

**Table S7.** Frequencies of mutated genes in 160 colorectal cancer patients identified by targeted capture sequencing.

Gene	missense	nonsense	splicing	frameshift_indel	nonframeshift_indel	mutated_sample_num	total_sample_num	mutation_frequency
APC	8	68	4	42	1	90	160	0.5625
TP53	49	11	5	4	2	67	160	0.41875
KRAS	51	1	0	0	0	52	160	0.325
SYNE1	51	7	2	3	0	28	160	0.175
FAT4	34	1	0	0	0	23	160	0.14375
ATM	18	2	2	5	0	17	160	0.10625
USH2A	27	4	1	0	0	16	160	0.1
CDH10	15	0	0	4	0	14	160	0.0875
MLL3	16	1	1	4	0	14	160	0.0875
HMCN1	23	3	0	1	0	13	160	0.08125
LRP2	18	0	0	3	0	13	160	0.08125
RYR1	19	1	0	0	1	13	160	0.08125
VCAN	19	2	1	1	0	13	160	0.08125
DMD	9	4	0	1	0	12	160	0.075
DOCK2	15	0	0	0	0	12	160	0.075
PCDH15	15	1	0	1	1	12	160	0.075
F8	12	1	0	3	0	10	160	0.0625
SMAD4	9	0	0	1	0	10	160	0.0625
AKAP9	11	1	0	3	2	9	160	0.05625
COL1A2	10	2	0	0	0	9	160	0.05625
COL6A3	11	1	0	0	0	9	160	0.05625
HERC2	15	0	1	1	0	9	160	0.05625
LAMA2	11	0	0	1	0	9	160	0.05625
NBAS	9	0	1	1	0	9	160	0.05625
COL5A1	12	0	0	0	0	8	160	0.05
EP400	10	1	0	0	1	8	160	0.05
FAT2	10	1	0	1	0	8	160	0.05
PDE10A	7	0	2	0	0	8	160	0.05
RELN	10	1	0	0	0	8	160	0.05
TMEM132D	12	1	0	0	0	8	160	0.05
CDH9	10	1	1	0	0	7	160	0.04375
COL3A1	5	1	1	1	0	7	160	0.04375
FLG	9	0	0	1	0	7	160	0.04375
GRM1	11	0	0	1	0	7	160	0.04375
LAMA1	8	0	2	1	0	7	160	0.04375
MUC17	12	0	0	0	0	7	160	0.04375
PCDH9	7	0	0	1	0	7	160	0.04375

SPTA1	9	0	1	2	0	7	160	0.04375
THBS2	12	0	0	0	0	7	160	0.04375
TNC	7	0	1	0	0	7	160	0.04375
VWF	7	0	0	1	0	7	160	0.04375
CTNNB1	6	0	0	0	0	6	160	0.0375
DCHS2	11	2	1	0	0	6	160	0.0375
FLNB	6	0	0	0	0	6	160	0.0375
IGSF10	11	3	1	0	0	6	160	0.0375
ITGAE	9	0	0	1	0	6	160	0.0375
LRRC7	9	2	0	0	0	6	160	0.0375
NF1	6	0	0	1	0	6	160	0.0375
PCDHA11	7	0	0	0	0	6	160	0.0375
RNF213	9	0	0	2	0	6	160	0.0375
SLC12A5	6	0	0	0	0	6	160	0.0375
ATP1A2	3	0	2	0	0	5	160	0.03125
CDH26	1	0	0	0	4	5	160	0.03125
CDH8	4	0	1	0	0	5	160	0.03125
CLSTN2	5	0	0	0	0	5	160	0.03125
DCC	4	0	1	1	0	5	160	0.03125
GUCY1A2	6	1	0	0	0	5	160	0.03125
GUCY1A3	6	0	0	0	0	5	160	0.03125
MTOR	5	0	0	0	0	5	160	0.03125
MYH4	11	0	0	1	0	5	160	0.03125
PCDHA2	6	0	0	0	0	5	160	0.03125
PPP1R3A	6	2	0	0	0	5	160	0.03125
PTPRM	8	1	0	0	0	5	160	0.03125
SOS2	8	1	0	0	0	5	160	0.03125
TAF1	6	0	0	1	0	5	160	0.03125
ARMC4	5	0	1	0	0	4	160	0.025
ATP2B2	4	0	0	0	0	4	160	0.025
ATR	8	0	1	1	0	4	160	0.025
BRCA1	4	0	0	0	0	4	160	0.025
CDH7	4	1	0	0	0	4	160	0.025
DPP10	4	0	0	0	0	4	160	0.025
EP300	4	1	1	1	0	4	160	0.025
ERBB4	6	1	0	0	0	4	160	0.025
GNAZ	3	0	0	1	0	4	160	0.025
ITGB4	4	0	0	0	0	4	160	0.025
MYH1	3	1	0	0	0	4	160	0.025
MYST3	7	3	0	0	0	4	160	0.025
PCDHA7	5	0	0	0	0	4	160	0.025
PCDHAC1	9	0	0	0	0	4	160	0.025

