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Mutational characterization of colorectal cancer from Korean patients with targeted sequencing

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Supplementary Table S1. List of genes covered by the targeted sequencing

ABL1, ABL2, ACVR1B, ADGRA2, AKT1, AKT2, AKT3, ALK, ALOX12B, AMER1, APC, APCDD1, APOBEC3A, APOBEC3B, AR, ARAF, ARFRP1, ARID1A, ARID1B, ARID2, ASXL1, ATM, ATR, ATRX, AURKA, AURKB, AXIN1, AXL, B2M, BACH1, BAP1, BARD1, BCL2, BCL2A1, BCL2L1, BCL2L2, BCL6, BCOR, BCORL1, BCR, BLM, BRAF, BRCA1, BRCA2, BRD2, BRD3, BRD4, BRIP1, BTG1, BTK, CARD11, CASP8, CBF, CBL, CCND1, CCND2, CCND3, CCNE1, CD79A, CD79B, CDC42, CDC73, CDH1, CDH2, CDH20, CDH5, CDK12, CDK4, CDK6, CDK8, CDKN2A, CDKN2B, CDKN2C, CDX2, CEBPA, CHD1, CHD2, CHD4, CHEK1, CHEK2, CHUK, CIC, CRBN, CREBBP, CRKL, CRLF2, CSF1R, CTCF, CTNNA1, CTNNB1, CUL4A, CUL4B, CYLD, CYP17A1, DAXX, DDR2, DIS3, DNMT1, DNMT3A, DOCK2, DOT1L, EGFR, ELMO1, EMSY, EP300, EPHA3, EPHA5, EPHA6, EPHA7, EPHB1, EPHB4, EPHB6, ERBB2, ERBB3, ERBB4, ERCC2, ERG, ESR1, ETV1, ETV4, ETV5, ETV6, EWSR1, EYA2, EZH2, FAM46C, FANCA, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FAT3, FBXW7, FGF10, FGF12, FGF14, FGF19, FGF23, FGF3, FGF4, FGF6, FGF7, FGFR1, FGFR2, FGFR3, FGFR4, FLT1, FLT3, FLT4, FOXA1, FOXL2, FUBP1, GATA1, GATA2, GATA3, GID4, GNA11, GNA13, GNAQ, GNAS, GRIN2A, GSK3B, GUCY1A2, H3F3A, HGF, HIST1H3B, HNF1A, HOXA3, HRAS, HSP90AA1, IDH1, IDH2, IGF1, IGF1R, IGF2R, IKBKE, IKZF1, IL7R, INHBA, INPP4B, INSR, IRF4, IRS2, ITK, JAK1, JAK2, JAK3, JUN, KAT6A, KDM5A, KDM5C, KDM6A, KDR, KEAP1, KIT, KLF4, KLHL6, KRAS, LMO1, LRP1B, LRP6, LTK, MAML1, MAP2K1, MAP2K2, MAP2K4, MAP3K1, MAP3K13, MCL1, MDM2, MDM4, MED12, MEF2B, MEN1, MET, MITF, MLH1, MPL, MRE11A, MSH2, MSH6, MTOR, MUTYH, MYC, MYCL, MYCN, MYD88, NCOA3, NCOR1, NF1, NF2, NFE2L2, NKFBIA, NKX2-1, NKX3-1, NOTCH1,

