SUPPLEMENTARY MATERIALS: TABLES

Elevated microsatellite alterations with allelic loss on 9p24.2 signify less aggressive metastasis in colorectal cancer

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SUPPLEMENTARY TABLES

Supplementary Table1: The distribution of clinical and genetic variables for the 79 LMs included in Tumor Set #1

Variables[a)]		Number of Cases (%)	Association with[b)] E/L	*KRAS/BRAF* Mutations	Overall Survival
Sample Source	Toho (DPOHTU) vs Korea (DPCNU)	28 vs 51	0.701	0.953	0.495
Age	<62 vs >62	41 vs 38	0.643	0.812	0.425
Sex	Female vs Male	26 vs 53	0.821	**0.046**	0.997
Primary Tumor Grade	G1 vs G2&G3	25 vs 54	0.882	0.424	0.138
Primary Tumor Sites	Proximal vs Distal	10 vs 69	0.502	0.656	0.088
Primary Tumor Type	Colon vs Rectum	36 vs 43	0.083	0.568	0.888
Metastasis	Metachronous vs Synchronous	38 vs 41	0.599	0.574	**0.0006**
MSI Status	MSI-H vs MSI-L vs MSS	1 vs 22 vs 56	N.A.	0.88	0.596
	EMAST vs non-EMAST	47 vs 32	N.A.	0.374	0.174
	E/L vs MS	56 vs 22	N.A.	0.69	0.843
***KRAS/BRAF* Mutation**	Mutated vs Wild-Type	26 vs 51	0.517	N.A.	0.867

[a)] Age: The average age of this set is ~62 years old. 62 was used as cut-off value for defining age group. Primary Tumor Grade, Sites and Type are those of primary CRC from which these 79 LMs were derived. KRAS mutations were examined in codons 12 and 13, and BRAF mutations were examined in codon 600.

[b)] Association between E/L or KRAS/BRAF mutations and each variable was examined by univariate logistic regression analysis.

Association between OS and each variable was examined by univariate Cox hazards regression analysis.

Each number represents p value. Undelined bolted numbers are significant. KRAS/BRAF mutations were associated with males. Shorter OS was associated with synchronous LM.

Supplementary Table 2. 141 loci examined for FS/LOH in 24 E/L positive LMs

Gene with dinucleotide repeats (44 genes)

Gene	Cancer[a]	Repeats	No. Unit	Posotion	Frame-shifts Freq.(%)[b]	LOH Freq.(%)
MNT	Y	CA	23	3'	0/24	12/14 (86)
SEMA6D	Y	CA	22	3'	1/24 (4)	11/18 (61)
FGF3	Y	CA	29	3'	0/24	8/19 (42)
MLH3	Y	CA	13	intron	0/24	5/14 (36)
IGF1	Y	CA	22	3'	0/23	1/13 (8)
PAX5	Y	CA	21	3'	0/24	4/12 (33)
ZEB1	Y	CA	19	3'	0/24	4/20 (20)
PTP4A2	Y	CA	25	3'	0/24	2/20 (10)
SNX20	Y	CA	21	3'	0/24	4/12 (33)
CNOT3	Y	CA	18	5'	0/24	4/17 (24)
PHF17	Y	CA	23	3'	0/24	4/21 (19)
STYK1	Y	CA	11	3'	1/24 (4)	9/15 (60)
MAPKAPK2	Y	CA	15	3'	0/14	1/7 (14)
NDRG4	Y	CA	14	3'	0/21	2/8 (25)
AKAP11	Y	CA	21	3'	0/22	0/6
MAP2	Y	CA	16	3'	0/21	1/10 (10)
BMP4	Y	CA	16	3'	0/24	0/1
RDX	Y	CA	15	3'	0/24	3/10 (30)
SATB1	Y	CA	18	3'	0/22	1/3 (33)
FASLG	Y	CA	15	3'	0/24	0/1
MACC1	Y	CA	49	3'	0/20	1/4 (25)
NLK	Y	CA	16	3'	0/24	1/11 (9)
PTGES	Y	CA	24	3'	0/24	5/19 (26)
HIF1β	Y	CA	15	3'	0/24	4/12 (33)
MAPK10	Y	CA	16	3'	0/23	0/20
EFNB1	Y	CA	14	3'	0/24	0/6
UBLCP1	N	CA	24	3'	0/21	0/13
ATF1	Y	CA	8	3'	0/24	0/0
SNAIL2	Y	CA	15	3'	0/24	0/0
SMAD7	Y	CA	11	3'	0/24	0/0
ENOS	Y	CA	34	intron	0/12	0/11
PTPRT	Y	CA	25	intron	0/23	1/14 (7)
DUSP10	Y	CA	20	intron	0/24	0/0
MSH3	Y	CA	20	intron	0/24	0/14
TMPRSS2	Y	CA	21	intron	0/24	0/0
PTEN	Y	CA	19	intron	0/24	4/12 (33)
EGFR	Y	CA	16	intron	0/22	0/8
MSH6	Y	CA	17	intron	0/24	0/0
DEC1	Y	CA	24	intron	0/24	5/15 (33)
LMO1	Y	CA	15	5'	1/24 (4)	5/19 (26)
BMP3	Y	CA	17	5'	0/24	0/0
CLEC2B	Y	CA	10	5'	0/24	6/14 (43)
XPO5	Y	CA	24	intron	2/24 (8)	1/3 (33)
MAF	Y	CA	23	3'	0/24	6/17 (35)

