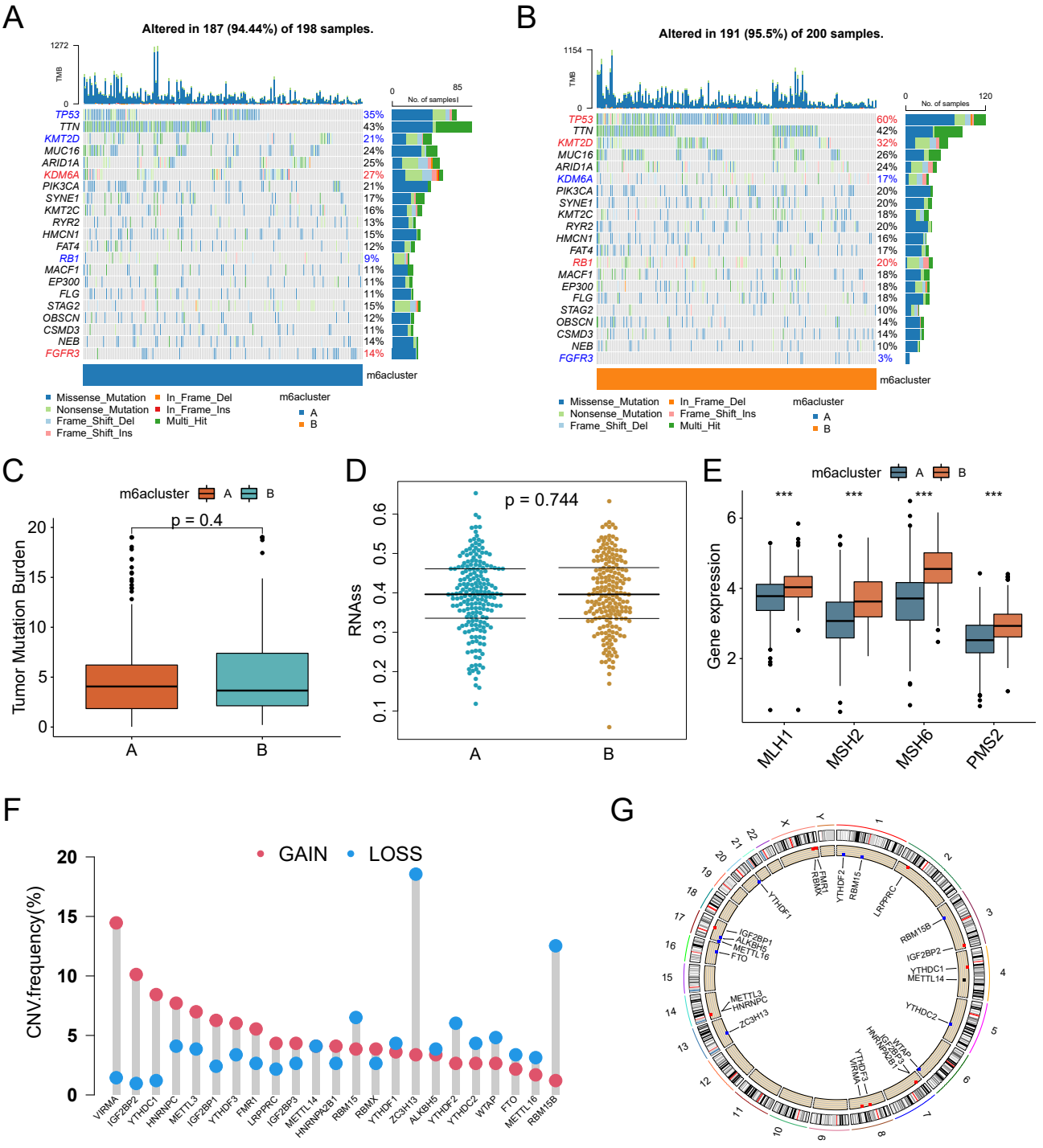
A
Altered in 187 (94.44%) of 198 samples.
TMB
No. of samples
TP53 35%
TTN 43%
KMT2D 21%
MUC16 24%
ARID1A 25%
KDM6A 27%
PIK3CA 21%
SYNE1 17%
KMT2C 16%
RYR2 13%
HMCN1 15%
FAT4 12%
RB1 9%
MACF1 11%
EP300 11%
FLG 11%
STAG2 15%
OBSCN 12%
CSMD3 11%
NEB 14%
FGFR3 14%
m6acluster
Missense_Mutation
Nonsense_Mutation
Frame_Shift_Del
Frame_Shift_Ins
In_Frame_Del
In_Frame_Ins
Multi_Hit
m6acluster
A
B
B
Altered in 191 (95.5%) of 200 samples.
TP53 60%
TTN 42%
KMT2D 32%
MUC16 26%
ARID1A 24%
KDM6A 17%
PIK3CA 20%
SYNE1 20%
KMT2C 18%
RYR2 20%
HMCN1 16%
FAT4 17%
RB1 20%
MACF1 18%
EP300 18%
FLG 18%
STAG2 10%
OBSCN 14%
CSMD3 14%
NEB 10%
FGFR3 3%
C
m6acluster A B
p = 0.4
Tumor Mutation Burden
D
p = 0.744
RNAss
E
m6acluster A B
Gene expression
MLH1
MSH2
MSH6
PMS2
F
GAIN
LOSS
CNV.frequency(%)
VIRMA
IGF2BP2
YTHDC1
HNRNPC
METTL3
IGF2BP1
YTHDF3
FMR1
LRPPRC
IGF2BP3
METTL14
HNRNPA2B1
RBM15
RBMX
YTHDF1
ZC3H13
ALKBH5
YTHDF2
YTHDC2
WTAP
FTO
METTL16
RBM15B
G