

Supplemental Table S4. List of 140 CRC-associated loci and associations with colorectal cancer in European-ancestry population

<b>LOCUS</b>	<b>RSID</b>	<b>VARIANT</b>	<b>CHR</b>	<b>POS</b>	<b>RISK ALLELE</b>	<b>RAF</b>	<b>BETA</b>
<b>1p34.3</b>	rs4360494	1:38455891_G/C	1	38455891	G	0.4539	0.0379
<b>1p32.3</b>	rs12144319	1:55246035_T/C	1	55246035	C	0.2548	0.0661
<b>1p36.12</b>	rs72647484	1:22587728_T/C	1	22587728	T	0.9107	0.0504
<b>1p31.3</b>	rs7542665	1:62673037_T/C	1	62673037	C	0.273	0.0334
<b>1q25.3</b>	rs6678517	1:183002639_A/G	1	183002639	A	0.5898	0.073
<b>1q41</b>	rs17011141	1:222112634_A/G	1	222112634	G	0.2087	0.0877
<b>2q24.2</b>	rs448513	2:159964552_T/C	2	159964552	C	0.326	0.0054
<b>2q33.1</b>	rs11884596	2:199612407_T/C	2	199612407	C	0.3823	0.0342
<b>2q33.1</b>	rs983402	2:199781586_T/C	2	199781586	T	0.3312	0.0622
<b>2p16.3</b>	rs7606562	2:48686695_T/A	2	48686695	T	0.813	0.0414
<b>2q11.2</b>	rs11692435	2:98275354_G/A	2	98275354	G	0.9	0.0492
<b>2q35</b>	rs3731861	2:219191256_T/C	2	219191256	T	0.6295	0.0613
<b>3q22.2</b>	rs10049390	3:133701119_G/A	3	133701119	A	0.7353	0.0455
<b>3q13.2</b>	rs13086367	3:112903888_A/G	3	112903888	A	0.5262	0.0463
<b>3q13.2</b>	rs72942485	3:112999560_G/A	3	112999560	G	0.9802	0.0545
<b>3p21.1</b>	rs9831861	3:53088285_T/G	3	53088285	G	0.59	0.0294
<b>3p22.1</b>	rs35470271	3:40915239_A/G	3	40915239	G	0.154	0.0994
<b>3q13.2</b>	rs12635946	3:112916918_C/T	3	112916918	C	0.62	0.0334
<b>3q22.2</b>	rs113569514	3:133748789_T/C	3	133748789	T	0.62	0.0414
<b>3q26.2</b>	rs9876206	3:169517436_C/T	3	169517436	C	0.7507	0.0453
<b>3p14.1</b>	rs6781752	3:66365163_G/A	3	66365163	A	0.205	0.0597
<b>4q31.21</b>	rs11727676	4:145659064_T/C	4	145659064	C	0.098	0.0093
<b>4q24</b>	rs1391441	4:106128760_G/A	4	106128760	A	0.672	0.0148
<b>4q22.2</b>	rs13149359	4:94938618_C/A	4	94938618	A	0.3663	0.052
<b>5p13.1</b>	rs7708610	5:40102443_G/A	5	40102443	A	0.3564	0.0384
<b>5p15.33</b>	rs78368589	5:1240204_C/T	5	1240204	T	0.0597	0.0786
<b>5q21.1</b>	rs145364999	5:98206082_T/A	5	98206082	T	0.9969	0.3496