Gene with tetranucleotide repeats (33 genes)

Gene	Cancer	Repeats	No. Unit	Posotion	Frame-shifts Freq.(%)	LOH Freq.(%)
SLC5A12	Y	AAAG	13	3'	1/24 (4)	2/13 (15)
RBM47	N	AAAG	16	3'	9/24 (38)	4/11 (36)
FZD4	Y	CAAA	8	3'	1/23 (4)	3/12 (25)
ANKRD5	N	ATGA,TAGA	5,10	3'	4/24 (17)	9/13 (69)
BCL2(D18S51)	Y	AAAG	18	intron	2/24 (8)	15/19 (79)
HDAC4	Y	TAGA	9	3'	0/21	4/13 (31)
KCNK2	Y	TAGA	13	3'	0/20	6/13 (46)

[a]Y: The locus has been associated with cancer; N: no association has been reported; N.A.:not applicable.

[b] Mutation frequency was calculated by dividing the number of mutated cases by the number of informative cases.

Supplementary Table 2. cont. 141 loci examined for FS/LOH in 24 E/L positive LMs

Gene with tetranucleotide repeats (33 genes) cont.

Gene	Cancer	Repeats	No. Unit	Posotion	Frame-shifts Freq.(%)	LOH Freq.(%)
D5S818	N.A.	AGAT	11	intergenic	2/24 (8)	11/19 (58)
D13S317	N.A.	TATC	11	intergeneic	0/24	5/21 (24)
KMO	N	TAGA	19	3'	2/24 (8)	6/17 (35)
D21S11	N.A.	TAGA	11	intergenic	6/24 (25)	10/15 (67)
DAP3	Y	AAAT	10	3'	2/23 (9)	0/13
TBX19	Y	AAAG	6	3'	0/24	2/19 (11)
SHROOM4	N	AAAG	15	3'	0/23	0/3
ORC6L	Y	TAGA	13	3'	0/24	3/8 (38)
TPOX	N.A.	TGAA	8	intron	1/24 (4)	2/14 (14)
NHLH1	Y	TTTA	13	3'	0/24	0/11
C20ORF56	N	AAAG	14	3'	1/24 (4)	1/13(8)
PMP2	N	TAGA	14	3'	0/24	0/0
SNX1	Y	GATA	16	3'	1/23 (4)	4/13 (31)
D2S1338	N.A.	AAGG	13	intergenic	2/24 (8)	0/15
D9S303	N.A.	GATA	12	intron	1/24 (4)	13/16 (81)
SNX27	N	AAAG	20	3'	0/27	1/5 (20)
D8S1179	N.A.	TAGA	11	intron	1/24 (4)	9/17 (53)
PLEKHG4B	N	TAGA	10	3'	0/24	2/13 (15)
KANK2	N	GGAT	13	3'	1/24 (4)	8/17 (47)
PLCXD3	N	GGAA	12	3'	0/24	7/19 (37)
ZFR2	N	CAAA	9	3'	0/24	0/0
RTKN2	N	AAGG	16	3'	1/20 (5)	4/14 (29)
C19orf2(D19S433)	N.A.	AGGA	13	intron	1/24 (4)	5/19 (26)
CDH1	Y	AAAG	20	intron	2/24 (8)	3/17 (18)

Genes with trinucleotide repeats (64 genes)