PCDHB13	5	0	0	0	0	4	160	0.025
SMAD3	4	0	0	0	0	4	160	0.025
TAF1L	4	0	0	1	0	4	160	0.025
TRRAP	5	1	0	0	0	4	160	0.025
ACACB	9	0	1	1	0	3	160	0.01875
ACSL6	2	0	0	1	0	3	160	0.01875
ADCY2	6	0	0	0	0	3	160	0.01875
ADCY6	4	0	0	0	0	3	160	0.01875
ADCY9	5	0	0	0	0	3	160	0.01875
ARHGAP5	2	1	0	2	0	3	160	0.01875
ATP1A4	3	0	0	1	0	3	160	0.01875
COL17A1	3	1	0	0	0	3	160	0.01875
COL18A1	4	0	0	0	0	3	160	0.01875
CTBP2	3	0	0	0	0	3	160	0.01875
CTNNA1	4	0	0	0	0	3	160	0.01875
DVL3	3	0	0	0	0	3	160	0.01875
ELMO1	4	0	0	0	0	3	160	0.01875
EPS15	3	1	0	0	0	3	160	0.01875
FANCC	2	1	0	0	0	3	160	0.01875
FYN	4	0	0	0	0	3	160	0.01875
HGF	2	0	0	1	0	3	160	0.01875
HTR2C	2	1	0	0	0	3	160	0.01875
MAP2K1	3	0	0	0	0	3	160	0.01875
MAP2K7	2	0	0	1	0	3	160	0.01875
MAP3K15	4	0	0	0	0	3	160	0.01875
MYLK	3	0	0	0	1	3	160	0.01875
PARP4	4	0	0	0	0	3	160	0.01875
PCDHA4	4	0	0	0	0	3	160	0.01875
PCDHB1	2	2	0	1	0	3	160	0.01875
PCDHB3	4	0	0	0	0	3	160	0.01875
PCDHB7	5	0	0	0	0	3	160	0.01875
PCMTD1	2	0	0	1	0	3	160	0.01875
PGCP	3	0	0	0	0	3	160	0.01875
PSG9	1	0	1	1	0	3	160	0.01875
RPS6KA5	3	0	0	0	0	3	160	0.01875
SCNN1G	3	0	0	0	0	3	160	0.01875
ST8SIA1	3	0	0	0	0	3	160	0.01875
ACTC1	2	0	0	0	0	2	160	0.0125
AKR1C4	3	0	0	0	0	2	160	0.0125
ANKFN1	2	0	1	0	0	2	160	0.0125
ARAF	2	0	0	0	0	2	160	0.0125
ATP2B3	2	0	0	0	0	2	160	0.0125

BACH2	4	0	0	0	0	2	160	0.0125
CASP8	1	0	0	2	0	2	160	0.0125
CBL	2	0	0	0	0	2	160	0.0125
CD44	2	0	1	0	0	2	160	0.0125
CDC27	1	0	0	0	1	2	160	0.0125
CPXM1	2	0	0	0	0	2	160	0.0125
CREBBP	2	0	0	0	0	2	160	0.0125
DCT	4	1	0	0	0	2	160	0.0125
FGF13	2	0	0	0	0	2	160	0.0125
GLB1L2	3	0	0	0	0	2	160	0.0125
INS-IGF2	1	0	0	1	0	2	160	0.0125
KIR2DS4	2	0	0	0	0	2	160	0.0125
MTMR8	2	0	0	0	0	2	160	0.0125
MYH2	5	0	0	0	0	2	160	0.0125
NCOA4	2	0	0	0	0	2	160	0.0125
NCOA6	2	0	0	0	0	2	160	0.0125
NLRP13	4	1	0	0	0	2	160	0.0125
NOX5	2	1	0	0	0	2	160	0.0125
NTN4	2	0	0	0	0	2	160	0.0125
OR2M5	3	0	0	0	0	2	160	0.0125
PAK1	2	0	0	0	0	2	160	0.0125
PAXIP1	1	0	0	0	1	2	160	0.0125
PCDHA12	2	0	0	0	0	2	160	0.0125
PCDHA6	2	0	0	0	0	2	160	0.0125
PCDHA8	2	0	0	0	0	2	160	0.0125
PCDHA9	2	0	0	0	0	2	160	0.0125
PCDHB14	2	0	0	0	0	2	160	0.0125
PCDHB15	2	0	0	0	0	2	160	0.0125
PCDHB2	2	0	0	0	0	2	160	0.0125
PCDHB5	2	0	0	0	0	2	160	0.0125
PCDHB6	1	1	0	0	0	2	160	0.0125
PDGFRA	3	0	0	0	0	2	160	0.0125
PHKA2	2	0	0	0	0	2	160	0.0125
PIK3R3	2	0	0	0	0	2	160	0.0125
PLAU	2	0	0	0	0	2	160	0.0125
PRPF8	3	0	0	0	0	2	160	0.0125
PSG1	2	0	0	0	0	2	160	0.0125
PSG3	2	0	0	0	0	2	160	0.0125
RPS6KB2	2	0	0	0	0	2	160	0.0125
RSPO2	2	0	0	0	0	2	160	0.0125
SH3KBP1	0	0	1	1	0	2	160	0.0125
SHC3	2	0	0	0	0	2	160	0.0125

