

**Supplementary Table 1 List of polymorphisms analyzed in this study and its dbSNP, primers sequence, and amplicon length**

Gene [variation bp]	dbSNP	Primers sequence (5'-3')	Amplicon length
ACE [288 bp]	rs4646994	F - ATCCTGTAAGCCACTGCTGGA R - GGCAGAACACATAAAAGTGA	94-382 bp
CASP8 [6 bp]	rs3834129	F - CTCTTCAATGCTTCCTTGAGGT R- TGCATGCCAGGAGCTAAGTAT	249-255 bp
SGSM3 [4 bp]	rs56228771	F - CTAGTAGGCTCCTGGCCTCTT R- CAGAACCTGGACCTGAATAC	117-121 bp
CYP2E1 [96 bp]	-	F- GTCCCAATAACAGTCACCTCTT R- GGCTTTATTGTTTGATCTG	397-493 bp
CYP19A1 [3 bp]	rs28892005	F- TGCATGAGAAAGGCATCATATT R- AGGCACATTCATAGACAAAAAA	122-125 bp
HLAG [14 p]	rs371194629	F- TGTTAAAGTGTCACCCCCTCAC R - CAGTCAGCATGAGGAAGAGG	192-206 bp
IL1A [4 bp]	rs3783553	F - TGGTCCAAGTTGTGCTTATCC R - ACAGTGGTCTCATGGTTGTCA	230-234 bp
IL4 [70 bp]	rs79071878	F - GGGTCAGTCTGGCTACTGTGT R - AAATCTGTTCACCTCAACTGC	217-287 bp
MDM2 [40 bp]	rs3730485	F - GGAAGTTCCCTTCTGGTAGGC R - TTTGATGCGGTCTCATAAATTG	192-232 bp
NFKB1 [4 bp]	rs28362491	F - ATGGACCGCATGACTCTATCA R - GGCTCTGGCATCCTAGCAG	366-370 bp
TP53 [16 bp]	rs17878362	F - GGGACTGACTTCTGCTCTGT R- GGACTGTAGATGGGTGAAAAG	148-164 bp
TP53 [6 bp]	rs17880560	F - TCCATTCAAACTCAGGAACCA R - TTAAATCCCGTAATCCTTGGTG	135-141 bp
TYMS [6 bp]	rs151264360	F- TCCAAACCAGAACATACAGCACA R- TCAAATCTGAGGGAGCTGAGT	213-219 bp
UCP2 [45 bp]	-	F - CCCACACTGTCAAATGTCAACT R - CCATGCTTCCCTTTCTTCCT	119-164 bp
UGT1A1 [2 bp]	rs8175347	F - CTCTGAAAGTGAACCTCCCTGCT R - AGAGGTTGCCCTCTCCTAT	135-137 bp
XRCC1 [4 bp]	rs3213239	F- AACCAGAACATCCAAAAGTGACC R- GGGAAAGAGAGAGAAGGAGAG	243-247 bp

dbSNP: Register of genetic variation; bp: Base pairs; F: Forward; R: Reverse.

**Supplementary Table 2 The logistic regression analyses between case-control and insertion-deletions polymorphism**

Gene	Genotype	Control	Case	OR [95%CI]	P value	power
ACE	Codominant	n = 140	n = 138			
	Del/Del	44 (31.4)	41 (29.7)	1 [Reference]	0.1790	0.373
	Del/Ins	76 (54.3)	68 (49.3)	1.24 [0.59-2.64]		
	Ins/Ins	20 (14.3)	29 (21.0)	2.37 [0.63-6.21]		
	Dominant					
	Del/Del	44 (31.4)	41 (29.7)	1 [Reference]	0.2920	0.19
	Del/Ins + Ins/Ins	96 (68.6)	97 (70.3)	1.46 [0.72-3.02]		
	Recessive					
	Del/Del + Del/Ins	120 (85.7)	109 (79.0)	1 [Reference]	0.0770	0.42
	Ins/Ins	20 (14.3)	29 (21.0)	2.05 [0.92-4.62]		
CASP8	log-Additive			1.51 [0.95-2.45]	0.0840	0.422
	Codominant	n = 140	n = 139			
	Ins/Ins	42 (30.0)	48 (34.5)	1 [Reference]	0.4670	0.183
	Del/Ins	65 (46.4)	64 (46.0)	0.90 [0.40-1.97]		
	Del/Del	33 (23.6)	27 (19.4)	1.42 [0.59-3.50]		
	Dominant					
	Ins/Ins	42 (30.0)	48 (34.5)	1 [Reference]	0.2290	0.228
	Del/Ins + Del/Del	98 (70.0)	91 (65.2)	1.54 [0.77-3.16]		
	Recessive					
	Ins/Ins + Del/Ins	107 (76.4)	112 (80.6)	1 [Reference]	0.8820	0.057
SGSM3	Del/Del	33 (23.6)	27 (19.4)	1.06 [0.50-2.22]		
	log-Additive			1.21 [0.78-1.89]	0.3970	0.142
	Codominant	n = 140	n = 139			
	Del/Del	84 (60.0)	87 (62.6)	1 [Reference]	0.8250	0.095
	Del/Ins	51 (36.4)	42 (30.2)	0.81 [0.42-1.57]		
	Ins/Ins	5 (3.6)	10 (7.2)	0.93 [0.21-4.37]		
	Dominant					
	Del/Del	84 (60.0)	87 (62.6)	1 [Reference]	0.5510	0.092
	Del/Ins + Ins/Ins	56 (40.0)	52 (37.4)	0.82 [0.43-1.55]		
	Recessive					
IL10	Del/Del + Del/Ins	135 (96.4)	129 (92.8)	1 [Reference]	0.9950	0.06
	Ins/Ins	5 (3.6)	10 (7.2)	1.01 [0.23-4.64]		
	log-Additive			0.87 [0.51-1.49]	0.6190	0.085

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**Supplementary Table 2 The logistic regression analyses between case-control and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Control	Case	OR [95%CI]	P value	Power
CYP19A1	Codominant	<i>n</i> = 140	<i>n</i> = 137			
	Ins/Ins	53 (37.9)	49 (35.8)	1 [Reference]	0.9750	0.061
	Del/Ins	70 (50.0)	68 (49.6)	1.11 [0.42-2.87]		
	Del/Del	17 (12.1)	20 (14.6)	1.06 [0.38-2.89]		
	Dominant					
	Ins/Ins	53 (37.9)	49 (35.8)	1 [Reference]	0.9410	0.053
	Del/Ins + Del/Del	87 (62.1)	88 (64.2)	0.98 [0.50-1.89]		
	Recessive					
	Ins/Ins + Del/Ins	123 (87.9)	117 (85.4)	1 [Reference]	0.8550	0.059
	Del/Del	17 (12.1)	20 (14.6)	1.09 [0.43-2.70]		
CYP2E1	log-Additive			1.01 [0.63-1.63]	0.9670	0.051
	Codominant	<i>n</i> = 140	<i>n</i> = 139			
	Del/Del	121 (86.4)	114 (82.0)	1 [Reference]	0.4880	0.196
	Del/Ins	18 (12.9)	24 (17.3)	1.68 [0.70-4.07]		
	Ins/Ins	1 (0.7)	1 (0.7)	0.73 [0.03-20.25]		
	Dominant					
	Del/Del	121 (86.4)	114 (82.0)	1 [Reference]	0.2850	0.192
	Del/Ins + Ins/Ins	19 (13.6)	25 (18.0)	1.59 [0.68-3.76]		
	Recessive					
	Del/Del + Del/Ins	139 (99.3)	138 (99.3)	1 [Reference]	0.7730	-
HLAG	Ins/Ins	1 (0.7)	1 (0.7)	0.65 [0.02-17.96]		
	log-Additive			1.43 [0.66-3.20]	0.3700	0.151
	Codominant	<i>n</i> = 140	<i>n</i> = 136			
	Del/Del	51 (36.4)	57 (41.9)	1 [Reference]	0.3540	0.246
	Del/Ins	70 (50.0)	59 (43.4)	0.68 [0.34-1.35]		
	Ins/Ins	19 (13.6)	20 (14.7)	1.24 [0.48-3.22]		
	Dominant					
	Del/Del	51 (36.4)	57 (41.9)	1 [Reference]	0.4750	0.11
	Del/Ins + Ins/Ins	89 (63.6)	79 (58.1)	0.79 [0.42-1.50]		
	Recessive					
CYP19A1	Del/Del + Del/Ins	121 (86.4)	116 (85.3)	1 [Reference]	0.3470	0.17
	Ins/Ins	19 (13.6)	20 (14.7)	1.52 [0.63-3.67]		
	log-Additive			0.99 [0.63-1.56]	0.9820	0.052

