

Supplemental Table 1. Selected prostate cancer risk loci and their association with prostate cancer risk in BPC3

SNP	Gene	Location	Chr	Position	Risk allele	Reference allele	allele frequency	allele frequency (cases)	BPC3 OR	BPC3 p-value
rs13385191	C2orf43	intronic	2	20751746	G	A	0.24	0.26	1.07(1.01-1.12)	0.01
rs1465618	THADA	intronic	2	43407453	T	C	0.21	0.23	1.11(1.05-1.16)	<.0001
rs721048	EHBP1	intronic	2	62985235	A	G	0.18	0.19	1.12(1.06-1.18)	<.0001
rs10187424	---	intergenic	2	85647808	A	G	0.58	0.58	1.02(0.96-1.07)	0.53
rs12621278	ITGA6	intronic	2	173019799	A	G	0.94	0.95	1.17(1.07-1.28)	0.0008
rs2292884	MLPH	non-synonymous	2	238107965	G	A	0.25	0.25	1.04(0.98-1.09)	0.17
rs2660753	---	intergenic	3	87193364	T	C	0.11	0.12	1.12(1.06-1.19)	0.0002
rs7629490	---	intergenic	3	87324187	T	C	0.34	0.36	1.10(1.05-1.15)	<.0001
rs6763931	---	intergenic	3	142585523	T	C	0.44	0.44	1.04(0.98-1.09)	0.20
rs10936632	---	intergenic	3	171612796	A	C	0.49	0.52	1.11(1.06-1.17)	<.0001
rs17021918	PDLIM5	intronic	4	95781900	C	T	0.66	0.68	1.08(1.04-1.13)	0.0003
rs7679673	---	intergenic	4	106280983	C	A	0.58	0.61	1.15(1.10-1.19)	<.0001
rs2242652	TERT	intronic	5	1333028	G	A	0.80	0.82	1.16(1.08-1.24)	<.0001
rs12653946	---	intergenic	5	1948829	T	C	0.42	0.45	1.10(1.05-1.15)	<.0001
rs2121875	FGF10	intronic	5	44401302	G	T	0.33	0.34	1.04(0.98-1.10)	0.15
rs130067	CCHCR1	non-synonymous	6	31226490	G	T	0.20	0.20	1.01(0.95-1.08)	0.67
rs1983891 (or rs9381080)	FOXP4	intronic	6	41644405	T	C	0.28	0.30	1.09(1.04-1.14)	0.0003
rs339331	RFXDC1	intronic	6	117316745	T	C	0.71	0.72	1.08(1.03-1.13)	0.002
rs9364554	SLC22A3	intronic	6	160753654	T	C	0.28	0.29	1.08(1.03-1.12)	0.001
rs12155172	---	intergenic	7	20961016	A	G	0.22	0.23	1.09(1.04-1.14)	0.0006
rs10486567	JAZF1	intronic	7	27943088	G	A	0.76	0.79	1.20(1.15-1.26)	<.0001
rs6465657	LMTK2	intronic	7	97654263	C	T	0.46	0.48	1.10(1.06-1.14)	<.0001
rs2928679 (or rs13264338)	---	intergenic	8	23494920	A	G	0.44	0.46	1.06(1.02-1.11)	0.003
rs1512268	---	intergenic	8	23582408	T	C	0.44	0.46	1.11(1.06-1.15)	<.0001
rs1016343	---	intergenic	8	128162479	T	C	0.20	0.24	1.25(1.19-1.31)	<.0001
rs16901979	---	intergenic	8	128194098	A	C	0.03	0.05	1.41(1.27-1.57)	<.0001
rs16902094	---	intergenic	8	128389528	G	A	0.16	0.18	1.17(1.11-1.24)	<.0001
rs620861	---	intergenic	8	128404855	C	T	0.63	0.66	1.16(1.11-1.21)	<.0001
rs6983267	---	intergenic	8	128482487	G	T	0.51	0.56	1.23(1.19-1.28)	<.0001
rs4242382	---	intergenic	8	128586755	A	G	0.10	0.14	1.39(1.31-1.48)	<.0001
rs1571801	DAB2IP	intronic	9	123467194	A	C	0.25	0.27	1.07(1.03-1.12)	0.002
rs10993994	MSMB	upstream	10	51219502	T	C	0.39	0.44	1.23(1.18-1.28)	<.0001
rs7127900	---	intergenic	11	2190150	A	G	0.20	0.22	1.14(1.08-1.20)	<.0001
rs12418451 (or rs10896438)	---	intergenic	11	68691995	A	G	0.30	0.32	1.12(1.08-1.17)	<.0001
rs10896449	---	intergenic	11	68751243	G	A	0.50	0.55	1.19(1.15-1.24)	<.0001
rs10875943	---	intergenic	12	47962277	C	T	0.30	0.32	1.06(1.00-1.12)	0.04
rs902774	---	intergenic	12	51560171	A	G	0.15	0.16	1.12(1.06-1.19)	0.0001
rs11649743	HNF1B	intronic	17	33149092	G	A	0.81	0.83	1.15(1.10-1.21)	<.0001
rs4430796	HNF1B	intronic	17	33172153	A	G	0.51	0.56	1.25(1.20-1.30)	<.0001
rs1859962	N/A	intergenic	17	66620348	G	T	0.48	0.53	1.19(1.15-1.24)	<.0001
rs8102476	N/A	intergenic	19	43427453	C	T	0.55	0.56	1.08(1.03-1.12)	0.0003
rs11672691 (or rs11673591)	N/A	intergenic	19	46677771	G	A	0.74	0.76	1.12(1.06-1.17)	<.0001
rs2735839	KLK3	downstream	19	56056435	G	A	0.85	0.87	1.16(1.10-1.23)	<.0001
rs5759167	---	intergenic	22	41830156	G	T	0.50	0.54	1.15(1.11-1.20)	<.0001
rs11704416	TNRC6B	upstream	22	38766919	G	C	0.19	0.21	1.09(1.03-1.15)	0.004
rs5945619	NUDT11	downstream	X (hg_17)	51074708	C	T	0.35	0.40	1.11(1.08-1.15)	<.0001
rs5919432	---	intergenic	X (hg_17)	66804571	A	G	0.79	0.81	1.06(1.01-1.11)	0.01

