

Table S1 Genomic alterations of 270 CCA patients

Gene	Fusion/rearrangement	Gene amplification	Gene homozygous deletion	Substitution/indel	Truncation	Total
TP53	0	4	0	111	48	159
KRAS	0	0	0	85	0	89
SMAD4	1	0	2	29	17	49
ARID1A	1	0	0	6	41	48
CDKN2A	6	0	6	14	17	43
ARID2	0	0	1	10	27	38
TERT	0	3	0	29	0	32
STK11	5	0	0	15	6	26
ERBB2	1	12	0	11	0	24
NF1	0	0	0	8	16	24
PIK3CA	0	1	0	21	0	22
BRAF	1	0	0	19	0	20
BRCA2	1	0	0	0	18	19
KMT2C	0	0	0	5	14	19
APC	0	0	0	4	14	18
KMT2D	0	0	0	7	10	17
LRP1B	0	0	0	12	5	17
RBM10	0	0	0	5	11	16
BAP1	0	0	0	7	8	15
FAT4	0	0	0	11	4	15
FGFR2	12	1	0	2	0	15
MUC16	0	0	0	15	0	15
OBSCN	0	0	0	10	5	15
PBRM1	0	0	0	4	10	14
CDK12	0	9	0	4	0	13
SPTA1	0	0	0	13	0	13
ATM	0	0	0	5	7	12
CCNE1	0	12	0	0	0	12
KDM6A	1	0	0	3	8	12
RNF43	0	0	0	1	11	12
FAT3	0	0	0	10	1	11
FBXW7	0	0	0	8	3	11
MDM2	0	10	0	1	0	11
ACVR1B	0	0	0	2	8	10
ACVR2A	0	0	0	2	8	10
FRS2	0	9	0	1	0	10
KEAP1	0	0	0	7	3	10
MLH1	0	0	1	7	2	10
AXIN1	0	0	0	2	7	9
B2M	0	0	0	3	6	9
EGFR	0	2	0	7	0	9
HMG2	0	9	0	0	0	9
MAP2K4	0	0	1	6	2	9
SMARCA4	1	0	0	7	1	9
ARID1B	2	0	0	2	4	8
ERBB3	0	0	0	8	0	8
PTEN	0	0	0	5	3	8
TGFBR2	0	0	0	2	6	8
CEBPA	0	5	0	2	0	7
EPHB1	0	0	0	5	2	7
ERBB4	0	0	0	5	2	7
MTAP	0	0	7	0	0	7
NRAS	0	0	0	7	0	7
SLIT2	0	0	0	6	1	7
TGFBR1	0	0	0	5	2	7
AKT2	0	4	0	2	0	6
BCOR	0	0	0	3	3	6
CCND1	0	5	0	1	0	6
CDKN2B	0	0	6	0	0	6
FAT1	0	0	0	4	2	6
FGF19	0	6	0	0	0	6
FGF3	0	5	0	1	0	6
GRIN2A	0	1	0	3	2	6
IDH1	0	0	0	6	0	6
MAP3K1	0	0	0	3	3	6
RB1	0	0	0	1	5	6
RGS1	0	0	0	6	0	6
UZAF1	0	0	0	6	0	6
CASP8	0	0	0	2	3	5
CDKN1B	0	0	0	0	5	5
CSK	0	0	0	2	3	5
FGF4	0	5	0	0	0	5
FLT4	0	2	0	3	0	5
GATA6	0	3	0	1	1	5
GNAS	0	1	0	4	0	5
KDM5A	0	2	0	3	0	5
LRP2	0	0	0	5	0	5
