

Supplement Table 1. Characteristics of selected single nucleotide polymorphisms (SNPs) in genes involved in the immune response, production of reactive oxygen species (ROS), detoxification of ROS, and repair of oxidative DNA damage evaluated in association with prostate cancer recurrence in men who underwent prostatectomy at Johns Hopkins Hospital, 1993-2001

Gene	dbSNP No.	Nucleotide change (major/minor)	Location	In controls		HapMap CEU	5' near seq 30 bp	3' near seq 30 bp
				Variant allele frequency	Hardy-Weinberg Equilibrium <i>P</i>			
Candidate SNPs								
<i>IL10</i>	rs1800872	C/A	-592 promoter	23.8%	0.36	21.2%	gcctggaacacatcct gtgaccccgcctgt	ctgtaggaagccagtc tctgaaagtaaaa
	rs1800896	G/A	-1082 promoter	49.3%	0.15	46.9%	caagacaacactact aaggctctttggga	ggggaagtagggata ggtaagaggaaagta
<i>CRP</i>	rs1205	C/T	Exon2	33.3%	0.03	33.3%	cctccactccagtttg cttctgtctca	agtctctccatgtgg caacaagatggc
	rs1800947	G/C	Exon2	8.2%	0.05	6.7%	tggaaatgtgaacatg tgggactttgtgct	tcaccagatgagatta acaccatctatctt
<i>GSTP1</i>	rs1695	A/G	Exon2	27.9%	0.13	40.7%	cctccactccagtttg cttctgtctca	agtctctccatgtgg caacaagatggc
<i>hOGG1</i>	rs293795	A/G	3'-UTR	16.8%	0.31	13.8%	gtttctctgccctgtccc ctcctcacctgc	tcctaccactcctcac tgcattttccata
<i>IL1B</i>	rs1143627	T/C	-31 promoter	39.2%	0.03	36.3%	tctcagcctcctacttct gctttgaaagc	ataaaaacagcgag ggagaaactggcag at
<i>IL6</i>	rs1800795 ^a	G/C	-237 promoter	35.5%	0.07	53.3%	gctgcacttttccccta gttggtctctgc	atgctaaaggacgtca cattgcacaatctt
<i>IL8</i>	rs4073	T/A	-251 promoter	46.3%	0.11	40.0%	taaagttatctagaaat aaaaaagcataca	ttgataattcaccaaatt gtggagcttca
<i>MPO</i>	rs12452417	G/A	5' near gene	16.5%	0.0003	17.3%	tactccaccctttatact gtggttatttg	ggagggggtaagctt ccacgagtcaaagtt

	rs12944679	C/T	5' near gene	27.1%	0.0002	27.4%	tgaatatgcttctatftta aatactgtgg	atagtgcaatfcattag ccttttgaaagg
	rs12451466	G/A	5' near gene	16.7%	0.0005	17.3%	gtagcccctagggtct ctctgcccctgttt	cactgctctagtcag aggcaacgtgcag
<i>NOS3</i>	rs1799983 ^a	G/T	Exon7	26.0%	0.36	34.2%	gctgcccctgtgctgc aggccccagatga	ccccagaactcttct tctgcccccgag
<i>SOD1</i>	rs2070424 ^a	A/G	Intron3	8.9%	0.07	7.6%	gccttgggacatagctt tgtagctatgcc	gtaattaacaggcata actcagtaactgag
<i>SOD2</i>	rs4880	T/C	Exon2	50.0%	0.89	44.7%	gtgtgcggcaccagc aggcagctgtccgg	ttggggatctgggctc caggcagaagca
<i>SOD3</i>	rs699473	T/C	Intron1	38.8%	0.50	34.4%	tatgacagcacagctc tggagcaaagcca	gcacattgcaagggtg cccatttccatgca
	rs1799895	C/G	Exon3	2.6%	<0.0001	3.3%	caggcgcgaggagca ctcagagcgcaagaa g	ggcggcgagagac gagtgaaggccgccc t
	rs2855262	C/T	Exon3	39.1%	0.99	38.3%	accctccactctgaggt ctcaccttcgct	tgctgaagtctccccgc agccctctccacc
<i>TLR4</i>	rs4986790	A/G	Exon4	7.5%	0.64	3.5%	gattagcatacttagac tactacctgatg	tattattgactatttaatt gkttgacaaa
<i>TNF</i>	rs1800629	G/A	-308 promoter	14.9%	0.49	17.3%	aatggaggcaatag gtttgaggggcatg	ggacgggggtcagcct ccagggtcctacac
<u>Tagging SNPs</u>								
<i>IL10</i>	rs3024498	A/G	3'-UTR	27.9%	0.78	29.3%	tgtctctgggcttgggg cttcctaactgct	caaatactcttaggaa gagaaaccaggagg
	rs3024496	T/C	3'-UTR	50.0%	0.36	52.2%	gcccttgagaaacct tattgtacctctct	atagaatatttacct ctgatacctcaa
	rs3024509	C/T	Intronic	7.9%	<0.0001	5.8%	cctcatgatgccacca gcttgtcccctaag	gtgatggacatggag ctggaagccaggatc
	rs1554286	C/T	Intronic	17.5%	0.92	17.3%	ctacggcgctgtgtaa gtagcagatcagtt	ttcccttgagctgccc ccaaaataccat
	rs3021094	A/C	Intronic	9.0%	0.29	6.2%	ccagatttttaataaac	ggaggacctgattaa