Gene	Cancer[a]	Repeats	No. Unit	Position	Frame-shifts Freq.(%)[b]	LOH Freq.(%)
WIPF2	Y	CGG	9	5'	3/24 (13)	1/4 (25)
KDM6B	Y	CCA	12	exon	0/24	5/7 (71)
SMARCA2	Y	CAG	20	exon	0/24	8/13 (62)
BCL6B	Y	CAG	9	exon	0/24	9/10 (90)
NADK	N	GGA	8	exon	0/20	3/9 (33)
UBE2B	Y	CGG	10	5'	0/19	2/6 (33)
PRKCSH	N	GAG	19	exon	1/23 (4)	3/9 (33)
KCNN3	Y	CAG	13, 14	exon	2/24 (8)	3/13 (23)
GABRA4	N	AAT	14	3'	0/20	2/10 (20)
MTMR9	N	GTT	8	3'	0/24	2/8 (25)
DMPK	Y	CAG	20	3'	0/21	2/12 (17)
GRIK2	Y	AAT	14	3'	0/21	0/0
PDCD1	Y	CAG	10	3'	0/24	1/3 (33)
SPRY4	Y	AAC	10	3'	0/24	0/11
PRDM10	N	AAG	10	3'	0/23	6/15 (40)
HERC5	N	AAC	9	3'	0/24	0/0
ARCN1	N	ATT	9	3'	0/22	0/0
ZNF516	N	AAC	9	3'	0/22	8/17 (47)
ZNF790	N	CAG	9	3'	0/22	0/8
SIRPA	Y	ACC	9	3'	0/22	0/0
RREB1	Y	ATT	8	3'	0/24	0/2
VKORC1L1	N	ATT	8	3'	0/23	2/13 (15)
NRP2	Y	TAT	10	3'	0/22	3/15 (20)
VANGL2	Y	ATT	10	3'	0/22	1/6 (17)

MOG	N	AAAT	11	3'	2/22 (9)	3/7 (43)
FGA	N	AAAG	14	intron	0/24	4/15 (27)
CRKL	Y	AAC	9	3'	0/22	0/6
HOXB6	Y	GAT	9	3'	0/19	0/0

[a] Y: The locus has been associated with cancer; N: no association has been reported; N.A.:not applicable

[b] Mutation frequency was calculated by dividing the number of mutated cases by the number of informative cases.

Supplementary Table 2. cont. 141 loci examined for FS/LOH in 24 E/L positive LMs

Genes with trinucleotide repeats (64 genes) cont.

Gene	Cancer[a]	Repeats	No. Unit	Posotion	Frame-shifts Freq.(%)[b]	LOH Freq.(%)
PAPSS2	Y	CAG	8	5'	1/23 (4)	0/2
BLMH	Y	CCG	9	5'	0/22	2/8 (25)
MTHFD1L	N	CCG	8	5'	0/24	1/7 (14)
MAB21L1	N	CAG	19	5'	0/23	0/15
GLS	Y	CAG	15	5'	0/23	2/17 (12)
STRC	N	CAG	11	5'	0/24	0/1
GRK5	Y	CGG	9	5'	0/22	0/0
GALNT5	N	CAG	8	5'	0/22	0/0
BPGM	N	CAG	8	5'	0/22	0/0
TRHDE	N	AGG	8	5'	0/21	0/2
MAF2	Y	CGG	8	5'	0/24	6/17 (35)
PCTK3	Y	AGG	8	5'	0/24	4/14 (29)
STC1	Y	CAG	6	3'	0/24	0/0
YEATS2	N	GGA	9	exon	0/24	2/12 (17)
TNRC6B	Y	CAG	8	exon	1/24 (4)	0/8
DACH1	Y	CAG	24	exon	1/12 (8)	0/1
NKD2	Y	CAC	9	exon	1/23 (4)	0/2
ASPN	N	TGA	14	exon	0/23	1/15 (7)
ATBF1	Y	GGA	24	exon	0/24	4/18 (22)
C19ORF2	Y	TGA	9	exon	0/23	0/6
CHAC	Y	TGA	11	exon	0/24	0/1
DIAPH1	Y	GGA	11	exon	0/24	1/4 (25)
HTT	N	GCC	10	exon	0/22	0/6
NCOA3	Y	GCA	20	exon	0/23	3/9 (33)
BMP2K	N	CAG	27	exon	0/22	0/0
MN1	Y	CAG	27	exon	0/23	0/4
ZNF384	Y	CAG	16	exon	0/21	0/5
BAIAP1	N	CAG	20	exon	0/24	2/10 (20)
SCA1	Y	CAG	29	exon	2/24 (8)	2/19 (11)
NCOR2	Y	CAG	12	exon	0/24	5/17 (29)
GATA6	Y	CCA	10	exon	0/24	0/0
PLCZ1	Y	GGA	15	exon	0/24	3/8 (38)
ZNF161	N	CAG, CAA	12, 6	exon	3/24 (13)	0/1

