

Nucleotide Excision Repair Gene *ERCC2* and *ERCC5* Variants Increase Risk of Uterine Cervical Cancer

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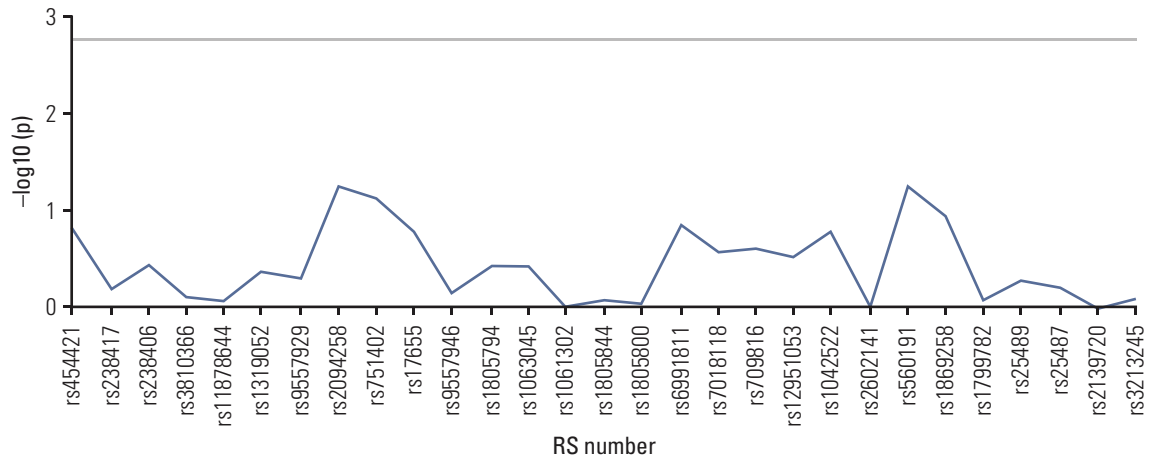
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Supplementary Data

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Supplementary Fig. S1. p-values from Hardy-Weinberg disequilibrium test. High p-value indicates no evident deviation from Hardy-Weinberg equilibrium (the horizontal line is the threshold of $\alpha=0.05/29=1.7\times 10^{-3}$ using the Bonferroni correction).

Supplementary Table 1. Crude and age-adjusted p-values of MIN2 for 29 SNPs determined using the Bonferroni correction

Gene	SNP	RS number	Genotype	No.		Crude		Age adjusted	
				Case	Control	OR	p-value	OR	p-value
ERCC2	ERCC2-T1	rs454421	G/G	107	293	1	0.0013	1	0.0009
			G/A	265	434	1.672		1.712	
			A/A	106	195	1.488		1.619	
	ERCC2-T2	rs238417	C/C	122	221	1	0.0171	1	0.0104
			C/G	262	453	1.048		1.013	
			G/G	94	248	0.687		0.644	
	ERCC2-T5	rs238406	C/C	135	247	1	0.0399	1	0.0391
			C/A	255	447	1.044		1.013	
			A/A	88	228	0.706		0.680	
	ERCC2-T8	rs3810366	G/G	102	257	1	0.0345	1	0.0238
			C/G	266	456	1.470		1.516	
			C/C	110	209	1.326		1.413	
	ERCC2-T9	rs11878644	T/T	102	248	1	0.0925	1	0.0647
			C/T	265	463	1.392		1.438	
C/C			111	211	1.279		1.350		
ERCC2-T14	rs1319052	A/A	271	556	1	0.3258	1	0.5327	
		A/G	178	314	1.163		1.145		
		G/G	29	52	1.144		1.044		
ERCC5	ERCC5-T1	rs9557929	G/G	134	242	1	0.7812	1	0.8482
			G/C	225	450	0.903		0.908	
			C/C	119	230	0.934		0.948	
	ERCC5-T4	rs2094258	C/C	162	301	1	0.6708	1	0.6532
			C/T	221	426	0.964		0.973	
			T/T	95	195	0.905		0.895	
	ERCC5-T6	rs751402	G/G	240	495	1	0.2122	1	0.4848
			G/A	187	346	1.115		1.065	
			A/A	51	81	1.299		1.196	
	ERCC5-T10	rs17655	G/G	101	276	1	0.0001	1	< 0.0001
			C/G	230	437	1.438		1.508	
			C/C	147	209	1.922		2.013	
ERCC5-T12	rs9557946	A/A	138	238	1	0.3955	1	0.5340	
		A/T	227	455	0.860		0.898		
		T/T	113	229	0.851		0.876		
NBS1	NBS1-185	rs1805794	G/G	140	268	1	0.9892	1	0.9000
			G/C	241	471	0.980		1.045	
			C/C	97	183	1.015		1.040	
	NBS1-34	rs1063045	C/C	140	276	1	0.7865	1	0.6829
			C/T	241	469	1.013		1.058	
			T/T	97	177	1.080		1.104	
	NBS1-672	rs1061302	A/A	140	272	1	0.9617	1	0.9312
			A/G	242	458	1.027		1.056	
			G/G	96	192	0.972		0.973	
	NBS1-i-800	rs1805844	A/A	139	267	1	0.8430	1	0.9525
			A/G	242	456	1.019		1.008	
			G/G	97	199	0.936		0.971	
NBS1-U-500	rs1805800	G/G	140	267	1	0.8271	1	0.9142	
		G/A	241	457	1.006		0.993		
		A/A	97	198	0.934		0.960		

