Systematic identification of interaction effects between genome- and environment-wide associations in Type 2 Diabetes Mellitus

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Supplementary Materials

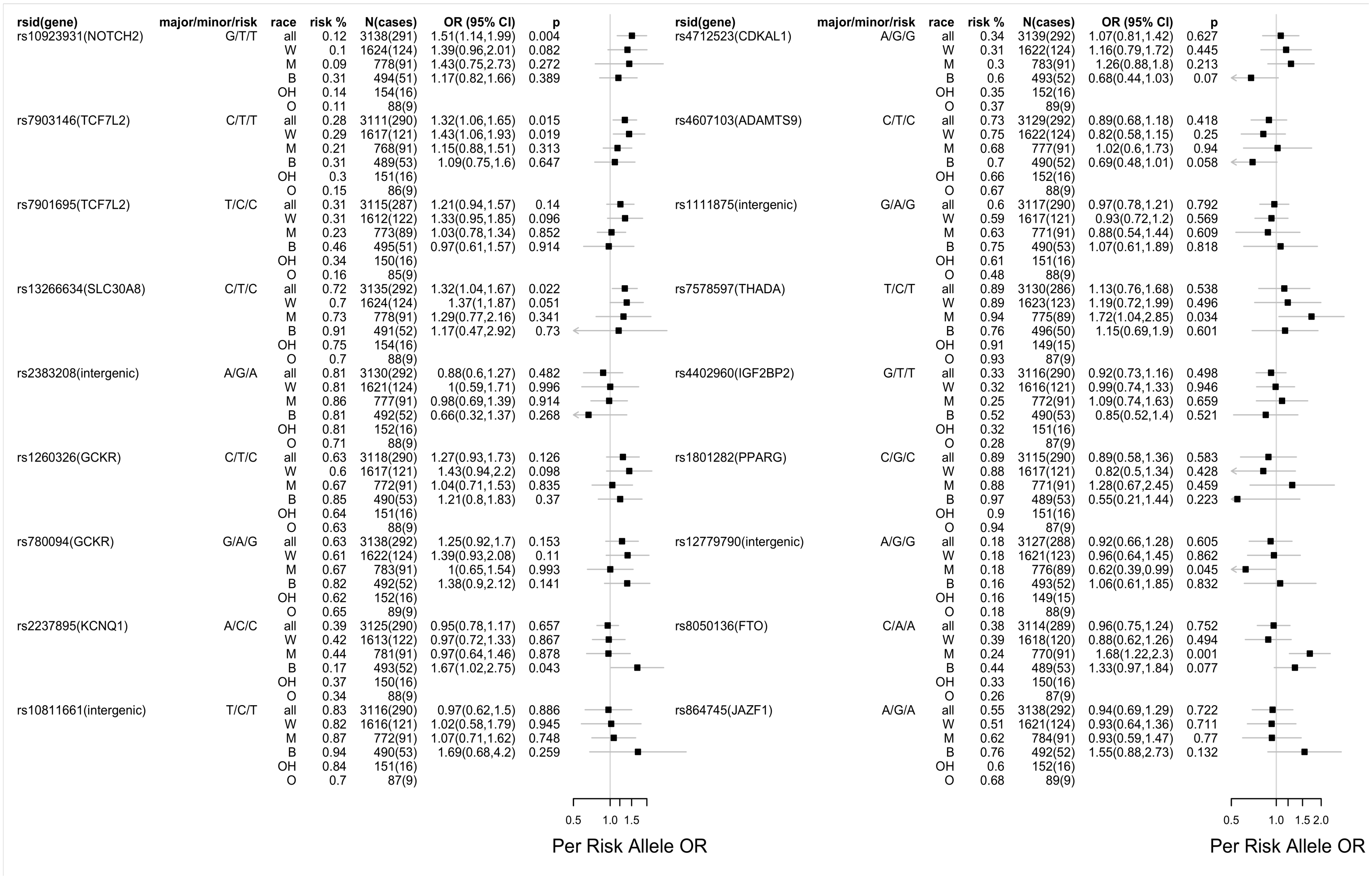
rsid (gene)	Population of sample(s)	OR/association p-value(s)	reference(s)
Rs10923931 (NOTCH2)	Caucasian (European)	1.13/1x10-8	(Zeggini et al. 2008)
Rs7903146 (TCF7L2)	Caucasian (European), Caucasian (American; European), Japanese, Indian	1.65(het)/3x10-10 , 1.4/1x10-48, 1.5/8x10-12 ,7x10-7	(Saxena et al. 2007; Sladek et al. 2007; Takeuchi et al. 2009; Zabaneh and Balding 2010)
Rs13266634 (SLC30A8)	Caucasian, Caucasian (American; European), Japanese	1.18(het)/6x10-8, 1.12/5x10-8, 1.2/2x10-14	(Saxena et al. 2007; Sladek et al. 2007; Takeuchi et al. 2009)
Rs7901695 (TCF7L2)	Caucasian (European), African American	1.37/1x10-48, 1.2/1x10-6	(Lettre et al. 2011; Zeggini et al. 2007)
Rs2383208 (CDKN2A)	Japanese	1.3/2x10-29	(Takeuchi et al. 2009)
Rs1260326 (GCKR)	European	0.07 (2-hour glucose)/7x10-11	(Saxena et al. 2010) (glucose challenge)
Rs780094 (GCKR)	European	1x10-9	(Dupuis et al. 2010)
Rs2237895 (KCNQ1)	Japanese, Chinese	1.4/2x10-42,1.29/1x10-9	(Yasuda et al. 2008),(Tsai et al. 2010)
Rs10811661 (unknown)	Caucasian (European), Caucasian (European; American), Korean	1.19/5x10-8, 1.2/8x10-15, 1.55/2x10-8	(Ng et al. 2008; Saxena et al. 2007; Scott et al. 2007)
Rs4712523 (CDKAL1)	Caucasian (European), Japanese	1.2/2x10-12, 1.27/7x10-20	(Rung et al. 2009; Takeuchi et al. 2009)
Rs4607103 (ADAMTS9)	Caucasian (European)	1.09/1x10-9	(Zeggini et al. 2008)
Rs1111875 (HHEX)	Caucasian, Japanese	1.13/6x10-10, 1.21/7x10-12	(Saxena et al. 2007; Takeuchi et al. 2009)
Rs7578597 (THADA)	Caucasian (European)	1.15/1x10-9	(Zeggini et al. 2008)
Rs4402960 (IGFBP2)	Caucasian (American; European)	1.17/1.7x10-9	(Saxena et al. 2007)
Rs1801282 (PPARG)	Caucasian (American;European), Caucasian	1.1/5x10-8,1.14/8x10-6	(Saxena et al. 2007; Voight et al. 2010)
Rs12779790 (CAMK1D)	Caucasian	1.11/1x10-10	(Zeggini et al. 2008)

Rs8050136 (FTO)	Caucasian (European), Caucasian (European)	1.23/9x10-16, 1.17/1x10-12	(Scott et al. 2007; Zeggini et al. 2007)
Rs864745 (JAZF1)	Caucasian (European), Caucasian	1.10/5x10-14, 1.12x10-8	(Voight et al. 2010; Zeggini et al. 2008)

Table S1. Examples of genome-wide association studies and publications for 18 selected SNPs.

