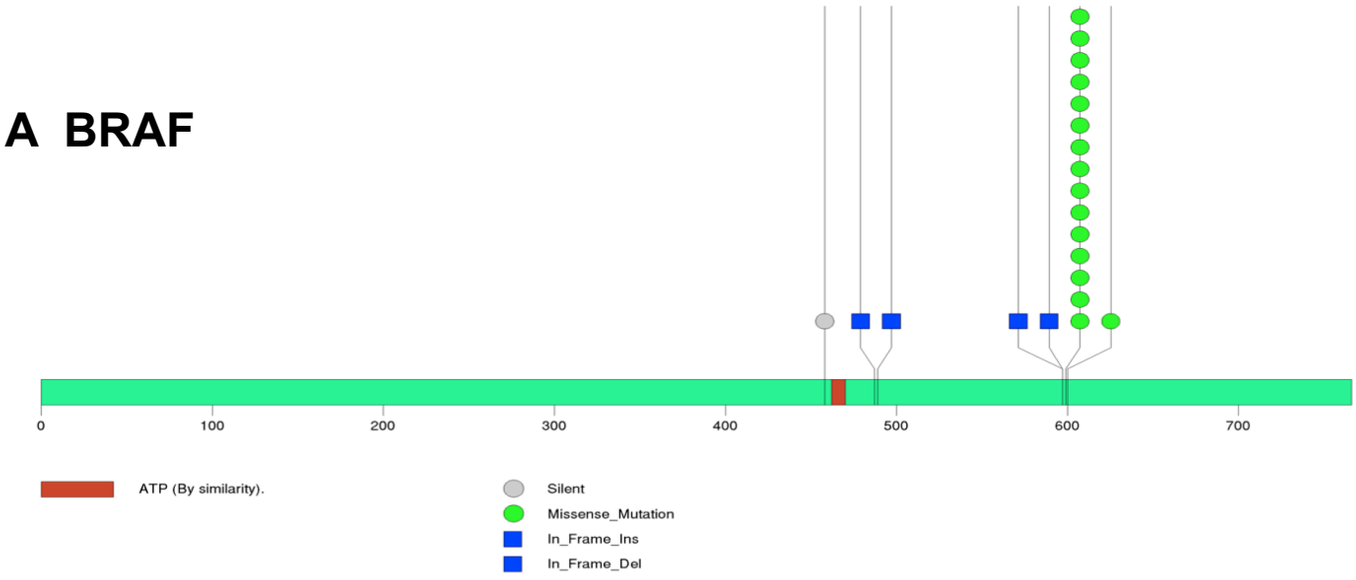
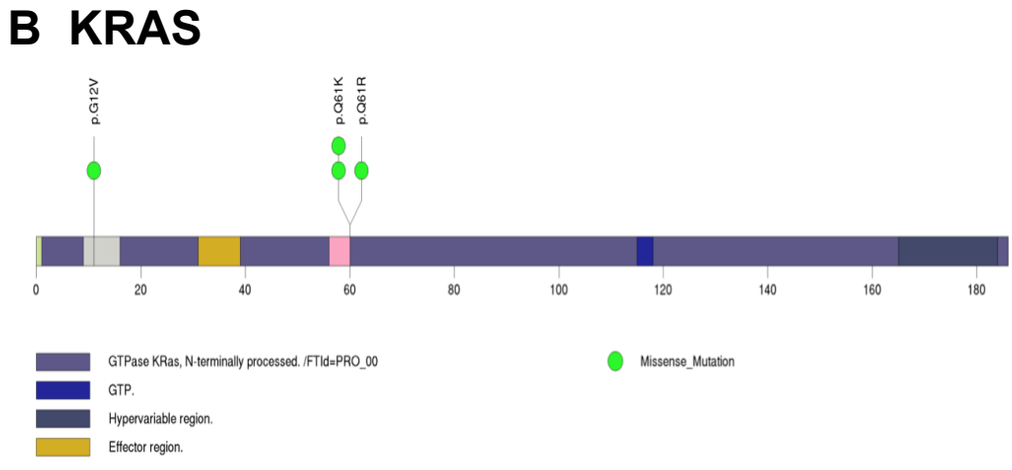
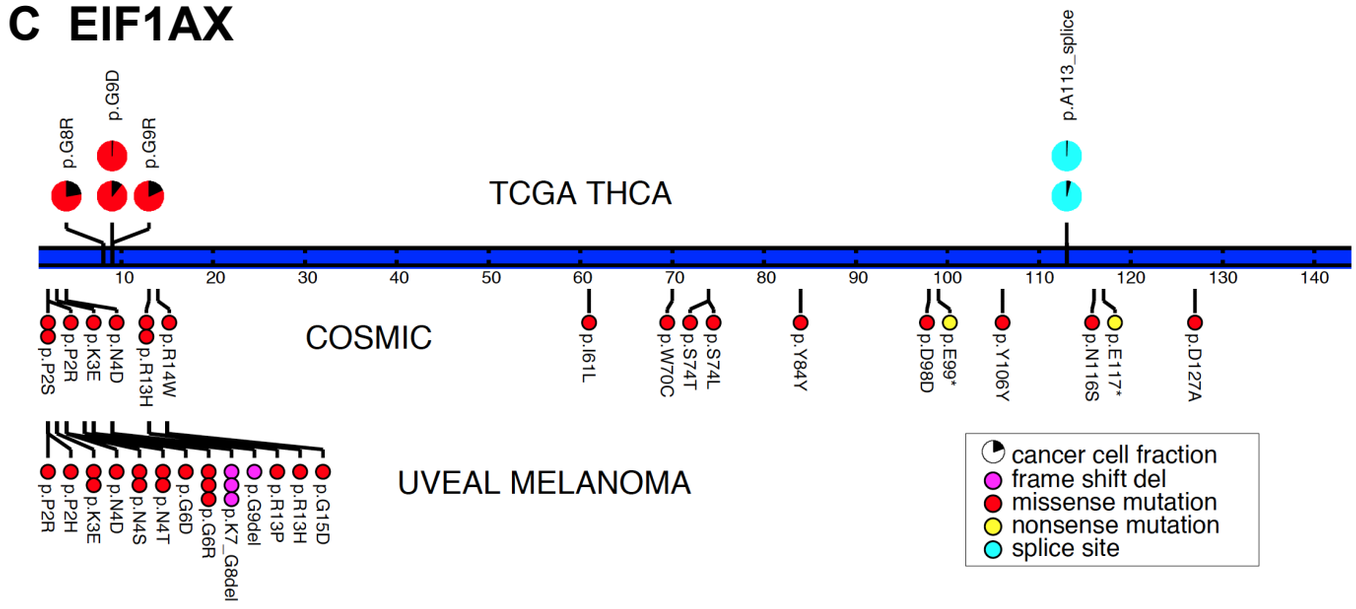