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**Supplementary Table 2 The logistic regression analyses between case-control and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Control	Case	OR [95%CI]	P value	power
<i>IL1A</i>	Codominant	<i>n</i> = 140	<i>n</i> = 139			
	Ins/Ins	73 (52.1)	64 (46.0)	1 [Reference]	0.1070	0.46
	Del/Ins	53 (37.9)	54 (38.8)	3.01 [1.08-8.73]		
	Del/Del	14 (10.0)	21 (15.2)	2.43 [0.91-6.70]		
	Dominant					
	Ins/Ins	73 (52.1)	64 (46.0)	1 [Reference]	0.8350	0.054
	Del/Ins + Del/Del	67 (47.9)	75 (54.0)	1.07 [0.57-1.99]		
	Recessive					
	Ins/Ins + Del/Ins	126 (90.0)	118 (84.8)	1 [Reference]	0.0430	0.533
	Del/Del	14 (10.0)	21 (15.2)	2.65 [1.03-7.04]		
<i>IL4</i>	log-Aditive			1.29 [0.82-2.03]	0.2660	0.198
	Codominant	<i>n</i> = 140	<i>n</i> = 139			
	Ins/Ins	84 (60.0)	68 (48.9)	1 [Reference]	< 0.0001	0.983
	Del/Ins	52 (37.1)	56 (40.3)	16.03 [3.69-86.64]		
	Del/Del	4 (2.9)	15 (10.8)	25.30 [5.91-135.27]		
	Dominant					
	Ins/Ins	84 (60.0)	68 (48.9)	1 [Reference]	0.0110	0.712
	Del/Ins + Del/Del	56 (40.0)	71 (51.1)	2.26 [1.20-4.31]		
	Recessive					
	Ins/Ins + Del/Ins	136 (97.1)	1124 (89.2)	1 [Reference]	< 0.0001	0.986
<i>MDM2</i>	Del/Del	4 (2.9)	15 (10.8)	20.92 [5.04-109.08]		
	log-Aditive			2.73 [1.62-4.72]	0.0001	0.964
	Codominant	<i>n</i> = 140	<i>n</i> = 139			
	Ins/Ins	71 (50.7)	70 (50.4)	1 [Reference]	0.4330	0.205
	Del/Ins	52 (37.1)	60 (43.2)	0.51 [0.16-1.53]		
	Del/Del	17 (12.2)	9 (6.5)	0.68 [0.21-2.02]		
	Dominant					
	Ins/Ins	71 (50.7)	70 (50.4)	1 [Reference]	0.6120	0.084
	Del/Ins + Del/Del	69 (49.3)	69 (49.6)	1.17 [0.63-2.20]		
	Recessive					
	Ins/Ins + Del/Ins	123 (87.8)	130 (93.5)	1 [Reference]	0.3370	0.167
	Del/Del	17 (12.1)	9 (6.5)	0.60 [0.19-1.69]		
	log-Aditive			0.99 [0.62-1.57]	0.9600	0.054

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**Supplementary Table 2 The logistic regression analyses between case-control and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Control	Case	OR [95%CI]	P value	power
NFKB1	Codominant	n = 140	n = 139			
	Ins/Ins	57 (40.7)	53 (38.1)	1 [Reference]	0.9480	0.06
	Del/Ins	59 (42.1)	64 (46.0)	1.02 [0.41-2.49]		
	Del/Del	24 (17.1)	22 (15.8)	0.91 [0.36-2.27]		
	Dominant					
	Ins/Ins	57 (40.7)	53 (38.1)	1 [Reference]	0.7440	0.064
	Del/Ins + Del/Del	83 (59.3)	86 (61.9)	0.90 [0.47-1.71]		
	Recessive					
	Ins/Ins + Del/Ins	116 (82.9)	117 (84.2)	1 [Reference]	0.9350	0.055
	Del/Del	24 (17.1)	22 (15.8)	0.97 [0.41-2.23]		
TP53 13 bp	log-Aditive			0.94 [0.60-1.47]	0.7890	0.06
	Codominant	n = 140	n = 139			
	Del/Del	93 (66.4)	96 (69.1)	1 [Reference]	0.8240	0.095
	Del/Ins	45 (32.2)	38 (27.3)	1.22 [0.62-2.41]		
	Ins/Ins	2 (1.4)	5 (3.6)	0.82 [0.12-7.33]		
	Dominant					
	Del/Del	93 (66.4)	96 (69.1)	1 [Reference]	0.6210	0.081
	Del/Ins + Ins/Ins	47 (33.6)	43 (30.9)	1.18 [0.61-2.29]		
	Recessive					
	Del/Del + Del/Ins	138 (98.6)	134 (96.4)	1 [Reference]	0.8010	-
TP53 6 bp	Ins/Ins	2 (1.4)	5 (3.6)	0.77 [0.11-6.88]		
	log-Aditive			1.12 [0.62-2.03]	0.7130	0.069
	Codominant	n = 140	n = 139			
	Del/Del	84 (60.0)	74 (53.2)	1 [Reference]	0.2560	0.303
	Del/Ins	46 (32.9)	55 (39.6)	1.69 [0.87-3.33]		
	Ins/Ins	10 (7.1)	10 (7.2)	0.88 [0.25-2.89]		
	Dominant					
	Del/Del	84 (60.0)	74 (53.2)	1 [Reference]	0.2000	0.252
	Del/Ins + Ins/Ins	56 (40.0)	65 (46.8)	1.50 [0.81-2.83]		
	Recessive					
TP53 6 bp	Del/Del + Del/Ins	130 (92.9)	129 (92.8)	1 [Reference]	0.5870	0.096
	Ins/Ins	10 (7.1)	10 (7.2)	0.72 [0.22-2.31]		
	log-Aditive			1.21 [0.74-1.97]	0.4410	0.127

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**Supplementary Table 2 The logistic regression analyses between case-control and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Control	Case	OR [95%CI]	P value	power
TYMS	Codominant	n = 140	n = 139			
	Ins/Ins	60 (42.9)	64 (46.0)	1 [Reference]	0.0330	0.642
	Del/Ins	59 (42.1)	61 (43.9)	0.29 [0.09-0.89]		
	Del/Del	21 (15.0)	14 (10.1)	0.23 [0.07-0.71]		
	Dominant					
	Ins/Ins	60 (42.9)	64 (46.0)	1 [Reference]	0.1500	0.309
	Del/Ins + Del/Del	80 (57.1)	75 (54.0)	0.63 [0.33-1.18]		
	Recessive					
	Ins/Ins + Del/Ins	119 (85.0)	125 (89.9)	1 [Reference]	0.0120	0.715
	Del/Del	21 (15.0)	14 (10.1)	0.26 [0.08-0.75]		
UCP2	log-Additive			0.58 [0.35-0.93]	0.0250	0.621
	Codominant	n = 140	n = 136			
	Del/Del	65 (46.4)	79 (58.1)	1 [Reference]	0.0700	0.526
	Del/Ins	62 (44.3)	48 (35.3)	0.47 [0.24-1.91]		
	Ins/Ins	13 (9.3)	9 (6.6)	0.51 [0.14-1.70]		
	Dominant					
	Del/Del	65 (46.4)	79 (58.1)	1 [Reference]	0.0210	0.629
	Del/Ins + Ins/Ins	75 (53.6)	57 (41.9)	0.48[0.25-0.90]		
	Recessive					
UGT1A1	Del/Del + Del/Ins	127 (90.7)	127 (93.4)	1 [Reference]	0.5660	0.097
	Ins/Ins	13 (9.3)	9 (6.6)	0.71 [0.20-2.26]		
	log-Additive			0.58 [0.34-0.97]	0.0380	0.546
	Codominant	n = 139	n = 139			
	Del/Del	60 (43.2)	61 (43.9)	1 [Reference]	0.6930	0.124
	Del/Ins	64 (46.0)	62 (44.6)	0.75 [0.39-1.46]		
	Ins/Ins	15 (10.8)	16 (11.5)	0.95 [0.31-2.81]		
	Dominant					
	Del/Del	60 (43.2)	61 (43.9)	1 [Reference]	0.4520	0.116
	Del/Ins + Ins/Ins	79 (56.8)	78 (56.1)	0.79 [0.41-1.47]		
	Recessive					
	Del/Del + Del/Ins	124 (89.2)	123 (88.5)	1 [Reference]	0.8600	0.062
	Ins/Ins	15 (10.8)	16 (11.5)	1.10 [0.38-3.07]		
	log-Additive			0.89 [0.54-1.43]	0.6220	0.08

