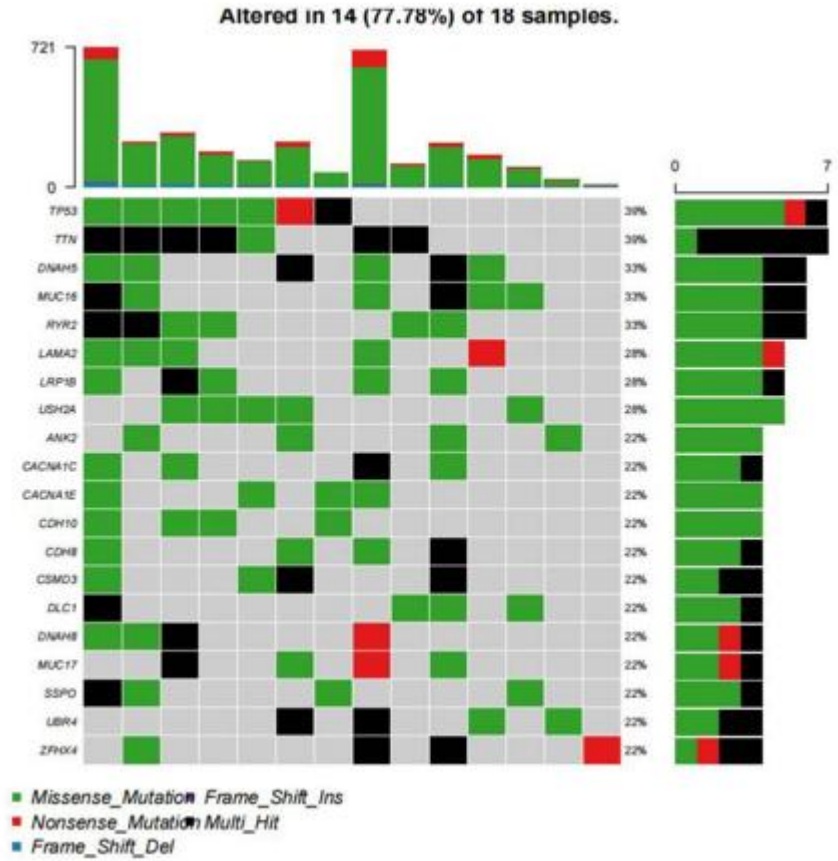
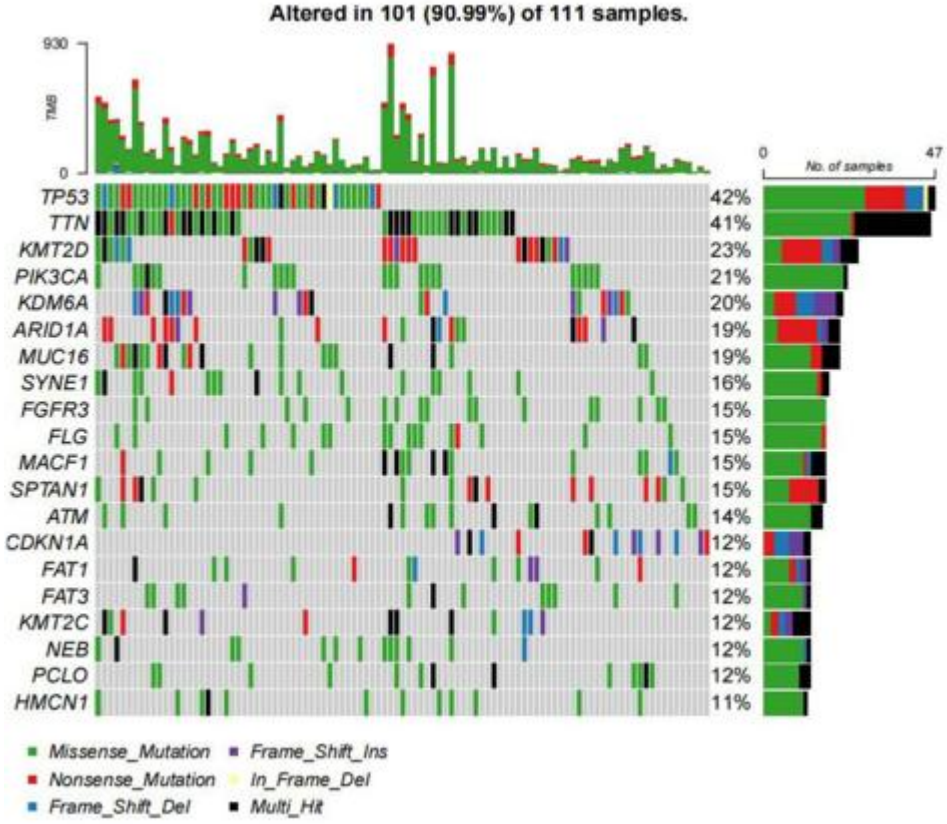