	Heptachlor Epoxide	PCB170	g-tocopherol	trans-b-carotene	cis-b-carotene
Heptachlor Epoxide	1	0.34	0.13	0.04	0.04
PCB170	0.34	1	0.03	0.19	0.2
g-tocopherol	0.13	0.03	1	-0.22	-0.2
trans-b-carotene	0.04	0.19	-0.22	1	0.96
cis-b-carotene	0.04	0.2	-0.2	0.96	1

Table S2. Correlation matrix (Pearson's ρ) of environmental factors.



rsid(gene)	major/minor/risk	race	risk %	N(cases)	OR (95% CI)	p
rs10923931(NOTCH2)	G/T/T	all	0.12	3138(291)	1.51(1.14,1.99)	0.004
		W	0.1	1624(124)	1.39(0.96,2.01)	0.082
		M	0.09	778(91)	1.43(0.75,2.73)	0.272
		B	0.31	494(51)	1.17(0.82,1.66)	0.389
		OH	0.14	154(16)		
		O	0.11	88(9)		
rs7903146(TCF7L2)	C/T/T	all	0.28	3111(290)	1.32(1.06,1.65)	0.015
		W	0.29	1617(121)	1.43(1.06,1.93)	0.019
		M	0.21	768(91)	1.15(0.88,1.51)	0.313
		B	0.31	489(53)	1.09(0.75,1.6)	0.647
		OH	0.3	151(16)		
		O	0.15	86(9)		
rs7901695(TCF7L2)	T/C/C	all	0.31	3115(287)	1.21(0.94,1.57)	0.14
		W	0.31	1612(122)	1.33(0.95,1.85)	0.096
		M	0.23	773(89)	1.03(0.78,1.34)	0.852
		B	0.46	495(51)	0.97(0.61,1.57)	0.914
		OH	0.34	150(16)		
		O	0.16	85(9)		
rs13266634(SLC30A8)	C/T/C	all	0.72	3135(292)	1.32(1.04,1.67)	0.022
		W	0.7	1624(124)	1.37(1,1.87)	0.051
		M	0.73	778(91)	1.29(0.77,2.16)	0.341
		B	0.91	491(52)	1.17(0.47,2.92)	0.73
		OH	0.75	154(16)		
		O	0.7	88(9)		
rs2383208(intergenic)	A/G/A	all	0.81	3130(292)	0.88(0.6,1.27)	0.482
		W	0.81	1621(124)	1(0.59,1.71)	0.996
		M	0.86	777(91)	0.98(0.69,1.39)	0.914
		B	0.81	492(52)	0.66(0.32,1.37)	0.268
		OH	0.81	152(16)		
		O	0.71	88(9)		
rs1260326(GCKR)	C/T/C	all	0.63	3118(290)	1.27(0.93,1.73)	0.126
		W	0.6	1617(121)	1.43(0.94,2.2)	0.098
		M	0.67	772(91)	1.04(0.71,1.53)	0.835
		B	0.85	490(53)	1.21(0.8,1.83)	0.37
		OH	0.64	151(16)		
		O	0.63	88(9)		
rs780094(GCKR)	G/A/G	all	0.63	3138(292)	1.25(0.92,1.7)	0.153
		W	0.61	1622(124)	1.39(0.93,2.08)	0.11
		M	0.67	783(91)	1(0.65,1.54)	0.993
		B	0.82	492(52)	1.38(0.9,2.12)	0.141
		OH	0.62	152(16)		
		O	0.65	89(9)		
rs2237895(KCNQ1)	A/C/C	all	0.39	3125(290)	0.95(0.78,1.17)	0.657
		W	0.42	1613(122)	0.97(0.72,1.33)	0.867
		M	0.44	781(91)	0.97(0.64,1.46)	0.878
		B	0.17	493(52)	1.67(1.02,2.75)	0.043
		OH	0.37	150(16)		
		O	0.34	88(9)		
rs10811661(intergenic)	T/C/T	all	0.83	3116(290)	0.97(0.62,1.5)	0.886
		W	0.82	1616(121)	1.02(0.58,1.79)	0.945
		M	0.87	772(91)	1.07(0.71,1.62)	0.748
		B	0.94	490(53)	1.69(0.68,4.2)	0.259
		OH	0.84	151(16)		
		O	0.7	87(9)		

rsid(gene)	major/minor/risk	race	risk %	N(cases)	OR (95% CI)	p
rs4712523(CDKAL1)	A/G/G	all	0.34	3139(292)	1.07(0.81,1.42)	0.627
		W	0.31	1622(124)	1.16(0.79,1.72)	0.445
		M	0.3	783(91)	1.26(0.88,1.8)	0.213
		B	0.6	493(52)	0.68(0.44,1.03)	0.07
		OH	0.35	152(16)		
		O	0.37	89(9)		
rs4607103(ADAMTS9)	C/T/C	all	0.73	3129(292)	0.89(0.68,1.18)	0.418
		W	0.75	1622(124)	0.82(0.58,1.15)	0.25
		M	0.68	777(91)	1.02(0.6,1.73)	0.94
		B	0.7	490(52)	0.69(0.48,1.01)	0.058
		OH	0.66	152(16)		
		O	0.67	88(9)		
rs1111875(intergenic)	G/A/G	all	0.6	3117(290)	0.97(0.78,1.21)	0.792
		W	0.59	1617(121)	0.93(0.72,1.2)	0.569
		M	0.63	771(91)	0.88(0.54,1.44)	0.609
		B	0.75	490(53)	1.07(0.61,1.89)	0.818
		OH	0.61	151(16)		
		O	0.48	88(9)		
rs7578597(THADA)	T/C/T	all	0.89	3130(286)	1.13(0.76,1.68)	0.538
		W	0.89	1623(123)	1.19(0.72,1.99)	0.496
		M	0.94	775(89)	1.72(1.04,2.85)	0.034
		B	0.76	496(50)	1.15(0.69,1.9)	0.601
		OH	0.91	149(15)		
		O	0.93	87(9)		
rs4402960(IGF2BP2)	G/T/T	all	0.33	3116(290)	0.92(0.73,1.16)	0.498
		W	0.32	1616(121)	0.99(0.74,1.33)	0.946
		M	0.25	772(91)	1.09(0.74,1.63)	0.659
		B	0.52	490(53)	0.85(0.52,1.4)	0.521
		OH	0.32	151(16)		
		O	0.28	87(9)		
rs1801282(PPARG)	C/G/C	all	0.89	3115(290)	0.89(0.58,1.36)	0.583
		W	0.88	1617(121)	0.82(0.5,1.34)	0.428
		M	0.88	771(91)	1.28(0.67,2.45)	0.459
		B	0.97	489(53)	0.55(0.21,1.44)	0.223
		OH	0.9	151(16)		
		O	0.94	87(9)		
rs12779790(intergenic)	A/G/G	all	0.18	3127(288)	0.92(0.66,1.28)	0.605
		W	0.18	1621(123)	0.96(0.64,1.45)	0.862
		M	0.18	776(89)	0.62(0.39,0.99)	0.045
		B	0.16	493(52)	1.06(0.61,1.85)	0.832
		OH	0.16	149(15)		
		O	0.18	88(9)		
rs8050136(FTO)	C/A/A	all	0.38	3114(289)	0.96(0.75,1.24)	0.752
		W	0.39	1618(120)	0.88(0.62,1.26)	0.494
		M	0.24	770(91)	1.68(1.22,2.3)	0.001
		B	0.44	489(53)	1.33(0.97,1.84)	0.077
		OH	0.33	150(16)		
		O	0.26	87(9)		
rs864745(JAZF1)	A/G/A	all	0.55	3138(292)	0.94(0.69,1.29)	0.722
		W	0.51	1621(124)	0.93(0.64,1.36)	0.711
		M	0.62	784(91)	0.93(0.59,1.47)	0.77
		B	0.76	492(52)	1.55(0.88,2.73)	0.132
		OH	0.6	152(16)		
		O	0.68	89(9)		

