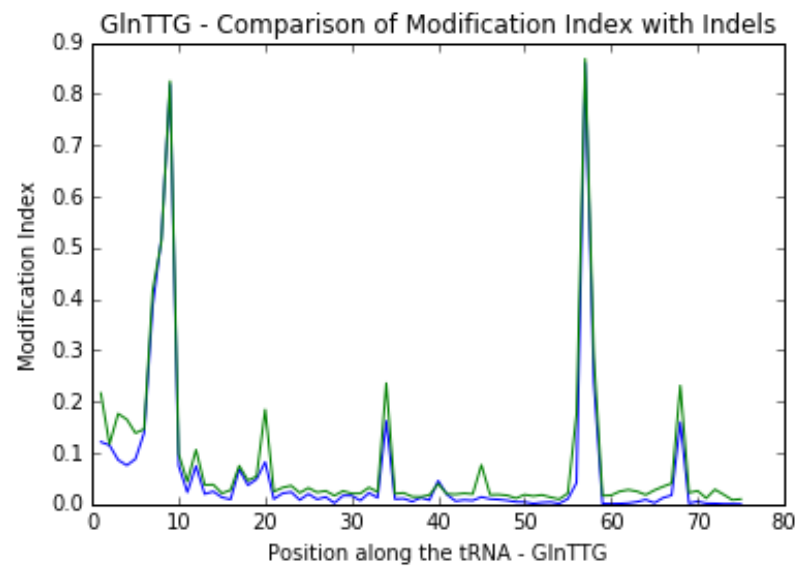
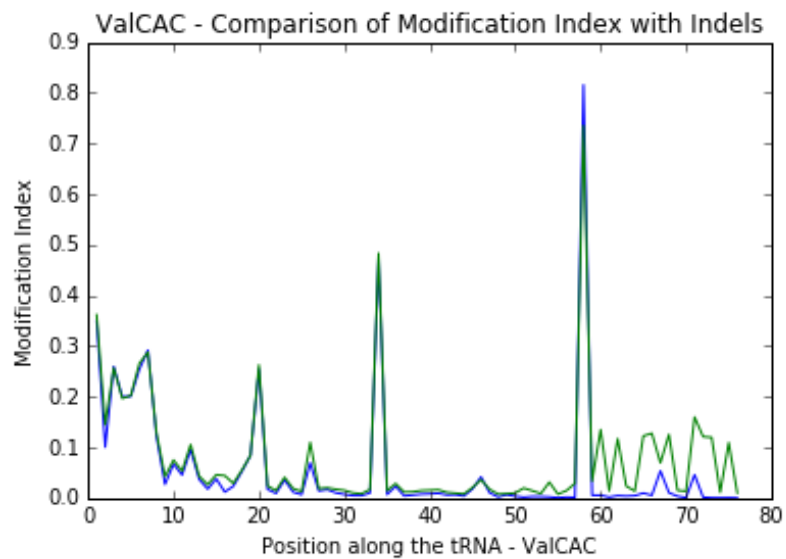
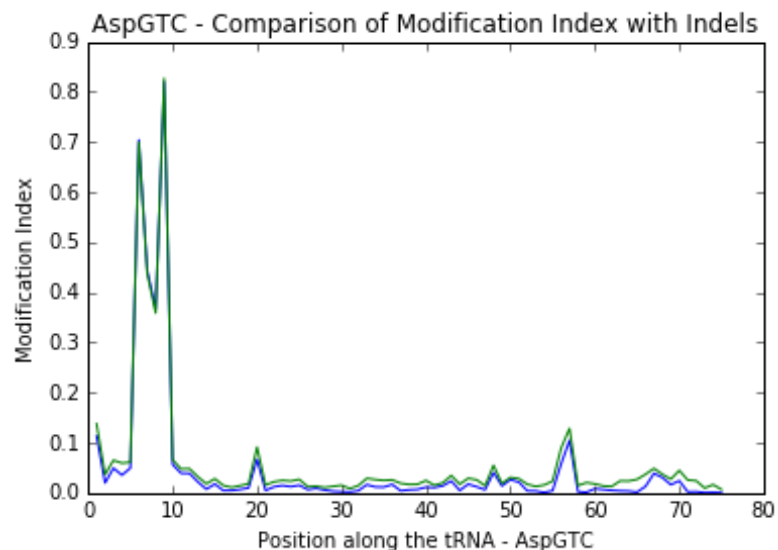
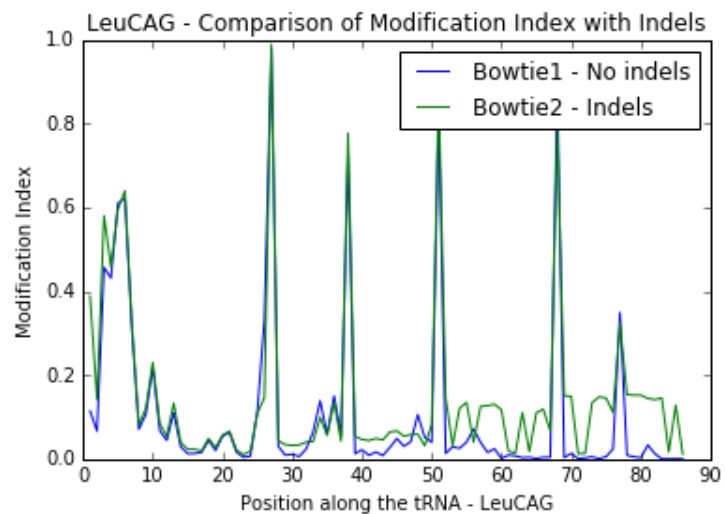
