

Supplemental Table S2. Associations of other DNA repair nonsynonymous polymorphisms and colon tumors\*

Polymorphism	MAF in controls	Genotype	Control <i>n</i>	Case <i>n</i>	All Cases** OR (95% CI)	Case <i>n</i>	MSI+ OR (95% CI)	Case <i>n</i>	CIMP high OR (95% CI)	Case <i>n</i>	<i>BRAF</i> V600E OR (95% CI)	Case <i>n</i>	<i>KRAS2</i> Mutation OR (95% CI)	Case <i>n</i>	<i>TP53</i> Mutation OR (95% CI)
<b>Double-strand break repair</b>															
XRCC3 T241M	0.38	CC	760	671	1.0	92	1.0	117	1.0	44	1.0	148	1.0	232	1.0
		CT	911	702	0.9 (0.8, 1.0)	75	0.7 (0.5, 0.9)	130	1.0 (0.8, 1.3)	41	0.8 (0.5, 1.2)	161	1.0 (0.8, 1.2)	229	0.9 (0.7, 1.0)
		TT	277	208	0.9 (0.7, 1.1)	23	0.8 (0.5, 1.2)	30	0.8 (0.5, 1.1)	11	0.7 (0.4, 1.4)	47	1.0 (0.7, 1.4)	66	0.9 (0.7, 1.2)
		<i>P trend</i>			0.12		0.04		0.19		0.14		0.53		0.08
<b>Nucleotide excision repair</b>															
ERCC2 D312N	0.34	GG	866	714	1.0	87	1.0	130	1.0	39	1.0	166	1.0	222	1.0
		GA	854	667	1.0 (0.8, 1.1)	77	0.9 (0.7, 1.2)	119	0.9 (0.7, 1.2)	51	1.3 (0.9, 1.9)	149	1.0 (0.8, 1.2)	238	1.1 (1.0, 1.4)
		AA	230	200	1.1 (0.9, 1.4)	26	1.2 (0.8, 1.8)	28	0.9 (0.6, 1.3)	6	0.6 (0.3, 1.5)	41	1.0 (0.7, 1.5)	67	1.3 (1.0, 1.7)
		<i>P trend</i>			0.51		0.85		0.62		0.86		0.94		0.10
ERCC2 K751Q	0.36	AA	793	667	1.0	82	1.0	128	1.0	39	1.0	159	1.0	209	1.0
		AC	893	689	0.9 (0.8, 1.1)	74	0.9 (0.6, 1.2)	107	0.8 (0.6, 1.0)	45	1.1 (0.7, 1.6)	156	0.9 (0.8, 1.2)	240	1.1 (0.9, 1.4)
		CC	267	226	1.1 (0.9, 1.3)	34	1.3 (0.9, 1.9)	42	1.0 (0.7, 1.4)	12	0.9 (0.5, 1.8)	41	0.8 (0.6, 1.1)	78	1.2 (0.9, 1.6)
		<i>P trend</i>			0.83		0.60		0.58		0.96		0.30		0.26
ERCC5 D1104I	0.22	GG	1189	947	1.0	121	1.0	163	1.0	60	1.0	202	1.0	293	1.0
		GC	658	540	1.1 (0.9, 1.2)	63	0.9 (0.7, 1.3)	97	1.1 (0.9, 1.4)	31	0.9 (0.6, 1.4)	124	1.1 (0.9, 1.4)	198	1.2 (1.03, 1.5)
		CC	104	94	1.1 (0.8, 1.4)	6	0.5 (0.2, 1.1)	17	1.1 (0.7, 1.7)	5	0.8 (0.3, 2.1)	29	1.5 (1.04, 2.2)	36	1.3 (0.9, 1.8)
		<i>P trend</i>			0.44		0.37		0.28		0.98		0.05		0.02
<b>Direct repair</b>															
MGMT L84F	0.13	CC	1467	1206	1.0	157	1.0	222	1.0	81	1.0	263	1.0	408	1.0
		CT/TT	485	375	0.9 (0.8, 1.1)	33	0.7 (0.5, 1.0)	54	0.8 (0.6, 1.0)	14	0.6 (0.3, 1.0)	93	1.2 (0.9, 1.5)	119	0.9 (0.8, 1.2)
MGMT I143V	0.14	AA	1451	1205	1.0	139	1.0	198	1.0	69	1.0	279	1.0	409	1.0
		AG/GG	500	376	0.9 (0.8, 1.1)	51	1.1 (0.8, 1.5)	78	1.2 (1.0, 1.6)	27	1.2 (0.8, 1.9)	76	0.8 (0.6, 1.1)	117	0.9 (0.7, 1.1)

\*Adjusted for age, sex, race, center, energy, BMI, activity, longterm alcohol, smoking, recent NSAIDs, and family history.

\*\*Includes cases without tumor marker data.