Figure S1. Allele specification, risk allele frequency, and marginal effect size (adjusted odds ratio) for 18 loci. Race key: "All": All races combined; "W": Non-Hispanic White; "M": Mexican-American; "B": Non-Hispanic Black. All effect sizes were adjusted by age, sex, BMI. The "All" model was adjusted by age, sex, BMI, and race. Risk allele specification determined from the literature.

factor	race	N(cases)	Diabetics Mean (95% CI) [units]	Controls Mean (95% CI) [units]	OR (95% CI)	p
PCB170	all	1710(97)	0.14(0.12,0.16) [ng/g]	0.08(0.07,0.08) [ng/g]	1.72(1.18,2.51)	0.011
	W	728(38)	0.14(0.11,0.16) [ng/g]	0.08(0.08,0.09) [ng/g]	1.59(1.04,2.43)	0.045
	M	491(28)	0.12(0.07,0.18) [ng/g]	0.05(0.04,0.05) [ng/g]	1.85(0.81,4.25)	0.172
	B	358(20)	0.17(0.11,0.23) [ng/g]	0.07(0.06,0.08) [ng/g]	2.15(0.72,6.41)	0.191
	OH	74(5)	0.1(0.05,0.15) [ng/g]	0.06(0.04,0.08) [ng/g]		
	O	59(6)	0.15(0.11,0.19) [ng/g]	0.06(0.04,0.07) [ng/g]		
trans-b-carotene	all	2847(186)	13.32(10.82,15.82) [ug/dL]	17.23(16.22,18.24) [ug/dL]	0.63(0.51,0.78)	0.003
	W	1320(82)	14.28(10.65,17.91) [ug/dL]	17.75(16.29,19.22) [ug/dL]	0.68(0.52,0.91)	0.022
	M	722(50)	15.69(12.24,19.13) [ug/dL]	16.9(14.83,18.97) [ug/dL]	0.76(0.55,1.04)	0.16
	B	601(36)	10.2(7.29,13.1) [ug/dL]	15.34(13.23,17.44) [ug/dL]	0.52(0.38,0.73)	0.005
	OH	99(9)	15.05(7.34,22.76) [ug/dL]	13.47(10.44,16.5) [ug/dL]		
	O	105(9)	7.68(2.79,12.57) [ug/dL]	17.79(14.16,21.42) [ug/dL]		
cis-b-carotene	all	2846(186)	0.82(0.7,0.94) [ug/dL]	1(0.95,1.05) [ug/dL]	0.62(0.48,0.79)	0.006
	W	1319(82)	0.85(0.67,1.03) [ug/dL]	1.02(0.95,1.09) [ug/dL]	0.67(0.49,0.9)	0.022
	M	722(50)	0.91(0.72,1.1) [ug/dL]	0.93(0.83,1.04) [ug/dL]	0.8(0.58,1.09)	0.231
	B	601(36)	0.71(0.56,0.86) [ug/dL]	0.99(0.86,1.11) [ug/dL]	0.47(0.26,0.83)	0.032
	OH	99(9)	0.92(0.62,1.22) [ug/dL]	0.77(0.62,0.92) [ug/dL]		
	O	105(9)	0.6(0.35,0.85) [ug/dL]	1.05(0.85,1.26) [ug/dL]		
g-tocopherol	all	5039(310)	327.94(295.49,360.39) [ug/dL]	225.72(216.78,234.65) [ug/dL]	1.47(1.25,1.73)	<0.001
	W	2193(131)	324.86(276.47,373.26) [ug/dL]	225.92(214.48,237.36) [ug/dL]	1.35(1.15,1.59)	0.001
	M	1343(84)	376.45(300.05,452.85) [ug/dL]	223.38(211.34,235.41) [ug/dL]	1.78(1.33,2.39)	0.002
	B	1087(64)	359.6(316.47,402.74) [ug/dL]	241.76(233.42,250.1) [ug/dL]	3.2(1.66,6.19)	0.002
	OH	241(18)	249.78(200.64,298.93) [ug/dL]	199.78(180.77,218.8) [ug/dL]		
	O	175(13)	343(194.47,491.53) [ug/dL]	225.95(201.01,250.88) [ug/dL]		
Heptachlor Epoxide	all	1618(93)	0.13(0.09,0.18) [ng/g]	0.05(0.05,0.06) [ng/g]	1.49(1.13,1.98)	0.011
	W	683(35)	0.14(0.07,0.21) [ng/g]	0.05(0.05,0.06) [ng/g]	1.66(1.17,2.35)	0.009
	M	488(29)	0.26(0,0.52) [ng/g]	0.05(0.04,0.06) [ng/g]	1.73(0.92,3.26)	0.122
	B	331(19)	0.08(0.06,0.11) [ng/g]	0.04(0.03,0.04) [ng/g]	1.61(0.84,3.07)	0.173
	OH	63(5)	0.12(-0.01,0.25) [ng/g]	0.04(0.03,0.05) [ng/g]		
	O	53(5)	0.04(0.02,0.05) [ng/g]	0.05(0.03,0.06) [ng/g]		

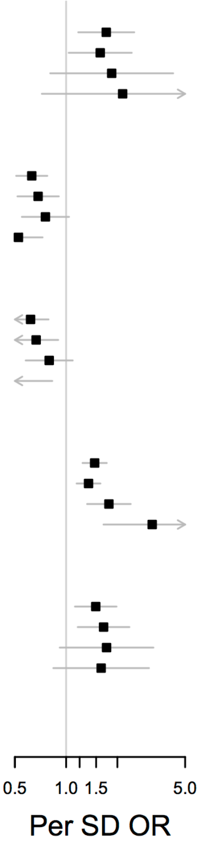


Figure S2. Serum levels of environmental factors and marginal effect sizes (adjusted odds ratio) for five factors. Race key: “All”: all races combined; “W”: Non-Hispanic White; “M”: Mexican American; “B”: Non-Hispanic Black, “OH”: Other Hispanic; “O”: Other.. Means are specified in their original units of measure (ng/g: nanogram per gram serum, ug/mL: microgram per milliliter). Adjusted odds ratios were adjusted by age, sex, and BMI; The “All” model was adjusted by age, sex, BMI, and race. Adjusted odds ratios are for a change in 1SD of logged exposure value.