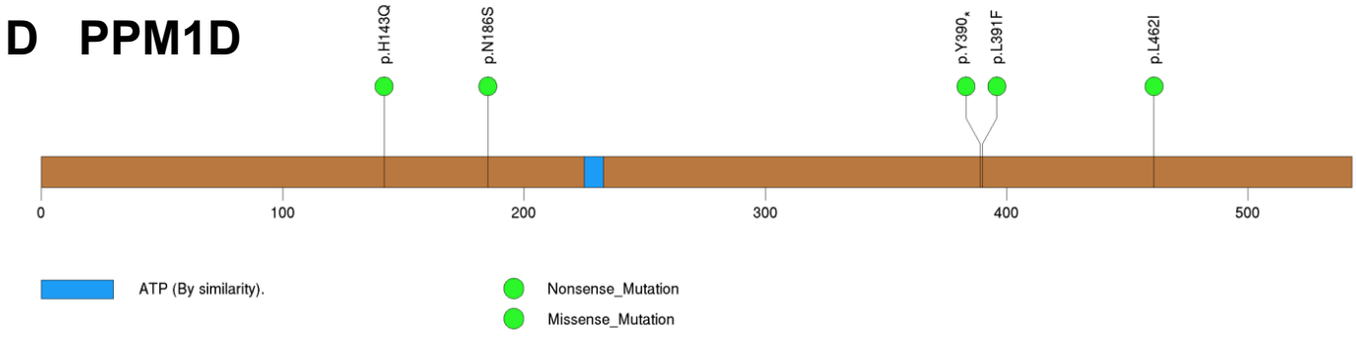
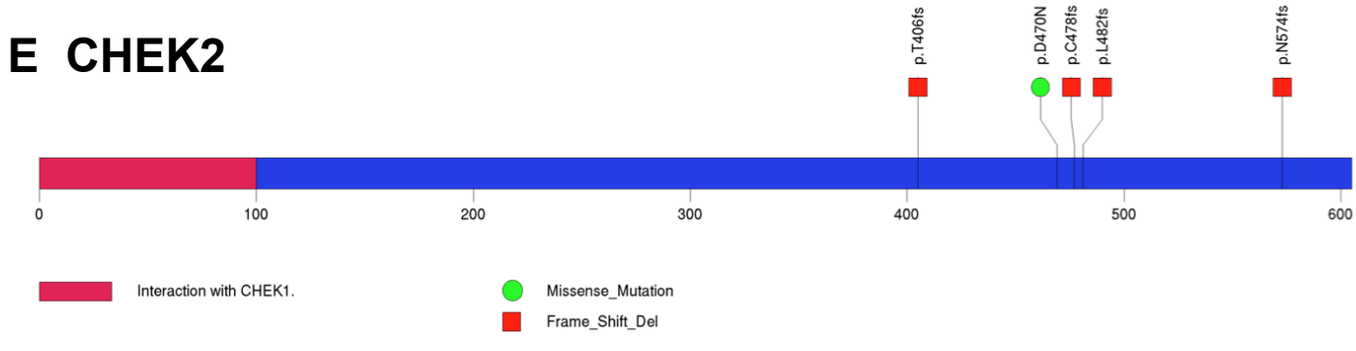