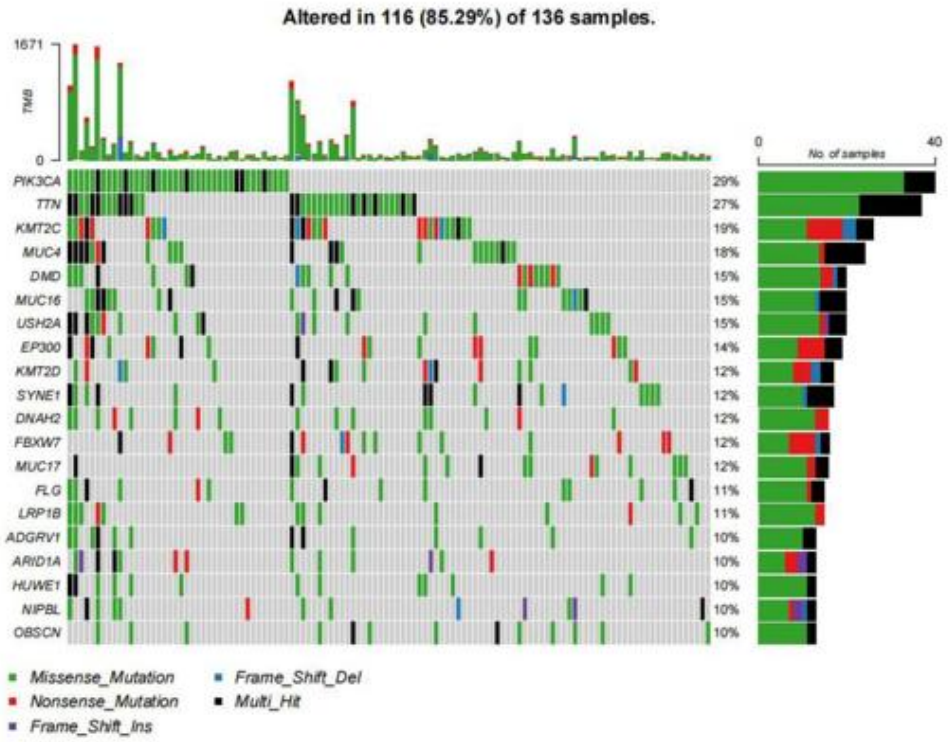
(A)