NOTCH2, NOTCH3, NOTCH4, NPM1, NRAS, NSD1, NTRK1, NTRK2, NTRK3, NUP93, NUTM1, PAK3, PAK7, PALB2, PARP1, PARP2, PARP3, PARP4, PAX5, PBRM1, PDGFRA, PDGFRB, PDK1, PGR, PHF6, PHLPP2, PIK3C3, PIK3CA, PIK3CG, PIK3R1, PIK3R2, PKHD1, PLCG1, PMS2, PNRC1, PPP2R1A, PRDM1, PRKAR1A, PRKDC, PRPF40B, PRSS8, PTCH1, PTCH2, PTEN, PTPN11, PTPRD, RAB35, RAC1, RAC2, RAD50, RAD51, RAD51B, RAD51C, RAD51D, RAD52, RAD54L, RAF1, RARA, RB1, REL, RET, RICTOR, RNF43, ROBO1, ROBO2, ROS1, RPA1, RPTOR, RUNX1, RUNX1T1, SEMA3A, SEMA3E, SETBP1, SETD2, SF3A1, SF3B1, SH2B3, SKP2, SLIT2, SMAD2, SMAD3, SMAD4, SMARCA1, SMARCA4, SMARCB1, SMARCD1, SMO, SOCS1, SOX10, SOX2, SOX9, SPEN, SPOP, SRC, SRSF1, SRSF2, SRSF7, STAG2, STAT3, STAT4, STK11, SUFU, SYK, TBX22, TBX3, TERT, TET2, TGFBR2, TIPARP, TMPRSS2, TNFAIP3, TNFRSF14, TNKS, TNKS2, TOP1, TP53, TRAF7, TRRAP, TSC1, TSC2, TSHR, U2AF1, U2AF2, USP9X, VHL, WHSC1L1, WISP3, WT1, WWP1, XBP1, XPO1, XRCC3, ZNF217, ZNF703, ZRSR2

Supplementary Table S2. Genes that show significantly different mutation frequencies by each clinical information criteria from tumors of the 172 Korean patients with colorectal cancer. Genes in boldface presentation are the common genes that also showed significantly different mutation frequencies from the Caucasian patients of the TCGA colorectal cancer data set.

Genes	Categorization by clinical variable		p-value
	Left-sided (N=125)	Right-sided (N=47)	
APC	97, 77.6%	27, 57.4%	0.013
APCDD1	0, 0.0%	3, 6.4%	0.019
ATRX	4, 3.2%	8, 17.0%	0.004
CASP5	0, 0.0%	3, 6.4%	0.019
CTNNB1	4, 3.2%	6, 12.8%	0.026
DDX27	0, 0.0%	3, 6.4%	0.019
FBXW7	25, 20.0%	3, 6.4%	0.036
HNF1A	2, 1.6%	4, 8.5%	0.048
INSR	4, 3.2%	6, 12.8%	0.026
JAK1	2, 1.6%	4, 8.5%	0.048
MCHR2	0, 0.0%	3, 6.4%	0.019
NSD1	6, 4.8%	8, 17.0%	0.023
NSD3	1, 0.8%	4, 8.5%	0.020
PIK3C3	0, 0.0%	3, 6.4%	0.019
PRKDC	19, 15.2%	16, 34.0%	0.010
RAF1	0, 0.0%	3, 6.4%	0.019

RB1	1, 0.8%	4, 8.5%	0.020
RPA1	4, 3.2%	6, 12.8%	0.026
SLC16A4	0, 0.0%	3, 6.4%	0.019
TMEM97	0, 0.0%	3, 6.4%	0.019
TP53	100, 80.0%	26, 55.3%	0.002
TTC3	0, 0.0%	3, 6.4%	0.019

	ages under 50	ages 50 or older	
	(N=157)	(N=15)	

ALOX12B	3, 1.9%	3, 20.0%	0.009
ASXL1	9, 5.7%	5, 33.3%	0.003
FANCE	0, 0.0%	2, 13.3%	0.007
FANCI	13, 8.3%	5, 33.3%	0.011
GID4	2, 1.3%	2, 13.3%	0.039
IGF2R	13, 8.3%	4, 26.7%	0.045
ITK	2, 1.3%	2, 13.3%	0.039
NOTCH1	15, 9.6%	6, 40.0%	0.004
PALB2	8, 5.1%	4, 26.7%	0.012
PIK3R2	2, 1.3%	2, 13.3%	0.039
RB1	2, 1.3%	3, 20.0%	0.005