LZTR1	0	3	0	1	1	5
MYC	0	3	0	2	0	5
NF2	0	0	0	0	5	5
NOTCH3	0	1	0	4	0	5
MSD1	0	0	0	4	1	5
RAD50	0	1	0	1	4	5
RPTOR	0	0	0	4	0	5
RUNX1T1	0	0	0	4	1	5
TAF1	0	0	0	4	1	5
TSC1	0	0	0	2	3	5
ASXL1	0	0	0	2	2	4
ATRX	0	0	0	2	2	4
BLM	0	0	0	3	1	4
CDK4	0	3	0	1	0	4
CFTR	0	1	0	2	1	4
CIC	0	0	0	2	2	4
CRKL	0	4	0	0	0	4
CTCF	0	0	0	2	2	4
CTNNB1	0	0	0	4	0	4
DNMT3A	0	0	0	4	0	4
FAS	1	0	0	2	1	4
FGFR3	0	2	0	2	0	4
GLI3	0	0	0	4	0	4
IRF1	0	0	0	2	2	4
JAK1	0	0	0	1	3	4
KAT6A	0	3	0	1	0	4
KMT2A	0	1	0	1	2	4
MECOM	0	3	0	1	0	4
MED12	0	0	0	2	2	4
NRG1	0	1	0	3	0	4
NRG3	0	1	0	3	0	4
NTRK3	0	0	0	4	0	4
PRKDC	0	1	0	3	0	4
PTCH1	0	0	0	4	0	4
RANBP2	0	0	0	1	3	4
SDHA	0	1	0	2	1	4
SETBP1	0	0	0	4	0	4
SF3B1	0	0	0	4	0	4
SMAD3	0	0	0	3	1	4
SOX9	0	3	0	0	1	4
SPINK1	0	2	0	2	0	4
TCF7L2	0	0	0	4	0	4
TFEB	0	4	0	0	0	4
ADAM29	0	0	0	3	0	3
ARAF	0	1	0	2	0	3
ARHGFE17	0	0	0	2	1	3
ATR	0	0	0	2	1	3
BRCA1	0	0	0	0	3	3
CCND2	0	1	0	2	0	3
CCND3	0	3	0	0	0	3
CD1A	0	1	0	2	0	3
CDH1	0	0	0	2	1	3
CHD4	0	1	0	1	1	3
CREBBP	0	0	0	1	2	3
CTNNA1	1	0	0	1	1	3
DDR2	0	1	0	2	0	3
DLC1	0	0	0	3	0	3
DNMT3B	0	0	0	3	0	3
EPHA2	0	0	0	2	1	3
FANCD2	0	0	0	3	0	3
FLT1	0	0	0	3	0	3
FOS	1	2	0	0	0	3
HDAC9	0	0	0	2	1	3
HGF	0	0	0	3	0	3
IKZF1	0	0	0	2	1	3
IL7R	0	1	0	2	0	3
JAK2	0	0	0	1	2	3
MCF2L	0	0	0	3	0	3
MET	0	1	0	2	0	3
MRE11	0	0	0	1	2	3
MSH2	0	0	0	1	2	3
MSH3	0	0	0	1	2	3
MSH6	1	0	0	1	1	3
NCOR1	1	0	0	0	2	3
NKX2-1	0	2	0	0	1	3
NOTCH1	0	0	0	3	0	3
NTRK1	0	1	0	2	0	3
PALB2	1	0	0	2	0	3
PAX5	0	2	0	0	1	3
PDGFRA	0	0	0	3	0	3
RARA	0	1	0	2	0	3
RET	0	0	0	3	0	3
RIT1	0	0	0	3	0	3
SRGAP1	0	1	0	2	0	3
SRMS	0	3	0	0	0	3
STAT3	0	2	0	1	0	3
TET2	0	0	0	2	1	3
TOP2A	0	2	0	1	0	3
TSPAN31	0	3	0	0	0	3
VEGFA	0	3	0	0	0	3