Altered in 14 (77.78%) of 18 samples.
721
0
0
7
TP53
TTN
DNAH5
MUC16
RYR2
LAMA2
LRP1B
USH2A
ANK2
CACNA1C
CACNA1E
CDH10
CDH8
CSMD3
DLC1
DNAH8
MUC17
SSPO
UBR4
ZFHX4
39%
39%
33%
33%
33%
28%
28%
28%
22%
22%
22%
22%
22%
22%
22%
22%
22%
22%
22%
Missense_Mutation
Frame_Shift_Ins
Nonsense_Mutation
Multi_Hit
Frame_Shift_Del

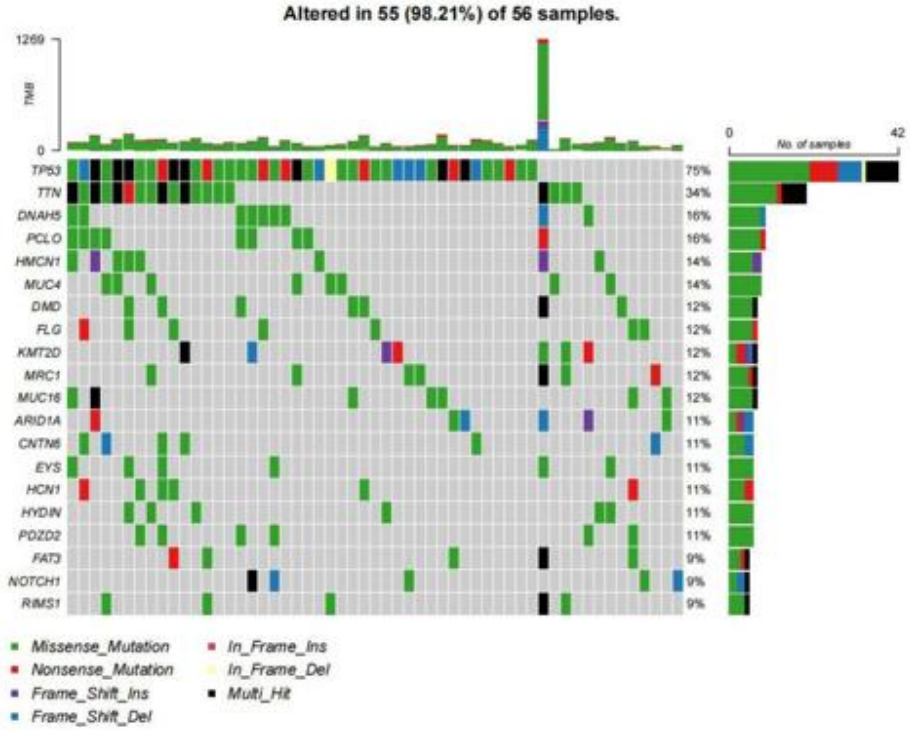
(B)


Altered in 101 (90.99%) of 111 samples.
930
TMB
0
0
47
No. of samples
TP53 42%
TTN 41%
KMT2D 23%
PIK3CA 21%
KDM6A 20%
ARID1A 19%
MUC16 19%
SYNE1 16%
FGFR3 15%
FLG 15%
MACF1 15%
SPTAN1 15%
ATM 14%
CDKN1A 12%
FAT1 12%
FAT3 12%
KMT2C 12%
NEB 12%
PCLO 12%
HMCN1 11%
Missense_Mutation
Frame_Shift_Ins
Nonsense_Mutation
In_Frame_Del
Frame_Shift_Del
Multi_Hit