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**Supplementary Table 2 The logistic regression analyses between case-control and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Control	Case	OR [95%CI]	P value	power
XRCC1	Codominant	<i>n</i> = 140	<i>n</i> = 139			
	Ins/Ins	60 (42.9)	58 (41.7)	1 [Reference]	0.8550	0.081
	Del/Ins	63 (45.0)	66 (47.5)	1.27 [0.47-3.34]		
	Del/Del	17 (12.1)	15 (10.8)	1.09 [0.40-2.94]		
	Dominant					
	Ins/Ins	60 (42.9)	58 (41.7)	1 [Reference]	0.7650	0.068
	Del/Ins + Del/Del	80 (57.1)	81 (58.3)	0.91 [0.48-1.72]		
	Recessive					
	Ins/Ins + Del/Ins	123 (87.9)	124 (89.2)	1 [Reference]	0.7190	0.075
	Del/Del	17 (12.1)	15 (10.8)	1.19 [0.46-2.97]		
log-Additive				0.99 [0.62-1.58]	0.9690	0.058

**Supplementary Table 3 The logistic regression analyses between outcome of colorectal cancer and insertion-deletions polymorphism**

Gene	Genotype	Anatomic localization of tumor				TNM Stage			
		Colon	Rectosigmoid	OR [95%CI]	P value	I and II	III and IV	OR [95%CI]	P value
ACE	Codominant	n = 24	n = 112			n = 73	n = 58		
	Del/Del	7 (29.2)	33 (29.5)	1 [Reference]	0.9742	29 (39.7)	11 (19.0)	1 [Reference]	0.0338
	Del/Ins	11 (45.8)	56 (50.0)	0.94 [0.30-2.92]		31 (42.5)	33 (56.9)	2.81 [1.20-6.56]	
	Ins/Ins	6 (25.0)	23 (20.5)	0.85 [0.22-3.33]		13 (17.8)	14 (24.1)	2.84 [1.02-7.92]	
	Dominant								
	Del/Del	7 (29.2)	33 (29.5)	1 [Reference]	0.8689	29 (39.7)	11 (19.0)	1 [Reference]	0.0092
	Del/Ins + Ins/Ins	16 (70.8)	79 (70.5)	0.91 [0.31-2.66]		44 (60.3)	47 (81.0)	2.82 [1.26-6.31]	
	Recessive								
	Del/Del + Del/Ins	18 (75.0)	89 (79.5)	1 [Reference]	0.8389	60 (82.2)	44 (75.9)	1 [Reference]	0.3749
	Ins/Ins	6 (25.0)	23 (20.5)	0.89 [0.28-2.79]		13 (17.8)	14 (24.1)	1.47 [0.63-3.43]	
CASP8	log-Additive			0.92 [0.47-1.83]	0.8216			1.74 [1.05-2.87]	0.0288
	Codominant	n = 24	n = 113			n = 74	n = 58		
	Ins/Ins	4 (16.7)	43 (38.0)	1 [Reference]	0.0457	28 (37.8)	17 (29.3)	1 [Reference]	0.2438
	Del/Ins	16 (66.6)	47 (41.6)	0.23 [0.06-0.82]		30 (40.5)	32 (55.2)	1.76 [0.80-3.84]	
	Del/Del	4 (16.7)	23 (20.4)	0.50 [0.10-2.41]		16 (21.6)	9 (15.5)	0.93 [0.34-2.56]	
	Dominant								
	Ins/Ins	4 (16.7)	43 (38.0)	1 [Reference]	0.0303	28 (37.8)	17 (29.3)	1 [Reference]	0.3033
	Del/Ins + Del/Del	20 (83.3)	70 (62.0)	0.28 [0.08-0.97]		46 (62.2)	41 (70.7)	1.47 [0.70-3.06]	
	Recessive								
	Ins/Ins + Del/Ins	20 (83.3)	90 (79.6)	1 [Reference]	0.6406	58 (78.4)	49 (84.5)	1 [Reference]	0.3710
	Del/Del	4 (16.7)	23 (20.4)	1.34 [0.38-4.67]		16 (21.6)	9 (15.5)	0.67 [0.27-1.64]	
	log-Additive			0.69 [0.35-1.35]	0.2753			1.05 [0.65-1.70]	0.8462

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**Supplementary Table 3 The logistic regression analyses between outcome of colorectal cancer and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Anatomic localization of tumor				TNM Stage			
		Colon	Rectosigmoid	OR [95%CI]	P value	I and II	III and IV	OR [95%CI]	P value
<i>SGSM3</i>	Codominant	n = 24	n = 113			n = 74	n = 58		
		12 (50.0)	73 (64.6)	1 [Reference]	0.2012	50 (67.6)	32 (55.2)	1 [Reference]	0.3431
		9 (37.5)	33 (29.2)	0.82 [0.28-2.37]		19 (25.7)	21 (36.2)	1.73 [0.81-3.70]	
	Dominant	3 (12.5)	7 (6.2)	0.20 [0.04-1.08]		5 (6.8)	5 (8.6)	1.56 [0.42-5.83]	
		12 (50.0)	73 (64.6)	1 [Reference]	0.3350	50 (67.6)	32 (55.2)	1 [Reference]	0.1454
	Recessive	12 (50.0)	40 (35.4)	0.62 [0.23-1.64]		24 (32.4)	26 (44.8)	1.69 [0.83-3.44]	
		21 (87.5)	106 (93.8)	1 [Reference]	0.0799	69 (93.2)	53 (91.4)	1 [Reference]	0.6889
	log-Additive	3 (12.5)	7 (6.2)	0.21 [0.04-1.11]		5 (6.8)	5 (8.6)	1.30 [0.36-4.73]	
				0.56 [0.26-1.19]	0.1354			1.43 [0.83-2.47]	0.1990
<i>CYP19A1</i>	Codominant	n = 23	n = 112			n = 73	n = 57		
		5 (21.7)	44 (39.3)	1 [Reference]	0.1645	26 (35.6)	21 (36.8)	1 [Reference]	0.7830
		15 (65.2)	51 (45.5)	0.34 [0.11-1.09]		37 (50.7)	26 (45.6)	0.87 [0.41-1.87]	
	Dominant	3 (13.0)	17 (15.2)	0.55 [0.11-2.90]		10 (13.7)	10 (17.5)	1.24 [0.43-3.53]	
		5 (21.7)	44 (39.3)	1 [Reference]	0.0749	26 (35.6)	21 (36.8)	1 [Reference]	0.8853
	Recessive	18 (78.2)	68 (60.7)	0.38 [0.12-1.17]		47 (64.4)	36 (63.2)	0.95 [0.46-1.95]	
		20 (86.9)	95 (84.8)	1 [Reference]	0.9057	63 (86.3)	47 (82.5)	1 [Reference]	0.5478
	log-Additive	3 (13.0)	17 (15.2)	1.09 [0.26-4.55]		10 (13.7)	10 (17.5)	1.34 [0.52-3.48]	
				0.65 [0.32-1.34]	0.2409			1.06 [0.64-1.75]	0.8293

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**Supplementary Table 3 The logistic regression analyses between outcome of colorectal cancer and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Anatomic localization of tumor				TNM Stage		
		Colon	Rectosigmoid	OR [95%CI]	P value	I and II	III and IV	OR [95%CI]
<i>CYP2E1</i>	Codominant	n = 24	n = 113			n = 74	n = 58	
	Del/Del	20 (83.3)	93 (82.3)	1 [Reference]	0.5637	62 (83.8)	49 (84.5)	1 [Reference]
	Del/Ins	4 (16.7)	19 (16.8)	1.84 [0.48-7.03]		12 (16.2)	9 (15.5)	0.95 [0.37-2.43]
	Ins/Ins	0 (0.0)	1 (0.9)	-		0 (0.0)	0 (0.0)	-
	Dominant							
	Del/Del	20 (83.3)	93 (82.3)	1 [Reference]	0.3290	-	-	1 [Reference]
	Del/Ins + Ins/Ins	4 (16.7)	20 (17.7)	1.90 [0.50-7.23]		-	-	-
	Recessive							
	Del/Del + Del/Ins	24 (100)	112 (99.1)	1 [Reference]	-	-	-	1 [Reference]
<i>HLAG</i>	Ins/Ins	0 (0.0)	1 (0.9)	-		-	-	-
	log-Additive			1.92 [0.52-7.09]	0.3081			-
	Codominant	n = 23	n = 111			n = 72	n = 57	
	Del/Del	12 (52.2)	45 (40.5)	1 [Reference]	0.4649	30 (41.7)	21 (36.8)	1 [Reference]
	Del/Ins	7 (30.4)	50 (45.0)	1.96 [0.66-5.76]		35 (48.6)	23 (40.4)	0.94 [0.44-2.02]
	Ins/Ins	4 (17.4)	16 (14.4)	1.27 [0.32-4.96]		7 (9.7)	13 (22.8)	2.65 [0.91-7.77]
	Dominant							
	Del/Del	12 (52.2)	45 (40.5)	1 [Reference]	0.2760	30 (41.7)	21 (36.8)	1 [Reference]
	Del/Ins + Ins/Ins	11 (47.8)	66 (59.4)	1.71 [0.65-4.51]		42 (58.3)	36 (63.2)	1.22 [0.60-2.50]
<i>HLAG</i>	Recessive							
	Del/Del + Del/Ins	19 (82.6)	95 (85.5)	1 [Reference]	0.9129	65 (90.3)	44 (77.2)	1 [Reference]
	Ins/Ins	4 (17.4)	16 (14.4)	0.93 [0.26-3.37]		7 (9.7)	13 (22.8)	2.74 [1.01-7.42]
	log-Additive			1.27 [0.64-2.53]	0.4842			1.44 [0.87-2.38]
0.1497								

Continue on next page.