<b>5p15.33</b>	rs2735940	5:1296486_A/G	5	1296486	G	0.4952	0.0865
<b>5p13.1</b>	rs12514517	5:40280076_G/A	5	40280076	A	0.288	0.1013
<b>5q22.2</b>	rs755229494	5:112097351_A/G	5	112097351	G	0.0011	0.6286
<b>5q23.2</b>	rs12659017	5:125988175_G/A	5	125988175	G	0.232	0.0374
<b>5q31.1</b>	rs4976270	5:134467220_C/T	5	134467220	C	0.5501	0.0693
<b>6p12.1</b>	rs13204733	6:55566108_A/G	6	55566108	G	0.141	0.0643
<b>6p21.33</b>	rs116685461	6:31315512_G/A	6	31315512	G	0.8755	0.0655
<b>6p21.32</b>	rs9271695	6:32593080_A/G	6	32593080	G	0.7954	0.0889
<b>6p21.33</b>	rs2516420	6:31449620_C/T	6	31449620	C	0.9263	0.1091
<b>6p21.33</b>	rs116353863	6:31010185_T/C	6	31010185	C	0.0165	0.1202
<b>6p21.31</b>	rs16878812	6:35569562_A/G	6	35569562	A	0.8861	0.0778
<b>6p21.2</b>	rs9470361	6:36623379_G/A	6	36623379	A	0.2488	0.054
<b>6p12.1</b>	rs62404966	6:55712124_C/T	6	55712124	C	0.7623	0.0724
<b>6p21.33</b>	rs3131043	6:30758466_A/G	6	30758466	G	0.43	0.0294
<b>6p24.1</b>	rs2070699	6:12292772_G/T	6	12292772	T	0.48	0.0294
<b>6p22.1</b>	rs1476570	6:29809860_G/A	6	29809860	A	0.376	0.0492
<b>6p21.32</b>	rs3830041	6:32191339_C/T	6	32191339	T	0.14	0.0645
<b>6q21</b>	rs6928864	6:105966894_C/A	6	105966894	C	0.91	0.0531
<b>6p21.1</b>	rs62396735	6:41702582_C/T	6	41702582	C	0.2908	0.033
<b>7p13</b>	rs12672022	7:45136423_T/C	7	45136423	T	0.8345	0.0067
<b>7p12.3</b>	rs80077929	7:46094089_C/T	7	46094089	T	0.1107	0.0093
<b>7p12.3</b>	rs10951878	7:46926695_C/T	7	46926695	C	0.91	0.0531
<b>7p12.3</b>	rs3801081	7:47511161_A/G	7	47511161	G	0.49	0.0253
<b>8q24.21</b>	rs7013278	8:128414892_T/C	8	128414892	T	0.3761	0.0091
<b>8q24.21</b>	rs4313119	8:128571855_G/T	8	128571855	G	0.7486	0.0518
<b>8q23.3</b>	rs16892766	8:117630683_A/C	8	117630683	C	0.0829	0.2099
<b>8q23.3</b>	rs6469654	8:117632965_G/C	8	117632965	G	0.2288	0.0677
<b>8q24.11</b>	rs117079142	8:117790914_C/A	8	117790914	A	0.0432	0.1139
<b>8q24.21</b>	rs6983267	8:128413305_G/T	8	128413305	G	0.5228	0.1052
<b>9q22.33</b>	rs34405347	9:101679752_T/G	9	101679752	T	0.9034	0.0089
<b>9p21.3</b>	rs1537372	9:22103183_G/T	9	22103183	G	0.5692	0.012