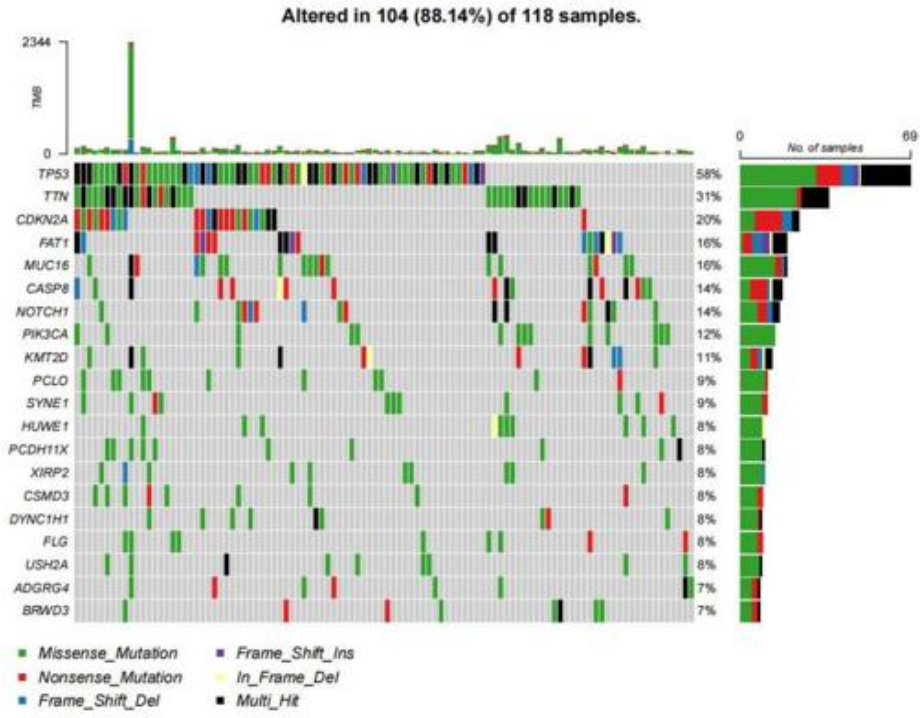
(C)


Altered in 116 (85.29%) of 136 samples.
TMB
1671
0
No. of samples
0
40
PIK3CA 29%
TTN 27%
KMT2C 19%
MUC4 18%
DMD 15%
MUC16 15%
USH2A 15%
EP300 14%
KMT2D 12%
SYNE1 12%
DNAH2 12%
FBXW7 12%
MUC17 12%
FLG 11%
LRP1B 11%
ADGRV1 10%
ARID1A 10%
HUWE1 10%
NIPBL 10%
OBSCN 10%
Missense_Mutation
Nonsense_Mutation
Frame_Shift_Ins
Frame_Shift_Del
Multi_Hit

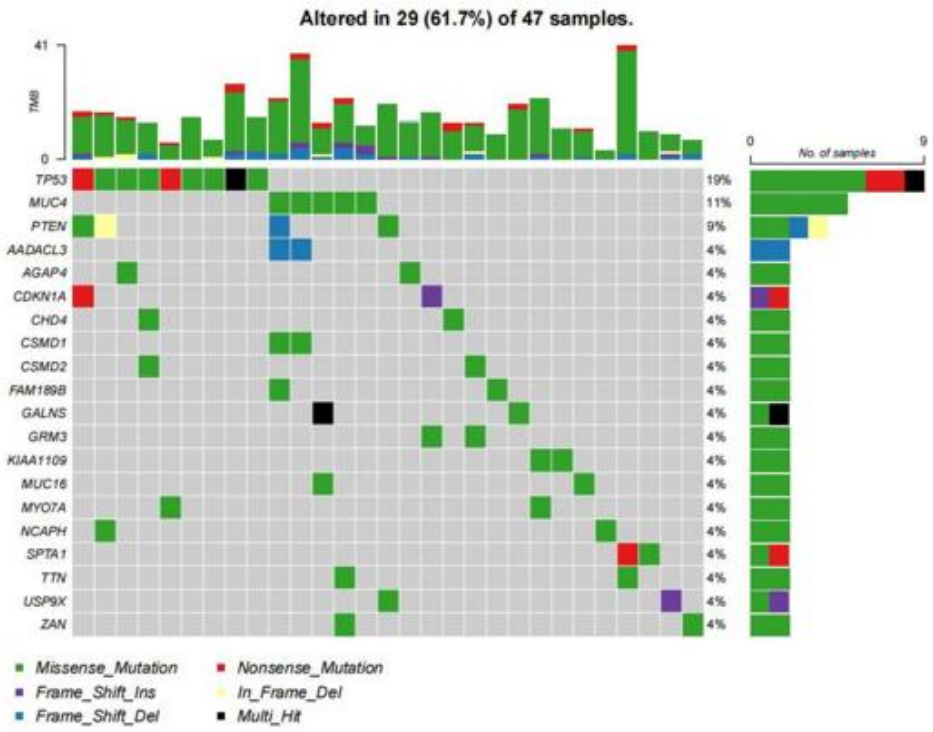
(D)