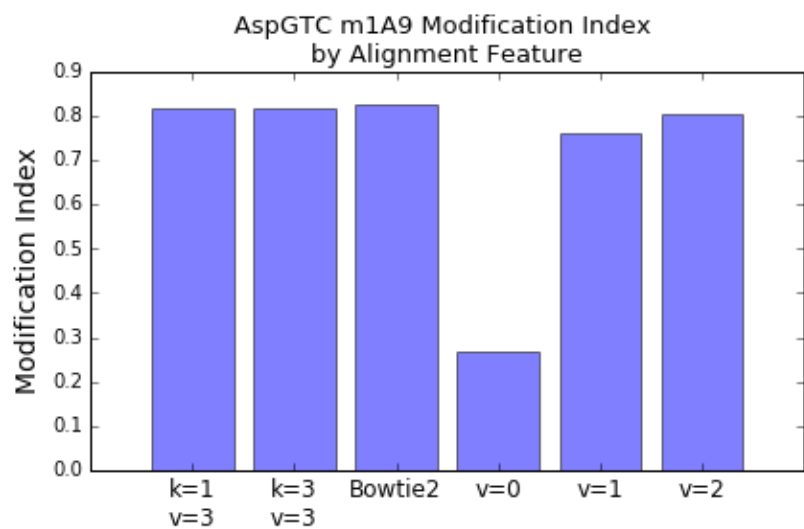
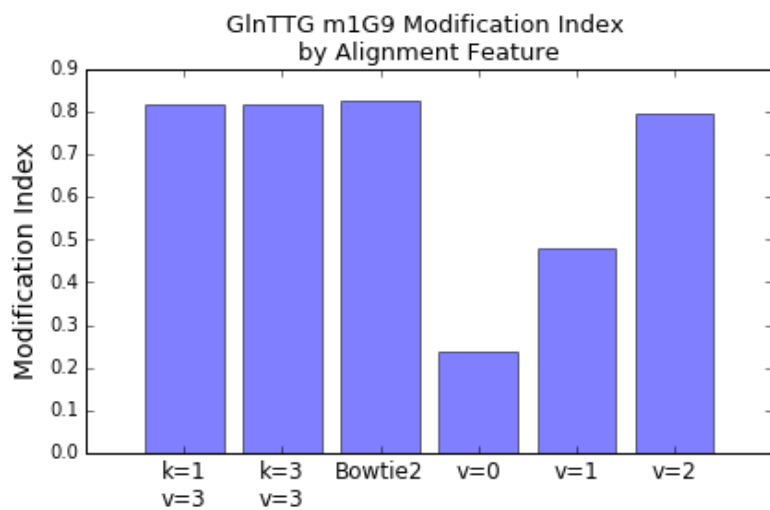
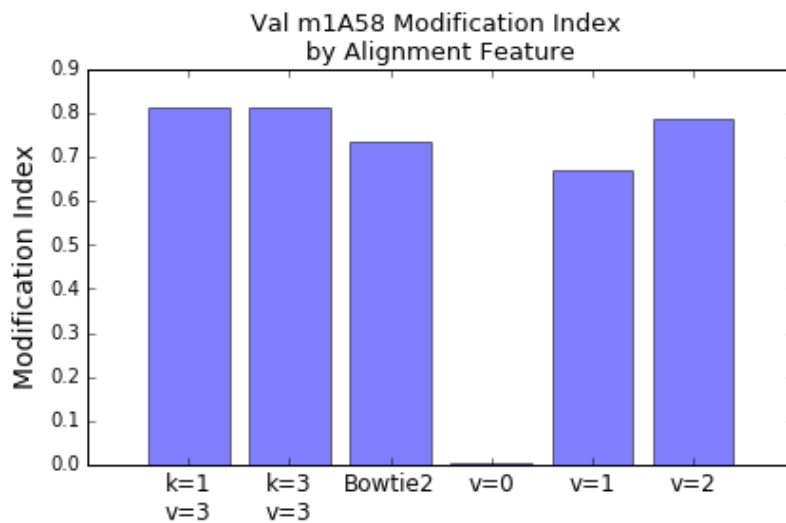
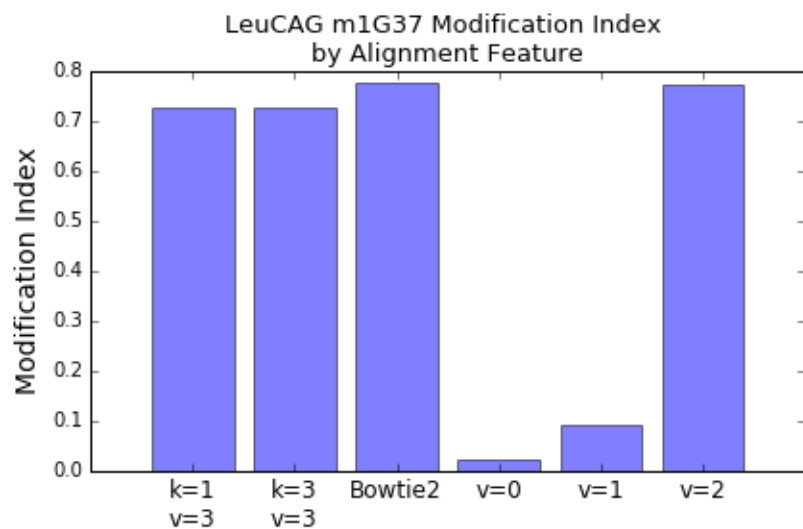