<b>9q31.3</b>	rs10980628	9:113671403_T/C	9	113671403	C	0.2106	0.0511
<b>10p14</b>	rs12217641	10:8663875_C/T	10	8663875	C	0.6981	0.0069
<b>10q24.2</b>	rs10786560	10:101315166_G/A	10	101315166	G	0.762	0.0082
<b>10q22.3</b>	rs1250567	10:81046265_T/C	10	81046265	C	0.4405	0.047
<b>10p14</b>	rs11255841	10:8739580_T/A	10	8739580	T	0.703	0.1064
<b>10q11.23</b>	rs10821907	10:52648454_C/T	10	52648454	C	0.8276	0.073
<b>10q22.3</b>	rs704017	10:80819132_A/G	10	80819132	G	0.5846	0.0765
<b>10q24.2</b>	rs11190164	10:101351704_A/G	10	101351704	G	0.2626	0.0889
<b>10q25.2</b>	rs12246635	10:114288619_T/C	10	114288619	C	0.0983	0.0975
<b>10q25.2</b>	rs11196170	10:114722621_G/A	10	114722621	A	0.2178	0.0527
<b>11q13.4</b>	rs7946853	11:74409077_T/C	11	74409077	C	0.8624	0.0119
<b>11q22.1</b>	rs55864876	11:100717136_G/A	11	100717136	G	0.9184	0.015
<b>11q22.1</b>	rs2186607	11:101656397_T/A	11	101656397	T	0.5178	0.0483
<b>11q13.4</b>	rs61389091	11:74427921_C/T	11	74427921	C	0.9606	0.1934
<b>11p15.4</b>	rs4450168	11:10286755_A/C	11	10286755	C	0.17	0.0413
<b>11q12.2</b>	rs174533	11:61549025_G/A	11	61549025	G	0.6739	0.0636
<b>11q13.4</b>	rs7121958	11:74280012_T/G	11	74280012	G	0.5105	0.078
<b>11q23.1</b>	rs3087967	11:111156836_T/C	11	111156836	T	0.2911	0.1122
<b>12q13.3</b>	rs4759277	12:57533690_C/A	12	57533690	A	0.3546	0.0285
<b>12q24.21</b>	rs1427760	12:115100714_T/C	12	115100714	C	0.5268	0.0424
<b>12p13.32</b>	rs3217874	12:4400808_C/T	12	4400808	T	0.4282	0.0453
<b>12p13.31</b>	rs10849433	12:6406904_T/C	12	6406904	C	0.267	0.0468
<b>12q12</b>	rs11610543	12:43134191_A/G	12	43134191	G	0.5013	0.0474
<b>12p13.32</b>	rs35808169	12:4368607_T/C	12	4368607	C	0.1721	0.089
<b>12p13.32</b>	rs3217810	12:4388271_C/T	12	4388271	T	0.1253	0.1181
<b>12p13.31</b>	rs2250430	12:6421174_A/T	12	6421174	T	0.7095	0.0597
<b>12p11.21</b>	rs77969132	12:31594813_C/T	12	31594813	T	0.015	0.1583
<b>12q13.12</b>	rs12372718	12:51171090_A/G	12	51171090	G	0.3924	0.0896
<b>12q24.12</b>	rs597808	12:111973358_A/G	12	111973358	G	0.5166	0.0737
<b>12q24.21</b>	rs7300312	12:115890922_T/C	12	115890922	C	0.5719	0.066
<b>12p13.2</b>	rs2710310	12:12035649_C/T	12	12035649	C	0.7596	0.0145

<b>13q22.1</b>	rs78341008	13:73791554_T/C	13	73791554	C	0.0719	0.0109
<b>13q34</b>	rs8000189	13:111075881_C/T	13	111075881	T	0.6401	0.0473
<b>13q22.1</b>	rs45597035	13:73649152_A/G	13	73649152	A	0.6506	0.0495
<b>13q22.1</b>	rs1924816	13:73997961_A/G	13	73997961	A	0.7737	0.0506
<b>13q13.3</b>	rs7333607	13:37462010_A/G	13	37462010	G	0.235	0.0758
<b>13q22.3</b>	rs1330889	13:78609615_T/C	13	78609615	C	0.87	0.0453
<b>13q13.2</b>	rs377429877	13:34092164_C/T	13	34092164	C	0.6117	0.0468
<b>14q22.2</b>	rs1951864	14:54369299_G/A	14	54369299	A	0.3722	0.0059
<b>14q23.1</b>	rs17094983	14:59189361_G/A	14	59189361	G	0.8773	0.0062
<b>14q23.1</b>	rs8020436	14:59208437_G/A	14	59208437	A	0.4016	0.0294
<b>14q22.2</b>	rs35107139	14:54419106_A/C	14	54419106	C	0.4235	0.0912
<b>14q22.2</b>	rs4901473	14:54445157_G/A	14	54445157	G	0.378	0.0465
<b>15q23</b>	rs745213	15:68060389_T/G	15	68060389	G	0.8102	0.0072
<b>15q22.31</b>	rs12594720	15:67007018_C/G	15	67007018	C	0.7218	0.0246
<b>15q22.33</b>	rs56324967	15:67402824_T/C	15	67402824	C	0.6757	0.0689
<b>15q13.3</b>	rs17816465	15:33156386_G/A	15	33156386	A	0.2055	0.069
<b>15q13.3</b>	rs12708491	15:32992836_G/A	15	32992836	G	0.5872	0.0464
<b>15q13.3</b>	rs2293581	15:33010736_G/A	15	33010736	A	0.2116	0.1248
<b>15q26.1</b>	rs7495132	15:91172901_C/T	15	91172901	T	0.12	0.0453
<b>16q23.2</b>	rs9930005	16:80043258_C/A	16	80043258	C	0.4303	0.0061
<b>16q24.1</b>	rs12447408	16:86252544_G/A	16	86252544	A	0.2535	0.0079
<b>16q22.1</b>	rs9924886	16:68743939_A/C	16	68743939	A	0.7321	0.055
<b>16q24.1</b>	rs12149163	16:86339315_T/C	16	86339315	T	0.4976	0.0487
<b>16q24.1</b>	rs62042090	16:86703949_C/T	16	86703949	T	0.2164	0.0481
<b>17q24.3</b>	rs983318	17:70413253_G/A	17	70413253	A	0.2526	0.0397
<b>17p13.3</b>	rs73975586	17:814243_A/T	17	814243	A	0.8732	0.0497
<b>17p12</b>	rs1078643	17:10707241_G/A	17	10707241	A	0.7636	0.0747
<b>17q25.3</b>	rs75954926	17:81061048_A/G	17	81061048	G	0.6568	0.0882
<b>17q25.3</b>	rs373585858	17:80394556_G/A	17	80394556	A	0.0016	0.1103
<b>17p13.3</b>	rs4968127	17:809643_G/A	17	809643	G	0.3684	0.0514
<b>18q21.1</b>	rs11874392	18:46453156_A/T	18	46453156	A	0.545	0.1606