*the risk allele is defined as the allele associated with an increased risk of prostate cancer incidence from the literature

Supplemental Table 2. Minor allele frequencies (MAF) of original and imputed data

SNP	MAF (nonimputed)	MAF(imputed)
rs13385191	0.26	0.25
rs1465618	0.23	0.23
rs721048	0.19	0.19
rs10187424	0.42	0.42
rs12621278	0.05	0.05
rs2292884	0.25	0.26
rs2660753	0.12	0.12
rs7629490	0.36	0.36
rs6763931	0.44	0.44
rs10936632	0.48	0.48
rs17021918	0.32	0.33
rs7679673	0.39	0.39
rs2242652	0.18	0.18
rs12653946	0.45	0.45
rs2121875	0.34	0.34
rs130067	0.20	0.20
rs1983891	0.30	0.30
rs339331	0.28	0.27
rs9364554	0.29	0.29
rs12155172	0.23	0.24
rs10486567	0.21	0.21
rs6465657	0.48	0.48
rs2928679	0.46	0.45
rs1512268	0.46	0.47
rs1016343	0.24	0.24
rs16901979	0.05	0.05
rs16902094	0.18	0.18
rs620861	0.34	0.34
rs6983267	0.44	0.44
rs4242382	0.14	0.13
rs1571801	0.27	0.26
rs10993994	0.44	0.43
rs7127900	0.22	0.22
rs12418451	0.32	0.32
rs10896449	0.45	0.45
rs10875943	0.32	0.31
rs902774	0.16	0.17
rs11649743	0.17	0.17
rs4430796	0.44	0.44
rs1859962	0.47	0.47
rs8102476	0.44	0.44
rs11672691	0.24	0.24
rs2735839	0.13	0.13
rs5759167	0.47	0.46
rs11704416	0.21	0.20
rs5945619	0.40	0.40
rs5919432	0.19	0.16