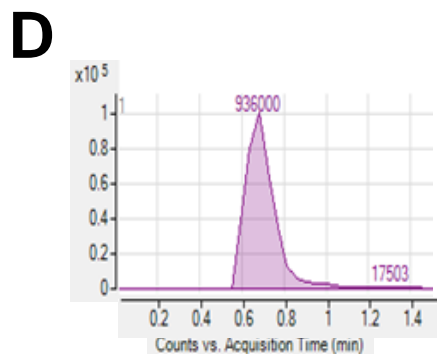
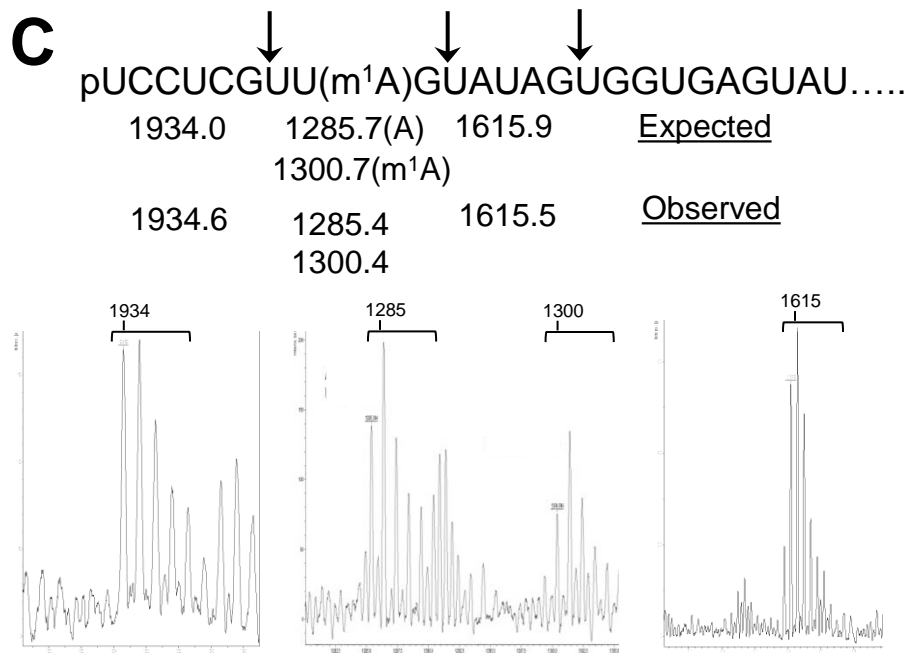
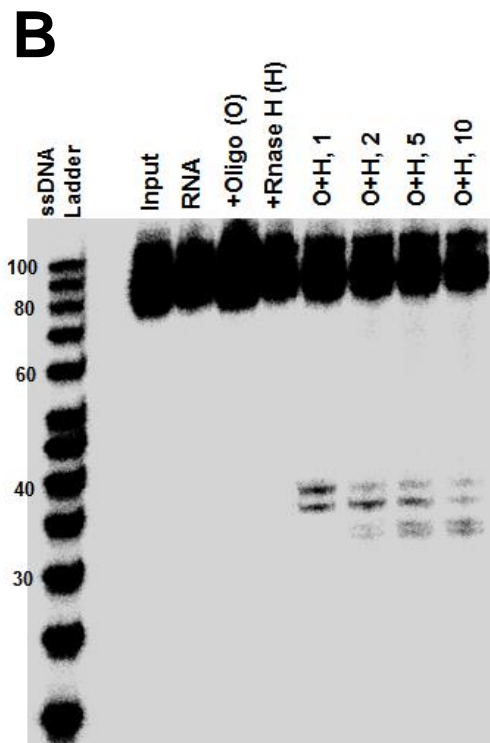
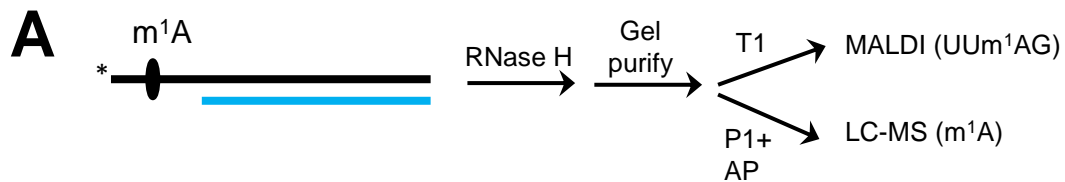


