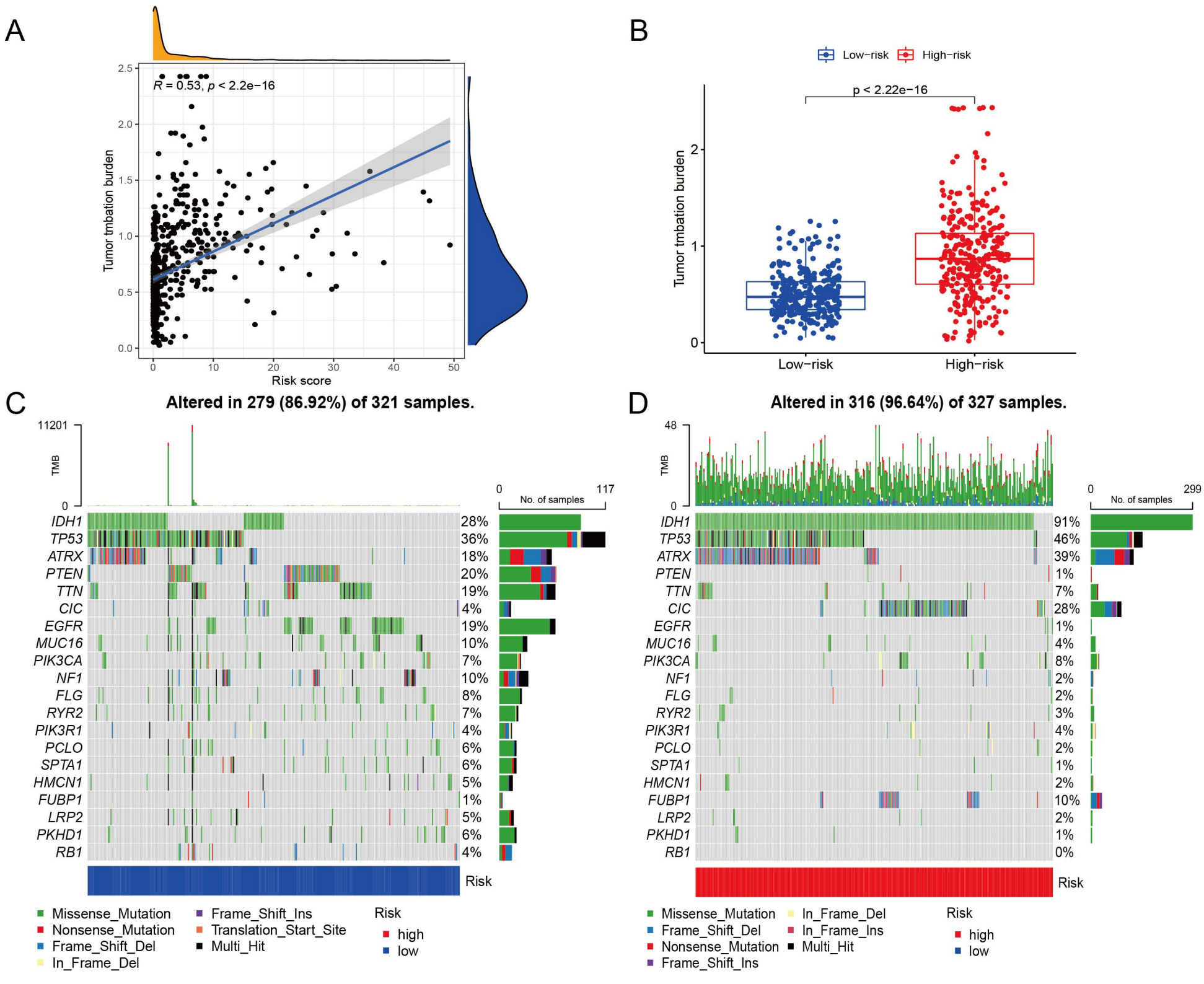
A
R = 0.53, p < 2.2e−16
Tumor tmbation burden
Risk score
B
Low−risk
High−risk
p < 2.22e−16
Tumor tmbation burden
Low−risk
High−risk
C
Altered in 279 (86.92%) of 321 samples.
TMB
11201
0
No. of samples
0
117
IDH1 28%
TP53 36%
ATRX 18%
PTEN 20%
TTN 19%
CIC 4%
EGFR 19%
MUC16 10%
PIK3CA 7%
NF1 10%
FLG 8%
RYR2 7%
PIK3R1 4%
PCLO 6%
SPTA1 6%
HMCN1 5%
FUBP1 1%
LRP2 5%
PKHD1 6%
RB1 4%
Risk
Missense_Mutation
Nonsense_Mutation
Frame_Shift_Del
In_Frame_Del
Frame_Shift_Ins
Translation_Start_Site
Multi_Hit
Risk
high
low
D
Altered in 316 (96.64%) of 327 samples.
TMB
48
0
No. of samples
0
299
IDH1 91%
TP53 46%
ATRX 39%
PTEN 1%
TTN 7%
CIC 28%
EGFR 1%
MUC16 4%
PIK3CA 8%
NF1 2%
FLG 2%
RYR2 3%
PIK3R1 4%
PCLO 2%
SPTA1 1%
HMCN1 2%
FUBP1 10%
LRP2 2%
PKHD1 1%
RB1 0%
Risk
Missense_Mutation
Frame_Shift_Del
Nonsense_Mutation
Frame_Shift_Ins
In_Frame_Del
In_Frame_Ins
Multi_Hit
Risk
high
low