**Supplementary Table 3 The logistic regression analyses between outcome of colorectal cancer and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Anatomic localization of tumor				TNM Stage			
		Colon	Rectosigmoid	OR [95%CI]	P value	I and II	III and IV	OR [95%CI]	P value
<i>IL1A</i>	Codominant	n = 24	n = 113			n = 74	n = 58		
	Ins/Ins	10 (41.7)	54 (47.8)	1 [Reference]	0.2307	34 (45.9)	25 (43.1)	1 [Reference]	0.6986
	Del/Ins	12 (50.0)	40 (35.4)	0.62 [0.22-1.74]		30 (40.5)	22 (37.9)	1.00 [0.47-2.12]	
	Del/Del	2 (8.3)	19 (16.8)	2.49 [0.43-14.26]		10 (13.5)	11 (19.0)	1.50 [0.55-4.07]	
	Dominant								
	Ins/Ins	10 (41.7)	54 (47.8)	1 [Reference]	0.7660	34 (45.9)	25 (43.1)	1 [Reference]	0.7443
	Del/Ins + Del/Del	14 (58.3)	59 (52.6)	0.86 [0.33-2.28]		40 (54.1)	33 (56.9)	1.12 [0.56-2.24]	
	Recessive								
	Ins/Ins + Del/Ins	22 (91.7)	94 (83.2)	1 [Reference]	0.1464	64 (86.5)	47 (81.0)	1 [Reference]	0.3970
	Del/Del	2 (8.3)	19 (16.8)	3.09 [0.58-16.46]		10 (13.5)	11 (19.0)	1.50 [0.59-3.82]	
<i>IL4</i>	log-Additive			1.18 [0.60-2.32]	0.6284			1.17 [0.73-1.88]	0.5134
	Codominant	n = 24	n = 113			n = 74	n = 58		
	Ins/Ins	10 (41.7)	56 (49.6)	1 [Reference]	0.7281	34 (45.9)	30 (51.7)	1 [Reference]	0.3224
	Del/Ins	10 (41.7)	46 (40.7)	0.90 [0.31-2.59]		34 (45.9)	20 (34.5)	0.67 [0.32-1.40]	
	Del/Del	4 (16.6)	11 (9.7)	0.54 [0.12-2.43]		6 (8.1)	8 (13.8)	1.51 [0.47-4.85]	
	Dominant								
	Ins/Ins	10 (41.7)	56 (49.6)	1 [Reference]	0.6504	34 (45.9)	30 (51.7)	1 [Reference]	0.5097
	Del/Ins + Del/Del	24 (58.4)	57 (50.4)	0.80 [0.30-2.12]		40 (54.1)	28 (48.3)	0.79 [0.40-1.58]	
	Recessive								
	Ins/Ins + Del/Ins	20 (83.4)	102 (90.3)	1 [Reference]	0.4394	68 (91.9)	50 (86.2)	1 [Reference]	0.2945
	Del/Del	4 (16.6)	11 (9.7)	0.56 [0.14-2.35]		6 (8.1)	8 (13.8)	1.81 [0.59-5.56]	
	log-Additive			0.78 [0.38-1.57]	0.4830			1.00 [0.60-1.67]	0.9937

Continue on next page.

**Supplementary Table 3 The logistic regression analyses between outcome of colorectal cancer and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Anatomic localization of tumor				TNM Stage			
		Colon	Rectosigmoid	OR [95%CI]	P value	I and II	III and IV	OR [95%CI]	P value
<i>MDM2</i>	Codominant	<i>n</i> = 24	<i>n</i> = 113			<i>n</i> = 74	<i>n</i> = 58		
	Ins/Ins	10 (41.7)	59 (52.2)	1 [Reference]	0.3521	39 (52.7)	29 (50.0)	1 [Reference]	0.7647
	Del/Ins	11 (45.8)	48 (42.5)	0.58 [0.20-1.68]		31 (41.9)	24 (41.4)	1.04 [0.51-2.13]	
	Del/Del	3 (12.5)	6 (5.3)	0.34 [0.07-1.74]		4 (5.4)	5 (8.6)	1.68 [0.41-6.82]	
	Dominant								
	Ins/Ins	10 (41.7)	59 (52.2)	1 [Reference]	0.1923	39 (52.7)	29 (50.0)	1 [Reference]	0.7578
	Del/Ins + Del/Del	14 (58.3)	54 (47.8)	0.52 [0.19-1.40]		35 (47.3)	29 (50.0)	1.11 [0.56-2.22]	
	Recessive								
	Ins/Ins + Del/Ins	21 (87.5)	107 (94.5)	1 [Reference]	0.3010	70 (94.6)	53 (91.4)	1 [Reference]	0.4690
<i>NFKB1</i>	Del/Del	3 (12.5)	6 (5.3)	0.43 [0.09-2.03]		4 (5.4)	5 (8.6)	1.65 [0.42-6.45]	
	log-Additive			0.58 [0.28-1.21]	0.1485			1.17 [0.67-2.03]	0.5861
	Codominant	<i>n</i> = 24	<i>n</i> = 113			<i>n</i> = 74	<i>n</i> = 58		
	Ins/Ins	6 (25.0)	46 (40.7)	1 [Reference]	0.0840	32 (43.2)	18 (31.0)	1 [Reference]	0.3311
	Del/Ins	14 (58.3)	49 (43.4)	0.29 [0.09-0.93]		30 (40.5)	30 (51.7)	1.78 [0.82-3.83]	
	Del/Del	4 (16.7)	18 (15.9)	0.37 [0.08-1.71]		12 (16.2)	10 (17.2)	1.48 [0.53-4.10]	
	Dominant								
	Ins/Ins	6 (25.0)	46 (40.7)	1 [Reference]	0.0276	32 (43.2)	18 (31.0)	1 [Reference]	0.1495
	Del/Ins + Del/Del	18 (75.0)	67 (59.3)	0.31 [0.10-0.93]		42 (56.8)	40 (69.0)	1.69 [0.82-3.48]	
<i>log-Additive</i>	Recessive								
	Ins/Ins + Del/Ins	20 (83.3)	95 (84.1)	1 [Reference]	0.6569	62 (83.8)	48 (82.8)	1 [Reference]	0.8755
	Del/Del	4 (16.7)	18 (15.9)	0.74 [0.20-2.74]		12 (16.2)	10 (17.2)	1.08 [0.43-2.70]	
	log-Additive			0.55 [0.27-1.09]	0.0842			1.30 [0.80-2.12]	0.2860