Fig. S1



k: # alignment for each read.
V: # mismatch





E

A: 0.204	A: 0.585
C: 0.042	C: 0.023
G: 0.007	G: 0.005
T: 0.748	T: 0.387
Stop: 0.153	Stop: 0.068
Untreated	+demethylase

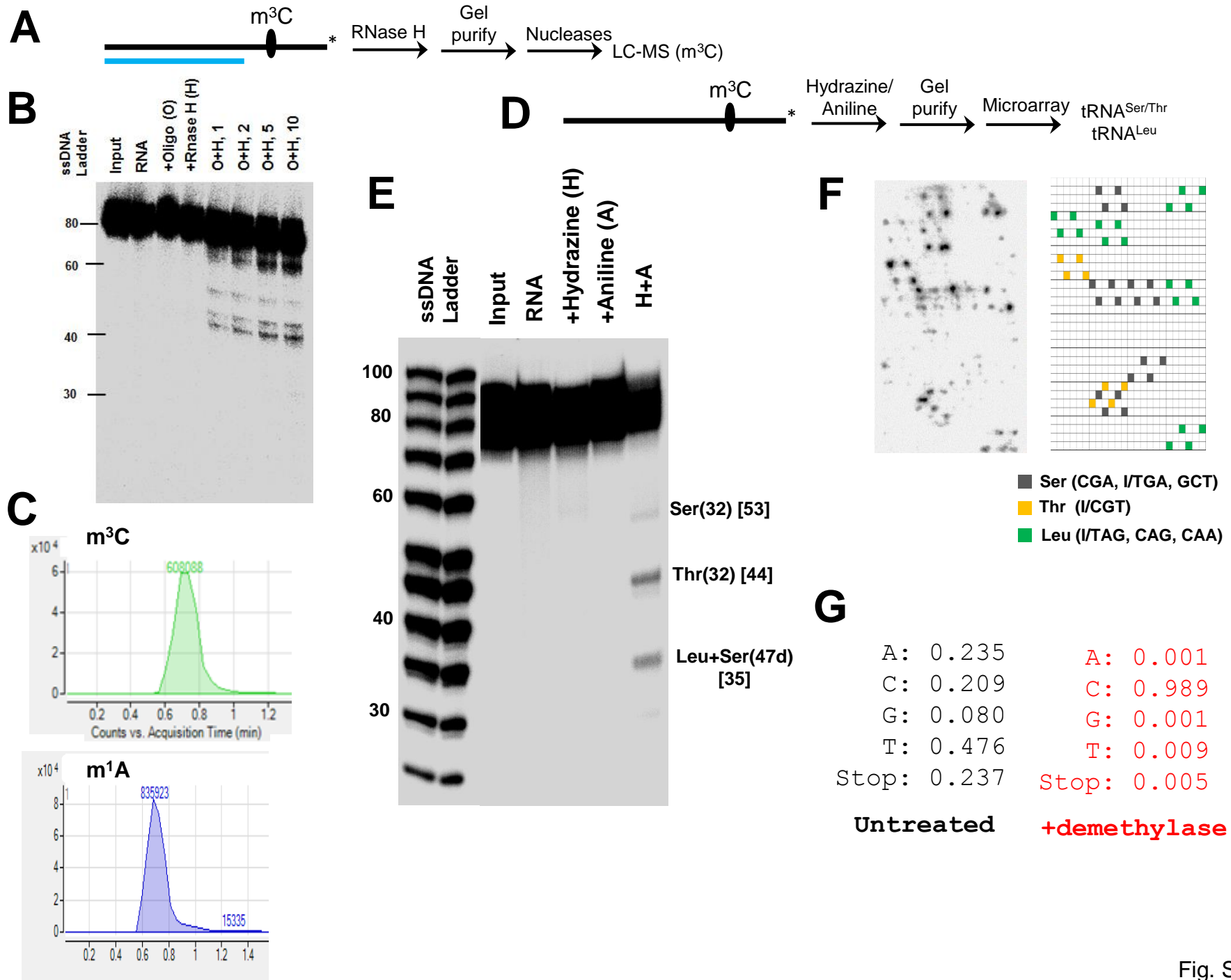


Fig. S5

AspGTC (lacking or low m1A58, but has m1A9)

TCCTCGTT (m1A) GTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAGCCA

AspGTC m1A58 primer (60-76) - ddGTP, dCTP, d*ATP, dTTP

TCCTCGTT (m1A) GTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAGCCA
GCTAAGGGGCTGCCCTCGGT 5'

AspGTC m1A9 primer (11-76) ddGTP, d*CTP, dTTP, dATP

TCCTCGTT (m1A) GTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAGCCA
GCAA T CATATCACCACCTCATAGGGGCGGACAGTGCGCCCTCTGGCCCCAAGCTAAGGGGCTGCCCTCGGT 5'

GlyGCC (high m1A58, known)

GCATGGGTGGTTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCG (m1A) TTCCCGGCCCATGCACCA

GlyGCC m1A58 primer(60-76) ddGTP, d*ATP, dTTP, dCTP

GCATGGGTGGTTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCG (m1A) TTCCCGGCCCATGCACCA
GC T AAGGGCCGGGTACGTGGT 5'

ArgTCG (high m1A58, not annotated)

GACCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCG (m1A) GTCCCTTCGTGGTCGCCA

ArgTCG m1A58 primer (60-76) ddATP, d*CTP, dTTP, dGTP

GACCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCG (m1A) GTCCCTTCGTGGTCGCCA
AGC T CAGGGAAGCACCAGCGGT 5'

