Supplemental material for "A large multi-ethnic genome-wide association study of prostate cancer identifies two novel risk variants and ethnic differences"

Thomas J. Hoffmann,[1,2] Stephen K. Van Den Eeden,[3,4] Lori C. Sakoda,[3] Eric Jorgenson,[3] Laurel A. Habel,[3] Rebecca E. Graff,[1] Michael N. Passarelli,[1] Clinton L. Cario,[1] Nima C. Emami,[1] Chun R. Chao,[5] Nirupa R. Ghai,[5] Jun Shan,[3] Dilrini K. Ranatunga,[3] Charles P. Quesenberry,[3] David Aaronson,[6] Joseph Presti,[6] Wang Zhaoming,[7] Sonja I. Berndt,[7] Stephen J. Chanock,[7] Shannon K. McDonnell,[8] Amy J French,[9] Daniel J Schaid,[8] Stephen N. Thibodeau,[9] Qiyuan Li,[10] Matthew L. Freedman,[11] Kathryn L. Penney,[12] Lorelei A. Mucci,[12] Christopher A. Haiman,[13] Brian E. Henderson,[13] Daniela Seminara,[14]Mark N. Kvale,[2] Pui-Yan Kwok,[2] Catherine Schaefer,[3] Neil Risch,[1,2,3] and John S. Witte[1,2,4,15]

[1]Department of Epidemiology and Biostatistics, University of California San Francisco, San Francisco, CA 94158, USA
[2]Institute for Human Genetics, University of California San Francisco, San Francisco, CA, 94143 USA
[3]Division of Research, Kaiser Permanente, Northern California, Oakland, CA 94612, USA
[4]Department of Urology, University of California San Francisco, San Francisco, CA 94158, USA
[5]Department of Research and Evaluation, Kaiser Permanente Southern California, Pasadena CA 91101, USA
[6]Department of Urology, Kaiser Oakland Medical Center, Northern California, Oakland, CA 94612, USA
[7]Laboratory of Translational Genomics, Division of Cancer Epidemiology and Genetics, Department of Health and Human Services, National Cancer Institute, National Institutes of Health, Bethesda MD, USA.
[8]Department of Health Science Research, Mayo Clinic, Rochester MN
[9]Department of Laboratory Medicine and Pathology, Mayo Clinic, Rochester MN
[10]Medical College, Xiamen University, Xiamen China 361102
[11]Department of Medical Oncology, Dana-Farber Cancer Institute and Harvard Medical School, Boston, MA 02115 and Center for Functional Cancer Epigenetics, Dana-Farber Cancer Institute, Boston, MA and The Eli and Edythe L. Broad Institute, Cambridge, MA
[12]Department of Epidemiology, Harvard T.H. Chan School of Public Health, Boston, MA and Channing Division of Network Medicine, Department of Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston, MA
[13]Department of Preventive Medicine, Keck School of Medicine and Norris Comprehensive Cancer Center, University of Southern California, Los Angeles, CA
[14]National Cancer Institute, National Institutes of Health, Bethesda, MD
[15]UCSF Helen Diller Family Comprehensive Cancer Center, University of California San Francisco, San Francisco, CA 94158, USA

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Table S1: Descriptive factors for KP study population, broken down by study, used in the genome-wide association study of prostate cancer.

	RPGEH				Men's Health Study				Pro Health Study			
	Cases		Controls		Cases		Controls		Cases		Controls	
	N	%	N	%	N	%	N	%	N	%	N	%
Total	4640		27601		2743		10903		400		91	
Race/ethnicity:												
African American	86	1.9%	622	2.3%	117	4.3%	937	8.6%	398	99.5%	91	100.0%
Asian	165	3.6%	1941	7.0%	123	4.5%	997	9.1%	0	0.0%	0	0.0%
non-Hispanic white	4183	90.2%	22857	82.8%	2222	81.0%	8009	73.5%	1	0.2%	0	0.0%
Latino	206	4.4%	2181	7.9%	281	10.2%	960	8.8%	1	0.2%	0	0.0%
Age:												
Age < 50	38	0.8%	4619	16.7%	30	1.1%	0	0.0%	18	4.5%	0	0.0%
$50 \leq$ Age < 60	520	11.2%	5050	18.3%	578	21.1%	2472	22.7%	126	31.5%	14	15.4%
$60 \leq$ Age < 70	1837	39.6%	7242	26.2%	1593	58.1%	4957	45.5%	174	43.5%	41	45.1%
$70 \leq$ Age	2245	48.4%	10690	38.7%	542	19.8%	3474	31.9%	82	20.5%	36	39.6%
PSA:												
Mean (SD)	13.6	(66.1)	2.5	(6.2)	8.5	(25.2)	2.4	(3.5)	12.2	(44.2)	2.8	(3.1)
Median (MAD)	6.9	(3.6)	1.5	(1.3)	5.8	(2.6)	1.5	(1.2)	6.5	(2.8)	1.7	(1.6)
Interquartile range	5.0-10.7		0.8-2.8		4.5-8.3		0.8-2.9		5.0-10.0		0.9-3.7	
Stage:												
Localized	3444	74.2%	—	—	1849	67.4%	—	—	334	83.5%	—	—
Regional	370	8.0%	—	—	245	8.9%	—	—	41	10.2%	—	—
Distant	82	2.0%	—	—	16	0.7%	—	—	5	1.3%	—	—
Unknown	158	3.9%	—	—	34	1.6%	—	—	16	4.0%	—	—
Gleason:												
≤ 5	116	2.5%	—	—	43	1.6%	—	—	8	2.0%	—	—
6	1889	55.6%	—	—	972	61.1%	—	—	206	54.1%	—	—
7	1062	31.3%	—	—	436	27.4%	—	—	143	37.5%	—	—
8	192	5.7%	—	—	84	5.3%	—	—	16	4.2%	—	—
9	119	3.5%	—	—	49	3.1%	—	—	6	1.6%	—	—
10	18	0.5%	—	—	7	0.4%	—	—	2	0.5%	—	—

Table S2: Genome-wide significant SNPs found in our cohort. Meta-analysis is given for the four RPGEH race/ethnicity groups for the fixed effects (FE) and random effects (RE) analysis. Information is given for each SNP's rs number, chromosomal location, chromosomal position, correlation with other previously reported SNPs in the vicinity (using KP non-Hispanic white race/ethnicity individuals), and type of region in the genome the SNP is located in. RAF, risk allele frequency.

Round / Condition	SNP	Risk Allele	Ref. Allele	Group	RAF	OR (95% CI)	P	r^2_{info}
0	rs3731827	T	C	KP NH white	0.584	1.11 (1.06, 1.16)	5.6e-06	1.00
	2p11.2			KP Latino	0.630	1.18 (1.00, 1.39)	0.046	1.00
	85806068			KP Asian	0.604	1.39 (1.14, 1.69)	0.0012	1.00
	$r^2_{\text{rs10187424}} = 0.99$			KP Af-Amer	0.413	1.23 (1.08, 1.41)	0.0025	1.00
	DHS			Kaiser Meta FE	—	1.13 (1.09, 1.18)	9.7e-10	—
				Kaiser Meta RE	—	1.19 (1.08, 1.30)	0.00026	—
0	rs13016083	T	C	KP NH white	0.696	1.14 (1.08, 1.19)	1.6e-07	0.99
	2q22.3			KP Latino	0.722	1.11 (0.93, 1.31)	0.26	0.98
	148570945			KP Asian	0.645	1.13 (0.92, 1.38)	0.24	1.00
	(no prev)			KP Af-Amer	0.880	1.18 (0.95, 1.47)	0.15	0.97
	intergenic			Kaiser Meta FE	—	1.13 (1.09, 1.19)	1.6e-08	—
				Kaiser Meta RE	—	1.13 (1.09, 1.19)	1.6e-08	—
				MEC	0.694	0.99 (0.87, 1.13)	0.79	0.81
				PEGASUS	0.693	1.03 (0.96, 1.11)	0.39	1.00
0	rs4646284							
	(See text)							
0	rs7808935	T	C	KP NH white	0.766	1.17 (1.11, 1.23)	2.4e-09	1.00
	7p15.2			KP Latino	0.606	1.21 (1.03, 1.41)	0.019	1.00
	27977363			KP Asian	0.155	1.00 (0.77, 1.29)	1	1.00
	$r^2_{\text{rs10486567}} = 0.99$			KP Af-Amer	0.700	1.18 (1.02, 1.37)	0.03	1.00
	intron			Kaiser Meta FE	—	1.17 (1.12, 1.22)	2.7e-11	—
				Kaiser Meta RE	—	1.17 (1.12, 1.22)	2.7e-11	—
0	rs142463603	A	C	KP NH white	0.417	1.17 (1.12, 1.22)	7.4e-13	0.99
	8p21.2			KP Latino	0.435	1.19 (1.01, 1.39)	0.035	0.99
	23507262			KP Asian	0.312	1.22 (1.00, 1.49)	0.048	0.99
	$r^2_{\text{rs142463603}} = 0.89$			KP Af-Amer	0.542	1.19 (1.04, 1.37)	0.011	0.98
	intergenic			Kaiser Meta FE	—	1.18 (1.13, 1.22)	4.1e-16	—
				Kaiser Meta RE	—	1.18 (1.13, 1.22)	4.1e-16	—
0	rs11986220	A	T	KP NH white	0.099	1.56 (1.46, 1.67)	2.3e-40	1.00
	8q24.21			KP Latino	0.083	1.09 (0.83, 1.43)	0.52	0.99
	128531689			KP Asian	0.136	1.83 (1.44, 2.33)	9.2e-07	0.99
	(exact)			KP Af-Amer	0.067	1.38 (1.06, 1.80)	0.016	1.00
	DHS			Kaiser Meta FE	—	1.54 (1.45, 1.63)	4.1e-45	—
				Kaiser Meta RE	—	1.47 (1.24, 1.74)	1e-05	—
0	9:33975799	CA	C	KP NH white	0.801	0.86 (0.82, 0.91)	1.1e-07	0.95
	9p13.3			KP Latino	0.874	0.83 (0.66, 1.04)	0.1	0.95
	33975799			KP Asian	0.968	0.59 (0.34, 1.03)	0.062	0.67
	(no prev)			KP Af-Amer	0.906	0.98 (0.76, 1.26)	0.87	0.89
	intron			Kaiser Meta FE	—	0.86 (0.82, 0.91)	2e-08	—
				Kaiser Meta RE	—	0.86 (0.82, 0.91)	2e-08	—
				MEC	0.906	1.05 (0.90, 1.22)	0.54	0.90
				PEGASUS	0.791	0.94 (0.90, 0.98)	0.13	0.99
0	rs10993994	T	C	KP NH white	0.401	1.21 (1.16, 1.26)	2.9e-18	1.00
	10q11.23			KP Latino	0.388	1.31 (1.12, 1.53)	0.00064	1.00
	51549496			KP Asian	0.498	1.18 (0.97, 1.43)	0.092	1.00
	(exact)			KP Af-Amer	0.600	1.08 (0.94, 1.24)	0.29	1.00
	DHS			Kaiser Meta FE	—	1.21 (1.16, 1.25)	6.5e-21	—
				Kaiser Meta RE	—	1.20 (1.13, 1.27)	6.8e-10	—

Round / Condition	SNP	Risk Allele	Ref. Allele	Group	RAF	OR (95% CI)	P	r^2_{info}
0	rs376592364	A	T	KP NH white	0.480	0.82 (0.79, 0.86)	6.5e-19	0.98
	11q13.3			KP Latino	0.607	0.84 (0.72, 0.98)	0.029	0.98
	69011693			KP Asian	0.901	0.88 (0.65, 1.20)	0.41	0.98
	$r^2_{\text{rs10875943}} = 0.99$			KP Af-Amer	0.446	0.91 (0.80, 1.05)	0.2	0.97
	intergenic			Kaiser Meta FE	—	0.83 (0.80, 0.86)	5.9e-20	—
				Kaiser Meta RE	—	0.83 (0.80, 0.86)	5.9e-20	—
0	12:49672714	A	G	KP NH white	0.746	0.90 (0.85, 0.94)	9.1e-06	1.00
	12q13.12			KP Latino	0.702	0.96 (0.81, 1.14)	0.64	1.00
	49672714			KP Asian	0.319	0.68 (0.55, 0.85)	0.0005	1.00
	$r^2_{\text{rs10875943}} = 0.84$			KP Af-Amer	0.472	0.81 (0.71, 0.92)	0.0018	1.00
	DHS			Kaiser Meta FE	—	0.88 (0.84, 0.92)	8e-09	—
				Kaiser Meta RE	—	0.85 (0.76, 0.95)	0.003	—
0	12:53309584	G	A	KP NH white	0.878	0.81 (0.76, 0.87)	1e-10	1.00
	12q13.13			KP Latino	0.916	0.81 (0.63, 1.05)	0.12	1.00
	53309584			KP Asian	0.992	—	—	1.00
	$r^2_{\text{rs902774}} = 0.77$			KP Af-Amer	0.846	0.69 (0.57, 0.82)	2.7e-05	1.00
	DHS			Kaiser Meta FE	—	0.80 (0.75, 0.85)	2e-14	—
				Kaiser Meta RE	—	0.78 (0.70, 0.87)	4.9e-06	—
0	rs34582366	G	T	KP NH white	0.959	1.42 (1.26, 1.59)	1.3e-08	0.98
	14q23.1			KP Latino	0.963	1.32 (0.83, 2.08)	0.24	0.96
	61933357			KP Asian	0.921	1.11 (0.77, 1.60)	0.58	0.98
	$r^2_{\text{rs7153648}}$ =2.1e-06			KP Af-Amer	0.880	1.13 (0.91, 1.41)	0.27	0.92
	DHS			Kaiser Meta FE	—	1.32 (1.20, 1.46)	2.3e-08	—
				Kaiser Meta RE	—	1.28 (1.12, 1.47)	0.00035	—
				MEC	0.865	0.96 (0.85, 1.09)	0.56	0.96
				PEGASUS	0.957	0.90 (0.76, 1.06)	0.19	
0	rs11263763	G	A	KP NH white	0.481	0.81 (0.78, 0.85)	1.8e-21	0.97
	17q12			KP Latino	0.434	0.84 (0.72, 0.99)	0.034	0.99
	36103565			KP Asian	0.293	0.80 (0.65, 1.00)	0.047	0.95
	$r^2_{\text{rs7501939}} = 0.71$			KP Af-Amer	0.399	0.87 (0.75, 1.00)	0.047	0.96
	DHS			Kaiser Meta FE	—	0.82 (0.78, 0.85)	5.3e-24	—
				Kaiser Meta RE	—	0.82 (0.78, 0.85)	5.3e-24	—
0	rs8071558	C	G	KP NH white	0.483	1.14 (1.09, 1.18)	6.8e-09	1.00
	17q24.3			KP Latino	0.543	1.19 (1.02, 1.38)	0.03	1.00
	69107673			KP Asian	0.400	1.03 (0.85, 1.25)	0.75	1.00
	$r^2_{\text{rs1859962}} = 0.99$			KP Af-Amer	0.199	1.21 (1.04, 1.40)	0.013	1.00
	DHS			Kaiser Meta FE	—	1.14 (1.09, 1.18)	7.2e-11	—
				Kaiser Meta RE	—	1.14 (1.09, 1.18)	7.2e-11	—
0	rs2659124							
	(See text)							
0	rs5759167	G	T	KP NH white	0.505	1.14 (1.09, 1.19)	5.2e-09	0.93
	22q13.2			KP Latino	0.575	1.00 (0.85, 1.17)	0.99	1.00
	43500212			KP Asian	0.681	1.15 (0.94, 1.41)	0.19	0.98
	(exact)			KP Af-Amer	0.731	1.14 (0.98, 1.33)	0.091	1.00
	DHS			Kaiser Meta FE	—	1.13 (1.09, 1.18)	1.8e-09	—
				Kaiser Meta RE	—	1.13 (1.09, 1.18)	1.8e-09	—
1	rs7679673	C	A	KP NH white	0.590	1.12 (1.07, 1.17)	4.4e-07	1.00
	4q24			KP Latino	0.498	1.16 (0.99, 1.36)	0.061	0.99
	106061534			KP Asian	0.233	1.12 (0.90, 1.40)	0.32	0.99
	(exact)			KP Af-Amer	0.399	1.09 (0.94, 1.25)	0.24	0.99
	intergenic			Kaiser Meta FE	—	1.12 (1.08, 1.17)	2.6e-08	—
				Kaiser Meta RE	—	1.12 (1.08, 1.17)	2.6e-08	—
1	rs12682374	C	G	KP NH white	0.506	1.26 (1.20, 1.31)	3.2e-24	1.00
	8q24.21			KP Latino	0.566	1.33 (1.13, 1.56)	0.00054	1.00
	128410948			KP Asian	0.408	1.02 (0.84, 1.24)	0.83	1.00
	$r^2_{\text{rs12682374}} = 0.95$			KP Af-Amer	0.834	1.22 (1.00, 1.48)	0.047	0.98
	intergenic			Kaiser Meta FE	—	1.25 (1.20, 1.30)	8.9e-27	—
				Kaiser Meta RE	—	1.23 (1.13, 1.33)	1.8e-06	—

Round / Condition	SNP	Risk Allele	Ref. Allele	Group	RAF	OR (95% CI)	P	r^2_{info}
1	rs71046513	ATT	A	KP NH white	0.817	0.86 (0.81, 0.91)	1.3e-07	0.92
	11q13.3			KP Latino	0.864	0.88 (0.70, 1.11)	0.29	0.95
	69009755			KP Asian	0.969	1.07 (0.53, 2.13)	0.85	0.74
	$r^2_{\text{rs12793759}} = 0.92$			KP Af-Amer	0.789	0.84 (0.71, 1.00)	0.048	0.94
	DHS			Kaiser Meta FE	—	0.86 (0.82, 0.91)	1.2e-08	—
				Kaiser Meta RE	—	0.86 (0.82, 0.91)	1.2e-08	—
2	rs630045	C	G	KP NH white	0.706	1.14 (1.09, 1.20)	7.1e-08	1.00
	6q22.1			KP Latino	0.722	1.01 (0.85, 1.21)	0.88	1.00
	117199790			KP Asian	0.647	1.23 (1.00, 1.51)	0.053	0.99
	$r^2_{rs339331} = 1.00$			KP Af-Amer	0.762	1.07 (0.91, 1.26)	0.42	1.00
	intron			Kaiser Meta FE	—	1.13 (1.08, 1.18)	3e-08	—
				Kaiser Meta RE	—	1.13 (1.08, 1.18)	3e-08	—
2	rs77541621	G	A	KP NH white	0.978	0.49 (0.43, 0.56)	2.1e-26	0.90
	8q24.21			KP Latino	0.987	0.75 (0.39, 1.46)	0.4	0.90
	128077146			KP Asian	0.998	—	—	0.85
	$r^2_{\text{rs6983561}} = 0.47$			KP Af-Amer	0.995	-	-	0.84
	intergenic			Kaiser Meta FE	—	0.50 (0.44, 0.57)	3.1e-26	—
				Kaiser Meta RE	—	0.53 (0.38, 0.75)	0.00024	—
				MEC	0.996	—	—	0.84
				PEGASUS	0.972	0.51 (0.41, 0.63)	8.6e-10	0.84
8q24 loci	rs77541621	G	A	KP NH white	0.978	0.61 (0.50, 0.74)	1.2e-06	0.90
				KP Latino	0.987	1.00 (0.47, 2.15)	0.99	0.90
				KP Asian	0.998	—	—	0.85
				KP Af-Amer	0.995	—	—	0.84
				MEC	0.996	—	—	0.84
				PEGASUS	0.972	0.68 (0.49, 0.94)	0.020	0.84
3	rs72725879	C	T	KP NH white	0.811	0.85 (0.80, 0.90)	7.4e-09	0.98
	8q24.21			KP Latino	0.756	0.83 (0.69, 0.98)	0.032	0.99
	128103969			KP Asian	0.333	0.52 (0.41, 0.65)	2.6e-08	0.99
	$r^2_{\text{rs72725879}} = 0.73$			KP Af-Amer	0.648	0.68 (0.59, 0.79)	2e-07	0.97
	DHS			Kaiser Meta FE	—	0.81 (0.77, 0.85)	1e-17	—
				Kaiser Meta RE	—	0.72 (0.59, 0.87)	0.00067	—
3	12:25430787	C	T	KP NH white	0.966	0.72 (0.64, 0.81)	2.3e-08	0.96
	12p12.1			KP Latino	0.974	0.86 (0.53, 1.39)	0.53	0.97
	25430787			KP Asian	0.998	-	-	0.61
	intergenic			KP Af-Amer	0.990	-	-	0.80
				Kaiser Meta FE	—	0.74 (0.66, 0.82)	4.8e-08	—
				Kaiser Meta RE	—	0.74 (0.65, 0.86)	4.7e-05	—
				MEC	0.991	—	—	0.81
				PEGASUS	0.957	1.10 (0.92, 1.33)	0.27	0.76
4	rs4527381	C	T	KP NH white	0.505	1.12 (1.07, 1.17)	6.9e-07	0.99
	3p11.2			KP Latino	0.595	1.13 (0.96, 1.32)	0.14	0.99
	87221370			KP Asian	0.678	1.10 (0.89, 1.36)	0.37	0.99
	$r^2_{\text{rs17181170}} = 0.79$,			KP Af-Amer	0.756	1.15 (0.97, 1.36)	0.1	0.98
	$r^2_{\text{rs7629490}} = 0.38$,			Kaiser Meta FE	—	1.12 (1.08, 1.17)	4.1e-08	—
	$r^2_{\text{rs17023900}} = 0.064$			Kaiser Meta RE	—	1.12 (1.08, 1.17)	4.1e-08	—
	DHS							
4	rs73351629	C	G	KP NH white	0.670	1.16 (1.11, 1.22)	5.6e-10	0.99
	8q24.21			KP Latino	0.657	1.17 (0.99, 1.38)	0.069	0.99
	128018466			KP Asian	0.807	1.06 (0.82, 1.36)	0.67	0.98
	$r^2_{\text{rs73351629}} = 0.84$			KP Af-Amer	0.748	1.30 (1.10, 1.54)	0.0018	0.98
	intergenic			Kaiser Meta FE	—	1.17 (1.12, 1.22)	2e-12	—
				Kaiser Meta RE	—	1.17 (1.12, 1.22)	2e-12	—
4	rs36004513	G	GA	KP NH white	0.998	-	-	0.54
	2p22.3			KP Latino	0.989	0.36 (0.19, 0.66)	0.0011	0.76
	34429966			KP Asian	0.992	-	-	0.87
	(no prev)			KP Af-Amer	0.874	0.61 (0.49, 0.75)	2.2e-06	0.97
	intergenic			Kaiser Meta FE	—	0.58 (0.47, 0.70)	3.1e-08	—
				Kaiser Meta RE	—	0.50 (0.31, 0.83)	0.0073	—
				MEC[5]	0.868	0.98 (0.87, 1.11)	0.80	0.99
				PEGASUS	—	—	—	—

Table S3: Cis-eQTL expression of the rs4646284 locus. Het, heterogeneity p-value.

			Normal prostate tissue				Tumor prostate tissue						
	Transcription		Mayo[1] (n=471, frozen, RNA-seq)		PHS+HPFS[2] (n=56, paraffin, array)		TCGA[3] (n=128, paraffin, RNA-seq)		PHS+HPFS42 (n=99, paraffin, RNA-seq)		Fixed Effects Meta-analysis of non-Mayo		
Gene	Start	End	Est (95% CI)	P	Est (95% CI)	P	Est (95% CI)	P	Est (95% CI)	P	Est (95% CI)	One-sided P	Het P
IGF2R	160390130	160527583	-0.023 (-0.043, -0.003)	0.024	-0.032 (-0.130, 0.067)	0.53	0.344 (0.017, 0.671)	0.041	-0.052 (-0.151, 0.047)	0.3	-0.025 (-0.093, 0.043)	0.24	0.074
LOC729603	160514113	160517244	-0.044 (-0.079, -0.008)	0.018	-0.132 (-0.229, -0.036)	0.0072	0.084 (-0.248, 0.416)	0.62	-0.014 (-0.107, 0.080)	0.77	-0.065 (-0.131, 0.001)	0.027	0.15
SLC22A1	160542862	160579750	-0.421 (-0.499, -0.343)	1.3e-23	0.007 (-0.110, 0.125)	0.9	-0.292 (-0.620, 0.036)	0.084	-0.097 (-0.198, 0.005)	0.063	-0.065 (-0.140, 0.010)	0.046	0.16
SLC22A2	160637793	160679963	-0.255 (-0.356, -0.154)	1.1e-06	0.002 (-0.106, 0.110)	0.97	-0.192 (-0.522, 0.138)	0.26	-0.020 (-0.106, 0.065)	0.64	-0.019 (-0.084, 0.047)	0.29	0.55
SLC22A3	160769404	160873611	-0.684 (-0.761, -0.607)	3.2e-52	-0.346 (-0.755, 0.062)	0.096	-0.256 (-0.585, 0.073)	0.13	-0.383 (-0.738, -0.029)	0.034	-0.323 (-0.531, -0.115)	0.0012	0.87
LPAL2	160888217	160932156	-0.060 (-0.102, -0.017)	0.006	-0.216 (-0.375, -0.057)	0.0079	-0.454 (-0.776, -0.132)	0.0066	-0.080 (-0.205, 0.044)	0.21	-0.159 (-0.253, -0.065)	0.00045	0.073
LPA	160952514	161087407	0.017 (-0.068, 0.102)	0.69	-0.082 (-0.230, 0.066)	0.28	0.206 (-0.123, 0.535)	0.22	0.016 (-0.092, 0.125)	0.77	-0.003 (-0.088, 0.081)	1.00	0.25

[1]Normal prostate tissue (fresh frozen) of 471 men with Gleason ≤ 7 undergoing radical prostatectomy or cystoprostatectomy from the Mayo Clinic, via RNA-seq.
[2]Normal prostate tissue (formalin-fixed paraffin embedded) of 56 prostate cancer cases from the Physicians Health Study (PHS) and the Health Professionals Follow-up Study (HPFS), via the Affymetrix GeneChip Human Gene 1.0 ST microarray.
[3]Prostate tumor tissue (formalin-fixed paraffin embedded) of 128 men from the The Cancer Genome Atlas (TCGA), via RNA-seq.
[4]Prostate tumor tissue (formalin-fixed praffin embedded) of 99 men from the PHS and HPFS from trans-urethral resection of the prostate (TURP) or radical prostatectomy specimens, via the Affymetrix GeneChip Human Gene 1.0 ST microarray.

Table S4: Results at the 105 loci previously found to be associated with prostate cancer. These risk variants were identified in GWAS of European ancestry, unless otherwise noted, as follows: [a]identified in a multi-ethnic sample, though mainly of European ancestry; [b]identified in an Asian ancestry sample; [c]identified in an African ancestry sample.