	CA19-9 level \geq 25	CA19-9 level < 25	
	(N=35)	(N=137)	

ARID1B	0, 0.0%	18, 13.1%	0.026
CHEK1	3, 8.6%	0, 0.0%	0.008
ETV5	3, 8.6%	1, 0.7%	0.027

KRAS	23, 65.7%	54, 39.4%	0.007
PRKDC	2, 5.7%	33, 24.1%	0.017
PTEN	3, 8.6%	1, 0.7%	0.027
	CEA level \geq 5	CEA level < 5	
	(N=53)	(N=119)	
CASP5	3, 5.7%	0, 0.0%	0.028
EP300	11, 20.8%	11, 9.2%	0.048
EPHB4	7, 13.2%	2, 1.7%	0.004
KDM6A	5, 9.4%	2, 1.7%	0.029
KRAS	31, 58.5%	46, 38.7%	0.020
MSH3	4, 7.6%	1, 0.8%	0.032
NUTM1	8, 15.1%	5, 4.2%	0.024
RAD51D	3, 5.7%	0, 0.0%	0.028
RNF43	7, 13.2%	4, 3.4%	0.036
SMAD3	5, 9.4%	0, 0.0%	0.002
SMARCA1	4, 7.6%	1, 0.8%	0.032
SOX2	3, 5.7%	0, 0.0%	0.028
	Low T stage(T1, T2)	High T stage(T3, T4)	
	(N=46)	(N=126)	
ALOX12B	4, 8.7%	2, 1.6%	0.045
BRAF	0, 0.0%	15, 11.9%	0.012
INHBA	4, 8.7%	2, 1.6%	0.045
LRP1B	8, 17.4%	43, 34.1%	0.038
MAP3K13	6, 13.0%	3, 2.4%	0.012

NF2	4, 8.7%	0, 0.0%	0.005
SEMA3E	5, 10.9%	2, 1.6%	0.015
TP53	26, 56.5%	100, 79.4%	0.006
XRCC3	3, 6.5%	0, 0.0%	0.018
	Without metastasis	With metastasis	
	(N=144)	(N=28)	
BRAF	9, 6.2%	6, 21.4%	0.019
EPHA6	7, 4.9%	5, 17.9%	0.028
GOT1L1	0, 0.0%	2, 7.1%	0.026
IKZF1	1, 0.7%	3, 10.7%	0.014
SMARCA1	2, 1.4%	3, 10.7%	0.031
	Without regional lymph node	With regional lymph node	
	metastasis	metastasis	
	(N=93)	(N=79)	
ACVR1B	9, 9.7%	1, 1.3%	0.022
ACVR2A	7, 7.5%	0, 0.0%	0.016
APC	61, 65.6%	63, 79.8%	0.042
ARID1A	19, 20.4%	6, 7.6%	0.018
ATRX	10, 10.8%	2, 2.5%	0.039
EPHB4	8, 8.6%	1, 1.3%	0.040
ETV4	0, 0.0%	7, 8.9%	0.004
FOXL2	0, 0.0%	4, 5.1%	0.043
MAP3K13	9, 9.7%	0, 0.0%	0.004
PIK3CA	20, 21.5%	4, 5.1%	0.002
PIK3CG	7, 7.5%	0, 0.0%	0.016