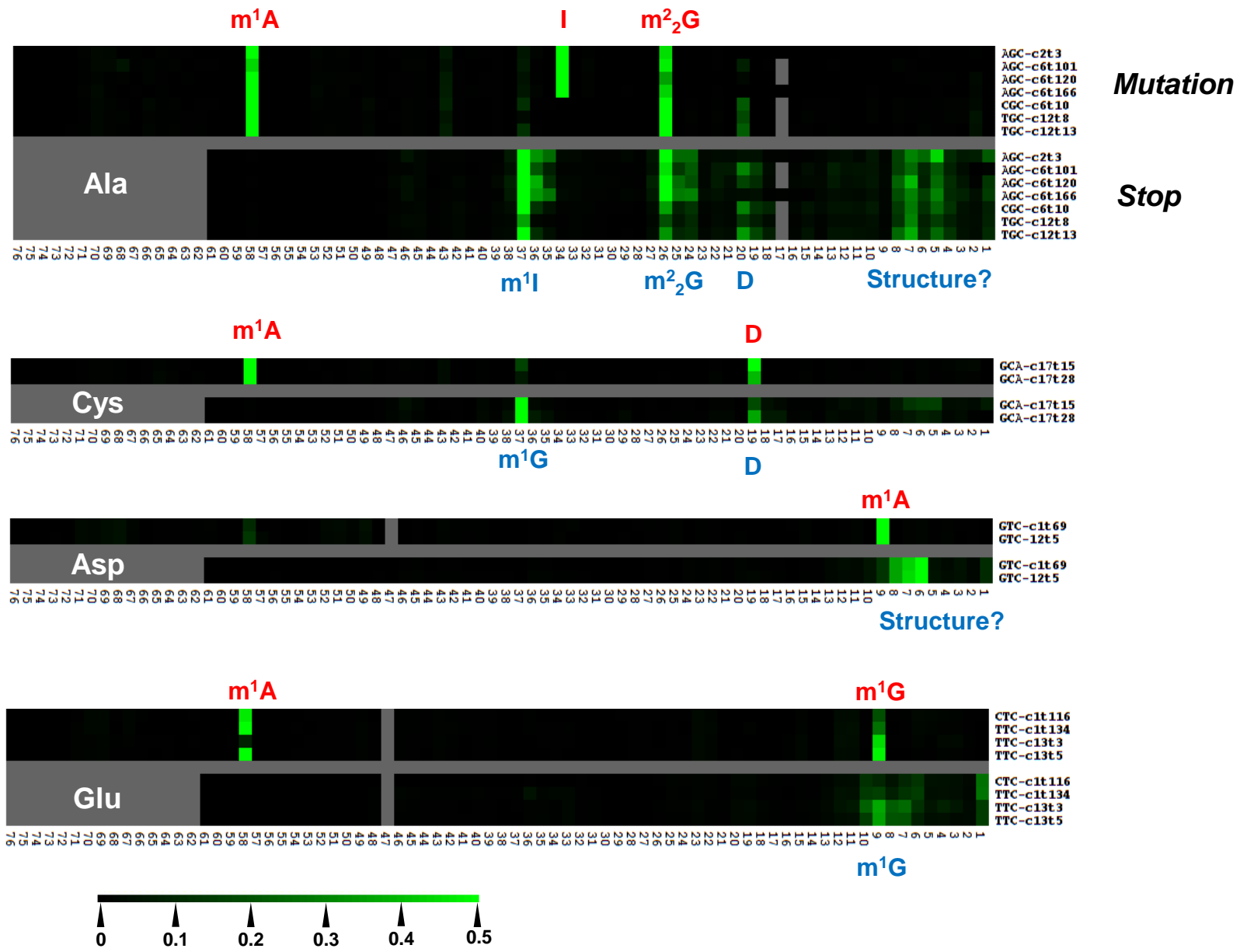
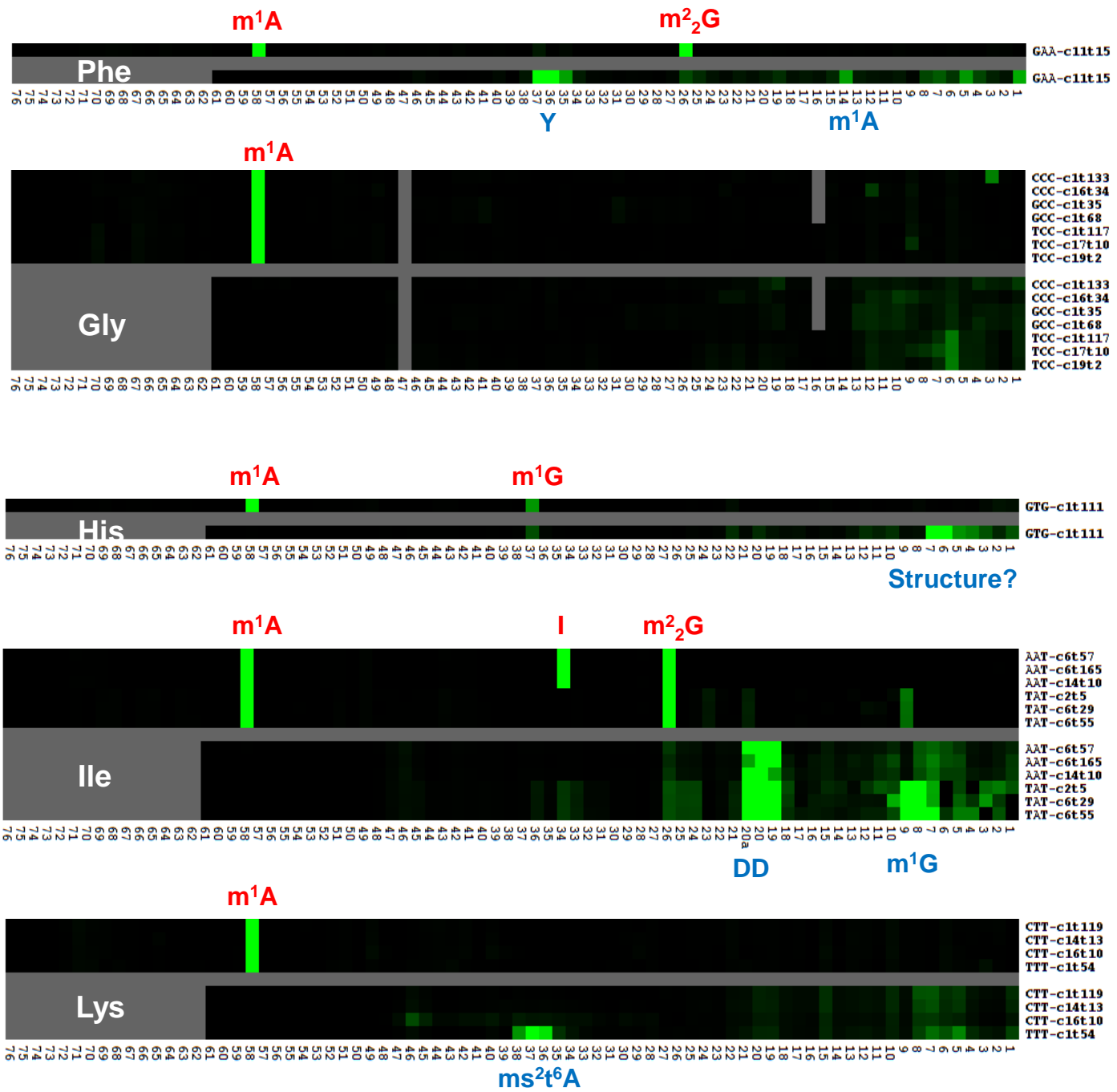