Altered in 55 (98.21%) of 56 samples.
TMB
1269
0
No. of samples
0
42
TP53 75%
TTN 34%
DNAH5 16%
PCLO 16%
HMCN1 14%
MUC4 14%
DMD 12%
FLG 12%
KMT2D 12%
MRC1 12%
MUC16 12%
ARID1A 11%
CNTN6 11%
EYS 11%
HCN1 11%
HYDIN 11%
PDZD2 11%
FAT3 9%
NOTCH1 9%
RIMS1 9%
Missense_Mutation
Nonsense_Mutation
Frame_Shift_Ins
Frame_Shift_Del
In_Frame_Ins
In_Frame_Del
Multi_Hit

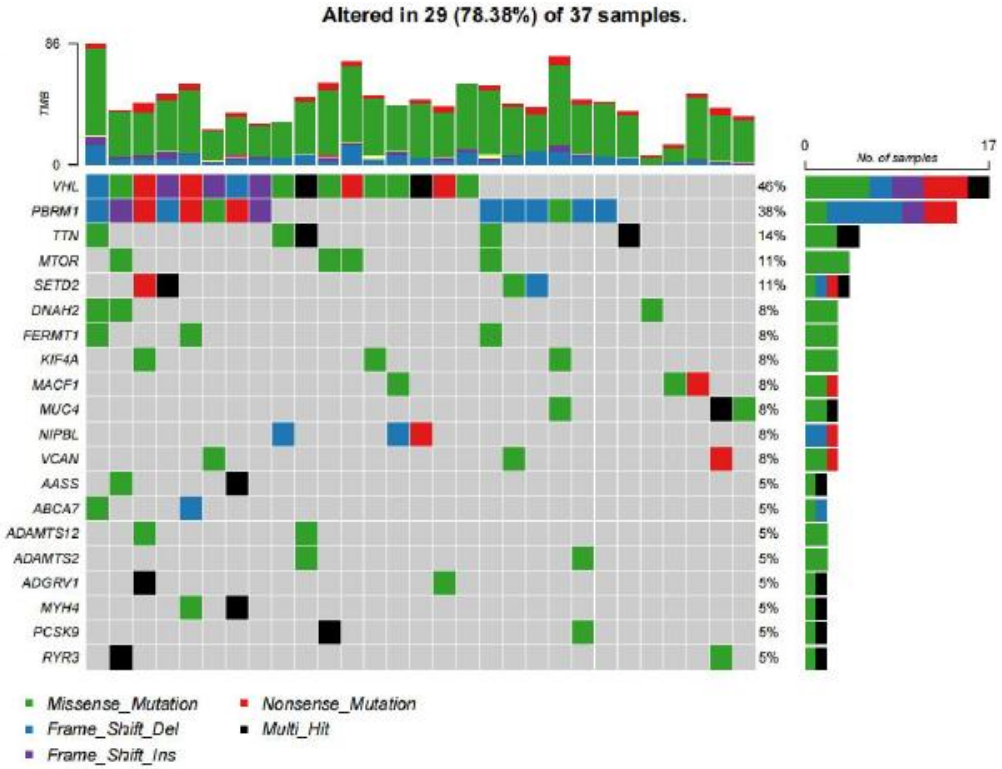
(E)


Altered in 104 (88.14%) of 118 samples.
TMB
2344
0
No. of samples
0
69
TP53 58%
TTN 31%
CDKN2A 20%
FAT1 16%
MUC16 16%
CASP8 14%
NOTCH1 14%
PIK3CA 12%
KMT2D 11%
PCLO 9%
SYNE1 9%
HUWE1 8%
PCDH11X 8%
XIRP2 8%
CSMD3 8%
DYNC1H1 8%
FLG 8%
USH2A 8%
ADGRG4 7%
BRWD3 7%
Missense_Mutation
Nonsense_Mutation
Frame_Shift_Del
Frame_Shift_Ins
In_Frame_Del
Multi_Hit