A BRAF
0
100
200
300
400
500
600
700
ATP (By similarity).
Silent
Missense_Mutation
In_Frame_Ins
In_Frame_Del


B KRAS
p.G12V
p.Q61K
p.Q61R
0
20
40
60
80
100
120
140
160
180
GTPase KRas, N-terminally processed. /FTId=PRO_00
GTP.
Hypervariable region.
Effector region.
Missense_Mutation


C EIF1AX
p.G8R
p.G9D
p.G9R
p.A113_splice
TCGA THCA
10
20
30
40
50
60
70
80
90
100
110
120
130
140
COSMIC
p.P2S
p.P2R
p.K3E
p.N4D
p.R13H
p.R14W
p.I61L
p.W70C
p.S74T
p.S74L
p.Y84Y
p.D98D
p.E99*
p.Y106Y
p.N116S
p.E117*
p.D127A
UVEAL MELANOMA
p.P2R
p.P2H
p.K3E
p.N4D
p.N4S
p.N4T
p.G6D
p.G6R
p.K7_G8del
p.G9del
p.R13P
p.R13H
p.G15D
cancer cell fraction
frame shift del
missense mutation
nonsense mutation
splice site


D PPM1D
p.H143Q
p.N186S
p.Y390*
p.L391F
p.L462I
0
100
200
300
400
500
ATP (By similarity).
Nonsense_Mutation
Missense_Mutation


E CHEK2
p.T406fs
p.D470N
p.C478fs
p.L482fs
p.N574fs
0
100
200
300
400
500
600
Interaction with CHEK1.
Missense_Mutation
Frame_Shift_Del