

Web Material

Web Table 1. Baseline Characteristics of Prostate Cancer Cases and Controls by Cohort in the BPC3 (Mean (SD) or Geometric Mean (95% CI)).

	ATBC ¹		EPIC ²		HPFS ³		PHS ⁴		PLCO ⁵	
	Cases	Controls	Cases	Controls	Cases	Controls	Cases	Controls	Cases	Controls
No. of participants	739	436	525	458	1,280	1,188	515	246	752	652
No. of dead cases	217		79		82		93		40	
Age at blood draw	64.4 (5.2)	64.7 (5.0)	61.1 (6.3)	61.2 (6.3)	64.0 (7.8)	63.9 (7.8)	59.3 (7.5)	60.9 (7.7)	64.6 (5.0)	64.3 (5.0)
Age at diagnosis	69.7 (5.6)	NA	65.3 (6.2)	NA	69.6 (7.5)	NA	68.4 (6.8)	NA	68.0 (5.3)	NA
BMI, kg/m ²	26.2 (3.4)	26.3 (3.4)	26.8 (3.3)	27.1 (3.5)	26.7 (3.3)	25.9 (3.6)	24.7 (2.5)	24.5 (2.6)	27. (3.6)	27.5 (3.9)
25(OH)D, ng/mL	14.1 (13.5-14.7)	16.4 (15.6-17.2)	21.5 (20.8-22.3)	20.9 (20.0-21.7)	27.2 (26.5-27.9)	26.9 (26.1-27.7)	29.8 (28.9-30.8)	27.4 (26.0-28.8)	22.2 (21.7-22.8)	21.6 (21.0-22.2)
Study duration	1985 – 2002		1992 – 2004		1993 – 2004		1982 – 2002		1993 - 2002	

Abbreviations: 25(OH)D, 25-hydroxyvitamin D; BMI, body mass index; BPC3, Breast and Prostate Cancer Cohort Consortium; CI, confidence interval; SD, standard deviation.

Web Table 2. Per Allele Association Between 46 GWAS-identified SNPs and Risk of Total Prostate Cancer in the BPC3.

SNP	Chromosome (gene)	Number of cases	Number of controls	Minor allele frequency (in controls)	Per allele OR ^a	95% CI	P-value
rs13385191	2 (<i>C2orf43</i>)	3,377	2,556	0.24 (G)	1.08	0.99, 1.17	0.09
rs1465618	2 (<i>THADA</i>)	3,648	2,816	0.21 (T)	1.11	1.02, 1.21	0.01
rs721048	2 (<i>EHBPI</i>)	3,675	2,849	0.17 (A)	1.16	1.06, 1.26	0.001
rs10187424	2 (<i>GGCX/VAMP8</i>)	2,252	1,782	0.42 (G)	1.06	0.97, 1.16	0.21
rs12621278	2 (<i>ITGA6</i>)	3,682	2,834	0.05 (G)	1.08	0.92, 1.26	0.37
rs2292884	2 (<i>MLPH</i>)	3,109	2,455	0.24 (G)	1.04	0.95, 1.13	0.41
rs2660753	3 (Unknown)	3,692	2,884	0.11 (T)	1.13	1.02, 1.26	0.03
rs7629490	3 (Unknown)	3,115	2,441	0.33 (T)	1.09	1.01, 1.18	0.02
rs6763931	3 (<i>ZBTB38</i>)	2,318	1,837	0.43 (T)	1.03	0.94, 1.12	0.56
rs10936632	3 (<i>CLDN11/SKIL</i>)	2,348	1,858	0.50 (C)	1.03	0.94, 1.12	0.49
rs17021918	4 (<i>PDLIM5</i>)	3,656	2,831	0.34 (T)	1.09	1.01, 1.17	0.02
rs7679673	4 (<i>TET2</i>)	3,677	2,824	0.42 (A)	1.14	1.07, 1.23	1.62·10 ⁻⁰⁴
rs2242652	5 (<i>TERT</i>)	2,350	1,858	0.21 (A)	1.25	1.12, 1.40	5.01·10 ⁻⁰⁵
rs12653946	5 (<i>IRX4</i>)	3,365	2,548	0.44 (T)	1.05	0.97, 1.13	0.21
rs2121875	5 (<i>FGF10</i>)	2,285	1,739	0.33 (G)	1.02	0.93, 1.13	0.63
rs130067	6 (<i>CCHCR1</i>)	2,340	1,856	0.19 (G)	1.07	0.96, 1.19	0.24
rs339331	6 (<i>RFX6</i>)	3,387	2,564	0.28 (C)	1.05	0.96, 1.13	0.27
rs9364554	6 (<i>SLC22A3</i>)	3,694	2,876	0.27 (T)	1.07	0.99, 1.15	0.11
rs12155172	7 (<i>SP8</i>)	3,650	2,830	0.23 (A)	1.04	0.96, 1.13	0.31
rs10486567	7 (<i>JAZF1</i>)	3,677	2,873	0.24 (A)	1.18	1.08, 1.28	1.07·10 ⁻⁰⁴
rs6465657	7 (<i>LMTK2</i>)	3,681	2,868	0.46 (C)	1.08	1.01, 1.16	0.02
rs2928679	8 (<i>SLC25A37</i>)	3,692	2,828	0.44 (A)	1.01	0.94, 1.08	0.77
rs1512268	8 (<i>NKX3.1</i>)	3,709	2,851	0.44 (T)	1.08	1.01, 1.16	0.03
rs1016343	8 (Unknown)	3,694	2,875	0.21 (T)	1.17	1.08, 1.27	2.01·10 ⁻⁰⁴
rs16901979	8 (Unknown)	3,655	2,852	0.03 (A)	1.48	1.23, 1.78	3.82·10 ⁻⁰⁵
rs16902094	8 (Unknown)	3,362	2,621	0.17 (G)	1.12	1.02, 1.23	0.02
rs620861	8 (Unknown)	3,460	2,673	0.37 (T)	1.09	1.02, 1.18	0.02
rs6983267	8 (Unknown)	3,670	2,847	0.49 (T)	1.21	1.13, 1.30	7.66·10 ⁻⁰⁸
rs4242382	8 (Unknown)	3,755	2,921	0.10 (A)	1.45	1.31, 1.62	8.15·10 ⁻¹²