			Risk	Ref.	Previous	KP non-Hispanic white			KP Latino				KP Asian				KP African Americon				KP Meta FE		KP Meta RE		Meta FE	
SNP	Region	Pos	Allele	Allele	OR (95% CI)	RAF	OR (95% CI)	P	r^2	RAF	OR (95% CI)	P	r^2	RAF	OR (95% CI)	P	r^2	RAF	OR (95% CI)	P	r^2	OR (95% CI)	P	OR (95% CI)	P	power	Type
rs636291	1p35	10556097	A	G	1.18 (1.12, 1.24)	0.69	1.05 (1.00, 1.10)	0.036	0.98	0.59	0.99 (0.85, 1.16)	0.89	0.99	0.72	0.96 (0.78, 1.18)	0.71	1.00	0.31	0.98 (0.85, 1.14)	0.83	0.97	1.04 (0.99, 1.08)	0.088	1.04 (0.99, 1.08)	0.088	1 / 1	intron
rs17599629	1q21	150658287	G	A	1.08 (1.06, 1.11)	0.21	1.14 (1.08, 1.20)	1e-06	0.97	0.22	0.85 (0.70, 1.04)	0.11	0.97	0.086	0.89 (0.64, 1.25)	0.51	0.98	0.089	1.22 (0.97, 1.54)	0.091	0.96	1.12 (1.06, 1.17)	9e-06	1.04 (0.88, 1.22)	0.68	0.98 / 0.71	DHS
rs1218582	1q21	154834183	G	A	1.06 (1.03, 1.09)	0.46	1.08 (1.03, 1.12)	0.001	0.95	0.59	0.90 (0.77, 1.05)	0.17	0.99	0.89	0.87 (0.64, 1.17)	0.35	0.94	0.65	0.91 (0.79, 1.05)	0.2	0.98	1.05 (1.00, 1.09)	0.031	0.96 (0.85, 1.09)	0.53	0.97 / 0.62	utr
rs4245739	1q32	204518842	A	C	1.10 (1.06, 1.14)	0.73	1.08 (1.03, 1.13)	0.0017	1.00	0.74	1.28 (1.07, 1.54)	0.0079	1.00	0.95	1.45 (0.89, 2.36)	0.13	1.00	0.75	0.98 (0.84, 1.15)	0.83	1.00	1.09 (1.04, 1.14)	0.0003	1.11 (0.99, 1.24)	0.066	1 / 0.98	intergenic
rs1775148	1q32	205757824	C	T	1.06 (1.04, 1.08)	0.36	1.02 (0.97, 1.07)	0.4	0.99	0.48	0.95 (0.82, 1.11)	0.55	0.99	0.44	1.19 (0.98, 1.44)	0.077	0.98	0.6	1.17 (1.02, 1.35)	0.029	0.98	1.03 (0.99, 1.08)	0.11	1.06 (0.97, 1.16)	0.19	0.97 / 0.61	intron
rs11902236	2p25	10117868	A	G	1.07 (1.03, 1.10)	0.29	1.01 (0.96, 1.05)	0.8	1.00	0.25	1.06 (0.89, 1.26)	0.51	1.00	0.17	1.01 (0.78, 1.31)	0.92	0.94	0.57	0.93 (0.81, 1.07)	0.33	0.93	1.00 (0.96, 1.05)	0.91	1.00 (0.96, 1.05)	0.91	0.98 / 0.73	intergenic
rs9287719	2p25	10710730	C	T	1.06 (1.04, 1.08)	0.49	1.06 (1.01, 1.11)	0.0092	1.00	0.47	0.91 (0.78, 1.06)	0.24	1.00	0.39	1.02 (0.83, 1.24)	0.88	1.00	0.3	0.99 (0.85, 1.15)	0.9	1.00	1.04 (1.00, 1.08)	0.038	1.02 (0.96, 1.09)	0.49	0.97 / 0.65	intron
rs13385191	2p24	20888265	G	A	1.07 (1.02, 1.12)	0.24	1.03 (0.98, 1.09)	0.2	1.00	0.27	1.00 (0.84, 1.19)	1	1.00	0.41	1.14 (0.95, 1.37)	0.17	1.00	0.069	0.88 (0.67, 1.17)	0.39	0.99	1.03 (0.99, 1.08)	0.16	1.03 (0.99, 1.08)	0.16	0.97 / 0.66	DHS
rs1465618[a]	2p21	43553949	A	G	1.08 (1.03, 1.12)	0.21	1.04 (0.99, 1.09)	0.15	0.99	0.37	1.10 (0.94, 1.28)	0.24	1.00	0.68	1.05 (0.86, 1.28)	0.64	0.99	0.13	1.16 (0.95, 1.42)	0.14	1.00	1.05 (1.00, 1.10)	0.037	1.05 (1.00, 1.10)	0.037	0.99 / 0.83	intron
rs721048	2p15	63131731	A	G	1.15 (1.10, 1.21)	0.19	1.07 (1.01, 1.13)	0.016	1.00	0.17	1.09 (0.89, 1.33)	0.41	1.00	0.052	1.22 (0.81, 1.83)	0.34	1.00	0.048	1.14 (0.83, 1.56)	0.42	1.00	1.07 (1.02, 1.13)	0.0063	1.07 (1.02, 1.13)	0.0063	1 / 1	intergenic
rs10187424[a]	2p11	85794297	A	G	1.09 (1.06, 1.12)	0.58	1.11 (1.06, 1.16)	5.4e-06	1.00	0.62	1.16 (0.99, 1.36)	0.075	1.00	0.6	1.38 (1.13, 1.68)	0.0015	0.99	0.37	1.20 (1.05, 1.38)	0.0082	1.00	1.13 (1.08, 1.17)	2.7e-09	1.17 (1.08, 1.27)	0.00021	1 / 0.99	DHS
rs12621278[a]	2q31	173311553	A	G	1.33 (1.24, 1.42)	0.94	1.25 (1.13, 1.38)	1.1e-05	1.00	0.93	1.23 (0.89, 1.71)	0.21	1.00	0.75	0.97 (0.78, 1.21)	0.8	1.00	0.98	1.08 (0.63, 1.86)	0.78	1.00	1.19 (1.10, 1.30)	4.7e-05	1.16 (1.01, 1.33)	0.036	1 / 1	coding
rs2292884	2q37	238443226	G	A	1.14 (1.09, 1.19)	0.24	1.07 (1.01, 1.13)	0.024	0.80	0.29	0.96 (0.81, 1.13)	0.62	1.00	0.27	0.94 (0.75, 1.18)	0.61	0.89	0.55	0.96 (0.83, 1.10)	0.54	1.00	1.04 (0.99, 1.09)	0.14	1.02 (0.95, 1.09)	0.56	1 / 1	DHS
rs3771570	2q37	242382864	A	G	1.12 (1.08, 1.17)	0.15	1.08 (1.01, 1.14)	0.017	0.99	0.13	1.16 (0.93, 1.45)	0.2	1.00	0.13	0.94 (0.71, 1.26)	0.7	0.97	0.036	0.74 (0.49, 1.10)	0.13	0.99	1.07 (1.01, 1.13)	0.022	1.04 (0.92, 1.18)	0.54	1 / 0.96	intergenic
rs2660753	3p12	87110674	T	C	1.13 (1.06, 1.20)	0.12	1.11 (1.04, 1.18)	0.0024	1.00	0.17	1.20 (0.99, 1.45)	0.066	1.00	0.24	1.15 (0.93, 1.42)	0.2	1.00	0.47	1.02 (0.89, 1.17)	0.8	0.98	1.10 (1.04, 1.16)	0.0005	1.10 (1.04, 1.16)	0.0005	1 / 0.99	intergenic
rs2055109[b]	3p11	87467332	C	T	1.20 (1.13, 1.29)	0.24	1.04 (0.99, 1.09)	0.13	1.00	0.19	1.00 (0.83, 1.22)	0.97	1.00	0.089	1.05 (0.77, 1.45)	0.74	1.00	0.13	1.06 (0.87, 1.29)	0.58	1.00	1.04 (0.99, 1.09)	0.11	1.04 (0.99, 1.09)	0.11	1 / 1	intergenic
rs7611694	3q13	113275624	A	C	1.10 (1.07, 1.13)	0.6	1.08 (1.03, 1.13)	0.0007	0.99	0.65	0.97 (0.83, 1.14)	0.75	0.99	0.3	1.17 (0.95, 1.43)	0.14	0.96	0.65	1.00 (0.87, 1.15)	0.99	0.98	1.07 (1.03, 1.11)	0.001	1.07 (1.03, 1.11)	0.0016	1 / 1	DHS
rs10934853	3q21	128038373	A	C	1.12 (1.08, 1.16)	0.29	1.07 (1.02, 1.12)	0.0079	0.96	0.38	0.94 (0.81, 1.11)	0.47	1.00	0.47	1.07 (0.88, 1.30)	0.47	0.96	0.69	1.04 (0.90, 1.20)	0.61	0.98	1.06 (1.01, 1.10)	0.013	1.06 (1.01, 1.10)	0.013	1 / 1	DHS
rs6763931[a]	3q23	141102833	T	C	1.04 (1.01, 1.07)	0.44	1.06 (1.01, 1.10)	0.012	1.00	0.41	1.02 (0.88, 1.19)	0.78	1.00	0.32	0.94 (0.77, 1.15)	0.52	1.00	0.79	1.12 (0.95, 1.33)	0.18	1.00	1.05 (1.01, 1.10)	0.01	1.05 (1.01, 1.10)	0.01	0.74 / 0.18	DHS
rs10936632[a]	3q26	170130102	A	C	1.11 (1.08, 1.14)	0.5	1.04 (1.00, 1.09)	0.055	0.96	0.4	1.14 (0.98, 1.34)	0.098	0.97	0.33	0.85 (0.69, 1.04)	0.12	0.97	0.26	1.03 (0.88, 1.21)	0.68	0.96	1.04 (1.00, 1.08)	0.05	1.03 (0.95, 1.12)	0.46	1 / 1	intergenic
rs10009409	4q13	73855253	T	C	1.08 (1.05, 1.10)	0.31	1.04 (0.99, 1.09)	0.13	1.00	0.44	0.97 (0.83, 1.13)	0.67	1.00	0.53	1.23 (1.01, 1.49)	0.04	1.00	0.35	1.06 (0.92, 1.22)	0.43	1.00	1.04 (1.00, 1.08)	0.058	1.05 (0.98, 1.11)	0.14	1 / 0.91	intergenic
rs1894292	4q13	74349158	G	A	1.10 (1.07, 1.13)	0.53	1.04 (1.00, 1.09)	0.052	1.00	0.62	1.00 (0.85, 1.18)	0.97	0.98	0.61	1.12 (0.92, 1.36)	0.26	1.00	0.67	1.06 (0.91, 1.22)	0.46	0.97	1.04 (1.00, 1.09)	0.028	1.04 (1.00, 1.09)	0.028	1 / 1	intron
rs12500426[a]	4q22	95514609	A	C	1.08 (1.05, 1.12)	0.46	1.07 (1.03, 1.12)	0.0012	1.00	0.52	1.22 (1.05, 1.42)	0.0095	1.00	0.54	1.02 (0.85, 1.24)	0.82	1.00	0.4	1.05 (0.91, 1.21)	0.48	1.00	1.08 (1.04, 1.12)	0.00013	1.08 (1.03, 1.13)	0.00038	1 / 0.95	intron
rs17021918[a]	4q22	95562877	C	T	1.11 (1.07, 1.15)	0.65	1.07 (1.02, 1.12)	0.0025	1.00	0.71	1.11 (0.94, 1.32)	0.22	1.00	0.66	1.01 (0.83, 1.23)	0.93	1.00	0.77	1.00 (0.85, 1.18)	1	1.00	1.07 (1.02, 1.11)	0.0022	1.07 (1.02, 1.11)	0.0022	1 / 1	DHS
rs7679673[a]	4q24	106061534	C	A	1.10 (1.06, 1.14)	0.59	1.12 (1.07, 1.17)	9.9e-07	1.00	0.5	1.15 (0.99, 1.35)	0.071	0.99	0.23	1.08 (0.87, 1.35)	0.48	0.99	0.4	1.11 (0.96, 1.27)	0.16	0.99	1.12 (1.07, 1.16)	5.5e-08	1.12 (1.07, 1.16)	5.5e-08	1 / 1	intergenic
rs2242652[a]	5p15	1280028	G	A	1.15 (1.11, 1.19)	0.81	1.05 (0.97, 1.13)	0.2	0.54	0.83	1.14 (0.92, 1.43)	0.23	0.95	0.84	0.99 (0.71, 1.39)	0.96	0.55	0.85	1.09 (0.89, 1.35)	0.4	0.85	1.06 (0.99, 1.13)	0.082	1.06 (0.99, 1.13)	0.082	1 / 0.98	intron
rs12653946	5p15	1895829	T	C	1.10 (1.06, 1.16)	0.44	1.05 (1.00, 1.11)	0.058	0.69	0.48	1.06 (0.91, 1.24)	0.45	1.00	0.36	1.03 (0.81, 1.31)	0.81	0.61	0.4	1.07 (0.92, 1.25)	0.35	0.85	1.05 (1.01, 1.10)	0.026	1.05 (1.01, 1.10)	0.026	1 / 0.97	DHS
rs2121875[a]	5p12	44365545	G	T	1.05 (1.02, 1.08)	0.33	0.98 (0.94, 1.03)	0.38	1.00	0.49	1.16 (0.99, 1.35)	0.059	1.00	0.49	1.06 (0.88, 1.28)	0.57	1.00	0.69	1.12 (0.96, 1.30)	0.15	0.97	1.00 (0.96, 1.05)	0.81	1.06 (0.96, 1.16)	0.25	0.88 / 0.37	DHS
rs6869841	5q35	172939426	A	G	1.07 (1.04, 1.11)	0.21	1.00 (0.94, 1.05)	0.86	1.00	0.18	1.04 (0.85, 1.28)	0.7	0.99	0.17	1.14 (0.89, 1.47)	0.3	0.96	0.36	1.08 (0.94, 1.25)	0.25	0.99	1.01 (0.97, 1.06)	0.61	1.01 (0.97, 1.06)	0.61	0.96 / 0.58	DHS
rs4713266	6p24	11219030	C	T	1.06 (1.04, 1.08)	0.51	1.02 (0.97, 1.06)	0.47	0.99	0.42	0.97 (0.83, 1.13)	0.71	0.99	0.22	1.04 (0.82, 1.31)	0.76	0.99	0.74	1.08 (0.92, 1.27)	0.35	0.92	1.02 (0.98, 1.06)	0.39	1.02 (0.98, 1.06)	0.39	0.97 / 0.65	DHS
rs115457135	6p22	30073776	A	G	1.07 (1.05, 1.10)	0.2	1.10 (1.04, 1.16)	0.0006	0.97	0.23	1.26 (1.06, 1.50)	0.0085	0.99	0.3	0.77 (0.62, 0.95)	0.015	0.99	0.15	0.87 (0.71, 1.06)	0.17	0.96	1.08 (1.02, 1.13)	0.0031	1.00 (0.83, 1.20)	0.96	0.95 / 0.55	intron
rs130067[a]	6p21	31118511	G	T	1.05 (1.02, 1.09)	0.19	1.00 (0.95, 1.06)	0.97	1.00	0.26	0.97 (0.82, 1.16)	0.74	1.00	0.32	1.19 (0.97, 1.45)	0.091	1.00	0.19	0.82 (0.69, 0.98)	0.033	1.00	0.99 (0.95, 1.04)	0.82	0.99 (0.88, 1.10)	0.8	0.75 / 0.19	coding
rs3096702	6p21	32192331	A	G	1.07 (1.04, 1.10)	0.35	1.02 (0.98, 1.07)	0.33	0.99	0.33	1.13 (0.96, 1.32)	0.14	1.00	0.24	0.92 (0.73, 1.16)	0.48	1.00	0.16	0.98 (0.81, 1.17)	0.8	1.00	1.02 (0.98, 1.07)	0.27	1.02 (0.98, 1.07)	0.27	0.99 / 0.78	intergenic
rs115306967	6p21	32400939	G	C	1.06 (1.04, 1.08)	0.7	1.01 (0.97, 1.06)	0.53	1.00	0.76	1.05 (0.87, 1.26)	0.6	1.00	0.78	0.90 (0.72, 1.12)	0.34	1.00	0.79	1.11 (0.94, 1.32)	0.23	1.00	1.02 (0.98, 1.06)	0.42	1.02 (0.98, 1.06)	0.42	0.94 / 0.5	intergenic
rs1983891	6p21	41536427	T	C	1.09 (1.04, 1.15)	0.27	1.10 (1.05, 1.16)	7.3e-05	0.99	0.37	1.11 (0.95, 1.30)	0.17	1.00	0.35	1.02 (0.84, 1.24)	0.81	0.99	0.47	1.06 (0.93, 1.22)	0.39	0.96	1.09 (1.05, 1.14)	2.6e-05	1.09 (1.05, 1.14)	2.6e-05	1 / 0.96	DHS
rs9443189	6q14	76495882	G	A	1.08 (1.05, 1.11)	0.14	0.94 (0.88, 1.00)	0.06	0.99	0.15	0.94 (0.76, 1.17)	0.6	0.99	0.37	1.09 (0.90, 1.33)	0.37	0.99	0.49	0.88 (0.77, 1.01)	0.062	0.96	0.94 (0.89, 0.99)	0.028	0.94 (0.89, 1.00)	0.056	0.97 / 0.65	intron
rs2273669	6q21	109285189	G	A	1.07 (1.03, 1.11)	0.14	1.12 (1.05, 1.18)	0.00034	0.98	0.12	1.07 (0.85, 1.36)	0.55	0.98	0.079	1.07 (0.75, 1.52)	0.7	0.99	0.31	0.95 (0.82, 1.10)	0.49	1.00	1.09 (1.03, 1.15)	0.0018	1.07 (0.98, 1.16)	0.14	0.88 / 0.36	intron
rs339331	6q22	117210052	T	C	1.08 (1.02, 1.13)	0.71	1.13 (1.07, 1.18)	1e-06	1.00	0.72	1.00 (0.85, 1.19)	0.97	1.00	0.64	1.21 (0.99, 1.48)	0.065	1.00	0.77	1.06 (0.90, 1.25)	0.49	1.00	1.12 (1.07, 1.17)	5.5e-07	1.12 (1.07, 1.17)	5.5e-07	1 / 0.87	DHS
rs1933488	6q25	153441079	A	G	1.12 (1.09, 1.16)	0.58	1.04 (1.00, 1.09)	0.067	1.00	0.57	1.08 (0.92, 1.25)	0.36	1.00	0.19	0.84 (0.65, 1.08)	0.17	1.00	0.56	1.13 (0.99, 1.29)	0.08	1.00	1.05 (1.00, 1.09)	0.028	1.05 (0.98, 1.12)	0.2	1 / 1	intron
rs9364554	6q25	160833664	T	C	1.08 (1.03, 1.12)	0.28	1.10 (1.05, 1.15)	6.6e-05	1.00	0.22	1.16 (0.97, 1.39)	0.1	1.00	0.32	1.06 (0.87, 1.29)	0.59	1.00	0.079	1.14 (0.89, 1.47)	0.3	1.00	1.10 (1.06, 1.15)	1.1e-05	1.10 (1.06, 1.15)	1.1e-05	1 / 0.86	DHS
rs12155172	7p15	20994491	A	G	1.11 (1.07, 1.15)	0.22	1.07 (1.02, 1.13)	0.0095	1.00	0.16	1.02 (0.83, 1.25)	0.86	1.00	0.26	0.82 (0.66, 1.03)	0.09	1.00	0.14	0.95 (0.78, 1.16)	0.63	1.00	1.05 (1.00, 1.10)	0.05	0.99 (0.89, 1.11)	0.9	1 / 0.99	DHS
rs10486567	7p15	27976563	G	A	1.19 (1.13, 1.25)	0.77	1.17 (1.11, 1.23)	2.6e-09	1.00	0.61	1.21 (1.03, 1.41)	0.019	1.00	0.16	0.99 (0.77, 1.28)	0.96	1.00	0.7	1.19 (1.02, 1.38)	0.025	1.00	1.17 (1.12, 1.22)	3.2e-11	1.17 (1.12, 1.22)	3.2e-11	1 / 1	DHS
rs56232506	7p12	47437244	A	G	1.06 (1.04, 1.08)	0.47	1.04 (1.00, 1.09)	0.077	0.98	0.49	1.11 (0.95, 1.30)	0.19	0.97	0.36	0.73 (0.59, 0.90)	0.003	0.94	0.14	1.29 (1.06, 1.56)	0.011	0.96	1.04 (1.00, 1.08)	0.054	1.03 (0.87, 1.21)	0.74	0.97 / 0.63	intron
rs6465657	7q21	97816327	C	T	1.11 (1.07, 1.16)	0.45	1.07 (1.02, 1.12)	0.0025	1.00	0.62	1.17 (1.00, 1.37)	0.05	1.00	0.84	1.52 (1.14, 2.02)	0.0044	1.00	0.85	1.00 (0.82, 1.21)	0.98	0.97	1.08 (1.04, 1.12)	0.0002	1.12 (1.00, 1.26)	0.048	1 / 1	DHS
rs29286794[a]	8p21	23438975	T	C	1.05 (1.01, 1.09)	0.46	1.01 (0.97, 1.06)	0.56	1.00	0.36	1.01 (0.86, 1.18)	0.93	1.00	0.18	1.22 (0.97, 1.54)	0.086	0.99	0.29	0.96 (0.83, 1.11)	0.59	0.99	1.01 (0.98, 1.06)	0.48	1.01 (0.97, 1.06)	0.51	0.9 / 0.39	DHS
rs15122684[a]	8p21	23526463	A	G	1.18 (1.14, 1.22)	0.43	1.17 (1.12, 1.22)	1.9e-12	1.00	0.45	1.20 (1.02, 1.40)	0.028	1.00	0.3	1.26 (1.03, 1.54)	0.022	1.00	0.63	1.13 (0.98, 1.30)	0.09	1.00	1.17 (1.12, 1.22)	4.4e-15	1.17 (1.12, 1.22)	4.4e-15	1 / 1	DHS
rs11135910	8p21	25892142	A	G	1.11 (1.07, 1.16)	0.16	1.06 (1.00, 1.12)	0.054	0.99	0.15	0.95 (0.77, 1.18)	0.66	0.99	0.047	0.87 (0.53, 1.42)	0.57	0.99	0.1	1.06 (0.85, 1.33)	0.59	0.98	1.05 (0.99, 1.11)	0.08	1.05 (0.99, 1.11)	0.08	1 / 0.93	DHS
rs12543663	8q24	127924659	C	A	1.08 (1.00, 1.16)	0.3	1.07 (1.02, 1.12)	0.0055	0.98	0.32	1.21 (1.03, 1.42)	0.022	0.97	0.075	1.13 (0.81, 1.59)	0.47	0.96	0.15	0.88 (0.72, 1.07)	0.19	0.97	1.07 (1.02, 1.12)	0.0027	1.07 (0.95, 1.19)	0.27	1 / 0.86	intergenic
rs10086908	8q24	128011937	T	C	1.15 (1.06, 1.24)	0.71	1.17 (1.12, 1.23)	1.5e-10	1.00	0.68	1.13 (0.95, 1.33)	0.16	0.99	0.8	1.02 (0.81, 1.29)	0.87	0.99	0.75	1.28 (1.09, 1.50)	0.0027	0.99	1.17 (1.12, 1.22)	2e-12	1.17 (1.12, 1.22)	2e-12	1 / 1	intergenic
rs1016343	8q24	128093297	T	C	1.25 (1.19, 1.31)	0.21	1.28 (1.21, 1.34)	5.4e-21	1.00	0.16	1.09 (0.89, 1.35)	0.39	1.00	0.3	1.27 (1.04, 1.54)	0.02	1.00	0.22	1.05 (0.89, 1.23)	0.58	0.97	1.25 (1.19, 1.30)	6.3e-21	1.19 (1.07, 1.32)	0.0018	1 / 1	DHS
rs13252298	8q24	128095156	A	G	1.19 (1.11, 1.28)	0.71	1.10 (1.05, 1.15)	9.5e-05	1.00	0.67	1.06 (0.90, 1.25)	0.51	1.00	0.66	1.38 (1.12, 1.69)	0.0023	1.00	0.91	1.23 (0.97, 1.58)	0.093	1.00	1.11 (1.06, 1.16)	2.3e-06	1.15 (1.04, 1.27)	0.0064	1 / 1	intergenic
rs6983561	8q24	128106880	C	A	1.47 (1.21, 1.79)	0.035	1.61 (1.45, 1.78)	4.6e-19	1.00	0.047	1.24 (0.89, 1.73)	0.21	1.00	0.23	1.32 (1.07, 1.63)	0.01	1.00	0.42	1.29 (1.12, 1.48)	0.00028	0.99	1.45 (1.34, 1.56)	5.6e-22	1.39 (1.21, 1.61)	5.4e-06	1 / 1	intergenic
rs116041037[c]	8q24	128131809	A	G	2.45 (1.65, 3.62)	0.0001	—	—	0.97	0.0023	—	—	0.95	0	—	—	0.05	0.043	2.67 (1.96, 3.64)	6e-10	0.95	2.67 (1.96, 3.64)	6e-10	2.67 (1.96, 3.64)	6e-10	1 / 1	intergenic
rs445114	8q24	128323181	T	C	1.14 (1.10, 1.19)	0.63	1.10 (1.05, 1.15)	3.5e-05	1.00	0.62	1.01 (0.86, 1.19)	0.86	1.00	0.53	1.00 (0.83, 1.20)	0.96	1.00	0.36	1.04 (0.91, 1.20)	0.54	1.00	1.08 (1.04, 1.13)	8.8e-05	1.08 (1.04, 1.13)	8.8e-05	1 / 1	DHS
rs16902104	8q24	128340908	T	C	1.21 (1.15, 1.26)	0.14	1.21 (1.14, 1.28)	5.3e-10	1.00	0.13	1.08 (0.87, 1.35)	0.5	0.99	0.23	1.06 (0.86, 1.32)	0.58	1.00	0.083	1.09 (0.86, 1.40)	0.47	0.99	1.18 (1.12, 1.25)	9.5e-10	1.18 (1.12, 1.25)	9.5e-10	1 / 1	DHS
rs16902104	8q24	128340908	—	—	—	1	—	—	0.91	1	—	—	0.99	1	—	—	0.04	0.96	0.87 (0.61, 1.24)	0.43	0.99	0.87 (0.61, 1.24)	0.43	0.87 (0.61, 1.24)	0.43	NA / NA	DHS
rs6983267	8q24	128413305	G	T	1.23 (1.19, 1.28)	0.51	1.25 (1.20, 1.31)	2.6e-24	1.00	0.57	1.31 (1.12, 1.54)	0.00079	1.00	0.41	1.02 (0.85, 1.23)	0.82	1.00	0.87	1.33 (1.07, 1.64)	0.0089	0.98	1.25 (1.20, 1.30)	3.2e-27	1.23 (1.13, 1.35)	1.9e-06	1 / 1	DHS
rs7000448	8q24	128441170	T	C	1.14 (0.93, 1.40)	0.37	1.08 (1.03, 1.13)	0.00053	1.00	0.33	1.14 (0.97, 1.34)	0.11	0.99	0.3	1.05 (0.86, 1.28)	0.66	1.00	0.65	1.15 (1.00, 1.33)	0.05	0.98	1.09 (1.05, 1.13)	3e-05	1.09 (1.05, 1.13)	3e-05	1 / 1	DHS
rs11986220	8q24	128531689	A	T	1.36 (0.99, 1.86)	0.099	1.56 (1.46, 1.67)	2.3e-40	1.00	0.083	1.09 (0.83, 1.43)	0.52	0.99	0.14	1.83 (1.44, 2.33)	9.2e-07	0.99	0.067	1.38 (1.06, 1.80)	0.016	1.00	1.54 (1.45, 1.63)	4.1e-45	1.47 (1.24, 1.74)	1e-05	1 / 1	DHS
rs17694493	9p21	22041998	G	C	1.08 (1.05, 1.11)	0.14	1.12 (1.06, 1.19)	0.00017	0.99	0.092	1.30 (1.02, 1.65)	0.036	0.99	0.016	0.69 (0.30, 1.55)	0.36	0.92	0.11	1.15 (0.92, 1.43)	0.22	0.98	1.13 (1.07, 1.20)	2e-05	1.13 (1.07, 1.20)	2e-05	0.93 / 0.47	DHS