CRP	rs1800894	C/T	-886 promoter	2.4%	<0.0001	4.0%	ttgactctgagg tacatcacctgtacaa gggtacaccagtgc	gtgatggcccac aactgagaattgggtt cctcacctactg	
	rs1800890	T/A	-3585 promoter	40.9%	0.25	40.0%	atttcccagttacatccc ccactggaaaaat	catftaaaatcagttata ataagcattgatt	
	rs3093077	A/C	3'intergenic	9.1%	<0.0001	5.3%	gagaaggaatccag gcaagtacgacaacc c	tctgagactagtgggc agttgtcctaggat	
	rs2808630	T/C	3'intergenic	26.4%	0.23	29.9%	tattaaggccagaggc tgtctaccagacta	gtatagtaagatgcaa gcaactgaattctg	
	rs1417938	T/A	Intron1	28.1%	0.98	33.1%	ttagacccccacccca tacctcagatcaaa	ctctccatagcctggg gtggcccttacct	
GPX1	rs1800668	C/T	5'-UTR	31.1%	0.69	23.3%	taaaaggaggcgctt gctggcctcccctta	agtgttgttcggggcg ctccgctggcttc	
	rs3448	C/T	5'-UTR	25.1%	0.05	27.4%	gagaaaagagcact gtgaattagagccag a	gcttaagtccagggtg agacaggttatgcc	
	rs3594	C/A	3' near gene	37.9%	0.88	38.8%	cagaaaaaataaa atgacaagaacacat a	aaatattgaaattatc attgaaactataaa	
GSR	rs2551715	G/A	Intron	34.3%	0.23	42.9%	tggtctgcccgaacaa tttgtaatctact	ggagtcttatggtttatt tccccccaga	
	rs8190996	C/T	Intron	41.0%	0.80	45.5%	tagttatttaagaatac taaccctctgct	gctgtcagccgcagc gtcattgttggtgc	
	rs3779647	T/C	Intron	49.9%	0.22	42.0%	tcttggttgctgatgcc aacacaattctc	gttttcaagttctgtag aacttctaact	
	rs2978663	A/G	Intron	42.5%	0.42	35.8%	caagtgtttattaagtg cccaccagctct	tgcatcatgatgtctag gcactttgcaaaa	
	rs17557435	T/C	Intron	23.8%	<0.0001	11.9%	cacaggcctcaagtc agacagataggagtt	gactctcagctctcca tttagtgctaga	
	rs8190893	G/A	Intron	5.4%	0.21	6.2%	gggtgttgacgattaa aatgctgtatccaa	aggaacctgggatttg ggataggttctcta	
	rs1002149	G/T	5' near gene	18.2%	0.50	16.4%	tccaggaagagaaat ttgcctctattcgaa	ggttgtttgcaggtttg ttccagagacc	
	IL1RN	rs878972	A/C	Intron1	26.4%	0.15	17.4%	tgaagacaatgctgac	tttttaggatccaagtttg