rs1571801	9 (<i>DAB2IP</i>)	3,598	2,773	0.25 (A)	1.11	1.02, 1.20	0.012
rs10993994	10 (<i>MSMB</i>)	3,653	2,852	0.39 (T)	1.19	1.11, 1.27	$1.75 \cdot 10^{-06}$
rs7127900	11 (Unknown)	3,666	2,815	0.20 (A)	1.18	1.08, 1.29	$1.62 \cdot 10^{-04}$
rs12418451	11 (Unknown)	3,773	2,932	0.30 (A)	1.11	1.03, 1.20	0.005
rs10896449	11 (Unknown)	3,635	2,850	0.50 (A)	1.20	1.12, 1.29	$1.41 \cdot 10^{-07}$
rs10875943	12 (<i>TUBA1C/PRPH</i>)	2,363	1,867	0.31 (C)	1.04	0.95, 1.14	0.433
rs902774	12 (<i>KRT8</i>)	3,574	2,752	0.15 (A)	1.09	0.99, 1.20	0.072
rs11649743	17 (<i>HNF1B</i>)	3,661	2,858	0.20 (A)	1.18	1.08, 1.29	$3.51 \cdot 10^{-04}$
rs4430796	17 (<i>HNF1B</i>)	3,596	2,802	0.49 (G)	1.25	1.17, 1.35	$3.58 \cdot 10^{-10}$
rs1859962	17 (Unknown)	3,701	2,882	0.48 (T)	1.21	1.13, 1.30	$3.38 \cdot 10^{-08}$
rs8102476	19 (Unknown)	3,622	2,796	0.45 (T)	1.01	0.94, 1.08	0.735
rs11672691	19 (Unknown)	3,338	2,549	0.26 (A)	1.09	1.00, 1.19	0.04
rs2735839	19 (<i>KLK2/KLK3</i>)	3,614	2,795	0.15 (A)	1.14	1.03, 1.26	0.01
rs5759167	22 (<i>BIL/TLL1</i>)	3,661	2,819	0.49 (T)	1.15	1.08, 1.24	$4.95 \cdot 10^{-05}$
rs11704416	22 (TNRC6B)	3,354	2,564	0.20 (C)	1.10	1.01, 1.20	0.034
rs5945619	X (<i>NUDT11</i>)	3,703	2,871	0.35 (C)	1.11	1.05, 1.17	$7.73 \cdot 10^{-05}$
rs5919432	X (<i>AR</i>)	2,336	1,851	0.21 (G)	1.06	0.99, 1.15	0.113

Abbreviations: BPC3, Breast and Prostate Cancer Cohort Consortium; CI, confidence interval; GWAS, genome-wide association study; OR, odds ratio; SNP, single nucleotide polymorphism.

