0.031)
Signature J (0.024)
Signature K (0.028)
Signature L (0.032)
Signature M (0.022)
Signature N (0.039)
Signature O (0.043)
Signature P (0.032)
Signature Q (0.025)
Signature R (0.032)
Signature S (0.038)
Signature T (0.034)
Signature U (0.054)
Signature V (0.022)
Signature W (0.032)
Signature X (0.027)
Signature Y (0.031)
Signature Z (0.037)
Signature AA (0.027)
Signature AB (0.025)
Signature AC (0.032)
Signature AD (0.031)


Mutational spectrum
Sample 194 (39 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
Reconstructed mutational spectrum
Cosine similarity = 0.705
Signature A (0.032)
Signature B (0.099)
Signature C (0.04)
Signature D (0.032)
Signature E (0.037)
Signature F (0.031)
Signature G (0.034)
Signature H (0.033)
Signature I (0.037)
Signature J (0.022)
Signature K (0.037)
Signature L (0.029)
Signature M (0.04)
Signature N (0.032)
Signature O (0.024)
Signature P (0.031)
Signature Q (0.02)
Signature R (0.025)
Signature S (0.038)
Signature T (0.034)
Signature U (0.028)
Signature V (0.017)
Signature W (0.038)
Signature X (0.027)
Signature Y (0.027)
Signature Z (0.027)
Signature AA (0.02)
Signature AB (0.02)
Signature AC (0.029)
Signature AD (0.06)


Mutational spectrum
Sample 195 (46 mutations)
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
ACA>AAA
ACC>AAC
ACG>AAG
ACT>AAT
CCA>CAA
CCC>CAC
CCG>CAG
CCT>CAT
GCA>GAA
GCC>GAC
GCG>GAG
GCT>GAT
TCA>TAA
TCC>TAC
TCG>TAG
TCT>TAT
ACA>AGA
ACC>AGC
ACG>AGG
ACT>AGT
CCA>CGA
CCC>CGC
CCG>CGG
CCT>CGT
GCA>GGA
GCC>GGC
GCG>GGG
GCT>GGT
TCA>TGA
TCC>TGC
TCG>TGG
TCT>TGT
ACA>ATA
ACC>ATC
ACG>ATG
ACT>ATT
CCA>CTA
CCC>CTC
CCG>CTG
CCT>CTT
GCA>GTA
GCC>GTC
GCG>GTG
GCT>GTT
TCA>TTA
TCC>TTC
TCG>TTG
TCT>TTT
ATA>AAA
ATC>AAC
ATG>AAG
ATT>AAT
CTA>CAA
CTC>CAC
CTG>CAG
CTT>CAT
GTA>GAA
GTC>GAC
GTG>GAG
GTT>GAT
TTA>TAA
TTC>TAC
TTG>TAG
TTT>TAT
ATA>ACA
ATC>ACC
ATG>ACG
ATT>ACT
CTA>CCA
CTC>CCC
CTG>CCG
CTT>CCT
GTA>GCA
GTC>GCC
GTG>GCG
GTT>GCT
TTA>TCA
TTC>TCC
TTG>TCG
TTT>TCT
ATA>AGA
ATC>AGC
ATG>AGG
ATT>AGT
CTA>CGA
CTC>CGC
CTG>CGG
CTT>CGT
GTA>GGA
GTC>GGC
GTG>GGG
GTT>GGT
TTA>TGA
TTC>TGC
TTG>TGG
TTT>TGT
Reconstructed mutational spectrum
Cosine similarity = 0.713
C>A
C>G
C>T
T>A
T>C
T>G
Mutations
0
2
4
6
8
Signature A (0.063)
Signature B (0.03)
Signature C (0.031)
Signature D (0.033)
Signature E (0.028)
Signature F (0.042)
Signature G (0.049)
Signature H (0.03)
Signature I (0.024)
Signature J (0.036)
Signature K (0.038)
Signature L (0.026)
Signature M (0.037)
Signature N (0.027)
Signature O (0.023)
Signature P (0.027)
Signature Q (0.023)
Signature R (0.022)
Signature S (0.045)
Signature T (0.029)
Signature U (0.036)
Signature V (0.027)
Signature W (0.046)
Signature X (0.023)
Signature Y (0.032)
Signature Z (0.027)
Signature AA (0.067)
Signature AB (0.018)
Signature AC (0.026)
Signature AD (0.038)