Supplementary Table 1. Continued

Gene	SNP	RS number	Genotype	No.		Crude		Age adjusted	
				Case	Control	OR	p-value	OR	p-value
	NBS1-U2200	rs6991811	G/G	139	265	1	0.9335	1	0.6717
			G/T	242	480	0.961		1.013	
			T/T	97	177	1.045		1.120	
	NBS1-U3500	rs7018118	T/T	139	274	1	0.7502	1	0.8782
			T/C	242	473	1.009		1.016	
			C/C	97	175	1.093		1.053	
	NBS1-399	rs709816	C/C	202	398	1	0.9441	1	0.9741
			C/T	216	403	1.056		1.035	
			T/T	60	121	0.977		0.964	
TP53	TP53-11	rs12951053	T/T	248	509	1	0.1206	1	0.0559
			T/G	190	361	1.080		1.141	
			G/G	40	52	1.579		1.662	
	TP53-72	rs1042522	G/G	190	383	1	0.1263	1	0.0854
			C/G	216	438	0.994		0.993	
			C/C	72	101	1.437		1.509	
TP53BP1	TP53BP1-1136	rs2602141	T/T	116	268	1	0.2001	1	0.2333
			T/G	255	457	1.289		1.264	
			G/G	107	197	1.255		1.248	
	TP53BP1-353	rs560191	C/C	114	235	1	0.5864	1	0.5513
			G/C	256	490	1.077		1.084	
			G/G	108	197	1.130		1.145	
	TP53BP1-U-1k	rs1869258	A/A	112	236	1	0.5030	1	0.5699
			A/C	256	485	1.112		1.057	
			C/C	110	201	1.153		1.141	
XRCC1	XRCC1-194	rs1799782	C/C	219	414	1	0.7387	1	0.8924
			C/T	211	406	0.982		1.012	
			T/T	48	102	0.890		0.916	
	XRCC1-280	rs25489	G/G	371	717	1	0.9207	1	0.8092
			G/A	100	195	0.991		0.982	
			A/A	7	10	1.353		1.558	
	XRCC1-399	rs25487	G/G	257	500	1	0.5352	1	0.6618
			A/G	194	354	1.066		1.056	
			A/A	27	68	0.773		0.795	
	XRCC1-i10-141	rs2139720	C/C	411	758	1	0.1096	1	0.2674
			C/T	64	156	0.757		0.819	
			T/T	3	8	0.692		0.673	
	XRCC1-77	rs3213245	T/T	401	754	1	0.4352	1	0.6355
			T/C	74	161	0.864		0.905	
			C/C	3	7	0.806		0.833	

ERCC, excision repair cross-complementing; XRCC, X-ray repair cross-complementing; SNP, single nucleotide polymorphism; OR, odds ratio.