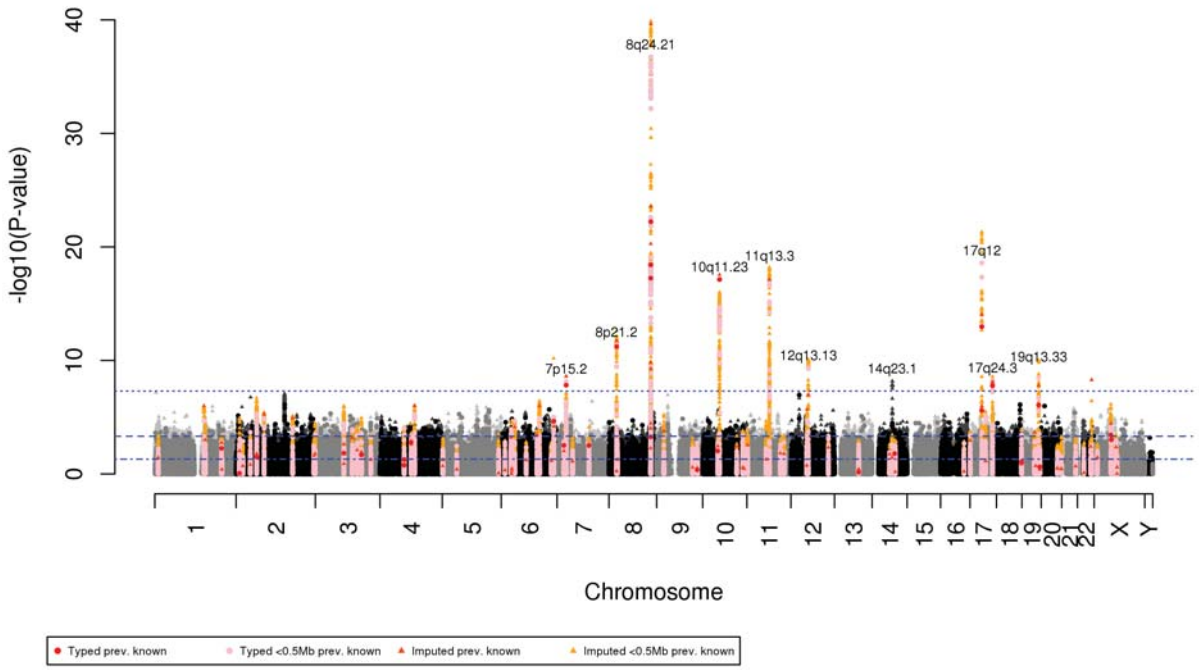
SNP	Region	Pos	Risk Allele	Ref. Allele	Previous OR (95% CI)	KP non-Hispanic white RAF	KP non-Hispanic white OR (95% CI)	KP non-Hispanic white P	KP non-Hispanic white r^2	KP Latino RAF	KP Latino OR (95% CI)	KP Latino P	KP Latino r^2	KP Asian RAF	KP Asian OR (95% CI)	KP Asian P	KP Asian r^2	KP African Americon RAF	KP African Americon OR (95% CI)	KP African Americon P	KP African Americon r^2	KP Meta FE OR (95% CI)	KP Meta FE P	KP Meta RE OR (95% CI)	KP Meta RE P	Meta FE power	Type
rs817826[b]	9q31	110156300	C	T	1.41 (1.29, 1.54)	0.15	0.97 (0.91, 1.03)	0.27	0.97	0.13	0.93 (0.73, 1.17)	0.53	0.96	0.11	1.08 (0.80, 1.45)	0.63	0.99	0.28	1.05 (0.90, 1.23)	0.52	0.94	0.98 (0.93, 1.03)	0.41	0.98 (0.93, 1.03)	0.41	1 / 1	intergenic
rs1571801	9q33	124427373	A	C	1.07 (1.02, 1.12)	0.25	1.03 (0.98, 1.08)	0.31	1.00	0.2	1.14 (0.94, 1.37)	0.19	1.00	0.086	1.27 (0.93, 1.72)	0.13	1.00	0.15	0.91 (0.75, 1.10)	0.34	1.00	1.03 (0.98, 1.08)	0.21	1.04 (0.95, 1.14)	0.4	0.97 / 0.62	intron
rs76934034	10q11	46082985	T	C	1.13 (1.09, 1.17)	0.92	1.13 (1.04, 1.22)	0.0036	0.99	0.92	0.95 (0.71, 1.26)	0.7	0.99	0.99	—	—	0.84	0.98	0.84 (0.52, 1.35)	0.46	0.77	1.10 (1.02, 1.19)	0.011	1.06 (0.92, 1.22)	0.4	0.98 / 0.73	intron
rs10993994	10q11	51549496	T	C	1.23 (1.18, 1.28)	0.4	1.21 (1.16, 1.26)	2.9e-18	1.00	0.39	1.31 (1.12, 1.53)	0.00064	1.00	0.5	1.18 (0.97, 1.43)	0.092	1.00	0.6	1.08 (0.94, 1.24)	0.29	1.00	1.21 (1.16, 1.25)	6.5e-21	1.20 (1.13, 1.27)	6.8e-10	1 / 1	DHS
rs3850699	10q24	104414221	A	G	1.10 (1.07, 1.13)	0.7	1.07 (1.02, 1.12)	0.0039	0.99	0.75	1.14 (0.95, 1.37)	0.15	0.99	0.81	0.96 (0.76, 1.22)	0.74	0.98	0.63	1.04 (0.90, 1.20)	0.57	0.98	1.07 (1.02, 1.12)	0.0022	1.07 (1.02, 1.12)	0.0022	1 / 0.99	intron
rs2252004[b]	10q26	122844709	G	T	1.16 (1.10, 1.22)	0.91	1.04 (0.97, 1.12)	0.28	0.99	0.75	1.10 (0.92, 1.31)	0.31	0.99	0.71	1.08 (0.88, 1.33)	0.45	1.00	0.54	1.10 (0.96, 1.26)	0.17	0.97	1.06 (1.00, 1.13)	0.044	1.06 (1.00, 1.13)	0.044	1 / 1	intergenic
rs4962416	10q26	126696872	C	T	1.09 (1.05, 1.14)	0.28	1.02 (0.98, 1.08)	0.33	0.90	0.24	1.11 (0.93, 1.33)	0.25	1.00	0.029	1.07 (0.57, 2.00)	0.83	0.79	0.18	1.00 (0.84, 1.19)	0.99	1.00	1.03 (0.98, 1.08)	0.23	1.03 (0.98, 1.08)	0.23	1 / 0.9	intron
rs7127900[a]	11p15	2233574	A	G	1.22 (1.17, 1.27)	0.2	1.10 (1.03, 1.17)	0.0029	0.70	0.27	1.07 (0.90, 1.27)	0.43	1.00	0.12	0.97 (0.69, 1.38)	0.88	0.68	0.36	1.07 (0.93, 1.24)	0.34	0.99	1.09 (1.03, 1.15)	0.0017	1.09 (1.03, 1.15)	0.0017	1 / 1	intergenic
rs1938781[b]	11q12	58915110	C	T	1.16 (1.11, 1.21)	0.21	1.05 (1.00, 1.11)	0.052	1.00	0.23	1.18 (0.99, 1.40)	0.073	1.00	0.26	1.00 (0.81, 1.24)	0.96	1.00	0.32	0.98 (0.85, 1.14)	0.83	0.99	1.05 (1.00, 1.10)	0.033	1.05 (1.00, 1.10)	0.033	1 / 1	intron
rs10896449	11q13	68994667	G	A	1.19 (1.15, 1.23)	0.52	1.21 (1.16, 1.26)	7.5e-18	1.00	0.4	1.19 (1.02, 1.38)	0.03	1.00	0.091	1.07 (0.78, 1.46)	0.69	1.00	0.69	1.11 (0.96, 1.29)	0.15	1.00	1.20 (1.15, 1.24)	4.7e-19	1.20 (1.15, 1.24)	4.7e-19	1 / 1	intergenic
rs11568818	11q22	102401661	A	G	1.10 (1.06, 1.14)	0.55	1.05 (1.01, 1.10)	0.015	1.00	0.64	1.19 (1.01, 1.40)	0.033	1.00	0.9	1.23 (0.87, 1.75)	0.24	0.95	0.55	1.03 (0.90, 1.18)	0.65	1.00	1.06 (1.02, 1.11)	0.0026	1.06 (1.02, 1.11)	0.0026	1 / 1	DHS
rs11214775[a]	11q23	113807181	G	A	1.07 (1.04, 1.09)	0.7	1.06 (1.01, 1.11)	0.017	1.00	0.76	1.13 (0.94, 1.36)	0.18	0.99	0.75	0.94 (0.76, 1.16)	0.55	1.00	0.71	1.06 (0.91, 1.22)	0.46	0.99	1.06 (1.01, 1.10)	0.0099	1.06 (1.01, 1.10)	0.0099	0.98 / 0.73	intron
rs80130819	12q13	48419618	A	C	1.14 (1.09, 1.18)	0.92	1.06 (0.98, 1.14)	0.18	0.98	0.93	0.90 (0.66, 1.23)	0.51	0.97	0.99	—	—	0.97	0.98	0.96 (0.61, 1.52)	0.86	0.93	1.04 (0.97, 1.12)	0.28	1.04 (0.97, 1.12)	0.28	0.99 / 0.82	intergenic
rs10875943	12q13	49676010	C	T	1.07 (1.04, 1.10)	0.29	1.12 (1.07, 1.18)	2.1e-06	0.95	0.33	1.03 (0.88, 1.21)	0.72	1.00	0.82	1.44 (1.10, 1.89)	0.0085	1.00	0.61	1.15 (1.00, 1.32)	0.043	1.00	1.12 (1.08, 1.17)	6.6e-08	1.13 (1.05, 1.22)	0.0013	0.99 / 0.77	intergenic
rs902774	12q13	53273904	A	G	1.17 (1.11, 1.24)	0.15	1.17 (1.11, 1.24)	1e-07	0.99	0.13	1.09 (0.87, 1.36)	0.45	0.99	0.027	1.18 (0.68, 2.02)	0.56	1.00	0.079	1.07 (0.84, 1.37)	0.58	1.00	1.16 (1.10, 1.23)	8.6e-08	1.16 (1.10, 1.23)	8.6e-08	1 / 1	DHS
rs1270884	12q24	114685571	A	G	1.07 (1.04, 1.10)	0.48	1.06 (1.02, 1.11)	0.0048	0.99	0.38	1.12 (0.96, 1.32)	0.15	0.99	0.28	0.93 (0.75, 1.15)	0.49	0.97	0.21	1.22 (1.03, 1.44)	0.018	0.97	1.07 (1.03, 1.11)	0.00067	1.08 (1.00, 1.17)	0.044	0.99 / 0.84	intergenic
rs9600079	13q22	73728139	T	G	1.01 (0.97, 1.06)	0.45	1.02 (0.98, 1.06)	0.37	1.00	0.41	1.09 (0.93, 1.27)	0.3	1.00	0.46	1.09 (0.90, 1.32)	0.37	1.00	0.51	0.98 (0.85, 1.13)	0.79	0.97	1.02 (0.98, 1.06)	0.24	1.02 (0.98, 1.06)	0.24	0.1 / 0.0023	intergenic
rs8008270	14q22	53372330	G	A	1.12 (1.08, 1.17)	0.81	1.07 (1.01, 1.13)	0.018	1.00	0.86	1.19 (0.94, 1.51)	0.14	1.00	0.99	—	—	0.98	0.74	1.09 (0.93, 1.28)	0.28	0.97	1.08 (1.02, 1.13)	0.0045	1.08 (1.02, 1.13)	0.0045	1 / 0.99	intron
rs7153648	14q23	61122526	C	G	1.11 (1.07, 1.14)	0.091	1.08 (1.01, 1.17)	0.036	0.95	0.11	1.11 (0.87, 1.43)	0.39	0.93	0.2	1.12 (0.88, 1.41)	0.36	0.97	0.33	0.97 (0.84, 1.12)	0.65	0.96	1.07 (1.00, 1.13)	0.046	1.07 (1.00, 1.13)	0.046	0.99 / 0.79	intergenic
rs7141529	14q24	69126744	G	A	1.09 (1.06, 1.12)	0.51	1.05 (1.01, 1.10)	0.017	1.00	0.55	0.98 (0.84, 1.14)	0.78	1.00	0.77	1.15 (0.91, 1.45)	0.24	1.00	0.53	1.01 (0.88, 1.15)	0.93	1.00	1.05 (1.01, 1.09)	0.02	1.05 (1.01, 1.09)	0.02	1 / 0.99	intergenic
rs8014671	14q24	71092256	G	A	1.06 (1.04, 1.08)	0.58	1.01 (0.97, 1.05)	0.66	0.99	0.57	1.02 (0.87, 1.19)	0.84	0.99	0.37	1.05 (0.86, 1.28)	0.63	0.97	0.47	1.00 (0.87, 1.14)	0.95	0.97	1.01 (0.97, 1.05)	0.6	1.01 (0.97, 1.05)	0.6	0.97 / 0.64	intergenic
rs12051443	16q22	71691329	A	G	1.06 (1.04, 1.08)	0.33	1.01 (0.97, 1.06)	0.62	1.00	0.44	1.04 (0.89, 1.21)	0.63	1.00	0.69	1.05 (0.86, 1.29)	0.63	1.00	0.27	1.06 (0.91, 1.23)	0.46	0.99	1.02 (0.98, 1.06)	0.38	1.02 (0.98, 1.06)	0.38	0.96 / 0.6	intron
rs684232	17p13	618965	G	A	1.10 (1.07, 1.14)	0.35	1.08 (1.03, 1.13)	0.0012	0.98	0.41	1.04 (0.89, 1.21)	0.64	0.98	0.59	0.96 (0.79, 1.16)	0.67	0.99	0.64	1.01 (0.87, 1.16)	0.93	1.00	1.06 (1.02, 1.11)	0.0028	1.06 (1.02, 1.11)	0.0028	1 / 1	DHS
rs11649743	17q12	36074979	G	A	1.15 (1.09, 1.21)	0.81	1.15 (1.09, 1.22)	1e-06	0.99	0.83	1.10 (0.89, 1.36)	0.37	0.99	0.67	1.18 (0.96, 1.44)	0.12	0.99	0.91	0.95 (0.73, 1.24)	0.69	0.82	1.14 (1.08, 1.20)	5.9e-07	1.14 (1.08, 1.20)	5.9e-07	1 / 1	DHS
rs7501939	17q12	36101156	C	T	1.22 (1.17, 1.27)	0.6	1.19 (1.14, 1.24)	9.9e-15	1.00	0.64	1.18 (1.00, 1.38)	0.05	1.00	0.72	1.13 (0.91, 1.39)	0.27	1.00	0.5	1.04 (0.91, 1.19)	0.55	1.00	1.17 (1.13, 1.22)	4.2e-15	1.16 (1.09, 1.23)	5.8e-07	1 / 1	DHS
rs11650494	17q21	47345186	A	G	1.15 (1.09, 1.22)	0.086	1.07 (0.99, 1.16)	0.072	0.99	0.068	0.91 (0.66, 1.24)	0.54	0.98	0.011	0.74 (0.27, 2.09)	0.58	0.98	0.24	0.93 (0.79, 1.09)	0.37	0.97	1.04 (0.97, 1.11)	0.29	1.02 (0.92, 1.12)	0.75	1 / 0.96	intergenic
rs7210100[c]	17q21	47436749	A	G	1.51 (1.35, 1.69)	0.0001	—	—	0.94	0.0034	—	—	1.00	0.0002	—	—	0.80	0.056	1.06 (0.79, 1.41)	0.71	1.00	1.06 (0.79, 1.41)	0.71	1.06 (0.79, 1.41)	0.71	0.87 / 0.34	intron
rs1859962	17q24	69108753	G	T	1.19 (1.14, 1.24)	0.48	1.13 (1.09, 1.18)	7.7e-09	1.00	0.55	1.16 (0.99, 1.36)	0.06	1.00	0.4	1.03 (0.85, 1.24)	0.79	1.00	0.32	1.08 (0.93, 1.24)	0.31	0.97	1.13 (1.08, 1.17)	1.6e-09	1.13 (1.08, 1.17)	1.6e-09	1 / 1	DHS
rs7241993	18q23	76773973	G	A	1.09 (1.05, 1.12)	0.69	1.04 (0.99, 1.09)	0.14	1.00	0.7	1.13 (0.95, 1.35)	0.15	1.00	0.61	0.93 (0.77, 1.13)	0.46	1.00	0.47	1.06 (0.92, 1.21)	0.43	1.00	1.04 (1.00, 1.08)	0.079	1.04 (1.00, 1.08)	0.079	1 / 0.97	intergenic
rs8102476	19q13	38735613	C	T	1.12 (1.08, 1.15)	0.56	1.09 (1.04, 1.14)	0.0002	0.98	0.53	1.02 (0.88, 1.19)	0.79	1.00	0.41	1.26 (1.04, 1.53)	0.02	0.98	0.73	1.12 (0.96, 1.31)	0.14	1.00	1.09 (1.05, 1.14)	1.8e-05	1.09 (1.05, 1.14)	1.8e-05	1 / 1	intergenic
rs11672691	19q13	41985587	G	A	1.08 (1.05, 1.12)	0.75	1.03 (0.98, 1.09)	0.2	0.95	0.76	1.01 (0.85, 1.22)	0.88	0.96	0.59	1.11 (0.91, 1.34)	0.3	0.99	0.26	1.04 (0.89, 1.21)	0.62	0.93	1.04 (0.99, 1.09)	0.12	1.04 (0.99, 1.09)	0.12	0.99 / 0.85	DHS
rs2735839	19q13	51364623	G	A	1.15 (1.08, 1.22)	0.85	1.20 (1.13, 1.28)	1.6e-08	1.00	0.79	1.21 (1.00, 1.47)	0.052	1.00	0.58	1.15 (0.95, 1.40)	0.15	1.00	0.7	1.02 (0.88, 1.18)	0.8	1.00	1.17 (1.11, 1.24)	5.7e-09	1.16 (1.07, 1.25)	0.00012	1 / 1	DHS
rs103294[b]	19q13	54797848	C	T	1.28 (1.21, 1.36)	0.8	0.98 (0.93, 1.03)	0.39	1.00	0.75	1.09 (0.91, 1.30)	0.35	1.00	0.55	0.98 (0.82, 1.17)	0.83	1.00	0.9	0.97 (0.78, 1.21)	0.78	1.00	0.98 (0.94, 1.03)	0.53	0.98 (0.94, 1.03)	0.53	1 / 1	intergenic
rs12480328	20q13	49527922	T	C	1.13 (1.10, 1.17)	0.93	1.04 (0.96, 1.14)	0.31	1.00	0.92	0.84 (0.64, 1.10)	0.19	0.99	0.91	0.84 (0.61, 1.15)	0.27	1.00	0.88	1.08 (0.87, 1.34)	0.47	0.98	1.02 (0.95, 1.10)	0.6	1.00 (0.89, 1.11)	0.95	0.99 / 0.77	DHS
rs2427345	20q13	61015611	G	A	1.06 (1.03, 1.10)	0.61	1.03 (0.97, 1.10)	0.36	0.48	0.61	1.05 (0.90, 1.23)	0.55	1.00	0.75	0.75 (0.55, 1.03)	0.072	0.46	0.5	1.04 (0.91, 1.20)	0.56	0.95	1.02 (0.97, 1.08)	0.37	1.02 (0.95, 1.10)	0.63	0.79 / 0.24	intergenic
rs6062509	20q13	62362563	A	C	1.12 (1.09, 1.16)	0.69	1.02 (0.98, 1.07)	0.36	0.99	0.7	1.01 (0.85, 1.19)	0.94	1.00	0.41	0.98 (0.81, 1.18)	0.81	0.99	0.88	1.08 (0.87, 1.34)	0.46	0.99	1.02 (0.98, 1.07)	0.34	1.02 (0.98, 1.07)	0.34	1 / 1	DHS
rs1041449	21q22	42901421	G	A	1.06 (1.04, 1.08)	0.42	1.03 (0.98, 1.08)	0.21	0.91	0.42	1.04 (0.89, 1.23)	0.62	0.95	0.22	0.68 (0.52, 0.89)	0.0053	0.86	0.39	1.03 (0.89, 1.19)	0.69	0.90	1.02 (0.98, 1.06)	0.34	0.98 (0.87, 1.10)	0.72	0.95 / 0.56	intergenic
rs2238776	22q11	19757892	G	A	1.08 (1.05, 1.11)	0.8	1.01 (0.95, 1.08)	0.79	0.68	0.74	1.00 (0.84, 1.19)	0.99	1.00	0.62	1.11 (0.88, 1.39)	0.38	0.69	0.94	0.98 (0.74, 1.30)	0.9	1.00	1.01 (0.96, 1.07)	0.66	1.01 (0.96, 1.07)	0.66	0.94 / 0.52	intron
rs2238776	22q11	19757892	—	—	—	1	—	—	0.34	1	—	—	0.75	1	—	—	0.09	0.99	—	—	0.88	—	—	—	—	NA / NA	intron
rs9623117	22q13	40452119	C	T	1.18 (1.11, 1.26)	0.23	1.08 (1.02, 1.13)	0.0038	0.98	0.19	0.99 (0.82, 1.20)	0.93	1.00	0.042	1.21 (0.78, 1.90)	0.4	0.96	0.72	0.94 (0.81, 1.09)	0.42	0.99	1.06 (1.01, 1.11)	0.014	1.04 (0.97, 1.12)	0.26	1 / 1	intron
rs5759167[a]	22q13	43500212	G	T	1.16 (1.13, 1.20)	0.51	1.14 (1.09, 1.19)	5.2e-09	0.93	0.57	1.00 (0.85, 1.17)	0.99	1.00	0.68	1.15 (0.94, 1.41)	0.19	0.98	0.73	1.14 (0.98, 1.33)	0.091	1.00	1.13 (1.09, 1.18)	1.8e-09	1.13 (1.09, 1.18)	1.8e-09	1 / 1	DHS
rs2405942	23p22	9814135	A	G	1.14 (1.08, 1.19)	0.79	1.04 (1.00, 1.08)	0.037	0.95	0.82	1.11 (0.95, 1.29)	0.17	0.93	0.89	0.96 (0.78, 1.19)	0.73	0.97	0.75	1.02 (0.91, 1.15)	0.7	0.82	1.04 (1.01, 1.08)	0.023	1.04 (1.01, 1.08)	0.023	1 / 1	—
rs5945572	23p11	51229683	A	G	1.23 (1.16, 1.30)	0.35	1.07 (1.04, 1.10)	3.6e-05	1.00	0.24	—	—	1.00	0.079	—	—	1.00	0.28	1.08 (0.97, 1.20)	0.16	1.00	1.07 (1.04, 1.10)	1.3e-05	1.07 (1.04, 1.10)	1.3e-05	1 / 1	—
rs2807031	23p11	52896949	C	T	1.07 (1.05, 1.09)	0.18	1.07 (1.03, 1.11)	0.00069	1.00	0.13	0.92 (0.78, 1.08)	0.31	1.00	0.037	1.18 (0.86, 1.62)	0.31	1.00	0.22	1.05 (0.93, 1.17)	0.42	1.00	1.06 (1.02, 1.10)	0.0011	1.05 (1.00, 1.11)	0.057	0.92 / 0.46	—
rs5919432[a]	23q12	67021550	A	G	1.06 (1.01, 1.11)	0.8	1.06 (1.02, 1.10)	0.0043	1.00	0.84	0.99 (0.86, 1.15)	0.94	1.00	0.99	1.79 (0.66, 4.85)	0.25	1.00	0.43	1.11 (1.01, 1.23)	0.031	0.96	1.06 (1.03, 1.10)	0.00075	1.06 (1.03, 1.10)	0.00075	0.88 / 0.35	—
rs6625711	23q13	70139850	A	T	1.04 (1.03, 1.06)	0.45	1.00 (0.97, 1.03)	0.95	0.69	0.57	1.05 (0.94, 1.18)	0.4	0.83	0.47	1.07 (0.93, 1.24)	0.33	0.79	0.77	1.02 (0.90, 1.16)	0.78	0.68	1.01 (0.98, 1.04)	0.58	1.01 (0.98, 1.04)	0.58	0.6 / 0.098	—
rs4844289	23q13	70407983	G	A	1.04 (1.03, 1.06)	0.4	1.02 (0.99, 1.05)	0.25	0.97	0.52	0.99 (0.89, 1.11)	0.87	0.99	0.74	0.89 (0.76, 1.05)	0.17	0.64	0.68	1.02 (0.92, 1.13)	0.71	0.93	1.01 (0.98, 1.04)	0.39	1.01 (0.98, 1.04)	0.39	0.72 / 0.17	—

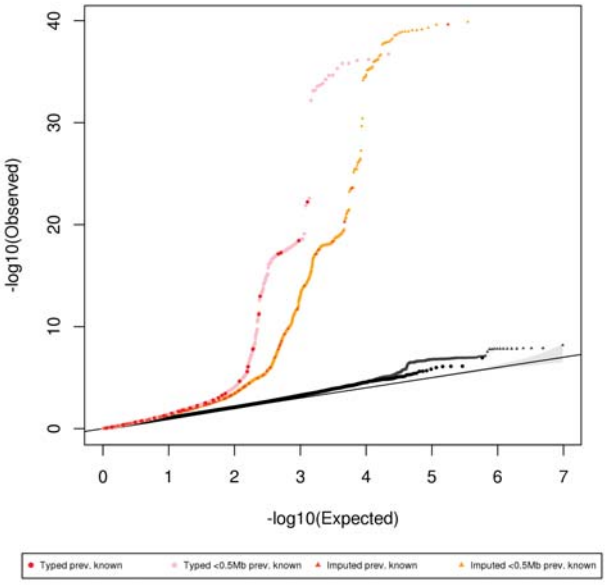
Table S5: Risk score of and variance explained by the 105 previously reported hits. PCs, top 10 principal components (for race/ethnicity group) for ancestry; *The KP Asian risk score excludes rs7210100 and rs6983561, as they have $r^2 = 0.87$ and $r^2 = 0.44$, respectively, to other previously reported SNPs in the risk score (there were no other SNPs with pairwise $r^2 > 0.3$ in any of the race/ethnicity groups).

	KP NH white	KP Latino	KP Asian*	KP Af-Amer
Risk score p	$2.0\text{x}10^{-211}$	$3.5\text{x}10^{-16}$	$1.0\text{x}10^{-8}$	$1.10\text{x}10^{-15}$
r^2 age, BMI	0.073	0.122	0.101	0.051
r^2 age, BMI, risk score	0.123	0.156	0.121	0.099
r^2 age, BMI, PCs	0.076	0.147	0.112	0.060
r^2 age, BMI, PCs, risk score	0.127	0.183	0.138	0.104

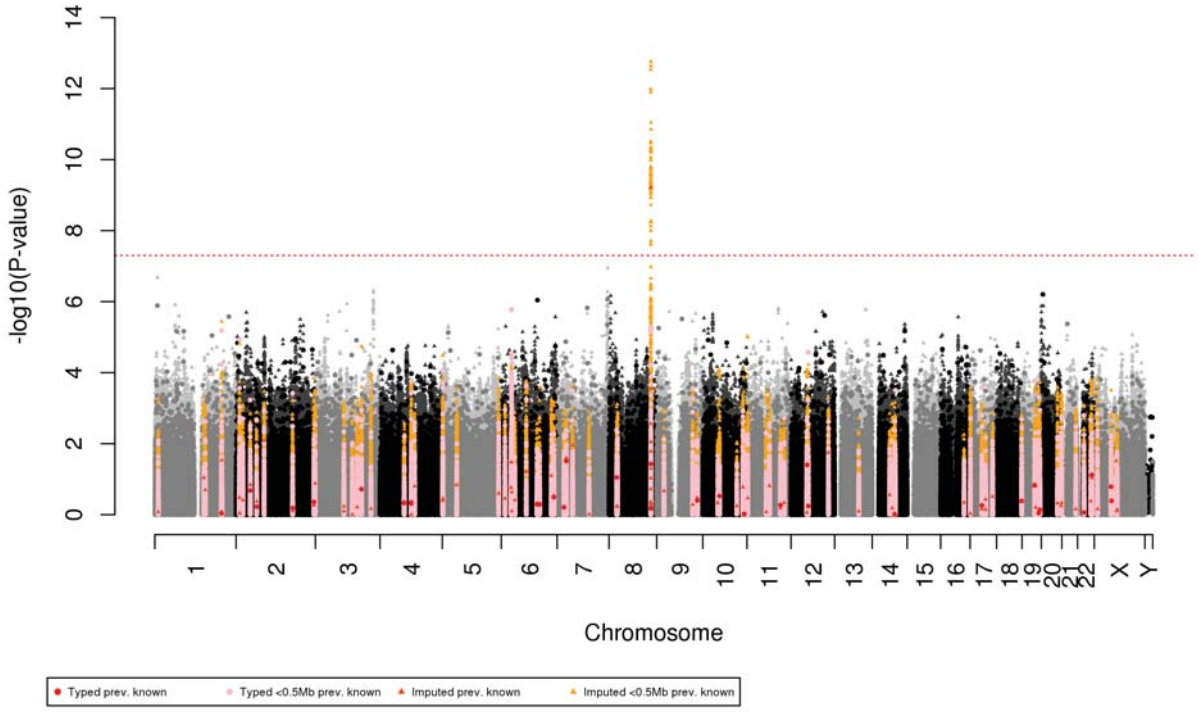
Figure S1: Manhattan plots and Q-Q plots of each race/ethnicity, and of the meta-analysis, followed by conditional analysis plots. In the race/ethnicity-specific plots, the triangles are imputed SNPs, whereas the circles are based on the genotyped SNPs; in the meta-analysis all points are imputed. The color coding of the plot is described in the legend, where "<0.5Mb prev. known" indicates that a SNP was previously identified to be a prostate cancer risk variant, and that the current SNP is within 0.5 megabases of that SNP (a 1 megabase window).

