Supplementary

Table S1 Prevalence of each mutation collected from the NGS of the study sample population

Mutation	N (%)
TP53	132 (82.0)
APC	129 (80.1)
KRAS	70 (43.5)
SMAD4	30 (18.6)
PIK3CA	26 (16.1)
MYC	18 (11.2)
FBXW7	16 (9.9)
ARID1A	15 (9.3)
PIK3R1	13 (8.1)
AMER1	11 (6.8)
DDX11	11 (6.8)
BRAF	9 (5.6)
CDKN2A	9 (5.6)
PTEN	9 (5.6)
FGFR1	8 (5.0)
CCND2	8 (5.0)
ATM	8 (5.0)
NRAS	7 (4.3)
RB1	7 (4.3)
HER2	7 (4.3)
GNAS	7 (4.3)
AURKA	7 (4.3)
PLCG1	7 (4.3)
RASA1	6 (3.7)
STK11	5 (3.1)
MAP2K4	5 (3.1)
CDK6	5 (3.1)
HER3	5 (3.1)
NF1	5 (3.1)
EGFR	4 (2.5)
ATRX	4 (2.5)
NBN	4 (2.5)
MTAP	4 (2.5)
TSC2	4 (2.5)
ARID2	4 (2.5)
SMARCA2	4 (2.5)
PLAG1	4 (2.5)
TCEB1	4 (2.5)
RNF139	4 (2.5)
POLE	3 (1.9)
CDH1	3 (1.9)
SMARCA4	3 (1.9)
TP53BP1	3 (1.9)
CHEK2	3 (1.9)
CTNNB1	3 (1.9)
ERCC2	3 (1.9)
LZTR1	2 (1.2)
FANCG	2 (1.2)
CCNE1	2 (1.2)
CCND3	2 (1.2)
RNF43	2 (1.2)
CDKN1B	2 (1.2)
MAP2K1	2 (1.2)
TERT	2 (1.2)
JAK2	2 (1.2)
CD274 (PD-L1)	2 (1.2)
PDCD1LG2	2 (1.2)
YAP1	2 (1.2)
BARD1	2 (1.2)
MSH3	2 (1.2)
MUTYH	2 (1.2)
PBRM1	2 (1.2)
IDO1	2 (1.2)
IDO2	2 (1.2)
B2M	2 (1.2)
RAD50	2 (1.2)
ERCC3	2 (1.2)
TSC1	2 (1.2)
SMARCB1	2 (1.2)
TRAF7	2 (1.2)
RAD52	2 (1.2)
CDK12	2 (1.2)
FANCD2	1 (0.6)
KEAP1	1 (0.6)
BRCA1	1 (0.6)
BRCA2	1 (0.6)
ERBB4	1 (0.6)
MET	1 (0.6)
FGFR2 amp	1 (0.6)
CCND1	1 (0.6)
MTOR	1 (0.6)
RICTOR	1 (0.6)
AXIN1	1 (0.6)
SETD2	1 (0.6)
RAF1	1 (0.6)
MSH6	1 (0.6)
MLH3	1 (0.6)
IDH1	1 (0.6)
RNG139	1 (0.6)
NTRK3	1 (0.6)
IRF1	1 (0.6)
CASP8	1 (0.6)
BAP1	1 (0.6)
SDHD	1 (0.6)
XRCC1	1 (0.6)
SOCS1	1 (0.6)
CAPZA2-MET fusion	1 (0.6)
AKT1	1 (0.6)
TAPBP	1 (0.6)
SPOP	1 (0.6)
PPM1D	1 (0.6)
ROS1	1 (0.6)
YES1	1 (0.6)
MAP3K1	1 (0.6)
MDC1	1 (0.6)
AKT2	1 (0.6)
BUB1B	1 (0.6)
IDH2	1 (0.6)
FGF3	1 (0.6)
FGF4	1 (0.6)
FGF19	1 (0.6)
MLH1	1 (0.6)

NGS, next-generation sequencing.

https://dx.doi.org/10.21037/jgo-23-809