Supplementary Materials to:

Genetic variants associated with colorectal-cancer risk: comprehensive research synopsis, meta-analysis, and epidemiological evidence

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Webappendix notes for Venice criteria

Amount of evidence

A: Large-scale evidence — minor genetic group (alleles or genotypes) in cases and controls>1,000.

B: Moderate amount of evidence — minor genetic group in cases and controls between 100 and 1,000.

C: Little evidence — minor genetic group in cases and controls<100.

Replication of association

A: Little between-study heterogeneity — I^2<25%.

B: Moderate between-study heterogeneity — I^2 between 25% and 50%.

C: Large between-study heterogeneity — I^2>50%.

Protection from bias

A: No observable bias and bias was unlikely to explain the presence of the association.

B: No obvious bias may affect the presence of the association, but there is considerable missing information on the identification of evidence.

C: Bias is demonstrable or is likely to explain the presence of the association.

General checks for bias

1) Association lost with exclusion of first study;

2) Association lost with exclusion of studies deviated from HWE;

3) Small magnitude of association (i.e., 0.87<OR<1.15);

4) Evidence of small-study effect ($p<0.10$ in modified Egger test);

5) Evidence is presented for an excess of individual studies with significant findings ($p<0.10$ in significant bias test).

Appendix Table 1. Associations of 267 genetic variants with colorectal-cancer risk in meta-analyses using different genetic models

						Number evaluated				Colorectal-cancer risk meta-analysis							Dominant model			Recessive model		
Genes	**Variant ID**	**Genetic variants**	**Category**	**Comparison**	**Ethinicity**	**Studies**	**Cases**	**Controls**	**Frequency (%)[a]**	**OR (95% CI)**	***P* value**	***I^2* (%)**	***Q***	***$P_{heterogeneity}$*[b]**	**Modified *P*[c]**	**Excess *P*[d]**	**OR (95% CI)**	***P* value**	***I^2* (%)**	**OR (95% CI)**	***P* value**	***I^2* (%)**
ABCB1	1	rs1128503 (Gly412Gly)	synonymous	T vs C	All	3	195	324	42.59	0.83 (0.52-1.33)	0.434	68	6	0.05	0.82	0.27						
ABCB1	2	rs1202168	intron	T vs C	White	4	6,318	5,805	41.25	1.05 (0.97-1.14)	0.191	55	7	0.08	0.65	0.13	1.1 (0.97-1.24)	0.134	60	1.04 (0.95-1.14)	0.421	0
ABCB1	3	rs2229109 (Ser400Asn)	non-synonymous	A vs G	White	3	4,242	4,178	5.19	0.99 (0.86-1.13)	0.866	0	1	0.57	0.47	1.00	0.99 (0.86-1.14)	0.892	0	0.92 (0.32-2.67)	0.876	2
ABCB1	4	rs868755	intron	T vs G	White	3	2,958	3,255	42.06	1.06 (0.99-1.14)	0.109	0	2	0.39	0.28	0.37	1.09 (0.96-1.24)	0.166	25	1.04 (0.9-1.2)	0.573	14
ABCB1	5	rs9282564 (Asn21Asp)	non-synonymous	G vs A	White	4	5,792	5,234	8.89	1.21 (0.78-1.88)	0.400	96	68	0.00	0.99	0.37	1.23 (0.75-2.02)	0.407	96	1.08 (0.65-1.8)	0.768	52
ABCB1/MDR1	6	rs1045642 (p.Ile1145Ile, c.3435T>C)	synonymous	C vs T	All	13	6,312	7,128	47.52	0.98 (0.89-1.07)	0.611	58	27	0.00	0.83	0.00	1 (0.88-1.13)	0.984	46	0.97 (0.83-1.14)	0.721	61
ABCB1/MDR1	7	rs2032582 (2677G>T)	non-synonymous	T vs G	All	4	558	672	47.02	0.94 (0.78-1.14)	0.555	22	4	0.28	0.02	1.00	0.86 (0.64-1.16)	0.327	25	1.03 (0.74-1.43)	0.865	23
ACE	8	287-bp repeat (I/D)	STR	ins vs del	White	3	509	6,895	47.28	1.01 (0.87-1.18)	0.857	0	1	0.76	0.11	1.00	1.09 (0.85-1.40)	0.509	0	1.08 (0.66-1.79)	0.511	67
ADH1B/ADH2	9	rs1229984 (ADH1B*2; HIS47ARG)	non-synonymous	G vs A	All	6	3,130	4,815	21.27	1.06 (0.89-1.25)	0.523	67	15	0.01	0.44	0.01	1.06 (0.83-1.34)	0.662	72	1.16 (0.93-1.43)	0.185	0
ADH1C/ADH3	10	rs698 (p.Ile350Phe/p.Ile350Val)	non-synonymous	G vs A	All	9	4,817	8,019	36.21	1.03 (0.93-1.15)	0.569	71	27	0.00	0.52	0.07	1.00 (0.87-1.16)	0.952	66	1.12 (0.93-1.34)	0.254	59
ADIPOQ	11	rs1501299	intron	T vs G	All	6	1,743	2,386	30.43	0.98 (0.88-1.09)	0.674	18	6	0.30	0.70	1.00	0.94 (0.80-1.11)	0.480	37	1.10 (0.87-1.37)	0.431	5
ADIPOQ	12	rs266729 (nearGene-5, C-11374G)	intergenic	G vs C	All	6	3,889	4,290	31.79	0.93 (0.84-1.03)	0.158	52	10	0.06	0.11	0.57	0.9 (0.78-1.04)	0.159	57	0.94 (0.81-1.09)	0.392	0
ADIPOR1	13	rs1342387	intron	A vs G	All	3	1,092	1,295	45.91	0.9 (0.8-1.01)	0.068	0	1	0.54	0.11	0.00	0.9 (0.75-1.07)	0.226	0	0.82 (0.67-1.01)	0.068	0
ADIPOR1	14	rs7539542	3' UTR	C vs G	All	3	1,098	1,301	57.23	1.01 (0.84-1.21)	0.950	53	4	0.12	0.88	1.00	1.05 (0.85-1.29)	0.669	0	1.03 (0.74-1.43)	0.861	66
ALDH2	15	rs671 (p.Glu487Lys/Glu504Lys, c.1510G>A)	non-synonymous	A vs G	All	8	4,359	6,078	12.38	1.02 (0.82-1.26)	0.865	70	23	0.00	0.47	0.00	0.98 (0.77-1.24)	0.841	64	1.12 (0.69-1.83)	0.638	67
ALOX12/12-LOX	16	rs1126667 (p.Gln261Arg, c.782G>A)	non-synonymous	A vs G	All	7	2,775	4,912	44.07	1.12 (0.95-1.31)	0.172	78	27	0.00	0.39	0.16	1.13 (0.89-1.43)	0.317	78	1.16 (0.95-1.42)	0.156	55
ALOX5	17	rs4986832 (nearGene-5, -1708 G>A, g.3400G>A)	intergenic	A vs G	All	3	452	723	14.73	0.86 (0.59-1.26)	0.441	58	5	0.09	0.28	0.23	0.87 (0.55-1.35)	0.522	67	0.69 (0.29-1.63)	0.395	0
APC	18	rs1801155 (I1307K, T3920A)	non-synonymous	carriers vs non-carriers	Jewish	3	804	6,188	6.80	1.96 (1.37-2.79)	**1.99×10^{-4}**	0	0	0.84	0.64	1.00	1.96 (1.37-2.79)	**1.99×10^{-4}**	0			
APC	19	rs1801166 (E1317Q)	non-synonymous	(CC+CG) vs GG	All	4	3,574	5,223	1.10	1.69 (0.85-3.35)	0.134	64	8	0.04	0.70	1.00	1.69 (0.85-3.35)	0.134	64			
APC	20	rs2229992 (p.Tyr486Tyr)	synonymous	T vs C	All	3	1,793	1,785	39.78	0.96 (0.87-1.05)	0.357	0	2	0.46	0.48	1.00	0.9 (0.76-1.05)	0.182	26	1.02 (0.85-1.22)	0.818	0
APC	21	rs2229995 (p.Gly2502Ser, c.7504G>A)	non-synonymous	A vs G	White	3	1,130	1,626	1.75	1.25 (0.85-1.85)	0.258	0	0	0.93	0.77	1.00	1.26 (0.85-1.87)	0.250	0			
APC	22	rs41115 (p.Thr1493Thr)	synonymous	C vs T	All	4	2,425	2,817	36.14	1 (0.92-1.1)	0.963	13	3	0.33	0.13	1.00	0.94 (0.82-1.08)	0.391	0	1.01 (0.83-1.23)	0.918	0
APC	23	rs42427 (p.Gly1678Gly)	synonymous	G vs A	All	4	2,543	2,790	35.63	1.01 (0.93-1.09)	0.879	5	3	0.37	0.06	1.00	0.95 (0.82-1.11)	0.529	20	1.01 (0.83-1.24)	0.909	0
APC	24	rs459552 (p.Val1822Asp, c.5465T>A)	non-synonymous	A vs T	All	8	6,654	7,117	22.27	0.96 (0.91-1.02)	0.205	0	5	0.66	0.19	1.00	0.95 (0.89-1.02)	0.171	0	0.98 (0.84-1.14)	0.752	0
APC	25	rs465899 (p.Pro1960Pro)	synonymous	C vs T	All	3	1,822	2,114	45.88	1.02 (0.93-1.12)	0.710	0	2	0.39	0.78	1.00						
APEX1/APEX	26	rs1048945 (p.Gln51His, c.153G>C)	non-synonymous	C vs G	White	3	3,224	3,369	4.05	0.89 (0.63-1.25)	0.497	41	3	0.19	0.57	1.00	0.90 (0.64-1.26)	0.535	39	0.4 (0.09-1.87)	0.242	0
APEX1/APEX	27	rs1130409 (p.Asp148Glu, c.444T>G)	non-synonymous	G vs T	All	9	4,374	5,422	45.57	1.05 (0.89-1.23)	0.582	80	40	0.00	0.64	0.02	1.11 (0.86-1.43)	0.412	82	1.00 (0.8-1.24)	0.976	64
ARLTS1/ARL11	28	rs34301344 (p.Trp149Stop, c.446G>A)	nonsense	(AA+AG) vs GG	White	3	1,367	1,862	0.99	1.00 (0.60-1.65)	0.992	0	0	0.83	0.69	1.00	1.00 (0.60-1.66)	0.992	0			
ARLTS1/ARL11	29	rs3803185 (p.Cys148Arg, T442C, T>C)	non-synonymous	C vs T	White	4	2,123	2,681	46.10	1.07 (0.99-1.17)	0.093	0	2	0.68	0.10	1.00	1.11 (0.89-1.37)	0.352	61	1.09 (0.88-1.34)	0.453	54
ATM	30	rs1801673 (Ex37+62A>T, Asp1853Val)	non-synonymous	A vs G	White	3	2,879	6,384	0.66	0.77 (0.54-1.10)	0.144	0	2	0.46	0.82	1.00	0.79 (0.54-1.14)	0.211	0			
AURKA/STK15	31	rs2273535 (p.Phe31Ile, c.91T>A)	non-synonymous	A vs T	All	6	5,374	4,953	23.70	1.07 (0.94-1.21)	0.308	60	13	0.03	0.66	0.51	1.02 (0.93-1.12)	0.646	11	1.22 (0.91-1.65)	0.184	60
AXIN2	32	rs2240308 (p.Pro50Ser, c.148C>T, G/A)	non-synonymous	A vs G	White	3	3,762	3,934	46.11	1.07 (0.98-1.17)	0.124	29	3	0.24	0.14	1.00	1.09 (0.98-1.20)	0.099	0	1.10 (0.93-1.31)	0.263	45
BLM	33	ASH non-carriers/carriers	frameshift	carriers vs non-carriers	All	3	1,741	11,043	0.84	1.89 (0.74-4.83)	0.184	60	5	0.08	0.76	0.54	1.89 (0.74-4.83)	0.184	60			
BMP4	34	rs17563 (p.Val152Ala, c.455T>C)	non-synonymous	T vs C	All	4	2,919	3,102	63.68	1.01 (0.88-1.15)	0.943	31	4	0.23	0.84	1.00				1.06 (0.87-1.29)	0.562	69
CASP8	35	rs3834129 (nearGene-5, -652 6N del, -/CTTACT)	intergenic	6 bp ins vs del	All	10	6,922	10,750	41.14	1.05 (0.92-1.20)	0.441	82	50	0.00	0.48	0.06	1.04 (0.86-1.27)	0.682	83	1.07 (0.91-1.25)	0.401	54
CASR	36	rs1042636 (p.Arg990Gly, c.2968A>G)	non-synonymous	G vs A	White	4	6,298	7,839	8.52	1.00 (0.92-1.09)	0.936	0	2	0.66	0.68	1.00	1.00 (0.91-1.09)	0.944	0	1.11 (0.71-1.74)	0.631	21
CASR	37	rs1801725 (p.Ala986Ser, c.2956G>T)	non-synonymous	T vs G	White	3	2,733	3,359	13.10	1.30 (0.99-1.72)	0.061	84	12	0.00	0.65	1.00	1.30 (0.96-1.76)	0.089	82	1.76 (0.86-3.61)	0.124	69
CBS	38	rs5742905 (Ile278Thr; CBS I278T)	non-synonymous	C vs T	All	4	3,042	4,374	7.41	1.04 (0.91-1.17)	0.589	0	1	0.76	0.30	1.00	1.04 (0.91-1.19)	0.529	0	0.93 (0.51-1.69)	0.803	0
CCND1	39	rs9344 (rs603965, p.Pro241Pro, c.723G>A/c.870G>A)	synonymous	A vs G	All	22	6,316	8,272	48.15	1.05 (0.98-1.13)	0.197	51	51	0.00	0.56	0.01	1.13 (1.01-1.26)	**0.035**	43	1.00 (0.86-1.17)	0.976	48
CDH1	40	rs16260 (UTR-5, -160C>A)	5' UTR	A vs C	All	9	7,220	7,045	28.09	0.94 (0.88-1.01)	0.116	21	10	0.26	0.22	0.21	0.97 (0.86-1.09)	0.575	40	0.88 (0.74-1.04)	0.129	19
CDKN1A	41	rs1059234 (UTR-3, c.*20C>T)	3' UTR	T vs C	All	3	1,036	1,512	30.29	1.01 (0.87-1.18)	0.912	4	2	0.35	0.91	1.00	1.05 (0.81-1.36)	0.719	29	0.93 (0.69-1.24)	0.596	0
CDKN1A	42	rs1801270 (p.Ser31Arg, c.93C>A)	non-synonymous	A vs C	All	3	1,037	1,511	29.85	0.92 (0.69-1.23)	0.582	55	4	0.11	0.62	0.21	0.87 (0.57-1.34)	0.535	68	0.91 (0.68-1.22)	0.535	0
CHEK2	43	1100delC (fs381X)	frameshift	carriers vs non-carriers	White	7	3,874	11,630	0.71	1.88 (1.29-2.73)	**0.001**	0	5	0.50	0.77	1.00	1.88 (1.29-2.73)	**0.001**	0			
CHEK2	44	rs17879961 (p.Ile200Thr)	non-synonymous	carriers vs non-carriers	White	6	6,042	17,051	3.91	1.56 (1.32-1.84)	**1.22×10^{-7}**	0	3	0.76	0.29	0.10	1.56 (1.32-1.84)	**1.22×10^{-7}**	0			
COMT	45	rs4680 (p.Val158Met, c.472G>A)	non-synonymous	A vs G	White	5	5,074	5,239	48.89	1.05 (0.94-1.16)	0.390	56	9	0.06	0.04	0.41	1.03 (0.9-1.19)	0.650	40	1.04 (0.92-1.18)	0.540	30
CRP	46	rs1205 (c.*1082G>A, 2042C>T)	3' UTR	T vs C	All	5	3,084	8,818	33.80	1.00 (0.87-1.15)	0.993	71	14	0.01	0.49	0.13	1.00 (0.84-1.19)	0.968	60	1.00 (0.76-1.34)	0.976	71
CRP	47	rs1417938 (29T>A)	intron	A vs T	White	3	2,422	3,146	29.83	0.95 (0.85-1.06)	0.322	34	3	0.22	0.65	1.00	0.94 (0.85-1.05)	0.254	0	0.93 (0.75-1.14)	0.478	10
CRP	48	rs1800947 (p.Leu184Leu, c.552G>C)	synonymous	C vs G	All	4	2,916	3,544	5.70	1.04 (0.89-1.20)	0.631	0	2	0.53	0.69	1.00	0.99 (0.84-1.15)	0.857	0	3.84 (1.38-10.74)	**0.010**	0
CTLA4	49	rs231775 (p.Thr17Ala, c.49A>G)	non-synonymous	G vs A	All	5	777	1,356	30.01	1.01 (0.84-1.20)	0.944	31	6	0.21	0.78	1.00	1.11 (0.88-1.39)	0.390	31	0.74 (0.43-1.28)	0.285	50
CX3CR1	50	rs3732378 (T280M)	non-synonymous	A vs G	White	3	3,143	3,269	16.95	1.00 (0.83-1.19)	0.968	44	4	0.17	0.83	1.00	0.99 (0.78-1.26)	0.944	57	0.97 (0.72-1.29)	0.810	0
CYP17A1	51	rs743572	intergenic	G vs A	White	3	4,376	4,588	39.56	1.04 (0.91-1.18)	0.592	67	6	0.05	0.06	0.25	1.08 (0.91-1.29)	0.366	60	0.96 (0.79-1.17)	0.705	52
CYP1A1	52	rs1048943 (*2C, m2, p.Ile462Val, c.1384A>C)	non-synonymous	G vs A	All	16	6,704	8,009	10.33	1.24 (1.05-1.47)	**0.014**	74	58	0.00	0.31	0.78	1.28 (1.02-1.62)	**0.035**	82	1.43 (1.15-1.79)	**0.002**	0
CYP1A1	53	rs1799814 (Thr461Asp)	non-synonymous	A vs C	All	4	3,225	3,492	4.38	0.86 (0.55-1.35)	0.522	71	10	0.02	0.68	0.37	0.85 (0.52-1.39)	0.516	74	1.05 (0.35-3.21)	0.928	0
CYP1A1	54	rs4646903 (m1, MspI, UTR-3, T3801C)	3' UTR	C vs T	All	15	7,258	8,154	14.42	1.05 (0.92-1.19)	0.500	65	40	0.00	0.08	0.52	1.09 (0.92-1.29)	0.339	74	0.95 (0.68-1.32)	0.754	42
CYP1A2	55	rs2069514 (CYP1A2*1C, -3860G>A)	intron	A vs G	All	5	1,289	1,305	20.27	1.12 (0.80-1.58)	0.516	58	10	0.05	0.36	0.42	1.00 (0.69-1.46)	0.984	51	1.62 (0.63-4.15)	0.317	72
CYP1A2	56	rs2470890 (CYP1A2*1B, Asn516Asn; 1545T>C)	synonymous	C vs T	All	4	3,648	3,888	46.18	1.05 (0.90-1.22)	0.547	78	14	0.00	0.03	0.00	1.06 (0.88-1.28)	0.525	65	1.02 (0.82-1.27)	0.870	69
CYP1A2	57	rs762551 (CYP1A2*1F, c.A-163C)	intron	C vs A	All	11	7,667	8,242	30.45	1.02 (0.94-1.1)	0.664	55	22	0.01	0.40	0.06	1.04 (0.93-1.16)	0.517	60	0.97 (0.88-1.09)	0.633	0
CYP1B1	58	rs10012 (p.Arg48Gly, c.142C>G)	non-synonymous	G vs C	White	4	3,825	3,926	29.43	0.03 (0.94-1.14)	0.524	44	5	0.15	0.15	0.22	1.01 (0.92-1.1)	0.901	0	1.13 (0.86-1.48)	0.397	59
CYP1B1	59	rs1056836 (CYP1B1*3, p.Leu432Val, c.1294C>G)	non-synonymous	G vs C	White	9	8,709	9,097	43.27	1.02 (0.97-1.06)	0.488	0	8	0.44	0.64	1.00	1.01 (0.95-1.08)	0.723	0	1.03 (0.96-1.11)	0.415	0
CYP1B1	60	rs1800440 (p.Asn453Ser, c.1358A>G)	non-synonymous	G vs A	White	6	6,679	6,923	18.36	0.97 (0.88-1.07)	0.580	53	11	0.06	0.84	0.26	0.98 (0.86-1.13)	0.810	66	0.94 (0.78-1.14)	0.546	0
CYP2C19	61	rs4244285 (Pro681Pro)	synonymous	T vs C	White	3	2,557	2,664	14.94	0.91 (0.75-1.1)	0.337	53	43	0.12	0.87	0.39	0.88 (0.69-1.11)	0.285	61	0.97 (0.66-1.43)	0.882	0
CYP2C9	62	R144C/I359L	Combined variant	mutation vs wild	All	5	2,885	3,974	18.97	0.91 (0.82-1.02)	0.098	21	5	0.28	0.00	1.00	0.88 (0.76-1.02)	0.079	37	0.97 (0.73-1.28)	0.813	0
CYP2C9	63	rs1057910 (p.Ile359Leu, c.1075A>C)	non-synonymous	G vs A	All	8	8,538	9,182	7.16	1 (0.86-1.16)	0.994	62	19	0.01	0.43	0.02	1.02 (0.87-1.19)	0.832	64	0.69 (0.42-1.12)	0.132	21
CYP2C9	64	rs1799853 (p.Arg144Cys, c.430C>T)	non-synonymous	T vs C	White	6	4,915	5,237	13.31	0.98 (0.91-1.07)	0.668	0	5	0.47	0.68	1.00	0.95 (0.87-1.04)	0.247	0	1.36 (1.02-1.83)	**0.038**	0
CYP2D6	65	rs3892097 (c.353-1G>A)	intron	A vs G	White	3	798	1,512	20.07	1.03 (0.88-1.21)	0.684	0	1	0.69	0.65	1.00						
CYP2E1	66	96-bp insertion	STR	insertion vs non-insertion	All	4	1,412	1,781	16.98	1.24 (1.03-1.49)	0.023	35	5	0.20	0.25	1.00	1.31 (1.03-1.67)	0.027	44	1.19 (0.79-1.8)	0.405	25
CYP2E1	67	rs2031920 (RsaI, c1>c2, C>T)	intergenic	T vs C	All	8	3,796	4,293	11.18	1.12 (0.93-1.34)	0.232	59	17	0.02	0.15	0.18	1.08 (0.9-1.3)	0.426	51	1.55 (0.87-2.74)	0.135	54
CYP2E1	68	rs3813867 (nearGene-5, g.3739G>C, c.-1293G>C)	intergenic	C vs G	White	4	2,345	2,867	3.56	0.84 (0.68-1.05)	0.131	0	1	0.69	0.44	1.00	0.85 (0.68-1.07)	0.174	0			
CYP2E1	69	rs6413432 (Intron, c.967+1143T>A, 7632T>A)	intron	A vs T	All	4	1,406	1,926	8.13	1.09 (0.67-1.76)	0.734	68	9	0.02	0.92	0.22	1.34 (0.72-2.51)	0.363	70			
CYP3A4	70	rs2740574	intergenic	G vs A	White	3	4,464	4,603	3.77	0.96 (0.83-1.12)	0.629	0	0	0.97	0.81	1.00	0.98 (0.84-1.15)	0.825	0	0.55 (0.23-1.3)	0.171	0
DNMT3B	71	rs1569686 (nearGene-5, c.-6-1045G>T, 39179G>T)	intergenic	G vs T	All	4	1,054	1,224	16.99	0.57 (0.47-0.68)	**1.86×10^{-9}**	0	0	0.99	0.81	1.00	0.44 (0.32-0.61)	**4.42×10^{-7}**	45	0.93 (0.54-1.58)	0.775	0
DNMT3B	72	rs2424913 (Intron, c.307-49C>T, -149C>T)	intron	T vs C	All	6	2,398	4,273	61.56	0.96 (0.88-1.05)	0.368	0	3	0.63	0.07	1.00	0.96 (0.84-1.10)	0.569	0	0.93 (0.80-1.09)	0.358	0
DNMT3b	73	rs406193	intergenic	T vs C	White	3	966	2,074	18.44	1.06 (0.84-1.33)	0.631	49	4	0.14	0.20	1.00	1.29 (0.75-2.21)	0.352	79	0.99 (0.72-1.37)	0.968	0
EPHX1	74	rs1051740 (p.Tyr113His, c.337T>C)	non-synonymous	C vs T	All	18	10,478	12,372	30.95	1.02 (0.97-1.08)	0.447	36	27	0.06	0.71	0.03	1.03 (0.97-1.09)	0.379	15	1.06 (0.92-1.23)	0.438	54
EPHX1	75	rs2234922 (p.His139Arg, c.416A>G)	non-synonymous	G vs A	All	13	5,329	6,700	19.38	0.95 (0.87-1.04)	0.241	29	17	0.15	0.86	0.50	0.91 (0.85-0.99)	**0.020**	0	1.18 (0.9-1.57)	0.237	41
ERCC1	76	rs11615 (rs3177700, p.Asn118Asn, c.354T>C)	synonymous	C vs T	White	5	1,060	1,659	37.97	0.98 (0.87-1.10)	0.722	0	4	0.47	0.83	1.00	0.95 (0.79-1.16)	0.617	21	0.98 (0.76-1.25)	0.865	14
ERCC1	77	rs3212986 (8092C>A)	3' UTR	(AA+AC) vs CC	All	3	653	656	41.46	1.04 (0.82-1.32)	0.728	12	2	0.32	0.55	1.00	1.04 (0.82-1.32)	0.728	12			
ERCC2/XPD	78	rs13181 (p.Lys751Gln, c.2251A>C)	non-synonymous	C vs A	All	17	6,039	8,749	30.25	0.99 (0.92-1.05)	0.649	24	21	0.17	0.72	0.40	0.97 (0.90-1.04)	0.379	0	0.96 (0.82-1.12)	0.610	37
ERCC2/XPD	79	rs1799793 (p.Asp312Asn, c.981G>A)	synonymous	A vs G	All	7	5,470	7,135	29.71	1.01 (0.96-1.07)	0.674	0	4	0.68	0.53	1.00	1.00 (0.93-1.08)	0.968	0	1.07 (0.92-1.23)	0.401	24
ERCC4/XPF	80	rs1800067 (R415Q)	non-synonymous	A vs G	White	3	3,173	3,206	10.61	1.01 (0.90-1.14)	0.826	0	1	0.64	0.24	1.00	1.01 (0.89-1.15)	0.889	0	1.03 (0.72-1.48)	0.857	7
ERCC5/XPG	81	rs17655 (p.Asp1104His, c.3310G>C)	non-synonymous	C vs G	All	9	6,322	7,537	24.73	1.05 (1-1.12)	0.064	0	7	0.54	0.71	0.53	1.13 (1.01-1.25)	0.027	38	0.97 (0.85-1.11)	0.647	0
ESR1	82	rs2077647 (Ser10Ser)	synonymous	C vs T	White	3	1,923	2,416	46.83	1.13 (0.85-1.5)	0.413	70	1	0.04	0.35	1.00	1.04 (0.87-1.26)	0.642	11	1.36 (0.7-2.66)	0.369	83
ESR1	83	rs2234693	intron	C vs T	White	5	2,122	2,616	45.47	0.95 (0.73-1.23)	0.678	71	14	0.01	0.89	0.31	1.01 (0.62-1.64)	0.980	80	0.97 (0.84-1.13)	0.701	0
ESR1	84	rs3798577	3' UTR	C vs T	White	3	1,920	2,430	46.48	0.99 (0.91-1.08)	0.820	0	2	0.37	0.67	1.00	0.93 (0.81-1.06)	0.269	0	1.07 (0.92-1.24)	0.410	0
ESR1	85	rs9340799	intron	G vs A	White	7	4,367	5,414	35.54	0.99 (0.93-1.05)	0.710	0	4	0.64	0.09	1.00	1 (0.88-1.13)	0.966	33	0.98 (0.86-1.11)	0.713	0
EXO1	86	rs4149963 (p.Thr439Met, c.1316C>T)	non-synonymous	T vs C	All	4	3,630	3,776	8.26	1.12 (0.83-1.53)	0.461	77	13	0.01	0.44	0.48	1.11 (0.83-1.48)	0.487	69	0.92 (0.33-2.55)	0.872	48
EXO1	87	rs9350 (p.Pro757Leu, c.2270C>T)	non-synonymous	T vs C	All	3	2,492	2,860	17.31	0.80 (0.54-1.17)	0.242	76	8	0.02	0.17	1.00	0.87 (0.61-1.24)	0.447	54	0.60 (0.25-1.43)	0.246	75
FOLH1	88	rs202676 (p.Tyr75His, c.223T>C)	non-synonymous	C vs T	White	3	3,135	3,914	21.27	0.94 (0.87-1.02)	0.165	0	0	0.90	0.33	1.00	0.94 (0.85-1.04)	0.238	0			
FRZB	89	rs288326 (p.Arg200Trp, c.598C>T)	non-synonymous	T vs C	White	3	2,967	4,851	12.02	0.95 (0.86-1.05)	0.312	0	1	0.60	0.71	1.00	0.93 (0.83-1.04)	0.215	0	1.12 (0.74-1.68)	0.603	0
FRZB	90	rs7775 (p.Arg324Gly, c.970C>G)	non-synonymous	G vs C	White	3	1,256	3,000	8.77	1.17 (0.88-1.56)	0.285	66	6	0.06	0.36	0.46	1.04 (0.84-1.28)	0.726	25	3.20 (1.17-8.73)	**0.023**	64
GH1	91	rs2665802 (c.456+90T>A)	intron	A vs T	All	7	3,275	3,848	45.39	0.89 (0.80-0.99)	**0.025**	49	**12**	**0.07**	**0.03**	1.00	0.89 (0.78-1.02)	0.103	36	0.83 (0.71-0.98)	**0.028**	37
GPX1	92	rs1050450 (p.Pro200Leu, c.599C>T)	non-synonymous	T vs C	White	3	1,222	1,813	29.51	1.01 (0.90-1.13)	0.920	0	2	0.45	0.92	1.00	1.04 (0.89-1.21)	0.638	5	0.90 (0.67-1.20)	0.465	0
GPX4	93	rs713041	3' UTR	T vs C	All	4	1,684	2,245	39.06	0.97 (0.82-1.14)	0.689	65	9	0.04	0.07	0.18	0.94 (0.71-1.25)	0.667	76	0.99 (0.83-1.18)	0.873	0
GSTA1	94	*A/*B	Combined variant	mutation vs wild	White	3	464	574	39.11	1.13 (0.84-1.53)	0.418	62	5	0.07	0.42	0.27	1.18 (0.86-1.60)	0.303	22	1.17 (0.52-2.61)	0.704	83
GSTA1	95	rs3957357	intergenic	A vs G	White	3	1,313	1,327	39.90	1 (0.9-1.12)	0.989	0	0	0.88	0.44	1.00	1 (0.85-1.17)	0.996	0	1 (0.81-1.22)	0.974	0
GSTM1	96	Present/Null	phenotype	null vs present	All	56	20,552	31,419	50.64	1.10 (1.04-1.17)	**0.001**	48	106	0.00	0.00	0.06						
GSTM3	97	rs1799735 (c.468+21delAGG, delAGG)	intron	AGG del vs ins	White	3	2,531	2,707	15.96	0.94 (0.72-1.23)	0.653	83	12	0.00	0.26	0.24	0.92 (0.68-1.25)	0.596	83	1.14 (0.68-1.90)	0.631	45
GSTP1	98	rs1138272 (p.Ala114Val, c.341C>T)	non-synonymous	T vs C	All	10	7,160	7,789	9.84	0.92 (0.8-1.06)	0.234	56	21	0.02	0.99	0.59	0.92 (0.79-1.08)	0.310	54	0.74 (0.51-1.06)	0.097	18