	Microsatellite stable (N=165)	Microsatellite instability (N=7)	
ACVR2A	1, 0.6%	6, 85.7%	0.000
ADD3	0, 0.0%	2, 28.6%	0.001
ADGRA2	5, 3.0%	3, 42.9%	0.002
ADNP	1, 0.6%	2, 28.6%	0.004
AIM2	0, 0.0%	1, 14.3%	0.041
AKAP7	0, 0.0%	1, 14.3%	0.041
ALOX12B	3, 1.8%	3, 42.9%	0.001
ANO10	0, 0.0%	1, 14.3%	0.041
APC	122, 73.9%	2, 28.6%	0.019
ARID1A	21, 12.7%	4, 57.1%	0.009
ARID1B	14, 8.5%	4, 57.1%	0.002
ARID2	10, 6.1%	4, 57.1%	0.001
ASH1L	0, 0.0%	1, 14.3%	0.041
ASTE1	3, 1.8%	4, 57.1%	0.000
ATM	18, 10.9%	4, 57.1%	0.006
ATR	7, 4.2%	2, 28.6%	0.045
ATRX	9, 5.4%	3, 42.9%	0.008
AXIN1	0, 0.0%	2, 28.6%	0.001
B2M	3, 1.8%	2, 28.6%	0.013
BACH1	4, 2.4%	2, 28.6%	0.020
BAX	1, 0.6%	3, 42.9%	0.000
BCL2L1	0, 0.0%	1, 14.3%	0.041
BCL2L2	0, 0.0%	1, 14.3%	0.041

BCL6	2, 1.2%	3, 42.9%	0.000
BCORL1	5, 3.0%	2, 28.6%	0.027
BMPR2	0, 0.0%	3, 42.9%	0.000
BORCS8	3, 1.8%	2, 28.6%	0.013
CARD11	15, 9.1%	5, 71.4%	0.000
CASP5	0, 0.0%	3, 42.9%	0.000
CASP8	4, 2.4%	2, 28.6%	0.020
CCDC168	0, 0.0%	1, 14.3%	0.041
CCDC43	0, 0.0%	1, 14.3%	0.041
CD3G	0, 0.0%	1, 14.3%	0.041
CHD4	9, 5.4%	3, 42.9%	0.008
CLOCK	0, 0.0%	2, 28.6%	0.001
COBLL1	0, 0.0%	2, 28.6%	0.001
CTCF	2, 1.2%	2, 28.6%	0.008
CTNNA1	3, 1.8%	2, 28.6%	0.013
CYHR1	2, 1.2%	3, 42.9%	0.000
DDX27	1, 0.6%	2, 28.6%	0.004
DOCK3	0, 0.0%	3, 42.9%	0.000
EGFR	7, 4.2%	2, 28.6%	0.045
EIF2B3	1, 0.6%	2, 28.6%	0.004
EMSY	5, 3.0%	2, 28.6%	0.027
EP300	19, 11.5%	3, 42.9%	0.046
EPHA5	13, 7.9%	5, 71.4%	0.000
EPHB1	11, 6.7%	3, 42.9%	0.013
EPHB4	5, 3.0%	4, 57.1%	0.000

EPHB6	15, 9.1%	3, 42.9%	0.026
ETV6	3, 1.8%	2, 28.6%	0.013
FANCL	3, 1.8%	2, 28.6%	0.013
FETUB	0, 0.0%	2, 28.6%	0.001
FGF14	2, 1.2%	2, 28.6%	0.008
FGF4	0, 0.0%	1, 14.3%	0.041
FGF6	0, 0.0%	1, 14.3%	0.041
GBP3	1, 0.6%	2, 28.6%	0.004
GRK4	0, 0.0%	1, 14.3%	0.041
HNF1A	4, 2.4%	2, 28.6%	0.020
IGF1	0, 0.0%	1, 14.3%	0.041
IGF2R	13, 7.9%	4, 57.1%	0.002
IKBKE	6, 3.6%	2, 28.6%	0.035
IKZF1	2, 1.2%	2, 28.6%	0.008
IL7R	4, 2.4%	2, 28.6%	0.020
IRF4	0, 0.0%	1, 14.3%	0.041
JAK1	4, 2.4%	2, 28.6%	0.020
JAK3	4, 2.4%	2, 28.6%	0.020
JPH4	0, 0.0%	1, 14.3%	0.041
KCNMA1	0, 0.0%	4, 57.1%	0.000
KDM5C	1, 0.6%	3, 42.9%	0.000
KDM6A	5, 3.0%	2, 28.6%	0.027
KIT	10, 6.1%	3, 42.9%	0.010
LARP4B	0, 0.0%	1, 14.3%	0.041
LMAN1	0, 0.0%	3, 42.9%	0.000

