

**S4 Table.** Associations of 50 SNPs in MMR genes and overall survival time in patients with rectal cancer receiving postoperative CRT

SNP	Gene	Variation	HR (95% CI) <sup>a)</sup>	p-value
rs1540354	<i>MLH1</i>	A>T	1.03 (0.71-1.51)	0.865
rs175057	<i>MLH3</i>	C>T	0.69 (0.42-1.15)	0.153
rs175068	<i>MLH3</i>	A>G	0.70 (0.41-1.18)	0.179
rs4026175	<i>MLH3</i>	A>C	0.91 (0.64-1.30)	0.592
rs56329719	<i>MLH3</i>	A>T	0.28 (0.04-2.07)	0.214
rs5809691	<i>MLH3</i>	ins>del	0.69 (0.41-1.16)	0.163
rs10188090	<i>MSH2</i>	A>G	0.86 (0.58-1.29)	0.474
rs10191478	<i>MSH2</i>	T>G	0.89 (0.56-1.41)	0.615
rs13019654	<i>MSH2</i>	G>T	1.05 (0.71-1.57)	0.798
rs1981929	<i>MSH2</i>	A>G	0.79 (0.45-1.39)	0.416
rs2042649	<i>MSH2</i>	T>C	1.06 (0.75-1.48)	0.760
rs2303428	<i>MSH2</i>	T>C	1.12 (0.77-1.62)	0.554
rs3771273	<i>MSH2</i>	T>A	0.96 (0.66-1.40)	0.824
rs4608577	<i>MSH2</i>	T>G	0.81 (0.49-1.34)	0.407
rs4952887	<i>MSH2</i>	C>T	0.99 (0.57-1.71)	0.965
rs6544991	<i>MSH2</i>	A>C	0.86 (0.59-1.25)	0.427
rs6544997	<i>MSH2</i>	A>G	1.01 (0.69-1.47)	0.979
rs12513549	<i>MSH3</i>	G>T	1.13 (0.75-1.69)	0.554
rs181747	<i>MSH3</i>	T>C	0.76 (0.51-1.13)	0.172
rs245346	<i>MSH3</i>	A>G	1.26 (0.92-1.72)	0.155
rs26279	<i>MSH3</i>	A>G	1.16 (0.75-1.78)	0.507
rs33008	<i>MSH3</i>	G>C	1.23 (0.80-1.88)	0.356
rs33013	<i>MSH3</i>	A>G	1.17 (0.79-1.72)	0.442
rs4703819	<i>MSH3</i>	C>G	0.72 (0.47-1.08)	0.115
rs6151627	<i>MSH3</i>	A>G	1.23 (0.81-1.89)	0.337
rs138593458	<i>MSH6</i>	del>ins	0.95 (0.54-1.67)	0.853
rs1800934	<i>MSH6</i>	G>T	0.82 (0.62-1.08)	0.154
rs2348244	<i>MSH6</i>	T>C	1.06 (0.76-1.48)	0.738
rs3136245	<i>MSH6</i>	T>C	0.86 (0.58-1.29)	0.469
rs3136289	<i>MSH6</i>	G>T	0.99 (0.63-1.54)	0.957
rs1233255	<i>PMS1</i>	A>C	1.46 (0.89-2.41)	0.136
rs1233258	<i>PMS1</i>	T>C	0.67 (0.45-1.02)	0.059
rs1233284	<i>PMS1</i>	G>A	0.79 (0.50-1.25)	0.308
<b>rs4920657</b>	<b><i>PMS1</i></b>	<b>T&gt;A</b>	<b>0.58 (0.36-0.94)</b>	<b>0.026</b>
<b>rs5743030</b>	<b><i>PMS1</i></b>	<b>G&gt;A</b>	<b>0.36 (0.16-0.84)</b>	<b>0.018</b>
rs5743035	<i>PMS1</i>	del>ins	0.89 (0.59-1.34)	0.572
<b>rs5743100</b>	<b><i>PMS1</i></b>	<b>G&gt;T</b>	<b>0.49 (0.24-0.98)</b>	<b>0.043</b>
rs5743112	<i>PMS1</i>	C>A	0.65 (0.39-1.07)	0.091
rs12536167	<i>PMS2</i>	A>G	0.88 (0.60-1.29)	0.512
rs140788589	<i>PMS2</i>	C>T	0.83 (0.49-1.40)	0.491
rs145874235	<i>PMS2</i>	ins>del	0.84 (0.52-1.36)	0.476

rs201018511	<i>PMS2</i>	G>A	0.94 (0.56-1.57)	0.815
rs58032887	<i>PMS2</i>	G>C	1.17 (0.86-1.58)	0.313
rs62456170	<i>PMS2</i>	G>C	1.14 (0.68-1.90)	0.626
rs62456182	<i>PMS2</i>	T>C	0.91 (0.62-1.33)	0.632
rs72363238	<i>PMS2</i>	ins>del	0.84 (0.58-1.22)	0.357
rs75973354	<i>PMS2</i>	A>G	1.02 (0.67-1.54)	0.934
rs7776504	<i>PMS2</i>	C>T	0.85 (0.58-1.24)	0.394
rs7797466	<i>PMS2</i>	G>A	0.76 (0.46-1.27)	0.298
rs79192116	<i>PMS2</i>	T>C	1.18 (0.80-1.74)	0.401

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SNP, single nucleotide polymorphism; MMR, mismatch repair; CRT, chemoradiotherapy; HR, hazard ratio; CI, confidence interval. <sup>a)</sup>Calculated by Cox regression model, adjusted for gender, age, KPS, clinical stage, tumor grade, surgical procedure and tumor location.