GSTP1	99	rs1695 (p.Ile105Val, c.313A>G)	non-synonymous	G vs A	All	33	9,986	15,562	27.54	0.98 (0.93-1.03)	0.487	25	43	0.10	0.50	0.27	0.99 (0.93-1.07)	0.868	29	0.95 (0.86-1.06)	0.361	12
GSTT1	100	Present/Null	phenotype	null vs present	All	43	15,144	23,847	29.53	1.15 (1.05-1.27)	**0.004**	68	131	0.00	0.28	**0.03**						
GSTZ1	101	rs3177427 (GLU32LYS)	non-synonymous	A vs G	All	3	2,860	3,271	29.27	0.93 (0.73-1.19)	0.569	57	5	0.10	0.16	1.00	0.93 (0.69-1.25)	0.624	61	1.02 (0.86-1.22)	0.826	0
HFE	102	rs1799945 (H63D)	non-synonymous	G vs C	White	7	3,729	4,079	14.70	1.03 (0.93-1.15)	0.581	7	7	0.37	0.42	1.00	1.03 (0.93-1.14)	0.608	0	1.18 (0.73-1.92)	0.494	30
HFE	103	rs1800562 (rs111535158, p.Cys282Tyr, c.1005G>A)	non-synonymous	A vs G	White	10	2,502	30,857	7.43	1.05 (0.92-1.21)	0.467	0	3	0.94	**0.06**	1.00	1.04 (0.9-1.2)	0.622	0	1.22 (0.52-2.87)	0.648	32
HIF1A	104	rs11549465 (p.Pro582Ser, c.1744C>T)	non-synonymous	T vs C	All	3	3,019	4,950	8.43	1.04 (0.74-1.46)	0.841	69	7	0.04	0.52	0.13	1.01 (0.69-1.50)	0.944	73			
HPGD	105	rs2612656	intron	G vs A	White	3	2,979	5,575	22.75	1.09 (0.97-1.24)	0.162	65	6	0.06	0.57	1.00	1.08 (0.93-1.25)	0.294	62	1.31 (1.05-1.64)	**0.016**	21
HPGD	106	rs7349744	intron	A vs G	White	3	3,014	5,622	30.54	1.00 (0.93-1.07)	0.897	0	2	0.44	0.40	1.00	0.96 (0.87-1.04)	0.308	0	1.13 (0.91-1.41)	0.258	51
HPGD	107	rs7349744	intron	C vs A	White	3	3,001	5,624	7.56	0.96 (0.84-1.09)	0.516	11	2	0.33	0.84	1.00	0.96 (0.81-1.13)	0.589	38	0.96 (0.32-2.86)	0.944	68
HPGD	108	rs8752	3' UTR	G vs A	White	3	3,008	5,632	41.98	1.01 (0.86-1.17)	0.936	22	11	0.00	0.43	**0.09**	0.96 (0.75-1.23)	0.749	85	1.09 (0.96-1.24)	0.201	23
HPGD	109	rs9312555	3' UTR	G vs A	White	3	3,015	5,634	15.42	0.93 (0.86-1.02)	0.134	0	2	0.44	**0.06**	1.00	0.92 (0.83-1.01)	0.091	0	1.00 (0.74-1.36)	0.992	0
ICAM1	110	rs5498 (p.Lys469Glu, c.1405A>G)	non-synonymous	G vs A	All	4	3,229	3,357	42.63	0.96 (0.79-1.17)	0.719	70	10	0.02	0.90	**0.02**	0.91 (0.72-1.16)	0.441	58	1.02 (0.80-1.31)	0.873	43
IGF1	111	(CA)n (R19>non-R19)	STR	non R19 vs R19	All	8	5,493	6,827	36.71	0.99 (0.89-1.09)	0.769	70	23	0.00	0.36	0.03	0.92 (0.73-1.16)	0.491	88	1.03 (0.92-1.15)	0.611	20
IGF1	112	rs35767	intergenic	T vs C	All	3	2,717	4,880	24.75	0.95 (0.8-1.14)	0.599	59	5	0.09	0.15	0.25	0.98 (0.79-1.21)	0.826	60	0.75 (0.62-0.91)	**0.003**	0
IGFBP1	113	rs4619 (p.Ile253Met,c.759A>G)	non-synonymous	G vs A	White	3	3,570	3,660	35.53	0.93 (0.75-1.16)	0.535	85	13	0.00	0.63	0.48	0.89 (0.63-1.26)	0.509	89	1.02 (0.89-1.17)	0.787	0
IGFBP3	114	rs2854744 (nearGene-5, C-202A, A>C)	intergenic	C vs A	All	9	6,872	10,606	46.30	1.03 (0.98-1.07)	0.284	0	2	0.98	**0.13**	1.00	1 (0.93-1.07)	0.985	0	1.07 (0.99-1.15)	0.078	0
IGFBP3	115	rs2854746 (p.Ala32Gly, c.95C>G)	non-synonymous	G vs C	All	5	4,282	7,365	46.08	1.07 (1.01-1.14)	0.016	0	2	0.07	0.68	1.00	1.12 (1.03-1.22)	**0.012**	0	1.05 (0.95-1.17)	0.327	15
IL10	116	rs1800872 (nearGene-5, g.4433A>C, -592C>A)	intergenic	A vs C	White	6	1,561	2,439	22.57	0.94 (0.81-1.1)	0.444	41	8	0.13	0.83	0.28	0.9 (0.78-1.05)	0.168	16	1.13 (0.73-1.76)	0.580	45
IL10	117	rs1800896 (nearGene-5, g.3943A>G, -1082A>G)	intergenic	G vs A	White	5	1,134	1,492	46.68	0.98 (0.84-1.15)	0.793	44	7	0.13	0.70	0.15	1.00 (0.8-1.24)	0.976	31	0.94 (0.76-1.16)	0.550	9
IL16	118	rs4072111 (p.Pro434Ser, c.1300C>T)	non-synonymous	T vs C	All	3	3,193	3,577	12.31	1.06 (0.9-1.25)	0.494	43	4	0.17	0.72	1.00	1.03 (0.87-1.23)	0.716	38	1.32 (0.82-2.14)	0.253	26
IL1B	119	rs1143627 (nearGene-5, g.4970C>T, -31T>C)	intergenic	C vs T	All	6	1,593	2,170	33.66	1.07 (0.97-1.19)	0.156	0	1	0.97	0.03	1.00	1.11 (0.96-1.27)	0.152	3	1.1 (0.83-1.44)	0.516	43
IL1B	120	rs16944	intergenic	G vs A	All	3	577	828	36.41	0.96 (0.82-1.13)	0.626	0	1	0.67	0.60	1.00	0.82 (0.55-1.24)	0.352	63	1.08 (0.78-1.48)	0.649	0
IL4	121	rs2243250 (nearGene-5, -509C>T)	intergenic	T vs C	White	6	1,225	1,754	18.93	0.92 (0.76-1.12)	0.401	42	9	0.12	0.48	0.30	0.91 (0.74-1.13)	0.401	35	0.88 (0.6-1.27)	0.484	0
IL4R	122	rs1801275 (p.Gln576Arg, c.1727A>G)	non-synonymous	G vs A	All	4	803	986	18.97	1.05 (0.88-1.24)	0.624	0	1	0.69	0.49	1.00	1.03 (0.84-1.27)	0.757	0	1.18 (0.71-1.95)	0.522	0
IL4R	123	rs1805012 (C431R)	non-synonymous	G vs A	White	3	2,840	3,233	11.18	0.95 (0.70-1.31)	0.764	59	5	0.09	0.25	0.16	0.93 (0.66-1.32)	0.697	60	1.32 (0.82-2.11)	0.250	0
IL4R	124	rs1805015 (S503P)	non-synonymous	C vs T	White	3	640	892	16.26	1.02 (0.84-1.25)	0.834	0	1	0.61	0.47	1.00	0.97 (0.78-1.22)	0.818	0	1.73 (0.85-3.51)	0.129	0
IL6	125	rs1800795	intergenic	C vs G	All	14	6,952	8,657	38.55	1.01 (0.93-1.11)	0.749	65	38	0.00	0.50	0.00	1.02 (0.91-1.14)	0.733	59	1 (0.89-1.13)	0.963	34
IL6	126	rs1800797	intergenic	(AA+AG) vs GG	White	4	2,612	3,381	60.75	0.96 (0.87-1.07)	0.468	0	2	0.57	0.61	1.00	0.96 (0.87-1.07)	0.468	0			
IL6R	127	rs2228145 (rs8192284, Asp358Val)	non-synonymous	C vs A	White	3	3,070	20,173	30.92	0.97 (0.91-1.04)	0.435	0	2	0.47	0.08	1.00	1.02 (0.87-1.20)	0.795	36	0.94 (0.82-1.07)	0.363	0
IL8	128	rs4073 (nearGene-5, T-251A)	intergenic	A vs T	White	10	3,520	4,381	45.88	1.04 (0.92-1.18)	0.525	70	30	0.00	0.52	0.09	1.05 (0.87-1.28)	0.620	71	1.04 (0.87-1.23)	0.638	55
IRS1	129	rs1801278 (p.Gly971Arg, c.2911G>A)	non-synonymous	A vs G	White	7	7,048	7,533	6.92	1.08 (0.96-1.22)	0.219	39	10	0.13	0.99	0.45	1.15 (0.95-1.39)	0.674	74	1.05 (0.66-1.68)	0.834	0
IRS2	130	rs1805097 (p.Gly1057Asp, c.3170G>A)	non-synonymous	A vs G	White	3	2,318	2,814	41.13	0.96 (0.89-1.04)	0.327	0	2	0.47	0.32	1.00	0.93 (0.74-1.17)	0.555	79	0.99 (0.87-1.13)	0.920	0
LCT	131	rs4988235 (c.1917+326C>T, 13910 C>T)	intron	T vs C	White	7	2,103	2,492	41.75	0.99 (0.87-1.14)	0.879	51	12	0.06	**0.06**	**0.02**	0.94 (0.79-1.10)	0.438	30	1.02 (0.78-1.33)	0.886	50
LEP	132	rs7799039	intergenic	A vs G	White	3	2,324	2,776	43.98	0.95 (0.88-1.03)	0.222	0	2	0.46	0.85	1.00	0.98 (0.87-1.10)	0.704	0	0.89 (0.77-1.02)	0.478	0
LEPR	133	rs1137101 (p.Gln223Arg, c.668A>G)	non-synonymous	G vs A	White	3	1,100	1,166	44.47	1.08 (0.96-1.22)	0.187	0	1	0.69	**0.09**	1.00	1.14 (0.92-1.40)	0.226	16	1.09 (0.89-1.34)	0.384	0
LIPC	134	rs6083 (N215S)	non-synonymous	A vs G	All	3	4,702	4,914	36.52	0.93 (0.86-1.01)	0.075	31	3	0.24	0.93	1.00	0.95 (0.87-1.03)	0.192	0	0.85 (0.74-0.99)	0.032	25
MBL2	135	rs11003125	intergenic	G vs C	All	3	822	872	32.17	0.91 (0.7-1.17)	0.465	53	4	0.12	0.74	1.00						
MBL2	136	rs1800450 (Gly54Asp)	non-synonymous	A vs G	All	4	3,395	3,546	13.85	0.97 (0.8-1.18)	0.775	42	5	0.16	0.03	1.00	0.83 (0.54-1.27)	0.381	61			
MBL2	137	rs1800451 (p.Gly57Glu)	non-synonymous	A vs G	All	3	819	843	6.17	1.31 (0.93-1.83)	0.120	0	2	0.43	0.48	1.00						
MBL2	138	rs5030737 (R52C)	non-synonymous	T vs C	All	4	1,185	1,199	6.21	1.03 (0.81-1.3)	0.805	0	1	0.81	0.40	1.00	1.13 (0.82-1.57)	0.453	0			
MBL2	139	rs7096206	intergenic	C vs G	All	3	826	873	19.82	0.98 (0.82-1.17)	0.795	0	0	0.81	0.34	1.00						
MDM2	140	rs2279744 (nearGene-5, SNP309, c.14+309T>G)	intergenic	G vs T	All	10	3,032	2,538	42.99	1.12 (0.94-1.34)	0.211	76	39	0.00	0.54	1.00	1.24 (0.92-1.67)	0.154	80	1.06 (0.86-1.29)	0.607	39
MGMT	141	rs12917 (p.Leu115Phe, c.343C>T)	non-synonymous	T vs C	All	7	4,127	7,284	12.99	1.00 (0.90-1.11)	0.992	13	7	0.33	0.23	1.00	0.94 (0.79-1.11)	0.459	49	1.54 (1.14-2.08)	**0.005**	0
MGMT	142	rs2308321 (p.Ile174Val, c.520A>G)	non-synonymous	G vs A	All	6	3,843	8,783	12.79	1.00 (0.80-1.25)	0.984	74	19	0.00	0.70	**0.01**	1.00 (0.79-1.26)	0.976	71	1.10 (0.61-1.99)	0.757	35
MLH1	143	rs121912963 (p.D132H, c.415G>C)	non-synonymous	C vs G	All	3	1,412	1,508	0.43	2.74 (1.31-5.75)	**0.008**	15	2	0.31	0.75	1.00	2.78 (1.34-5.74)	**0.006**	12			
MLH1	144	rs1799977 (p.Ile219Val, c.655A>G)	non-synonymous	G vs A	All	10	6,384	8,972	29.56	1.01 (0.92-1.11)	0.904	58	21	0.01	0.66	0.26	1.03 (0.92-1.16)	0.589	55	0.95 (0.81-1.11)	0.509	29
MLH1	145	rs1800734 (nearGene-5/UTR-5, -93G>A)- MSI+ CRC	5' UTR	A vs G	White	5	801	10,890	21.11	1.51 (1.34-1.69)	**6.74×10^{-12}**	46	7	0.11	**0.02**	1.00	1.46 (1.27-1.69)	**2.75×10^{-7}**	40	2.45 (1.92-3.12)	**6.97×10^{-13}**	0
MLH1	145	rs1800734 (nearGene-5/UTR-5, -93G>A)	5' UTR	A vs G	White	7	17,783	13,777	21.31	1.05 (1.01-1.09)	**0.014**	0	5	0.52	0.57	1.00	1.06 (1.01-1.11)	**0.014**	0	1.06 (0.95-1.18)	0.290	0
MLH1	146	rs63750447 (p.Val384Asp, 1151 T>A)	non-synonymous	A vs T	Asian	3	937	919	1.96	2.14 (1.12-4.12)	**0.022**	41	3	0.18	**0.04**	1.00	2.17 (1.14-4.15)	**0.019**	38			
MLH1	147	rs9876116 (Intron 14, c.1668-19A>G)	intron	G vs A	White	3	2,024	2,143	44.47	0.93 (0.85-1.02)	0.631	15	2	0.31	0.56	1.00	0.96 (0.84-1.09)	0.516	0	0.85 (0.70-1.02)	0.077	26
MMP1	148	rs1799750 (nearGene-5, -1607 1G/2G)	intergenic	2G vs 1G	All	8	1,477	1,751	39.63	0.76 (0.64-0.92)	**0.004**	61	18	0.01	0.09	0.15	0.70 (0.54-0.89)	**0.004**	60	0.80 (0.64-0.99)	**0.041**	8
MMP2	149	rs243865 (-1306C/T)	intergenic	T vs C	All	4	786	868	21.43	0.96 (0.67-1.36)	0.805	60	8	0.06	0.86	0.17	0.91 (0.62-1.35)	0.645	56	1.16 (0.74-1.81)	0.520	0
MMP3	150	rs3025058	intergenic	5A vs 6A	All	7	1,119	1,493	33.19	1.01 (0.84-1.22)	0.922	42	10	0.11	0.67	0.19	0.94 (0.71-1.26)	0.691	55	1.15 (0.91-1.45)	0.240	8
MMP7	151	rs11568818 (nearGene-5, -181A>G)	intergenic	G vs A	All	4	652	828	16.00	0.86 (0.5-1.47)	0.576	72	11	0.01	0.02	0.03	0.85 (0.44-1.65)	0.629	75			
MMP9	152	rs3918242 (nearGene-5, g.3430C>T, -1562 C>T)	intergenic	T vs C	All	4	644	792	13.26	0.87 (0.66-1.14)	0.303	25	4	0.26	**0.07**	0.25	0.91 (0.67-1.22)	0.522	26	0.36 (0.11-1.14)	0.080	0
MSH2	153	rs2303425 (nearGene-5, g.4951T>C, c.-118T>C)	intergenic	C vs T	White	3	1,775	2,206	12.78	1.01 (0.87-1.17)	0.944	14	2	0.31	0.99	1.00	0.97 (0.78-1.20)	0.764	47	2.34 (0.56-9.81)	0.246	74
MSH2	154	rs2303428 (c.2006-6T>C)	intron	C vs T	All	5	4,371	4,697	11.42	0.96 (0.87-1.06)	0.450	0	3	0.54	0.78	1.00	0.95 (0.86-1.06)	0.391	0	1.03 (0.71-1.49)	0.890	0
MSH2	155	rs4987188 (p.Gly322Asp, c.965G>A)	non-synonymous	A vs G	All	7	4,004	3,849	1.52	1.24 (0.97-1.58)	0.086	0	3	0.77	0.77	0.39	1.24 (0.97-1.59)	0.093	0			
MSH3	156	rs184967 (p.Arg949Gln, c.3099G>A)	non-synonymous	A vs G	White	3	5,085	7,136	15.25	1.11 (1.03-1.20)	**0.005**	0	2	0.38	**0.09**	1.00	1.11 (1.02-1.21)	**0.016**	0	1.31 (1.03-1.66)	**0.026**	0
MSH3	157	rs26279 (p.Ala1045Thr,c.3133G>A)	non-synonymous	G vs A	White	4	5,691	7,665	28.13	1.1 (1.03-1.17)	**0.006**	17	4	0.31	0.71	0.60	1.09 (1.01-1.17)	**0.023**	0	1.23 (1.06-1.43)	**0.007**	18
MSH6	158	rs1042821 (p.Gly39Glu, c.116G>A)	non-synonymous	A vs G	White	4	3,136	6,063	17.22	0.99 (0.86-1.13)	0.832	59	7	0.06	0.45	1.00	0.99 (0.84-1.16)	0.865	60	0.98 (0.75-1.27)	0.856	0
MSH6	159	rs1800935 (p.Asp180Asp, c.540T>C)	synonymous	C vs T	White	3	5,132	4,709	29.45	0.96 (0.90-1.02)	0.159	0	2	0.42	0.70	1.00	0.95 (0.88-1.03)	0.197	0	0.94 (0.81-1.08)	0.358	0
MTHFD1	160	rs1950902 (p.Arg134Lys, c.401G>A)	non-synonymous	A vs G	White	3	3,822	5,452	18.78	0.90 (0.84-0.98)	**0.010**	0	0	0.79	0.71	1.00	0.88 (0.81-0.97)	**0.007**	0	0.91 (0.72-1.16)	0.447	0
MTHFD1	161	rs2236225 (p.Arg653Gln, c.1958G>A)	non-synonymous	A vs G	White	6	6,535	9,347	45.19	0.98 (0.90-1.07)	0.603	67	15	0.01	0.47	**0.04**	0.96 (0.89-1.04)	0.280	15	1.01 (0.86-1.17)	0.952	70
MTHFR	162	rs1801131 (p.Ala429Glu, c.1286A>C)	non-synonymous	C vs A	All	34	14,965	22,017	30.14	0.99 (0.94-1.03)	0.514	32	49	0.04	0.87	**0.00**	1 (0.95-1.05)	0.880	20	0.94 (0.86-1.03)	0.207	22
MTHFR	163	rs1801133 (p.Ala222Val, c.C677T)	non-synonymous	T vs C	All	68	32,608	44,383	33.50	0.99 (0.95-1.03)	0.683	64	188	0.00	**0.04**	**0.00**	1.01 (0.96-1.07)	0.638	63	0.92 (0.85-1)	**0.036**	52
MTR	164	rs1805087 (A2756G)	non-synonymous	G vs A	All	19	12,945	17,655	19.42	0.99 (0.94-1.05)	0.717	33	26	0.09	0.57	0.44	0.98 (0.92-1.03)	0.412	15	1.03 (0.88-1.21)	0.692	32
MTRR	165	rs10380 (p.His595Tyr, c.1783C>T)	non-synonymous	T vs C	White	4	3,869	5,141	9.31	1.05 (0.87-1.26)	0.638	57	7	0.07	0.95	1.00	1.01 (0.83-1.22)	0.952	53	1.61 (1.02-2.52)	**0.039**	6
MTRR	166	rs1532268 (Ser175Leu)	non-synonymous	T vs C	White	3	3,496	4,809	36.48	1.01 (0.94-1.08)	0.779	5	2	0.35	0.78	1.00	1.05 (0.96-1.15)	0.317	0	0.91 (0.74-1.13)	0.384	48
MTRR	167	rs162036 (Ile22Met)	non-synonymous	G vs A	White	3	3,506	4,793	11.14	1.01 (0.83-1.23)	0.936	65	6	0.06	0.63	1.00	1.01 (0.83-1.22)	0.960	57	1.20 (0.78-1.84)	0.401	14
MTRR	168	rs1801394 (Ile22Met)	non-synonymous	A vs G	All	16	7,674	11,593	48.33	0.96 (0.91-1.01)	0.110	37	22	0.12	0.23	1.00	0.95 (0.89-1.03)	0.218	12	0.94 (0.85-1.03)	0.187	42
MUTYH	169	rs3219484 (p.Val22Met, c.64G>A)	non-synonymous	A vs G	White	3	5,391	5,222	8.20	0.95 (0.68-1.34)	0.787	91	21	0.00	0.90	0.20	0.94 (0.65-1.38)	0.764	91	1.06 (0.61-1.84)	0.826	0
MUTYH	170	rs3219489 (p.Gln324His, c.972G>C)	non-synonymous	C vs G	All	4	5,082	5,280	28.44	1.09 (0.92-1.28)	0.317	81	16	0.00	0.13	1.00	1.04 (0.88-1.23)	0.660	67	1.21 (0.87-1.67)	0.263	78
MUTYH	171	rs34612342 (p.Tyr165Cys, c.494A>G, Tyr179Cys)	non-synonymous	GG vs AA	White	17	27,041	19,641	0.01	3.32 (1.13-9.81)	**0.030**	0	0	1.00	0.10	0.39						
MUTYH	172	rs36053993 (p.Gly382Asp, c.1178G>A)/ss49785896, G396D	non-synonymous	AA vs GG	White	17	26,957	19,870	0.00	6.49 (2.57-1.35)	**7.49×10^{-5}**	0	5	0.85	0.80	0.76						
MUTYH	173	Biallelic mutation	Combined variant	Carriers vs wild homozygotes	White	17	25,981	18,811	0.01	10.19 (5.00-22.04)	**5.30×10-10**	0	7	0.88	0.23	0.16						
MUTYH	174	Monoallelic mutation	Combined variant	Carriers vs wild homozygotes	White	17	25,981	18,811	1.69	1.17 (1.01-1.34)	**0.036**	0	10	0.84	0.15	1.00						
NAT1	175	Phenotype	Phenotype	Fast vs slow	All	15	7,336	9,825	44.37	1.03 (0.92-1.16)	0.596	61	36	0.00	0.46	**0.02**						
NAT2	176	Fast/slow	phenotype	Slow vs fast	All	35	11,684	15,348	47.39	0.94 (0.89-0.99)	**0.023**	1	34	0.45	0.79	0.69						
NAT2	177	rs1799930 (NAT2*6B, G590A)	non-synonymous	A vs G	White	3	3,793	4,021	28.66	1.05 (0.98-1.13)	0.144	0	0	0.79	**0.07**	1.00	1.09 (1.00-1.19)	0.061	0	1.00 (0.85-1.18)	0.984	0
NBS1	178	rs1805794 (E185Q)	non-synonymous	G vs C	White	4	3,185	3,424	33.63	0.85 (0.63-1.14)	0.276	86	22	0.00	0.44	1.00	0.89 (0.65-1.21)	0.441	65	0.70 (0.43-1.16)	0.168	79
NFKB1	179	rs28362491 (-94ins/delATTG)	intergenic	ATTG del vs ins	All	8	2,393	4,597	42.32	1.17 (0.96-1.43)	0.125	85	46	0.00	0.08	0.24	1.5 (1.02-2.21)	0.041	89	1.07 (0.84-1.36)	0.578	62
NFkBIA	180	rs696	3' UTR	A vs G	All	3	1,355	2,020	43.19	1.01 (0.89-1.15)	0.881	24	3	0.27	0.50	1.00	1.01 (0.69-1.47)	0.984	79	1.10 (0.92-1.32)	0.289	0
NOD2/CARD15	181	rs2066844 (p.Arg702Trp, c.2104C>T)	non-synonymous	(TT+CT) vs CC	White	9	3,297	3,088	6.15	1.35 (1.02-1.78)	**0.038**	34	12	0.14	**0.02**	**0.02**	1.35 (1.02-1.78)	**0.038**	34			
NOD2/CARD15	182	rs2066845 (p.Gly908Arg, c.2722G>C)	non-synonymous	C vs G	White	8	3,252	2,988	1.10	1.31 (0.93-1.85)	0.124	0	7	0.44	0.90	0.36	1.31 (0.91-1.87)	0.144	4			
NOD2/CARD15	183	rs2066847 (frameshift, 3020insC, WT/insC, L1007fs)	frameshift	Ins carriers vs wild homozygotes	White	11	4,337	5,395	6.21	1.30 (1.02-1.65)	**0.032**	33	15	0.13	0.53	0.35	1.30 (1.02-1.65)	**0.032**	33			
NOS3	184	rs1799983 (p.Asp298Glu, c.894G>T)	non-synonymous	T vs G	All	4	1,599	1,750	27.91	0.99 (0.75-1.31)	0.957	80	17	0.00	0.78	0.00	1.03 (0.77-1.37)	0.860	69	0.91 (0.53-1.57)	0.726	69
NQO1	185	rs1131341 (rs4986998, p.Arg139Trp, c.415C>T)	non-synonymous	T vs C	White	4	4,436	4,725	4.07	0.99 (0.86-1.15)	0.914	0	2	0.51	0.19	1.00	0.97 (0.83-1.13)	0.699	0			
NQO1	186	rs1800566 (p.Pro187Ser/p.Pro153Ser, c.648C>T)	non-synonymous	T vs C	All	12	7,209	8,783	22.90	1.07 (0.99-1.15)	0.090	32	16	0.13	0.74	0.28	1.09 (1.00-1.20)	0.064	0	1.06 (0.90-1.24)	0.507	6
OGG1	187	rs1052133 (p.Ser326Cys, c.977C>G)	non-synonymous	G vs C	All	18	6,654	8,599	25.79	1.10 (0.99-1.23)	0.085	71	58	0.00	0.18	0.46	1.08 (0.95-1.23)	0.254	66	1.25 (1.00-1.57)	0.054	55
PARP1	188	rs1136410 (p.Val762Ala, c.2285T>C)	non-synonymous	C vs T	All	4	3,536	4,586	22.57	1.05 (0.97-1.14)	0.222	0	2	0.59	0.54	1.00	1.05 (0.95-1.16)	0.337	0	1.14 (0.91-1.43)	0.254	0
PGR	189	rs1042838 (Val496Leu)	non-synonymous	T vs G	White	3	2,266	2,668	14.24	1.1 (0.96-1.26)	0.171	14	2	0.31	0.02	1.00	1.14 (0.96-1.35)	0.132	24	0.99 (0.69-1.43)	0.968	0
PLA2G2A	190	rs11677 (G>A)	3' UTR	A vs G	White	3	2,803	3,825	11.76	1.00 (0.83-1.20)	0.976	64	6	0.06	0.96	1.00	1.01 (0.83-1.23)	0.944	61	0.88 (0.57-1.37)	0.569	0
PMS2	191	rs1805319 (rs2228005/rs6463524, p.Ser260Ser)	synonymous	G vs C	White	3	3,713	3,374	18.55	1.06 (0.85-1.33)	0.596	80	10	0.01	0.17	0.31	1.05 (0.81-1.36)	0.697	80	1.09 (0.83-1.43)	0.549	10
PPARG	192	rs1801282 (p.Pro12Ala, c.36C>G)	non-synonymous	G vs C	All	18	13,758	20,300	9.10	0.97 (0.91-1.03)	0.339	18	21	0.24	0.32	0.15	0.97 (0.9-1.04)	0.400	21	0.89 (0.72-1.12)	0.324	0
PPARG	193	rs3856806 (p.His447His,c.1431C>T)	non-synonymous	T vs C	All	10	6,189	8,707	11.39	1.03 (0.96-1.11)	0.412	2	9	0.42	0.74	0.33	1.07 (0.98-1.16)	0.115	0	0.77 (0.39-1.52)	0.446	72
PTGS1/COX1	194	rs1236913 (p.Trp8Arg, c.22C>T)	non-synonymous	T vs C	White	4	4,033	6,783	7.27	0.95 (0.85-1.06)	0.327	0	1	0.70	0.22	1.00	0.96 (0.85-1.07)	0.441	0	0.67 (0.29-1.52)	0.332	18
PTGS1/COX1	195	rs5788 (p.Gly213Gly, c.639C>A)	synonymous	A vs C	White	4	3,989	6,659	13.35	1.13 (1.04-1.22)	**0.004**	0	2	0.64	0.27	1.00	1.16 (1.06-1.27)	**0.001**	0	1.04 (0.78-1.39)	0.779	0
PTGS2/COX2	196	rs20417	intergenic	C vs G	All	13	3,637	5,964	9.80	1.07 (0.95-1.19)	0.265	24	16	0.20	0.23	0.12	1.07 (0.93-1.24)	0.339	40	1.15 (0.83-1.59)	0.417	0
PTGS2/COX2	197	rs4648298	3' UTR	(GG+AG) vs AA	White	5	2,261	2,636	5.31	0.88 (0.52-1.52)	0.653	71	14	0.01	0.51	0.20	0.88 (0.52-1.52)	0.653	71			
PTGS2/COX2	198	rs5275 (UTR-3, c.*427T>C, 8473T>C)	3' UTR	C vs T	All	10	6,059	8,084	33.17	1.01 (0.97-1.07)	0.579	0	4	0.98	**0.90**	1.00	1.01 (0.95-1.08)	0.701	0	1.03 (0.93-1.15)	0.565	0
PTGS2/COX2	199	rs5277 (p.Val102Val, c.306G>C)	synonymous	C vs G	White	8	4,246	5,675	16.21	0.99 (0.91-1.07)	0.764	10	3	0.79	0.80	1.00	1.00 (0.90-1.10)	0.912	11	0.92 (0.69-1.24)	0.589	10