EPHB6	Y	AGG	8	exon	0/24	0/0
CBX4	N	GTG	11	exon	0/24	0/2
C14ORF4	N	CAG	21	exon	0/24	1/4 (25)
HRC	N	GAT	13	exon	0/24	5/17 (29)
SNAPC4	N	GCA	9	exon	0/24	0/0

[a] Y: The locus has been associated with cancer; N: no association has been reported; N.A.:not applicable

[b] Mutation frequency was calculated by dividing the number of mutated cases by the number of informative cases.

Supplementary Table 3: Loci associated with E/L in LM from primary CRC

Genes	Cancer[a]	Repeats	No. Unit	Repeats Positin	Gene Location	Frame-shift or LOH Freq. in 24 MSI-L/EMAST LMs (%)[b]	Frame-shift or LOH Freq. in Total LMs (%)[c]	Association with E/L[d]
(MSI Loci)								
RBM47	N	AAAG	16	3'	4p14	9/24 (38)	18/76 (24)	No
D21S11	N.A.	TAGA	11	intergenic	21q21.1	6/24 (25)	12/77 (16)	Yes (0.04)
ANKRD5	N	ATGA, TAGA	5,10	3'	20p12.2	4/24 (17)	13/77 (17)	Yes (0.049)
WIPF2	Y	CGG	9	5'	17q21	3/24 (13)	13/76 (17)	No
ZNF161	N	CAG, CAA	12, 6	exon	17q22	3/24 (13)	4/76(5)	No
(LOH Loci)								
BCL6B	Y	CAG	9	exon	17p13.1	9/10 (90)	24/29 (83)	No
MNT	Y	CA	23	3'	17p13.3	12/14 (86)	40/52 (77)	No
D9S303	N.A.	GATA	12	intron	9q21.32	13/16 (81)	29/54 (54)	No
BCL2 (D18S51)	Y	AAAG	18	intron	18q21.33	15/19 (79)	46/58 (79)	No
KDM6B	Y	CCA	12	exon	17p13.1	5/7 (71)	19/23 (83)	No
D21S11	N.A.	TAGA	11	intergenic	21q21.1	10/15 (67)	32/48 (67)	No
SMARCA2	Y	CAG	20	exon	9p24.3	8/13 (62)	15/39 (38)	Yes (0.017)
SEMA6D	Y	CA	22	3'	15q21.1	11/18 (61)	35/57 (61)	No
STYK1	Y	CA	11	3'	12p13.2	9/15 (60)	20/45 (44)	No
D5S818	N.A.	AGAT	11	intergenic	5q23.2	11/19 (58)	41/61 (67)	No
D8S1179	N.A.	TAGA	11	intron	8q24.13	9/17 (53)	26/55 (47)	No

[a] Each gene locus was examined for its association with cancer by accessing NCBI PubMed data base.

Y: the locus has been associated with cancer; N: no association has been reported. N.A. not applicable.

[b] A mutation frequency was determined in 24 E/L positive LMs by ratio between the number of mutated cases divided by the number of informative cases.

[c] Frame-shift mutation or LOH frequency for each locus was determined in 78 LMs.

[d] P values were obtained by multivariate logistic regression analysis. P values for *D21S11* and *ANKRD5* were obtained by Firth's logistic regression method.

The associations were adjusted by age, sex, LM type (metachronous vs synchronous), primary tumor's grade and sites, and source of samples (DPOHTU vs DPCNU).

Supplementary Table 4: Characteristics of 88 Stage II/III primary CRC that experienced recurrence