Supplemental Table 3. Per-allele hazard ratio (HR) for each SNP and the multi-marker kernel test for associations with time to prostate cancer death

SNP	Gene	Location	Chr	Risk allele	Reference allele	Model 1: adjusted for age and cohort		Model 2: Model 1 + Gleason grade and clinical stage	
						HR (95% CI)	P-value	HR (95% CI)	P-value
rs13385191	C2orf43	intronic	2	G	A	0.88(0.78-1.00)	0.05	0.94(0.84-1.06)	0.33
rs1465618	THADA	intronic	2	T	C	0.99(0.89-1.10)	0.84	0.98(0.88-1.09)	0.73
rs721048	EHBP1	intronic	2	A	G	0.96(0.85-1.07)	0.44	1.01(0.91-1.14)	0.80
rs10187424	---	intergenic	2	A	G	1.04(0.93-1.17)	0.48	1.07(0.95-1.20)	0.28
rs12621278	ITGA6	intronic	2	A	G	0.93(0.75-1.15)	0.52	0.86(0.69-1.06)	0.16
rs2292884	MLPH	non-synonymous	2	G	A	1.03(0.91-1.16)	0.64	1.02(0.90-1.15)	0.75
rs2660753	---	intergenic	3	T	C	1.05(0.92-1.20)	0.46	1.02(0.89-1.16)	0.81
rs7629490	---	intergenic	3	T	C	0.93(0.84-1.04)	0.21	0.93(0.83-1.04)	0.20
rs6763931	---	intergenic	3	T	C	1.02(0.92-1.15)	0.68	1.02(0.91-1.14)	0.77
rs10936632	---	intergenic	3	A	C	1.12(0.99-1.26)	0.07	1.11(0.98-1.25)	0.10
rs17021918	PDLIM5	intronic	4	C	T	0.89(0.81-0.97)	0.01	0.91(0.82-1.00)	0.04
rs7679673	---	intergenic	4	C	A	1.04(0.95-1.14)	0.40	1.03(0.94-1.13)	0.49
rs2242652	TERT	intronic	5	G	A	1.03(0.90-1.19)	0.64	0.95(0.82-1.10)	0.49
rs12653946	---	intergenic	5	T	C	1.03(0.93-1.15)	0.52	1.00(0.90-1.11)	0.98
rs2121875	FGF10	intronic	5	G	T	0.98(0.87-1.11)	0.77	0.99(0.88-1.11)	0.83
rs130067	CCHCR1	non-synonymous	6	G	T	0.95(0.83-1.09)	0.46	0.97(0.84-1.11)	0.63
rs1983891	FOXP4	intronic	6	T	C	0.96(0.86-1.07)	0.46	0.95(0.85-1.07)	0.41
rs339331	RFXDC1	intronic	6	T	C	0.99(0.88-1.10)	0.80	0.96(0.86-1.07)	0.46
rs9364554	SLC22A3	intronic	6	T	C	0.99(0.90-1.09)	0.78	1.01(0.91-1.11)	0.89
rs12155172	---	intergenic	7	A	G	1.02(0.91-1.14)	0.69	1.08(0.96-1.21)	0.18
rs10486567	JAZF1	intronic	7	G	A	0.85(0.76-0.94)	0.001	0.87(0.79-0.97)	0.008
rs6465657	LMTK2	intronic	7	C	T	0.90(0.82-0.98)	0.02	0.92(0.85-1.01)	0.08