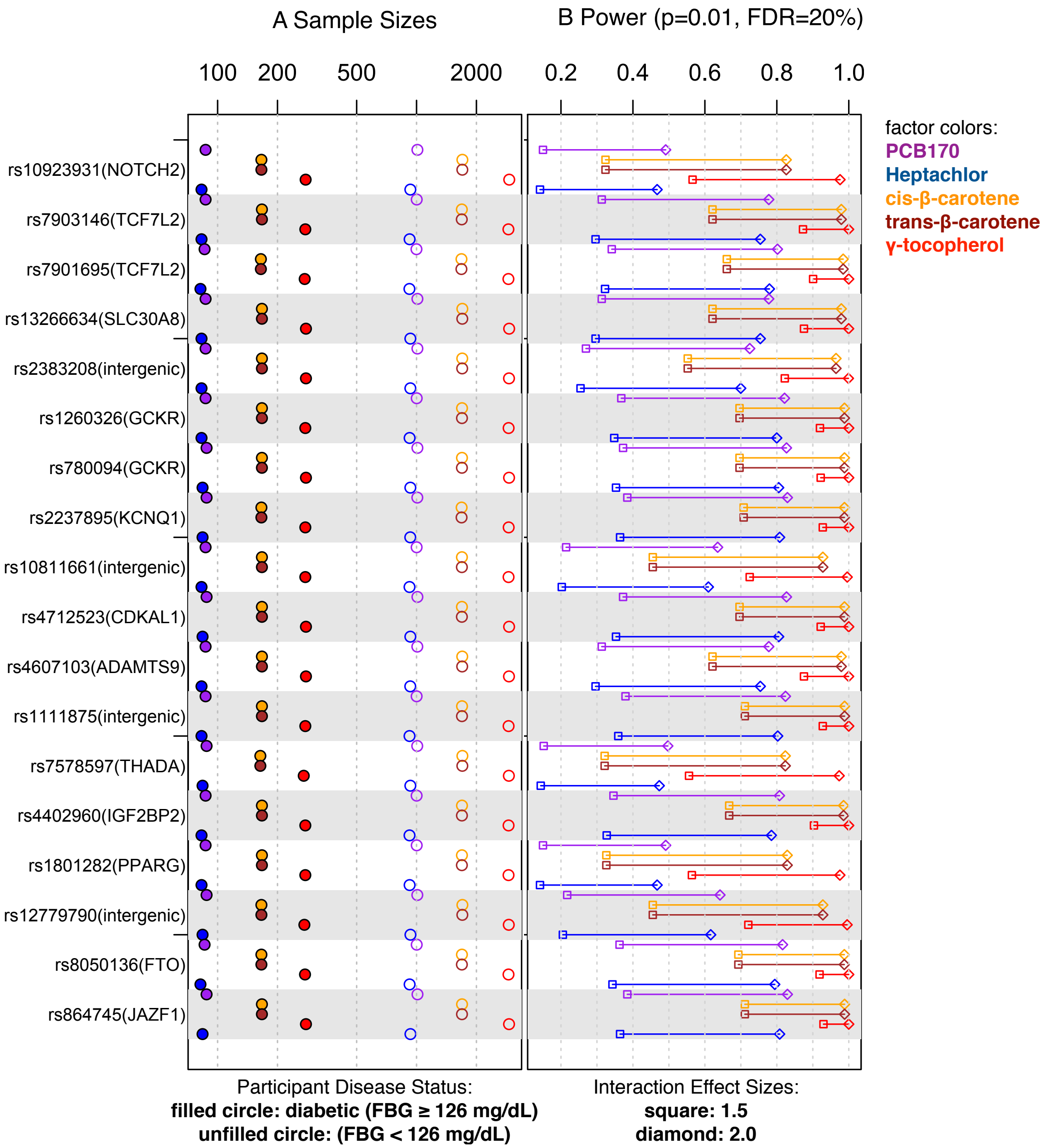


Figure S3. Sample sizes and power for detection of interaction per SNP by environmental factor pair. A) Sample size for each SNP and environmental factor pair. Filled markers correspond to diabetics. B) Power estimate for detection of interaction for each genetic locus and environmental factor pair tested against T2D. Assumptions include an interaction odds ratio of 1.5 and 2.0, a main effect of the SNP of 1.0 (additive model) and environmental factor OR of 1.5, the minor allele frequencies as in Figure 2 (combined races), 10 controls per case, environmental factor SD of 1, and p-value of 0.01 (FDR of 18%). FBG: fasting blood glucose.