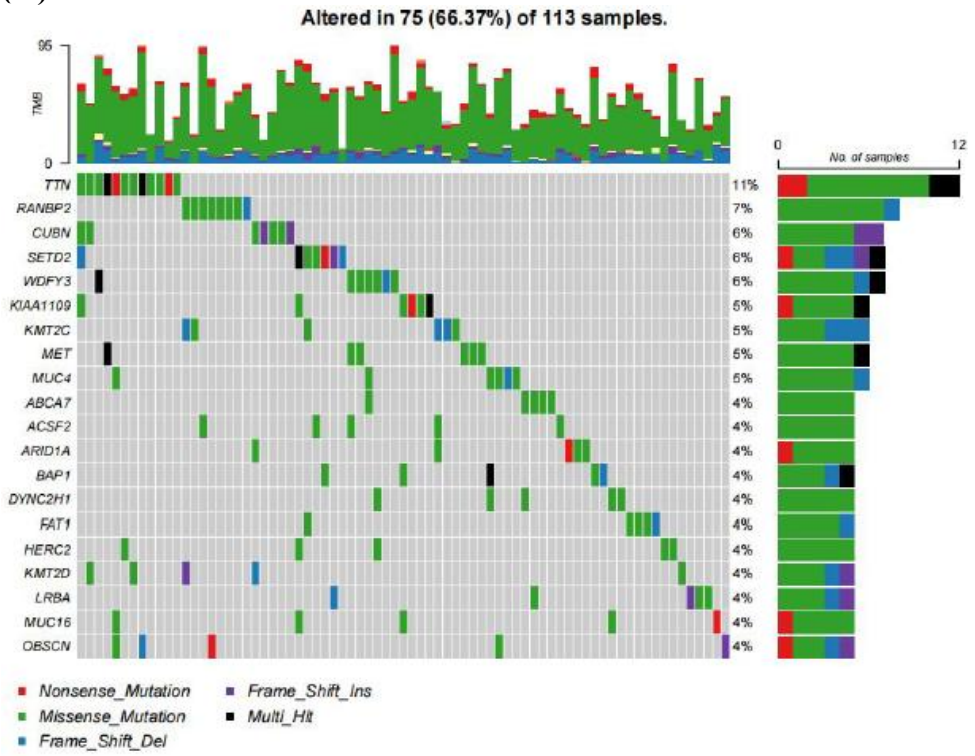
(F)


Altered in 29 (61.7%) of 47 samples.
TMB
41
0
No. of samples
0
9
TP53 19%
MUC4 11%
PTEN 9%
AADACL3 4%
AGAP4 4%
CDKN1A 4%
CHD4 4%
CSMD1 4%
CSMD2 4%
FAM189B 4%
GALNS 4%
GRM3 4%
KIAA1109 4%
MUC16 4%
MYO7A 4%
NCAPH 4%
SPTA1 4%
TTN 4%
USP9X 4%
ZAN 4%
Missense_Mutation
Nonsense_Mutation
Frame_Shift_Ins
In_Frame_Del
Frame_Shift_Del
Multi_Hit