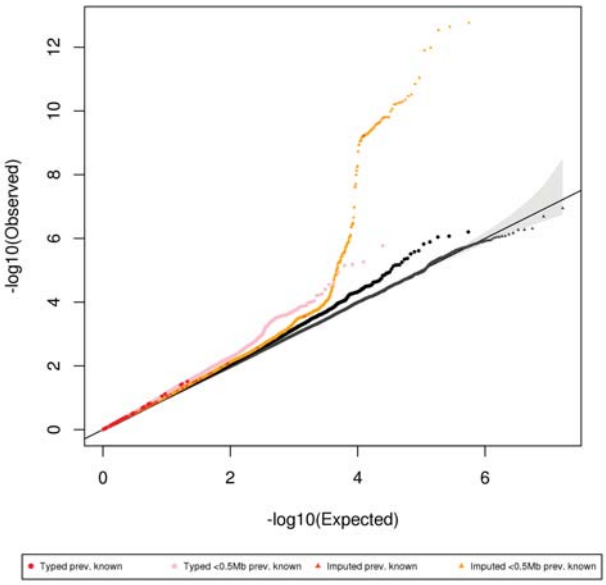
(S1.1) Round 0 of non-Hispanic white race/ethnicity. $\lambda_{\text{typed}} = 1.063$, $\lambda_{\text{imputed}} = 1.058$



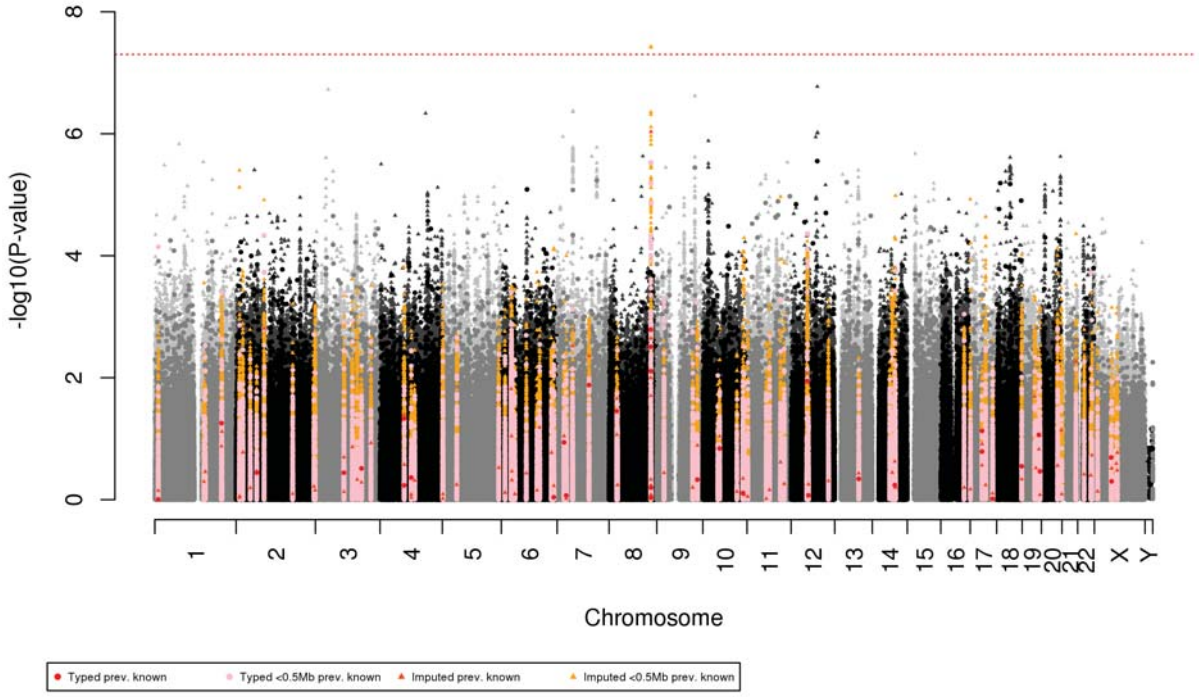


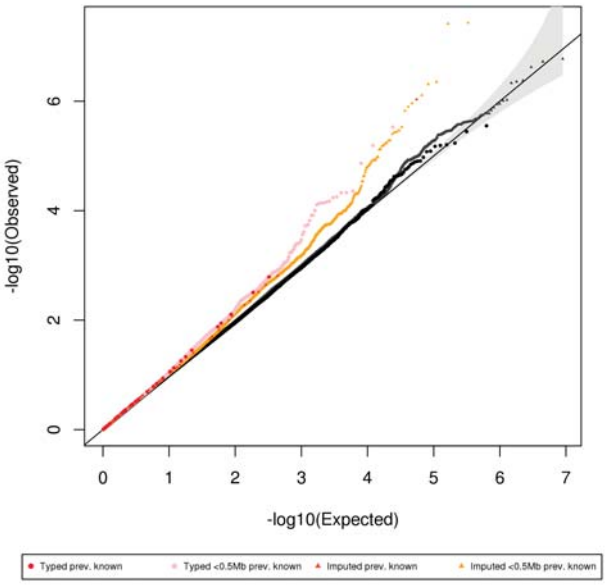
(S1.2) Round 0 of African American race/ethnicity. $\lambda_{\text{typed}} = 1.040$, $\lambda_{\text{imputed}} = 1.009$



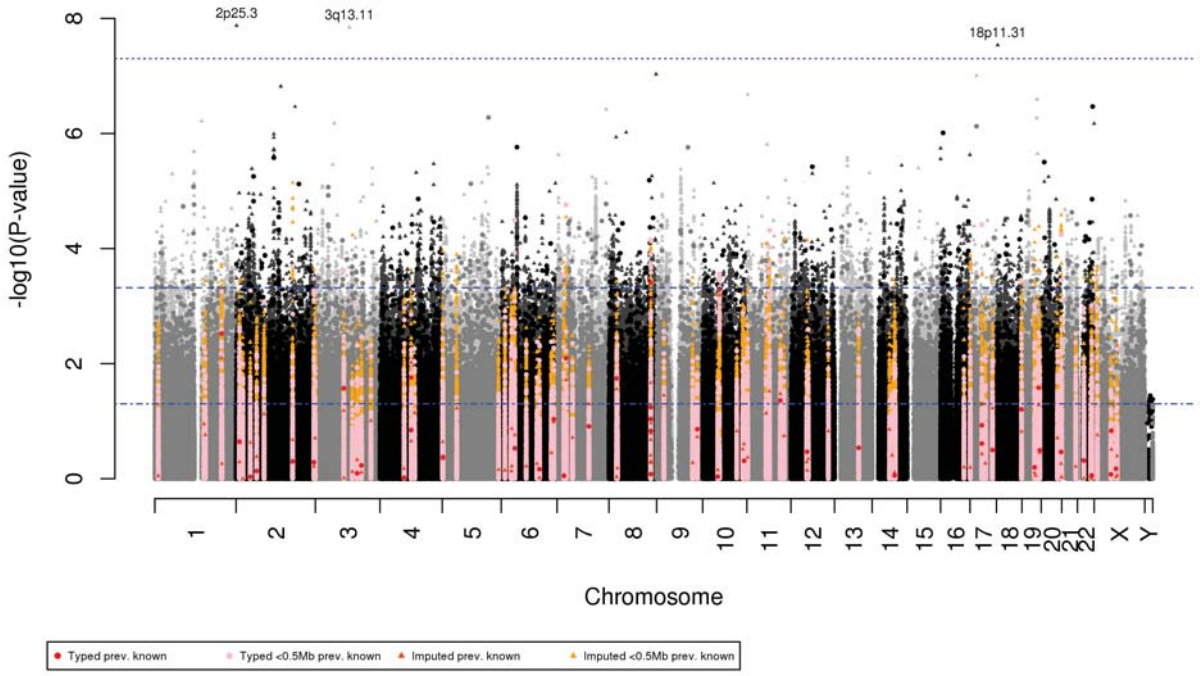


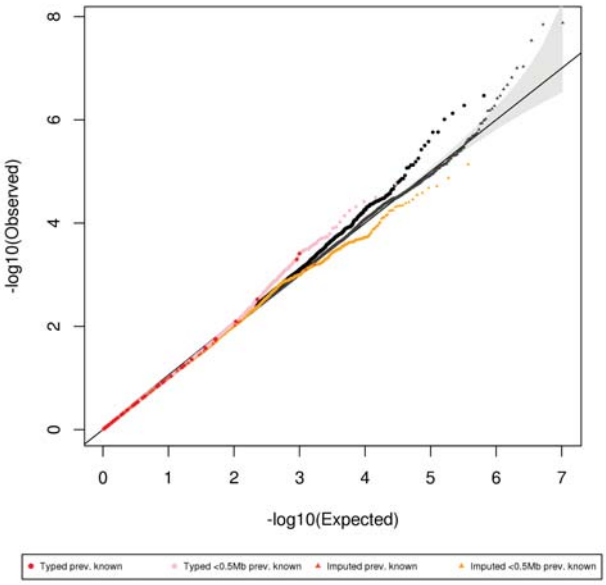
(S1.3) Round 0 of Asian race/ethnicity. $\lambda_{\text{typed}} = 1.025$, $\lambda_{\text{imputed}} = 1.015$



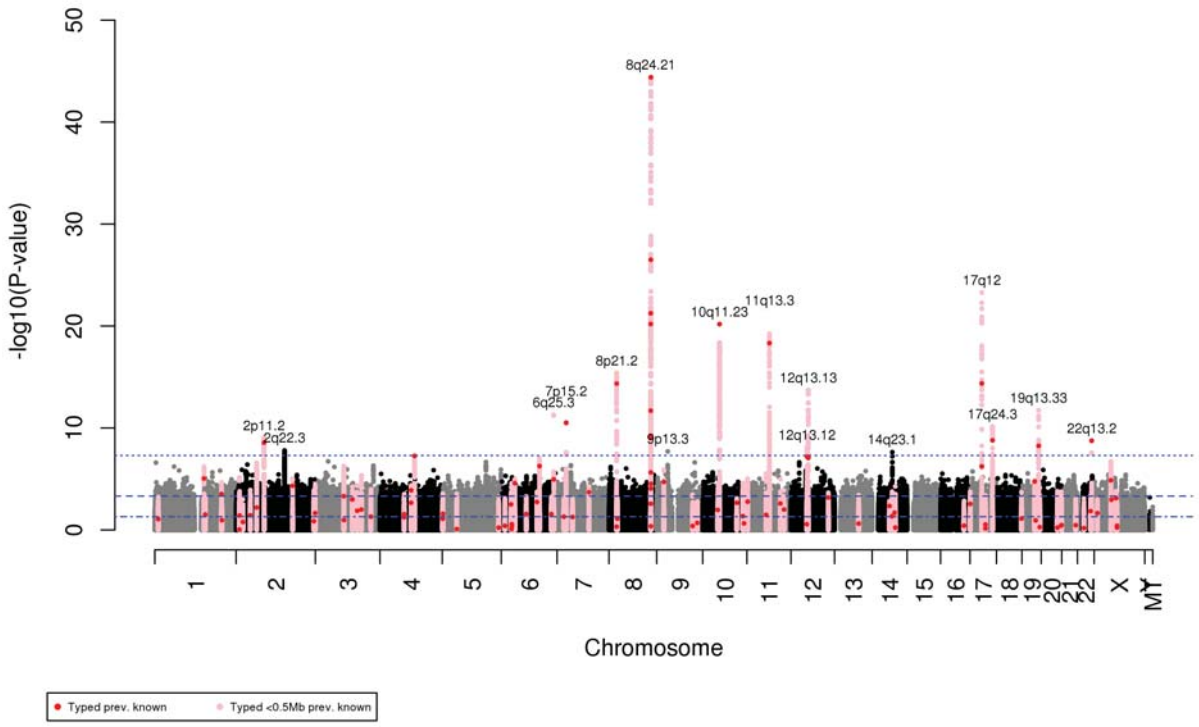


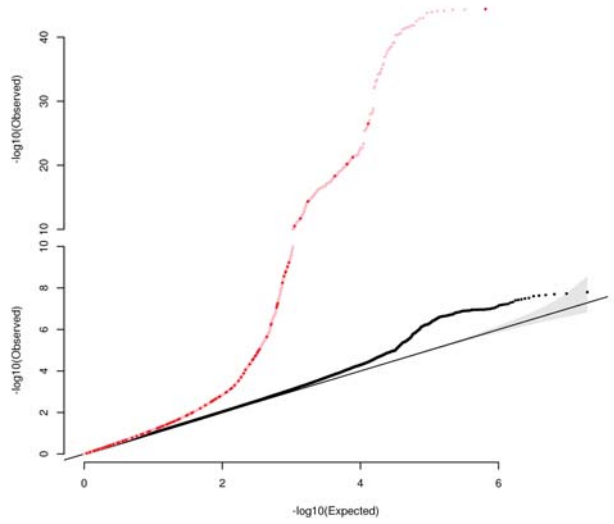
(S1.4) Round 0 of Latino race/ethnicity. $\lambda_{\text{typed}} = 1.035$, $\lambda_{\text{imputed}} = 1.017$



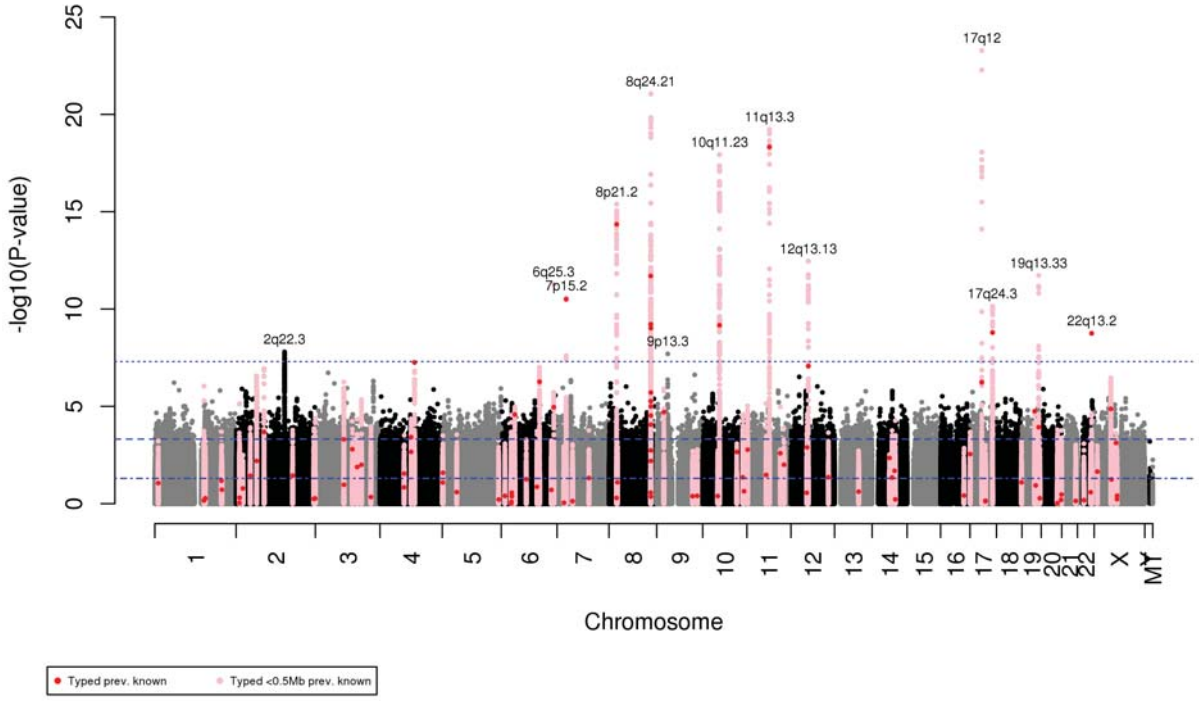


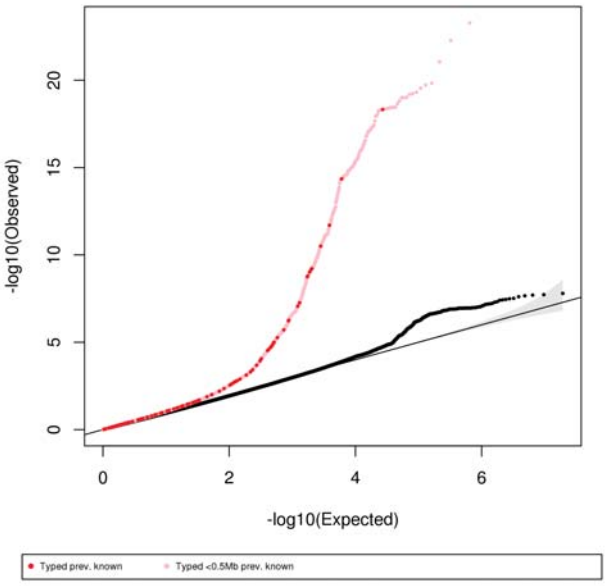
(S1.5) Round 0 of Meta-analysis fixed effects. $\lambda = 1.052$



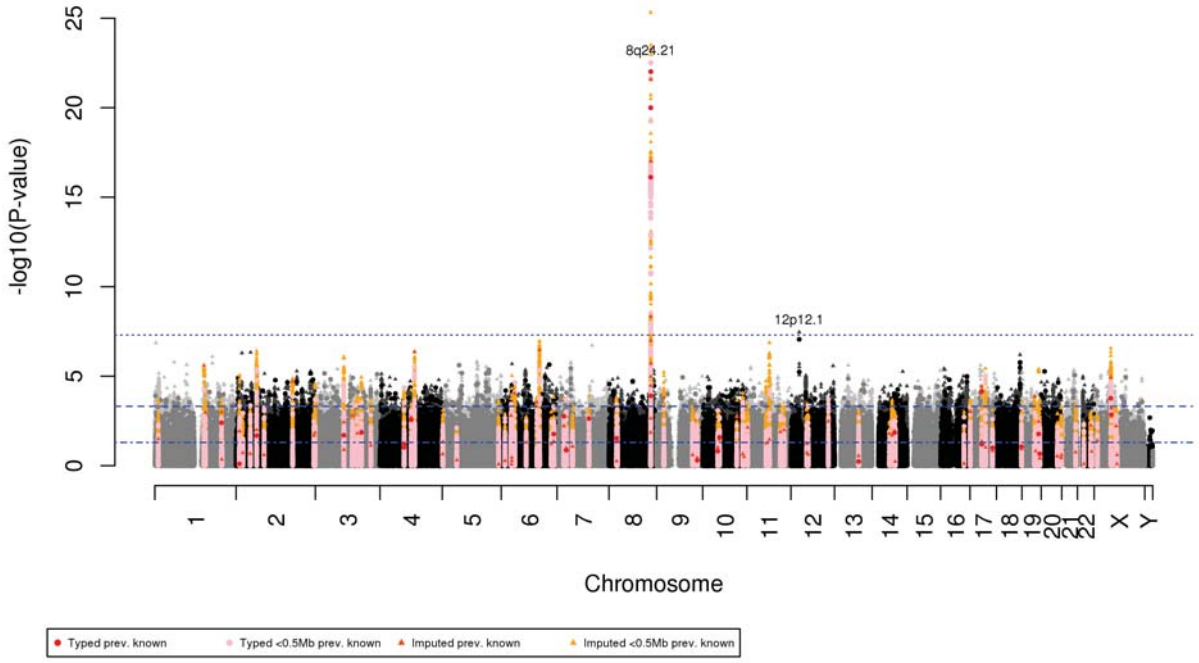


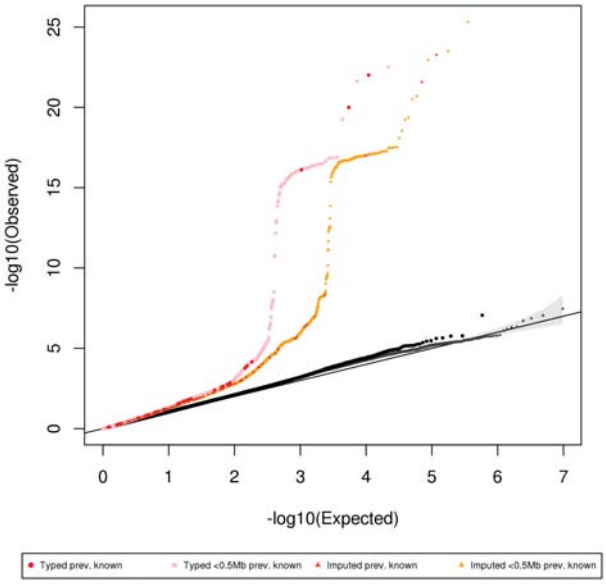
(S1.6) Round 0 of Meta-analysis random effects. $\lambda = 0.872$



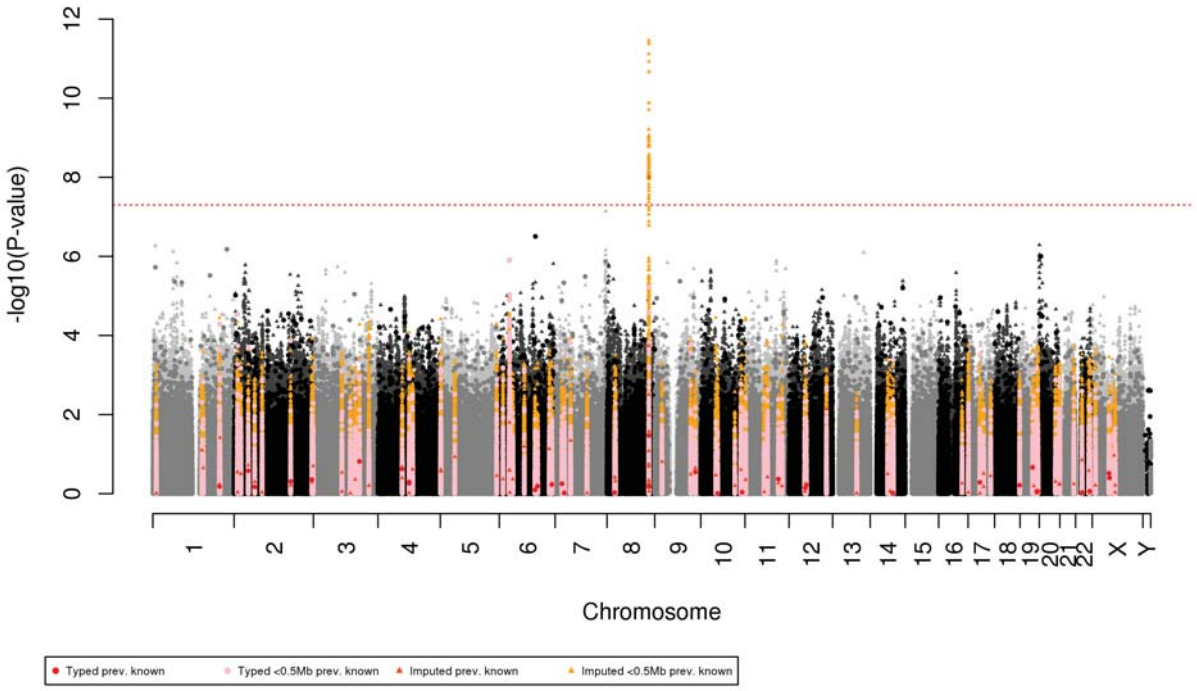


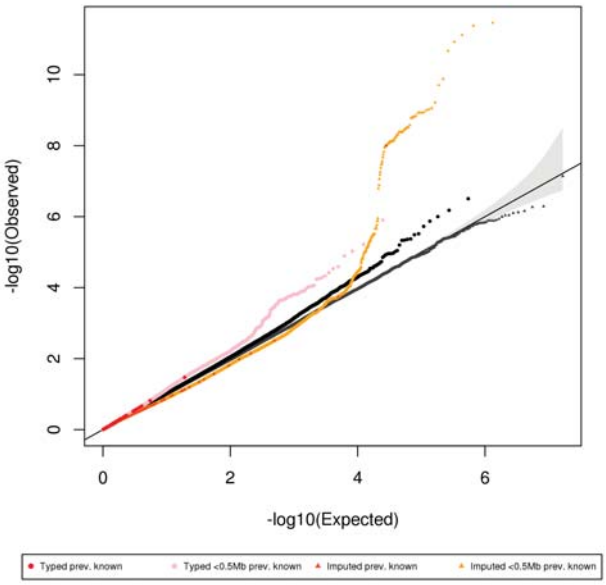
(S1.7) Round 1 of non-Hispanic white race/ethnicity. $\lambda_{\text{typed}} = 1.065$, $\lambda_{\text{imputed}} = 1.047$



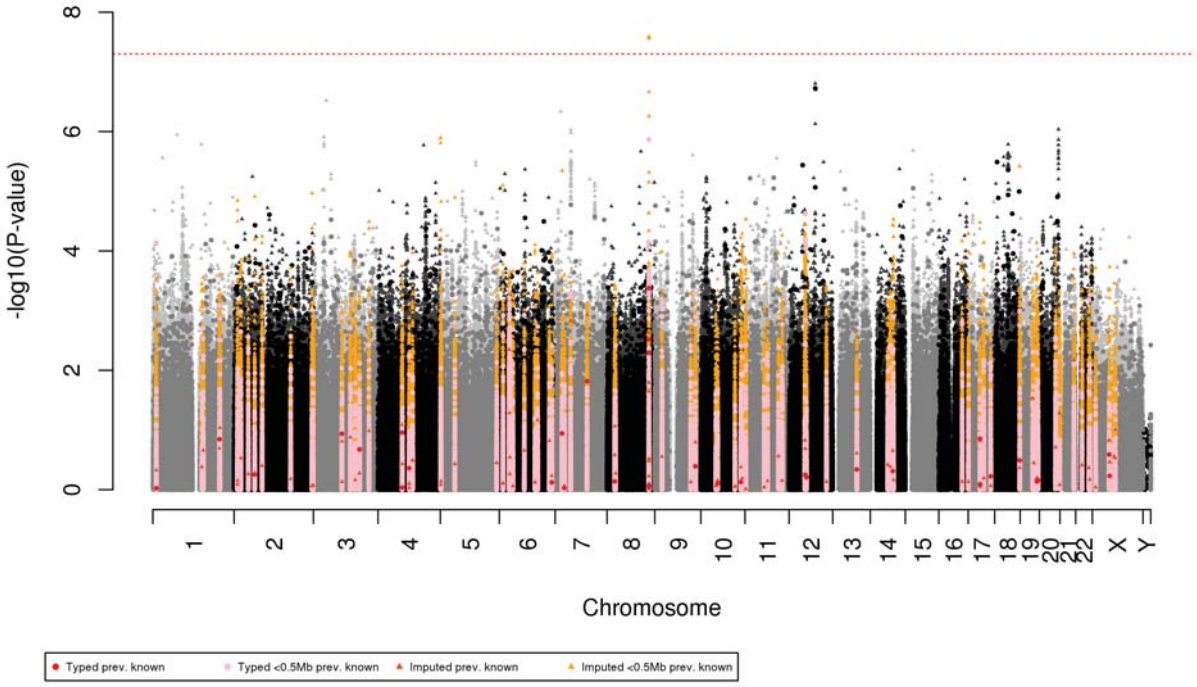


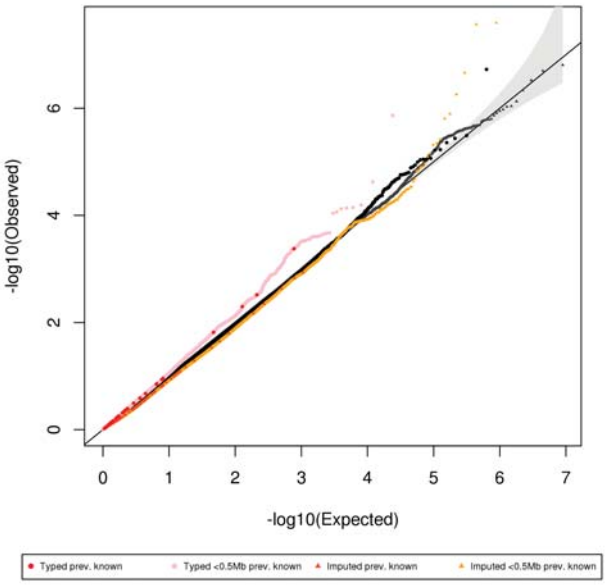
(S1.8) Round 1 of African American race/ethnicity. $\lambda_{\text{typed}} = 1.039$, $\lambda_{\text{imputed}} = 0.999$



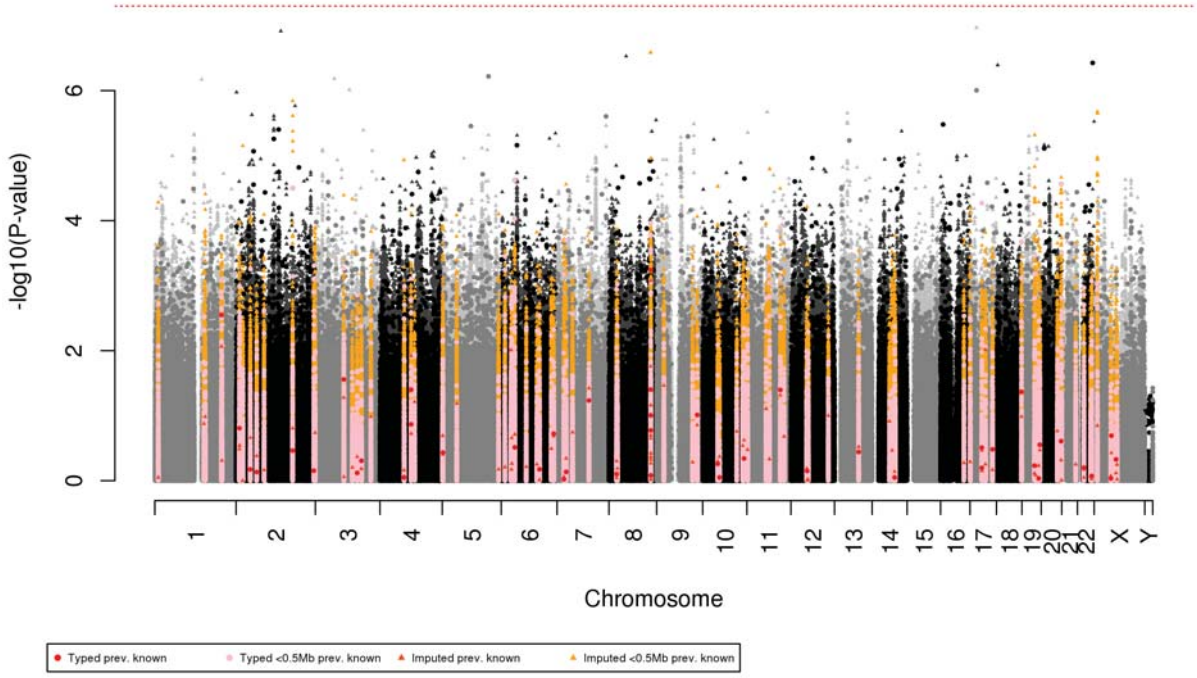


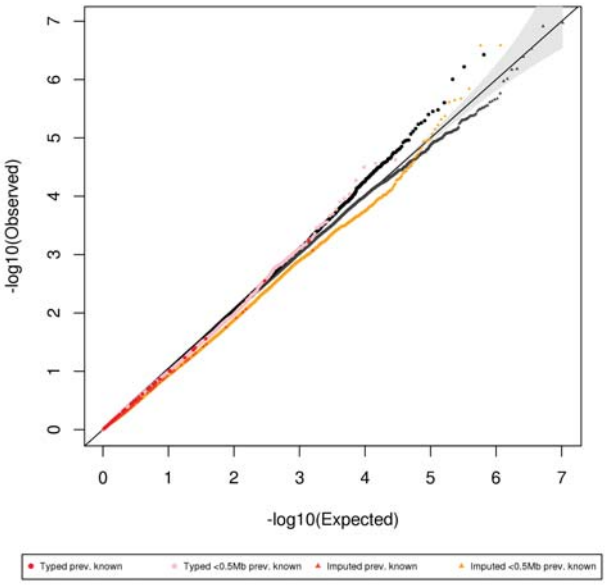
(S1.9) Round 1 of Asian race/ethnicity. $\lambda_{\text{typed}} = 1.026$, $\lambda_{\text{imputed}} = 0.982$



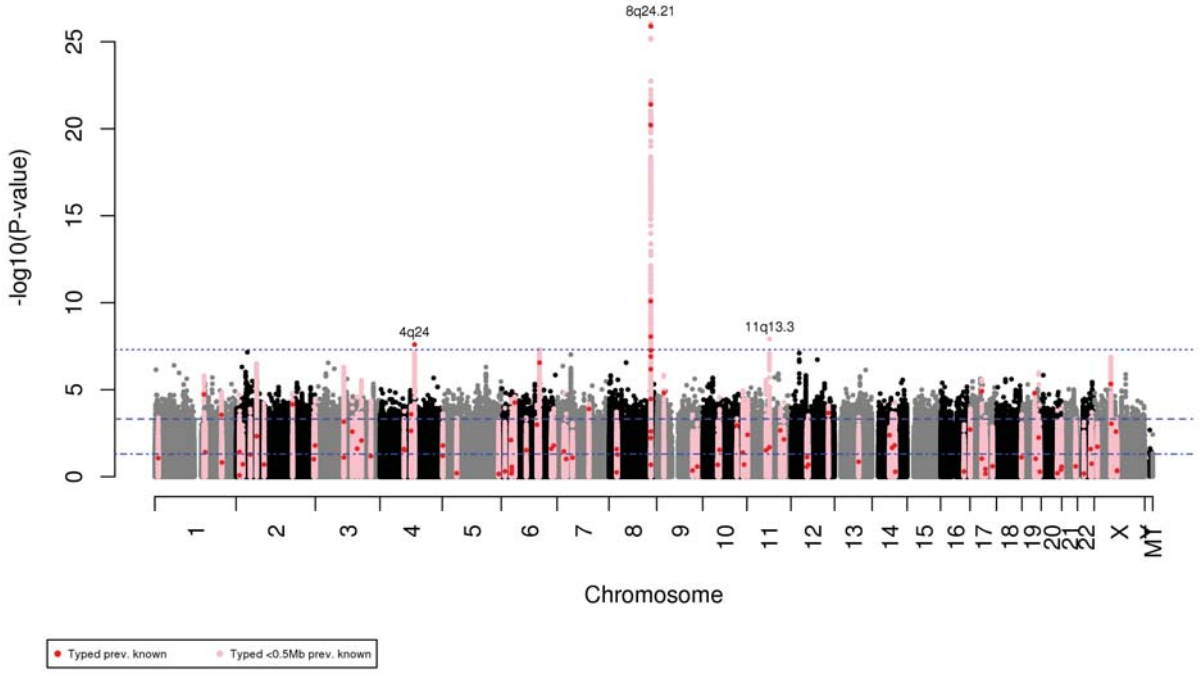


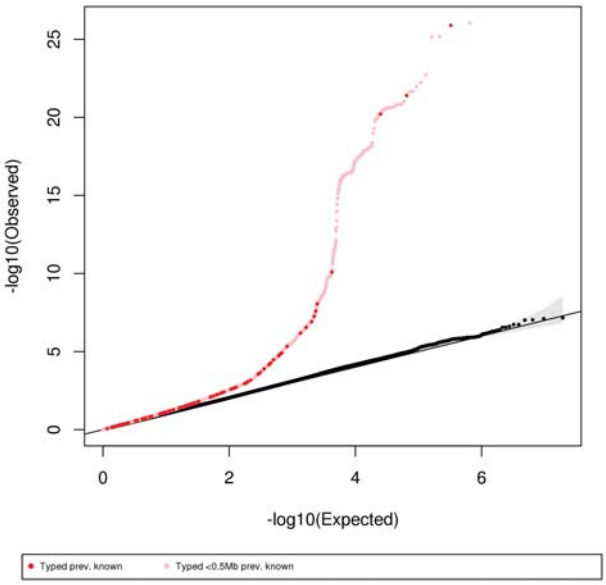
(S1.10) Round 1 of Latino race/ethnicity. $\lambda_{\text{typed}} = 1.029$, $\lambda_{\text{imputed}} = 0.996$