IL6	rs3087263	G/A	Intron2	6.6%	<0.0001	9.3%	tcaaagggtaaatt cgctgtgacatctgtg	aaaacaatfff ataactcctgtgtgcct
	rs315951	G/C	3'-UTR	29.6%	0.02	26.3%	acatgagagtcac gaagaggaggcaga	tacaggggtgtt ttgtgacgccttctgag
	rs1474348	G/C	Intron2	34.7%	0.20	45.7%	gtcctgtgaccagggt	gtgcccccctca
	rs2069845	G/A	Intron4	41.0%	0.79	45.8%	ccacctctggactccat cagtaaaattggg	gtggactaggtgatctc atagatccttct
	rs2069860	A/T	Exon5	100%	N/A	1.7%	aaggtgtttcccagtc tcttacaccacc	gatcagtggtcttcaa cagatcctaaagg
MPO	rs4401102	C/T	5' near gene	28.0%	0.003	27.9%	ctttcatttccttcaggc aagaatctag	tgcaataaccaccct gaccaaccacaaa
	rs12949848	A/G	5' near gene	16.8%	0.0009	17.3%	gtcaacctgagtatgc ttgagtgccttt	gctctttaagggaaatt gtcaaggctcaac
	rs12949848	A/G	5' near gene	16.8%	0.0009	17.3%	cagagtaaccagggg aatgcagctcaaggg	gtgggagggattcaa ataagctttgtccc
NOS2	rs8081248	G/A	3' near gene	39.1%	0.12	49.1%	tggtccacaacaccca gatcaacaactctt	ggggctgatgagag gggcacagctgggga
	rs12450521	C/A	3' near gene	24.4%	0.0004	21.7%	gtccctcaggcgagg atgctgtggcccaca	tcgcctcgacacgctg ccttcccagggacc
	rs9906835	A/G	Intron	48.8%	<0.0001	36.7%	tagctgagtgagttaa tgaataatcaatgc	gaatctcccctgcgttc aggctgcatgatt
	rs2297515	A/C	Intron	0.6%	<0.0001	15.9%	ggagcagatgctcag agtccaagctggaaa	gtggctcgtggttaacc aagagtagacgta
	rs2314810	G/C	Intron	5.6%	0.69	10.6%	aggatgtgtggtgcaa agccagcccttccc	aaacaccggggggct cttctgttccatct
	rs12944039	G/A	Intron	20.5%	0.04	19.0%	ccctgccccatggagc ttacattctagtg	ggaaacaaacaata aagaaagctggcccg
	rs4795067	A/G	Intron	35.8%	0.19	32.3%	tcatgcactcattcattc atgcaaacctat	ttaagctcaagtatgt gccaggctctgtg
	rs944725	C/T	Intron	37.4%	0.46	37.5%	gtgctttgatattatcct gcaacaaatga	tccccacaaaaaga tggcctaggaggcta
	rs17722851	T/A	Intron	13.1%	0.08	9.2%	accaggtcgcctga tgccaagcccagggt	cttaactgtcagcaac gtgaccttccatct
	rs3794764	G/A	Intron	20.8%	0.27	19.5%	tccccaaaggacacc ctgccataaggagct	ctgggtgaggtggga accaccccactgctg
	rs3794766	C/T	Intron	23.1%	0.02	19.9%	cattggctctcattgctt	ccctttgacaggctgctt

	rs10459953	G/C	5'-UTR	29.6%	0.12	45.7%	caggatgaaat ttaaagcaggaatga ggctgagttctctg	tctctacagta ggccggagcctcagtt ttcgactcgctaca
	rs2779248	T/C	5' near gene	40.8%	0.69	32.3%	ggcagttcatcagcag ggtggctgctaaga	agaggcaccacgga gccaggtttatttg
	rs11080358	G/A	5' near gene	13.8%	0.42	11.6%	tctggttccttagcctg aaaggfccag	ttcaggcacagcttc actgctgacctacc
	rs2779252	G/T	5' near gene	3.3%	0.46	5.8%	ttctgatgatggatgca gcaggtgaattct	ctggggagaaatcaa agagcacctgaagg
<i>NOS3</i>	rs2373961	G/A	5' near gene	36.6%	0.42	37.2%	ctcagttgtcacctg ggctgccctccct	gtttctgctgagcctgc cgtaaagtattt
	rs6951150	C/T	5' near gene	33.7%	0.12	40.2%	agccatccaagga tcatcagctgctgag	cagccaacaccaag gacctgagaagaga ac
	rs12703107	G/T	5' near gene	26.2%	0.58	25.8%	caagtcaccaatgact gaaggttctccagg	cttgaagtcaggatttc cacatctcacaga
	rs3918227	C/A	Intron	8.0%	0.51	13.7%	tattgtgtgaatatccc cagttgtttac	cattctctgttggtgac actgggctgtt
	rs2373929	T/C	Intron	39.9%	0.51	49.1%	gggtcacttccctcctg tgctctcgtgcc	tcgtctgtcagatggca acaatggcaatgt
<i>SOD1</i>	rs1041740	C/T	Intron4	26.6%	0.21	23.2%	cctggggaactgcatc tggttctgcaaaa	accaagtagacaggc tctctttacctccc
<i>SOD2</i>	rs5746136	G/A	Intron	22.9%	0.25	32.7%	ggctttctatagaaaat tgcacttttgc	agtaatcctctgcagtg atactctggtag
	rs2758331	C/A	Intron	48.3%	0.88	43.8%	cttcagtgacatttttaa atccaattagg	tcaacagcaaagtattt ggtgagcccagcc
<i>TLR4</i>	rs11536889	G/C	3'-UTR	12.3%	0.80	12.5%	gggcaatgctccttga ccacatttgggaa	agtggatgttatcattg agaaaacaatgtg