rs2928679	---	intergenic	8	A	G	1.01(0.92-1.10)	0.87	1.03(0.94-1.12)	0.56
rs1512268	---	intergenic	8	T	C	0.93(0.85-1.02)	0.12	0.96(0.88-1.05)	0.39
rs1016343	---	intergenic	8	T	C	1.08(0.98-1.20)	0.13	1.09(0.99-1.21)	0.09
rs16901979	---	intergenic	8	A	C	1.03(0.84-1.27)	0.78	1.06(0.87-1.29)	0.58
rs16902094	---	intergenic	8	G	A	1.04(0.92-1.17)	0.56	1.05(0.93-1.18)	0.45
rs620861	---	intergenic	8	C	T	0.97(0.88-1.07)	0.49	0.96(0.87-1.06)	0.45
rs6983267	---	intergenic	8	G	T	1.00(0.92-1.09)	0.99	1.02(0.94-1.12)	0.62
rs4242382	---	intergenic	8	A	G	1.00(0.89-1.13)	0.94	0.98(0.87-1.11)	0.77
rs1571801	DAB2IP	intronic	9	A	C	1.09(0.99-1.20)	0.08	1.10(1.00-1.21)	0.06
rs10993994	MSMB	upstream	10	T	C	0.90(0.83-0.98)	0.02	0.87(0.80-0.95)	0.002
rs7127900	---	intergenic	11	A	G	0.86(0.77-0.97)	0.01	0.87(0.78-0.97)	0.02
rs12418451	---	intergenic	11	A	G	1.00(0.91-1.10)	0.96	1.02(0.93-1.12)	0.69
rs10896449	---	intergenic	11	G	A	0.92(0.85-1.01)	0.08	0.92(0.85-1.01)	0.07
rs10875943	---	intergenic	12	C	T	0.97(0.86-1.09)	0.59	0.98(0.87-1.10)	0.72
rs902774	---	intergenic	12	A	G	1.11(0.98-1.25)	0.10	1.10(0.98-1.25)	0.12
rs11649743	HNF1B	intronic	17	G	A	0.99(0.88-1.11)	0.80	0.97(0.86-1.09)	0.59
rs4430796	HNF1B	intronic	17	A	G	1.02(0.93-1.11)	0.70	1.05(0.96-1.15)	0.31
rs1859962	N/A	intergenic	17	G	T	1.03(0.94-1.12)	0.56	1.05(0.96-1.15)	0.28
rs8102476	N/A	intergenic	19	C	T	1.03(0.94-1.13)	0.54	1.03(0.94-1.13)	0.47
rs11672691	N/A	intergenic	19	G	A	1.18(1.05-1.34)	0.007	1.16(1.02-1.31)	0.02
rs2735839	KLK3	downstream	19	G	A	0.82(0.73-0.93)	0.002	0.85(0.75-0.96)	0.01
rs5759167	---	intergenic	22	G	T	0.99(0.91-1.08)	0.85	0.97(0.89-1.06)	0.54
rs11704416	TNRC6B	upstream	22	G	C	1.10(0.98-1.25)	0.11	1.05(0.93-1.18)	0.47
rs5945619	NUDT11	downstream	X (hg_17)	C	T	1.01(0.95-1.08)	0.74	1.02(0.96-1.09)	0.55
rs5919432	---	intergenic	X (hg_17)	A	G	1.00(0.90-1.10)	0.95	0.99(0.90-1.09)	0.84
						kernel machine p-value	0.05	kernel machine p-value	0.08