LRP6	3, 1.8%	2, 28.6%	0.013
LRRIQ3	0, 0.0%	2, 28.6%	0.001
MAP3K13	6, 3.6%	3, 42.9%	0.003
MCHR2	1, 0.6%	2, 28.6%	0.004
MDM2	1, 0.6%	2, 28.6%	0.004
MED12	3, 1.8%	3, 42.9%	0.001
MFSD4B	1, 0.6%	3, 42.9%	0.000
MLH1	6, 3.6%	4, 57.1%	0.000
MRE11	1, 0.6%	2, 28.6%	0.004
MSH3	1, 0.6%	4, 57.1%	0.000
MSH6	9, 5.4%	3, 42.9%	0.008
MYCN	4, 2.4%	2, 28.6%	0.020
NDUFC2	1, 0.6%	2, 28.6%	0.004
NF1	16, 9.7%	4, 57.1%	0.004
NOTCH1	18, 10.9%	3, 42.9%	0.040
NSD1	10, 6.1%	4, 57.1%	0.001
NSD3	2, 1.2%	3, 42.9%	0.000
NUP93	5, 3.0%	2, 28.6%	0.027
OR6C75	0, 0.0%	1, 14.3%	0.041
PBRM1	6, 3.6%	3, 42.9%	0.003
PGR	6, 3.6%	3, 42.9%	0.003
PHACTR4	0, 0.0%	1, 14.3%	0.041
PIK3C3	1, 0.6%	2, 28.6%	0.004
PIK3CA	19, 11.5%	5, 71.4%	0.001
PRDM2	0, 0.0%	1, 14.3%	0.041

PRRG1	1, 0.6%	2, 28.6%	0.004
PTPRD	7, 4.2%	3, 42.9%	0.004
RAC1	0, 0.0%	1, 14.3%	0.041
RAD50	10, 6.1%	3, 42.9%	0.010
RAF1	1, 0.6%	2, 28.6%	0.004
RB1	3, 1.8%	2, 28.6%	0.013
RBBP8	0, 0.0%	1, 14.3%	0.041
RBM27	0, 0.0%	3, 42.9%	0.000
RBM43	0, 0.0%	1, 14.3%	0.041
RNF43	6, 3.6%	5, 71.4%	0.000
ROBO1	11, 6.7%	4, 57.1%	0.001
ROBO2	8, 4.8%	3, 42.9%	0.006
RPL22	0, 0.0%	3, 42.9%	0.000
RUNX1T1	5, 3.0%	2, 28.6%	0.027
SEC31A	6, 3.6%	2, 28.6%	0.035
SEC63	0, 0.0%	2, 28.6%	0.001
SETD2	7, 4.2%	3, 42.9%	0.004
SLC16A4	0, 0.0%	3, 42.9%	0.000
SLC22A9	0, 0.0%	2, 28.6%	0.001
SMARCA4	4, 2.4%	5, 71.4%	0.000
SMC6	0, 0.0%	2, 28.6%	0.001
SPOUT1	0, 0.0%	1, 14.3%	0.041
SRPRA	0, 0.0%	3, 42.9%	0.000
TBC1D23	0, 0.0%	1, 14.3%	0.041
TBX22	3, 1.8%	3, 42.9%	0.001