PTGS2/COX2	200	rs689466 (nearGene-5, g.38139393T>C)	intergenic	G vs A	All	9	4,076	7,610	30.34	0.88 (0.80-0.98)	**0.018**	56	18	**0.02**	0.23	1.00	0.85 (0.74-0.97)	**0.014**	58	0.86 (0.71-1.05)	0.140	30
RAD18	201	rs373572 (p.Arg302Gln, c.905G>A)	non-synonymous	C vs T	All	3	3,174	3,397	29.22	1.19 (1-1.43)	0.055	67	6	0.05	0.19	1.00	1.18 (1.01-1.37)	0.033	27	1.27 (0.87-1.86)	0.221	72
RAD51	202	rs1801320 (135G/C)	5' UTR	C vs G	White	4	753	720	32.15	1.01 (0.31-3.27)	0.987	97	109	0.00	0.18	0.01	0.89 (0.43-1.88)	0.768	89	1.27 (0.1-16.43)	0.854	95
RNASEL	203	rs486907 (p.Arg462Gln, c.1385G/A)	non-synonymous	A vs G	White	3	808	1,132	35.03	1.05 (0.92-1.2)	0.469	0	1	0.61	0.21	1.00	1.03 (0.85-1.24)	0.789	0	1.22 (0.8-1.87)	0.353	55
SCD	204	rs7849	3' UTR	G vs A	All	3	2,011	2,580	18.49	0.85 (0.73-0.98)	0.025	29	3	0.25	0.11	1.00	0.85 (0.72-1.02)	0.084	33	0.64 (0.4-1.02)	0.058	41
SELS	205	rs34713741	intergenic	T vs C	All	3	1,442	2,071	33.22	1.13 (0.96-1.33)	0.139	60	5	0.08	0.66	0.17	1.21 (1.05-1.39)	**0.008**	0	1.07 (0.63-1.83)	0.795	80
(SEP15)	206	rs5859	3' UTR	T vs C	All	3	1,409	2,086	7.48	1.04 (0.87-1.23)	0.689	0	0	0.80	0.39	1.00	1.03 (0.84-1.26)	0.779	0			
SEPP1	207	rs3877899 (Ala264Thr)	non-synonymous	T vs C	All	3	1,441	2,079	7.07	1.12 (0.94-1.33)	0.211	0	1	0.52	0.30	1.00	1.19 (0.96-1.48)	0.105	0			
SEPP1	208	rs7579	3' UTR	T vs C	All	3	1,346	1,967	29.05	1.03 (0.86-1.22)	0.779	60	5	0.08	**0.02**	0.12	1.04 (0.86-1.26)	0.660	42	1.06 (0.72-1.58)	0.757	57
SERPINE1/PAI-1	209	rs1799889 (nearGene-5, -675 4G/5G)	intergenic	5G vs 4G	White	4	2,241	4,534	44.94	0.97 (0.90-1.04)	0.368	0	1	0.73	0.58	1.00	0.87 (0.78-0.97)	**0.014**	0	1.09 (0.96-1.23)	0.208	0
SHBG	210	rs6259 (D356N)	non-synonymous	A vs G	White	3	4,677	4,823	11.60	1.04 (0.95-1.14)	0.383	0	1	0.71	0.22	1.00	1.03 (0.94-1.14)	0.509	0	1.22 (0.85-1.75)	0.278	0
SHMT1	211	rs1979276 (UTR-3, C1420T)	3' UTR	T vs C	All	5	1,697	1,994	31.97	0.93 (0.82-1.05)	0.215	30	6	0.22	0.13	0.37	0.94 (0.83-1.08)	0.379	0	0.84 (0.60-1.18)	0.322	57
SLC19A1/RFC1	212	rs1051266 (p.His27Arg, c.80A>G, 80G>A)	non-synonymous	A vs G	White	5	3,775	5,340	43.66	1.02 (0.91-1.14)	0.757	61	10	0.04	0.94	0.18	1.05 (0.88-1.24)	0.603	63	1.00 (0.88-1.13)	0.968	18
SLC22A4/OCTN1	213	rs1050152 (L503F)	non-synonymous	T vs C	White	3	3,110	3,243	53.39	1.06 (0.94-1.21)	0.342	38	3	0.20	0.29	1.00	1.12 (0.94-1.34)	0.194	29	1.02 (0.84-1.23)	0.849	21
SOD2	214	rs4880 (rs1799725, Ala16Val)	non-synonymous	T vs C	All	5	2,400	3,003	69.08	0.97 (0.89-1.06)	0.478	0	0	1.00	0.92	1.00	0.99 (0.85-1.16)	0.928	0	0.94 (0.82-1.07)	0.332	0
SULT1A1	215	rs9282861 (p.Arg213His, c.638G>A)	non-synonymous	A vs G	All	11	3,802	5,042	33.40	1.02 (0.92-1.12)	0.757	51	20	0.03	0.78	**0.04**	1.02 (0.93-1.11)	0.726	0	0.99 (0.75-1.32)	0.960	74
SULT1A2	216	rs1059491 (p.Asn235Thr, c.714A>C)	non-synonymous	C vs A	White	3	1,806	1,986	31.80	1.05 (0.95-1.17)	0.308	6	2	0.35	0.21	1.00	1.08 (0.95-1.23)	0.219	0	1.03 (0.82-1.30)	0.779	15
TCF7L2	217	rs7903146	intron	T vs C	All	4	3,899	20,299	26.32	1.07 (0.94-1.22)	0.293	66	9	0.03	0.20	1.00	1.07 (0.91-1.27)	0.393	68	1.08 (0.92-1.27)	0.324	5
TCN2	218	rs1801198 (p.Arg259Pro, c.776C>G)	non-synonymous	G vs C	White	3	2,582	5,117	43.70	0.96 (0.86-1.07)	0.453	54	4	0.11	0.59	1.00	0.95 (0.85-1.06)	0.322	13	0.97 (0.81-1.15)	0.697	46
TERT	219	rs2736100	intron	T vs G	White	8	16,176	18,135	49.34	1.07 (1.04-1.1)	**2.92×10^{-5}**	0	6	0.53	0.30	0.44	1.14 (1.08-1.2)	**2.03×10^{-6}**	0	1.06 (1-1.13)	0.069	15
TGFB1	220	rs1800469 (nearGene-5, C-509T)	intergenic	T vs C	All	10	4,405	5,383	38.74	0.88 (0.79-0.97)	**0.013**	55	20	0.02	0.97	0.71	0.83 (0.71-0.97)	**0.018**	58	0.83 (0.73-0.95)	**0.006**	8
TGFB1	221	rs1800470 (p.Leu10Pro, c.29C>T, c.T29C)	non-synonymous	C vs T	All	5	1,204	2,191	45.14	1.17 (0.95-1.44)	0.142	66	12	0.02	0.31	1.00	1.12 (0.90-1.38)	0.312	29	1.26 (0.89-1.78)	0.197	68
TGFB1	222	rs4803455	intron	A vs C	All	3	2,786	3,516	47.48	1.10 (0.99-1.22)	0.066	46	4	0.16	0.47	1.00	1.15 (0.99-1.34)	0.066	39	1.14 (1.01-1.28)	**0.030**	0
TGFBR1	223	rs11466445 (Frameshift in exon 1, *6A/9A)	frameshift	9 bp del vs ins	All	10	6,338	6,689	9.19	1.04 (0.96-1.13)	0.379	1	9	0.43	0.39	1.00	1.06 (0.96-1.16)	0.246	7	0.85 (0.58-1.23)	0.373	0
TGFBR1	224	rs334354 (Intron, IVS7G+24A, c.1024+24G>A)	intron	A vs G	All	4	1,226	2,776	26.71	1.08 (0.88-1.33)	0.472	68	9	0.03	0.53	0.30	1.03 (0.78-1.36)	0.834	71	1.38 (1.04-1.84)	**0.029**	8
TLR3	225	rs3775291 (Leu412Phe)	non-synonymous	AA vs (AG+GG)	White	3	4,867	5,604	9.23	0.94 (0.80-1.11)	0.465	30	3	0.24	0.21	1.00				0.94 (0.80-1.11)	0.465	30
TLR4	226	rs11536898	intergenic	AA vs (AC+CC)	White	3	2,501	3,239	1.85	0.79 (0.37-1.67)	0.529	53	4	0.12	0.61	0.20				0.79 (0.37-1.67)	0.529	53
TLR4	227	rs1927911	intron	T vs C	White	3	2,512	3,276	27.79	0.99 (0.91-1.07)	0.757	0	1	0.61	0.12	1.00	0.97 (0.88-1.08)	0.575	0	1.03 (0.85-1.25)	0.757	0
TLR4	228	rs4986790 (p.Asp299Gly)	non-synonymous	T vs C	White	3	714	1,156	4.28	1.27 (0.67-2.4)	0.459	68	6	0.04	0.38	0.31	1.2 (0.66-2.19)	0.542	62			
TLR4	229	rs4986791 (Thr399Ile)	non-synonymous	T vs C	All	4	3,054	3,632	5.37	1.07 (0.84-1.37)	0.564	16	4	0.31	0.28	1.00	1.08 (0.83-1.41)	0.583	20			
TNF	230	rs1799724 (nearGene-5, -857C>T)	intergenic	T vs C	White	3	745	732	13.05	0.97 (0.72-1.30)	0.818	36	3	0.21	0.89	1.00	0.96 (0.69-1.34)	0.795	40			
TNF	231	rs1800629 (nearGene-5, G-308A)	intergenic	A vs G	All	11	2,296	2,283	13.78	1.28 (1-1.62)	**0.046**	71	34	0.00	0.39	0.48	1.27 (0.99-1.64)	0.065	67	1.41 (0.81-2.46)	0.222	51
TP53	232	rs1042522 (p.Pro72Arg, c.215C>G)	non-synonymous	C vs G	All	31	10,515	12,909	31.28	1 (0.92-1.1)	0.922	72	107	0.00	0.48	**0.00**	1.01 (0.9-1.12)	0.906	67	1.01 (0.87-1.17)	0.875	52
TP53	233	rs17878362 (nearGene-5, IVS3 16bp Del/Ins)	intergenic	16 bp ins vs del	White	5	1,569	1,891	15.49	0.96 (0.73-1.28)	0.787	73	15	0.01	0.69	**0.01**	0.96 (0.70-1.32)	0.810	72	0.92 (0.57-1.48)	0.719	0
TP73	234	G4C14/A4T14	Combined variant	mutation vs wild	All	4	858	1,168	24.02	1.20 (1.04-1.40)	**0.015**	6	3	0.36	0.11	1.00	1.10 (0.83-1.45)	0.509	55	1.74 (1.22-2.48)	**0.002**	0
TYMS/TS	235	28-bp tandem repeat	STR	3R vs 2R	All	7	3,220	3,900	37.17	1.13 (0.97-1.32)	0.215	66	18	0.01	**0.03**	0.64	1.13 (0.93-1.36)	0.213	55	1.17 (0.89-1.52)	0.264	56
TYMS/TS	236	rs16430 (UTR-3, 1494 ins/del6, -/CTTTAA)	3' UTR	6 bp del vs ins	All	5	3,796	3,963	32.35	0.99 (0.89-1.09)	0.310	38	6	0.17	0.56	1.00	1.01 (0.92-1.1)	0.903	0	0.9 (0.69-1.18)	0.430	59
UBD	237	rs2076485 (I68T)	non-synonymous	C vs T	White	3	4,281	6,157	26.07	1.07 (1.01-1.14)	**0.034**	0	1	0.77	0.63	1.00	1.08 (0.99-1.16)	0.073	0	1.15 (0.97-1.35)	0.103	12
UGT1A1	238	rs10929302 (Intron, c.862-9898G>A, c.-3156G>A)	intron	A vs G	All	3	1,560	1,987	35.68	1.03 (0.93-1.14)	0.535	0	0	0.85	0.52	1.00	1.03 (0.89-1.19)	0.689	0	1.07 (0.87-1.32)	0.509	0
UGT1A1	239	rs4124874 (Intron, c.862-10021T>G, c.-3279T>G)	intron	G vs T	All	3	1,560	1,987	50.35	1.05 (0.91-1.22)	0.472	42	3	0.18	0.80	1.00	1.06 (0.72-1.57)	0.772	70	1.03 (0.88-1.21)	0.741	0
UGT1A1	240	rs8175347	STR	TA7 vs TA6	All	8	3,345	4,177	32.46	1.00 (0.90-1.1)	0.920	43	12	0.09	0.67	0.02	0.99 (0.85-1.15)	0.860	55	1.02 (0.88-1.19)	0.761	0
UGT1A6	241	rs1105879 (p.Arg184Ser, c.552A>C)	non-synonymous	C vs A	White	3	4,006	4,295	34.33	0.97 (0.91-1.04)	0.401	0	0	0.97	0.47	1.00	0.95 (0.87-1.03)	0.222	0	1.01 (0.88-1.15)	0.897	0
UGT1A6	242	T181A/R184S	Combined variant	mutation vs wild	White	4	3,066	3,915	34.41	1.04 (0.97-1.12)	0.303	10	3	0.35	0.89	1.00	1.07 (0.96-1.18)	0.238	11	1.03 (0.89-1.18)	0.719	0
UGT1A7	243	Phenotype	phenotype	low vs high	All	5	1,174	1,533	30.37	1.23 (0.97-1.55)	0.084	73	15	0.01	0.53	0.64	1.25 (0.95-1.65)	0.110	65	1.32 (0.88-1.97)	0.177	59
UGT1A7	244	rs17868323 (N129K)	non-synonymous	T vs G	All	3	1,545	1,930	31.37	0.90 (0.77-1.05)	0.168	31	3	0.24	0.53	0.48	0.88 (0.77-1.01)	0.070	0	0.83 (0.56-1.22)	0.337	43
VDR	245	rs11568820	5' UTR	(AA+AG) vs GG	White	4	3,228	3,455	36.61	1.15 (1.04-1.27)	**0.005**	0	0	0.93	0.42	0.58	1.15 (1.04-1.27)	**0.005**	0			
VDR	246	rs1544410 (Intron, BsmI, b>B, c.1024+283G>A)	intron	A vs G	All	17	11,687	12,301	38.96	0.85 (0.72-0.99)	**0.040**	93	242	93.40	0.38	**0.05**	0.78 (0.62-0.96)	**0.022**	91	0.72 (0.55-0.94)	**0.015**	88
VDR	247	rs2228570 (Fok1)	non-synonymous	A vs G	All	20	13,631	15,155	37.32	1.00 (0.94-1.06)	0.959	53	41	0.00	0.74	**0.02**	1 (0.9-1.12)	0.974	1	0.98 (0.87-1.09)	0.665	41
VDR	248	rs2238136	intron	A vs G	All	7	3,435	3,176	23.36	1.01 (0.93-1.1)	0.779	8	7	0.37	0.75	0.18						
VDR	249	rs731236 (TaqI, T>t, p.Ile352Met, c.1056T>C)	non-synonymous	C vs T	All	12	4,360	4,193	33.17	1.02 (0.94-1.09)	0.680	15	13	0.29	0.34	0.31	1 (0.87-1.15)	0.976	10	1.1 (0.81-1.51)	0.545	63
VDR	250	rs7975232 (ApaI)	intron	A vs C	All	9	5,421	5,377	43.08	1.08 (0.98-1.19)	0.105	58	19	0.02	0.31	0.12	1.10 (0.91-1.35)	0.327	59	1.15 (0.92-1.43)	0.226	53
VEGF	251	rs1570360 (-1154G>A)	intergenic	A vs G	All	4	1,150	1,342	28.20	0.98 (0.87-1.12)	0.798	0	1	0.74	**0.05**	1.00	0.98 (0.83-1.16)	0.816	0	0.98 (0.74-1.29)	0.869	0
VEGF	252	rs2010963 (UTR-5, 634G>C)	5' UTR	C vs G	All	6	2,200	2,126	33.00	1.02 (0.88-1.17)	0.836	55	11	0.05	0.64	0.16	0.98 (0.76-1.26)	0.867	75	1.04 (0.86-1.25)	0.686	0
VEGF	253	rs3025039 (UTR-3, C936T)	3' UTR	T vs C	All	6	1,925	1,884	19.43	1.19 (1.04-1.37)	**0.014**	29	7	0.22	0.94	1.00	1.21 (1.01-1.45)	**0.037**	38	1.27 (0.96-1.68)	0.097	0
VEGF	254	rs699947 (−2578 C/A)	intergenic	A vs C	All	8	3,313	4,082	43.15	1.02 (0.91-1.14)	0.710	52	15	0.04	0.67	1.00	0.99 (0.87-1.13)	0.898	24	1.09 (0.89-1.33)	0.413	44
VEGF	255	rs833061	intergenic	C vs T	All	3	766	633	33.65	1.36 (0.93-2.00)	0.116	81	11	0.01	0.75	0.60	1.44 (0.90-2.30)	0.129	74	1.61 (0.85-3.03)	0.144	74
WRN	256	rs1346044 (p.Cys1367Arg, c.4099T>C)	non-synonymous	C vs T	White	3	4,693	4,840	26.02	1.05 (0.99-1.12)	0.114	0	1	0.54	0.22	1.00	1.08 (1.00-1.17)	0.064	0	1.02 (0.87-1.19)	0.810	0
WRN	257	rs1801195 (rs2725362, p.Leu1074Phe, c.3222G>T)	non-synonymous	T vs G	White	3	4,681	4,833	44.93	0.95 (0.89-1.02)	0.129	18	2	0.29	0.95	0.42	0.95 (0.87-1.03)	0.234	0	0.91 (0.81-1.02)	0.116	16
WRN	258	rs2230009 (rs4987236, p.Val114Ile, c.340G>A)	non-synonymous	A vs G	White	3	4,695	4,842	6.29	0.95 (0.84-1.07)	0.368	0	0	0.96	1.00	1.00	0.95 (0.84-1.08)	0.418	0	0.86 (0.49-1.49)	0.582	0
XPA	259	rs1800975	5' UTR	A vs G	White	3	593	1,137	36.46	0.82 (0.70-0.96)	**0.016**	4	2	0.36	**0.06**	0.57	0.78 (0.57-1.06)	0.107	37	0.64 (0.45-0.91)	**0.012**	0
XPC	260	rs2228000 (A499V)	non-synonymous	T vs C	All	3	779	2,035	35.72	0.93 (0.76-1.14)	0.472	58	5	0.09	0.71	0.23	0.87 (0.67-1.11)	0.258	50	1.09 (0.64-1.84)	0.757	67
XPC	261	rs2228001 (p.Gln939Lys, c.2815C>A)	non-synonymous	C vs A	All	9	2,978	5,204	37.38	1.08 (1.01-1.16)	0.021	0	4	0.83	0.58	0.61	1.2 (1.09-1.33)	**1.84×10^{-4}**	0	0.96 (0.84-1.1)	0.529	0
XPC	262	rs2279017	intron	(AA+AC) vs CC	All	3	439	458	62.23	1.21 (0.83-1.77)	0.312	44	4	0.17	**0.09**	0.27	1.21 (0.83-1.77)	0.312	44			
XRCC1	263	rs1799782 (p.Arg194Trp, c.580C>T)	non-synonymous	T vs C	All	14	3,170	6,441	14.87	1.07 (0.91-1.27)	0.392	54	28	0.01	0.30	0.52	1.09 (0.91-1.3)	0.369	49	0.97 (0.77-1.22)	0.787	0
XRCC1	264	rs25487 (p.Gln399Arg, c.1196A>G)	non-synonymous	G vs A	All	25	9,541	14,448	31.87	1.04 (0.97-1.11)	0.281	49	47	0.00	0.30	**0.03**	1.02 (0.95-1.11)	0.570	32	1.12 (0.95-1.32)	0.195	60
XRCC1	265	rs25489 (p.Arg280His, c.839G>A)	non-synonymous	A vs G	All	6	4,270	4,760	7.63	1.02 (0.91-1.15)	0.690	0	4	0.62	**0.03**	1.00	1.01 (0.89-1.15)	0.893	0	1.21 (0.8-1.82)	0.372	0
XRCC2	266	rs3218536 (p.Arg188His, c.563G>A)	non-synonymous	A vs G	White	4	4,219	4,488	8.17	1.09 (0.96-1.24)	0.174	15	4	0.32	0.19	0.37	1.11 (0.99-1.24)	0.080	0	1.00 (0.49-2.05)	0.992	50
XRCC3	267	rs861539 (p.Thr241Met, c.722C>T)	non-synonymous	T vs C	All	11	4,157	5,534	25.55	1.16 (0.91-1.47)	0.237	88	85	0.00	0.22	**0.04**	1.22 (0.9-1.64)	0.202	87	1.3 (0.93-1.81)	0.124	62