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**Supplementary Table 3 The logistic regression analyses between outcome of colorectal cancer and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Anatomic localization of tumor				TNM Stage		
		Colon	Rectosigmoid	OR [95%CI]	P value	I and II	III and IV	OR [95%CI]
<i>TP53</i> 13 bp	Codominant	n = 24	n = 113			n = 74	n = 58	
	Del/Del	15 (62.5)	80 (70.8)	1 [Reference]	0.8733	53 (71.6)	36 (62.1)	1 [Reference]
	Del/Ins	8 (33.3)	29 (25.7)	0.84 [0.29-2.41]		18 (24.3)	20 (34.5)	1.64 [0.76-3.51]
	Ins/Ins	1 (4.2)	4 (3.5)	0.57 [0.05-6.39]		3 (4.1)	2 (3.4)	0.98 [0.16-6.17]
	Dominant							
	Del/Del	15 (62.5)	80 (70.8)	1 [Reference]	0.6709	53 (71.6)	36 (62.1)	1 [Reference]
	Del/Ins + Ins/Ins	9 (37.5)	33 (29.2)	0.80 [0.30-2.19]		21 (28.4)	22 (37.9)	1.54 [0.74-3.21]
	Recessive							
	Del/Del + Del/Ins	23 (95.8)	109 (96.5)	1 [Reference]	0.6804	71 (95.9)	56 (96.6)	1 [Reference]
<i>TP53</i> 6 bp	Ins/Ins	1 (4.2)	4 (3.5)	0.59 [0.05-6.57]		3 (4.1)	2 (3.4)	0.85 [0.14-5.23]
	log-Additive			0.80 [0.35-1.87]	0.6172			1.34 [0.72-2.48]
	Codominant	n = 24	n = 113			n = 74	n = 58	
	Del/Del	15 (62.5)	58 (51.3)	1 [Reference]	0.6058	46 (62.2)	23 (39.7)	1 [Reference]
	Del/Ins	8 (33.3)	47 (41.6)	1.62 [0.58-4.55]		23 (31.1)	30 (51.7)	2.61 [1.25-5.46]
	Ins/Ins	1 (4.2)	8 (7.1)	1.97 [0.17-23.47]		5 (6.8)	5 (8.6)	2.00 [0.53-7.61]
	Dominant							
	Del/Del	15 (62.5)	58 (51.3)	1 [Reference]	0.3226	46 (62.2)	23 (39.7)	1 [Reference]
	Del/Ins + Ins/Ins	8 (37.7)	55 (48.7)	1.65 [0.60-4.52]		28 (37.8)	35 (60.3)	2.50 [1.23-5.06]
<i>TP53</i> 8 bp	Recessive							
	Del/Del + Del/Ins	23 (95.8)	105 (92.9)	1 [Reference]	0.7070	69 (93.2)	53 (91.4)	1 [Reference]
	Ins/Ins	1 (4.2)	8 (7.1)	1.57 [0.14-17.88]		5 (6.8)	5 (8.6)	1.30 [0.36-4.73]
	log-Additive			1.54 [0.64-3.67]	0.3257			1.86 [1.06-3.26]

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**Supplementary Table 3 The logistic regression analyses between outcome of colorectal cancer and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Anatomic localization of tumor				TNM Stage			
		Colon	Rectosigmoid	OR [95%CI]	P value	I and II	III and IV	OR [95%CI]	P value
TYMS	Codominant	n = 24	n = 113			n = 74	n = 58		
	Ins/Ins	13 (54.2)	50 (44.3)	1 [Reference]	0.6889	40 (54.1)	23 (39.7)	1 [Reference]	0.2406
	Del/Ins	9 (37.5)	52 (46.0)	1.51 [0.55-4.13]		27 (36.5)	29 (50.0)	1.87 [0.90-3.89]	
	Del/Del	2 (8.3)	11 (9.7)	0.90 [0.15-5.23]		7 (9.5)	6 (10.3)	1.49 [0.45-4.97]	
	Dominant								
	Ins/Ins	13 (54.2)	50 (44.3)	1 [Reference]	0.5023	40 (54.1)	23 (39.7)	1 [Reference]	0.0994
	Del/Ins + Del/Del	11 (45.8)	63 (55.7)	1.39 [0.53-3.60]		34 (45.9)	35 (60.3)	1.79 [0.89-3.59]	
	Recessive								
	Ins/Ins + Del/Ins	22 (91.7)	102 (90.3)	1 [Reference]	0.7450	67 (90.5)	52 (89.7)	1 [Reference]	0.8656
UCP2	Del/Del	2 (8.3)	11 (9.7)	0.75 [0.14-4.14]		7 (9.5)	6 (10.3)	1.10 [0.35-3.48]	
	log-Additive			1.17 [0.54-2.54]	0.6890			1.43 [0.84-2.41]	0.1850
	Codominant	n = 23	n = 111			n = 72	n = 57		
	Del/Del	12 (52.2)	66 (59.5)	1 [Reference]	0.6724	40 (55.6)	34 (59.6)	1 [Reference]	0.2193
	Del/Ins	10 (43.5)	37 (33.3)	0.75 [0.27-2.05]		26 (36.1)	22 (38.6)	1.00 [0.48-2.06]	
	Ins/Ins	1 (4.3)	8 (7.2)	1.93 [0.16-22.57]		6 (8.3)	1 (1.8)	0.20 [0.02-1.71]	
	Dominant								
	Del/Del	12 (52.2)	66 (59.5)	1 [Reference]	0.7013	40 (55.6)	34 (59.6)	1 [Reference]	0.6404
	Del/Ins + Ins/Ins	11 (47.8)	45 (40.5)	0.82 [0.31-2.21]		32 (44.4)	23 (40.4)	0.85 [0.42-1.71]	
TYMS	Recessive								
	Del/Del + Del/Ins	22 (95.7)	103 (92.8)	1 [Reference]	0.4915	66 (91.7)	56 (98.2)	1 [Reference]	0.0815
	Ins/Ins	1 (4.3)	8 (7.2)	2.22 [0.20-24.76]		6 (8.3)	1 (1.8)	0.20 [0.02-1.68]	
	log-Additive			0.98 [0.43-2.21]	0.9563			0.74 [0.41-1.34]	0.3122

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**Supplementary Table 3 The logistic regression analyses between outcome of colorectal cancer and insertion-deletions polymorphism (Continued)**

Gene	Genotype	Anatomic localization of tumor			P value	TNM Stage			P value
		Colon	Rectosigmoid	OR [95%CI]		I and II	III and IV	OR [95%CI]	
<i>UGT1A1</i>	Codominant	n = 24	n = 113			n = 74	n = 58		
	Del/Del	11 (45.8)	49 (43.4)	1 [Reference]	0.9527	37 (50.0)	20 (34.5)	1 [Reference]	0.1948
	Del/Ins	11 (45.8)	51 (45.1)	0.85 [0.31-2.37]		30 (40.5)	30 (51.7)	1.85 [0.88-3.89]	
	Ins/Ins	2 (8.4)	13 (11.5)	0.87 [0.15-5.15]		7 (9.5)	8 (13.8)	2.11 [0.67-6.68]	
	Dominant								
	Del/Del	11 (45.8)	49 (43.4)	1 [Reference]	0.7561	37 (50.0)	20 (34.5)	1 [Reference]	0.0728
	Del/Ins + Ins/Ins	13 (54.1)	64 (56.6)	0.85 [0.32-2.31]		37 (50.0)	38 (65.5)	1.90 [0.94-3.86]	
	Recessive								
	Del/Del + Del/Ins	22 (91.6)	100 (88.5)	1 [Reference]	0.9535	67 (90.5)	50 (86.2)	1 [Reference]	0.4381
	Ins/Ins	2 (8.4)	13 (11.5)	0.95 [0.18-5.09]		7 (9.5)	8 (13.8)	1.53 [0.52-4.50]	
	log-Additive			0.90 [0.42-1.94]	0.7881			1.57 [0.93-2.65]	0.0890
<i>XRCC1</i>	Codominant	n = 24	n = 113			n = 74	n = 58		
	Ins/Ins	10 (41.7)	47 (41.6)	1 [Reference]	0.6822	34 (45.9)	21 (36.2)	1 [Reference]	0.2127
	Del/Ins	13 (54.2)	52 (46.0)	0.96 [0.36-2.59]		35 (47.3)	28 (48.3)	1.30 [0.62-2.71]	
	Del/Del	1 (4.2)	14 (12.4)	2.38 [0.25-22.92]		5 (6.8)	9 (15.5)	2.91 [0.86-9.88]	
	Dominant								
	Ins/Ins	10 (41.7)	47 (41.6)	1 [Reference]	0.9015	34 (45.9)	21 (36.2)	1 [Reference]	0.2589
	Del/Ins + Del/Del	14 (58.4)	66 (58.4)	1.06 [0.40-2.81]		40 (54.1)	37 (63.8)	1.50 [0.74-3.03]	
	Recessive								
	Ins/Ins + Del/Ins	23 (95.9)	99 (87.6)	1 [Reference]	0.3837	69 (93.2)	49 (84.5)	1 [Reference]	0.1055
	Del/Del	1 (4.2)	14 (12.4)	2.44 [0.27-21.80]		5 (6.8)	9 (15.5)	2.53 [0.80-8.03]	
	log-Additive			1.20 [0.55-2.63]	0.6429			1.55 [0.91-2.64]	0.1057