TCERG1	0, 0.0%	1, 14.3%	0.041
TEAD2	0, 0.0%	2, 28.6%	0.001
TGFBR2	8, 4.8%	4, 57.1%	0.000
TM9SF3	0, 0.0%	2, 28.6%	0.001
TMEM97	1, 0.6%	2, 28.6%	0.004
TNKS	8, 4.8%	6, 85.7%	0.000
TNKS2	6, 3.6%	3, 42.9%	0.003
TOP1	1, 0.6%	2, 28.6%	0.004
TP53	124, 75.2%	2, 28.6%	0.015
TRRAP	24, 14.6%	4, 57.1%	0.014
TTC3	0, 0.0%	3, 42.9%	0.000
TTK	0, 0.0%	2, 28.6%	0.001
TVP23A	0, 0.0%	2, 28.6%	0.001
USF3	1, 0.6%	3, 42.9%	0.000
USP9X	6, 3.6%	3, 42.9%	0.003
VEPH1	0, 0.0%	1, 14.3%	0.041
VHL	0, 0.0%	1, 14.3%	0.041
WWP1	4, 2.4%	3, 42.9%	0.001
XPOT	0, 0.0%	1, 14.3%	0.041
ZFR	0, 0.0%	1, 14.3%	0.041
ZNF609	0, 0.0%	1, 14.3%	0.041
ZNF703	3, 1.8%	2, 28.6%	0.013

	Without lymphovascular invasion (N=81)	With lymphovascular invasion (N=91)	
ABL2	8, 9.9%	2, 2.2%	0.048

DNMT3A	4, 4.9%	0, 0.0%	0.047
INSR	1, 1.2%	9, 9.9%	0.020
MAP3K13	8, 9.9%	1, 1.1%	0.014
MED12	0, 0.0%	6, 6.6%	0.030
NF2	4, 4.9%	0, 0.0%	0.047
NTRK2	4, 4.9%	0, 0.0%	0.047
PALB2	2, 2.5%	10, 11.0%	0.036
TP53	51, 63.0%	75, 82.4%	0.006

	Without diabetes mellitus (N=134)	With diabetes mellitus (N=38)	
ADD3	0, 0.0%	2, 5.3%	0.048
ARID1B	10, 7.5%	8, 21.0%	0.031
ASTE1	3, 2.2%	4, 10.5%	0.043
BRD4	5, 3.7%	5, 13.2%	0.044
CTCF	1, 0.8%	3, 7.9%	0.034
CYHR1	1, 0.8%	4, 10.5%	0.009
DDX27	0, 0.0%	3, 7.9%	0.010
ELOA	0, 0.0%	2, 5.3%	0.048
EPHB4	4, 3.0%	5, 13.2%	0.026
FGF19	0, 0.0%	2, 5.3%	0.048
GRIN2A	13, 9.7%	9, 23.7%	0.030
H3F3A	0, 0.0%	2, 5.3%	0.048
HRAS	1, 0.8%	3, 7.9%	0.034
KDM5C	1, 0.8%	3, 7.9%	0.034
LRP1B	46, 34.3%	5, 13.2%	0.015

MBD4	0, 0.0%	2, 5.3%	0.048
MRE11	0, 0.0%	3, 7.9%	0.010
NDUFC2	0, 0.0%	3, 7.9%	0.010
SETD2	5, 3.7%	5, 13.2%	0.044
SRPRA	0, 0.0%	3, 7.9%	0.010
SUFU	0, 0.0%	2, 5.3%	0.048
TEAD2	0, 0.0%	2, 5.3%	0.048
TM9SF3	0, 0.0%	2, 5.3%	0.048
TNKS2	2, 1.5%	7, 18.4%	0.000
TTK	0, 0.0%	2, 5.3%	0.048
USF3	1, 0.8%	3, 7.9%	0.034

	BMI \geq 25	BMI < 25	
	(N=45)	(N=127)	
ELMO1	4, 8.9%	2, 1.6%	0.041
GNAQ	3, 6.7%	0, 0.0%	0.017
IRS2	4, 8.9%	2, 1.6%	0.041
JAK2	3, 6.7%	0, 0.0%	0.017
RAD50	7, 15.6%	6, 4.7%	0.042
ROS1	8, 17.8%	8, 6.3%	0.034

Supplementary Table S3. Genes that show significantly different mutation frequencies by each clinical information criteria from tumors of the Caucasian patients of the TCGA colorectal cancer data set. Genes in boldface presentation are the common genes that also showed significantly different mutation frequencies from tumors of the 172 Korean patients with colorectal cancer.