^aFrom a logistic regression model adjusted for age at blood draw, cohort and country (within EPIC).

Web Table 3. Per Allele Association Between 46 GWAS-identified SNPs and Risk of Fatal Prostate Cancer in the BPC3.

SNP	Chromosome (gene)	Number of cases	Number of controls	Minor allele frequency (in controls)	Per allele OR ^a	95% CI	P-value
rs13385191	2 (<i>C2orf43</i>)	419	2,556	0.24 (G)	1.01	0.85, 1.21	0.87
rs1465618	2 (<i>THADA</i>)	459	2,816	0.21 (T)	1.14	0.96, 1.35	0.14
rs721048	2 (<i>EHBPI</i>)	489	2,849	0.17 (A)	1.06	0.88, 1.27	0.53
rs10187424	2 (<i>GGCX/VAMP8</i>)	307	1,782	0.42 (G)	1.16	0.96, 1.40	0.13
rs12621278	2 (<i>ITGA6</i>)	475	2,834	0.05 (G)	1.06	0.76, 1.47	0.75
rs2292884	2 (<i>MLPH</i>)	403	2,455	0.24 (G)	1.05	0.88, 1.27	0.57
rs2660753	3 (Unknown)	486	2,884	0.11 (T)	0.96	0.76, 1.21	0.71
rs7629490	3 (Unknown)	400	2,441	0.33 (T)	1.03	0.88, 1.21	0.73
rs6763931	3 (<i>ZBTB38</i>)	321	1,837	0.43 (T)	0.98	0.82, 1.18	0.86
rs10936632	3 (<i>CLDN11/SKIL</i>)	315	1,858	0.50 (C)	1.04	0.86, 1.25	0.68
rs17021918	4 (<i>PDLIM5</i>)	469	2,831	0.34 (T)	0.96	0.82, 1.11	0.57
rs7679673	4 (<i>TET2</i>)	472	2,824	0.42 (A)	1.25	1.08, 1.45	0.002
rs2242652	5 (<i>TERT</i>)	324	1,858	0.21 (A)	1.10	0.88, 1.37	0.42
rs12653946	5 (<i>IRX4</i>)	420	2,548	0.44 (T)	1.12	0.96, 1.31	0.14
rs2121875	5 (<i>FGF10</i>)	309	1,739	0.33 (G)	1.11	0.91, 1.35	0.31
rs130067	6 (<i>CCHCR1</i>)	323	1,856	0.19 (G)	0.89	0.71, 1.12	0.33
rs339331	6 (<i>RFX6</i>)	421	2,564	0.28 (C)	0.98	0.83, 1.16	0.81
rs9364554	6 (<i>SLC22A3</i>)	489	2,876	0.27 (T)	1.08	0.92, 1.26	0.34
rs12155172	7 (<i>SP8</i>)	472	2,830	0.23 (A)	1.05	0.89, 1.25	0.54
rs10486567	7 (<i>JAZF1</i>)	500	2,873	0.24 (A)	0.97	0.83, 1.14	0.75
rs6465657	7 (<i>LMTK2</i>)	478	2,868	0.46 (C)	0.98	0.85, 1.13	0.81
rs2928679	8 (<i>SLC25A37</i>)	477	2,828	0.44 (A)	1.00	0.87, 1.16	0.99
rs1512268	8 (<i>NKX3.1</i>)	482	2,851	0.44 (T)	0.99	0.86, 1.15	0.94
rs1016343	8 (Unknown)	487	2,875	0.21 (T)	1.30	1.10, 1.53	0.002
rs16901979	8 (Unknown)	490	2,852	0.03 (A)	1.46	1.02, 2.08	0.039
rs16902094	8 (Unknown)	450	2,621	0.17 (G)	1.29	1.07, 1.55	0.008
rs620861	8 (Unknown)	463	2,673	0.37 (T)	1.04	0.89, 1.21	0.61
rs6983267	8 (Unknown)	498	2,847	0.49 (T)	1.23	1.07, 1.41	0.004
rs4242382	8 (Unknown)	505	2,921	0.10 (A)	1.42	1.17, 1.74	1.17