^a Both a candidate and tagging SNP.

Supplement Table 2. Matched odds ratios and 95% confidence intervals of prostate cancer recurrence for tagging single nucleotide polymorphisms (SNPs) in genes involved in immune response, production of reactive oxygen species (ROS), detoxification of ROS, and repair of oxidative DNA damage, men who underwent prostatectomy at John Hopkins Hospital, 1993-2001

Gene	dbSNP	Number of minor alleles					<i>P</i> ^a	At least 1 minor allele		
		None	1 copy		2 copies			Cases/ controls (genotype)	OR (95% CI)	
		Cases/ controls (genotype)	Cases/ controls (genotype)	OR (95% CI)	Cases/ controls (genotype)	OR (95% CI)		Cases/ controls (genotype)	OR (95% CI)	
<i>IL10</i>	rs3024498	276/243 (AA)	153/181 (AG)	0.75 (0.57-0.98)	31/36 (GG)	0.75 (0.45-1.25)	0.05	184/217 (G-carrier)	0.75 (0.58-0.97)	
	rs3024496	147/111 (TT)	201/234 (CT)	0.65 (0.48-0.89)	99/102 (CC)	0.74 (0.51-1.06)	0.08	300/336 (C-carrier)	0.68 (0.51-0.91)	
	rs3024509	414/428 (TT)	-/-	N/A	53/39 (CC)	1.42 (0.91-2.22)	0.12	53/39 (C-carrier)	1.42 (0.91-2.22)	
	rs1554286	295/304 (CC)	135/133 (CT)	1.04 (0.79-1.38)	21/14 (TT)	1.52 (0.77-3.01)	0.35	156/147 (T-carrier)	1.09 (0.83-1.42)	
	rs3021094	371/373 (AA)	72/76 (CA)	0.94 (0.66-1.33)	8/2 (CC)	4.00 (0.85-18.84)	0.53	80/78 (C-carrier)	1.03 (0.74-1.44)	
	rs1800894	442/456 (CC)	-/-	N/A	26/12 (TT)	2.27 (1.12-4.62)	0.02	26/12 (T-carrier)	2.27 (1.12-4.62)	
	rs1800890	204/162 (TT)	200/232 (AT)	0.67 (0.50-0.90)	58/68 (AA)	0.68 (0.46-1.02)	0.01	258/300 (A-carrier)	0.67 (0.51-0.89)	
	<i>CRP</i>	rs3093077	377/391 (TT)	81/63 (GT)	1.33 (0.93-1.89)	8/12 (GG)	0.65 (0.25-1.67)	0.47	89/75 (G-carrier)	1.22 (0.88-1.70)
		rs2808630	239/230 (AA)	169/183 (AG)	0.89 (0.68-1.17)	33/28 (GG)	1.12 (0.67-1.88)	0.83	202/211 (G-carrier)	0.92 (0.71-1.20)
rs1417938		239/240 (AA)	191/194 (AT)	0.99 (0.76-1.30)	38/34 (TT)	1.12 (0.68-1.85)	0.79	229/228 (T-carrier)	1.01 (0.78-1.31)	
<i>GPX1</i>	rs1800668	215/215 (CC)	202/186 (CT)	1.10 (0.83-1.44)	31/47 (TT)	0.66 (0.41-1.08)	0.41	233/233 (T-carrier)	1.00 (0.77-1.30)	
	rs3448	225/255 (GG)	184/153 (AG)	1.33 (1.01-1.73)	29/30 (AA)	1.09 (0.64-1.85)	0.13	213/183 (A-carrier)	1.29 (1.00-1.67)	
<i>GSR</i>	rs3594	170/173 (GG)	224/208 (GT)	1.09 (0.82-1.45)	51/64 (TT)	0.82 (0.53-1.26)	0.61	275/272 (T-carrier)	1.03 (0.78-1.36)	
	rs2551715	186/188	191/206	0.94	63/46	1.40	0.36	254/252	1.02	