	Stage	*KRAS* Mutation	*BRAF* Mutations	9p24$^-$	E/L	E/L/9p24$^-$	Recurence-free survival (months)	Survival		Outcome			No. of	Simulotenous	Adjuvant
primary CRC with	Stage II (2)	positive (+)	positive (+)	positive (+)	positive (+)	positive (+)		after recurrence	Overall survival	Dead (D)	Metachronous	Hepatectomy	Metastasis	metastasis	chemotherapy
recurence	Stage III (3)	negative (-)	negative (-)	negative (-)	negative (-)	negative (-)		(months)	(months)	alive (A)	LM (L) or other	yes (Y), no (N)	0: <3, 1: ≥3	yes (Y), no (N)	yes (Y), no (N)
59T	3	-	-	+	+	+	13	47	60	A	L	Y	0	N	Y
61T	3	+	-	+	+	+	9	51	60	A	L	Y	0	Y	Y
78T	3	-	-	+	+	+	33	12	45	D	L	Y	0	N	Y
80T	3	-	-	+	+	+	16	44	60	A	L	Y	0	N	Y
122T	3	-	-	+	+	+	8	35	43	D	L	Y	0	N	Y
110T	3	-	-	+	+	+	3	57	60	A	L	Y	0	N	Y
77T	2	-	-	+	+	+	11	49	60	A	L	Y	0	N	Y
63T	2	+	-	+	+	+	13	47	60	A	L	Y	0	N	Y
65T	3	+	-	+	+	+	31	2	33	A	L	N	1	N	Y
123T	3	-	-	+	+	+	40	20	60	A	L	N	1	Y	Y
155T	3	-	-	+	+	+	11	9	20	D	lung	N.A	1	N	Y
2T	3	+	-	+	+	+	42	17	59	D	lung	N.A	1	Y	Y
168T	2	-	-	+	+	+	14	31	45	D	lung	N.A	1	N	Y
27T	3	+	-	+	+	+	33	27	60	A	lung	N.A	1	N	Y
4026	3	-	-	+	+	+	5	38	43	D	lung	N.A	1	N	N
776	3	-	-	+	+	+	9	1	10	A	lung	N.A	0	N	Y
2303	3	-	-	+	+	+	21	39	60	A	lung	N.A	0	N	Y
3634	3	-	-	+	+	+	12	48	60	A	lung	N.A	0	N	N
944	3	-	-	+	+	+	5	19	24	A	lung	N.A	0	N	Y
1105	3	+	-	+	+	+	6	5	11	A	lung	N.A	0	Y	N
1024	3	+	-	+	+	+	11	3	14	A	ovary	N.A	0	N	N
3873	2	-	-	+	+	+	44	16	60	A	peritoneal	N.A	0	N	Y
1101	3	-	-	+	+	+	7	28	35	D	peritoneal	N.A	0	Y	Y
108T	3	-	-	+	+	+	10	50	60	A	pelvic	N.A	0	N	Y
56	2	-	-	+	+	+	11	37	48	D	pelvic	N.A	0	N	N
810	2	+	+	+	+	+	13	13	26	D	para-aortic nodes	N.A	1	Y	N
2781	2	+	-	+	+	+	13	47	60	A	anastomotic site	N.A	0	N	N
948	3	-	-	+	+	+	5	18	23	A	anastomotic site	N.A	0	Y	Y
69T	3	-	-	+	+	+	18	42	60	A	T8 vertebra	N.A	0	N	Y
104T	2	-	-	+	+	+	10	50	60	A	rectum	N.A	0	N	Y
13T	2	-	-	+	+	+	16	44	60	A	colon	N.A	0	N	Y
19T	3	-	-	-	+	-	14	1	15	D	L	N	1	Y	N
23T	3	+	-	-	+	-	12	21	33	D	L	N	1	N	Y
82T	3	+	-	-	+	-	6	10	16	D	L	N	1	N	Y
119T	3	-	-	-	+	-	7	6	13	D	L	N	1	N	Y
132T	3	-	-	-	+	-	18	23	41	D	L	N	1	Y	Y
20T	2	-	-	-	+	-	51	9	60	A	L	N	1	Y	Y

25T	2	-	-	-	+	-	10	17	27	D	L	N	1	Y	Y
81T	3	-	-	-	+	-	18	36	54	D	L	N	0	Y	Y
113T	3	+	-	-	+	-	12	6	18	D	L	N	0	Y	Y
115T	3	+	-	-	+	-	8	9	17	D	L	N	0	Y	Y
56T	3	-	-	-	+	-	12	11	23	D	L	N	0	N	N
58T	3	-	-	-	+	-	4	37	41	A	L	N	0	N	N
84T	2	-	-	-	+	-	8	46	54	D	L	Y	0	N	Y
76T	3	-	-	-	+	-	47	13	60	D	L	N	0	Y	Y
121T	2	-	-	-	+	-	15	45	60	A	L	Y	1	N	Y

Supplementary Table 4 cont.