rs1571801	9 (<i>DAB2IP</i>)	482	2,773	0.25 (A)	1.18	1.01, 1.39	0.038
rs10993994	10 (<i>MSMB</i>)	494	2,852	0.39 (T)	1.12	0.98, 1.30	0.11
rs7127900	11 (Unknown)	474	2,815	0.20 (A)	1.07	0.90, 1.27	0.47
rs12418451	11 (Unknown)	504	2,932	0.30 (A)	1.10	0.95, 1.29	0.20
rs10896449	11 (Unknown)	493	2,850	0.50 (A)	1.12	0.97, 1.28	0.12
rs10875943	12 (<i>TUBA1C/PRPH</i>)	321	1,867	0.31 (C)	1.11	0.92, 1.34	0.26
rs902774	12 (<i>KRT8</i>)	469	2,752	0.15 (A)	1.21	1.00, 1.45	0.05
rs11649743	17 (<i>HNF1B</i>)	496	2,858	0.20 (A)	1.25	1.03, 1.50	0.02
rs4430796	17 (<i>HNF1B</i>)	489	2,802	0.49 (G)	1.36	1.17, 1.57	3.73·10 ⁻⁰⁵
rs1859962	17 (Unknown)	495	2,882	0.48 (T)	1.20	1.04, 1.38	0.01
rs8102476	19 (Unknown)	495	2,796	0.45 (T)	0.97	0.85, 1.12	0.71
rs11672691	19 (Unknown)	418	2,549	0.26 (A)	1.24	1.03, 1.49	0.02
rs2735839	19 (<i>KLK2/KLK3</i>)	483	2,795	0.15 (A)	0.95	0.78, 1.17	0.65
rs5759167	22 (<i>BIL/TLL1</i>)	471	2,819	0.49 (T)	1.11	0.97, 1.28	0.13
rs11704416	22 (TNRC6B)	422	2,564	0.20 (C)	1.24	1.04, 1.48	0.02
rs5945619	X (<i>NUDT11</i>)	490	2,871	0.35 (C)	1.16	1.05, 1.29	0.003
rs5919432	X (<i>AR</i>)	320	1,851	0.21 (G)	1.01	0.86, 1.18	0.92

Abbreviations: BPC3, Breast and Prostate Cancer Cohort Consortium; CI, confidence interval; GWAS, genome-wide association study; OR, odds ratio; SNP, single nucleotide polymorphism.

^aFrom a logistic regression model adjusted for age at blood draw, cohort and country (within EPIC).

Web Table 4. Association Between 25(OH)D Concentrations and Risk of Prostate Cancer in the BPC3.

	Number of cases	Number of controls	Tertile of 25(OH)D concentrations						<i>P</i> -trend	<i>P</i> -heterogeneity (by cohort) ^b
			First		Second		Third			
			OR ^a	95% CI	OR ^a	95% CI	OR ^a	95% CI		
Total prostate cancer	3,811	2,980	1.00	Reference	1.11	0.99, 1.25	1.16	1.03, 1.31	0.01	0.41
Fatal prostate cancer	511	2,980	1.00	Reference	0.93	0.73, 1.19	0.96	0.75, 1.22	0.73	0.71

Abbreviations: 25(OH)D, 25-hydroxyvitamin D; BPC3, Breast and Prostate Cancer Cohort Consortium; CI, confidence interval; OR, odds ratio.

^aFrom a logistic regression model across “cohort, batch and season-specific” tertiles of 25(OH)D concentrations adjusted for age at blood draw, year of blood draw, diabetes, body mass index, alcohol, cohort and country (within EPIC). The p-value for trend uses the ordinal (0, 1, 2) 25(OH)D variable.

^bLikelihood ratio tests were used to evaluate heterogeneity between cohorts.