	rs8190996	(GG) 148/158	(AG) 233/215	(0.71-1.23) 1.16	(AA) 67/75	(0.91-2.17) 0.96	0.92	(A-carrier) 300/290	(0.79-1.31) 1.11
	rs3779647	(CC) 114/121	(CT) 227/214	(0.86-1.56) 1.13	(TT) 116/121	(0.64-1.43) 1.02	0.96	(T-carrier) 343/334	(0.84-1.47) 1.09
	rs2978663	(GG) 157/162	(AG) 236/223	(0.81-1.58) 1.09	(AA) 79/87	(0.70-1.48) 0.93	0.89	(A-carrier) 315/310	(0.80-1.50) 1.05
	rs17557435	(AA) 353/342	(AG) -/-	(0.82-1.44) N/A	(GG) 92/103	(0.63-1.37) 0.87	0.38	(G-carrier) 92/103	(0.80-1.37) 0.87
	rs8190893	(AA) 408/409	51/52	0.98	(GG) 2/0	(0.64-1.19) N/A	0.76	(G-carrier) 53/52	(0.64-1.19) 1.02
	rs1002149	(GG) 325/309	(AG) 120/143	(0.64-1.49) 0.80	(AA) 20/13	1.46	0.58	(A-carrier) 140/156	(0.68-1.55) 0.85
		(CC)	(AC)	(0.59-1.07)	(AA)	(0.70-3.04)		(A-carrier)	(0.64-1.12)
<i>IL1RN</i>	rs878972	275/250	154/165	0.84	22/36	0.54	0.03	176/201	0.80
		(AA)	(AC)	(0.64-1.11)	(CC)	(0.31-0.96)		(C-carrier)	(0.61-1.04)
	rs3087263	384/394	60/45	1.38	3/8	0.40	0.65	63/53	1.23
		(GG)	(AG)	(0.90-2.11)	(AA)	(0.11-1.50)		(A-carrier)	(0.82-1.84)
	rs315951	231/216	191/210	0.84	36/32	1.05	0.55	227/242	0.87
		(CC)	(CG)	(0.64-1.11)	(GG)	(0.62-1.78)		(G-carrier)	(0.67-1.14)
<i>IL6</i>	rs1474348	204/207	202/192	1.07	54/61	0.89	0.85	256/253	1.03
		(GG)	(CG)	(0.81-1.42)	(CC)	(0.59-1.36)		(C-carrier)	(0.79-1.34)
	rs2069845	173/160	216/219	0.92	65/75	0.80	0.28	281/294	0.89
		(AA)	(AG)	(0.70-1.21)	(GG)	(0.54-1.19)		(G-carrier)	(0.68-1.16)
<i>MPO</i>	rs4401102	267/255	147/153	0.92	41/47	0.84	0.38	188/200	0.90
		(GG)	(AG)	(0.70-1.22)	(AA)	(0.54-1.31)		(A-carrier)	(0.70-1.17)
	rs12949848	334/324	103/106	0.95	16/23	0.69	0.32	119/129	0.90
		(TT)	(CT)	(0.70-1.31)	(CC)	(0.37-1.31)		(C-carrier)	(0.68-1.20)
<i>NOS2</i>	rs8081248	161/159	220/229	0.95	69/62	1.10	0.80	289/271	0.98
		(CC)	(CT)	(0.71-1.27)	(TT)	(0.73-1.65)		(T-carrier)	(0.74-1.30)
	rs12450521	272/253	174/205	0.81	26/14	1.88	0.69	200/219	0.86
		(GG)	(GT)	(0.63-1.05)	(TT)	(0.91-3.91)		(T-carrier)	(0.67-1.10)
	rs9906835	153/143	151/162	0.88	135/134	0.95	0.71	186/296	0.91
		(TT)	(CT)	(0.64-1.20)	(CC)	(0.68-1.32)		(C-carrier)	(0.69-1.19)
	rs2297515	469/466	-/-	N/A	0/3	N/A	0.99	0/3	N/A
		(TT)			(GG)			(G-carrier)	