Stage II/III	Stage	*KRAS* Mutation	*BRAF* Mutations	9p24.2 LOH	E/L	E/L/9p24$^-$	Recurence-free survival (months)	Survival after recurrence (months)	Overall survival (months)	Outocome	Metachronous	Hepatectomy	No. of Metastasis	Simulotenous metastasis	Adjuvant chemotherapy
primary CRC with	Stage II (2)	positive (+)	positive (+)	positive (+)	positive (+)	positive (+)				Dead (D)					
recurence	Stage III (3)	negative (-)	negative (-)	negative (-)	negative (-)	negative (-)				alive (A)	LM (L) or other	yes (Y), no (N)	0: <3, 1: ≥3	yes (Y), no (N)	yes (Y), no (N)
118T	3	-	-	-	+	-	1	22	23	D	L	N	1	N	Y
109T	3	-	-	-	+	-	42	14	56	A	L	N	0	N	N
503	3	-	-	-	+	-	20	1	21	D	L	N	1	N	Y
83T	3	+	-	-	-	-	2	20	22	D	L	N	0	Y	Y
85T	3	-	-	-	-	-	11	22	33	D	L	N	0	Y	Y
86T	3	-	-	-	-	-	7	20	27	D	L	N	1	N	Y
87T	3	+	-	-	-	-	15	14	29	D	L	N	0	N	Y
112T	3	+	-	-	-	-	37	23	60	A	L	N	0	N	Y
116T	3	-	-	+	-	-	10	17	27	D	L	N	1	Y	Y
117T	3	+	-	+	-	-	15	36	51	D	L	N	0	N	Y
21T	3	+	-	+	-	-	6	3	9	D	L	N	0	Y	Y
29T	3	+	-	+	-	-	16	15	31	D	L	Y	0	Y	Y
67T	3	-	-	+	-	-	28	9	37	A	L	N	0	Y	Y
60T	3	+	-	+	-	-	11	39	50	D	L	N	0	N	Y
111T	3	-	-	+	-	-	7	28	35	D	L	Y	0	N	Y
525	3	+	-	+	-	-	21	20	41	A	L	N	0	N	Y
1045	3	+	-	+	-	-	8	4	12	A	L	N	1	N	N
16T	3	-	+	-	-	-	8	1	9	D	L	N	1	Y	Y
126T	3	-	-	-	-	-	12	11	28	D	L	N	1	Y	Y
144T	3	-	-	-	-	-	36	6	42	D	L	N	1	Y	Y
22T	2	-	-	-	-	-	43	14	57	D	L	N	1	Y	Y
114T	2	-	-	-	-	-	40	9	49	D	L	N	0	Y	Y
44T	2	-	-	-	-	-	25	33	58	A	L	Y	0	N	Y
935	3	-	-	-	-	-	8	12	20	D	L	N	1	N	Y
1018	3	-	-	-	-	-	7	28	35	D	L	N	0	N	Y
31T	3	-	-	-	+	-	16	37	53	A	lung	N.A	0	N	Y
603	3	-	-	-	+	-	3	28	31	D	lung	N.A	0	N	Y
47T	3	+	-	-	-	-	15	36	51	D	lung	N.A	1	N	Y
5195	2	+	-	-	-	-	23	37	60	A	lung	N.A	0	N	Y
610	3	-	-	-	-	-	11	33	44	D	lung	N.A	0	N	N

SUPPLEMENTARY MATERIALS: TABLES

717	**3**	**-**	**-**	**-**	**-**	**-**	**14**	**11**	**25**	**D**	**lung**	**N.A**	**0**	**N**	**Y**
947	**3**	**+**	**-**	**-**	**-**	**-**	**7**	**30**	**37**	**D**	**lung**	**N.A**	**0**	**N**	**Y**
1066	**2**	**-**	**-**	**+**	**-**	**-**	**14**	**38**	**52**	**D**	**lung**	**N.A**	**0**	**N**	**Y**
1002	**3**	**-**	**-**	**+**	**-**	**-**	**18**	**5**	**23**	**A**	**lung**	**N.A**	**0**	**N**	**Y**
518	**2**	**-**	**-**	**+**	**-**	**-**	**21**	**23**	**44**	**A**	**lung**	**N.A**	**0**	**N**	**Y**
1039	**2**	**+**	**-**	**-**	**+**	**-**	**10**	**3**	**13**	**A**	**peritoneal**	**N.A**	**0**	**N**	**Y**
801	**3**	**+**	**-**	**-**	**+**	**-**	**21**	**17**	**38**	**A**	**ovary**	**N.A**	**0**	**Y**	**Y**
51T	**2**	**+**	**-**	**-**	**-**	**-**	**41**	**15**	**56**	**A**	**prostatal**	**N.A**	**0**	**N**	**Y**
41T	**3**	**+**	**-**	**-**	**-**	**-**	**18**	**2**	**20**	**D**	**pelvic and other**	**N.A**	**1**	**Y**	**Y**
1023	**3**	**-**	**-**	**-**	**-**	**-**	**12**	**28**	**40**	**D**	**para-aortic nodes**	**N.A**	**0**	**N**	**Y**
617	**3**	**-**	**-**	**-**	**+**	**-**	**24**	**10**	**34**	**A**	**rectum**	**N.A**	**1**	**Y**	**Y**
2295	**3**	**-**	**-**	**-**	**-**	**-**	**1**	**21**	**22**	**D**	**rectum**	**N.A**	**0**	**N**	**Y**
Average							**16**	**23**	**39**						