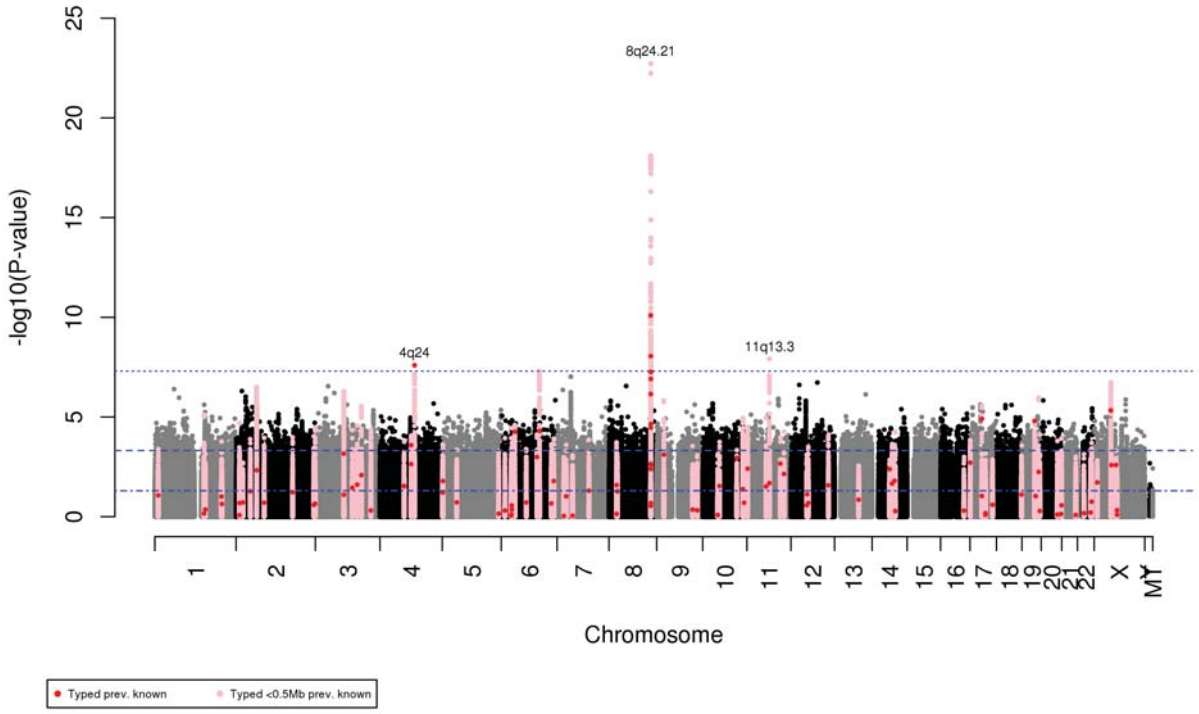


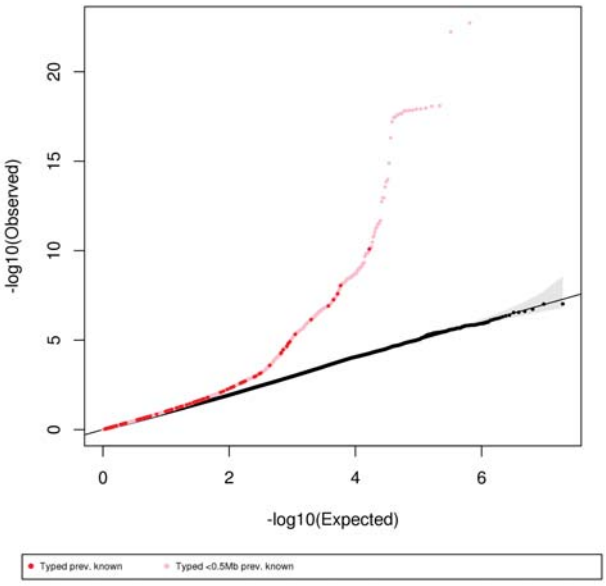
(S1.11) Round 1 of Meta-analysis fixed effects. $\lambda = 1.053$



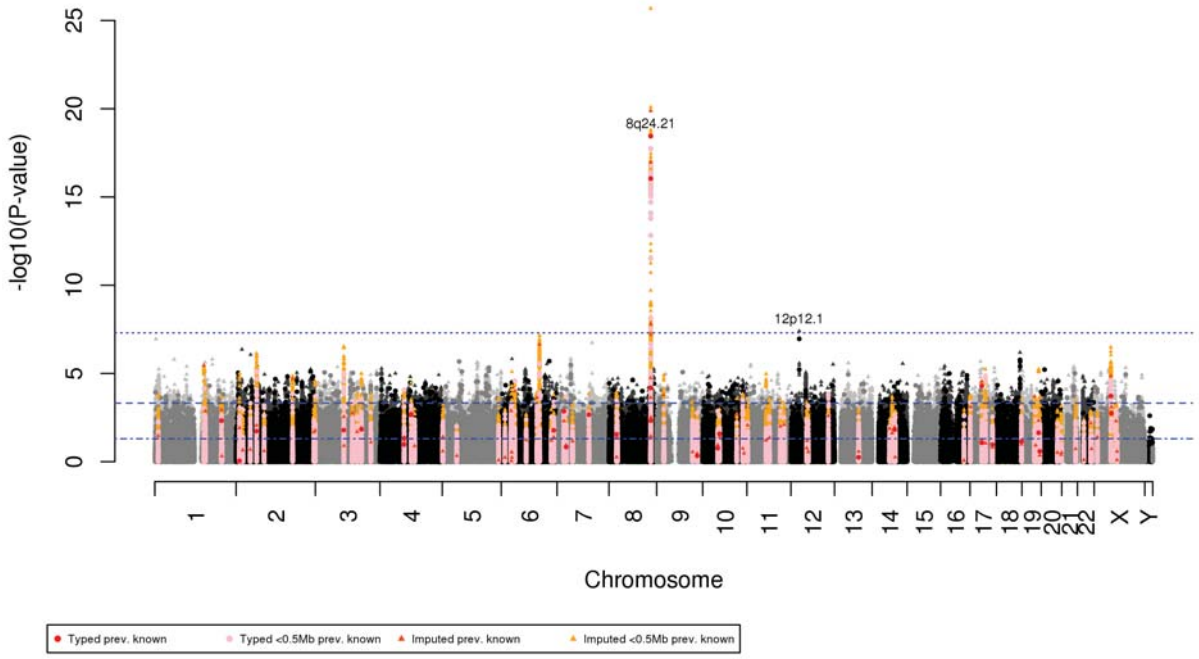


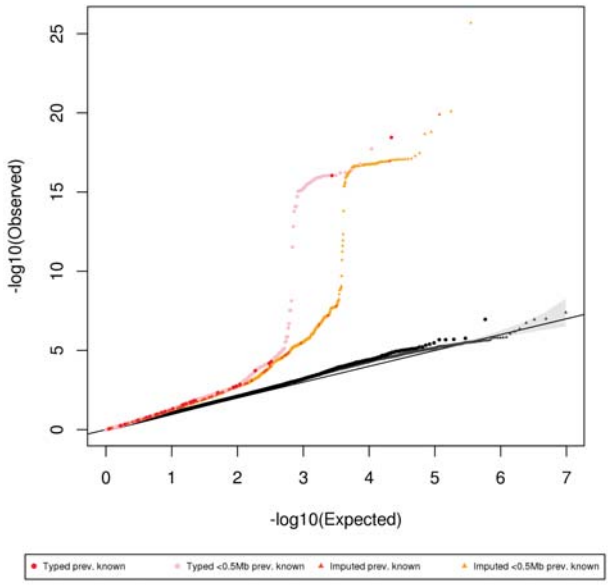
(S1.12) Round 1 of Meta-analysis random effects. $\lambda = 0.872$



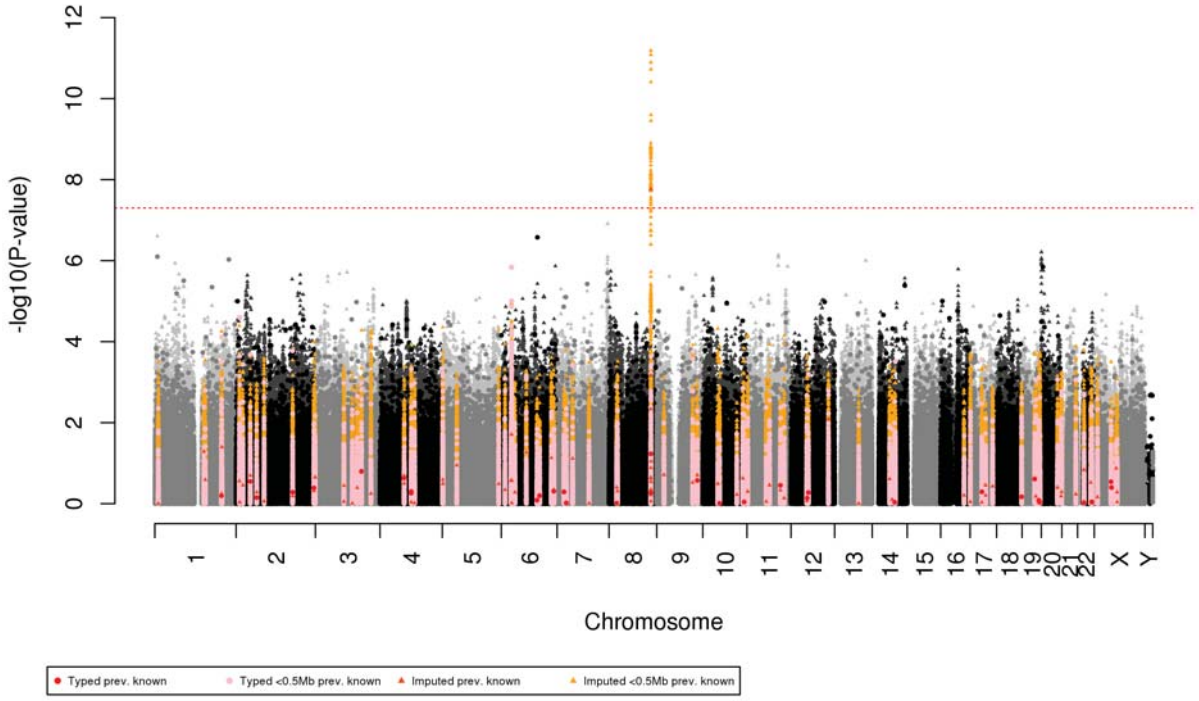


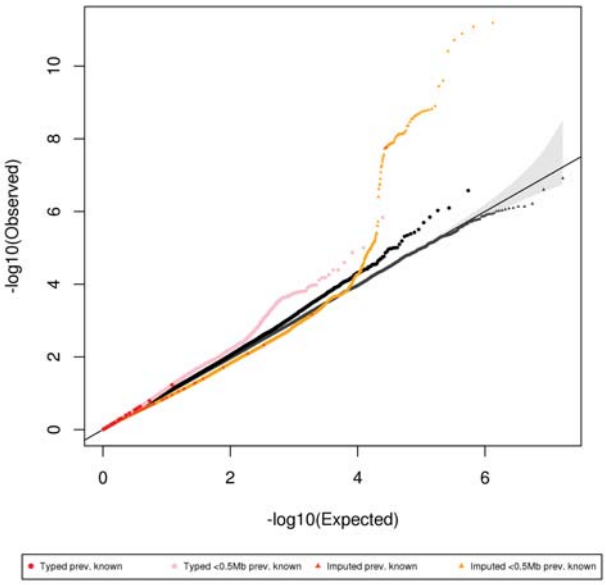
(S1.13) Round 2 of non-Hispanic white race/ethnicity. $\lambda_{\text{typed}} = 1.065$, $\lambda_{\text{imputed}} = 1.047$



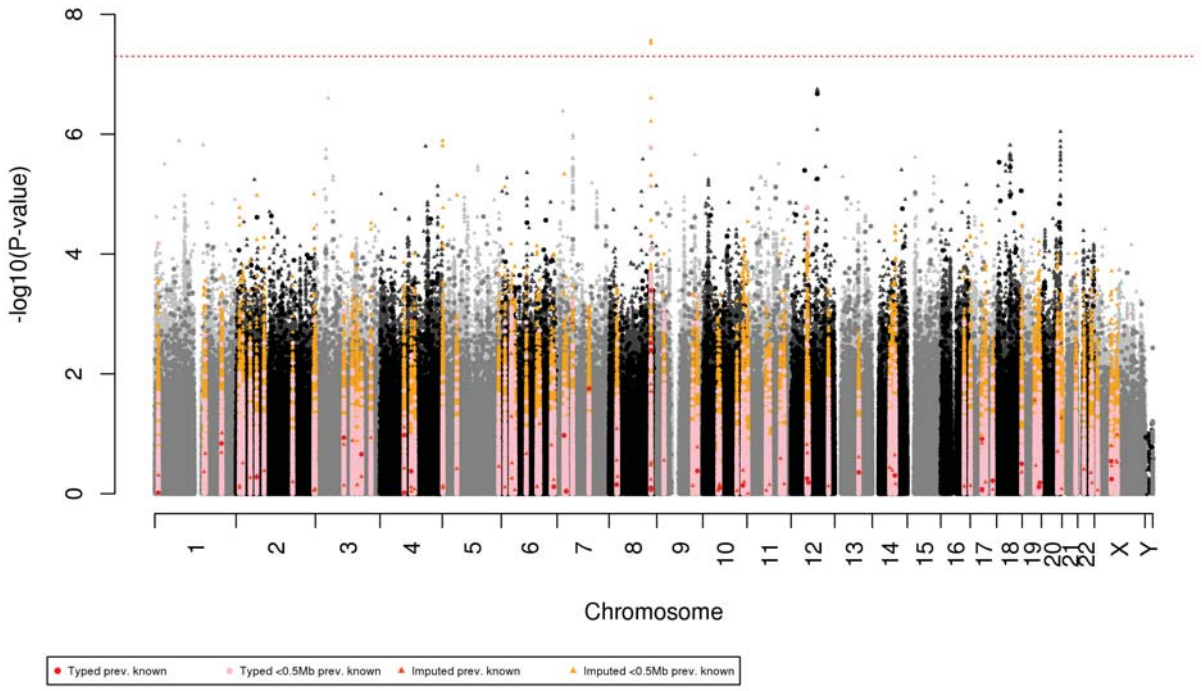


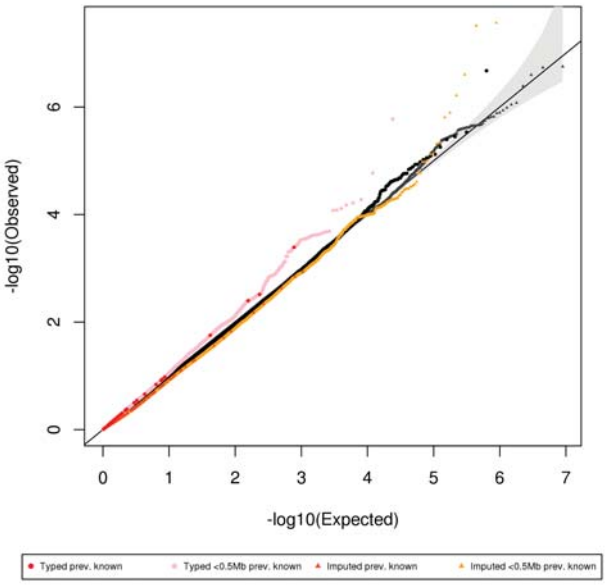
(S1.14) Round 2 of African American race/ethnicity. $\lambda_{\text{typed}} = 1.039$, $\lambda_{\text{imputed}} = 0.999$



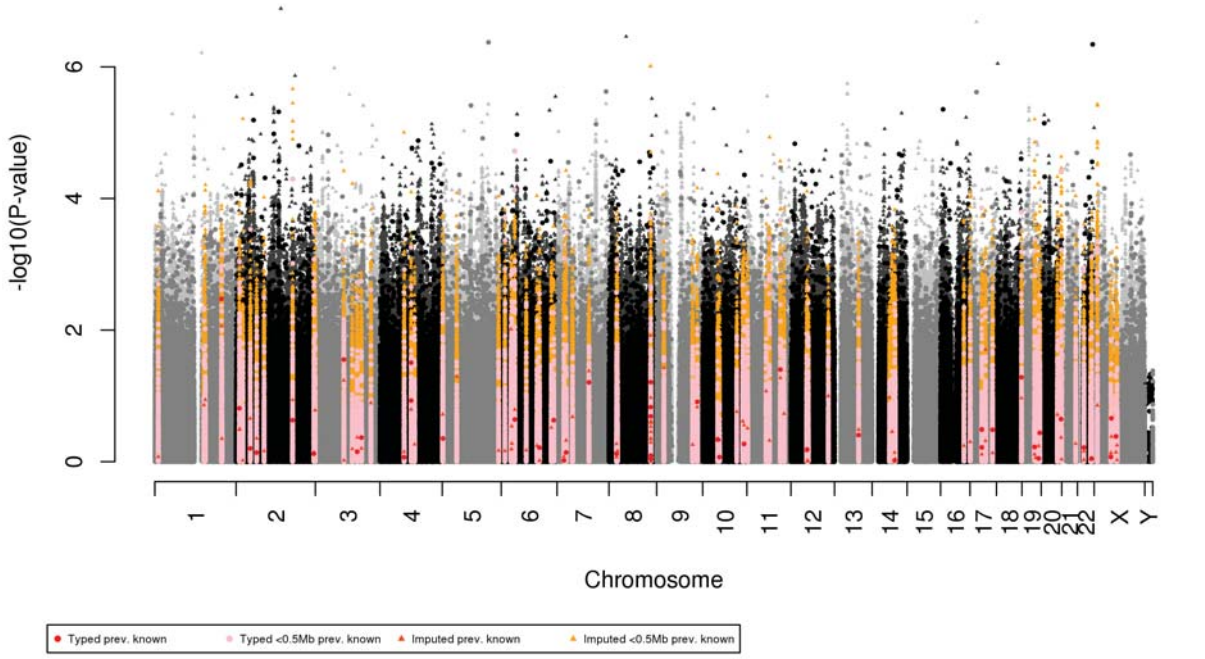


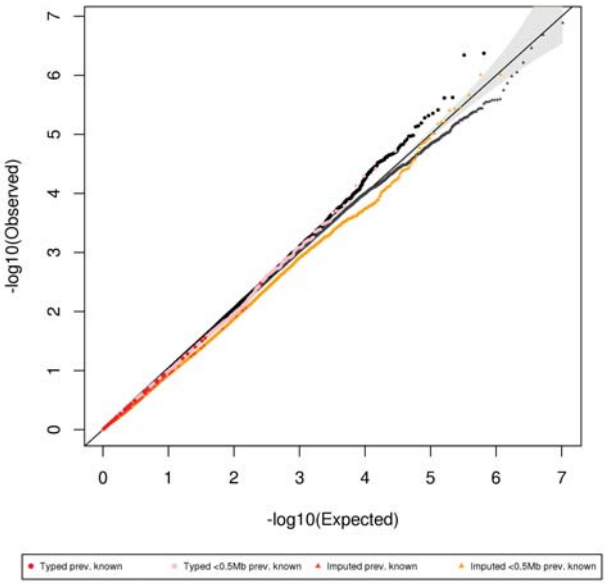
(S1.15) Round 2 of Asian race/ethnicity. $\lambda_{\text{typed}} = 1.025$, $\lambda_{\text{imputed}} = 0.981$



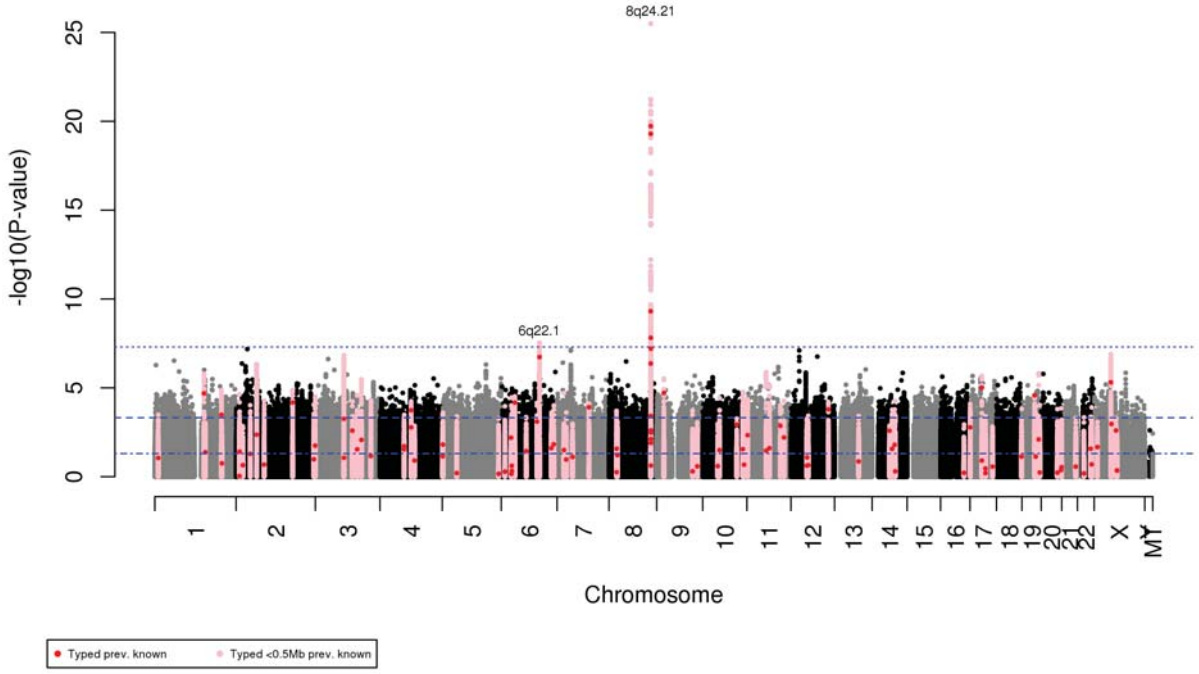


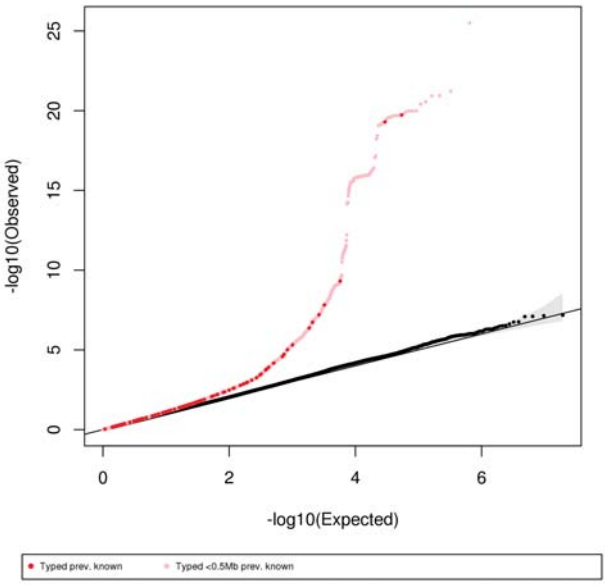
(S1.16) Round 2 of Latino race/ethnicity. $\lambda_{\text{typed}} = 1.030$, $\lambda_{\text{imputed}} = 0.997$



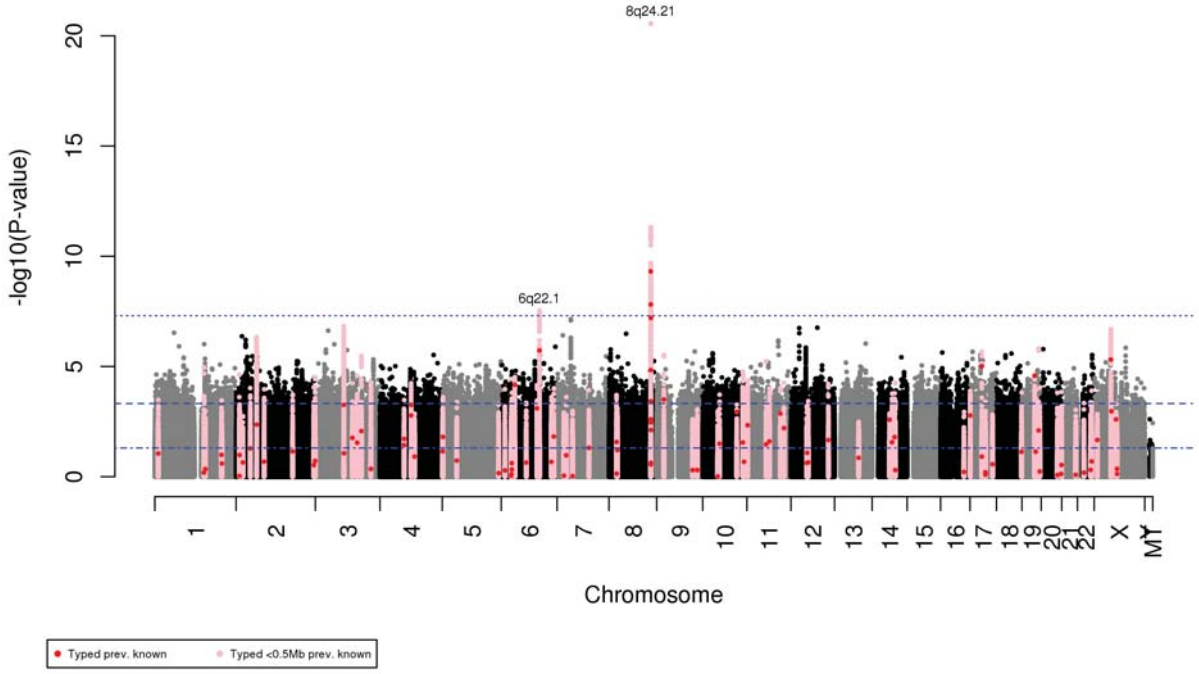


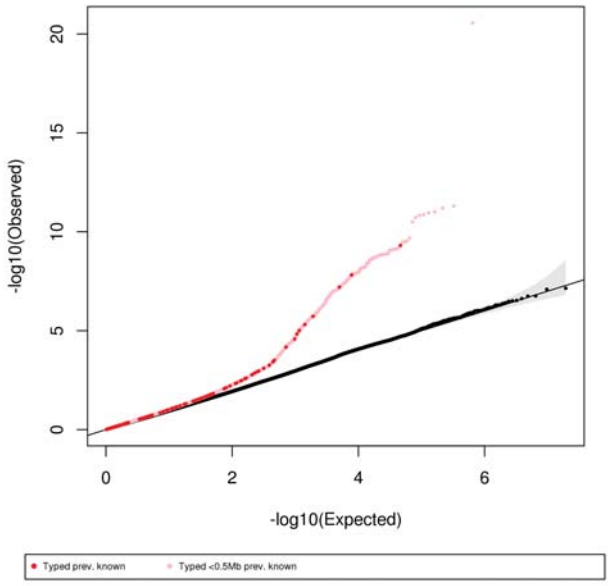
(S1.17) Round 2 of Meta-analysis fixed effects. $\lambda = 1.053$