**Supplementary Table 4 The insertion-deletions polymorphism frequency of cancer recurrence, according to follow-up**

Genotype	1 yr Follow-up		2 yr Follow-up		3 yr Follow-up		4 yr Follow-up		5 yr Follow-up		6 yr Follow-up		7 yr Follow-up		8 yr Follow-up	
	No	Yes														
ACE	n = 121	n = 14	n = 91	n = 30	n = 60	n = 37	n = 35	n = 42	n = 25	n = 44	n = 17	n = 45	n = 11	n = 46	n = 6	n = 47
Del/Del	28.1	42.9	22.0	46.7	20.0	40.5	20.0	35.7	16.0	36.4	11.8	37.8	9.1	37.0	0.0	36.2
Del/Ins	52.1	28.6	52.7	36.7	53.3	35.1	54.3	38.1	56.0	38.6	70.6	37.8	72.7	39.1	83.3	40.4
Ins/Ins	19.8	28.6	25.3	16.7	26.7	24.3	25.7	26.2	28.0	25.0	17.6	24.4	18.2	23.9	16.7	23.4
CASP8	n = 121	n = 15	n = 91	n = 31	n = 60	n = 38	n = 35	n = 43	n = 25	n = 45	n = 17	n = 46	n = 11	n = 47	n = 6	n = 48
Ins/Ins	35.5	40.0	35.2	45.2	41.7	36.8	45.7	34.9	40.0	37.8	23.5	39.1	27.3	38.3	33.3	37.5
Del/Ins	46.3	33.3	46.2	35.5	38.3	44.7	37.1	44.2	40.0	42.2	52.9	41.3	54.5	42.6	50.0	43.8
Del/Del	18.2	26.7	18.7	19.4	20.0	18.4	17.1	20.9	20.0	20.0	23.5	19.6	18.2	19.1	16.7	18.8
SGSM3	n = 121	n = 15	n = 91	n = 31	n = 60	n = 38	n = 35	n = 43	n = 25	n = 45	n = 17	n = 46	n = 11	n = 47	n = 6	n = 48
Del/Del	62.8	66.7	58.2	67.7	63.3	65.8	77.1	62.8	76.0	64.4	76.5	65.2	81.8	66.0	83.3	66.7
Del/Ins	30.6	26.7	35.2	25.8	30.0	26.3	20.0	25.6	24.0	24.4	23.5	23.9	18.2	23.4	16.7	22.9
Ins/Ins	6.6	6.7	6.6	6.5	6.7	7.9	2.9	11.6	0.0	11.1	0.0	10.9	0.0	10.6	0.0	10.4
CYP19A1	n = 120	n = 14	n = 90	n = 30	n = 60	n = 36	n = 35	n = 41	n = 25	n = 43	n = 17	n = 44	n = 11	n = 45	n = 6	n = 46
Ins/Ins	37.5	28.6	35.6	36.7	31.7	38.9	34.3	36.6	28.0	37.2	29.4	36.4	18.2	37.8	16.7	37.0
Del/Ins	49.2	42.9	48.9	46.7	50.0	44.4	51.4	43.9	56.0	44.2	58.8	45.5	72.7	44.4	66.6	45.7
Del/Del	13.3	28.6	15.6	16.7	18.3	16.7	14.3	19.5	16.0	18.6	11.8	18.2	9.1	17.8	16.7	17.4
CYP2E1	n = 121	n = 15	n = 91	n = 31	n = 60	n = 38	n = 35	n = 43	n = 25	n = 45	n = 17	n = 46	n = 11	n = 47	n = 6	n = 48
Del/Del	81.0	86.7	85.7	71.0	86.6	71.1	80.0	74.4	84.0	71.1	82.4	71.7	90.9	72.3	83.3	72.9
Del/Ins	18.2	13.3	13.2	29.0	11.7	28.9	17.1	25.6	12.0	28.9	17.6	28.3	9.1	27.7	16.7	27.1
Ins/Ins	0.8	0.0	1.1	0.0	11.7	0.0	2.9	0.0	4.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

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**Supplementary Table 4 The insertion-deletions polymorphism frequency of cancer recurrence, according to follow-up (Continued)**

Genotype	1 yr Follow-up		2 yr Follow-up		3 yr Follow-up		4 yr Follow-up		5 yr Follow-up		6 yr Follow-up		7 yr Follow-up		8 yr Follow-up	
	No	Yes														
<i>HLAG</i>	n = 119	n = 14	n = 90	n = 29	n = 60	n = 35	n = 35	n = 40	n = 25	n = 42	n = 17	n = 43	n = 11	n = 44	n = 6	n = 45
Del/Del	42.1	35.7	46.7	24.1	43.3	25.7	48.6	25.0	52.0	23.8	47.1	23.3	45.5	22.7	50.0	24.4
Del/Ins	44.5	42.9	42.2	51.7	43.3	54.3	37.1	57.5	32.0	59.5	35.3	60.5	45.5	59.1	33.3	57.8
Ins/Ins	13.4	21.4	11.1	24.1	13.3	20.0	14.3	17.5	16.0	16.7	17.6	16.3	9.1	18.2	16.7	17.8
<i>IL1A</i>	n = 121	n = 15	n = 91	n = 31	n = 60	n = 38	n = 35	n = 43	n = 25	n = 45	n = 17	n = 46	n = 11	n = 47	n = 6	n = 48
Ins/Ins	43.0	53.3	46.2	41.9	40.0	39.5	34.3	39.5	36.0	37.8	47.1	37	36.4	38.3	16.7	39.6
Del/Ins	41.3	33.4	37.4	41.9	41.7	42.1	37.1	44.2	32.0	44.4	29.4	45.7	36.4	44.7	50.0	43.8
Del/Del	15.7	13.3	16.5	16.1	18.3	18.4	28.6	16.3	32.0	17.8	23.5	17.4	27.3	17	33.3	16.7
<i>IL4</i>	n = 121	n = 15	n = 91	n = 31	n = 60	n = 38	n = 35	n = 43	n = 25	n = 45	n = 17	n = 46	n = 11	n = 47	n = 6	n = 48
Ins/Ins	47.1	53.3	45.1	48.4	48.3	47.4	48.6	46.5	40.0	46.7	41.2	47.8	36.4	46.8	50.0	45.8
Del/Ins	42.1	33.3	41.8	45.2	40.0	39.4	34.3	41.9	44.0	42.2	41.2	41.3	54.5	40.4	50.0	41.7
Del/Del	10.7	13.3	13.2	6.5	11.7	13.2	17.1	11.6	16.0	11.1	17.6	10.9	9.1	12.8	0.0	12.5
<i>MDM2</i>	n = 121	n = 15	n = 91	n = 31	n = 60	n = 38	n = 36	n = 42	n = 25	n = 45	n = 17	n = 46	n = 11	n = 47	n = 6	n = 48
Ins/Ins	47.9	60	49.5	51.6	48.3	52.6	52.8	50.0	44.0	48.9	35.3	50.0	54.5	48.9	66.7	47.9
Del/Ins	45.5	33.3	42.9	41.9	41.7	42.1	41.7	45.2	48.0	46.7	58.8	45.7	45.5	46.8	33.3	47.9
Del/Del	6.6	6.7	7.7	6.5	10.0	5.3	5.6	4.8	8.0	4.4	5.9	4.3	0.0	4.3	0.0	4.2

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**Supplementary Table 4 The insertion-deletions polymorphism frequency of cancer recurrence, according to follow-up (Continued)**

Genotype	1 yr Follow-up		2 yr Follow-up		3 yr Follow-up		4 yr Follow-up		5 yr Follow-up		6 yr Follow-up		7 yr Follow-up		8 yr Follow-up	
	No	Yes														
<i>NFKB1</i>	<i>n</i> = 121	15	91	31	60	38	35	43	25	45	17	46	11	47	6	48
Ins/Ins	40.5	26.7	41.8	35.5	43.3	42.1	45.7	41.9	40	40	35.3	41.3	27.3	42.6	33.3	41.7
Del/Ins	45.5	40	42.9	45.2	45	42.1	45.7	44.2	48	46.7	58.8	45.7	72.7	44.7	66.7	45.8
Del/Del	14.0	33.3	15.4	19.4	11.7	15.8	8.6	14.0	12.0	13.3	5.9	13.0	0.0	12.8	0.0	12.5
<i>TP53 13 bp</i>	<i>n</i> = 121	15	91	31	60	38	35	43	25	45	17	46	11	47	6	48
Del/Del	69.4	53.3	65.9	64.5	66.7	63.2	65.7	62.8	64.0	60.0	58.8	58.7	54.5	59.6	66.7	58.3
Del/Ins	26.4	46.7	30.8	32.3	28.3	34.2	34.3	30.2	36.0	33.3	41.2	34.8	45.5	34.0	33.3	35.4
Ins/Ins	4.1	0.0	3.3	3.2	5.0	2.6	0.0	7.0	0.0	6.7	0.0	6.5	0.0	6.4	0.0	6.2
<i>TP53 6 bp</i>	<i>n</i> = 121	15	91	31	60	38	35	43	25	45	17	46	11	47	6	48
Del/Del	55.4	46.7	54.9	48.4	50.0	47.4	51.4	46.5	56.0	46.7	58.8	47.8	63.6	46.8	66.7	47.9
Del/Ins	36.4	53.3	37.4	45.2	41.7	44.7	42.9	41.9	44.0	42.2	41.2	41.3	36.4	42.6	33.3	41.7
Ins/Ins	8.3	0.0	7.7	6.5	8.3	7.9	5.7	11.6	0.0	11.1	0.0	10.9	0.0	10.6	0.0	10.4
<i>TYMS</i>	<i>n</i> = 121	15	91	31	60	38	35	43	25	45	17	46	11	47	6	48
Ins/Ins	49.6	26.7	53.8	25.8	55.0	26.3	54.3	32.6	48.0	33.3	52.9	34.8	45.5	36.2	33.3	35.4
Del/Ins	41.3	53.3	36.3	61.3	35.0	57.9	37.1	53.5	48.0	51.1	41.2	50.0	45.5	48.9	50.0	50.0
Del/Del	9.1	20.0	9.9	12.9	10.0	15.8	8.6	14.0	4.0	15.6	5.9	15.2	9.1	14.9	16.7	14.6