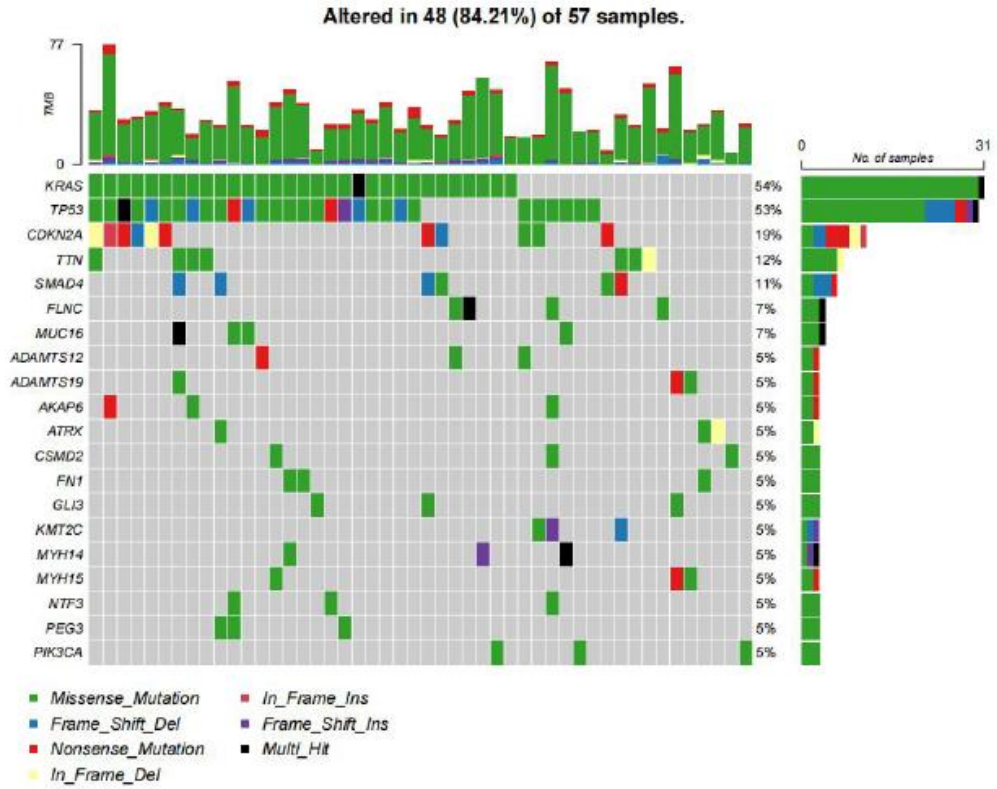
(G)


Altered in 29 (78.38%) of 37 samples.
TMB
86
0
No. of samples
0
17
VHL 46%
PBRM1 38%
TTN 14%
MTOR 11%
SETD2 11%
DNAH2 8%
FERMT1 8%
KIF4A 8%
MACF1 8%
MUC4 8%
NIPBL 8%
VCAN 8%
AASS 5%
ABCA7 5%
ADAMTS12 5%
ADAMTS2 5%
ADGRV1 5%
MYH4 5%
PCSK9 5%
RYR3 5%
Missense_Mutation
Nonsense_Mutation
Frame_Shift_Del
Multi_Hit
Frame_Shift_Ins

(H)


Altered in 75 (66.37%) of 113 samples.
TMB
95
0
No. of samples
0
12
TTN 11%
RANBP2 7%
CUBN 6%
SETD2 6%
WDFY3 6%
KIAA1109 5%
KMT2C 5%
MET 5%
MUC4 5%
ABCA7 4%
ACSF2 4%
ARID1A 4%
BAP1 4%
DYNC2H1 4%
FAT1 4%
HERC2 4%
KMT2D 4%
LRBA 4%
MUC16 4%
OBSCN 4%
Nonsense_Mutation
Frame_Shift_Ins
Missense_Mutation
Multi_Hit
Frame_Shift_Del

(I)



S2 Fig. Mutation landscape of nonsmoking cancers in The Cancer Genome Atlas (TCGA) dataset. (A) TCGA-LUSC. (B) TCGA-BLCA. (C) TCGA-CESC. (D) TCGA-ESCA. (E) TCGA-HNSC. (F) TCGA-KICH. (G) TCGA-KIRC. (H) TCGA-KIRP. (I) TCGA-PAAD. BLCA, bladder urothelial carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; ESCA, esophageal carcinoma; HNSC, head and neck squamous cell carcinoma; KICH, kidney chromophobe; KIRC, kidney renal clear cell carcinoma; KIRP, kidney renal papillary cell carcinoma; LUSC, lung squamous cell carcinoma; PAAD, pancreatic adenocarcinoma.