Fig. S7 (A,C,D,E)



Mutation Stop

Structure?

Fig. S7 (F,G,H,I,K)

Leu: see Figure 4.

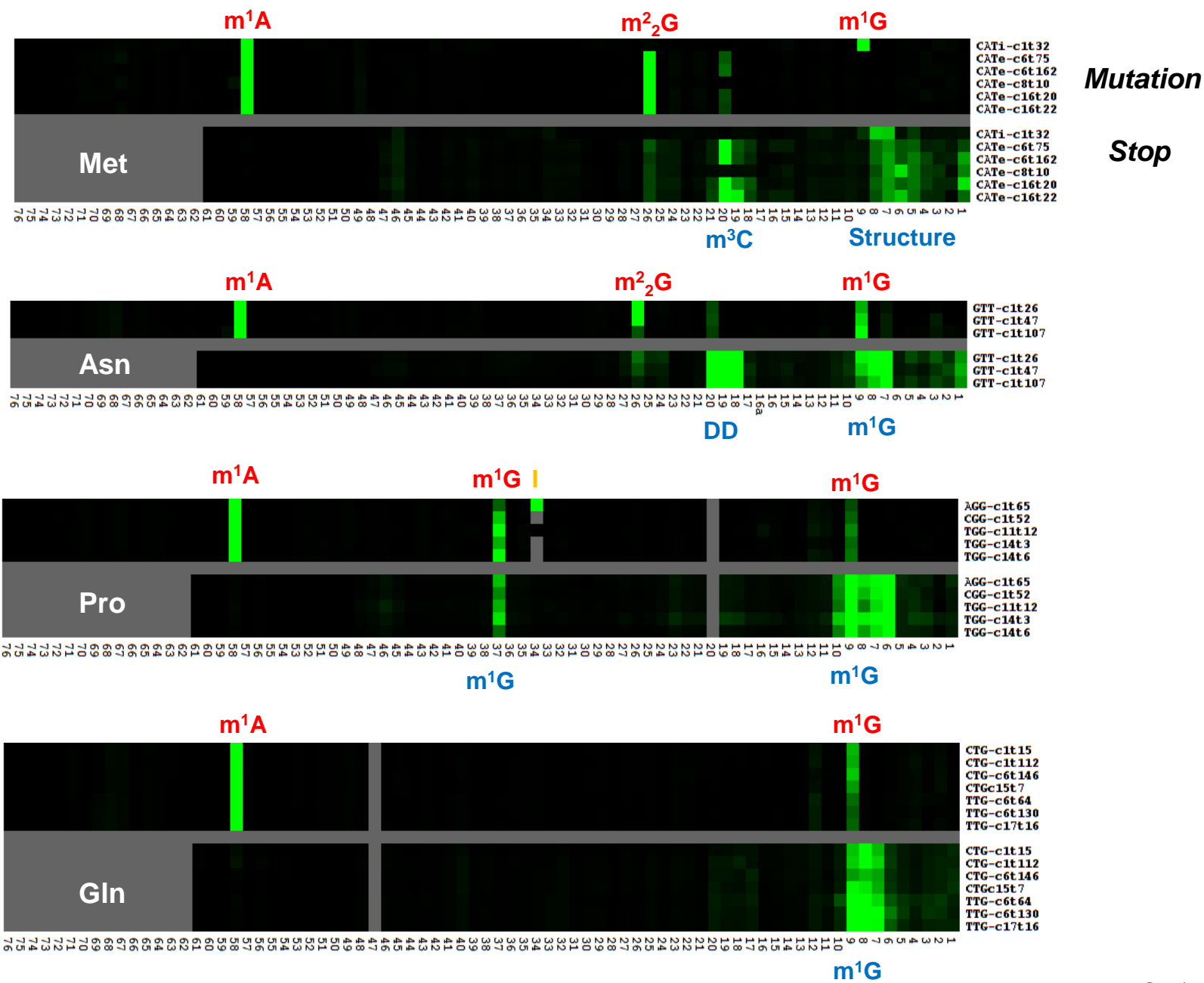


Fig. S7 (L,M,N,P,Q)