[a] *Frequency of effect allele or effect genotype(s) in controls based on primary meta-analysis.*
[b] *P for heterogeneity was calculated using a Cochran's Q test.*
[c] *P value of Harbord's modified test for small-study effects*
[d] *P value of test for disagreements in the number of observed and expected significant studies*

Webappendix table 2. Included studies for the genetic variants showing a statistically significant association with colorectal-cancer risk from meta-analyses, based on all available data or ethnicity-specific data

Gene	Variant	Ethnicity	Studies	References
37 variants in table 3				
APC	rs1801155 (I1307K, T3920A)	Jewish	3	1-3
CHEK2	rs17879961 (Ile200Thr)	White	6	4-8
CHEK2	1100delC (fs381X)	White	7	4, 6, 9-13
CYP1A1	rs1048943 (*2C, Ile462Val)	All	16	14-28
CYP2E1	96-bp insertion	All	4	29-32
DNMT3B	rs1569686 (39179G>T)	All	4	33-36
GH1	rs2665802 (c.456+90T>A)	All	7	37-40
GSTM1	Present/Null	All	56	14, 15, 18, 19, 22-25, 38, 41-82
GSTT1	Present/Null	All	43	14, 15, 18, 22, 25, 38, 41, 42, 44-46, 48-58, 60, 61, 64-70, 73, 75, 76, 78, 79, 81-83
IGFBP3	rs2854746 (Ala32Gly)	All	5	84-88
MLH1	rs63750447 (Val384Asp)	Asian	3	89-91
MLH1	rs1800734 (-93G>A)	White	5	92-96
MLH1	rs121912963 (D132H)	All	3	90, 97
MMP1	rs1799750 (-1607 1G/2G)	All	8	98-105
MSH3	rs184967 (Arg949Gln)	White	3	7, 94, 106
MSH3	rs26279 (Ala1045Thr)	White	4	7, 94, 106, 107
MTHFD1	rs1950902 (Arg134Lys)	White	3	7, 108, 109
MUTYH	rs34612342 (Tyr165Cys)	White	17	110-124
MUTYH	rs36053993 (Gly382Asp)	White	17	110-124
MUTYH	Monoallelic mutation	White	17	110-124
MUTYH	Biallelic mutation	White	17	110-124
NAT2	Phenotype	All	35	15, 16, 19, 23, 24, 47, 57, 62, 71, 125-149
NOD2/CARD15	rs2066847 (L1007fs)	White	11	150-160
NOD2/CARD15	rs2066844 (Arg702Trp)	White	9	150-158
PTGS1/COX1	rs5788 (Gly213Gly)	White	4	38, 161, 162
PTGS2/COX2	rs689466	All	9	161, 163-168
SCD	rs7849	All	3	161, 169
TERT	rs2736100	White	8	170, 171
TGFB1	rs1800469 (C-509T)	All	10	172-180
TNF	rs1800629	All	11	153, 180-188
TP73	G4C14/A4T14	All	4	189-192
UBD	rs2076485 (I68T)	White	3	7, 162
VDR	rs11568820	White	4	193-196
VDR	rs1544410 (BsmI)	All	17	38, 194, 197-207
VEGF	rs3025039 (C936T)	All	6	175, 208-212

XPA	rs1800975	White	3	213-215
XPC	rs2228001 (Gln939Lys)	All	9	213, 215-220
8 variants in table 4				
CDH1	rs16260 (-160C>A)	White	6	221-225
MTRR	rs1801394 (Ile22Met)	Asian	3	226-228
NFKB1	rs28362491 (-94ins/delATTG)	White	6	229-231
OGG1	rs1052133 (Ser326Cys)	White	14	38, 114, 117, 213, 217, 218, 232-238
PTGS2/COX2	rs20417	Asian	4	167, 239, 240
NQO1	rs1800566 (Pro187Ser)	White	8	7, 25, 38, 46, 241-244
TCF7L2	rs7903146	White	3	182, 245, 246
TP53	rs1042522	Asian	8	192, 247-253

Appendix table 3 Detailed information for genetic variants nominally significantly associated with colorectal-cancer risk in meta-analyses of all available data or ethnicity-specific data