Supplemental Table 4. Per-risk allele odds ratios for fatal vs. non-fatal prostate cancer

SNP	Gene	Location	Chr	Risk allele	Reference allele	OR (95% CI)	p-value
rs13385191	C2orf43	intronic	2	G	A	0.89(0.78-1.01)	0.08
rs1465618	THADA	intronic	2	T	C	0.99(0.88-1.11)	0.83
rs721048	EHBP1	intronic	2	A	G	0.94(0.84-1.07)	0.36
rs10187424	---	intergenic	2	A	G	1.04(0.92-1.18)	0.55
rs12621278	ITGA6	intronic	2	A	G	0.95(0.76-1.19)	0.66
rs2292884	MLPH	non-synonymous	2	G	A	1.03(0.91-1.18)	0.63
rs2660753	---	intergenic	3	T	C	1.04(0.90-1.20)	0.59
rs7629490	---	intergenic	3	T	C	0.94(0.83-1.05)	0.28
rs6763931	---	intergenic	3	T	C	1.03(0.91-1.16)	0.62
rs10936632	---	intergenic	3	A	C	1.13(0.99-1.28)	0.06
rs17021918	PDLIM5	intronic	4	C	T	0.89(0.80-0.98)	0.02
rs7679673	---	intergenic	4	C	A	1.05(0.95-1.16)	0.36
rs2242652	TERT	intronic	5	G	A	1.03(0.88-1.20)	0.75
rs12653946	---	intergenic	5	T	C	1.06(0.95-1.19)	0.28
rs2121875	FGF10	intronic	5	G	T	0.96(0.84-1.09)	0.52
rs130067	CCHCR1	non-synonymous	6	G	T	0.97(0.83-1.13)	0.71
rs1983891	FOXP4	intronic	6	T	C	0.94(0.83-1.06)	0.33
rs339331	RFXDC1	intronic	6	T	C	0.97(0.86-1.09)	0.61
rs9364554	SLC22A3	intronic	6	T	C	0.99(0.90-1.10)	0.90
rs12155172	---	intergenic	7	A	G	1.00(0.89-1.13)	0.99
rs10486567	JAZF1	intronic	7	G	A	0.86(0.77-0.96)	0.006
rs6465657	LMTK2	intronic	7	C	T	0.88(0.80-0.97)	0.008
rs2928679	---	intergenic	8	A	G	1.01(0.91-1.11)	0.89
rs1512268	---	intergenic	8	T	C	0.93(0.84-1.02)	0.13
rs1016343	---	intergenic	8	T	C	1.09(0.97-1.22)	0.15
rs16901979	---	intergenic	8	A	C	1.07(0.86-1.35)	0.53
rs16902094	---	intergenic	8	G	A	1.08(0.95-1.23)	0.25
rs620861	---	intergenic	8	C	T	0.96(0.86-1.07)	0.47
rs6983267	---	intergenic	8	G	T	0.99(0.90-1.09)	0.90
rs4242382	---	intergenic	8	A	G	1.01(0.89-1.16)	0.86
rs1571801	DAB2IP	intronic	9	A	C	1.10(0.99-1.23)	0.06
rs10993994	MSMB	upstream	10	T	C	0.89(0.81-0.98)	0.02
rs7127900	---	intergenic	11	A	G	0.86(0.76-0.97)	0.01
rs12418451	---	intergenic	11	A	G	1.00(0.90-1.11)	0.98
rs10896449	---	intergenic	11	G	A	0.92(0.84-1.01)	0.09
rs10875943	---	intergenic	12	C	T	0.96(0.85-1.09)	0.56
rs902774	---	intergenic	12	A	G	1.11(0.97-1.26)	0.14
rs11649743	HNF1B	intronic	17	G	A	0.98(0.87-1.11)	0.77
rs4430796	HNF1B	intronic	17	A	G	1.02(0.92-1.12)	0.72
rs1859962	N/A	intergenic	17	G	T	1.03(0.93-1.13)	0.60
rs8102476	N/A	intergenic	19	C	T	1.04(0.94-1.14)	0.48
rs11672691	N/A	intergenic	19	G	A	1.17(1.02-1.33)	0.02
rs2735839	KLK3	downstream	19	G	A	0.81(0.71-0.92)	0.002
rs5759167	---	intergenic	22	G	T	1.00(0.91-1.10)	0.96
rs11704416	TNRC6B	upstream	22	G	C	1.13(0.99-1.29)	0.07
rs5945619	NUDT11	downstream	X (hg_17)	C	T	1.00(0.93-1.07)	0.97
rs5919432	---	intergenic	X (hg_17)	A	G	0.98(0.88-1.10)	0.75

Supplemental Table 5. Per-risk allele odds ratio (OR) for each risk SNP and fatal prostate cancer vs. controls and non-fatal prostate cancer vs controls*