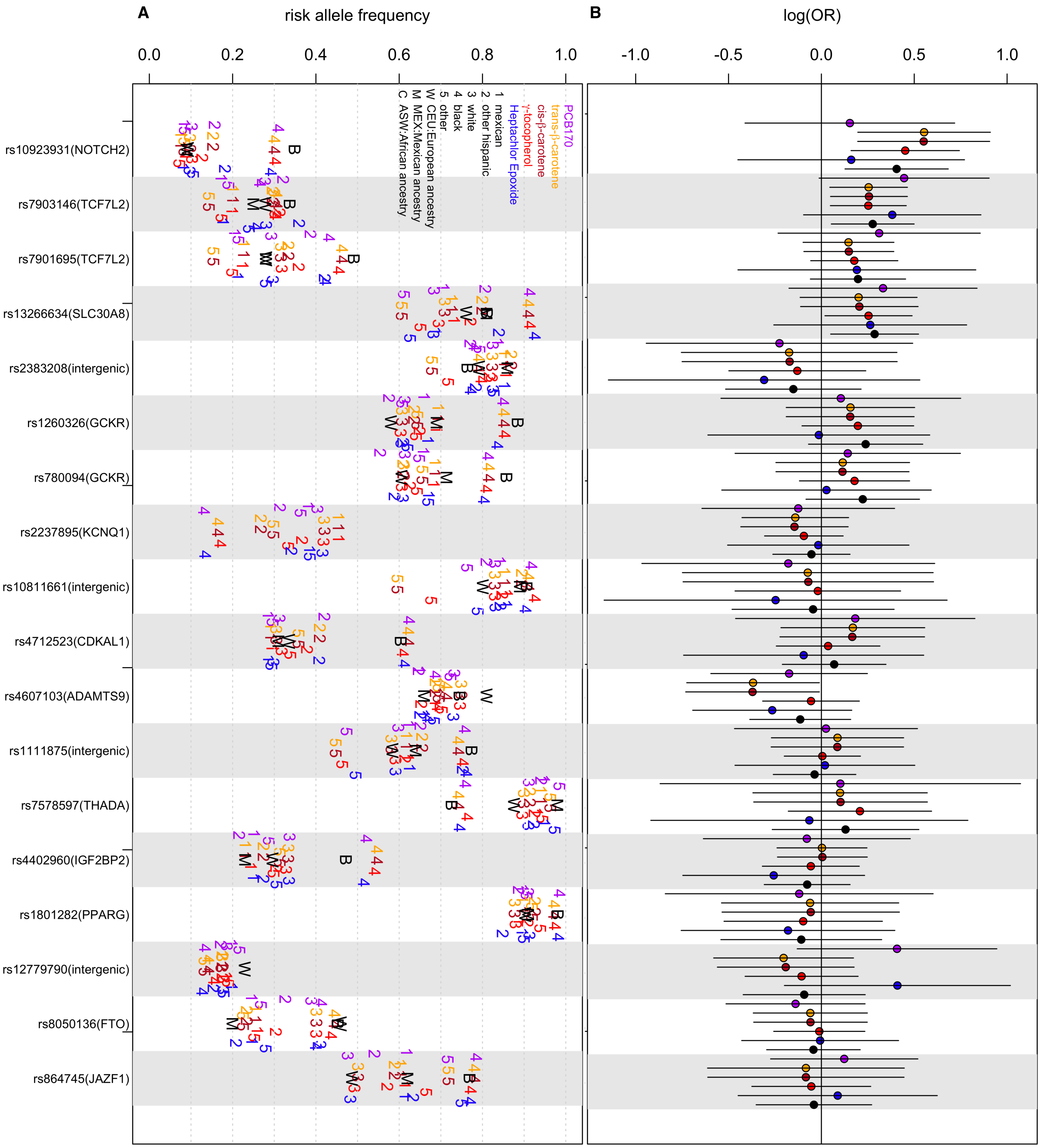
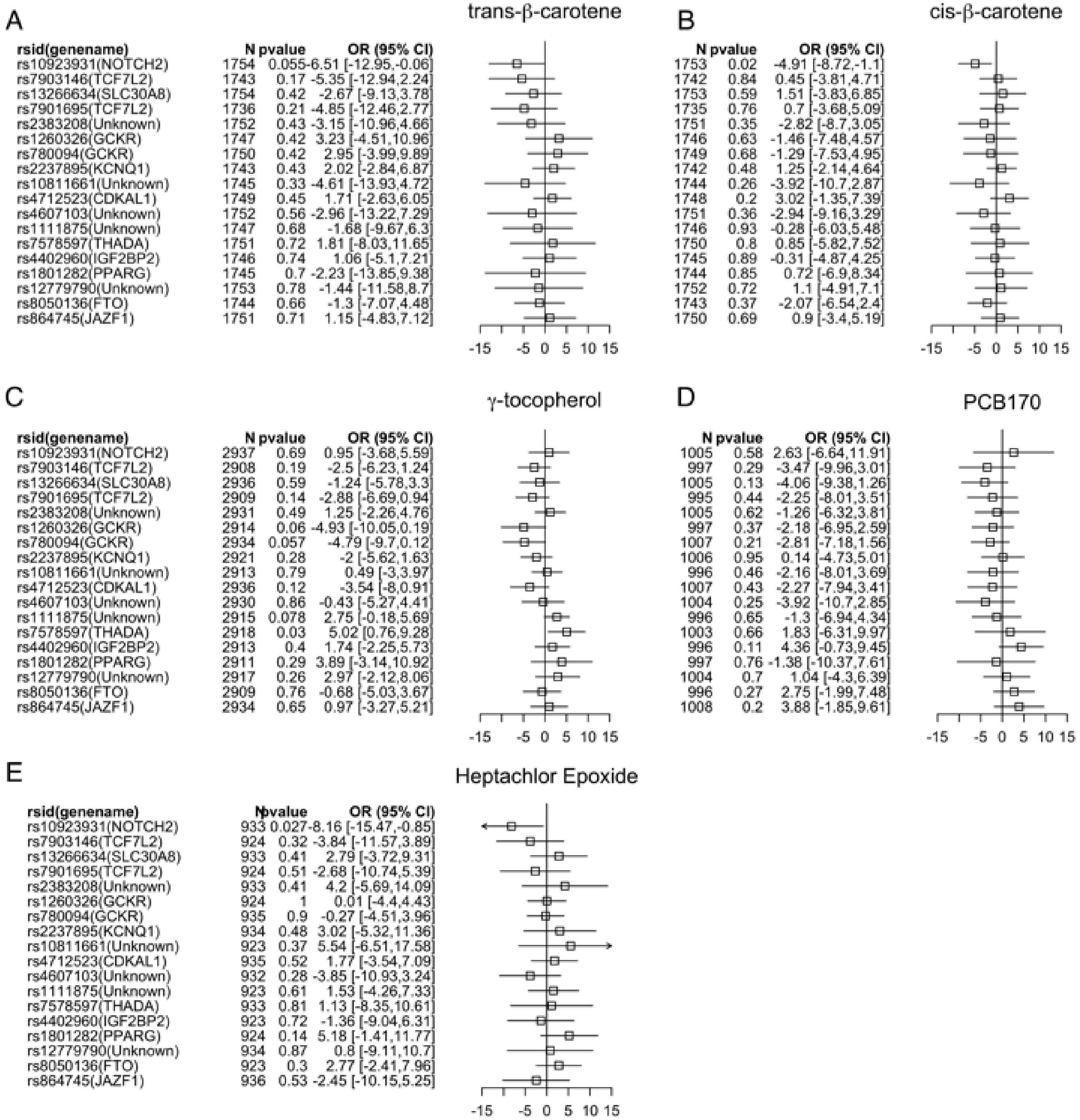


Figure S4. Risk allele frequency and genetic marginal effect sizes per subsample with joint measures for genetic variation and environmental factors. A) Risk allele frequency by race. Numbers indicate ancestry (1: Mexican American; 2: Other Hispanic; 3: Non-Hispanic White; 4: Non-Hispanic Black; 5: Other); letter indicates minor allele frequency in HapMap populations (W: CEU, European; M: MEX, Mexican; B: ASW, African). 2) Marginal effect size (log(odds ratio)) adjusted by sex, age, race, BMI. The black marker denotes the overall genetic effect size in the full sample. Colored markers indicate environmental factors: red: γ-tocopherol, blue: heptachlor epoxide, purple: PCB170, brown: cis-β-carotene, orange: trans-β-carotene.



A trans-β-carotene

rsid(genename)	N	pvalue	OR (95% CI)
rs10923931(NOTCH2)	1754	0.055	-6.51 [-12.95,-0.06]
rs7903146(TCF7L2)	1743	0.17	-5.35 [-12.94,2.24]
rs13266634(SLC30A8)	1754	0.42	-2.67 [-9.13,3.78]
rs7901695(TCF7L2)	1736	0.21	-4.85 [-12.46,2.77]
rs2383208(Unknown)	1752	0.43	-3.15 [-10.96,4.66]
rs1260326(GCKR)	1747	0.42	3.23 [-4.51,10.96]
rs780094(GCKR)	1750	0.42	2.95 [-3.99,9.89]
rs2237895(KCNQ1)	1743	0.43	2.02 [-2.84,6.87]
rs10811661(Unknown)	1745	0.33	-4.61 [-13.93,4.72]
rs4712523(CDKAL1)	1749	0.45	1.71 [-2.63,6.05]
rs4607103(Unknown)	1752	0.56	-2.96 [-13.22,7.29]
rs1111875(Unknown)	1747	0.68	-1.68 [-9.67,6.3]
rs7578597(THADA)	1751	0.72	1.81 [-8.03,11.65]
rs4402960(IGF2BP2)	1746	0.74	1.06 [-5.1,7.21]
rs1801282(PPARG)	1745	0.7	-2.23 [-13.85,9.38]
rs12779790(Unknown)	1753	0.78	-1.44 [-11.58,8.7]
rs8050136(FTO)	1744	0.66	-1.3 [-7.07,4.48]
rs864745(JAZF1)	1751	0.71	1.15 [-4.83,7.12]