						Number evaluated			Colorectal-cancer risk meta-analysis					Venice criteria gards‡	False-positive report probability§	Cumulative evidence of association	Amount of Evidence		Replication	Protection from Bias	Reason for Bias	Reason for bias exemption	Initial study influence		Deviation from HWE	Identified by GWAS if common variants	OR>1.15	Modified p	Excess p
Genes	**Variants**	**Alleles ***	**Chromosome**	**Frequency (%)†**	**Ethnicity**	**Studies**	**Cases**	**Controls**	**Genetic models**	**OR (95% CI)**	***P*** **value**	I^2 (%)	$P_{heterogeneity}$				**Numbers**	**Grade**					**OR (95% CI)**	**p value**					
Associations identified by analysis of all available data																													
APC	rs1801155	A/T	5	6.80	Jewish	3	804	6,188	Dominant	1.96 (1.37-2.79)	1.99×10^{-4}	0	0.84	BAA	0.007	Strong	492	B	A	A	NA	NA	2.11 (1.31-3.39)	0.002	Not tested	NA	No	0.64	1.00
CHEK2	1100delC	1100delC/–	22	0.71	White	7	3,874	11,630	Dominant	1.88 (1.29-2.73)	0.001	0	0.50	×AA	0.036	Strong	142	×	A	A	NA	NA	1.28 (1.05-2.38)	0.029	Not tested	NA	No	0.77	1.00
CHEK2	rs17879961	C/T	22	3.91	White	6	6,042	17,051	Dominant	1.56 (1.32-1.84)	1.22×10-7	0	0.76	BAA	<0.001	Strong	898	B	A	A	NA	NA	1.58 (1.30-1.91)	4.43×10^{-6}	Not tested	NA	No	0.29	0.10
CYP1A1	rs1048943	G/A	15	10.33	All	16	6,704	8,009	Additive	1.24 (1.05-1.47)	0.014	74	0.00	ACC	0.338	Weak	3,194	A	C	C	HWE, GWAS	NA	1.21 (1.01-1.43)	0.034	Yes	No	No	0.31	0.78
CYP2E1	96-bp insertion	96-bp ins/–	10	16.98	All	4	1,412	1,781	Additive	1.24 (1.03-1.49)	0.023	35	0.20	ABA	0.462	Weak	1,175	A	B	A	NA	NA	1.38 (1.01-1.89)	0.044	No	NA	No	0.25	1.00
DNMT3B	rs1569686	G/T	20	16.99	All	4	1,054	1,224	Additive	0.57 (0.47-0.68)	1.86×10-9	0	0.99	BAA	<0.001	Strong	657	B	A	A	exempted	Highly consistent of OR	0.56 (0.45-0.70)	2.22×10^{-7}	No	No	No	0.81	1.00
GH1	rs2665802	A/T	17	45.39	All	7	3,275	3,848	Additive	0.89 (0.80-0.99)	0.025	49	0.07	ABC	0.508	Weak	6,323	A	B	C	Low OR, GWAS, Small study	NA	0.93 (0.87-0.99)	0.024	No	No	Yes	0.03	1.00
GSTM1	Present/Null	NA	1	50.64	All	56	20,552	31,419	null vs present	1.10 (1.04-1.17)	0.001	48	0.00	ABC	0.046	Moderate	26,715	A	B	C	low OR, Small study, excess of significant studies	NA	1.10 (1.04-1.17)	0.001	NA	NA	Yes	0.00	0.06
GSTT1	Present/Null	NA	22	29.53	All	43	15,144	23,847	null vs present	1.15 (1.05-1.27)	0.004	68	0.00	ACC	0.144	Weak	11,515	A	C	C	excess of significant studies	NA	1.16 (1.05-1.27)	0.004	NA	NA	No	0.28	0.03
IGFBP3	rs2854746	G/C	7	46.08	All	5	4,282	7,365	Additive	1.07 (1.01-1.14)	0.016	0	0.07	AAC	0.447	Weak	10,895	A	A	C	First study, HWE, GWAS	NA	1.06 (1.00-1.13)	0.064	Yes	No	Yes	0.68	1.00
MLH1	rs121912963	C/G	3	0.43	All	3	1,412	1,508	Additive	2.74 (1.31-5.75)	0.008	15	0.31	×AC	0.231	Weak	48	×	A	C	First study	NA	1.95 (0.86-4.42)	0.108	No	NA	No	0.75	1.00
MLH1	rs1800734	A/G	3	21.11	White	5	801	10,890	Additive	1.51 (1.34-1.69)	6.74×10^{-12}	46	0.11	AAA	<0.001	Strong	5,061	A	B	A	Small study, exempted	Highly consistent of OR	1.47 (1.30-1.66)	7.75×10^{-16}	No	No GWAS for MSI-H	No	0.02	1.00
MLH1	rs63750447	A/T	3	1.96	Asian	3	937	919	Additive	2.14 (1.12-4.12)	0.022	41	0.18	BBC	0.458	Weak	102	B	B	C	First study, Small study	NA	1.61 (0.89-2.91)	0.117	No	NA	No	0.04	1.00
MMP1	rs1799750	2G/1G	11	39.63	All	8	1,477	1,751	Additive	0.76 (0.64-0.92)	0.004	61	0.01	ACC	0.138	Weak	2,439	A	C	C	Small study, GWAS	NA	0.78 (0.64-0.95)	0.012	No	No	No	0.09	0.15
MSH3	rs184967	A/G	5	15.25	White	3	5,085	7,136	Additive	1.11 (1.03-1.20)	0.005	0	0.38	AAC	0.182	Weak	3,857	A	A	C	GWAS, Low OR, Small study	NA	1.09 (1.01-1.18)	0.023	No	No	Yes	0.09	1.00
MSH3	rs26279	G/A	5	28.13	White	4	5,691	7,665	Additive	1.1 (1.03-1.17)	0.006	17	0.31	AAC	0.157	Weak	7,697	A	A	C	First study, GWAS, Low OR		1.11 (0.99-1.24)	0.085	No	No	Yes	0.71	0.60
MTHFD1	rs1950902	A/G	14	18.78	White	3	3,822	5,452	Additive	0.90 (0.84-0.98)	0.010	0	0.79	AAC	0.275	Weak	3,389	A	A	C	First study, GWAS, Low OR	NA	0.93 (0.82-1.06)	0.265	No	No	Yes	0.71	1.00
MUTYH	Monoallelic mutation	NA	1	1.69	White	17	25,981	18,811	Carriers vs wild homozygotes	1.17 (1.01-1.34)	0.036	0	0.84	BAC	0.546	Weak	829	B	A	C	First study	NA	1.11 (0.95-1.30)	0.184	Not tested	NA	No	0.15	1.00
MUTYH	Biallelic mutation	NA	1	0.01	White	17	25,981	18,811	Carriers vs wild homozygotes	10.19 (5.00-22.04)	5.30×10-10	0	0.88	×AA	<0.001	Strong	105	×	A	A	NA	NA	9.29 (4.29-20.11)	1.51×10^{-6}	Not tested	NA	No	0.23	0.16
MUTYH	rs34612342	G/A	1	0.01	White	17	27,041	19,641	GG vs AA	3.32 (1.13-9.81)	0.030	0	1.00	×AA	0.533	Strong	18	×	A	A	NA	NA	3.32 (1.13-9.81)	0.030	Not tested	NA	No	0.10	0.39
MUTYH	rs36053993	A/G	1	0.00	White	17	26,957	19,870	AA vs GG	6.49 (2.57-1.35)	7.49×10-5	0	0.85	×AA	0.003	Strong	40	×	A	A	NA	NA	5.22 (1.94-14.01)	0.001	Not tested	NA	No	0.80	0.76
NAT2	Fast/slow	NA	8	47.39	All	35	11,684	15,348	Slow vs fast	0.94 (0.89-0.99)	0.023	1	0.45	AAC	0.47	Weak	12,622	A	A	C	First study, Low OR	NA	0.96 (0.91-1.01)	0.096	Not tested	NA	Yes	0.79	0.69
NOD2	rs2066844	T/C	16	6.15	White	9	3,297	3,088	Dominant	1.35 (1.02-1.78)	0.038	34	0.14	BBC	0.581	Weak	436	B	B	C	First study, Small study, excess of significant studies	NA	1.25 (0.98-1.60)	0.072	Not tested	NA	No	0.02	0.02
NOD2	rs2066847	C/–	16	6.21	White	11	4,337	5,395	Dominant	1.30 (1.02-1.65)	0.032	33	0.13	BBC	0.546	Weak	641	B	B	C	First study	NA	1.23 (0.98-1.55)	0.074	Not tested	NA	No	0.53	0.35
PTGS1	rs5788	A/C	9	13.35	White	4	3,989	6,659	Additive	1.13 (1.04-1.22)	0.004	0	0.64	AAC	0.113	Weak	2,953	A	A	C	GWAS, Low OR	NA	1.11 (1.01-1.22)	0.027	No	No	Yes	0.27	1.00
PTGS2	rs689466	G/A	1	30.34	All	9	4,076	7,610	Additive	0.88 (0.80-0.98)	0.018	56	0.02	ACC	0.405	Weak	6,664	A	C	C	HWE, GWAS, Low OR	NA	0.91 (0.84-0.99)	0.032	Yes	No	Yes	0.23	1.00
SCD	rs7849	G/A	10	18.49	All	3	2,011	2,580	Additive	0.85 (0.73-0.98)	0.025	29	0.25	ABC	0.488	Weak	1,631	A	B	C	HWE, GWAS	NA	0.76 (0.62-0.92)	0.005	Yes	No	No	0.11	1.00
TERT	rs2736100	T/G	5	49.34	White	8	16,176	18,135	Additive	1.07 (1.04-1.1)	2.92×10-5	0	0.53	AAC	0.001	Moderate	34,514	A	A	C	low OR	NA	1.07 (1.04-1.11)	2.34×10^{-5}	No	No	Yes	0.30	0.44
TGFB1	rs1800469	T/C	19	38.74	All	10	4,405	5,383	Additive	0.88 (0.79-0.97)	0.013	55	0.02	ACC	0.33	Weak	7,257	A	C	C	GWAS, Low OR	NA	0.90 (0.81-0.99)	0.031	Yes	No	Yes	0.97	0.71
TNF	rs1800629	A/G	6	13.78	All	11	2,296	2,283	Additive	1.28 (1-1.62)	0.046	71	0.00	ACC	0.625	Weak	1,403	A	C	C	First study, HWE, GWAS	NA	1.27 (0.99-1.63)	0.055	Yes	No	No	0.39	0.48
TP73	G4C14/A4T14	NA	1	24.02	All	4	858	1,168	Additive	1.20 (1.04-1.40)	0.015	6	0.36	AAC	0.363	Weak	1,037	A	A	C	First study	NA	1.10 (0.91-1.32)	0.350	Yes	NA	No	0.11	1.00
UBD	rs2076485	C/T	6	26.07	White	3	4,281	6,157	Additive	1.07 (1.01-1.14)	0.034	0	0.77	AAC	0.563	Weak	5,523	A	A	C	First study, GWAS, Low OR	NA	1.08 (0.98-1.18)	0.109	No	No	Yes	0.63	1.00
VDR	rs11568820	A/G	12	36.61	White	4	3,228	3,455	Dominant	1.15 (1.04-1.27)	0.005	0	0.93	AAB	0.165	Weak	2,551	A	A	B	GWAS	NA	1.14 (1.03-1.27)	0.010	Not tested	No	No	0.42	0.58
VDR	rs1544410	A/G	12	38.96	All	17	11,687	12,301	Additive	0.85 (0.72-0.99)	0.040	93	93.40	ACC	0.87	Weak	18,394	A	C	C	First study, HWE, GWAS, excess of significant studies	NA	0.97 (0.93-1.02)	0.271	Yes	No	No	0.38	0.05
VEGF	rs3025039	T/C	6	19.43	All	6	1,925	1,884	Additive	1.19 (1.04-1.37)	0.014	29	0.22	ABC	0.347	Weak	1,558	A	B	C	HWE, GWAS	NA	1.15 (1.00-1.33)	0.046	Yes	No	No	0.94	1.00
XPA	rs1800975	A/G	9	36.46	White	3	593	1,137	Additive	0.82 (0.70-0.96)	0.016	4	0.36	AAC	0.379	Weak	1,218	A	A	C	GWAS, Small study	NA	0.70 (0.53-0.92)	0.011	No	No	No	0.06	0.57
XPC	rs2228001	C/A	3	37.38	All	9	2,978	5,204	Additive	1.08 (1.01-1.16)	0.021	0	0.83	AAC	0.486	Weak	6,248	A	A	C	low OR, GWAS	NA	1.09 (1.01-1.17)	0.029	No	No	Yes	0.58	0.61
Associations identified from additional analyses by ethnic group																													
CDH1	rs16260	A/C	16	28.02	White	6	6,761	6,646	Additive	0.93 (0.87-1.00)	0.048	23	0.26	AAC	0.642	Weak	7,296	A	A	C	First study, Low OR	NA	0.95 (0.85-1.07)	0.408	No	Yes (rs9929218, r^2=0.915)	Yes	0.53	0.28
MTRR	rs1801394	A/G	5	44.65	White	10	6,430	9,746	Additive	0.98 (0.93-1.02)	0.030	4	0.41	AAC	0.535	Weak	1,510	A	A	C	First study, HWE, GWAS	NA	0.82 (0.61-1.12)	0.212	Yes	No	No	0.84	1.00
NQO1	rs1800566	T/C	16	17.88	White	8	6,293	6,566	Additive	1.09 (1.03-1.16)	0.006	0	0.50	AAC	0.183	Weak	4,765	A	A	C	Low OR, GWAS	NA	1.08 (1.01-1.15)	0.026	No	No	Yes	0.28	0.34
OGG1	rs1052133	G/C	3	21.59	White	14	5,908	7,355	Additive	1.15 (1.01-1.32)	0.033	74	0.00	ACC	0.558	Weak	5,879	A	C	C	First study, HWE, GWAS	NA	1.16 (1.00-1.35)	0.055	Yes	No	No	0.15	1.00
PTGS2	rs20417	C/G	1	2.76	Asian	4	1,285	3,040	Additive	1.44 (1.06-1.95)	0.019	28	0.25	BBC	0.420	Weak	276	B	B	C	First study, GWAS	NA	1.27 (0.84-1.94)	0.251	No	No	No	0.43	0.28
NFKB1	rs28362491	–/ATTG	4	41.05	White	6	1,199	3,134	Additive	1.29 (1.11-1.50)	0.001	55	0.05	ACB	0.036	Weak	3,670	A	C	B	GWAS	NA	1.20 (1.05-1.36)	0.007	No	No	No	0.91	1.00
TCF7L2	rs7903146	T/C	10	29.08	White	3	1,960	14,290	Additive	1.12 (1.02-1.22)	0.015	0	0.47	AAC	0.335	Weak	9,486	A	A	C	First study, GWAS, Low OR	NA	1.10 (1.00-1.21)	0.061	No	No	Yes	0.11	0.57
TP53	rs1042522	C/G	17	37.15	Asian	8	3,993	4,943	Additive	1.14 (1.02-1.27)	0.021	60	0.02	ACC	0.430	Weak	6,851	A	C	C	GWAS, Low OR	NA	1.13 (1.01-1.28)	0.037	No	No	Yes	0.64	1.00

* Minor alleles/major alleles (Per Caucasian)

† Frequency of minor allele or effect genotype(s) in controls in primary meta-analysis

‡ Venice criteria grades are for amount of evidence, replication of the association, and protection from bias.

§ False-positive report probability (FPRP) was determined based on OR and P value of each variant from meta-analysis and a prior probability of 0.05.

Cumulative epidemiological evidence as graded by combination of results from Venice criteria and FPRP for association with colorectal-cancer risk.

Appendix table 4 Detailed information for additional genetic variants nominally significantly associated with colorectal-cancer risk in meta-analyses using dominant or recessive models

						Number evaluated			Colorectal-cancer risk meta-analysis					Venice criteria garde‡	False-positive report probability§	Cumulative evidence of association	Amount of Evidence			Protection from Bias	Reason for Bias	Reason for bias exemption	Initial study influence		Deviation from HWE	Validated by GWAS if common variants			
Genes	**Variants**	**Alleles ***	**Chromosome**	**MAF (%)†**	**Ethnicity**	**Studies**	**Cases**	**Controls**	**Genetic models**	**OR (95% CI)**	***P*** value	I^2 (%)	$P_{heterogeneity}$				**Numbers**	**Grade**	**Replication**				**OR (95% CI)**	**p value**			**OR<1.15**	**Modified p**	**Excess p**
SELS	rs34713741	T/C	15	33.22	All	3	1,442	2,071	Dominant	1.21 (1.05-1.39)	0.008	0	0.40	AAC	0.235	Weak	2,046	A	A	C	First study, HWE, GWAS	NA	1.15 (0.98-1.36)	0.086	Yes	No	No	0.96	1.00
SERPINE1/PAI-1	rs1799889	5G/4G	7	44.94	White	4	2,241	4,534	Dominant	0.87 (0.78-0.97)	0.014	0	0.56	AAC	0.337	Weak	4,705	A	A	C	First study, GWAS, Low OR	NA	0.90 (0.77-1.04)	0.144	No	No	Yes	0.84	1.00
EPHX1	rs2234922	G/A	1	19.38	All	13	5,329	6,700	Dominant	0.91 (0.85-0.99)	0.020	0	0.50	AAC	0.46	Weak	4,113	A	A	C	GWAS, Low OR	NA	0.91 (0.84-0.99)	0.025	No	No	Yes	0.45	0.28
ERCC5/XPG	rs17655	C/G	13	24.73	All	9	6,322	7,537	Dominant	1.13 (1.01-1.25)	0.027	38	0.12	ABC	0.48	Weak	6,138	A	B	C	GWAS, Low OR	NA	1.14 (1.02-1.27)	0.026	No	No	Yes	0.58	1.00
RAD18	rs373572	C/T	3	29.22	All	3	3,174	3,397	Dominant	1.18 (1.01-1.37)	0.033	27	0.25	ABC	0.55	Weak	3,333	A	B	C	GWAS, small study	NA	1.33 (1.06-1.67)	0.015	No	No	No	0.00	0.29
CCND1	rs9344	A/G	11	48.15	All	22	6,316	8,272	Dominant	1.13 (1.01-1.26)	0.035	43	0.00	ABC	0.569	Weak	10,655	A	B	C	studies	NA	1.11 (0.99-1.24)	0.071	Yes	No	Yes	0.42	0.08
IGF1	rs35767	T/C	12	24.75	All	3	2,717	4,880	Recessive	0.75 (0.62-0.91)	0.003	0	0.57	BAC	0.11	Weak	528	B	A	C	HWE	NA	0.73 (0.60-0.89)	0.002	Yes	NA	No	0.77	1.00
MGMT	rs12917	T/C	10	12.99	All	7	4,127	7,284	Recessive	1.54 (1.14-2.08)	0.005	0	0.47	BAA	0.158	Weak	208	B	A	A	NA	NA	1.61 (1.14-2.28)	0.007	Yes	NA	No	0.96	1.00
CRP	rs1800947	C/G	1	5.70	All	4	2,916	3,544	Recessive	3.84 (1.38-10.74)	0.010	0	0.47	CAC	0.277	Weak	32	C	A	C	First study	NA	2.78 (0.84-9.18)	0.093	No	NA	No	0.30	1.00
HPGD	rs2612656	G/A	4	22.75	White	3	2,979	5,575	Recessive	1.31 (1.05-1.64)	0.016	21	0.28	BAC	0.380	Weak	450	B	A	C	First study	NA	1.17 (0.91-1.50)	0.220	No	NA	No	0.45	1.00
FRZB	rs7775	C/C	2	8.77	White	3	1,256	3,000	Recessive	3.20 (1.17-8.73)	0.023	64	0.06	CCC	0.468	Weak	55	C	C	C	First study	NA	3.12 (0.61-15.94)	0.171	No	NA	No	0.28	1.00
TGFBR1	rs334354	A/G	9	26.71	All	4	1,226	2,776	Recessive	1.38 (1.04-1.84)	0.029	8	0.35	BAC	0.516	Weak	325	B	A	C	First study	NA	1.24 (0.92-1.67)	0.158	No	NA	No	0.24	0.56
TGFB1	rs4803455	A/C	19	47.48	All	3	2,786	3,516	Recessive	1.14 (1.01-1.28)	0.030	0	0.37	AAC	0.536	Weak	1,483	A	A	C	First study, Low OR	NA	1.04 (0.87-1.24)	0.646	No	NA	Yes	0.50	0.53
LIPC	rs6083	A/G	15	36.52	All	3	4,702	4,914	Recessive	0.85 (0.74-0.99)	0.032	25	0.27	AAA	0.56	Weak	1,248	A	A	A	NA	NA	0.78 (0.65-0.94)	0.008	No	NA	No	0.98	1.00
MTHFR	rs1801133	T/C	1	33.50	All	68	32,608	44,383	Recessive	0.92 (0.85-1)	0.036	52	0.00	ACC	**0.61**	Weak	9,072	A	C	C	Low OR, small study, excess of significant studies	NA	0.92 (0.86-1.00)	0.043	No	NA	Yes	0.06	0.00
CYP2C9	rs1799853	T/C	10	13.31	White	6	4,915	5,237	Recessive	1.36 (1.02-1.83)	0.038	0	0.76	BAA	0.60	Weak	190	B	A	A	NA	NA	1.36 (1.01-1.83)	0.046	No	NA	No	0.31	0.47
MTRR	rs10380	T/C	5	9.31	White	4	3,869	5,141	Recessive	1.61 (1.02-2.52)	0.039	6	0.36	BAA	0.597	Weak	93	C	A	A	NA	NA	2.24 (1.14-4.43)	0.020	No	NA	No	0.31	0.50

* Minor alleles/major alleles (Per Caucasian)

† MAF=minor allele frequency in controls.

‡ Venice criteria grades are for amount of evidence, replication of the association, and protection from bias.

§ False-positive report probability (FPRP) was determined based on OR and P value of each variant from meta-analysis and a prior probability of 0.05.

Cumulative epidemiological evidence as graded by combination of results from Venice criteria and FPRP for association with colorectal-cancer risk.