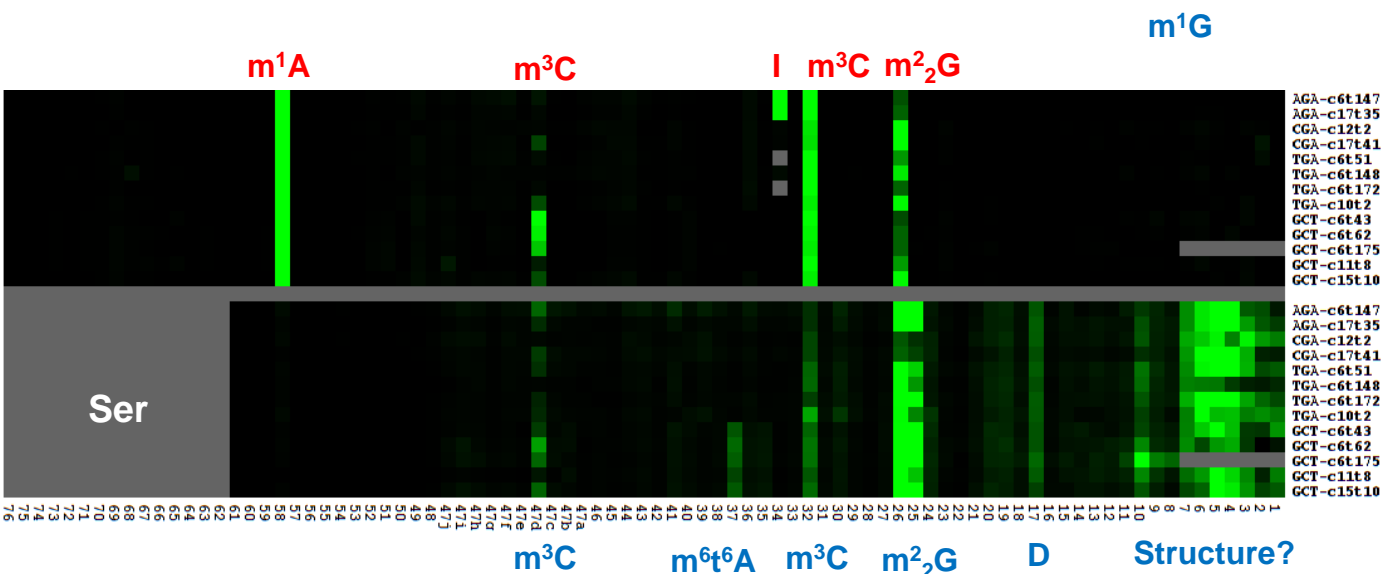
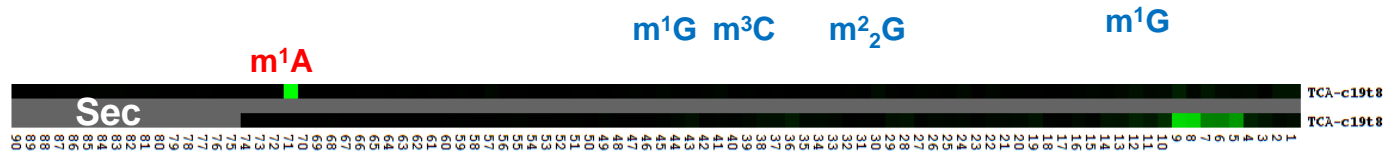
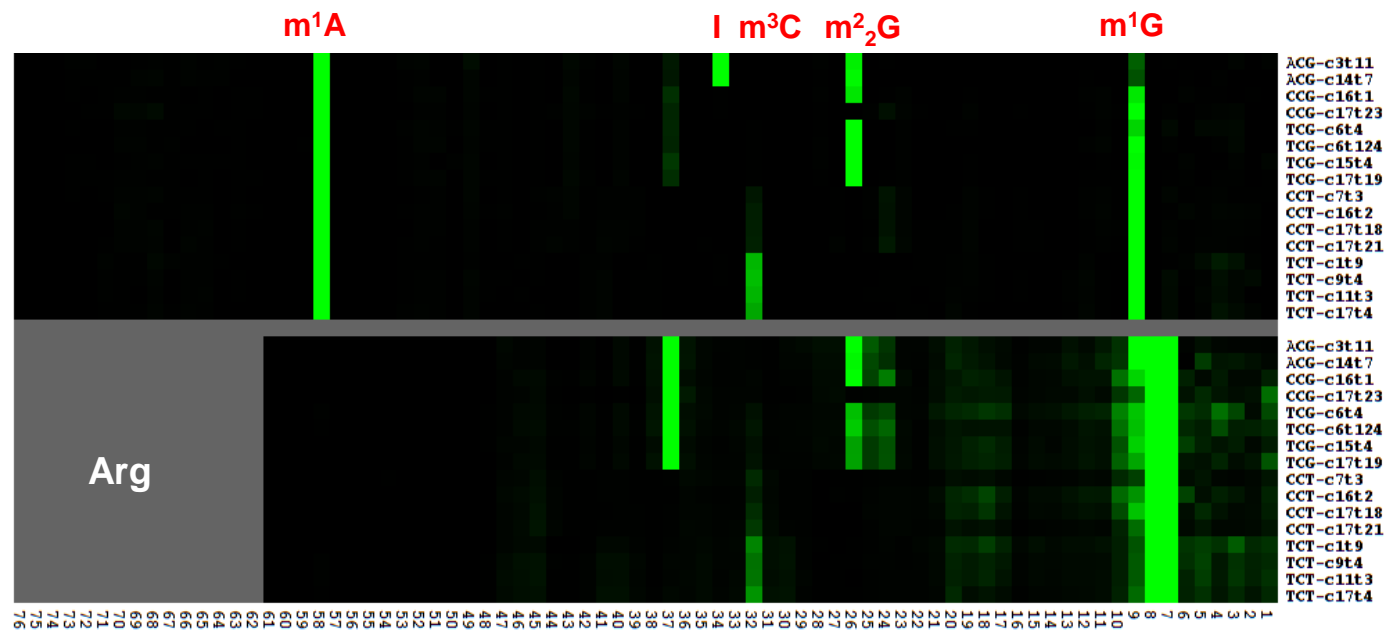