B cis-β-carotene

N	pvalue	OR (95% CI)
1753	0.02	-4.91 [-8.72,-1.1]
1742	0.84	0.45 [-3.81,4.71]
1753	0.59	1.51 [-3.83,6.85]
1735	0.76	0.7 [-3.68,5.09]
1751	0.35	-2.82 [-8.7,3.05]
1746	0.63	-1.46 [-7.48,4.57]
1749	0.68	-1.29 [-7.53,4.95]
1742	0.48	1.25 [-2.14,4.64]
1744	0.26	-3.92 [-10.7,2.87]
1748	0.2	3.02 [-1.35,7.39]
1751	0.36	-2.94 [-9.16,3.29]
1746	0.93	-0.28 [-6.03,5.48]
1750	0.8	0.85 [-5.82,7.52]
1745	0.89	-0.31 [-4.87,4.25]
1744	0.85	0.72 [-6.9,8.34]
1752	0.72	1.1 [-4.91,7.1]
1743	0.37	-2.07 [-6.54,2.4]
1750	0.69	0.9 [-3.4,5.19]

C γ-tocopherol

rsid(genename)	N	pvalue	OR (95% CI)
rs10923931(NOTCH2)	2937	0.69	0.95 [-3.68,5.59]
rs7903146(TCF7L2)	2908	0.19	-2.5 [-6.23,1.24]
rs13266634(SLC30A8)	2936	0.59	-1.24 [-5.78,3.3]
rs7901695(TCF7L2)	2909	0.14	-2.88 [-6.69,0.94]
rs2383208(Unknown)	2931	0.49	1.25 [-2.26,4.76]
rs1260326(GCKR)	2914	0.06	-4.93 [-10.05,0.19]
rs780094(GCKR)	2934	0.057	-4.79 [-9.7,0.12]
rs2237895(KCNQ1)	2921	0.28	-2 [-5.62,1.63]
rs10811661(Unknown)	2913	0.79	0.49 [-3,3.97]
rs4712523(CDKAL1)	2936	0.12	-3.54 [-8,0.91]
rs4607103(Unknown)	2930	0.86	-0.43 [-5.27,4.41]
rs1111875(Unknown)	2915	0.078	2.75 [-0.18,5.69]
rs7578597(THADA)	2918	0.03	5.02 [0.76,9.28]
rs4402960(IGF2BP2)	2913	0.4	1.74 [-2.25,5.73]
rs1801282(PPARG)	2911	0.29	3.89 [-3.14,10.92]
rs12779790(Unknown)	2917	0.26	2.97 [-2.12,8.06]
rs8050136(FTO)	2909	0.76	-0.68 [-5.03,3.67]
rs864745(JAZF1)	2934	0.65	0.97 [-3.27,5.21]

D PCB170

N	pvalue	OR (95% CI)
1005	0.58	2.63 [-6.64,11.91]
997	0.29	-3.47 [-9.96,3.01]
1005	0.13	-4.06 [-9.38,1.26]
995	0.44	-2.25 [-8.01,3.51]
1005	0.62	-1.26 [-6.32,3.81]
997	0.37	-2.18 [-6.95,2.59]
1007	0.21	-2.81 [-7.18,1.56]
1006	0.95	0.14 [-4.73,5.01]
996	0.46	-2.16 [-8.01,3.69]
1007	0.43	-2.27 [-7.94,3.41]
1004	0.25	-3.92 [-10.7,2.85]
996	0.65	-1.3 [-6.94,4.34]
1003	0.66	1.83 [-6.31,9.97]
996	0.11	4.36 [-0.73,9.45]
997	0.76	-1.38 [-10.37,7.61]
1004	0.7	1.04 [-4.3,6.39]
996	0.27	2.75 [-1.99,7.48]
1008	0.2	3.88 [-1.85,9.61]

E Heptachlor Epoxide

rsid(genename)	N	pvalue	OR (95% CI)
rs10923931(NOTCH2)	933	0.027	-8.16 [-15.47,-0.85]
rs7903146(TCF7L2)	924	0.32	-3.84 [-11.57,3.89]
rs13266634(SLC30A8)	933	0.41	2.79 [-3.72,9.31]
rs7901695(TCF7L2)	924	0.51	-2.68 [-10.74,5.39]
rs2383208(Unknown)	933	0.41	4.2 [-5.69,14.09]
rs1260326(GCKR)	924	1	0.01 [-4.4,4.43]
rs780094(GCKR)	935	0.9	-0.27 [-4.51,3.96]
rs2237895(KCNQ1)	934	0.48	3.02 [-5.32,11.36]
rs10811661(Unknown)	923	0.37	5.54 [-6.51,17.58]
rs4712523(CDKAL1)	935	0.52	1.77 [-3.54,7.09]
rs4607103(Unknown)	932	0.28	-3.85 [-10.93,3.24]
rs1111875(Unknown)	923	0.61	1.53 [-4.26,7.33]
rs7578597(THADA)	933	0.81	1.13 [-8.35,10.61]
rs4402960(IGF2BP2)	923	0.72	-1.36 [-9.04,6.31]
rs1801282(PPARG)	924	0.14	5.18 [-1.41,11.77]
rs12779790(Unknown)	934	0.87	0.8 [-9.11,10.7]
rs8050136(FTO)	923	0.3	2.77 [-2.41,7.96]
rs864745(JAZF1)	936	0.53	-2.45 [-10.15,5.25]

Figure S5. Correlation of SNP by environmental factor. Each locus was evaluated for differences in levels of A) PCB170, B) heptachlor epoxide, C) γ-tocopherol, D) cis-β-carotene, and E) trans-β-carotene, depending on the number of risk alleles at each locus, while adjusting for sex, age, self-report race, and BMI. X-axis: units of percent change of exposure for 1 risk allele. All p-values are uncorrected for multiple hypotheses.