Appendix table 5. Meta-analysis of associations between 267 genetic variants and colorectal-cancer risk by ethnicity

				Meta-analyses in Whites							Meta-analyses in Asians						
Gene	**Variant ID**	**Genetic variant (Variation)**	**Comparison**	**Studies**	**Cases**	**Controls**	**Frequency (%)[a]**	**OR (95% CI)**	***P* value**	**I^2 (%)**	**Studies**	**Cases**	**Controls**	**Frequency (%)[a]**	**OR (95% CI)**	***P* value**	**I^2 (%)**
ABCB1	1	rs1128503 (Gly412Gly)	T vs C														
ABCB1	2	rs1202168	T vs C	4	6,318	5,805	41.25	1.05 (0.97-1.14)	0.191	55							
ABCB1	3	rs2229109 (Ser400Asn)	A vs G	3	4,242	4,178	5.19	0.99 (0.86-1.13)	0.866	0							
ABCB1	4	rs868755	T vs G	3	2,958	3,255	42.06	1.06 (0.99-1.14)	0.109	0							
ABCB1	5	rs9282564 (Asn21Asp)	G vs A	4	5,792	5,234	8.89	1.21 (0.78-1.88)	0.400	96							
ABCB1/MDR1	6	rs1045642 (p.Ile1145Ile, c.3435T>C)	C vs T	9	5,983	6,669	47.20	1.00 (0.91-1.10)	0.977	64							
ABCB1/MDR1	7	rs2032582 (2677G>T)	T vs G	3	510	518	44.02	0.89 (0.74-1.06)	0.355	3							
ACE	8	287-bp repeat (I/D)	ins vs del	3	509	6,895	47.28	1.01 (0.87-1.18)	0.857	0							
ADH1B/ADH2	9	rs1229984 (ADH1B*2; HIS47ARG)	G vs A								5	1,899	2,833	32.83	1.087 0.901	0.384	68
ADH1C/ADH3	10	rs698 (p.Ile350Phe/p.Ile350Val)	G vs A	8	4,132	7,242	39.59	1.02 (0.91-1.15)	0.732	74							
ADIPOQ	11	rs1501299	T vs G														
ADIPOQ	12	rs266729 (nearGene-5, C-11374G)	G vs C	3	2,795	2,979	33.28	0.97 (0.90-1.04)	0.411	0							
ADIPOR1	13	rs1342387	A vs G														
ADIPOR1	14	rs7539542	C vs G														
ALDH2	15	rs671 (p.Glu487Lys/Glu504Lys, c.1510G>A)	A vs G								7	1,799	3,385	22.20	1.03 (0.83-1.27)	0.811	73
ALOX12/12-LOX	16	rs1126667 (p.Gln261Arg, c.782G>A)	A vs G	3	1,559	1,804	41.88	1.00 (0.8-1.16)	0.972	46							
ALOX5	17	rs4986832 (nearGene-5, -1708 G>A, g.3400G>A)	A vs G														
APC	18	rs1801155 (I1307K, T3920A)	carriers vs non-carriers														
APC	19	rs1801166 (E1317Q)	(CC+CG) vs GG														
APC	20	rs2229992 (p.Tyr486Tyr)	T vs C														
APC	21	rs2229995 (p.Gly2502Ser, c.7504G>A)	A vs G	3	1,130	1,626	1.75	1.25 (0.85-1.85)	0.258	0							
APC	22	rs41115 (p.Thr1493Thr)	C vs T														
APC	23	rs42427 (p.Gly1678Gly)	G vs A														
APC	24	rs459552 (p.Val1822Asp, c.5465T>A)	A vs T	7	6,388	6,859	22.77	0.97 (0.91-1.03)	0.267	0							
APC	25	rs465899 (p.Pro1960Pro)	C vs T														
APEX1/APEX	26	rs1048945 (p.Gln51His, c.153G>C)	C vs G	3	3,224	3,369	4.05	0.89 (0.63-1.25)	0.497	41							
APEX1/APEX	27	rs1130409 (p.Asp148Glu, c.444T>G)	G vs T	8	4,306	5,301	46.04	1.01 (0.86-1.19)	0.901	36							
ARLTS1/ARL11	28	rs34301344 (p.Trp149Stop, c.446G>A)	(AA+AG) vs GG	3	1,367	1,862	0.99	1.00 (0.60-1.65)	0.992	0							
ARLTS1/ARL11	29	rs3803185 (p.Cys148Arg, T442C, T>C)	C vs T	4	2,123	2,681	46.10	1.07 (0.99-1.17)	0.093	0							
ATM	30	rs1801673 (Ex37+62A>T, Asp1853Val)	A vs G	3	2,879	6,384	0.66	0.77 (0.54-1.10)	0.144	0							
AURKA/STK15	31	rs2273535 (p.Phe31Ile, c.91T>A)	A vs T	5	5,091	4,670	21.45	1.02 (0.94-1.10)	0.652	8							
AXIN2	32	rs2240308 (p.Pro50Ser, c.148C>T, G/A)	A vs G	3	3,762	3,934	46.11	1.07 (0.98-1.17)	0.124	29							
BLM	33	ASH non-carriers/carriers	carriers vs non-carriers														
BMP4	34	rs17563 (p.Val152Ala, c.455T>C)	T vs C														
CASP8	35	rs3834129 (nearGene-5, -652 6N del, -/CTTACT)	6 bp ins vs del	5	5,086	6,464	47.41	1.01 (0.94-1.09)	0.706	20	3	1,563	2,893	21.90	1.13 (0.68-1.90)	0.632	95
CASR	36	rs1042636 (p.Arg990Gly, c.2968A>G)	G vs A	4	6,298	7,839	8.52	1.00 (0.92-1.09)	0.936	0							
CASR	37	rs1801725 (p.Ala986Ser, c.2956G>T)	T vs G	3	2,733	3,359	13.10	1.30 (0.99-1.72)	0.061	84							
CBS	38	rs5742905 (Ile278Thr; CBS I278T)	C vs T	3	2,504	3,723	8.22	1.05 (0.92-1.19)	0.489	0							
CCND1	39	rs9344 (rs603965, p.Pro241Pro, c.723G>A/c.870G>A)	A vs G	10	2,789	2,595	47.76	1.05 (0.95-1.16)	0.369	35	4	1,758	3,160	45.55	0.95 (0.82-1.09)	0.462	56
CDH1	40	rs16260 (UTR-5, -160C>A)	A vs C	6	6,761	6,646	28.02	0.93 (0.87-1.00)	**0.048**	23							
CDKN1A	41	rs1059234 (UTR-3, c.*20C>T)	T vs C														
CDKN1A	42	rs1801270 (p.Ser31Arg, c.93C>A)	A vs C														
CHEK2	43	1100delC (fs381X)	carriers vs non-carriers	7	3,874	11,630	0.71	1.88 (1.29-2.73)	**0.001**	0							
CHEK2	44	rs17879961 (p.Ile200Thr)	carriers vs non-carriers	6	6,042	17,051	3.91	1.56 (1.32-1.84)	**1.22×10^{-7}**	0							
COMT	45	rs4680 (p.Val158Met, c.472G>A)	A vs G	5	5,074	5,239	48.89	1.05 (0.94-1.16)	0.390	56							
CRP	46	rs1205 (c.*1082G>A, 2042C>T)	T vs C	3	2,393	8,064	32.08	1.07 (0.99-1.16)	0.091	0							
CRP	47	rs1417938 (29T>A)	A vs T	3	2,422	3,146	29.83	0.95 (0.85-1.06)	0.322	34							
CRP	48	rs1800947 (p.Leu184Leu, c.552G>C)	C vs G														
CTLA4	49	rs231775 (p.Thr17Ala, c.49A>G)	G vs A														
CX3CR1	50	rs3732378 (T280M)	A vs G	3	3,143	3,269	16.95	1.00 (0.83-1.19)	0.968	44							
CYP17A1	51	rs743572	G vs A	3	4,376	4,588	39.56	1.04 (0.91-1.18)	0.592	67							
CYP1A1	52	rs1048943 (*2C, m2, p.Ile462Val, c.1384A>C)	G vs A	10	5,000	5,751	5.29	1.19 (1.04-1.36)	**0.011**	17	5	1,661	2,211	23.34	1.08 (0.90-1.28)	0.425	48
CYP1A1	53	rs1799814 (Thr461Asp)	A vs C	3	3,155	3,394	4.36	0.75 (0.46-1.20)	0.227	74							
CYP1A1	54	rs4646903 (m1, MspI, UTR-3, T3801C)	C vs T	11	6,418	7,152	11.57	1.03 (0.88-1.21)	0.686	72							
CYP1A2	55	rs2069514 (CYP1A2*1C, -3860G>A)	A vs G								3	901	937	27.59	1.06 (0.79-1.42)	0.697	54
CYP1A2	56	rs2470890 (CYP1A2*1B, Asn516Asn; 1545T>C)	C vs T														
CYP1A2	57	rs762551 (CYP1A2*1F, c.A-163C)	C vs A	7	5,608	5,968	29.46	1.02 (0.95-1.11)	0.547	42	3	279	429	36.25	1.03 (0.59-1.78)	0.924	82
CYP1B1	58	rs10012 (p.Arg48Gly, c.142C>G)	G vs C	4	3,825	3,926	29.43	0.03 (0.94-1.14)	0.524	44							
CYP1B1	59	rs1056836 (CYP1B1*3, p.Leu432Val, c.1294C>G)	G vs C	9	8,709	9,097	43.27	1.02 (0.97-1.06)	0.488	0							
CYP1B1	60	rs1800440 (p.Asn453Ser, c.1358A>G)	G vs A	6	6,679	6,923	18.36	0.97 (0.88-1.07)	0.580	53							
CYP2C19	61	rs4244285 (Pro681Pro)	T vs C	3	2,557	2,664	14.94	0.91 (0.75-1.1)	0.337	53							
CYP2C9	62	R144C/I359L	mutation vs wild	3	2,424	3,053	18.54	0.94 (0.81-1.08)	0.362	38							
CYP2C9	63	rs1057910 (p.Ile359Leu, c.1075A>C)	G vs A	6	6,474	6,835	6.82	0.95 (0.86-1.05)	0.307	0							
CYP2C9	64	rs1799853 (p.Arg144Cys, c.430C>T)	T vs C	6	4,915	5,237	13.31	0.98 (0.91-1.07)	0.668	0							
CYP2D6	65	rs3892097 (c.353-1G>A)	A vs G	3	798	1,512	20.07	1.03 (0.88-1.21)	0.684	0							
CYP2E1	66	96-bp insertion	insertion vs non-insertion														
CYP2E1	67	rs2031920 (RsaI, c1>c2, C>T)	T vs C	4	2,146	2,237	3.93	1.21 (0.85-1.71)	0.284	56							
CYP2E1	68	rs3813867 (nearGene-5, g.3739G>C, c.-1293G>C)	C vs G	4	2,345	2,867	3.56	0.84 (0.68-1.05)	0.131	0							
CYP2E1	69	rs6413432 (Intron, c.967+1143T>A, 7632T>A)	A vs T	3	1,352	1,858	8.32	1.13 (0.67-1.92)	0.649	78							
CYP3A4	70	rs2740574	G vs A	3	4,464	4,603	3.77	0.96 (0.83-1.12)	0.629	0							
DNMT3B	71	rs1569686 (nearGene-5, c.-6-1045G>T, 39179G>T)	G vs T								3	929	1,089	12.35	0.56 (0.45-0.70)	**2.60×10^{-7}**	0
DNMT3B	72	rs2424913 (Intron, c.307-49C>T, -149C>T)	T vs C	3	1,717	2,899	43.83	0.96 (0.88-1.04)	0.298	0	3	681	1,374	98.98	1.67 (0.75-3.72)	0.209	0
DNMT3b	73	rs406193	T vs C	3	966	2,074	18.44	1.06 (0.84-1.33)	0.631	49							
EPHX1	74	rs1051740 (p.Tyr113His, c.337T>C)	C vs T	13	9,176	10,366	29.84	1.02 (0.96-1.08)	0.475	34							
EPHX1	75	rs2234922 (p.His139Arg, c.416A>G)	G vs A	9	4,132	4,922	19.69	1.00 (0.91-1.09)	0.930	24							
ERCC1	76	rs11615 (rs3177700, p.Asn118Asn, c.354T>C)	C vs T	5	1,060	1,659	37.97	0.98 (0.87-1.10)	0.722	0							
ERCC1	77	rs3212986 (8092C>A)	(AA+AC) vs CC														
ERCC2/XPD	78	rs13181 (p.Lys751Gln, c.2251A>C)	C vs A	14	4,717	6,564	36.77	0.96 (0.90-1.03)	0.285	21							
ERCC2/XPD	79	rs1799793 (p.Asp312Asn, c.981G>A)	A vs G	6	5,069	5,967	34.74	1.02 (0.96-1.07)	0.593	0							
ERCC4/XPF	80	rs1800067 (R415Q)	A vs G	3	3,173	3,206	10.61	1.01 (0.90-1.14)	0.826	0							
ERCC5/XPG	81	rs17655 (p.Asp1104His, c.3310G>C)	C vs G	8	5,294	6,452	21.33	1.04 (0.98-1.11)	0.184	0							
ESR1	82	rs2077647 (Ser10Ser)	C vs T	3	1,923	2,416	46.83	1.13 (0.85-1.5)	0.413	70							
ESR1	83	rs2234693	C vs T	5	2,122	2,616	45.47	0.95 (0.73-1.23)	0.678	71							
ESR1	84	rs3798577	C vs T	3	1,920	2,430	46.48	0.99 (0.91-1.08)	0.820	0							
ESR1	85	rs9340799	G vs A	7	4,367	5,414	35.54	0.99 (0.93-1.05)	0.710	0							
EXO1	86	rs4149963 (p.Thr439Met, c.1316C>T)	T vs C	3	3,531	3,666	8.21	0.98 (0.82-1.17)	0.812	35							
EXO1	87	rs9350 (p.Pro757Leu, c.2270C>T)	T vs C														

FOLH1	88	rs202676 (p.Tyr75His, c.223T>C)	C vs T	3	3,135	3,914	21.27	0.94 (0.87-1.02)	0.165	0										
FRZB	89	rs288326 (p.Arg200Trp, c.598C>T)	T vs C	3	1,260	3,006	12.38	0.95 (0.86-1.05)	0.312	0										
FRZB	90	rs7775 (p.Arg324Gly, c.970C>G)	G vs C	3	1,256	3,000	8.77	1.17 (0.88-1.56)	0.285	66										
GH1	91	rs2665802 (c.456+90T>A)	A vs T																	
GPX1	92	rs1050450 (p.Pro200Leu, c.599C>T)	T vs C	3	1,222	1,813	29.51	1.01 (0.90-1.13)	0.920	0										
GPX4	93	rs713041	T vs C																	
GSTA1	94	*A/*B	mutation vs wild	3	464	574	39.11	1.13 (0.84-1.53)	0.418	62										
GSTA1	95	rs3957357	A vs G	3	1,313	1,327	39.90	1 (0.9-1.12)	0.989	0										
GSTM1	96	Present/Null	null vs present	35	14,650	19,818	52.43	1.08 (1.01-1.16)	**0.037**	53	12	4,739	9,929	50.10	1.04 (0.96-1.19)	0.360	0			
GSTM3	97	rs1799735 (c.468+21delAGG, delAGG)	AGG del vs ins	3	2,531	2,707	15.96	0.94 (0.72-1.23)	0.653	83										
GSTP1	98	rs1138272 (p.Ala114Val, c.341C>T)	T vs C	8	6,858	7,207	10.23	0.89 (0.77-1.02)	0.084	55										
GSTP1	99	rs1695 (p.Ile105Val, c.313A>G)	G vs A	19	7,433	8,487	33.35	0.99 (0.94-1.06)	0.855	28	7	1,622	5,660	18.74	0.89 (0.80-1.00)	0.057	0			
GSTT1	100	Present/Null	null vs present	26	9,684	12,638	19.20	1.24 (1.08-1.44)	**0.003**	74	9	4,354	9,301	44.52	1.08 (0.99-1.18)	0.104	13			
GSTZ1	101	rs3177427 (GLU32LYS)	A vs G																	
HFE	102	rs1799945 (H63D)	G vs C	7	3,729	4,079	14.70	1.03 (0.93-1.15)	0.581	7										
HFE	103	rs1800562 (rs111535158, p.Cys282Tyr, c.1005G>A)	A vs G	10	2,502	30,857	7.43	1.05 (0.92-1.21)	0.467	0										
HIF1A	104	rs11549465 (p.Pro582Ser, c.1744C>T)	T vs C																	
HPGD	105	rs7349744	C vs A	3	3,001	5,624	7.56	0.96 (0.84-1.09)	0.516	11										
HPGD	106	rs2612656	G vs A	3	2,979	5,575	22.75	1.09 (0.97-1.24)	0.162	65										
HPGD	107	rs7349744	A vs G	3	3,014	5,622	30.54	1.00 (0.93-1.07)	0.897	0										
HPGD	108	rs8752	G vs A	3	3,008	5,632	41.98	1.01 (0.86-1.17)	0.936	22										
HPGD	109	rs9312555	G vs A	3	3,015	5,634	15.42	0.93 (0.86-1.02)	0.134	0										
ICAM1	110	rs5498 (p.Lys469Glu, c.1405A>G)	G vs A	3	3,142	3,255	42.83	1.02 (0.85-1.24)	0.819	70										
IGF1	111	(CA)n (R19>non-R19)	non R19 vs R19	6	4,979	5,658	35.22	0.97 (0.85-1.10)	0.594	78										
IGF1	112	rs35767	T vs C																	
IGFBP1	113	rs4619 (p.Ile253Met,c.759A>G)	G vs A	3	3,570	3,660	35.53	0.93 (0.75-1.16)	0.535	85										
IGFBP3	114	rs2854744 (nearGene-5, C-202A, A>C)	C vs A	6	4,406	6,873	50.23	1.03 (0.98-1.09)	0.240	0										
IGFBP3	115	rs2854746 (p.Ala32Gly, c.95C>G)	G vs C	3	1,509	2,783	42.49	1.08 (0.97-1.20)	0.174	0										
IL10	116	rs1800872 (nearGene-5, g.4433A>C, -592C>A)	A vs C	6	1,561	2,439	22.57	0.94 (0.81-1.1)	0.444	41										
IL10	117	rs1800896 (nearGene-5, g.3943A>G, -1082A>G)	G vs A	5	1,134	1,492	46.68	0.98 (0.84-1.15)	0.793	44										
IL16	118	rs4072111 (p.Pro434Ser, c.1300C>T)	T vs C																	
IL1B	119	rs1143627 (nearGene-5, g.4970C>T, -31T>C)	C vs T	5	1,524	2,034	32.72	1.07 (0.96-1.18)	0.209	0										
IL1B	120	rs16944	G vs A																	
IL4	121	rs2243250 (nearGene-5, -509C>T)	T vs C	6	1,225	1,754	18.93	0.92 (0.76-1.12)	0.401	42										
IL4R	122	rs1801275 (p.Gln576Arg, c.1727A>G)	G vs A	3	633	887	19.90	1.05 (0.87-1.26)	0.629	0										
IL4R	123	rs1805012 (C431R)	G vs A	3	2,840	3,233	11.18	0.95 (0.70-1.31)	0.764	59										
IL4R	124	rs1805015 (S503P)	C vs T	3	640	892	16.26	1.02 (0.84-1.25)	0.834	0										
IL6	125	rs1800795	C vs G	13	6,683	8,121	39.73	1.01 (0.92-1.11)	0.822	68										
IL6	126	rs1800797	(AA+AG) vs GG	4	2,612	3,381	60.75	0.96 (0.87-1.07)	0.468	0										
IL6R	127	rs2228145 (rs8192284, Asp358Val)	C vs A	3	3,070	20,173	30.92	0.97 (0.91-1.04)	0.435	0										
IL8	128	rs4073 (nearGene-5, T-251A)	A vs T	10	3,520	4,381	45.88	1.04 (0.92-1.18)	0.525	70										
IRS1	129	rs1801278 (p.Gly971Arg, c.2911G>A)	A vs G	7	7,048	7,533	6.92	1.08 (0.96-1.22)	0.219	39										
IRS2	130	rs1805097 (p.Gly1057Asp, c.3170G>A)	A vs G	3	2,318	2,814	41.13	0.96 (0.89-1.04)	0.327	0										
LCT	131	rs4988235 (c.1917+326C>T, 13910 C>T)	T vs C	7	2,103	2,492	41.75	0.99 (0.87-1.14)	0.879	51										
LEP	132	rs7799039	A vs G	3	2,324	2,776	43.98	0.95 (0.88-1.03)	0.222	0										
LEPR	133	rs1137101 (p.Gln223Arg, c.668A>G)	G vs A	3	1,100	1,166	44.47	1.08 (0.96-1.22)	0.187	0										
LIPC	134	rs6083 (N215S)	A vs G																	
MBL2	135	rs11003125	G vs C																	
MBL2	136	rs1800450 (Gly54Asp)	A vs G	3	3,294	3,357	14.43	1.01 (0.85-1.19)	0.936	37										
MBL2	137	rs1800451 (p.Gly57Glu)	A vs G																	
MBL2	138	rs5030737 (R52C)	T vs C	3	1,083	1,023	7.09	1.02 (0.81-1.30)	0.845	0										
MBL2	139	rs7096206	C vs G																	
MDM2	140	rs2279744 (nearGene-5, SNP309, c.14+309T>G)	G vs T	6	1,613	886	37.36	1.03 (0.90-1.18)	0.671	2	3	1,252	1,485	46.13	1.01 (0.90-1.12)	0.933	0			
MGMT	141	rs12917 (p.Leu115Phe, c.343C>T)	T vs C	5	3,635	5,917	12.95	1.02 (0.93-1.11)	0.745	0										
MGMT	142	rs2308321 (p.Ile174Val, c.520A>G)	G vs A	5	3,642	8,583	12.76	0.94 (0.75-1.17)	0.565	74										
MLH1	143	rs121912963 (p.D132H, c.415G>C)	C vs G																	
MLH1	144	rs1799977 (p.Ile219Val, c.655A>G)	G vs A	8	6,117	8,385	31.41	1.00 (0.92-1.12)	0.952	63										
MLH1	145	rs1800734 (nearGene-5/UTR-5, -93G>A)	A vs G	7	17,783	13,777	21.31	1.05 (1.01-1.09)	**0.014**	0										
MLH1	146	rs63750447 (p.Val384Asp, 1151 T>A)	A vs T								3	937	919	1.96	2.14 (1.12-4.12)	**0.022**	41			
MLH1	147	rs9876116 (Intron 14, c.1668-19A>G)	G vs A	3	2,024	2,143	44.47	0.93 (0.85-1.02)	0.631	15										
MMP1	148	rs1799750 (nearGene-5, -1607 1G/2G)	2G vs 1G	3	678	842	50.30	0.80 (0.61-1.05)	0.107	62	4	649	809	26.89	0.78 (0.58-1.06)	0.113	67			
MMP2	149	rs243865 (-1306C/T)	T vs C																	
MMP3	150	rs3025058	5A vs 6A	3	660	869	47.07	1.03 (0.89-1.19)	0.709	0	4	459	624	13.86	1.01 (0.64-1.62)	0.947	68			
MMP7	151	rs11568818 (nearGene-5, -181A>G)	G vs A								3	468	623	6.50	0.69 (0.40-1.18)	0.171	39			
MMP9	152	rs3918242 (nearGene-5, g.3430C>T, -1562 C>T)	T vs C								3	517	584	14.13	0.80 (0.60-1.09)	0.155	22			
MSH2	153	rs2303425 (nearGene-5, g.4951T>C, c.-118T>C)	C vs T	3	1,775	2,206	12.78	1.01 (0.87-1.17)	0.944	14										
MSH2	154	rs2303428 (c.2006-6T>C)	C vs T	4	4,264	4,260	9.62	0.96 (0.866-1.07)	0.496	4										
MSH2	155	rs4987188 (p.Gly322Asp, c.965G>A)	A vs G	5	3,697	3,491	1.49	1.22 (0.94-1.58)	0.141	0										
MSH3	156	rs184967 (p.Arg949Gln, c.3099G>A)	A vs G	3	5,085	7,136	15.25	1.11 (1.03-1.20)	**0.005**	0										
MSH3	157	rs26279 (p.Ala1045Thr,c.3133G>A)	G vs A	4	5,691	7,665	28.13	1.1 (1.03-1.17)	**0.006**	17										
MSH6	158	rs1042821 (p.Gly39Glu, c.116G>A)	A vs G	4	3,136	6,063	17.22	0.99 (0.86-1.13)	0.832	59										
MSH6	159	rs1800935 (p.Asp180Asp, c.540T>C)	C vs T	3	5,132	4,709	29.45	0.96 (0.90-1.02)	0.159	0										
MTHFD1	160	rs1950902 (p.Arg134Lvs, c.401G>A)	A vs G	3	3,822	5,452	18.78	0.90 (0.84-0.98)	**0.010**	0										
MTHFD1	161	rs2236225 (p.Arg653Gln, c.1958G>A)	A vs G	6	6,535	9,347	45.19	0.98 (0.90-1.07)	0.603	67										
MTHFR	162	rs1801131 (p.Ala429Glu, c.1286A>C)	C vs A	19	11,550	17,286	32.18	1.00 (0.95-1.05)	0.895	29	8	1,886	2,868	19.37	0.95 (0.83-1.09)	0.449	29			
MTHFR	163	rs1801133 (p.Ala222Val, c.C677T)	T vs C	37	23,411	31,990	32.80	0.98 (0.94-1.02)	0.230	52	15	5,731	6,920	41.49	0.95 (0.87-1.03)	0.181	52			
MTR	164	rs1805087 (A2756G)	G vs A	14	11,730	15,669	19.51	0.97 (0.92-1.05)	0.529	45										
MTRR	165	rs10380 (p.His595Tyr, c.1783C>T)	T vs C	4	3,869	5,141	9.31	1.05 (0.87-1.26)	0.638	57										
MTRR	166	rs1532268 (Ser175Leu)	T vs C	3	3,496	4,809	36.48	1.01 (0.94-1.08)	0.779	5										
MTRR	167	rs162036 (Ile22Met)	G vs A	3	3,506	4,793	11.14	1.01 (0.83-1.23)	0.936	65										
MTRR	168	rs1801394 (Ile22Met)	A vs G	10	6,430	9,746	44.65	0.98 (0.93-1.02)	**0.030**	4	3	355	687	74.09	0.80 (0.66-0.98)	0.373	0			
MUTYH	169	rs3219484 (p.Val22Met, c.64G>A)	A vs G	3	5,391	5,222	8.20	0.95 (0.68-1.34)	0.787	91										
MUTYH	170	rs3219489 (p.Gln324His, c.972G>C)	C vs G																	
MUTYH	171	Monoallelic mutation	Carriers vs wild homozygotes	17	25,981	18,811	1.69	1.17 (1.01-1.34)	**0.036**	0										
MUTYH	172	Biallelic mutation	Carriers vs wild homozygotes	17	25,981	18,811	0.01	10.19 (5.00-22.04)	**5.30×10^{-10}**	0										
MUTYH	173	rs34612342 (p.Tyr165Cys, c.494A>G, Tyr179Cys)	GG vs AA	17	25,981	18,811	0.22	3.32 (1.13-9.81)	**0.030**	0										
MUTYH	174	rs36053993 (p.Gly382Asp, c.1178G>A)/ss49785896, G396D	AA vs GG	17	25,981	18,811	0.62	6.49 (2.57-1.35)	**7.49×10^{-5}**											
NAT1	175	Phenotype	Fast vs slow	11	5,559	7,326	36.95	1.08 (0.0.99-1.18)	0.102	24										
NAT2	176	Phenotype	Slow vs fast	23	8,699	11,339	54.88	0.92 (0.87-0.98)	**0.011**	1	9	1,802	2,276	18.80	0.92 (0.78-1.09)	0.352	0			
NAT2	177	rs1799930 (NAT2*6B, G590A)	A vs G	3	3,793	4,021	28.66	1.05 (0.98-1.13)	0.144	0										
NBS1	178	rs1805794 (E185Q)	G vs C	4	3,185	3,424	33.63	0.85 (0.63-1.14)	0.276	86										