	rs2314810	414/415 (CC)	49/49 (CG)	1.00 (0.67-1.50)	3/2 (GG)	1.50 (0.25-8.98)	0.85	52/51 (G-carrier)	1.02 (0.69-1.51)
	rs12944039	285/275 (CC)	144/164 (CT)	0.86 (0.65-1.13)	20/10 (TT)	1.87 (0.87-4.04)	1.00	164/174 (T-carrier)	0.91 (0.70-1.19)
	rs4795067	193/180 (TT)	196/210 (CT)	0.87 (0.66-1.15)	50/49 (CC)	0.96 (0.62-1.50)	0.55	246/259 (C-carrier)	0.89 (0.68-1.16)
	rs944725	160/174 (GG)	214/214 (AG)	1.10 (0.82-1.48)	72/58 (AA)	1.37 (0.90-2.09)	0.16	286/272 (A-carrier)	1.156 (0.87-1.53)
	rs17722851	355/344 (AA)	99/109 (AT)	0.88 (0.64-1.20)	3/4 (TT)	0.74 (0.17-3.29)	0.37	102/113 (T-carrier)	0.87 (0.64-1.19)
	rs3794764	264/262 (CC)	132/144 (CT)	0.91 (0.68-1.21)	25/15 (TT)	1.67 (0.86-3.24)	0.65	157/159 (T-carrier)	0.98 (0.75-1.29)
	rs3794766	267/279 (GG)	163/143 (AG)	1.19 (0.90-1.59)	25/33 (AA)	0.79 (0.46-1.37)	0.83	188/176 (A-carrier)	1.12 (0.86-1.46)
	rs10459953	199/233 (CC)	208/178 (CG)	1.38 (1.05-1.82)	53/49 (GG)	1.34 (0.85-2.10)	0.05	261/227 (G-carrier)	1.37 (1.05-1.80)
	rs2779248	154/160 (AA)	223/218 (AG)	1.07 (0.80-1.43)	77/76 (GG)	1.06 (0.72-1.56)	0.73	300/294 (G-carrier)	1.06 (0.80-1.41)
	rs11080358	329/329 (CC)	104/109 (CT)	0.96 (0.71-1.30)	12/7 (CC)	1.69 (0.66-4.32)	0.74	116/116 (C-carrier)	1.00 (0.74-1.35)
	rs2779252	420/435 (CC)	46/31 (AC)	1.48 (0.94-2.34)	-/-	N/A	0.09	46/32 (A-carrier)	1.48 (0.94-2.34)
NOS3	rs2373961	188/186 (CC)	228/209 (CT)	1.09 (0.82-1.43)	48/69 (TT)	0.68 (0.44-1.04)	0.26	276/278 (T-carrier)	0.98 (0.76-1.28)
	rs6951150	197/205 (CC)	201/185 (CT)	1.14 (0.85-1.54)	49/57 (TT)	0.91 (0.59-1.40)	1.00	250/242 (T-carrier)	1.09 (0.82-1.44)
	rs12703107	231/254 (GG)	192/173 (GT)	1.20 (0.93-1.56)	34/30 (TT)	1.25 (0.74-2.12)	0.16	226/203 (T-carrier)	1.21 (0.94-1.56)
	rs3918227	387/382 (CC)	58/65 (AC)	0.88 (0.61-1.29)	4/2 (AA)	1.96 (0.36-10.72)	0.79	62/67 (A-carrier)	0.92 (0.63-1.32)
	rs2373929	169/166 (CC)	228/215 (CT)	1.05 (0.78-1.40)	60/76 (TT)	0.78 (0.53-1.16)	0.36	288/291 (T-carrier)	0.97 (0.74-1.28)
SOD1	rs1041740	251/255 (CC)	177/170 (CT)	1.07 (0.80-1.42)	34/37 (TT)	0.94 (0.58-1.52)	0.96	211/207 (T-carrier)	1.04 (0.79-1.36)
SOD2	rs5746136	226/273 (GG)	180/154 (AG)	1.38 (1.04-1.82)	48/27 (AA)	2.11 (1.26-3.53)	0.001	228/181 (A-carrier)	1.50 (1.15-1.94)

<i>TLR4</i>	rs2758331	134/124 (GG)	227/223 (GT)	0.94 (0.69-1.29)	94/108 (TT)	0.80 (0.54-1.16)	0.25	321/331 (T-carrier)	0.90 (0.67-1.20)
	rs11536889	370/353 (GG)	85/99 (CG)	0.82 (0.59-1.14)	5/8 (CC)	0.61 (0.20-1.86)	0.15	90/107 (C-carrier)	0.80 (0.58-1.10)

^a For the additive model