SORBS1	1	0	0	1	0	2	160	0.0125
SOS1	2	0	0	0	0	2	160	0.0125
TRAF1	2	0	0	0	0	2	160	0.0125
WDR59	0	1	0	1	0	2	160	0.0125
AKR1C3	1	0	0	0	0	1	160	0.00625
ANAPC4	1	0	0	0	0	1	160	0.00625
ATP1A3	1	0	0	0	0	1	160	0.00625
BTK	2	0	0	0	0	1	160	0.00625
C10orf81	0	0	1	0	0	1	160	0.00625
CDH11	1	0	0	0	0	1	160	0.00625
CSTL1	1	0	0	0	0	1	160	0.00625
EPS15L1	2	0	0	0	0	1	160	0.00625
FGR	1	0	0	0	0	1	160	0.00625
FZD1	1	0	0	0	0	1	160	0.00625
FZD7	1	0	0	0	0	1	160	0.00625
FZD8	2	0	0	0	0	1	160	0.00625
G6PC	2	0	0	0	0	1	160	0.00625
GDPD3	2	0	0	0	0	1	160	0.00625
GFI1B	1	0	0	0	0	1	160	0.00625
HSD11B1	1	0	0	0	0	1	160	0.00625
IFNA10	1	0	0	0	0	1	160	0.00625
IFNA5	0	1	0	0	0	1	160	0.00625
KIR2DL1	0	0	1	0	0	1	160	0.00625
KIR3DL1	1	0	0	0	0	1	160	0.00625
KIR3DL3	0	0	1	0	0	1	160	0.00625
KPNB1	1	0	0	0	0	1	160	0.00625
KRT3	0	0	0	0	1	1	160	0.00625
LIPT1	0	0	0	1	0	1	160	0.00625
LRRC27	1	0	0	0	0	1	160	0.00625
MAP2K2	1	0	0	0	0	1	160	0.00625
MAPK4	1	0	0	0	0	1	160	0.00625
MED15	0	0	0	0	1	1	160	0.00625
MMP2	1	0	0	0	0	1	160	0.00625
MYH13	1	0	0	0	0	1	160	0.00625
MYH3	1	0	0	0	0	1	160	0.00625
MYH8	1	0	0	0	0	1	160	0.00625
OR2M2	1	0	0	0	0	1	160	0.00625
OR2M3	1	0	0	0	0	1	160	0.00625
OR2M7	1	0	0	0	0	1	160	0.00625
OR8B12	1	0	0	0	0	1	160	0.00625
PCDHA10	1	0	0	0	0	1	160	0.00625
PCDHA1	1	0	0	0	0	1	160	0.00625

PCDHA3	1	0	0	0	0	1	160	0.00625
PCDHB10	1	0	0	0	0	1	160	0.00625
PCDHB12	1	0	0	0	0	1	160	0.00625
PCDHB16	1	0	0	0	0	1	160	0.00625
PCDHB4	0	0	0	1	0	1	160	0.00625
PCDHB8	1	0	0	0	0	1	160	0.00625
PFKM	1	0	0	0	0	1	160	0.00625
PKD1L1	1	0	0	0	0	1	160	0.00625
PLK3	1	0	0	0	0	1	160	0.00625
PPP3CB	1	0	0	0	0	1	160	0.00625
PRKAA1	1	0	0	0	0	1	160	0.00625
PRKG1	0	1	0	0	0	1	160	0.00625
PRKG2	4	0	0	0	0	1	160	0.00625
PSG11	1	0	0	0	0	1	160	0.00625
PSG2	1	0	0	0	0	1	160	0.00625
PSG6	1	0	0	0	0	1	160	0.00625
PSG8	0	0	1	0	0	1	160	0.00625
PTPRU	1	0	0	0	0	1	160	0.00625
RAD1	1	0	0	0	0	1	160	0.00625
RYR3	1	0	0	0	0	1	160	0.00625
SLC12A4	1	0	0	0	0	1	160	0.00625
SLC12A7	1	0	0	0	0	1	160	0.00625
SPESP1	1	0	0	0	0	1	160	0.00625
TALDO1	1	0	0	0	0	1	160	0.00625
TGFB2	1	0	0	0	0	1	160	0.00625
TMEM132C	1	0	0	0	0	1	160	0.00625
TSNARE1	0	0	0	0	1	1	160	0.00625
USPL1	1	0	0	0	0	1	160	0.00625

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