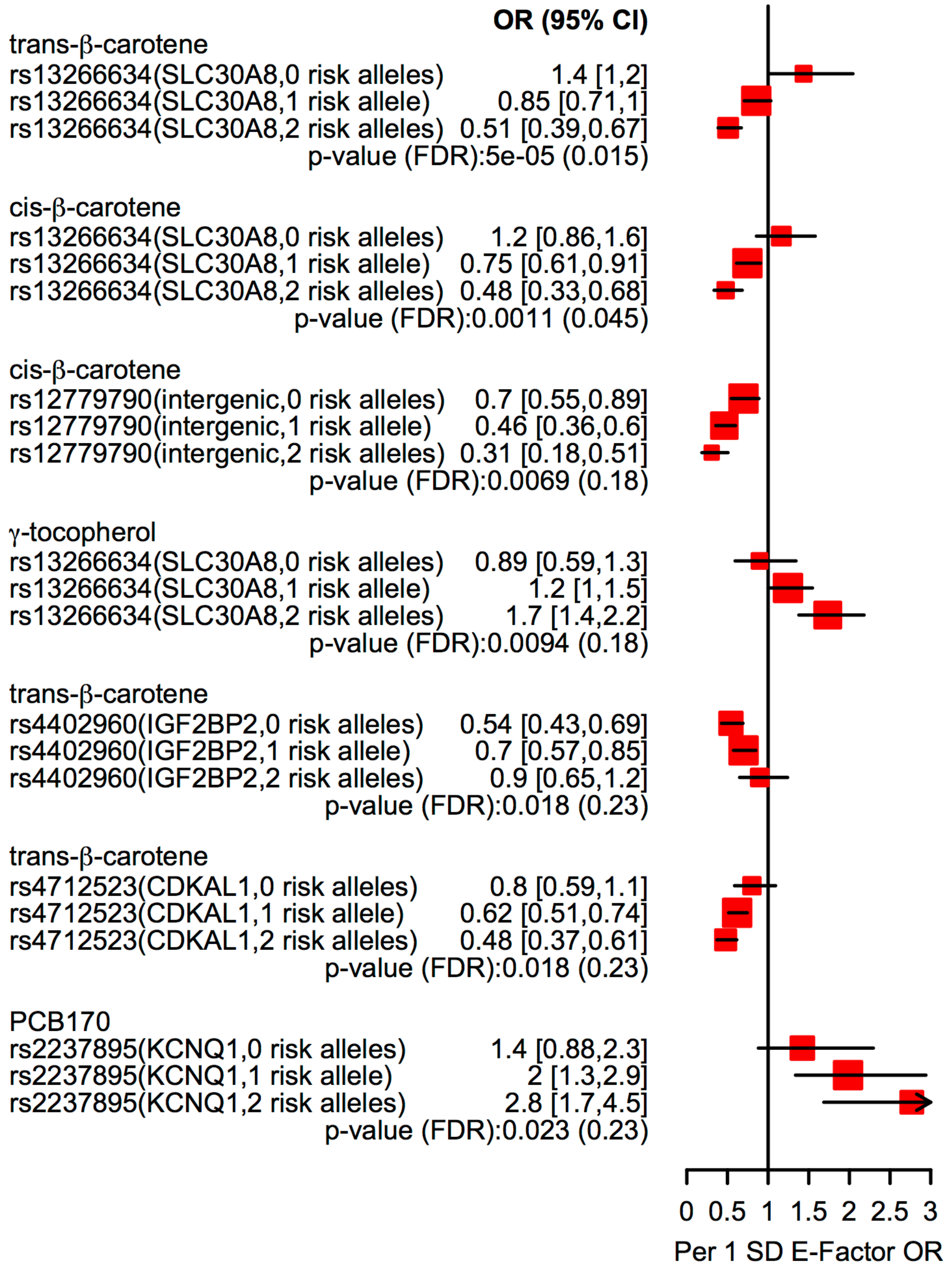


Figure S6. Per-SD environmental factor OR for top interactions. Red markers indicate effects computed conditional on 0, 1, or 2 risk alleles respectively. Marker sizes are proportional to inverse variance.

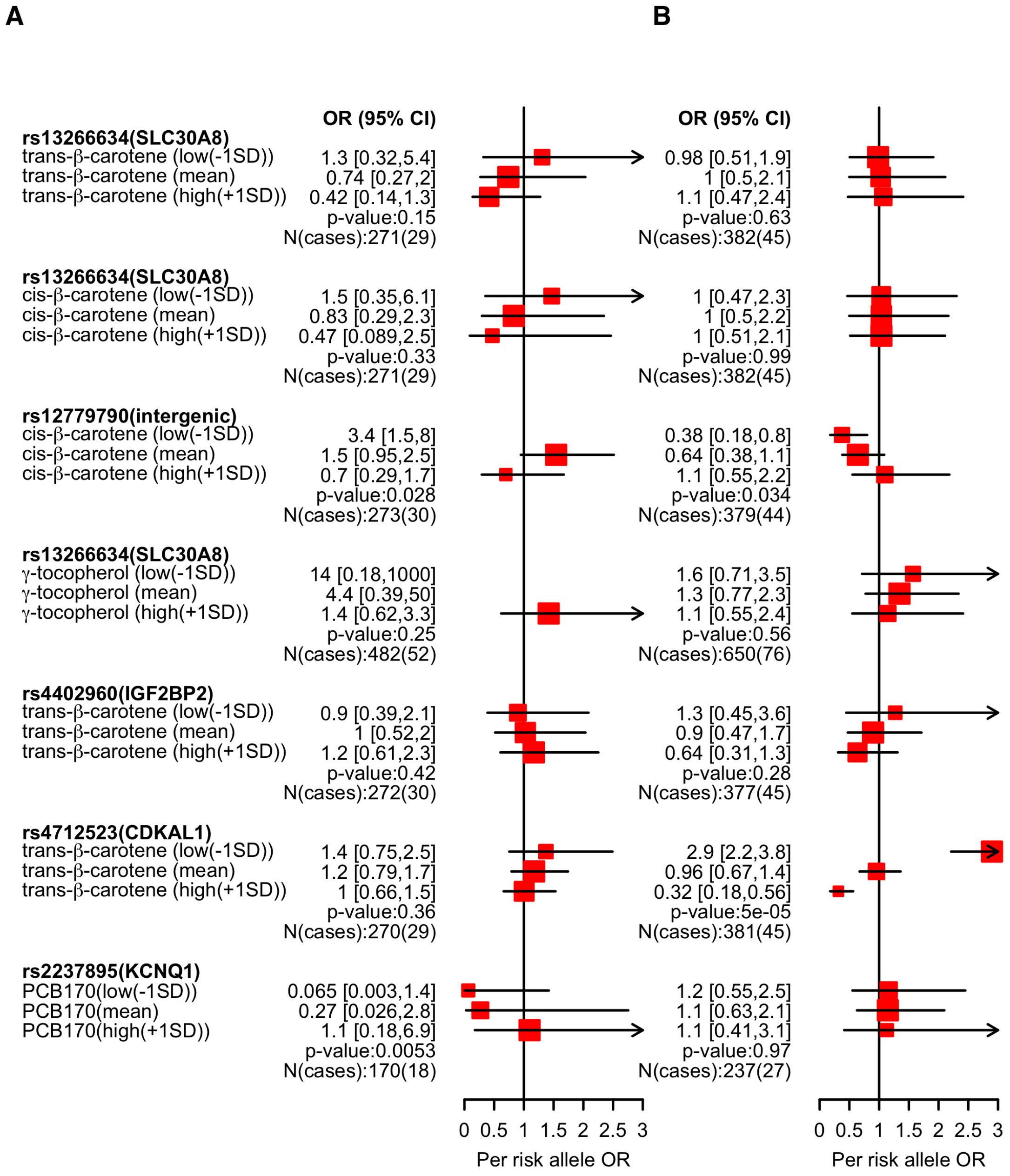


Figure S7. Per-risk allele effect sizes for Mexican-Americans and Non-Hispanic Blacks. (**A**) Non-Hispanic Blacks, (**B**) Mexican Americans. Markers denote interaction OR computed at 1SD below mean exposure levels, at the mean, or at 1SD above the mean. Marker sizes are proportional to inverse variance.