Supplementary Table 5 Clinico-pathological characteristics and genetic alterations of 50 primary CRC that gave rise to LMs

			Association with[b]			
Variables[a]		**Number of Cases**	**E/L (O.R.)**	**$9p24^-$ (O.R.)**	**$E/L/9p24^-$ (O.R.)**	**KRAS/BRAF (O.R.)**
Age	≤62 vs >62	29 vs 21	0.66	0.25	0.13	0.93
Sex	Female vs Male	19 vs 31	0.7	0.89	0.56	0.12
Stage	II vs III	9 vs 41	0.48	0.29	0.85	0.14
Tumor Grade	G1 vs G2&G3	13 vs 37	0.86	0.21	0.63	**0.04 (9.14)**
Tumor Sites	Proximal vs Distal	8 vs 42	0.07	0.45	0.57	0.82
Tumor Type	Colon vs Rectum	21 vs 29	0.11	0.56	0.39	0.6
Hepatectomy	No vs Yes	35 vs 15	0.32	**0.002 (9.28)**	**0.001 (18.85)**	0.48
Sample Source	Mie (DPMU) vs Korea (DPCNU)	5 vs 45	0.12	0.9	1	0.77
Adjuvant Chemotherapy	No vs Yes	5 vs 45	0.28	0.4	1	0.5
MSI Status	E/L vs MS	22 vs 28	N.A.	0.7	N.A.	0.13
9p24.2 LOH status	$9p24^-$ vs $9p24^+$	19 vs 31	0.7	N.A.	N.A.	0.12
$E/L/9p24.2^-$	No vs Yes	40 vs 10	N.A.	N.A.	N.A.	0.77
KRAS/BRAF Mutations	No vs Yes	33 vs 17	0.13	0.12	0.77	N.A.
RFS	≤17 vs >17	36 vs 14	0.59	0.84	0.87	0.25
SFR	≤19 vs >19	30 vs 20	0.3	**0.01 (4.93)**	**0.01 (9.33)**	0.63
OS	≤36 vs >36	25 vs 25	0.09	0.15	**0.02 (13.5)**	0.14
Simulotaneous Metastasis	No vs Yes	30 vs 20	0.2	0.12	0.057	0.63
Number of Metastasis	≤3 vs >3	33 vs 17	0.77	0.14	0.31	0.62
Liver Lobe affected	One vs Two	30 vs 20	**0.03 (3.92)**	0.34	0.47	0.63
Aggressiveness	No vs Yes	23 vs 27	0.52	0.06	**0.03 (0.15)**	0.62
LM recurrence after hepatectomy	No vs Yes	42 vs 8	0.69	0.45	0.19	0.99

[a] The average years of age in this cohort was 62, which was used as a cut-off criteria for dividing a chort into 2 groups according to the age. The avarage months of RFS, SFR and OS was 17, 19 and 36 months respectively and was used as a cut-off criteria for dividing a cohort into 2 groups.

[b] To determine the association between 2 variables, an univariate logistic regression analysis was used. The each number represents a p value.

When p value is less than 0.05, the association is considered to be a significant (underlined bolted numbers). N.A.: Not applicable. O.R.: Odds Ratio.