NFKB1	179	rs28362491 (-94ins/delATTG)	ATTG del vs ins	6	1,199	3,134	41.05	1.29 (1.11-1.50)	**0.001**	55								
NFkBIA	180	rs696	A vs G															
NOD2/CARD15	181	rs2066844 (p.Arg702Trp, c.2104C>T)	(TT+CT) vs CC	9	3,297	3,088	6.15	1.35 (1.02-1.78)	**0.038**	34								
NOD2/CARD15	182	rs2066845 (p.Gly908Arg, c.2722G>C)	C vs G	8	3,252	2,988	1.10	1.31 (0.93-1.85)	0.124	0								
NOD2/CARD15	183	rs2066847 (frameshift, 3020insC, WT/insC, L1007fs)	Ins carriers vs wild homozygotes	11	4,337	5,395	6.21	1.30 (1.02-1.65)	**0.032**	33								
NOS3	184	rs1799983 (p.Asp298Glu, c.894G>T)	T vs G															
NQO1	185	rs1131341 (rs4986998, p.Arg139Trp, c.415C>T)	T vs C	4	4,436	4,725	4.07	0.99 (0.86-1.15)	0.914	0								
NQO1	186	rs1800566 (p.Pro187Ser/p.Pro153Ser, c.648C>T)	T vs C	8	6,293	6,566	17.88	1.09 (1.03-1.16)	**0.006**	0	3	830	2,057	39.52	0.91 (0.80-1.05)	0.194	4	
OGG1	187	rs1052133 (p.Ser326Cys, c.977C>G)	G vs C	14	5,908	7,355	21.59	1.15 (1.01-1.32)	**0.033**	74	3	632	1,044	54.98	0.93 (0.81-1.07)	0.334	0	
PARP1	188	rs1136410 (p.Val762Ala, c.2285T>C)	C vs T	3	3,229	3,413	15.38	1.05 (0.95-1.15)	0.335	0								
PGR	189	rs1042838 (Val496Leu)	T vs G	3	2,266	2,668	14.24	1.1 (0.96-1.26)	0.171	14								
PLA2G2A	190	rs11677 (G>A)	A vs G	3	2,803	3,825	11.76	1.00 (0.83-1.20)	0.976	64								
PMS2	191	rs1805319 (rs2228005/rs6463524, p.Ser260Ser)	G vs C	3	3,713	3,374	18.55	1.06 (0.85-1.33)	0.596	80								
PPARG	192	rs1801282 (p.Pro12Ala, c.36C>G)	G vs C	13	9,310	11,127	11.70	0.96 (0.88-1.05)	0.384	39								
PPARG	193	rs3856806 (p.His447His,c.1431C>T)	T vs C	6	3,742	5,544	12.27	1.02 (0.93-1.12)	0.715	6								
PTGS1/COX1	194	rs1236913 (p.Trp8Arg, c.22C>T)	T vs C	4	4,033	6,783	7.27	0.95 (0.85-1.06)	0.327	0								
PTGS1/COX1	195	rs5788 (p.Gly213Gly, c.639C>A)	A vs C	4	3,989	6,659	13.35	1.13 (1.04-1.22)	**0.004**	0								
PTGS2/COX2	196	rs20417	C vs G	8	2,242	2,804	16.49	0.99 (0.88-1.10)	0.786	0	4	1,285	3,040	2.76	1.44 (1.06-1.95)	**0.019**	28	
PTGS2/COX2	197	rs4648298	(GG+AG) vs AA	5	2,261	2,636	5.31	0.88 (0.52-1.52)	0.653	71								
PTGS2/COX2	198	rs5275 (UTR-3, c.*427T>C, 8473T>C)	C vs T	9	4,279	6,220	33.07	1.04 (0.98-1.10)	0.230	0								
PTGS2/COX2	199	rs5277 (p.Val102Val, c.306G>C)	C vs G	7	3,862	5,272	16.16	0.99 (0.91-1.07)	0.764	10								
PTGS2/COX2	200	rs689466 (nearGene-5, g.38139393T>C)	G vs A	7	3,076	5,010	20.30	0.94 (0.87-1.02)	0.132	0								
RAD18	201	rs373572 (p.Arg302Gln, c.905G>A)	C vs T															
RAD51	202	rs1801320 (135G/C)	C vs G	4	753	720	32.15	1.01 (0.31-3.27)	0.987	97								
RNASEL	203	rs486907 (p.Arg462Gln, c.1385G/A)	A vs G	3	808	1,132	35.03	1.05 (0.92-1.2)	0.469	0								
SCD	204	rs7849	G vs A															
SELS	205	rs34713741	T vs C															
(SEP15)	206	rs5859	T vs C															
SEPP1	207	rs3877899 (Ala264Thr)	T vs C															
SEPP1	208	rs7579	T vs C															
SERPINE1/PAI-1	209	rs1799889 (nearGene-5, -675 4G/5G)	5G vs 4G	4	2,241	4,534	44.94	0.97 (0.90-1.04)	0.368	0								
SHBG	210	rs6259 (D356N)	A vs G	3	4,677	4,823	11.60	1.04 (0.95-1.14)	0.383	0								
SHMT1	211	rs1979276 (UTR-3, C1420T)	T vs C	4	1,458	1,672	31.91	0.90 (0.79-1.02)	0.109	27								
SLC19A1/RFC1	212	rs1051266 (p.His27Arg, c.80A>G, 80G>A)	A vs G	5	3,775	5,340	43.66	1.02 (0.91-1.14)	0.757	61								
SLC22A4/OCTN1	213	rs1050152 (L503F)	T vs C	3	3,110	3,243	53.39	1.06 (0.94-1.21)	0.342	38								
SOD2	214	rs4880 (rs1799725, Ala16Val)	T vs C	3	1,677	1,563	49.94	0.97 (0.88-1.07)	0.484	0								
SULT1A1	215	rs9282861 (p.Arg213His, c.638G>A)	A vs G	10	3,760	4,942	33.41	1.01 (0.91-1.12)	0.839	55								
SULT1A2	216	rs1059491 (p.Asn235Thr, c.714A>C)	C vs A	3	1,806	1,986	31.80	1.05 (0.95-1.17)	0.308	6								
TCF7L2	217	rs7903146	T vs C	3	1,960	14,290	29.08	1.12 (1.02-1.22)	**0.015**	0								
TCN2	218	rs1801198 (p.Arg259Pro, c.776C>G)	G vs C	3	2,582	5,117	43.70	0.96 (0.86-1.07)	0.453									
TERT	219	rs2736100	T vs G	8	16,176	18,135	49.34	1.07 (1.04-1.1)	**2.92×10^{-5}**	0								
TGFB1	220	rs1800469 (nearGene-5, C-509T)	T vs C	5	2,923	3,399	31.36	0.95 (0.85-1.07)	0.382	37	3	861	1,238	54.56	0.80 (0.62-1.04)	0.091	68	
TGFB1	221	rs1800470 (p.Leu10Pro, c.29C>T, c.T29C)	C vs T															
TGFB1	222	rs4803455	A vs C															
TGFBR1	223	rs11466445 (Frameshift in exon 1, *6A/9A)	9 bp del vs ins	9	5,571	5,923	9.48	1.03 (0.94-1.13)	0.524	10								
TGFBR1	224	rs334354 (Intron, IVS7G+24A, c.1024+24G>A)	A vs G	3	1,020	1,938	18.78	1.09 (0.81-1.48)	0.557	0								
TLR3	225	rs3775291 (Leu412Phe)	AA vs (AG+GG)	3	4,867	5,604	9.23	0.94 (0.80-1.11)	0.465	30								
TLR4	226	rs11536898	AA vs (AC+CC)	3	2,501	3,239	1.85	0.79 (0.37-1.67)	0.529	53								
TLR4	227	rs1927911	T vs C	3	2,512	3,276	27.79	0.99 (0.91-1.07)	0.757	0								
TLR4	228	rs4986790 (p.Asp299Gly)	T vs C	3	714	1,156	4.28	1.27 (0.67-2.4)	0.459	68								
TLR4	229	rs4986791 (Thr399Ile)	T vs C	3	2,994	3,582	5.44	1.07 (0.82-1.39)	0.629	28								
TNF	230	rs1799724 (nearGene-5, -857C>T)	T vs C	3	745	732	13.05	0.97 (0.72-1.30)	0.818	36								
TNF	231	rs1800629 (nearGene-5, G-308A)	A vs G	8	2,042	1,944	15.41	1.25 (0.96-1.64)	0.096	79	3	254	339	4.42	1.55 (0.93-2.59)	0.095	0	
TP53	232	rs1042522 (p.Pro72Arg, c.215C>G)	C vs G	20	6,054	7,393	26.42	0.92 (0.85-1.00)	0.063	38	8	3,993	4,943	37.15	1.14 (1.02-1.27)	**0.021**	60	
TP53	233	rs17878362 (nearGene-5, IVS3 16bp Del/Ins)	16 bp ins vs del	5	1,569	1,891	15.49	0.96 (0.73-1.28)	0.787	73								
TP73	234	G4C14/A4T14	mutation vs wild															
TYMS/TS	235	28-bp tandem repeat	3R vs 2R	5	2,648	2,690	46.30	1.214	0.978	0.079	77							
TYMS/TS	236	rs16430 (UTR-3, 1494 ins/del6, -/CTTTAA)	6 bp del vs ins	4	3,481	3,524	32.36	1.00 (0.90-1.11)	0.960	41								
UBD	237	rs2076485 (I68T)	C vs T	3	4,281	6,157	26.07	1.07 (1.01-1.14)	**0.034**	0								
UGT1A1	238	rs10929302 (Intron, c.862-9898G>A, c.-3156G>A)	A vs G															
UGT1A1	239	rs4124874 (Intron, c.862-10021T>G, c.-3279T>G)	G vs T															
UGT1A1	240	rs8175347	TA7 vs TA6	6	2,850	3,411	33.77	1.00 (0.89-1.13)	0.906	51								
UGT1A6	241	rs1105879 (p.Arg184Ser, c.552A>C)	C vs A	3	4,006	4,295	34.33	0.97 (0.91-1.04)	0.401	0								
UGT1A6	242	T181A/R184S	mutation vs wild	4	3,066	3,915	34.41	1.04 (0.97-1.12)	0.303	10								
UGT1A7	243	Phenotype	low vs high															
UGT1A7	244	rs17868323 (N129K)	T vs G															
VDR	245	rs11568820	(AA+AG) vs GG	4	3,228	3,455	36.61	1.15 (1.04-1.27)	**0.005**	0								
VDR	246	rs1544410 (Intron, BsmI, b>B, c.1024+283G>A)	A vs G	11	9,917	10,250	40.27	0.96 (0.92-1.00)	**0.032**	0								
VDR	247	rs2228570 (Fok1)	A vs G	14	11,777	12,309	38.06	1.00 (0.95-1.05)	0.936	32	3	607	1,409	46.06	0.90 (0.56-1.44)	0.658	91	
VDR	248	rs2238136	A vs G	4	2,313	1,864	29.91	0.99 (0.90-1.09)	0.809	0								
VDR	249	rs731236 (TaqI, T>t, p.Ile352Met, c.1056T>C)	C vs T	7	3,189	2,658	37.11	1.02 (0.93-1.12)	0.641	32								
VDR	250	rs7975232 (ApaI)	A vs C	5	4,276	3,894	47.28	1.01 (0.95-1.07)	0.830	1								
VEGF	251	rs1570360 (-1154G>A)	A vs G	3	760	850	35.35	0.98 (0.85-1.13)	0.757	0								
VEGF	252	rs2010963 (UTR-5, 634G>C)	C vs G	4	1,345	1,221	35.05	1.00 (0.89-1.13)	0.977	7								
VEGF	253	rs3025039 (UTR-3, C936T)	T vs C	4	1,198	1,242	19.97	1.24 (1.07-1.43)	**0.003**	0								
VEGF	254	rs699947 (−2578 C/A)	A vs C	5	2,567	3,277	47.16	1.03 (0.56-1.88)	0.468	50								
VEGF	255	rs833061	C vs T	3	766	633	33.65				3	746	805	26.83	0.97 (0.73-1.30)	0.850	55	
WRN	256	rs1346044 (p.Cys1367Arg, c.4099T>C)	C vs T	3	4,693	4,840	26.02	1.05 (0.99-1.12)	0.114	0								
WRN	257	rs1801195 (rs2725362, p.Leu1074Phe, c.3222G>T)	T vs G	3	4,681	4,833	44.93	0.95 (0.89-1.02)	0.129	18								
WRN	258	rs2230009 (rs4987236, p.Val114Ile, c.340G>A)	A vs G	3	4,695	4,842	6.29	0.95 (0.84-1.07)	0.368	0								
XPA	259	rs1800975	A vs G	3	593	1,137	36.46	0.82 (0.70-0.96)	**0.016**	4								
XPC	260	rs2228000 (A499V)	T vs C															
XPC	261	rs2228001 (p.Gln939Lys, c.2815C>A)	C vs A	6	1,530	2,435	40.27	1.03 (0.94-1.13)	0.505	0	3	1,448	2,769	34.85	1.14 (1.03-1.26)	**0.009**	0	
XPC	262	rs2279017	(AA+AC) vs CC															
XRCC1	263	rs1799782 (p.Arg194Trp, c.580C>T)	T vs C	9	1,816	4,126	6.86	1.17 (0.89-1.55)	0.261	59	3	1,199	2,147	30.46	0.99 (0.89-1.11)	0.872	0	
XRCC1	264	rs25487 (p.Gln399Arg, c.1196A>G)	G vs A	15	6,532	9,776	34.23	1.01 (0.94-1.08)	0.892	27	6	2,460	4,105	26.60	1.03 (0.88-1.21)	0.712	69	
XRCC1	265	rs25489 (p.Arg280His, c.839G>A)	A vs G	4	3,377	3,773	7.26	1.02 (0.89-1.17)	0.810	0								
XRCC2	266	rs3218536 (p.Arg188His, c.563G>A)	A vs G	4	4,219	4,488	8.17	1.09 (0.96-1.24)	0.174	15								
XRCC3	267	rs861539 (p.Thr241Met, c.722C>T)	T vs C	7	2,510	3,259	37.85	1.05 (0.84-1.31)	0.683	80	3	1,345	1,984	6.50	1.63 (0.76-3.52)	0.213	92	

[a] Frequency of effect allele or effect genotype(s) in controls based on primary meta-analysis.