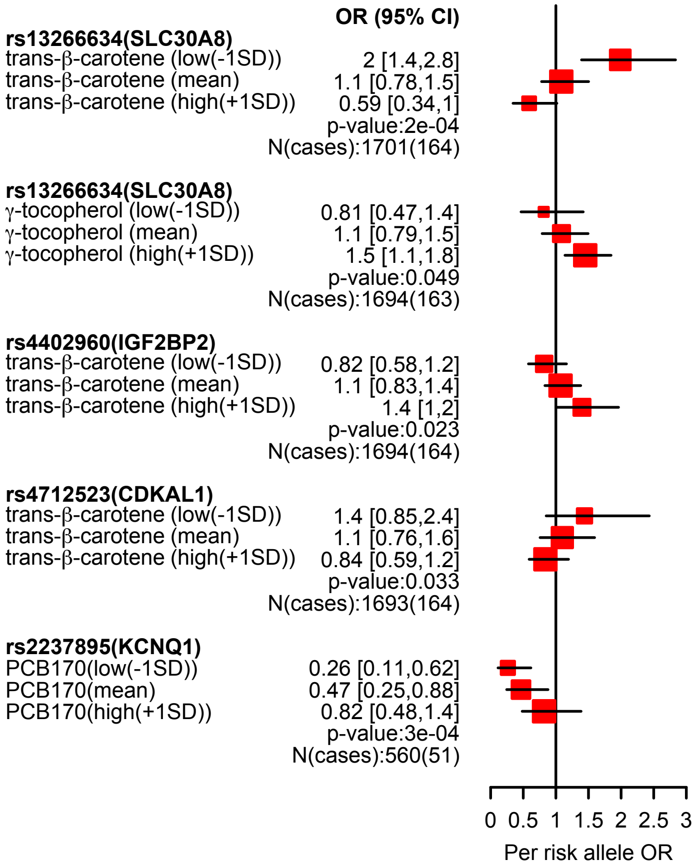


Figure S8. Per-risk allele effect sizes adjusting for cis-β-carotene. Markers denote interaction OR computed at 1SD below mean exposure levels, at the mean, or at 1SD greater than the mean. Marker sizes are proportional to inverse variance. Models were adjusted by age, sex, race, BMI, and cis-β-carotene.

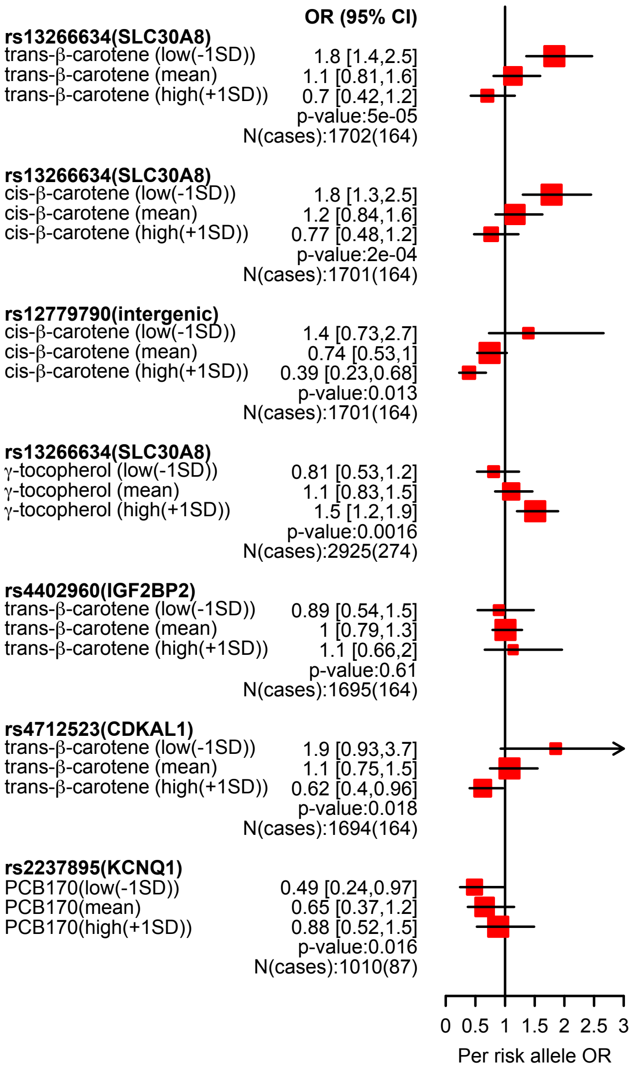


Figure S9. Per-risk allele effect sizes at non-logged levels of environmental factors. Markers denote interaction OR computed at 1SD below mean exposure levels, at the mean, or at 1SD greater than the mean. Marker sizes are proportional to inverse variance.

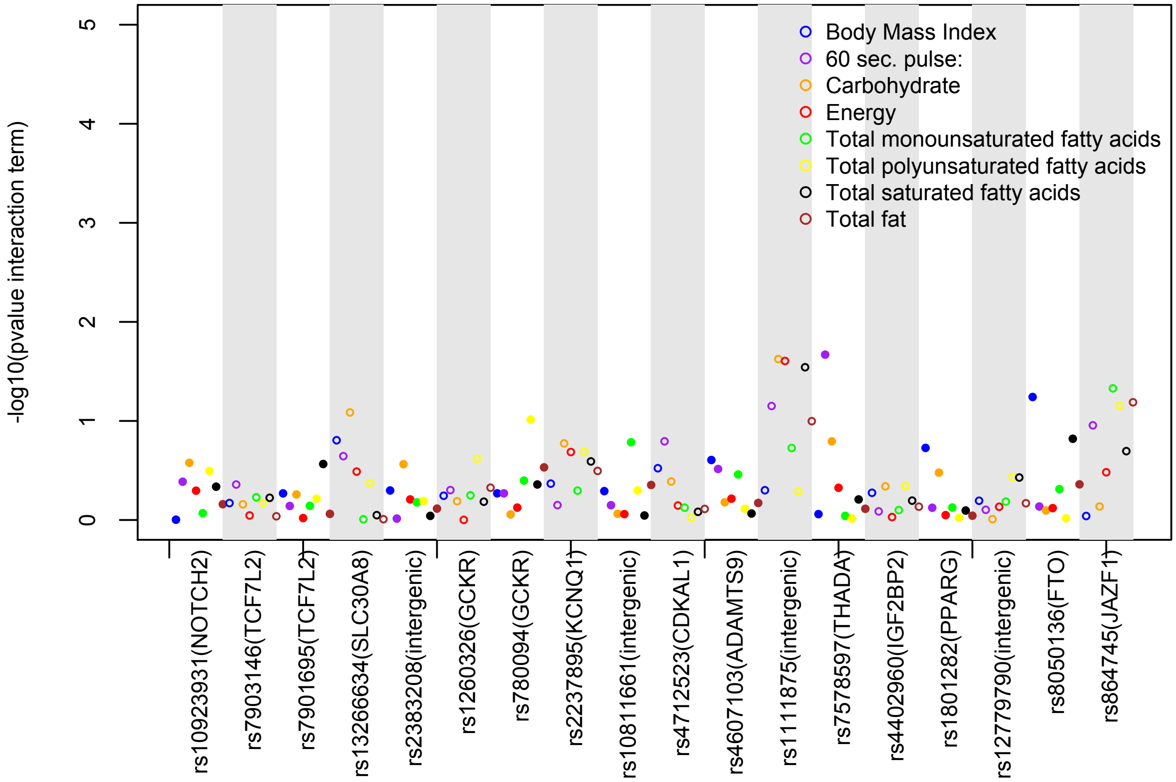


Figure S10. –log10(p-values) for interaction between SNPs and other factors. Blue: Body Mass Index, Purple: 60 second pulse rate, Orange: Total 24-hour carbohydrate intake, Red: Total 24-hour energy intake, Green: Total 24-hour monounsaturated fat intake, Yellow: Total 24-hour polyunsaturated fat intake, Black: Total 24-hour saturated fat intake, Brown: Total 24-hour fat intake.

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