AMER1	0	0	0	1	1	2
AR	0	0	0	2	0	2
ARFRP1	0	2	0	0	0	2
ARHGAP6	0	0	0	1	1	2
ARHGFE25	0	2	0	0	0	2
AURKA	0	1	0	1	0	2
BCORL1	0	1	0	1	1	2
BMPR1A	0	0	0	1	0	2
CAMTA1	0	0	0	1	1	2
CARD11	0	1	0	1	0	2
CD22	0	2	0	0	0	2
CDK6	0	2	0	0	0	2
CHD2	0	0	0	1	1	2
CHEK1	0	0	0	1	1	2
CREB3L1	0	0	0	2	0	2
DOT1L	0	0	0	2	0	2
DPYD	0	0	0	1	1	2
EP300	0	0	0	2	0	2
EPHA5	0	1	0	1	0	2
EPHA7	0	0	0	2	0	2
EPHA8	0	0	0	2	0	2
ETV6	1	1	0	0	0	2
EZH2	0	0	0	2	0	2
FAM135B	0	1	0	1	0	2
FANCA	0	0	0	2	0	2
FANCE	0	0	0	2	0	2
FGF12	0	0	0	2	0	2
FGF23	0	1	0	1	0	2
FLCN	0	0	0	0	2	2
GATA3	0	1	0	1	0	2
GLI2	0	0	0	2	0	2
H3F3A	0	0	0	2	0	2
INPP4B	0	0	0	0	2	2
IRF4	0	0	0	2	0	2
ITK	0	0	0	2	0	2
KDM5B	0	0	0	2	0	2
KDR	0	0	0	2	0	2
KLHL6	0	2	0	0	0	2
LRP1	0	0	0	1	1	2
MAP2K1	0	0	0	2	0	2
MAPK1	0	1	0	1	0	2
MEN1	1	0	0	1	0	2
MTOR	0	0	0	2	0	2
MYD88	0	1	0	1	0	2
MYH11	0	0	0	2	0	2
NETE1	0	2	0	0	0	2
NFE2L2	0	1	0	1	0	2
NOTCH4	0	0	0	2	0	2
PARP1	0	0	0	2	0	2
PAX3	0	0	0	2	0	2
PDGFB	2	0	0	0	0	2
PIK3CB	0	0	0	2	0	2
PIK3CG	0	0	0	2	0	2
PIM1	0	0	0	2	0	2
POLB	0	2	0	0	0	2
POLE	0	0	0	0	2	2
PPP2R1A	0	1	0	1	0	2
PREX2	0	0	0	2	0	2
PRKACA	0	2	0	0	0	2
PTK6	0	2	0	0	0	2
RAD21	0	0	0	1	1	2
RAD54B	0	1	0	1	0	2
REV3L	0	0	0	2	0	2
RICTOR	0	1	0	1	0	2
ROCK1	0	0	0	2	0	2
RUNX1	0	0	0	2	0	2
SLC6A2	0	0	0	2	0	2
SMARCB1	0	0	0	2	0	2
SOX2	0	2	0	0	0	2
SRC	0	0	0	2	0	2
TET1	0	0	0	2	0	2
TET3	0	0	0	0	2	2
TIE1	0	1	0	1	0	2
TOP1	0	1	0	1	0	2
TSC2	1	0	0	1	0	2
WRN	0	1	0	1	0	2
JUN	0	0	0	1	0	1
ABL2	0	0	0	0	1	1
AKT1	0	1	0	0	0	1
ALK	0	0	0	1	0	1
ALOX12B	0	0	0	1	0	1
APEX1	0</					

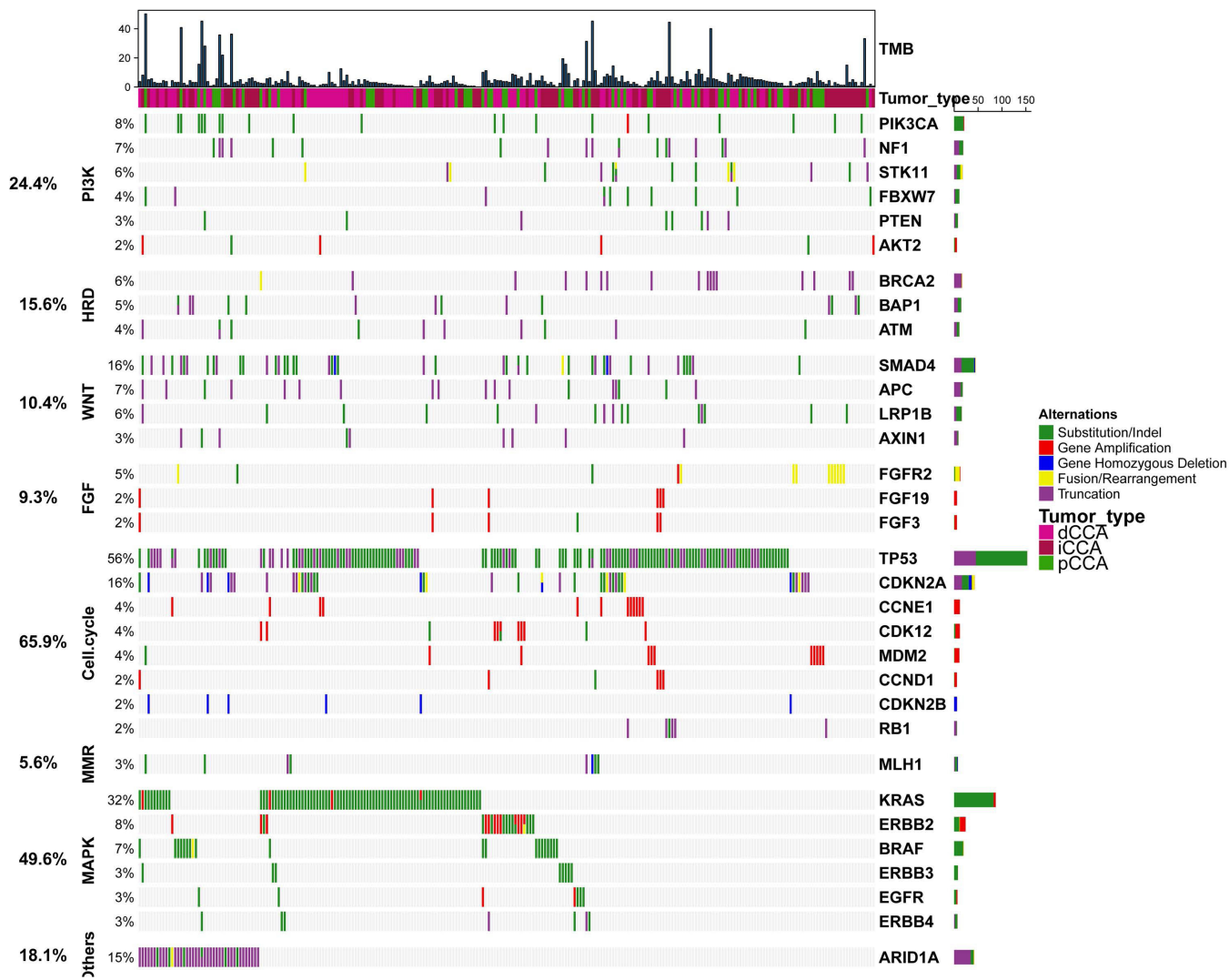


Figure S1 Pathway mutational landscape of 270 CCAs. CCA, cholangiocarcinoma.