Appendix table 6. Results of previously published meta-analysis compared to meta-analyses performed in this study

		Prior meta-analyses													Current study							
Genes	**Variant**	**PubMed ID**	**Reference**	**First author**	**Year**	**Retrieved databases**	**Close date**	**Ethinicity**	**Studies**	**Cases**	**Controls**	**Comparison**	**OR (95% CI)**	***P* value**	$P_{heterogeneity}$	**Comparison**	**Ethinicity**	**Studies**	**Cases**	**Controls**	**OR (95% CI)**	***P* value**	$P_{heterogeneity}$	**Comments for prior meta-analyses**
APEX1	rs1130409	19762350	(1)	Gu	2009	PubMed and Embase	5/30/2009	All	3	1,629	1,599	GG versus TT	1.25 (1.03–1.52)	NA	0.574	G vs T	All	9	4,374	5,422	1.05 (0.89-1.23)	0.582	0.00	
CCND1	rs9344	18843022	(2)	Pabalan	2008	PubMed	NA	All	16	4,638	6,157	AA + AG vs GG	1.10 (0.96-1.26)	0.180	0.010	AA + AG vs GG	All	22	6,316	8,272	1.13 (1.01-1.26)	0.035	0.02	
CDH1	rs16260	21997289	(3)	Wang	2011	Medline/PubMed, CNKI, Wanfang Med Online	Jan, 2011	All	8	4,652	4,428	AA vs CC	0.86 (0.75–0.98)	0.020	0.100	A vs C	All	9	7,220	7,045	0.94 (0.88-1.01)	0.116	0.26	
CYP1A1	rs1048943	21246002	(4)	Jin	2011	PubMed	Sep, 2010	All	13	5,336	6,226	GG vs AA	1.47 (1.16-1.86)	0.002	0.440	G vs A	All	16	6,704	8,009	1.24 (1.05-1.47)	0.014	0.00	
		21710246	(5)	Zheng	2011	PubMed	10/31/2010	All	14	6,654	7,859	GG vs AA	1.40 (1.12–1.76)	0.003	0.872	G vs A	All	16	6,704	8,009	1.24 (1.05-1.47)	0.014	0.00	
	rs4646903	21710246	(5)	Zheng	2011	PubMed	10/31/2010	All	13	5,468	6,492	CC vs. TT	0.95 (0.68–1.33)	0.758	0.079	C vs T	All	14	5,491	6,371	1.06 (0.92-1.23)	0.412	0.00	Included 1 studies published in Chinese
ERCC2	rs13181	21541661	(6)	Zhang	2011	PubMed and Medline	Dec, 2010	All	15	3,042	4,627	C vs A	1.02 (0.94–1.11)	0.623	0.593	C vs A	All	17	6,039	8,749	0.99 (0.92-1.05)	0.649	0.17	
	rs1799793	21541661	(6)	Zhang	2011	PubMed and Medline	Dec, 2010	All	7	1,581	2,846	A vs G	1.07 (0.95-1.20)	0.275	0.057	A vs G	All	7	5,470	7,135	1.01 (0.96-1.07)	0.674	0.68	Included 1 studies published in Chinese
GSTM1	Present/Null	14523342	(7)	Ye	2003	MEDLINE	2002	All	20	4,010	5,099	null vs present	0.99 (0.91-1.07)	NA	>0.1	null vs present	All	54	18,601	29,433	1.11 (1.04-1.18)	0.001	0.00	
		20123161	(8)	Gao	2010	Pubmed, Embase and HuGENet	Dec, 2008	All	36	10,009	15,070	null vs present	1.13 (1.03–1.23)	NA	<0.001	null vs present	All	54	18,601	29,433	1.11 (1.04-1.18)	0.001	0.00	
		20207535	(9)	Economopoulos	2010	MEDLINE	Jul, 2009	All	44	11,998	17,552	null vs present	1.11 (1.04-1.19)	NA	NA	null vs present	All	54	18,601	29,433	1.11 (1.04-1.18)	0.001	0.00	
GSTP1	rs1695	19643601	(10)	Gao	2009	Pubmed, Embase and HuGENet	Jan, 2009	All	16	4,386	7,127	G vs A	0.98 (0.92–1.04)	NA	0.310	G vs A	All	29	7,857	13,413	0.99 (0.93-1.05)	0.676	0.07	
		20207535	(9)	Economopoulos	2010	MEDLINE	Jul, 2009	All	19	5,421	7,671	GG vs AA	0.91 (0.76-1.08)	NA	0.078	G vs A	All	29	7,857	13,413	0.99 (0.93-1.05)	0.676	0.07	
GSTT1	Present/Null	19798506	(11)	Liao	2010	PUBMED, EMBASE, Cochrane Library and HuGENet	Feb, 2009	All	23	5,058	5,999	null vs present	1.23 (1.02–1.49)	0.032	<0.001	null vs present	All	41	13,201	21,862	1.16 (1.04-1.28)	0.006	0.00	
		20061204	(12)	Wan	2010	Pubmed, Embase	May, 2009	All	30	7,635	12,911	null vs present	1.20 (1.03–1.40)	0.020	<0.001	null vs present	All	41	13,201	21,862	1.16 (1.04-1.28)	0.006	0.00	
		20207535	(9)	Economopoulos	2010	MEDLINE	Jul, 2009	All	34	8,596	13,589	null vs present	1.20 (1.05-1.38)	NA	NA	null vs present	All	41	13,201	21,862	1.16 (1.04-1.28)	0.006	0.00	
		21916987	(13)	Zhong	2012	PubMed, Embase and Chinese biomedical database	2011	Asian	12	4,517	6,607	null vs present	1.1 (1.02-1.19)	0.020	NA	null vs present	All	41	13,201	21,862	1.16 (1.04-1.28)	0.006	0.00	
IGF1	CA repeat	18188667	(14)	Chen	2008	PubMed	NA	All	3	NA	NA	R19 vs non R19	0.96 (0.89–1.03)	0.270	0.360	non R19 vs R19	All	6	5,081	6,020	1.03 (0.97-1.10)	0.322	0.30	
MDM2	rs2279744	20503107	(15)	Fang	2010	PubMed, Web of Science, EBSCO, and CNKI	3/1/2010	All	7	2,543	2,115	TT vs GG	0.86 (0.57-1.30)	NA	0.006	G vs T	All	8	2,421	1,802	1.00 (0.91-1.10)	0.976	0.53	Included 1 studies published in Chinese
MGMT	rs12917	19892775	(16)	Zhong	2010	MEDLINE	Apr, 2009	All	4	1,618	4,685	TT vs CT+CC	1.05 (0.44–2.49)	0.911	0.084	TT vs CT+CC	All	7	4,127	7,284	1.54 (1.14-2.08)	0.005	0.47	
	rs2308321	19892775	(16)	Zhong	2010	MEDLINE	Apr, 2009	All	4	1,618	4,685	G vs A	0.89 (0.63–1.25)	0.490	0.005	G vs A	All	6	3,843	8,783	1.00 (0.80-1.25)	0.984	0.00	
MMP1	rs1799750	19507256	(17)	McColgan	2009	PubMed, Embase, Google Scholar and Yahoo	July, 2008	All	4	539	765	2G/2G+1G/2G vs 1G/1G	1.66 (1.14–2.42)	0.008	NA	2G vs 1G	All	7	987	1,281	0.72 (0.60-0.87)	6.74×10^{-4}	0.07	
		21538057	(18)	Liu	2011	PubMed, Embase, ISI Web of Knowledge, and Medline	July, 2010	All	7	987	1,281	2G/2G+1G/2G vs 1G/1G	1.23 (1.01–1.49)	NA	0.420	2G vs 1G	All	7	987	1,281	0.72 (0.60-0.87)	6.74×10^{-4}	0.07	
MMP2	rs243865	19507256	(17)	McColgan	2009	PubMed, Embase, Google Scholar and Yahoo	July, 2008	All	3	379	460	TT+TC vs CC	0.97 (0.49–1.93)	0.810	NA	T vs C	All	3	300	401	0.99 (0.49-2.00)	0.976	0.03	Included 1 studies published in Chinese
		21538057	(18)	Liu	2011	PubMed, Embase, ISI Web of Knowledge, and Medline	July, 2010	All	3	NA	NA	TT+TC vs CC	0.83 (0.59–1.17)	NA	0.080	T vs C	All	3	300	401	0.99 (0.49-2.00)	0.976	0.03	
MMP3	rs3025058	19507256	(17)	McColgan	2009	PubMed, Embase, Google Scholar and Yahoo	July, 2008	All	4	473	803	5A/5A+5A/6A vs 6A/6A	0.93 (0.50–1.71)	0.810	NA	5A vs 6A	All	6	649	996	0.98 (0.76-1.27)	0.881	0.08	
		21538057	(18)	Liu	2011	PubMed, Embase, ISI Web of Knowledge, and Medline	July, 2010	All	5	NA	NA	6A/6A+5A/6A vs 5A/5A	1.02 (0.73–1.42)	NA	0.150	5A vs 6A	All	6	649	996	0.98 (0.76-1.27)	0.881	0.08	
MMP9	rs3918242	19507256	(17)	McColgan	2009	PubMed, Embase, Google Scholar and Yahoo	July, 2008	All	5	700	963	TT+TC vs CC	0.9 (0.68–1.17)	0.430	NA	T vs C	All	4	644	792	0.87 (0.66-1.14)	0.303	0.26	Included 1 studies published in Chinese
		21538057	(18)	Liu	2011	PubMed, Embase, ISI Web of Knowledge, and Medline	July, 2010	All	4	NA	NA	TT+TC vs CC	0.85 (0.67–1.08)	NA	0.430	T vs C	All	4	644	792	0.87 (0.66-1.14)	0.303	0.26	
MTHFR	rs1801133	17131337	(19)	Hubner	2006	PubMed	4/21/2006	All	25	12,243	17,688	TT vs CC	0.83 (0.75–0.93)	0.001	0.120	T vs C	All	63	31,091	42,993	0.99 (0.95-1.03)	0.611	0.00	
		17089070	(20)	Huang	2007	PubMed	Aug, 2006	All	23	10,131	15,362	T vs C	0.93 (0.89–0.98)	0.004	0.220	T vs C	All	63	31,091	42,993	0.99 (0.95-1.03)	0.611	0.00	
		19846566	(21)	Taioli	2009	CINAHL, MEDLINE	4/30/2008	All	29	11,936	18,714	TT vs CC	0.83 (0.77-0.90)	<0.001	0.106	T vs C	All	63	31,091	42,993	0.99 (0.95-1.03)	0.611	0.00	
		20473868	(22)	Zacho	2010	PubMed, Embase and web-of-science	Dec, 2008	All	37	9,345	18,887	TT vs CC	0.85 (0.77–0.94)	NA	NA	T vs C	All	63	31,091	42,993	0.99 (0.95-1.03)	0.611	0.00	
	rs1801131	17089070	(20)	Huang	2007	PubMed	Aug, 2006	All	14	4,764	6,592	C vs A	0.94 (0.88–0.99)	0.090	0.030	C vs A	All	32	14,715	21,684	0.99 (0.95-1.03)	0.562	0.10	
MTR	rs1805087	19826453	(23)	Yu	2010	PubMed	May, 2008	All	12	6,452	8,184	G vs A	0.99 (0.90–1.08)	NA	NA	G vs A	All	18	12,832	17,467	0.99 (0.93-1.04)	0.653	0.08	
MTRR	rs1801394	21547363	(24)	Han	2011	PubMed and CNKI	7/16/2010	All	10	NA	NA	G vs A	1.06 (0.99–1.13)	0.105	0.698	A vs G	All	15	7,561	11,405	0.95 (0.91-1.00)	0.052	0.25	
MUTYH	rs34612342	21063410	(25)	Theodoratou	2010	Web of Science, PubMed	NA	All	15	25,231	18,285	GG vs AA	3.35 (1.14-9.89)	0.030	0.990	G vs A	White	17	27,041	19,641	3.32 (1.13-9.81)	0.030	1.00	
	rs36053993	21063410	(25)	Theodoratou	2010	Web of Science, PubMed	NA	All	15	25,231	18,285	AA vs GG	6.47 (2.33-17.97)	<0.0005	0.730	A vs G	White	17	26,957	19,870	6.49 (2.57-1.35)	7.49×10^{-5}	0.85	
NOD2	rs2066844	19787357	(26)	Tian	2010	Web of Science, PubMed, EMBASE	Mar, 2009	All	5	1,436	1,109	TT+TC vs CC	1.59 (1.09–2.32)	0.020	0.140	TT+TC vs CC	White	9	3,297	3,088	1.35 (1.02-1.78)	0.038	0.14	
	rs2066845	19787357	(26)	Tian	2010	Web of Science, PubMed, EMBASE	Mar, 2009	All	5	1,442	1,109	CC+CG vs GG	1.98 (1.14–3.44)	0.010	0.660	C vs G	White	8	3,252	2,988	1.31 (0.93-1.85)	0.124	0.44	
	rs2066847	19787357	(26)	Tian	2010	Web of Science, PubMed, EMBASE	Mar, 2009	All	7	2,571	1,856	ins vs wild	1.44 (1.13–1.84)	0.003	0.670	ins vs wild	White	11	4,337	5,395	1.30 (1.02-1.65)	0.032	0.13	
OGG1	rs1052133	21695387	(27)	Zhang	2011	PubMed	9/22/2010	All	12	NA	NA	GG VS CC	1.19 (0.92-1.53)	NA	0.028	G vs C	All	18	6,654	8,599	1.10 (0.99-1.23)	0.085	0.00	
PPARG	rs1801282	20440859	(28)	Lu	2010	PubMed and Google	Jan, 2010	All	9	4,533	6,483	CG + GG vs CC	0.84 (0.69-1.01)	0.070	0.009	G vs C	All	16	11,775	18,067	0.97 (0.90-1.04)	0.368	0.16	
		20596649	(29)	XU	2010	PubMed, Embase, Web of Science, and CNKI	1/1/2010	All	10	6,878	9,391	CG+GG vs. CC	0.84 (0.72-0.98)	NA	0.014	G vs C	All	16	11,775	18,067	0.97 (0.90-1.04)	0.368	0.16	
	rs3856806	20596649	(29)	XU	2010	PubMed, Embase, Web of Science, and CNKI	1/1/2010	All	3	486	941	CT+TT vs. CC	1.11 (0.89, 1.39)	NA	0.337	T vs C	All	9	4,427	6,842	1.04 (0.95-1.13)	0.435	0.33	
PTGS2	rs20417	19669667	(30)	Zhu	2010	Pubmed, Embase	3/26/2009	Asian	4	1,595	2,917	CC+GC vs GG	1.44 (1.09–1.91)	0.010	0.140	C vs G	All	12	3,527	5,844	1.06 (0.94-1.20)	0.337	0.16	
		20808059	(31)	Cao	2010	Web of Science, MEDLINE, EMBASE and Chinese biomedical database	Jan, 2010	All	10	3,222	5,166	CC+GC vs GG	1.06 (0.94-1.19)	NA	0.073	C vs G	All	12	3,527	5,844	1.06 (0.94-1.20)	0.337	0.16	
SULT1A1	rs9282861	21695189	(32)	Zhang	2011	Pubmed, Elsevier Science Direct, Embase and Chinese biomedical database	Sep, 2010	All	12	3,549	5,610	A vs G	1.04 (0.94–1.16)	0.460	0.009	A vs G	All	11	3,802	5,042	1.02 (0.92-1.12)	0.757	0.03	Included 1 studies published in Chinese
TGFB1	rs1800469	20012233	(33)	Fang	2010	PubMed, Web of Science and CNKI	10/16/2009	All	5	994	2,335	CC vs. TT	1.62 (1.30,2.02)	NA	0.118	T vs C	All	10	4,405	5,383	0.88 (0.79-0.97)	0.013	0.02	
TGFBR1	rs11466445	12947057	(34)	Kaklamani	2003	MEDLINE, CANCERLIT	Apr, 2002	All	3	546	642	6a/6a vs 9a/9a	2.19 (1.08-4.45)	NA	NA	9 bp del vs ins	All	10	6,338	6,689	1.04 (0.96-1.13)	0.379	0.43	
		19882361	(35)	Liao	2010	MEDLINE, PubMed	1/28/2009	All	9	2,346	3,578	6A/6A vs. 9A/9A	1.45 (0.87–2.43)	0.150	0.170	9 bp del vs ins	All	10	6,338	6,689	1.04 (0.96-1.13)	0.379	0.43	
TNF	rs1800629	21248737	(36)	Wang	2011	PubMed, Cochrane and Embase	NA	All	7	1,372	1,458	AA+AG vs GG	0.94 (0.59–1.49)	0.210	<0.001	A vs G	All	10	2,092	1,911	1.31 (1.00-1.72)	0.051	0.00	
TP53	rs1042522	20615891	(37)	Dahabreh	2010	MEDLINE, HUGENet, NIH Genetic Association Database	7/31/2009	All	23	6,514	9,334	C vs G	0.99 (0.89–1.09)	0.800	<0.001	C vs G	All	29	9,724	11,852	0.99 (0.90-1.09)	0.826	0.00	
		20363586	(38)	Tang	2010	Pubmed, Embase	Jan, 2010	All	20	3,537	5,168	CC vs GG	1.02 (0.80-1.29)	NA	0.010	C vs G	All	29	9,724	11,852	0.99 (0.90-1.09)	0.826	0.00	
		21124037	(39)	Economopoulos	2010	MEDLINE	7/20/2010	All	27	7,414	9,872	CC vs GG	1.04 (0.82–1.31)	0.766	<0.001	C vs G	All	29	9,724	11,852	0.99 (0.90-1.09)	0.826	0.00	
		21140221	(40)	Wang	2011	Medline, Google scholar, and Ovid database	May, 2010	All	21	3,603	5,524	CC vs GG	0.97 (0.76–1.25)	NA	0.005	C vs G	All	29	9,724	11,852	0.99 (0.90-1.09)	0.826	0.00	
TP73	rs2273953/rs1801173	21502193	(41)	Liu	2011	PubMed, Embase, CNKI and Chinese biomedical database	12/25/2010	All	5	919	1,234	A4T14 vs G4C14	1.97(1.41–2.75)	NA	0.210	A4T14 vs G4C14	All	4	858	1,168	1.20 (1.04-1.40)	0.015	0.36	Included 1 studies published in Chinese
		21672615	(42)	Yu	2011	PubMed, Web of Science, and EBSCO	10/12/2010	All	4	858	1,168	GC/GC versus AT/AT	0.55 (0.38-0.79)	NA	0.668	A4T14 vs G4C14	All	4	858	1,168	1.20 (1.04-1.40)	0.015	0.36	
		22011187	(43)	Hu	2011	PubMed	Sep, 2010	All	3	712	933	A4T14 vs G4C14	1.23 (1.01–1.50)	0.040	0.110	A4T14 vs G4C14	All	4	858	1,168	1.20 (1.04-1.40)	0.015	0.36	
NQO1	rs1800566	16702380	(44)	Chao	2006	Web of Science, PubMed	Jan, 2006	All	6	1,781	2,494	CT vs CC	1.15 (1.01-1.32)	NA	0.330	T vs C	All	12	7,209	8,783	1.07 (0.99-1.15)	0.090	0.13	
VEGF	rs699947	20635170	(45)	Cao	2010	Medline, EMBASE, OVID, and CNKI	Feb, 2010	All	3	1,047	904	CC vs. AA	0.70 (0.53-0.92)	0.580	0.010	A vs C	All	7	2,923	3,590	1.04 (0.91-1.18)	0.569	0.03	
		22058001	(46)	Zhou	2011	PubMed, Embase, and Chinese biomedical database	Jan, 2011	All	4	1,293	1,107	C vs A	0.91 (0.74-1.11)	0.340	0.050	A vs C	All	7	2,923	3,590	1.04 (0.91-1.18)	0.569	0.03	
	rs2010963	21174216	(47)	Liu	2011	Medline, Embase and CNKI	10/1/2011	All	5	1,354	1,557	GG vs CC	1.17 (0.93–1.47)	0.970	NA	C vs G	All	5	1,810	1,634	0.96 (0.86-1.08)	0.497	0.28	
		22058001	(46)	Zhou	2011	PubMed, Embase, and Chinese biomedical database	Jan, 2011	All	3	1,209	1,205	G vs C	1.07 (0.95-1.20)	0.240	0.470	C vs G	All	5	1,810	1,634	0.96 (0.86-1.08)	0.497	0.28	
	rs1570360	22058001	(46)	Zhou	2011	PubMed, Embase, and Chinese biomedical database	Jan, 2011	All	2	464	518	G vs A	1.03 (0.85-1.23)	0.780	0.270	A vs G	White	3	760	850	0.98 (0.85-1.13)	0.757	0.54	
	rs3025039	22058001	(46)	Zhou	2011	PubMed, Embase, and Chinese biomedical database	Jan, 2011	All	5	1,623	1,548	C vs T	0.95 (0.76-1.20)	0.680	0.020	T vs C	All	6	1,925	1,884	1.19 (1.04-1.37)	0.014	0.22	
	rs833061	22058001	(46)	Zhou	2011	PubMed, Embase, and Chinese biomedical database	Jan, 2011	All	3	766	633	C vs T	1.32 (0.87-2.01)	0.190	0.002	C vs T	All	3	766	633	1.36 (0.93-2.00)	0.116	0.01	
VDR	rs1544410	19403841	(48)	Raimondi	2009	Web of Science, PubMed, EMBASE	Jan, 2009	All	8	6,401	7,162	AA vs GG	0.63 (0.29-1.39)	NA	<0.001	A vs G	All	17	11,687	12,301	0.85 (0.72-0.99)	0.040	0.00	
		21378269	(49)	Touvier	2011	PubMed	Jun, 2010	All	8	NA	NA	AA vs GG	0.57 (0.36–0.89)	NA	<0.001	A vs G	All	17	11,687	12,301	0.85 (0.72-0.99)	0.040	0.00	
	rs2228570	19403841	(48)	Raimondi	2009	Web of Science, PubMed, EMBASE	Jan, 2009	All	10	6,759	8,293	AA vs GG	1.00 (0.76–1.31)	NA	<0.001	A vs G	All	19	13,432	14,964	1.00 (0.94-1.06)	0.865	0.00	
		21378269	(49)	Touvier	2011	PubMed	Jun, 2010	All	10	NA	NA	AA vs GG	0.98 (0.74–1.30)	NA	<0.001	A vs G	All	19	13,432	14,964	1.00 (0.94-1.06)	0.865	0.00	
	rs2238136	21378269	(49)	Touvier	2011	PubMed	Jun, 2010	All	4	NA	NA	AA vs GG	.11 (0.94–1.32)	NA	0.980	A vs G	All	6	3,108	2,849	0.98 (0.90-1.07)	0.689	0.79	
	rs731236	21378269	(49)	Touvier	2011	PubMed	Jun, 2010	All	4	NA	NA	CC vs TT	1.34 (0.80–2.24)	NA	0.040	C vs T	All	11	4,161	4,011	1.01 (0.94-1.10)	0.734	0.23	
	rs7975232	21378269	(49)	Touvier	2011	PubMed	Jun, 2010	All	5	NA	NA	AA vs CC	0.91 (0.67–1.23)	NA	0.020	A vs C	All	9	5,421	5,377	1.08 (0.98-1.19)	0.105	0.02	
XRCC1	rs25487	19915856	(50)	Jiang	2010	PubMed	Mar, 2009	All	11	3,514	4,686	G vs A	0.96 (0.86–1.06)	0.430	0.020	G vs A	All	22	8,267	12,402	1.02 (0.94-1.09)	0.704	0.01	
		20033188	(51)	Wang	2010	PubMed, Embase, and Chinese biomedical database	7/6/2009	All	14	2,776	4,402	GG+AG vs AA	1.02 (0.80, 1.30)	0.880	<0.00001	G vs A	All	22	8,267	12,402	1.02 (0.94-1.09)	0.704	0.01	
	rs1799782	20033188	(51)	Wang	2010	PubMed, Embase, and Chinese biomedical database	7/6/2009	All	9	1,709	3,233	TT+CT vs CC	1.14 (0.87, 1.51)	0.340	0.002	T vs C	All	12	2,378	5,545	1.14 (0.94-1.39)	0.187	0.01	
	rs25489	20033188	(51)	Wang	2010	PubMed, Embase, and Chinese biomedical database	7/6/2009	All	4	931	1,547	AA+AG vs GG	1.11 (0.87, 1.40)	0.400	0.250	A vs G	All	5	3,586	3,982	1.04 (0.91-1.19)	0.555	0.51	
XRCC3	rs861539	19915856	(52)	Jiang	2010	PubMed	Mar, 2009	All	8	3,183	3,926	T vs C	1.00 (0.82–1.21)	0.830	<0.001	T vs C	All	10	3,673	4,564	1.05 (0.87-1.27)	0.624	0.00	

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