Supplementary Table 6: 67 Stage II/III primary CRC without recurrence from DPCNU

Stage II/III Primary CRC	Stage	*KRAS* Mutation	*BRAF* Mutations	$9p24.2^-$	E/L	E/L/$9p24.2^-$	Recurrence-	
without recurence	Stage II (2) Stage III (3)	positive (+) negative (-)	positive (+) negative (-)	positive (+) negative (-)	positive (+) negative (-)	positive (+) negative (-)	free survival (months)	Dead/alive
161T	3	+	-	+	+	+	60	A
106T	3	-	-	+	+	+	60	A
34T	3	+	-	+	+	+	60	A
98T	3	+	-	+	+	+	60	A
3T	3	-	-	+	+	+	60	A
10T	3	+	-	+	+	+	60	A
75T	2	-	-	+	+	+	60	A
165T	2	-	-	+	+	+	0	A
143T	2	+	-	+	+	+	23	A
40T	2	-	-	+	+	+	60	A
49T	2	-	-	+	+	+	17	A
125T	2	-	-	+	+	+	35	A
151T	2	-	-	+	+	+	60	A
152T	2	-	-	+	+	+	58	A
50T	3	-	-	+	-	-	38	A
131T	3	+	-	+	-	-	60	A
105T	3	+	-	+	-	-	60	A
164T	2	-	-	+	-	-	60	A
134T	2	+	-	+	-	-	59	A
127T	2	+	-	+	-	-	57	A
129T	2	-	-	+	-	-	59	A
11T	2	-	-	+	-	-	60	A
145T	2	+	-	+	-	-	39	A
24T	2	-	-	-	+	-	60	A
71T	2	-	-	-	+	-	54	A
139T	2	+	-	-	+	-	44	A
142T	2	-	-	-	+	-	60	A
88T	2	+	-	-	+	-	60	A
158T	2	+	-	-	+	-	37	A
162T	3	-	-	-	+	-	1	A
166T	3	-	-	-	+	-	23	A
171T	3	-	-	-	+	-	60	A
154T	3	-	-	-	+	-	55	A
72T	3	+	-	-	+	-	9	A
90T	2	+	-	-	-	-	60	A
99T	2	+	-	-	-	-	0	A
7T	2	-	-	-	-	-	60	A
42T	2	-	-	-	-	-	59	A
45T	2	-	-	-	-	-	48	A
130T	2	+	-	-	-	-	47	A
148T	2	-	-	-	-	-	60	A
64T	2	+	-	-	-	-	60	A
68T	2	-	-	-	-	-	3	A
70T	2	+	-	-	-	-	13	A
100T	2	+	-	-	-	-	60	A
107T	2	-	-	-	-	-	48	A
136T	2	+	-	-	-	-	11	A
141T	2	-	-	-	-	-	60	A
160T	2	+	-	-	-	-	60	A
33T	3	-	-	-	-	-	60	A
170T	3	+	-	-	-	-	0	A
66T	3	-	-	-	-	-	29	A
35T	3	+	-	-	-	-	58	A
36T	3	-	-	-	-	-	0	A
52T	3	-	-	-	-	-	60	A
128T	3	-	-	-	-	-	58	A
156T	3	-	-	-	-	-	60	A
157T	3	-	-	-	-	-	58	A
30T	3	+	-	-	-	-	60	A
89T	3	-	-	-	-	-	50	A
8T	3	-	-	-	-	-	59	A
147T	3	-	-	-	-	-	60	A
48T	2	-	-	-	-	-	60	A

101T	3	-	-	-	+	-	2	A
95T	3	+	-	-	+	-	54	A
53T	3	+	-	-	+	-	60	A
79T	2	-	-	-	+	-	60	A

Supplementary Table 7

A: 61 cases of LMs

	No. of Cases with			
	E/L/9p24^{-}	non-E/L/9p24^{-}	Total	P value
mutated: *KRAS/BRAF* (%)	10/1 (32%)	9/1*	20	
no mutation in both	23	18	41	0.93
Total	34	27	61	

*One case had both KRAS and BRAF mutations

B: 61 cases of matched primary CRC

	No. of Cases with			
	E/L/9p24^{-}	non-E/L/9p24^{-}	Total	P value
mutated: *KRAS/BRAF* (%)	9/1 (37%)	8/1	18	
no mutation in both	17	26	43	0.33
Total	27	34	61	

C: 67 cases of Stage III primary CRC with recurrence

	No. of Cases with			
	E/L/9p24^{-}	non-E/L/9p24^{-}	Total	P value
mutated: *KRAS/BRAF* (%)	6/0 (18%)	17/1	24	
no mutation in both	16	27	43	0.31
Total	34	27	67	

D: 74 cases of Stage III primary CRC with and without recurrence

	No. of Cases with			
	E/L/9p24^{-}	non-E/L/9p24^{-}	Total	P value
mutated: *KRAS/BRAF* (%)	8/0 (42%)	21/1	30	
no mutation in both	11	33	44	0.87
Total	19	55	74	