SNP	Gene	Location	Chr	Risk allele	Reference allele	Fatal			Fatal		Non-Fatal		
						cases (n)	Non-fatal cases (n)	Controls (n)	OR (95% CI)	p-value	OR (95% CI)	p-value	p-contrast
rs13385191	C2orf43	intronic	2	G	A	722	7079	8201	0.95(0.84-1.08)	0.47	1.08(1.02-1.14)	0.004	0.06
rs1465618	THADA	intronic	2	T	C	937	8808	9811	1.08(0.97-1.22)	0.17	1.11(1.06-1.17)	<.0001	0.69
rs721048	EHBP1	intronic	2	A	G	1011	9135	10655	1.06(0.93-1.19)	0.38	1.12(1.07-1.18)	<.0001	0.31
rs10187424	---	intergenic	2	A	G	592	4833	5429	1.06(0.94-1.20)	0.35	1.01(0.96-1.07)	0.66	0.47
rs12621278	ITGA6	intronic	2	A	G	958	8851	9851	1.12(0.90-1.40)	0.31	1.17(1.07-1.29)	0.0008	0.71
rs2292884	MLPH	non-synonymous	2	G	A	711	6759	7615	1.06(0.94-1.21)	0.35	1.03(0.98-1.09)	0.21	0.68
rs2660753	---	intergenic	3	T	C	1007	8979	10682	1.15(1.00-1.33)	0.05	1.12(1.05-1.19)	0.0003	0.69
rs7629490	---	intergenic	3	T	C	720	6897	7836	1.03(0.92-1.15)	0.63	1.11(1.05-1.16)	<.0001	0.22
rs6763931	---	intergenic	3	T	C	622	4968	5591	1.06(0.94-1.20)	0.31	1.03(0.98-1.09)	0.26	0.62
rs10936632	---	intergenic	3	A	C	557	4777	5430	1.24(1.09-1.40)	0.0009	1.10(1.04-1.16)	0.0007	0.07
rs17021918	PDLIM5	intronic	4	C	T	952	8827	9885	0.97(0.88-1.07)	0.55	1.09(1.05-1.14)	<.0001	0.02
rs7679673	---	intergenic	4	C	A	9800	8808	9800	1.20(1.08-1.32)	0.0004	1.14(1.09-1.19)	<.0001	0.34
rs2242652	TERT	intronic	5	G	A	624	4987	5615	1.16(0.99-1.35)	0.06	1.16(1.08-1.24)	<.0001	1.00
rs12653946	---	intergenic	5	T	C	723	7047	8157	1.15(1.03-1.29)	0.01	1.10(1.05-1.15)	<.0001	0.38
rs2121875	FGF10	intronic	5	G	T	605	4932	5336	1.01(0.89-1.15)	0.82	1.05(0.99-1.11)	0.13	0.65
rs130067	CCHCR1	non-synonymous	6	G	T	625	4979	5577	0.98(0.85-1.14)	0.80	1.02(0.95-1.09)	0.60	0.62
rs1983891	FOXP4	intronic	6	T	C	733	7098	8216	1.02(0.91-1.15)	0.69	1.10(1.05-1.15)	0.0002	0.25
rs339331	RFXDC1	intronic	6	T	C	728	7089	8214	1.05(0.94-1.19)	0.39	1.08(1.03-1.14)	0.002	0.66
rs9364554	SLC22A3	intronic	6	T	C	1012	8968	10644	1.07(0.97-1.19)	0.19	1.08(1.03-1.12)	0.001	0.93
rs12155172	---	intergenic	7	A	G	876	8361	9788	1.08(0.96-1.21)	0.21	1.09(1.04-1.15)	0.0007	0.84
rs10486567	JAZF1	intronic	7	G	A	1032	9196	10744	1.04(0.94-1.16)	0.46	1.22(1.16-1.28)	<.0001	0.004
rs6465657	LMTK2	intronic	7	C	T	1001	8979	10643	0.98(0.90-1.08)	0.73	1.11(1.07-1.16)	<.0001	0.009
rs2928679	---	intergenic	8	A	G	967	8865	9881	1.07(0.97-1.17)	0.19	1.06(1.02-1.11)	0.004	0.97
rs1512268	---	intergenic	8	T	C	970	8866	9917	1.05(0.95-1.15)	0.33	1.11(1.07-1.16)	<.0001	0.21
rs1016343	---	intergenic	8	T	C	942	8680	10296	1.34(1.20-1.49)	<.0001	1.24(1.18-1.30)	<.0001	0.19
rs16901979	---	intergenic	8	A	C	937	8169	9256	1.49(1.19-1.87)	0.0006	1.40(1.26-1.56)	<.0001	0.59
rs16902094	---	intergenic	8	G	A	853	7542	8563	1.28(1.13-1.45)	0.0002	1.16(1.09-1.23)	<.0001	0.13
rs620861	---	intergenic	8	C	T	890	8193	9785	1.13(1.02-1.25)	0.02	1.16(1.11-1.21)	<.0001	0.57
rs6983267	---	intergenic	8	G	T	1025	9147	10693	1.23(1.13-1.35)	<.0001	1.23(1.19-1.28)	<.0001	0.99
rs4242382	---	intergenic	8	A	G	1036	9246	10810	1.39(1.22-1.58)	<.0001	1.39(1.31-1.48)	<.0001	0.98
rs1571801	DAB2IP	intronic	9	A	C	998	8949	10005	1.16(1.05-1.28)	0.005	1.07(1.02-1.12)	0.0077	0.11
rs10993994	MSMB	upstream	10	T	C	1018	8950	10615	1.11(1.01-1.22)	0.03	1.24(1.19-1.29)	<.0001	0.02