Genes	Categorization by clinical variable		p-value
	Left-sided (N=70)	Right-sided (N=97)	
APC	59, 84.3%	59, 60.8%	0.001
TRRAP	2, 2.9%	18, 18.6%	0.002
PIK3CG	0, 0.0%	13, 13.4%	0.001
APCDD1	0, 0.0%	6, 6.2%	0.041
ASXL1	3, 4.3%	14, 14.4%	0.038
ERBB4	4, 5.7%	17, 17.5%	0.032
JAK1	0, 0.0%	10, 10.3%	0.005
ABL2	0, 0.0%	6, 6.2%	0.041
MSH2	0, 0.0%	9, 9.3%	0.011
ATR	1, 1.4%	9, 9.3%	0.046
KDR	0, 0.0%	6, 6.2%	0.041
CTNNA1	0, 0.0%	6, 6.2%	0.041
BRAF	5, 7.1%	25, 25.8%	0.002
WT1	1, 1.4%	12, 12.4%	0.008
FAT3	9, 12.9%	29, 29.9%	0.014
FGF23	0, 0.0%	6, 6.2%	0.041

ARID2	1, 1.4%	10, 10.3%	0.026
SH2B3	0, 0.0%	6, 6.2%	0.041
FANCM	0, 0.0%	7, 7.2%	0.042
BLM	0, 0.0%	9, 9.3%	0.011
NF1	0, 0.0%	16, 16.5%	0.000
CDK12	1, 1.4%	12, 12.4%	0.008
RNF43	2, 2.9%	16, 16.5%	0.005
SOX9	4, 5.7%	17, 17.5%	0.032
BRD4	1, 1.4%	9, 9.3%	0.046
ERG	0, 0.0%	7, 7.2%	0.042
BCOR	0, 0.0%	15, 15.5%	0.000
BCORL1	1, 1.4%	13, 13.4%	0.008
KLHL6	1, 1.4%	10, 10.3%	0.026
MET	1, 1.4%	9, 9.3%	0.046
MPL	0, 0.0%	6, 6.2%	0.041
PARP1	1, 1.4%	9, 9.3%	0.046
EPHA7	0, 0.0%	6, 6.2%	0.041
TNKS	0, 0.0%	7, 7.2%	0.042
WWP1	1, 1.4%	9, 9.3%	0.046
NKX2-1	0, 0.0%	7, 7.2%	0.042
CTCF	1, 1.4%	9, 9.3%	0.046
CDH1	0, 0.0%	8, 8.2%	0.021
FANCA	0, 0.0%	13, 13.4%	0.001
RPTOR	1, 1.4%	9, 9.3%	0.046
AKT2	0, 0.0%	6, 6.2%	0.041

CIC	3, 4.3%	15, 15.5%	0.024
ADGRA2	0, 0.0%	7, 7.2%	0.042
CHD1	1, 1.4%	9, 9.3%	0.046
ALOX12B	1, 1.4%	9, 9.3%	0.046
IKBKE	0, 0.0%	7, 7.2%	0.042
DNMT3A	1, 1.4%	10, 10.3%	0.026
BAP1	0, 0.0%	6, 6.2%	0.041
PBRM1	1, 1.4%	10, 10.3%	0.026
RICTOR	0, 0.0%	6, 6.2%	0.041
DAXX	0, 0.0%	8, 8.2%	0.021
SEMA3E	1, 1.4%	9, 9.3%	0.046
PTCH1	1, 1.4%	14, 14.4%	0.004
IRS2	0, 0.0%	6, 6.2%	0.041
ABL1	0, 0.0%	8, 8.2%	0.021
EWSR1	0, 0.0%	7, 7.2%	0.042
INSR	0, 0.0%	8, 8.2%	0.021
SLIT2	1, 1.4%	11, 11.3%	0.015
HNF1A	0, 0.0%	10, 10.3%	0.005

	ages under 50 (N=28)	ages 50 or older (N=179)	
APC	15, 53.6%	132, 73.7%	0.042
ERBB4	0, 0.0%	25, 14.0%	0.030
HOXA3	4, 14.3%	7, 3.9%	0.045
SMAD4	0, 0.0%	27, 15.1%	0.030
NCOA3	3, 10.7%	3, 1.7%	0.034