Web Table 5. Additive Scale Interactions Between 46 GWAS-identified SNPs and Risk of Total Prostate Cancer by 25(OH)D Concentrations in the BPC3.

SNP	Number of cases/controls	RERI ^a	95% CI ^a	RERI ^b	95% CI ^b
rs13385191	3377/2556	-0.017	-0.165, 0.122	-0.005	-0.203, 0.006
rs1465618	3648/2816	-0.025	-0.166, 0.129	-0.003	-0.018, 0.008
rs721048	3675/2849	0.059	-0.103, 0.189	0.003	-0.010, 0.012
rs10187424	2252/1782	-0.059	-0.324, 0.119	-0.003	-0.021, 0.012
rs12621278	3682/2834	0.267 ^c	DNC ^c	0.021 ^c	DNC ^c
rs2292884	3109/2455	0.004	-0.157, 0.129	-0.001	-0.015, 0.009
rs2660753	3692/2884	0.061	-0.111, 0.225	0.007	-0.007, 0.016
rs7629490	3115/2441	-0.018	-0.205, 0.120	-0.004	-0.019, 0.007
rs6763931	2318/1837	0.051	-0.152, 0.174	0.005	-0.009, 0.017
rs10936632	2348/1858	0.161 ^d	0.002, 0.288 ^d	0.008	-0.005, 0.020
rs17021918	3656/2831	0.129	-0.031, 0.290	0.009	-0.006, 0.024
rs7679673	3677/2824	-0.022	-0.217, 0.146	-0.004	-0.020, 0.009
rs2242652	2350/1858	0.018	-0.483, 0.299	0.001	-0.030, 0.028
rs12653946	3365/2548	-0.074	-0.260, 0.054	-0.004	-0.018, 0.007
rs2121875	2285/1739	0.024	-0.157, 0.159	0.005	-0.007, 0.016
rs130067	2340/1856	-0.082	-0.261, 0.101	-0.010	-0.032, 0.006
rs339331	3387/2564	-0.114	-0.443, 0.107	-0.009	-0.031, 0.010
rs9364554	3694/2876	-0.011	-0.115, 0.14	0.006	-0.004, 0.013
rs12155172	3650/2830	0.024	-0.121, 0.142	0.001	-0.011, 0.009
rs10486567	3677/2873	0.131	-0.161, 0.357	0.007	-0.014, 0.029
rs6465657	3681/2868	-0.102	-0.249, 0.051	-0.005	-0.018, 0.006
rs2928679	3692/2828	0.024	-0.120, 0.151	0.002	-0.009, 0.012
rs1512268	3709/2851	-0.027	-0.188, 0.103	-0.004	-0.018, 0.007
rs1016343	3694/2875	0.004	-0.146, 0.142	-0.003	-0.017, 0.008
rs16901979	3655/2852	0.183	-0.154, 0.484	0.015	-0.005, 0.024
rs16902094	3362/2621	0.056	-0.087, 0.201	0.012	-0.003, 0.018
rs620861	3460/2673	0.179	-0.023, 0.320	0.010	-0.006, 0.024
rs6983267	3670/2847	0.069	-0.114, 0.210	0.002	-0.013, 0.013
rs4242382	3755/2921	0.133	-0.083, 0.304	0.001	-0.021, 0.014

rs1571801	3598/2773	-0.007	-0.137, 0.137	-0.002	-0.015, 0.008
rs10993994	3653/2852	0.020	-0.151, 0.131	0.0003	-0.013, 0.010
rs7127900	3666/2815	0.089	-0.026, 0.238	0.008	-0.002, 0.015
rs12418451	3773/2932	0.017	-0.140, 0.121	-0.008	-0.021, 0.003
rs10896449	3635/2850	-0.059	-0.242, 0.092	-0.003	-0.018, 0.009
rs10875943	2363/1867	0.015	-0.135, 0.174	0.002	-0.013, 0.118
rs902774	3574/2752	-0.008	-0.171, 0.138	-0.004	-0.020, 0.008
rs11649743	3661/2858	-0.089	-0.503, 0.290	0.003	-0.026, 0.029
rs4430796	3596/2802	-0.041	-0.226, 0.134	0.003	-0.013, 0.014
rs1859962	3701/2882	-0.034	-0.196, 0.121	0.003	-0.011, 0.013
rs8102476	3622/2796	0.178	-0.003, 0.289	0.011	-0.001, 0.022
rs11672691	3338/2549	-0.086	-0.446, 0.209	-0.011	-0.037, 0.015
rs2735839	3614/2795	-0.027	-0.659, 0.353	-0.006	-0.043, 0.031
rs5759167	3661/2819	0.092	-0.049, 0.232	0.009	-0.003, 0.020
rs11704416	3354/2564	-0.056	-0.220, 0.084	-0.006	-0.023, 0.006
rs5945619	3703/2871	-0.058	-0.229, 0.087	-0.007	-0.024, 0.006
rs5919432	2336/1851	0.136	-0.056, 0.295	0.010	-0.005, 0.023
Additive SNP score ^e	3811/2980	0.017	-0.046, 0.091	0.001	-0.004, 0.009