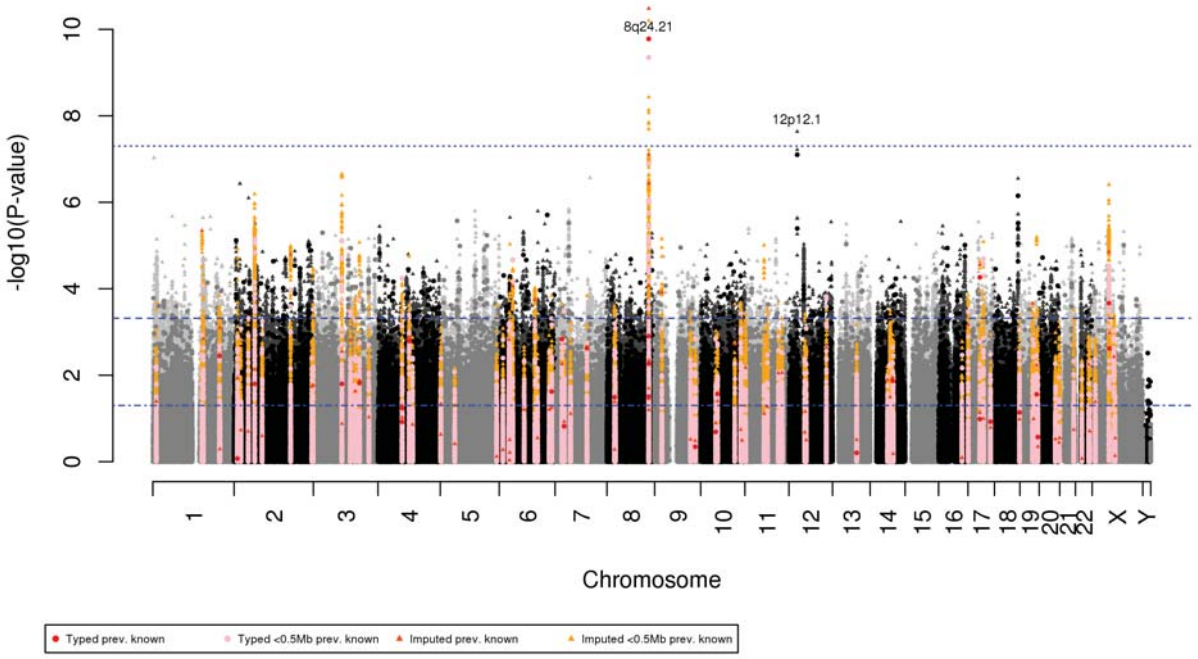


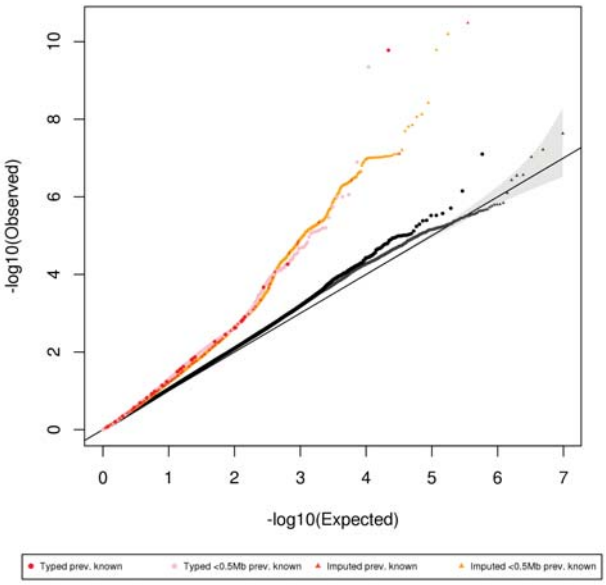
(S1.18) Round 2 of Meta-analysis random effects. $\lambda = 0.872$



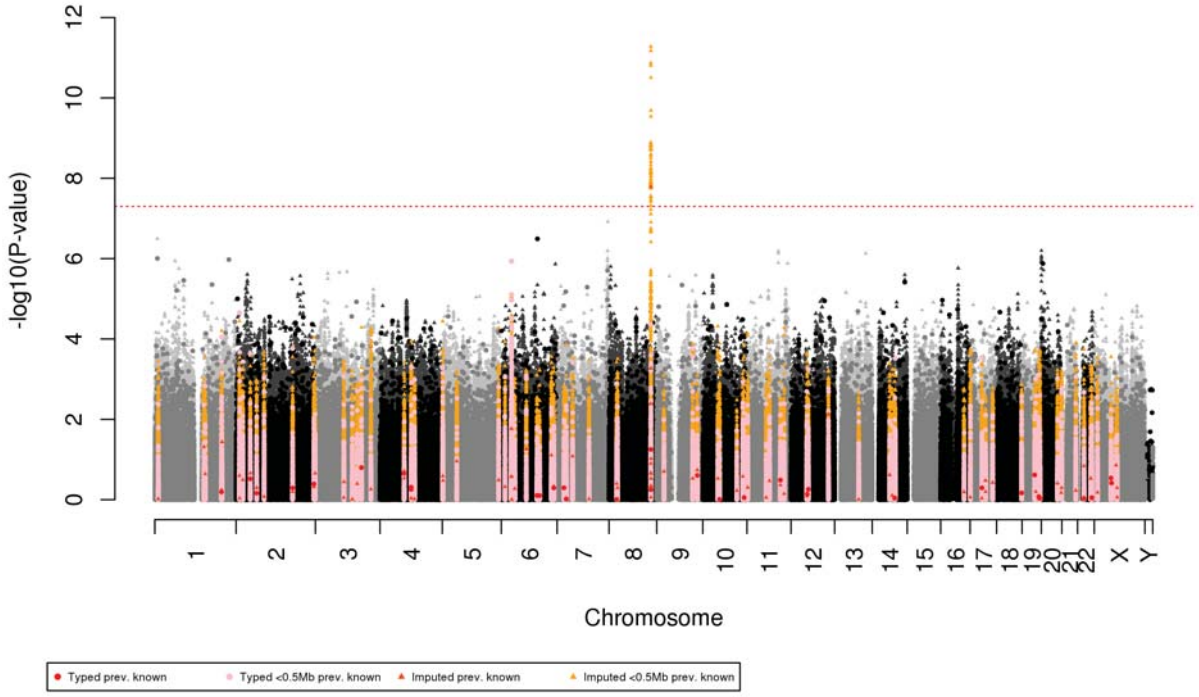


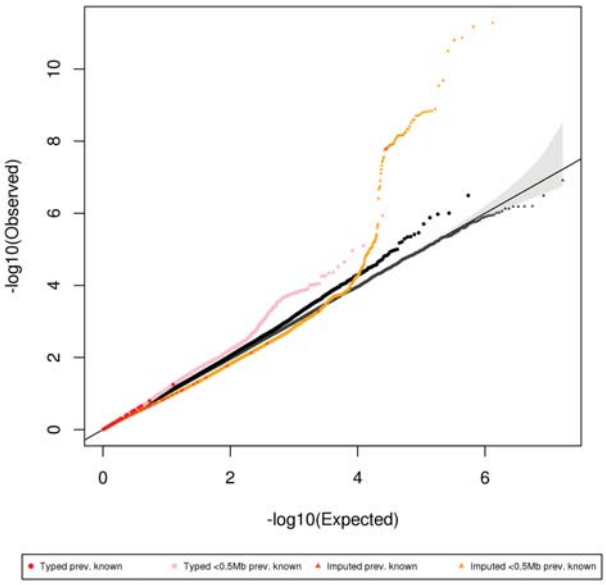
(S1.19) Round 3 of non-Hispanic white race/ethnicity. $\lambda_{\text{typed}} = 1.065$, $\lambda_{\text{imputed}} = 1.046$



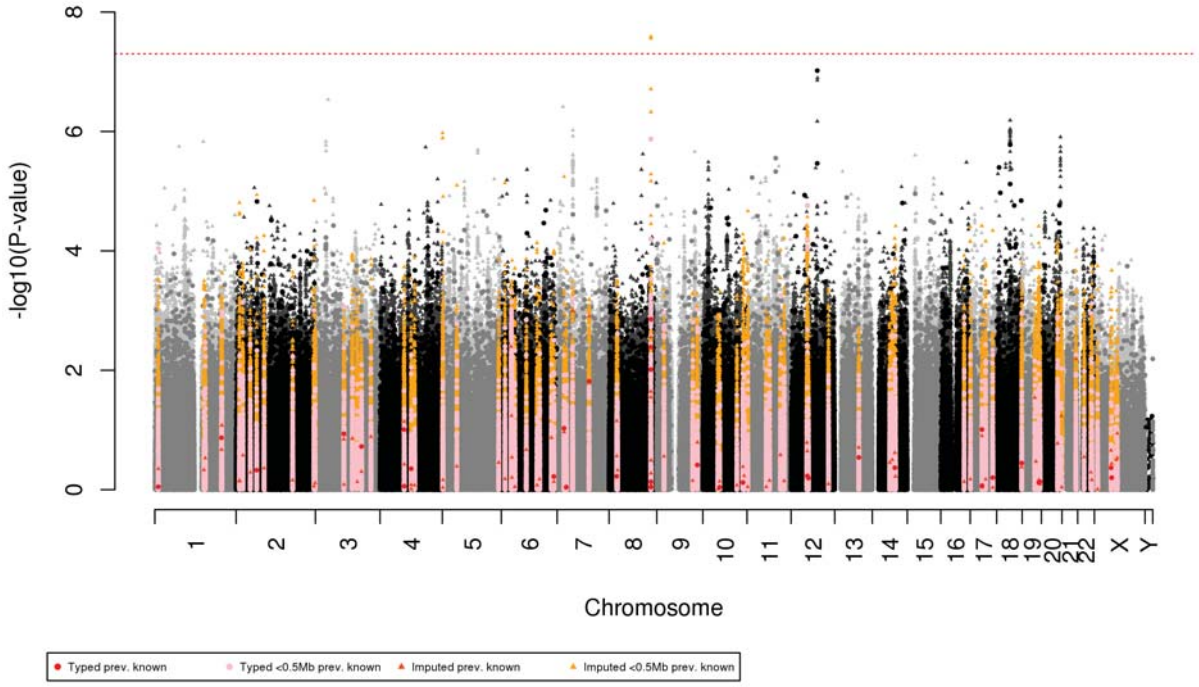


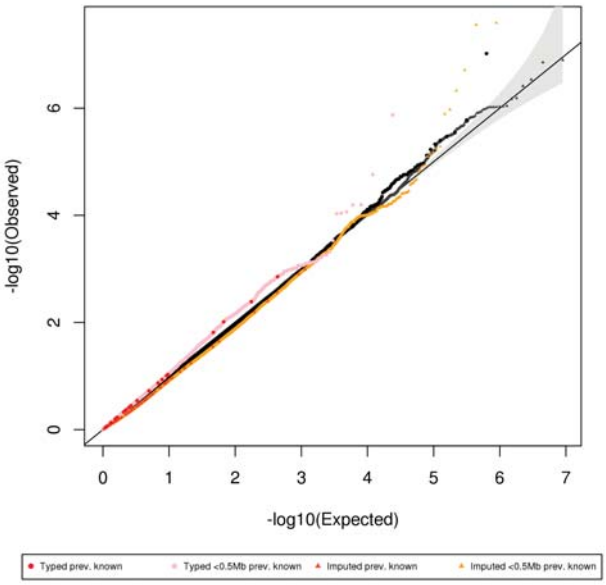
(S1.20) Round 3 of African American race/ethnicity. $\lambda_{\text{typed}} = 1.038$, $\lambda_{\text{imputed}} = 1.000$



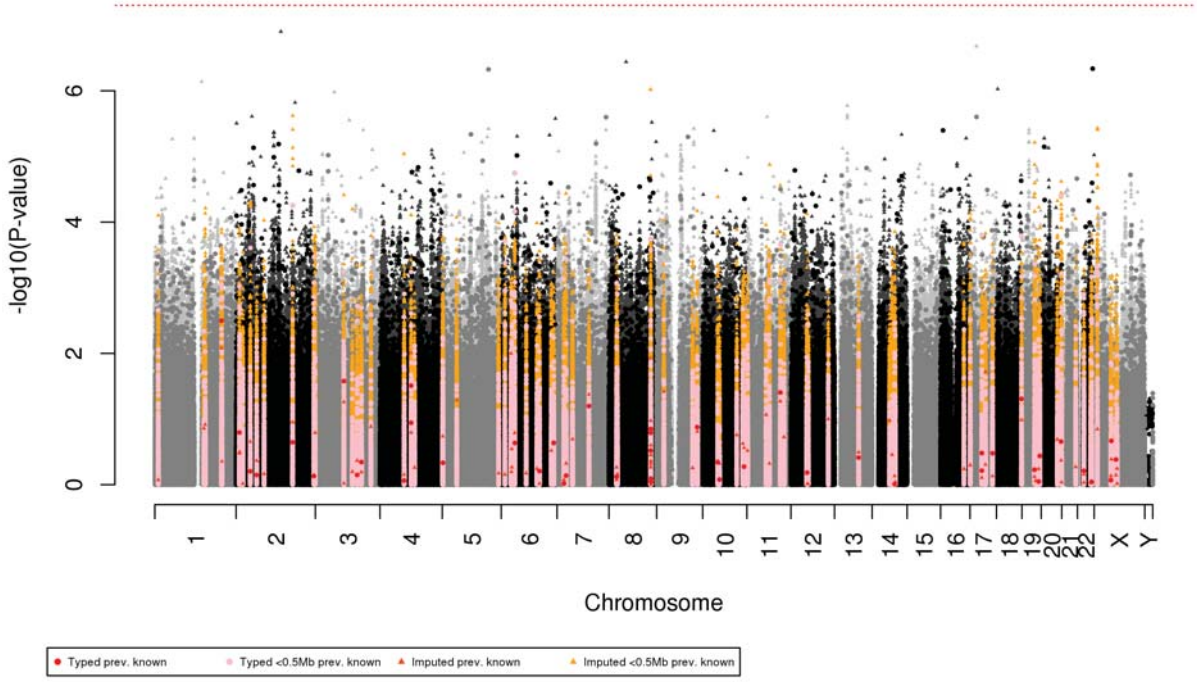


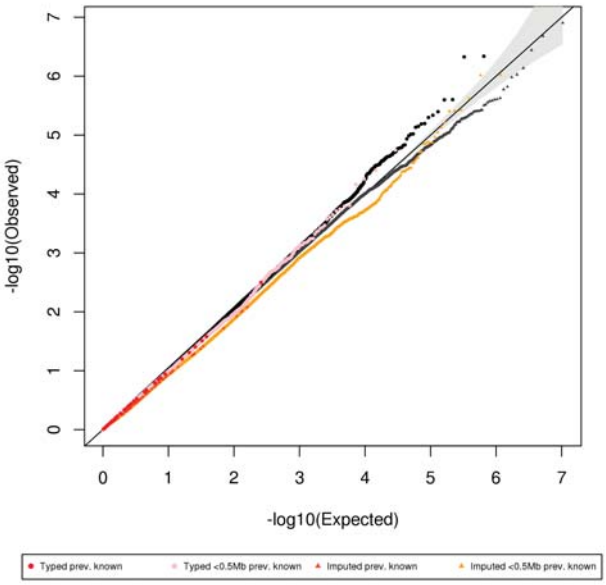
(S1.21) Round 3 of Asian race/ethnicity. $\lambda_{\text{typed}} = 1.029$, $\lambda_{\text{imputed}} = 0.983$



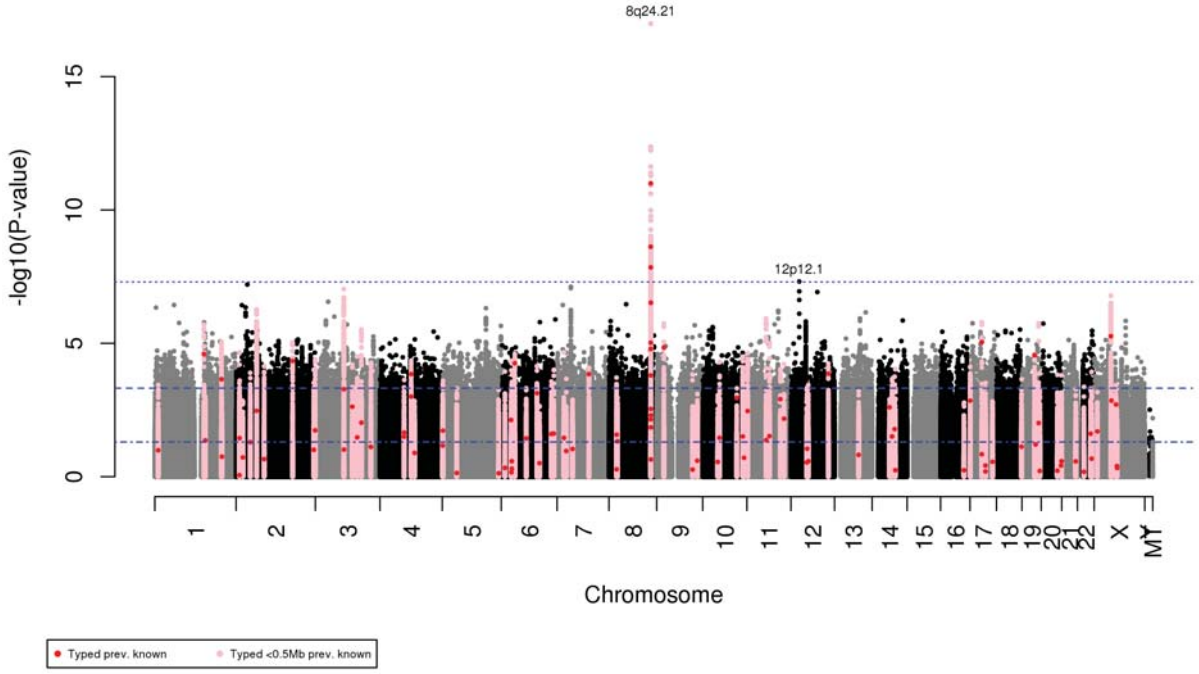


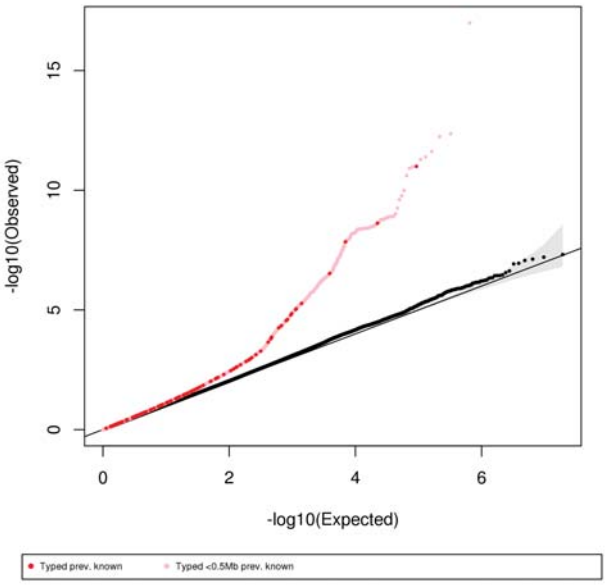
(S1.22) Round 3 of Latino race/ethnicity. $\lambda_{\text{typed}} = 1.030$, $\lambda_{\text{imputed}} = 0.996$



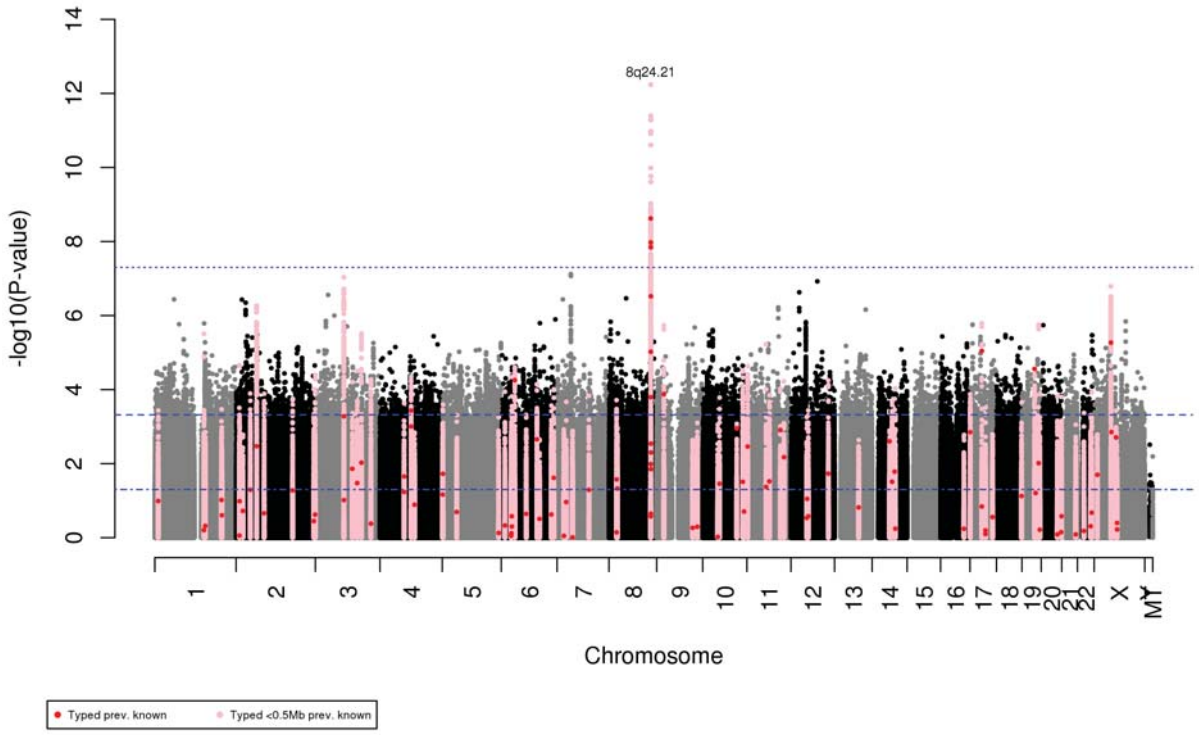


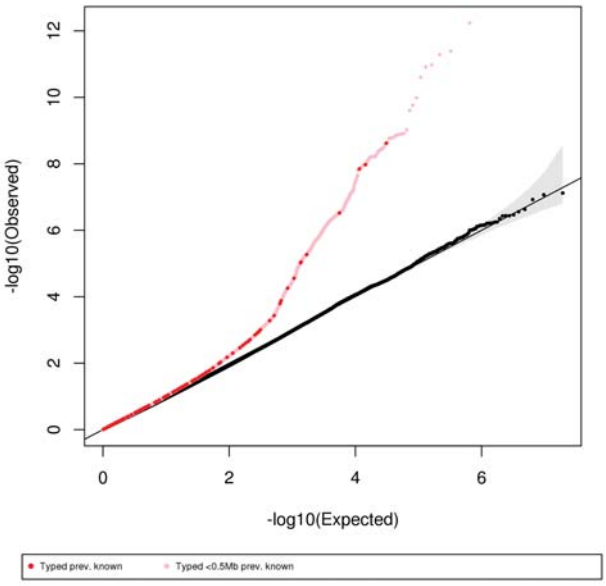
(S1.23) Round 3 of Meta-analysis fixed effects. $\lambda = 1.053$



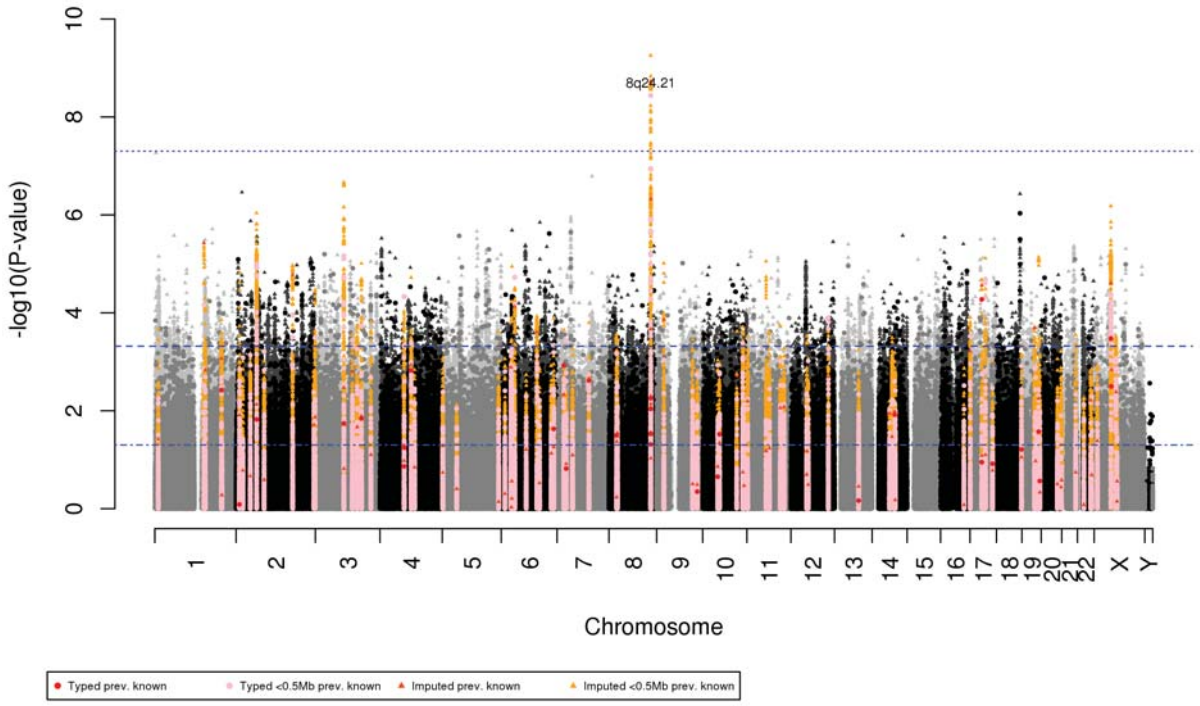


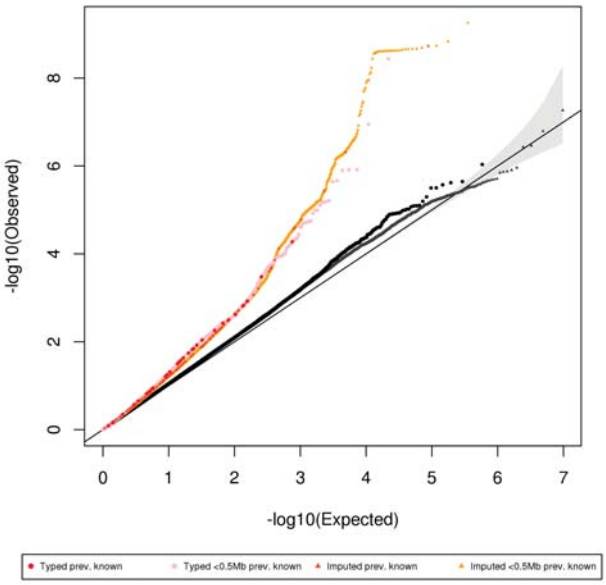
(S1.24) Round 3 of Meta-analysis random effects. $\lambda = 0.872$



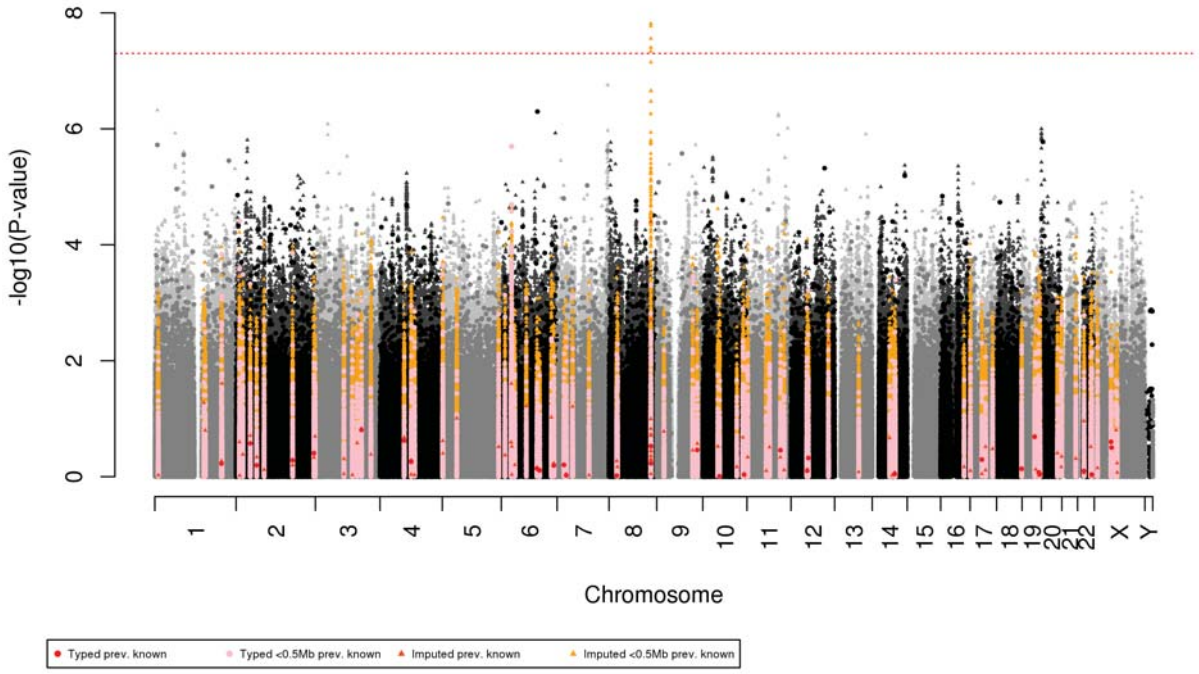


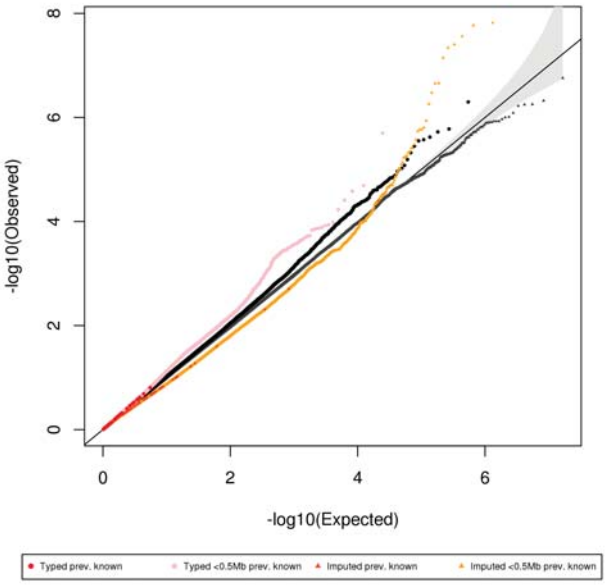
(S1.25) Round 4 of non-Hispanic white race/ethnicity. $\lambda_{\text{typed}} = 1.065$, $\lambda_{\text{imputed}} = 1.046$