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**Supplementary Table 4 The insertion-deletions polymorphism frequency of cancer recurrence, according to follow-up (Continued)**

Genotype	1 yr Follow-up		2 yr Follow-up		3 yr Follow-up		4 yr Follow-up		5 yr Follow-up		6 yr Follow-up		7 yr Follow-up		8 yr Follow-up	
	No	Yes														
<i>UCP2</i>	n = 119	n = 14	n = 90	n = 29	n = 60	n = 35	n = 35	n = 40	n = 25	n = 42	n = 17	n = 43	n = 11	n = 44	n = 6	n = 45
Del/Del	58.0	50.0	55.6	58.6	65.0	54.3	62.9	52.5	68.0	54.8	64.7	55.8	54.5	56.8	33.3	55.6
Del/Ins	34.5	50.0	34.4	41.4	28.3	45.7	31.4	47.5	24.0	45.2	29.4	44.2	36.4	43.2	50.0	44.4
Ins/Ins	7.6	0.0	10.0	0.0	6.7	0.0	5.7	0.0	8.0	0.0	5.9	0.0	9.1	0.0	16.7	0.0
<i>UGT1A1</i>	n = 121	n = 15	n = 91	n = 31	n = 60	n = 38	n = 35	n = 43	n = 25	n = 45	n = 17	n = 46	n = 11	n = 47	n = 6	n = 48
Del/Del	45.5	40.0	46.2	45.2	55.0	36.8	65.7	37.2	68.0	37.8	58.8	39.1	63.6	40.4	66.7	41.7
Del/Ins	43.8	46.7	41.7	45.2	30.0	55.3	20.0	53.5	20.0	51.1	23.6	50.0	36.4	48.9	33.3	47.9
Ins/Ins	10.7	13.3	12.1	9.7	15.0	7.9	14.3	9.3	12.0	11.1	17.6	10.9	0.0	10.6	0.0	10.4
<i>XRCC1</i>	n = 121	n = 15	n = 91	n = 41	n = 60	n = 38	n = 35	n = 43	n = 25	n = 45	n = 17	n = 46	n = 11	n = 47	n = 6	n = 48
Ins/Ins	41.3	46.7	44.0	38.7	41.7	44.7	42.9	46.5	44.0	46.7	41.2	45.7	18.2	44.7	33.3	43.8
Del/Ins	47.1	46.7	45.1	45.4	45.0	44.7	42.9	41.9	44.0	42.2	52.9	43.5	72.7	44.7	50.0	45.8
Del/Del	11.6	6.7	11.0	12.0	13.3	10.6	14.2	11.6	12.0	11.1	5.9	10.9	9.1	10.6	16.7	10.4

**Supplementary Table 5** The insertion-deletions polymorphism frequency of death cancer patients, according to follow-up

Genotype	2 yr Follow-up		3 yr Follow-up		4 yr Follow-up		5 yr Follow-up		6 yr Follow-up		7 yr Follow-up		8 yr Follow-up	
	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes
ACE	n = 135	n = 4	n = 118	n = 7	n = 85	n = 11	n = 60	n = 12	n = 40	n = 15	n = 27	n = 16	n = 17	n = 17
Del/Del	28.9	50.0	26.3	57.1	23.5	45.5	25.0	41.7	27.5	40.0	29.6	37.5	23.5	41.2
Del/Ins	50.4	25.0	50.0	28.6	47.1	45.5	48.3	41.7	50.0	40.0	55.6	43.8	64.7	41.2
Ins/Ins	20.7	25.0	23.7	14.3	29.4	9.1	26.7	16.7	22.5	20.0	14.8	18.8	11.8	17.6
CASP8	n = 136	n = 4	n = 119	n = 7	n = 86	n = 11	n = 61	n = 12	n = 41	n = 15	n = 28	n = 16	n = 18	n = 17
Ins/Ins	35.3	25.0	36.1	42.9	36.0	36.4	36.1	41.7	39.0	33.3	32.1	31.2	33.3	29.4
Del/Ins	45.6	50.0	44.5	42.9	41.9	54.5	41.0	50.0	41.5	60.0	46.4	62.6	50.0	58.8
Del/Del	19.1	25.0	19.3	14.3	22.1	9.1	23.0	8.3	19.5	6.7	21.4	6.2	16.7	11.8
SGSM3	n = 136	n = 4	n = 119	n = 7	n = 86	n = 11	n = 61	n = 12	n = 41	n = 15	n = 28	n = 16	n = 18	n = 17
Del/Del	64	25.0	61.3	42.9	64.0	54.5	72.1	50.0	80.5	53.3	82.1	50.0	83.3	52.9
Del/Ins	28.7	75.0	31.1	57.1	27.9	36.4	18.0	41.7	17.1	40.0	17.9	37.5	16.7	35.5
Ins/Ins	7.4	0.0	7.6	0.0	8.1	9.1	9.8	8.3	2.4	6.7	0.0	12.5	0.0	11.8
CYP19A1	n = 134	n = 4	n = 117	n = 7	n = 84	n = 11	n = 59	n = 12	n = 39	n = 15	n = 27	n = 16	n = 17	n = 17
Ins/Ins	36.6	0.0	35.9	14.3	34.5	9.1	32.2	8.3	35.9	13.3	33.3	12.5	29.4	17.6
Del/Ins	48.5	75.0	48.7	57.1	48.8	63.6	50.8	66.7	48.7	60.0	55.6	62.5	58.8	58.8
Del/Del	14.9	25.0	15.4	28.6	16.7	27.3	16.9	25.0	15.4	26.7	11.1	25.0	11.8	23.5
CYP2E1	n = 136	n = 4	n = 119	n = 7	n = 86	n = 11	n = 61	n = 12	n = 41	n = 15	n = 28	n = 16	n = 18	n = 17
Del/Del	82.4	75.0	84.0	57.1	82.6	63.6	78.7	66.7	80.5	60.0	78.6	62.5	77.8	64.7
Del/Ins	16.9	25.0	15.1	42.9	16.3	36.4	19.7	33.3	17.1	40.0	21.4	37.5	22.2	35.3
Ins/Ins	0.7	0.0	0.8	0.0	1.2	0.0	1.6	0.0	2.4	0.0	0.0	0.0	0.0	0.0
HLAG	n = 133	n = 4	n = 116	n = 7	n = 83	n = 11	n = 58	n = 12	n = 39	n = 14	n = 27	n = 15	n = 17	n = 15
Del/Del	41.4	50.0	42.2	28.6	39.8	27.3	43.1	25.0	48.7	21.4	37.0	26.7	37.0	26.7
Del/Ins	44.4	25.0	44.0	42.9	44.6	45.5	41.4	50.0	33.3	57.1	40.7	53.3	40.7	53.3
Ins/Ins	14.3	25.0	13.8	28.6	15.7	27.3	15.5	25.0	17.9	21.4	22.2	20.0	22.2	20.0

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**Supplementary Table 5 The insertion-deletions polymorphism frequency of death cancer patients, according to follow-up (Continued)**