Abbreviations: 25(OH)D, 25-hydroxyvitamin D; BPC3, Breast and Prostate Cancer Cohort Consortium; CI, confidence interval; GWAS, genome-wide association study; RERI, relative excess risk due to interaction; SNP, single nucleotide polymorphism.

^aRelative excess risk due to interaction (RERIs) were calculated to infer about interactions at the additive scale for “cohort, batch and season-specific” tertiles of 25(OH)D and dichotomized SNP using logistic regression models adjusted for age at blood draw, year of blood draw, cohort and country (within EPIC). CIs were calculated using bootstrap.

^bRelative excess risk due to interaction (RERIs) were calculated to infer about interactions at the additive scale for “Rosner-standardized” continuous 25(OH)D and dichotomized SNP using logistic regression models adjusted for age at blood draw, year of blood draw, cohort and country (within EPIC). CIs were calculated using bootstrap.

^cDid not calculate CIs due to small sample size.

^dP-value=0.027, which did not remain significant after adjustment for multiple testing.

^eRelative excess risk due to interaction (RERIs) were calculated using a dichotomized (at the median among controls) additive genetic score (after summing the number of risk alleles across the 46 SNPs for each participant).

Web Table 6. Additive Scale Interactions Between 46 GWAS-identified SNPs and Risk of Fatal Prostate Cancer by 25(OH)D Concentrations in the BPC3.

SNP	Number of cases/controls	RERI ^a	95% CI ^a	RERI ^b	95% CI ^b
rs13385191	419/2556	0.011	-0.287, 0.273	-0.003	-0.035, 0.017
rs1465618	459/2816	-0.033	-0.324, 0.294	-0.006	-0.054, 0.016
rs721048	489/2849	0.134	-0.149, 0.385	0.010	-0.016, 0.022
rs10187424	307/1782	-0.059	-0.768, 0.411	0.007	-0.038, 0.042
rs12621278	475/2834	0.890 ^c	DNC ^c	0.213 ^c	DNC ^c
rs2292884	403/2455	0.015	-0.297, 0.290	0.001	-0.029, 0.019
rs2660753	486/2884	0.013	-0.364, 0.271	0.012	-0.014, 0.022
rs7629490	400/2441	-0.008	-0.376, 0.258	-0.003	-0.038, 0.016
rs6763931	321/1837	0.215	-0.131, 0.420	0.015	-0.007, 0.033
rs10936632	315/1858	0.130	-0.210, 0.422	0.009	-0.019, 0.036
rs17021918	469/2831	-0.039	-0.440, 0.344	-0.001	-0.038, 0.029
rs7679673	472/2824	-0.054	-0.529, 0.266	-0.008	-0.051, 0.025
rs2242652	324/1858	-0.017	-1.421, 0.572	-0.032	-0.166, 0.045
rs12653946	420/2548	-0.095	-0.513, 0.200	-0.0001	-0.033, 0.021
rs2121875	309/1739	0.123	-0.274, 0.369	0.012	-0.013, 0.028
rs130067	323/1856	-0.097	-0.557, 0.203	-0.004	-0.039, 0.015
rs339331	421/2564	-0.170	-0.925, 0.249	-0.019	-0.072, 0.023
rs9364554	489/2876	-0.033	-0.309, 0.255	0.002	-0.025, 0.019
rs12155172	472/2830	0.065	-0.202, 0.333	0.002	-0.025, 0.019
rs10486567	500/2873	0.180	-0.424, 0.508	0.003	-0.041, 0.039
rs6465657	478/2868	-0.236	-0.705, 0.073	-0.012	-0.048, 0.010
rs2928679	477/2828	0.027	-0.321, 0.266	0.008	-0.018, 0.025
rs1512268	482/2851	-0.187	-0.538, 0.130	-0.017	-0.062, 0.007
rs1016343	487/2875	0.385	-0.742, 0.052	-0.028	-0.098, 0.003
rs16901979	490/2852	0.271	-0.362, 0.764	0.022	-0.010, 0.032
rs16902094	450/2621	0.279 ^d	0.032, 0.531 ^d	0.026 ^e	0.015, 0.038 ^e
rs620861	463/2673	0.511 ^e	0.247, 0.695 ^e	0.047 ^d	0.006, 0.090 ^d
rs6983267	498/2847	-0.054	-0.492, 0.215	-0.001	-0.034, 0.021
rs4242382	505/2921	0.105	-0.333, 0.369	0.009	-0.034, 0.025