Supplementary Table 2. Subgroup analyses of rs454421 and rs17655

Subgroup	RS number	Genotype	No.		Additive		Dominant		Recessive	
			Case	Control	OR	p-value	OR	p-value	OR	p-value
Age (yr)										
≤ 40	rs454421	G/G	16	293	1	0.1538	1	0.0287	1	0.9832
		G/A	47	434	1.260		1.863		1	
		A/A	17	195	1.589		1.863		1.006	
	rs17655	G/G	17	276	1	0.0281	1	0.1014	1	0.0465
		C/G	37	437	1.425		1.583		1	
		C/C	26	209	2.032		1.583		1.643	
> 40	rs454421	G/G	91	293	1	0.0170	1	0.0011	1	0.6228
		G/A	218	434	1.224		1.571		1	
		A/A	89	195	1.499		1.571		1.074	
	rs17655	G/G	84	276	1	0.0001	1	0.0009	1	0.0029
		C/G	193	437	1.376		1.597		1	
		C/C	121	209	1.894		1.597		1.490	
Histology										
Squamous cell carcinoma	rs454421	G/G	89	293	1	0.0117	1	0.0004	1	0.6867
		G/A	224	434	1.238		1.638		1	
		A/A	89	195	1.534		1.638		1.060	
	rs17655	G/G	88	276	1	0.0002	1	0.0026	1	0.0022
		C/G	191	437	1.358		1.524		1	
		C/C	123	209	1.845		1.524		1.504	
Adenocarcinomas	rs454421	G/G	16	293	1	0.5474	1	0.3659	1	0.9761
		G/A	32	434	1.117		1.310		1	
		A/A	13	195	1.247		1.310		1.010	
	rs17655	G/G	11	276	1	0.0326	1	0.0477	1	0.1286
		C/G	31	437	1.481		1.942		1	
		C/C	19	209	2.194		1.942		1.543	
HPV 18 type										
Yes	rs454421	G/G	11	293	1	0.3384	1	0.3442	1	0.5424
		G/A	22	434	1.226		1.397		1	
		A/A	11	195	1.504		1.397		1.243	
	rs17655	G/G	6	276	1	0.0127	1	0.0202	1	0.0794
		C/G	23	437	1.714		2.705		1	
		C/C	15	209	2.936		2.705		1.765	
No	rs454421	G/G	77	293	1	0.0613	1	0.0043	1	0.9614
		G/A	182	434	1.185		1.524		1	
		A/A	70	195	1.404		1.524		1.008	
	rs17655	G/G	75	276	1	0.0009	1	0.0134	1	0.0027
		C/G	152	437	1.342		1.447		1	
		C/C	102	209	1.802		1.447		1.533	

Subgroup analyses were performed according to age (≤ 40, > 40), histology (squamous, adeno carcinomas), and HPV 18 type (HPV 18 type, others). OR, odds ratio; HPV, human papillomavirus.

Supplementary Table 3. Proportional odds model for rs454421 in ERCC2 and rs17655 in ERCC5 according to age (≤ 40 , > 40 , control for 1, 2, 3), histology (adenocarcinoma, squamous cell carcinoma, control for 1, 2, 3), and HPV 18 type (HPV 18 type, others, control for 1,2,3)

Subgroup	RS number	Genotype	No.			Additive		Dominant		Recessive	
			1	2	3	OR	p-value	OR	p-value	OR	p-value
Age	rs454421	G/G	16	91	293	1	0.0087	1	0.0002	1	0.6866
		G/A	47	218	434	1.231		1.616		1	
		A/A	17	89	195	1.514		1.616		1.056	
	rs17655	G/G	17	84	276	1	< 0.0001	1	0.0005	1	0.0009
		C/G	37	193	437	1.378		1.581		1	
		C/C	26	121	209	1.898		1.581		1.508	
Histology	rs454421	G/G	16	89	293	1	0.0167	1	0.0007	1	0.7241
		G/A	32	224	434	1.212		1.561		1	
		A/A	13	89	195	1.469		1.561		1.050	
	rs17655	G/G	11	88	276	1	< 0.0001	1	0.0006	1	0.0013
		C/G	31	191	437	1.372		1.577		1	
		C/C	19	123	209	1.882		1.577		1.497	
HPV18 type	rs454421	G/G	11	77	293	1	0.0430	1	0.0039	1	0.7749
		G/A	22	182	434	1.191		1.498		1	
		A/A	11	70	195	1.419		1.498		1.044	
	rs17655	G/G	6	75	276	1	0.0001	1	0.0018	1	0.0010
		C/G	23	152	437	1.388		1.563		1	
		C/C	15	102	209	1.927		1.563		1.560	

ERCC, excision repair cross-complementing; HPV, human papillomavirus; OR, odds ratio.