Genotype	2 yr Follow-up		3 yr Follow-up		4 yr Follow-up		5 yr Follow-up		6 yr Follow-up		7 yr Follow-up		8 yr Follow-up	
	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes
<i>IL1A</i>	<i>n</i> = 136	<i>n</i> = 4	<i>n</i> = 119	<i>n</i> = 7	<i>n</i> = 86	<i>n</i> = 11	<i>n</i> = 61	<i>n</i> = 12	<i>n</i> = 41	<i>n</i> = 15	<i>n</i> = 28	<i>n</i> = 16	<i>n</i> = 18	<i>n</i> = 17
Ins/Ins	45.6	50.0	47.1	42.9	39.5	54.5	37.7	58.3	41.5	53.3	46.4	56.2	33.3	52.9
Del/Ins	39.7	25.0	37.8	28.6	41.9	27.3	44.3	25.0	31.7	33.3	28.6	31.2	38.9	29.4
Del/Del	14.7	25.0	15.1	28.6	18.6	18.2	18.0	16.7	26.8	13.3	25.0	12.5	27.8	17.6
<i>IL4</i>	<i>n</i> = 136	<i>n</i> = 4	<i>n</i> = 119	<i>n</i> = 7	<i>n</i> = 86	<i>n</i> = 11	<i>n</i> = 61	<i>n</i> = 12	<i>n</i> = 41	<i>n</i> = 15	<i>n</i> = 28	<i>n</i> = 16	<i>n</i> = 18	<i>n</i> = 17
Ins/Ins	47.1	100	45.4	71.4	47.7	63.6	49.2	58.3	46.3	60.0	42.9	62.5	38.9	58.8
Del/Ins	41.9	0.0	42.9	28.6	39.5	27.3	37.7	33.3	41.5	33.3	42.9	31.3	50.0	35.3
Del/Del	11.0	0.0	11.8	0.0	12.8	9.1	13.1	8.3	12.2	6.7	14.2	6.2	11.1	5.9
<i>MDM2</i>	<i>n</i> = 136	<i>n</i> = 4	<i>n</i> = 119	<i>n</i> = 7	<i>n</i> = 86	<i>n</i> = 11	<i>n</i> = 61	<i>n</i> = 12	<i>n</i> = 41	<i>n</i> = 15	<i>n</i> = 28	<i>n</i> = 16	<i>n</i> = 18	<i>n</i> = 17
Ins/Ins	50.0	50.0	51.3	42.9	53.5	36.4	50.8	41.7	48.8	46.7	42.9	50.0	55.6	52.9
Del/Ins	43.4	50.0	41.2	57.1	37.2	63.6	42.6	58.3	46.3	53.3	53.6	50.0	44.4	47.1
Del/Del	6.6	0.0	7.6	0.0	9.3	0.0	6.6	0.0	4.9	0.0	3.6	0.0	0.0	0.0
<i>NFKB1</i>	<i>n</i> = 136	<i>n</i> = 4	<i>n</i> = 119	<i>n</i> = 7	<i>n</i> = 86	<i>n</i> = 11	<i>n</i> = 61	<i>n</i> = 12	<i>n</i> = 41	<i>n</i> = 15	<i>n</i> = 28	<i>n</i> = 16	<i>n</i> = 18	<i>n</i> = 17
Ins/Ins	38.2	50.0	38.7	57.1	39.5	54.5	36.1	50.0	34.1	46.7	28.6	43.8	27.8	41.2
Del/Ins	46.3	25.0	45.4	28.6	46.5	36.4	50.8	41.7	56.1	40.0	64.3	43.8	66.7	47.1
Del/Del	15.4	25.0	16	14.3	14.0	9.1	13.1	8.3	9.8	13.3	7.1	12.5	5.6	11.8
<i>TP53 13 bp</i>	<i>n</i> = 136	<i>n</i> = 4	<i>n</i> = 119	<i>n</i> = 7	<i>n</i> = 86	<i>n</i> = 11	<i>n</i> = 61	<i>n</i> = 12	<i>n</i> = 41	<i>n</i> = 15	<i>n</i> = 28	<i>n</i> = 16	<i>n</i> = 18	<i>n</i> = 17
Del/Del	68.4	75.0	67.2	57.1	65.1	72.7	65.6	75.0	63.4	73.3	60.7	75	55.6	76.5
Del/Ins	27.9	25.0	29.4	42.9	30.2	27.3	29.5	25.0	34.1	26.7	39.3	25	44.4	23.5
Ins/Ins	3.7	0.0	3.4	0.0	4.7	0.0	4.9	0.0	2.4	0.0	0.0	0.0	0.0	0.0

TP53 6 bp	<i>n</i> = 136	<i>n</i> = 4	<i>n</i> = 119	<i>n</i> = 7	<i>n</i> = 86	<i>n</i> = 11	<i>n</i> = 61	<i>n</i> = 12	<i>n</i> = 41	<i>n</i> = 15	<i>n</i> = 28	<i>n</i> = 16	<i>n</i> = 18	<i>n</i> = 17
Del/Del	52.9	75.0	50.4	85.7	46.5	72.7	49.2	66.7	53.7	60.0	53.6	56.2	55.6	52.9
Del/Ins	40.4	0.0	42.9	0.0	46.5	18.2	42.6	25.0	43.9	33.3	42.9	37.5	38.9	41.2
Ins/Ins	6.6	25.0	6.7	14.3	7.0	9.1	8.2	8.3	2.4	6.7	3.6	6.2	5.6	5.9

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**Supplementary Table 5 The insertion-deletions polymorphism frequency of death cancer patients, according to follow-up (Continued)**

Genotype	2 yr Follow-up		3 yr Follow-up		4 yr Follow-up		5 yr Follow-up		6 yr Follow-up		7 yr Follow-up		8 yr Follow-up	
	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes	No	Yes
TYMS	<i>n</i> = 136	<i>n</i> = 4	<i>n</i> = 119	<i>n</i> = 7	<i>n</i> = 86	<i>n</i> = 11	<i>n</i> = 61	<i>n</i> = 12	<i>n</i> = 41	<i>n</i> = 15	<i>n</i> = 28	<i>n</i> = 16	<i>n</i> = 18	<i>n</i> = 17
Ins/Ins	47.8	0.0	46.2	42.9	46.5	27.3	47.5	25.0	46.3	26.7	50.0	31.2	50.0	29.4
Del/Ins	41.9	100	42.9	57.1	41.9	63.6	41.0	66.7	43.9	66.7	39.3	62.5	33.3	64.7
Del/Del	10.3	0.0	10.9	0.0	11.6	9.1	11.5	8.3	9.8	6.7	10.7	6.2	16.7	5.9
UCP2	<i>n</i> = 133	<i>n</i> = 4	<i>n</i> = 116	<i>n</i> = 7	<i>n</i> = 83	<i>n</i> = 11	<i>n</i> = 58	<i>n</i> = 12	<i>n</i> = 39	<i>n</i> = 14	<i>n</i> = 27	<i>n</i> = 15	<i>n</i> = 17	<i>n</i> = 16
Del/Del	57.9	50.0	57.8	42.9	62.7	54.5	60.3	58.3	66.7	50.0	66.7	53.3	70.6	56.2
Del/Ins	35.3	50.0	34.5	57.1	32.5	45.5	36.2	41.7	28.2	50.0	29.6	46.7	23.5	43.8
Ins/Ins	6.8	0.0	7.8	0.0	4.8	0.0	3.4	0.0	5.1	0.0	3.7	0.0	5.9	0.0
UGT1A1	<i>n</i> = 136	<i>n</i> = 4	<i>n</i> = 119	<i>n</i> = 7	<i>n</i> = 86	<i>n</i> = 11	<i>n</i> = 61	<i>n</i> = 12	<i>n</i> = 41	<i>n</i> = 15	<i>n</i> = 28	<i>n</i> = 16	<i>n</i> = 18	<i>n</i> = 17
Del/Del	44.9	25.0	45.4	42.9	51.2	27.3	55.7	25.0	65.9	26.7	60.7	25.0	66.7	23.5
Del/Ins	44.1	50.0	42.9	42.9	34.9	63.6	31.1	58.3	22.0	60.0	25.0	56.2	27.8	58.8
Ins/Ins	11.0	25.0	11.8	14.2	14.0	9.1	13.1	16.7	12.2	13.3	14.3	18.8	5.6	17.6
XRCC1	<i>n</i> = 136	<i>n</i> = 4	<i>n</i> = 119	<i>n</i> = 7	<i>n</i> = 86	<i>n</i> = 11	<i>n</i> = 61	<i>n</i> = 12	<i>n</i> = 41	<i>n</i> = 15	<i>n</i> = 28	<i>n</i> = 16	<i>n</i> = 18	<i>n</i> = 17
Ins/Ins	41.9	50.0	42.0	57.1	40.7	63.6	41.0	58.3	41.5	53.3	42.9	56.2	27.8	52.9
Del/Ins	47.1	50.0	46.2	42.9	47.7	36.4	49.2	33.3	51.2	40.0	53.6	37.5	66.7	41.2
Del/Del	11.0	0.0	11.8	0.0	11.6	0.0	9.8	8.3	7.3	6.7	3.6	6.2	5.6	5.9

TNM: tumor node metastasis