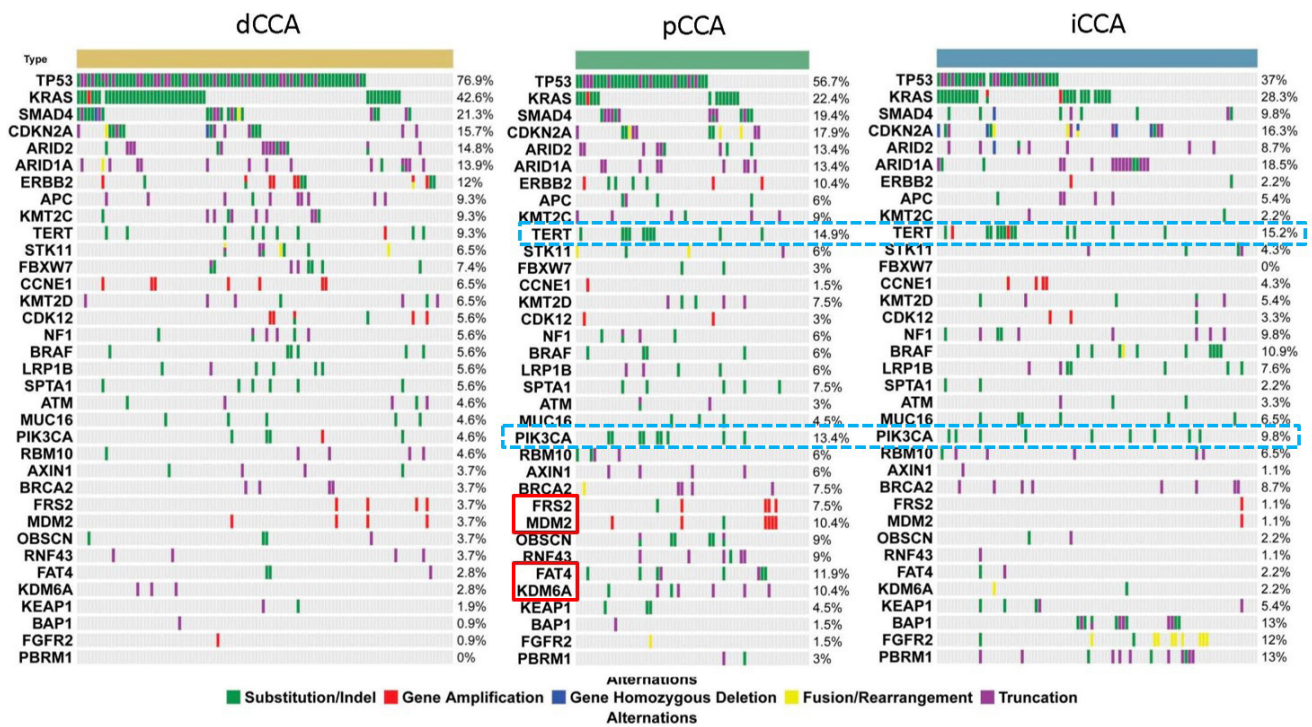


Figure S2 The most commonly mutated genes (>10%) in different CCA subtypes. CCA, cholangiocarcinoma.