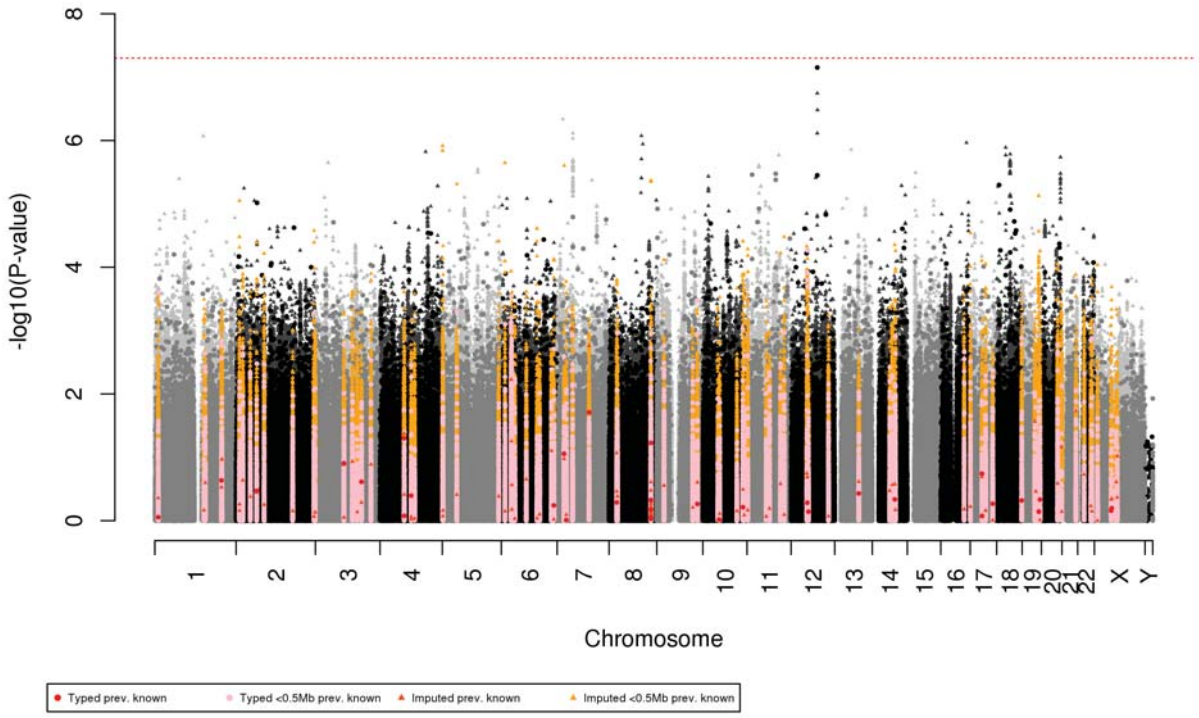


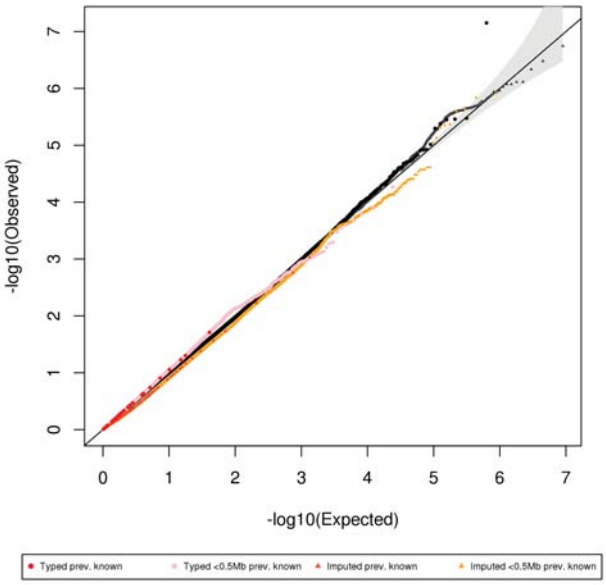
(S1.26) Round 4 of African American race/ethnicity. $\lambda_{\text{typed}} = 1.035$, $\lambda_{\text{imputed}} = 0.999$



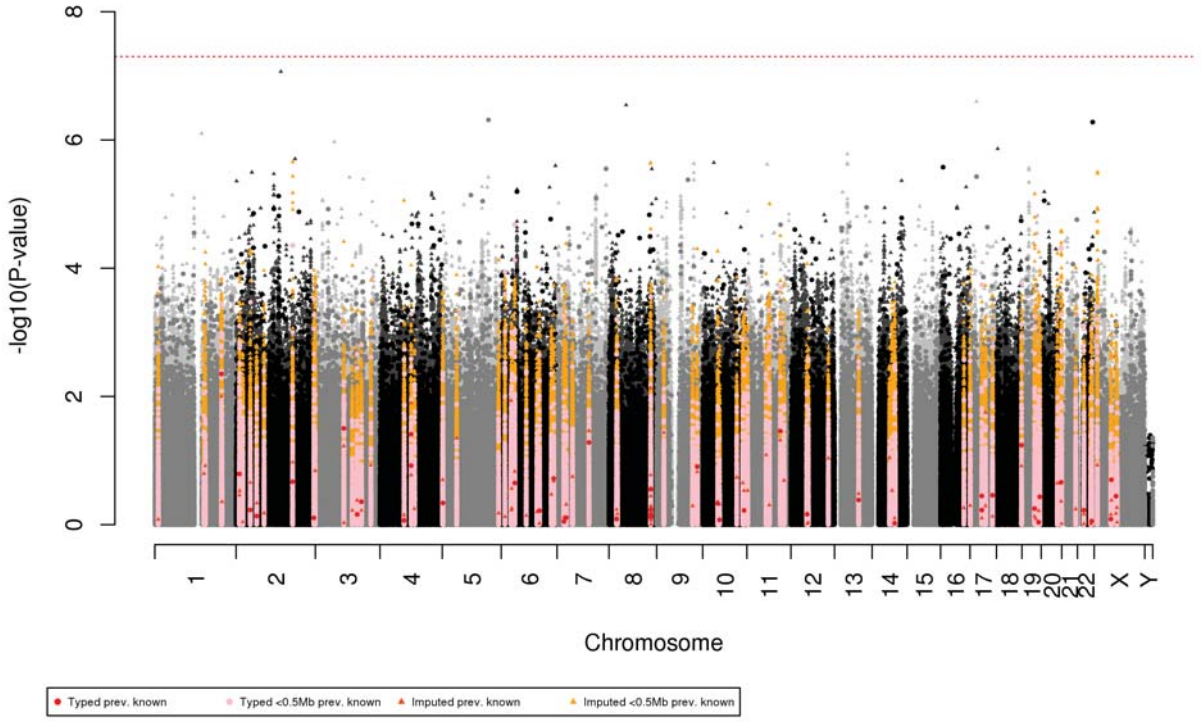


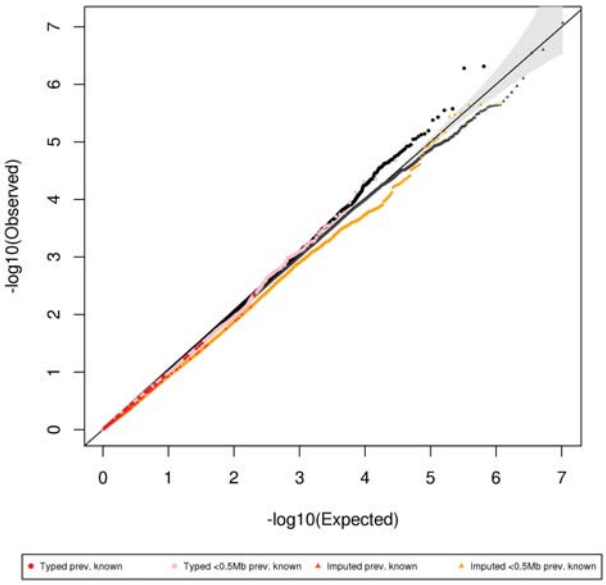
(S1.27) Round 4 of Asian race/ethnicity. $\lambda_{\text{typed}} = 1.032$, $\lambda_{\text{imputed}} = 0.985$



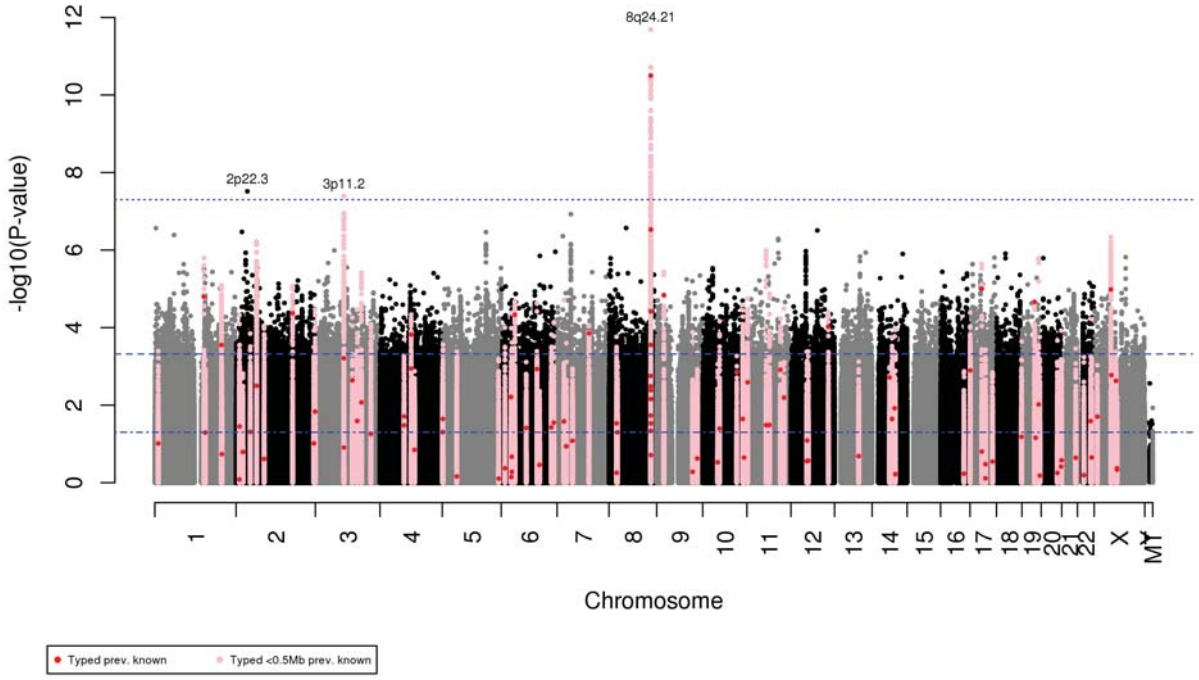


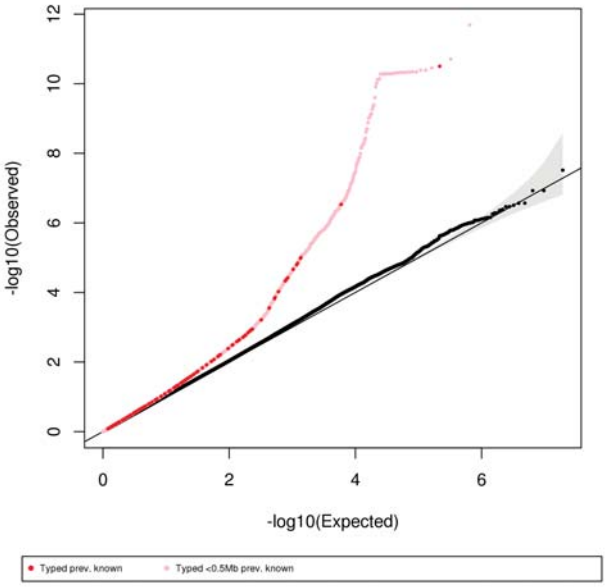
(S1.28) Round 4 of Latino race/ethnicity. $\lambda_{\text{typed}} = 1.028$, $\lambda_{\text{imputed}} = 0.997$



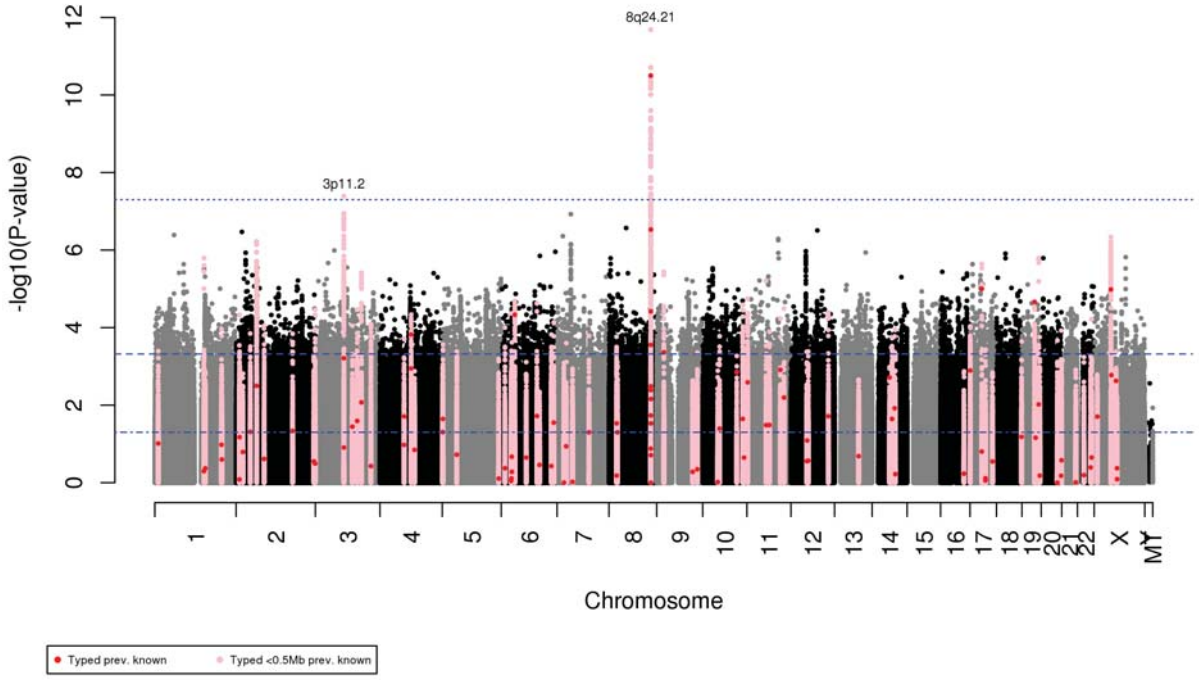


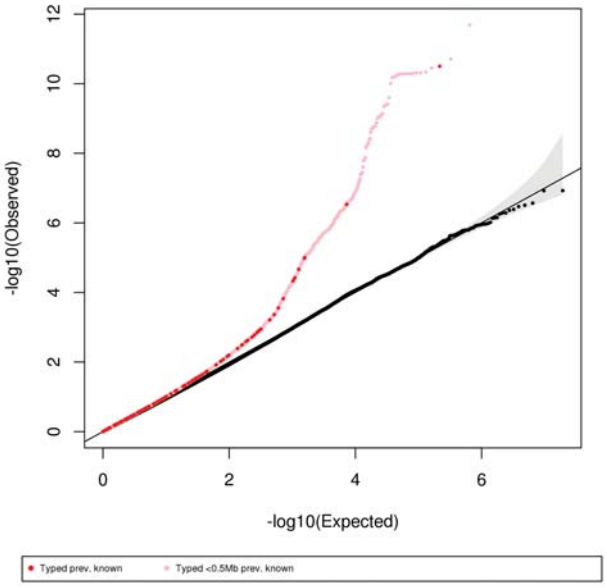
(S1.29) Round 4 of Meta-analysis fixed effects. $\lambda = 1.055$



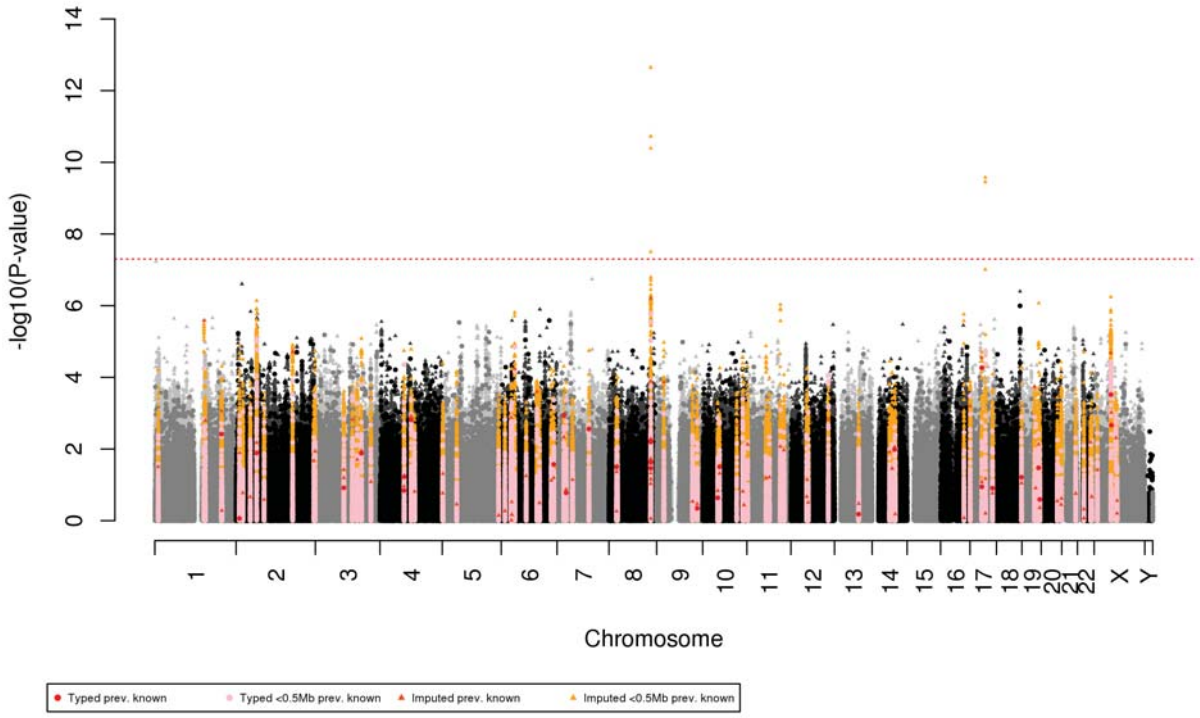


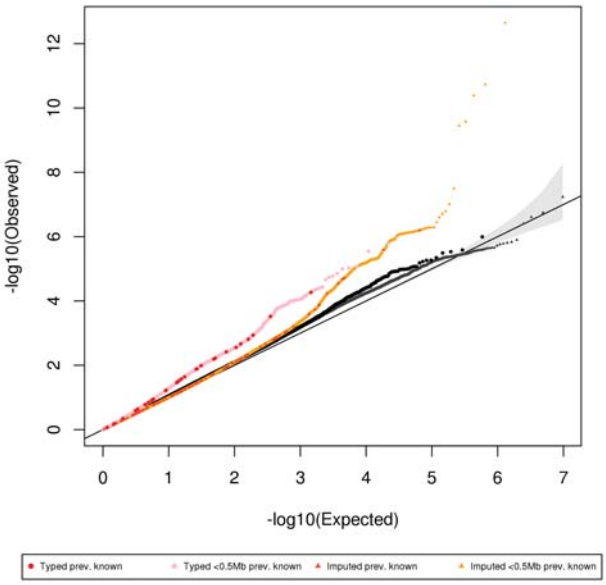
(S1.30) Round 4 of Meta-analysis random effects. $\lambda = 0.874$



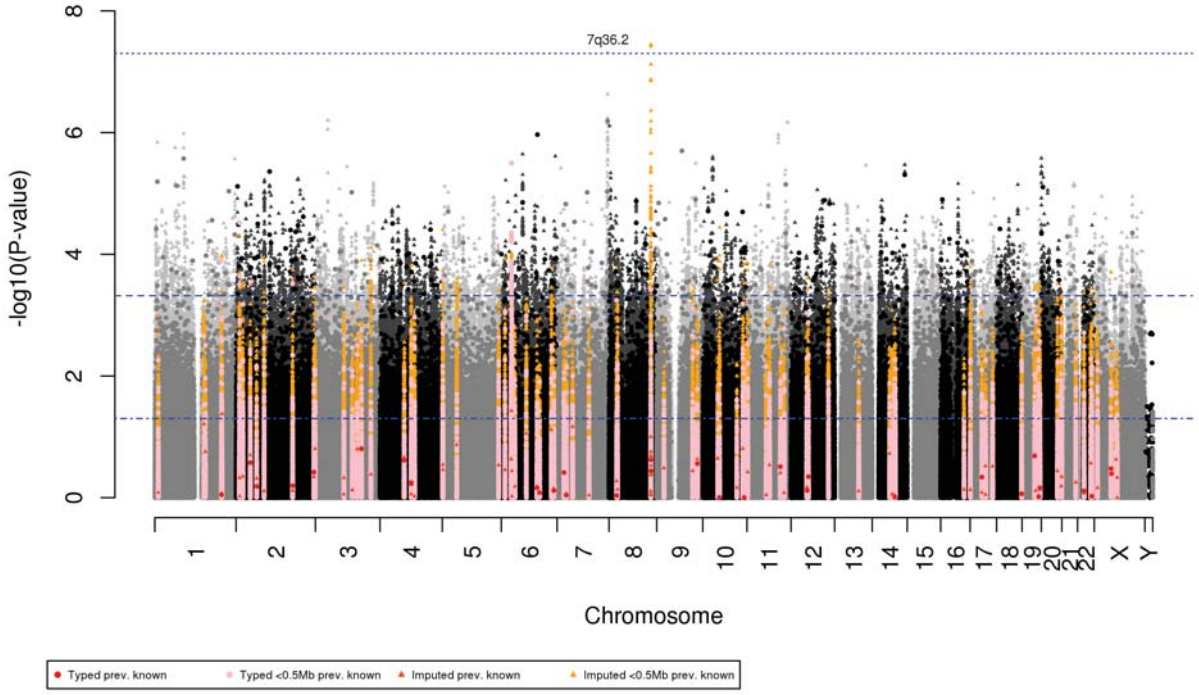


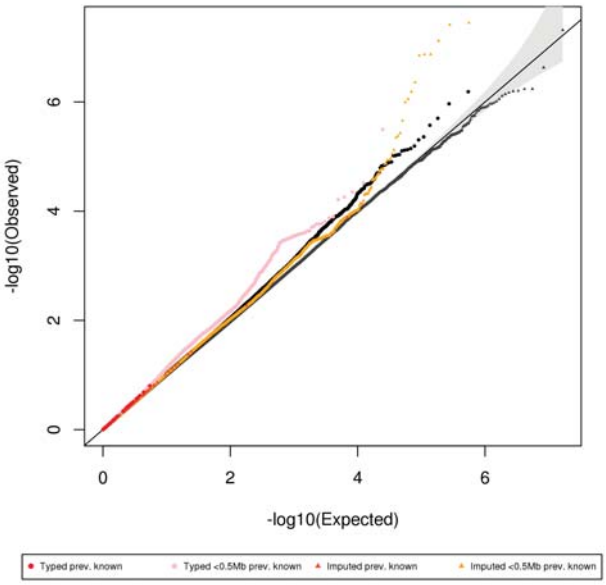
(S1.31) Round 5 of non-Hispanic white race/ethnicity. $\lambda_{\text{typed}} = 1.063$, $\lambda_{\text{imputed}} = 1.045$



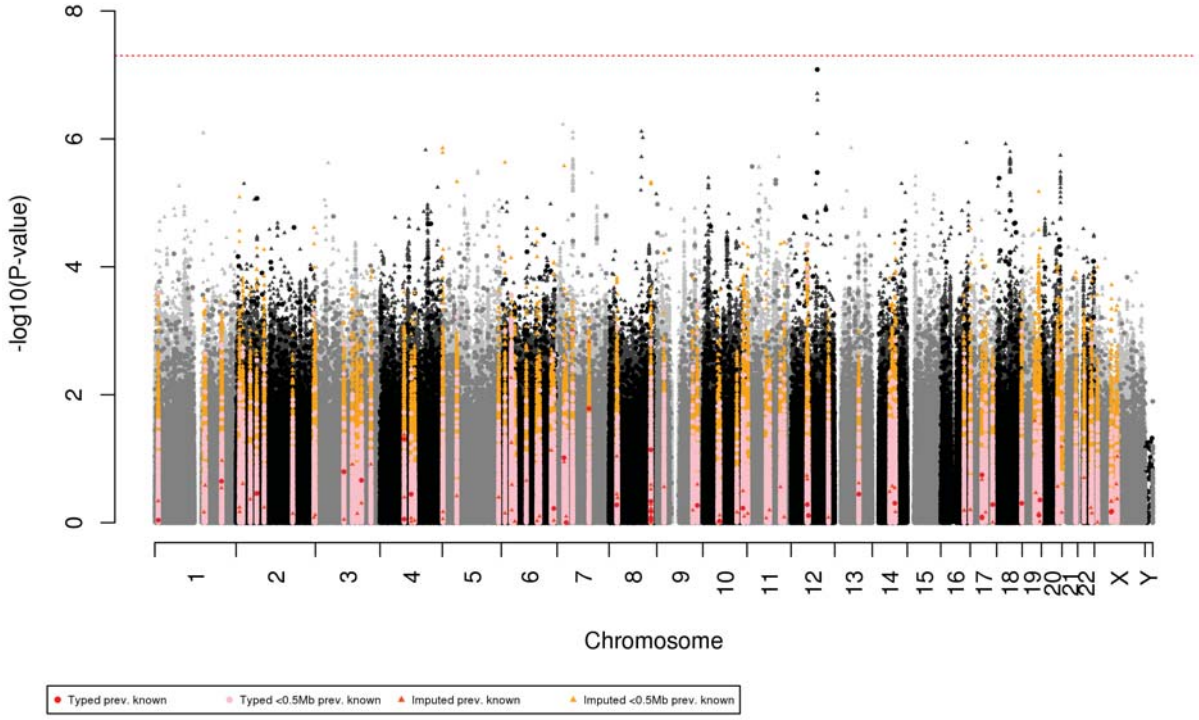


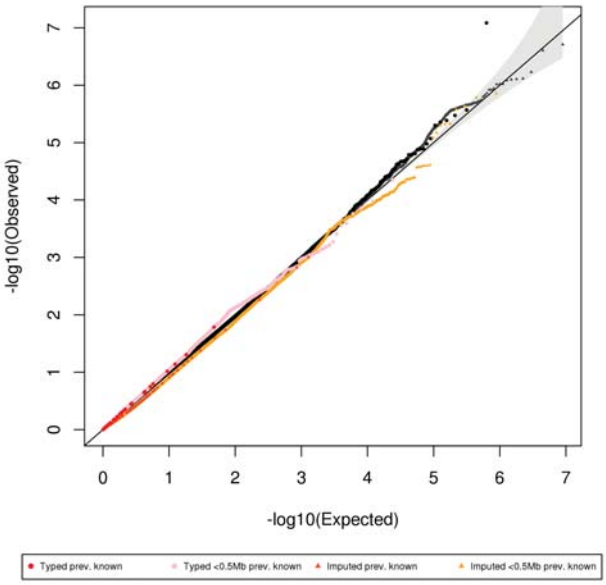
(S1.32) Round 5 of African American race/ethnicity. $\lambda_{\text{typed}} = 1.037$, $\lambda_{\text{imputed}} = 0.999$