<b>19q13.43</b>	rs73068325	19:59079096_C/T	19	59079096	T	0.1826	0.0066
<b>19p13.11</b>	rs34797592	19:16417198_C/T	19	16417198	T	0.1182	0.0824
<b>19q13.11</b>	rs28840750	19:33519927_T/G	19	33519927	T	0.948	0.1939
<b>19q13.2</b>	rs1963413	19:41871573_G/A	19	41871573	A	0.6119	0.0441
<b>19q13.33</b>	rs12979278	19:49218602_C/T	19	49218602	T	0.53	0.0293
<b>20q13.33</b>	rs2738783	20:62308612_T/G	20	62308612	T	0.2029	0.006
<b>20q13.13</b>	rs6067417	20:48983697_C/T	20	48983697	C	0.5635	0.0331
<b>20q13.12</b>	rs6031311	20:42666475_C/T	20	42666475	T	0.7591	0.0362
<b>20q13.13</b>	rs6091189	20:49256285_C/T	20	49256285	T	0.1529	0.0549
<b>20p12.3</b>	rs994308	20:6603622_C/T	20	6603622	C	0.5939	0.0626
<b>20p12.3</b>	rs28488	20:6762221_C/T	20	6762221	T	0.6388	0.0714
<b>20p12.3</b>	rs556532366	20:8568071_C/T	20	8568071	T	0.0029	0.0715
<b>20p12.3</b>	rs189583	20:6376457_G/C	20	6376457	G	0.3298	0.0795
<b>20p12.3</b>	rs4813802	20:6699595_T/G	20	6699595	G	0.3561	0.0819
<b>20p12.3</b>	rs11087784	20:7740976_A/G	20	7740976	G	0.1523	0.0874
<b>20q13.13</b>	rs6066825	20:47340117_A/G	20	47340117	A	0.6448	0.0719
<b>20q13.13</b>	rs6063514	20:49055318_C/T	20	49055318	C	0.6086	0.0547
<b>20q13.32</b>	rs13831	20:57475191_A/G	20	57475191	G	0.684	0.0334
<b>20q13.33</b>	rs1741640	20:60932414_T/C	20	60932414	C	0.7652	0.1146
<b>20q11.22</b>	rs6058093	20:33213196_A/C	20	33213196	C	0.4942	0.045

Supplemental Table S4a. Surrogate loci and their association with colorectal cancer in European-ancestry population

<b>Reference Variant</b>	<b>Surrogate Variant</b>	<b>Risk Allele</b>	<b>BETA</b>	<b>RAF</b>	<b>R2</b>
<b>5:112097351_A/G</b>	5:112436261_C/T	T	0.5477	0.0026	0.4027
<b>17:80394556_G/A</b>	17:80364244_C/T	T	0.1643	0.0043	1
<b>20:8568071_C/T</b>	20: 9549539_G/T	T	0.0941	0.0015	0.4494