rs1571801	482/2773	-0.179	-0.426, 0.181	0.001	-0.030, 0.018
rs10993994	494/2852	0.186	-0.097, 0.377	0.020 ^d	0.0005, 0.037 ^d
rs7127900	474/2815	0.013	-0.251, 0.283	0.002	-0.030, 0.019
rs12418451	504/2932	0.033	-0.274, 0.281	0.001	-0.028, 0.020
rs10896449	493/2850	0.025	-0.302, 0.339	0.008	-0.017, 0.030
rs10875943	321/1867	-0.150	-0.548, 0.184	-0.006	-0.049, 0.018
rs902774	469/2752	0.067	-0.285, 0.365	0.004	-0.033, 0.021
rs11649743	496/2858	0.287	-1.079, 0.889	0.034	-0.028, 0.110
rs4430796	489/2802	-0.749 ^d	-1.655, -0.104 ^d	-0.018	-0.076, 0.009
rs1859962	495/2882	-0.083	-0.583, 0.258	0.007	-0.024, 0.031
rs8102476	495/2796	0.296	-0.062, 0.423	0.022 ^d	0.001, 0.045 ^d
rs11672691	418/2549	-0.145	-1.220, 0.399	-0.001	-0.070, 0.045
rs2735839	483/2795	-0.031	-2.208, 0.778	0.002	-0.107, 0.113
rs5759167	471/2819	0.189	-0.105, 0.422	0.022 ^d	0.0002, 0.045 ^d
rs11704416	422/2564	-0.050	-0.482, 0.246	-0.003	-0.047, 0.017
rs5945619	490/2871	0.041	-0.342, 0.304	-0.004	-0.043, 0.017
rs5919432	320/1851	0.290	-0.017, 0.567	0.025 ^d	0.002, 0.051 ^d
Additive SNP score ^f	511/2980	0.164	-0.039, 0.383	0.027 ^d	0.001, 0.059 ^d

Abbreviations: 25(OH)D, 25-hydroxyvitamin D; BPC3, Breast and Prostate Cancer Cohort Consortium; CI, confidence interval; GWAS, genome-wide association study; RERI, relative excess risk due to interaction; SNP, single nucleotide polymorphism.

^a Relative excess risk due to interaction (RERIs) were calculated to infer about interactions at the additive scale for “cohort, batch and season-specific” tertiles of 25(OH)D and dichotomized SNP using logistic regression models adjusted for age at blood draw, year of blood draw, cohort and country (within EPIC). CIs were calculated using bootstrap.

^b Relative excess risk due to interaction (RERIs) were calculated to infer about interactions at the additive scale for “Rosner-standardized” continuous 25(OH)D and dichotomized SNP using logistic regression models adjusted for age at blood draw, year of blood draw, cohort and country (within EPIC). CIs were calculated using bootstrap.

^c Did not calculate CIs due to small sample size.

^d Unadjusted p-value between 0.01 and 0.05. All p-values were non-significant after allowance for multiple testing.

^e Unadjusted p-value=0.00001, which remained significant after allowance for multiple testing.

^f Relative excess risk due to interaction (RERIs) were calculated using a dichotomized (at the median among controls) additive genetic score (after summing the number of risk alleles across the 46 SNPs for each participant).

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