RAF1	3, 10.7%	3, 1.7%	0.034
CHD2	4, 14.3%	7, 3.9%	0.045
CCNE1	2, 7.1%	1, 0.6%	0.049
	Low T stage(T1, T2)	High T stage(T3, T4)	
	(N=40)	(N=167)	
ABL1	5, 12.5%	6, 3.6%	0.040
ARFRP1	3, 7.5%	1, 0.6%	0.023
	Without regional lymph node	With regional lymph node	
	metastasis	metastasis	
	(N=116)	(N=91)	
TRRAP	23, 19.8%	3, 3.3%	0.000
PIK3CG	14, 12.1%	2, 2.2%	0.008
GATA3	9, 7.8%	1, 1.1%	0.045
ASXL1	16, 13.8%	3, 3.3%	0.013
PDGFRA	11, 9.5%	2, 2.2%	0.042
TBX3	13, 11.2%	2, 2.2%	0.014
CDK12	14, 12.1%	1, 1.1%	0.002
BRD4	11, 9.5%	2, 2.2%	0.042
FOXL2	6, 5.2%	0, 0.0%	0.036
CSF1R	9, 7.8%	1, 1.1%	0.045
ETV1	8, 6.9%	0, 0.0%	0.010
FGFR2	10, 8.6%	1, 1.1%	0.025
ERCC2	6, 5.2%	0, 0.0%	0.036
ACVR1B	10, 8.6%	1, 1.1%	0.025
FANCI	6, 5.2%	0, 0.0%	0.036

PKHD1	16, 13.8%	3, 3.3%	0.013
CIC	18, 15.5%	3, 3.3%	0.004
EPHA5	16, 13.8%	4, 4.4%	0.031
ALOX12B	10, 8.6%	1, 1.1%	0.025
BAP1	6, 5.2%	0, 0.0%	0.036
BCL6	7, 6.0%	0, 0.0%	0.019
DAXX	8, 6.9%	0, 0.0%	0.010
PTCH1	15, 12.9%	3, 3.3%	0.023
KDM5A	9, 7.8%	1, 1.1%	0.045
FAM46C	9, 7.8%	1, 1.1%	0.045
EPHA6	16, 13.8%	3, 3.3%	0.013
GNAQ	6, 5.2%	0, 0.0%	0.036
TNKS2	10, 8.6%	1, 1.1%	0.025
CDH5	8, 6.9%	0, 0.0%	0.010
HNF1A	10, 8.6%	1, 1.1%	0.025

	BMI \geq 25 (N=113)	BMI < 25 (N=52)	
APCDD1	0, 0.0%	3, 5.8%	0.030
RAD54L	1, 0.9%	4, 7.7%	0.035
SRSF7	0, 0.0%	3, 5.8%	0.030
SRC	1, 0.9%	4, 7.7%	0.035
BCORL1	4, 3.5%	8, 15.4%	0.010
RPTOR	5, 4.4%	8, 15.4%	0.026
PBRM1	3, 2.6%	6, 11.5%	0.029
NOTCH4	3, 2.6%	8, 15.4%	0.005

IRS2	1, 0.9%	4, 7.7%	0.035
AKT1	3, 2.6%	6, 11.5%	0.029
GNA11	0, 0.0%	4, 7.7%	0.009
ITK	0, 0.0%	3, 5.8%	0.030
AXL	1, 0.9%	7, 13.5%	0.001
MEN1	0, 0.0%	4, 7.7%	0.009
CD79B	0, 0.0%	3, 5.8%	0.030