Fig. S7 (R,Sec,S)

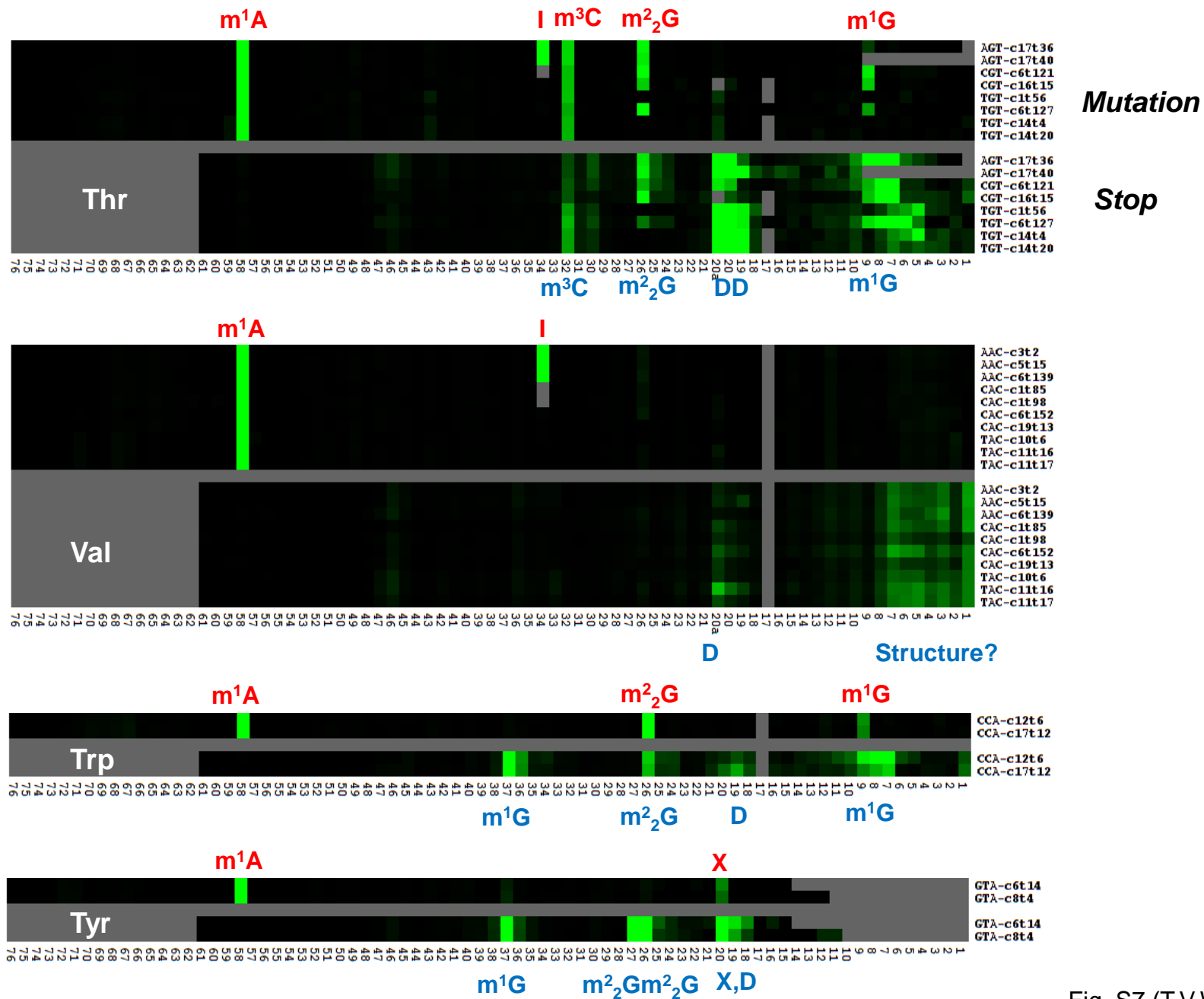


Fig. S7 (T,V,W,Y)