rs7127900	---	intergenic	11	A	G	959	8821	9876	1.01(0.89-1.13)	0.92	1.16(1.10-1.22)	<.0001	0.02
rs12418451	---	intergenic	11	A	G	963	8747	10382	1.12(1.01-1.25)	0.02	1.12(1.07-1.17)	<.0001	0.97
rs10896449	---	intergenic	11	G	A	1020	9088	10624	1.12(1.02-1.22)	0.02	1.20(1.15-1.25)	<.0001	0.13
rs10875943	---	intergenic	12	C	T	621	5003	5593	1.04(0.92-1.19)	0.50	1.06(1.00-1.13)	0.04	0.77
rs902774	---	intergenic	12	A	G	851	7876	8882	1.22(1.07-1.39)	0.004	1.11(1.05-1.18)	0.0006	0.17
rs11649743	HNF1B	intronic	17	G	A	1025	9145	10711	1.14(1.01-1.29)	0.03	1.15(1.09-1.21)	<.0001	0.91
rs4430796	HNF1B	intronic	17	A	G	1012	8958	9958	1.29(1.17-1.41)	<.0001	1.25(1.20-1.30)	<.0001	0.54
rs1859962	N/A	intergenic	17	G	T	1023	9165	10728	1.23(1.12-1.34)	<.0001	1.19(1.14-1.24)	<.0001	0.54
rs8102476	N/A	intergenic	19	C	T	942	8477	10044	1.10(1.00-1.21)	0.05	1.07(1.03-1.12)	0.0007	0.63
rs11672691	N/A	intergenic	19	G	A	722	7034	7844	1.26(1.11-1.43)	0.0005	1.10(1.05-1.16)	0.0003	0.05
rs2735839	KLK3	downstream	19	G	A	995	8853	10543	0.96(0.84-1.09)	0.50	1.19(1.12-1.26)	<.0001	0.001
rs5759167	---	intergenic	22	G	T	963	8868	9915	1.16(1.05-1.27)	0.003	1.15(1.10-1.20)	<.0001	0.92
rs11704416	TNRC6B	upstream	22	G	C	729	7047	7890	1.21(1.06-1.38)	0.004	1.07(1.01-1.14)	0.01	0.07
rs5945619	NUDT11	downstream	X (hg_17)	C	T	1011	8975	10630	1.11(1.04-1.19)	0.002	1.11(1.08-1.15)	<.0001	0.99
rs5919432	---	intergenic	X (hg_17)	A	G	621	4975	5579	1.05(0.94-1.17)	0.38	1.06(1.01-1.11)	0.02	0.83

*1053 fatal cases, 9434 non-fatal cases, 11024 controls; model adjusted for age and study cohort