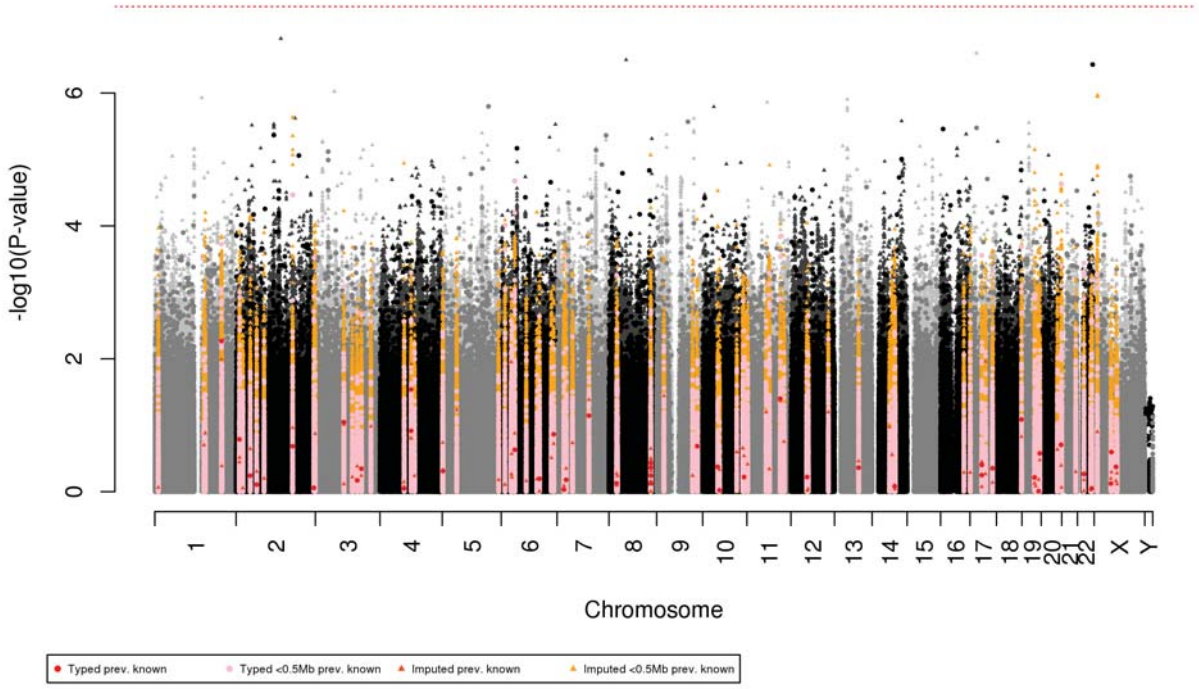


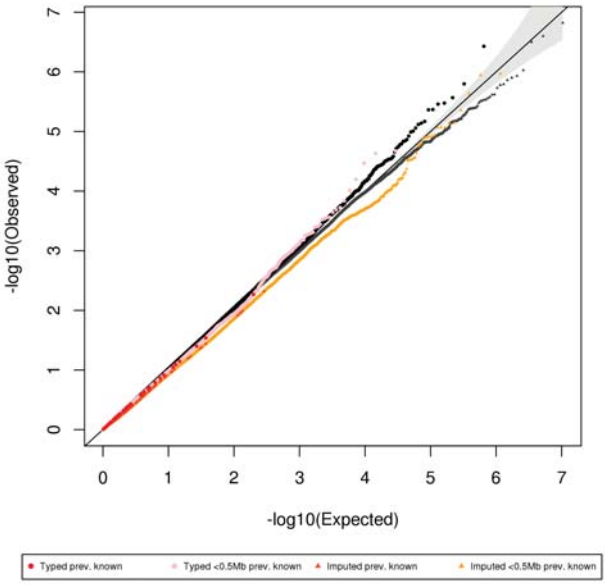
(S1.33) Round 5 of Asian race/ethnicity. $\lambda_{\text{typed}} = 1.032$, $\lambda_{\text{imputed}} = 0.984$



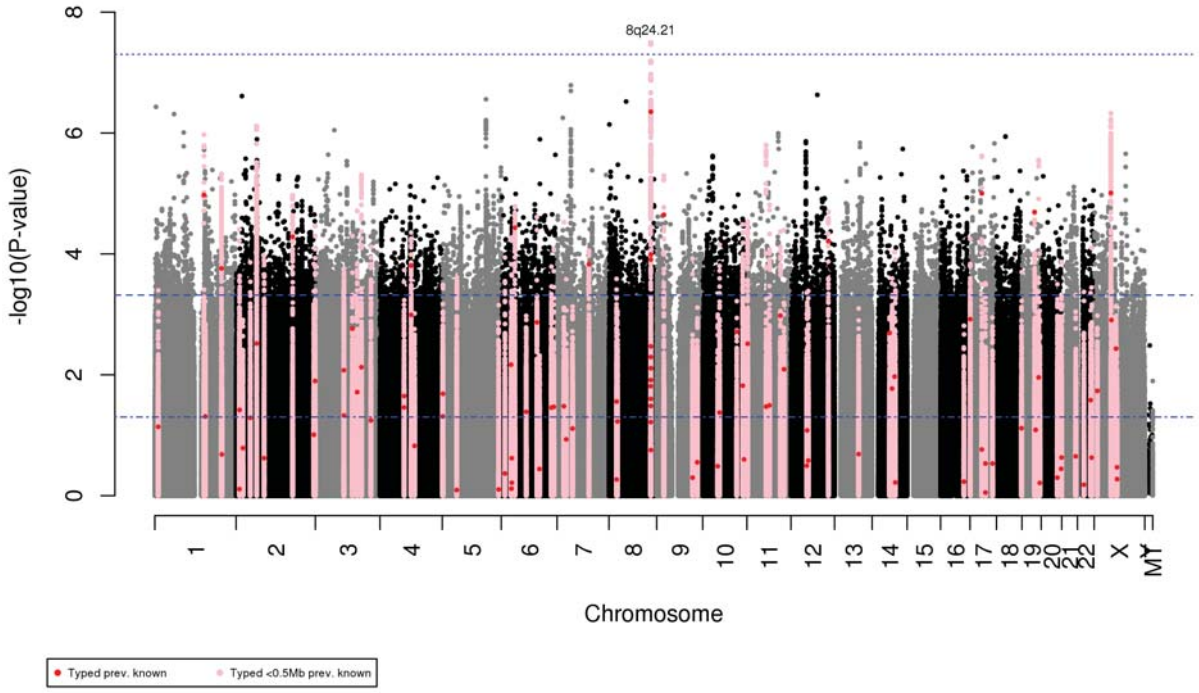


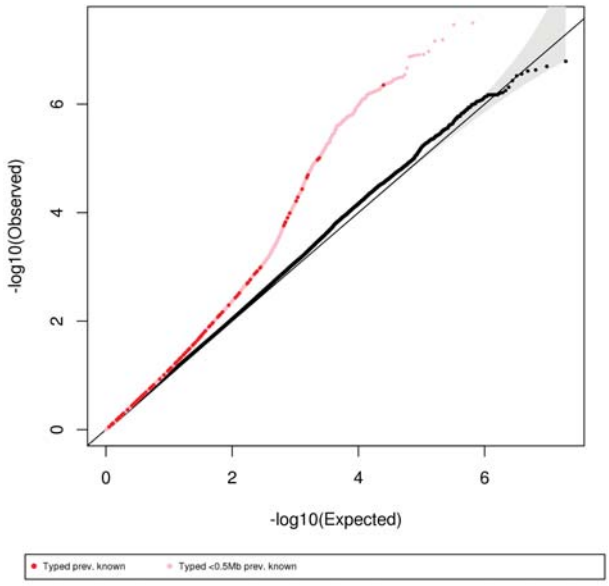
(S1.34) Round 5 of Latino race/ethnicity. $\lambda_{\text{typed}} = 1.024$, $\lambda_{\text{imputed}} = 0.995$



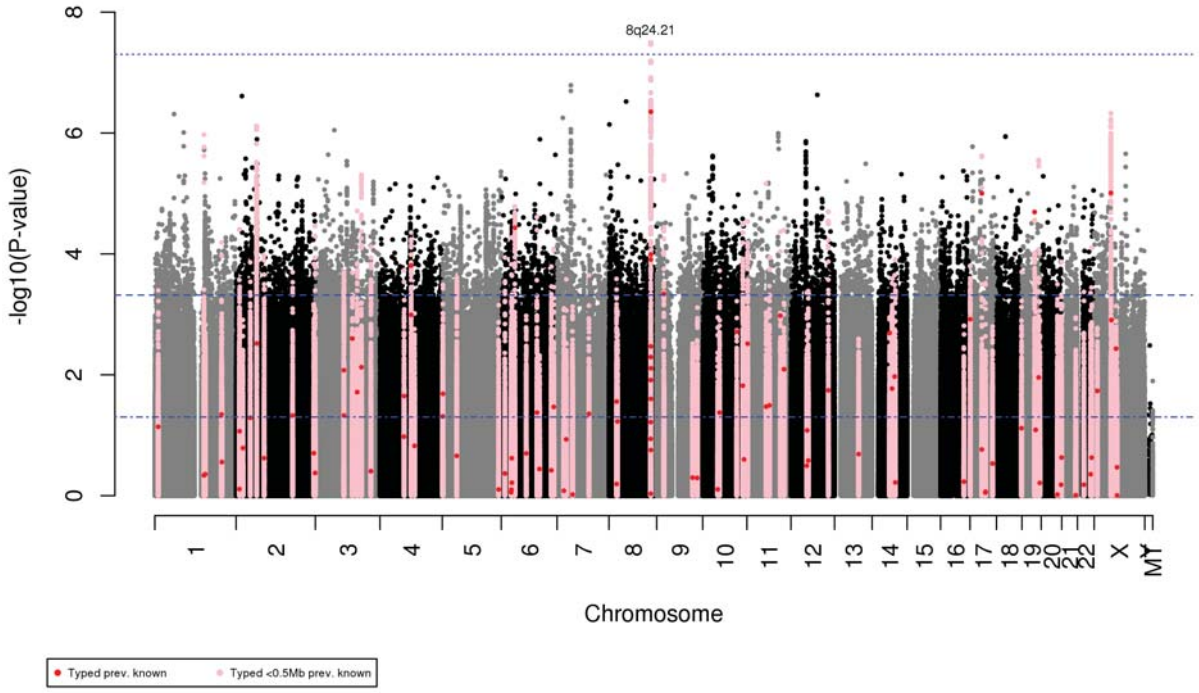


(S1.35) Round 5 of Meta-analysis fixed effects. $\lambda = 1.057$





(S1.36) Round 5 of Meta-analysis random effects. $\lambda = 0.873$



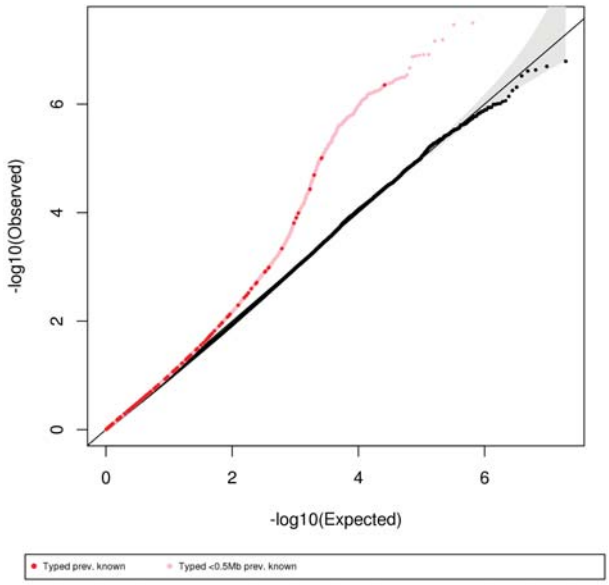
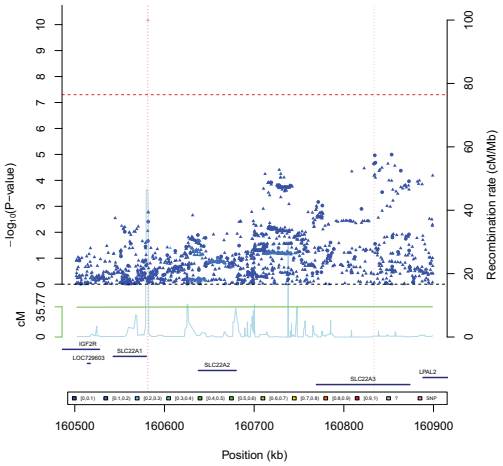
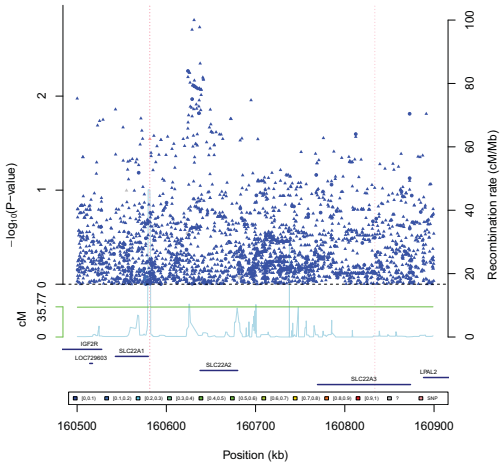


Figure S2: Local plots of the novel replicated hit (rs4646284), and the suggestive locus (rs2659124), in the four Kaiser groups and the meta-analysis of the Kaiser groups. FE, fixed effects; RE, random effects.

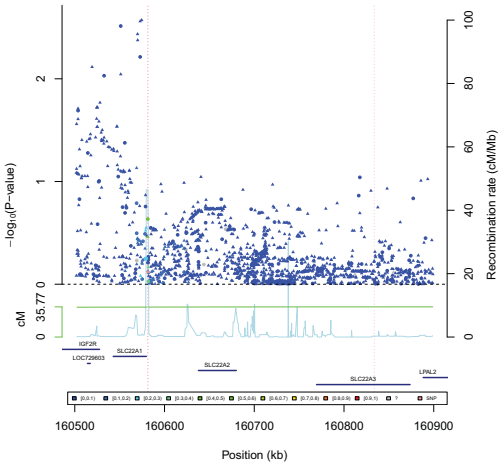
(S2.1) rs4646284 (Unconditional) - KP NH white



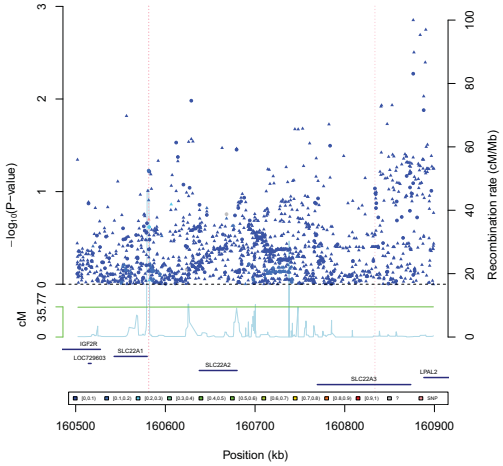
(S2.2) rs4646284 (Unconditional) - KP Af-Amer



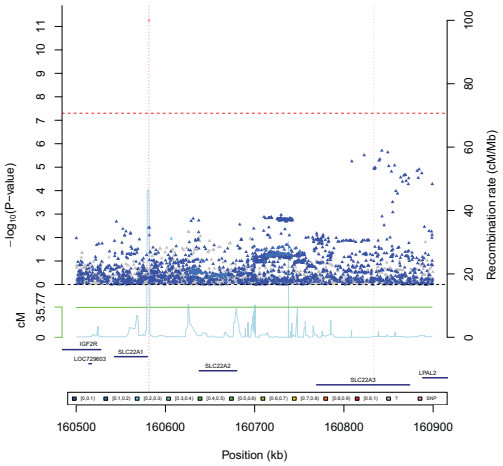
(S2.3) rs4646284 (Unconditional) - KP Asian



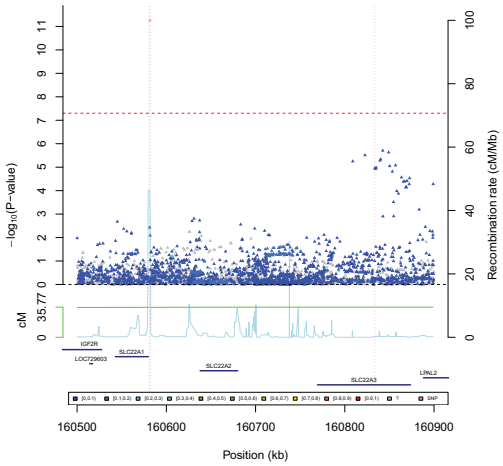
(S2.4) rs4646284 (Unconditional) - KP Latino



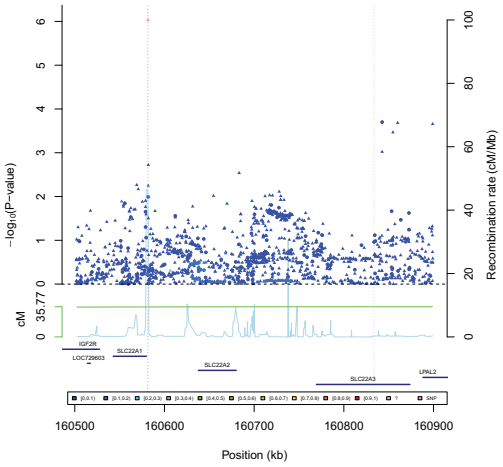
(S2.5) rs4646284 (Unconditional) - KP Meta FE (LD pattern EUR)



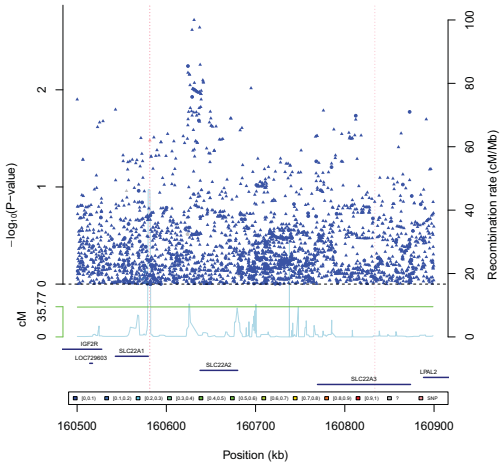
(S2.6) rs4646284 (Unconditional) - KP Meta RE (LD pattern EUR)



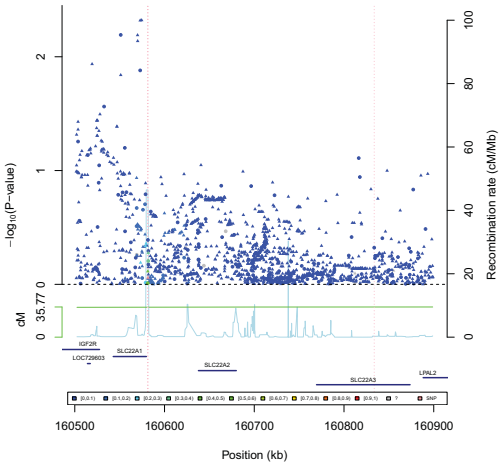
(S2.7) rs4646284 (Condition on rs9364554 and rs651164) - KP NH white



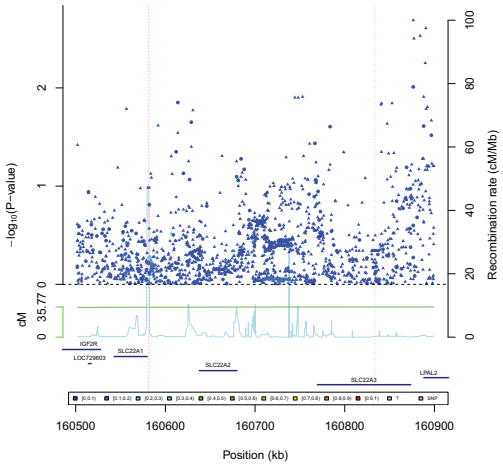
(S2.8) rs4646284 (Condition on rs9364554 and rs651164) - KP Af-Amer



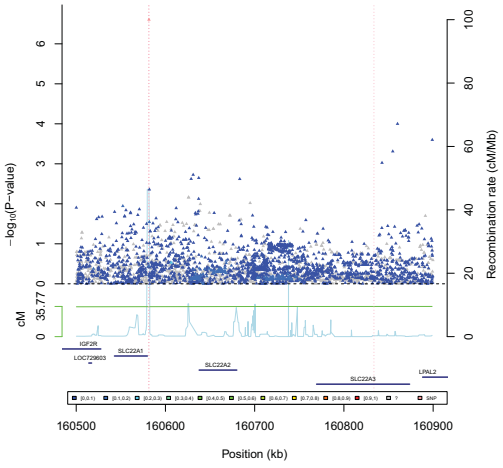
(S2.9) rs4646284 (Condition on rs9364554 and rs651164) - KP Asian



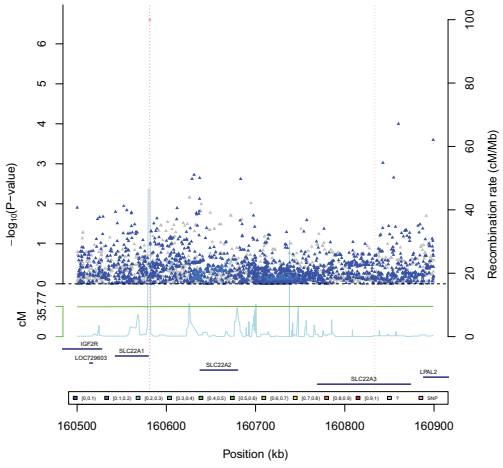
(S2.10) rs4646284 (Condition on rs9364554 and rs651164) - KP Latino



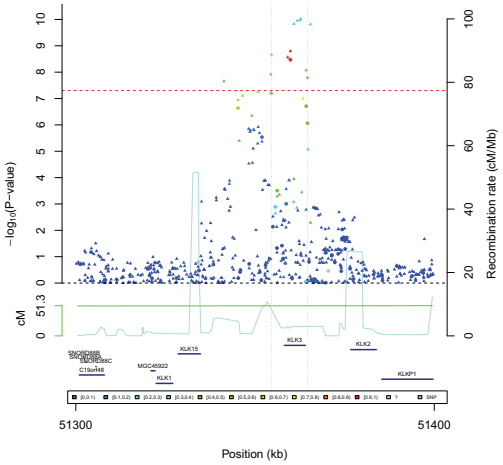
(S2.11) rs4646284 (Condition on rs9364554 and rs651164) - KP Meta FE
(LD pattern EUR)



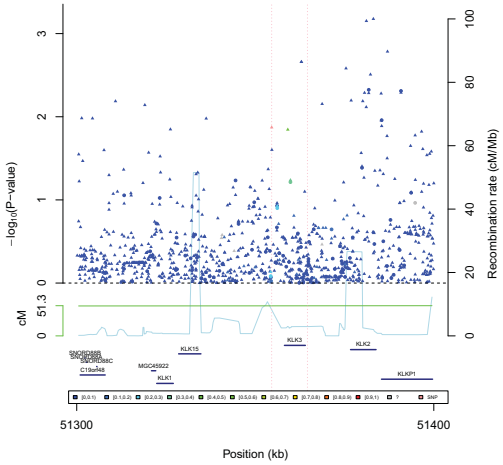
(S2.12) rs4646284 (Condition on rs9364554 and rs651164) - KP Meta RE
(LD pattern EUR)



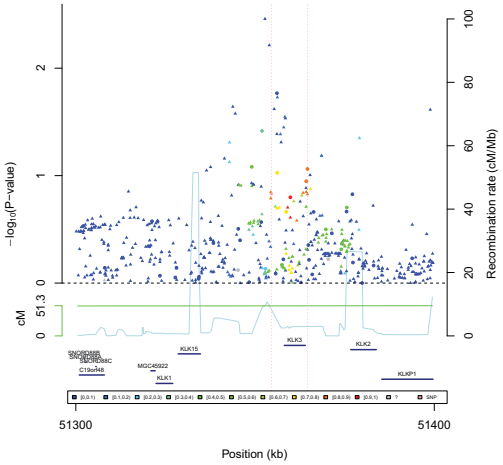
(S2.13) rs2659124 (Unconditional) - KP NH white



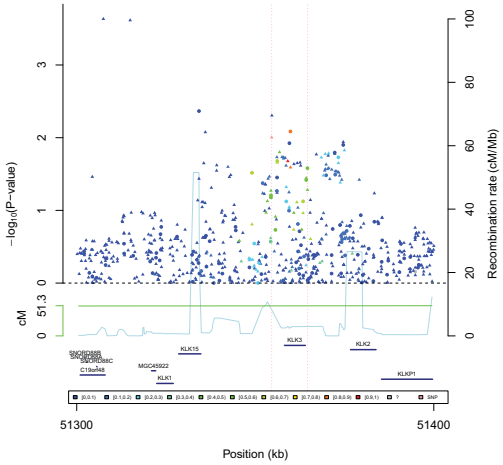
(S2.14) rs2659124 (Unconditional) - KP Af-Amer



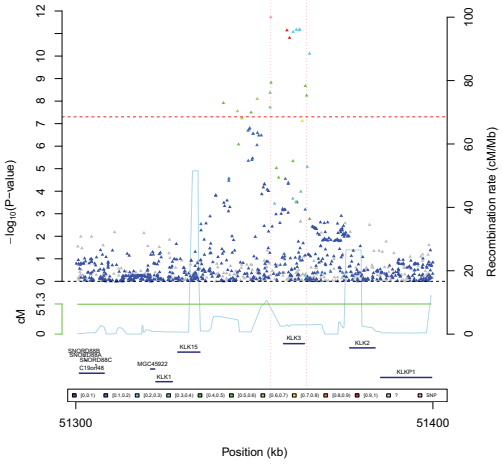
(S2.15) rs2659124 (Unconditional) - KP Asian



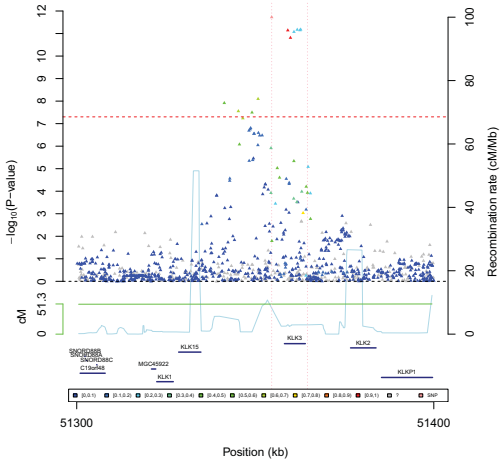
(S2.16) rs2659124 (Unconditional) - KP Latino



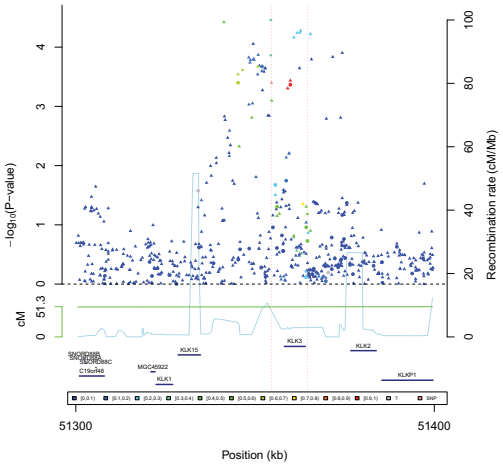
(S2.17) rs2659124 (Unconditional) - KP Meta FE (LD pattern EUR)



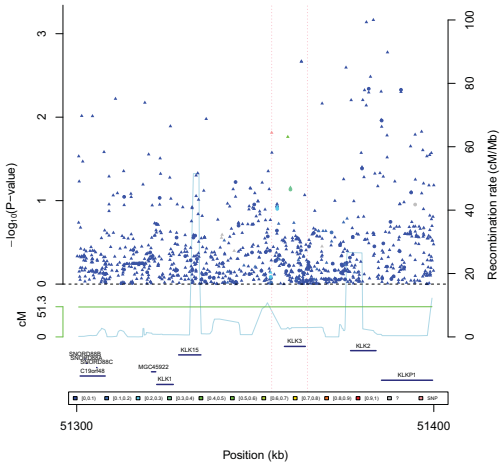
(S2.18) rs2659124 (Unconditional) - KP Meta RE (LD pattern EUR)



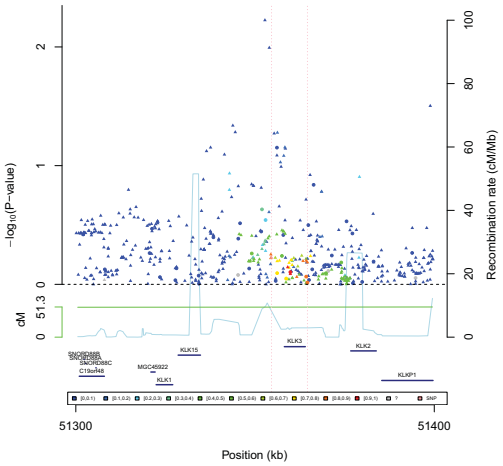
(S2.19) rs2659124 (Condition on rs2735839) - KP NH white



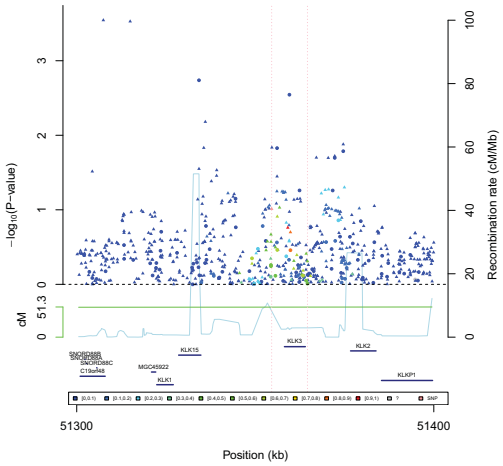
(S2.20) rs2659124 (Condition on rs2735839) - KP Af-Amer



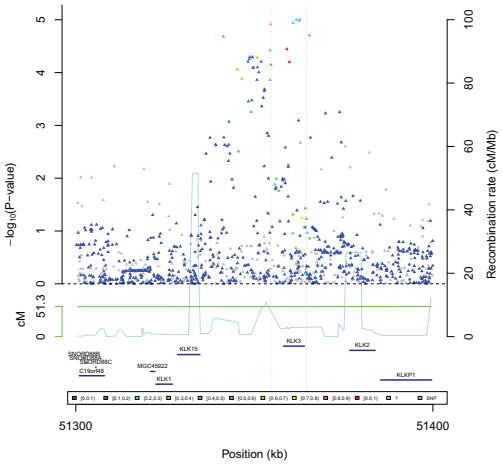
(S2.21) rs2659124 (Condition on rs2735839) - KP Asian



(S2.22) rs2659124 (Condition on rs2735839) - KP Latino



(S2.23) rs2659124 (Condition on rs2735839) - KP Meta FE (LD pattern EUR)



(S2.24) rs2659124 (Condition on rs2735839) - KP Meta RE (LD pattern EUR)

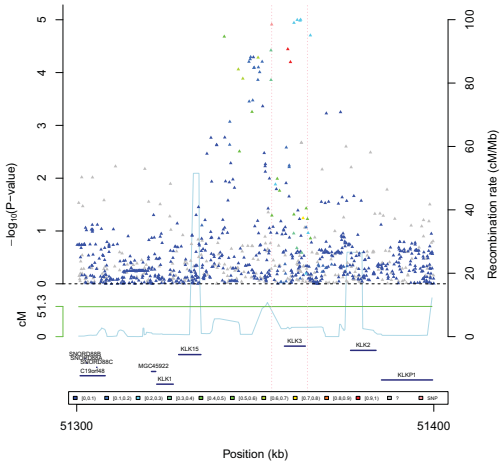
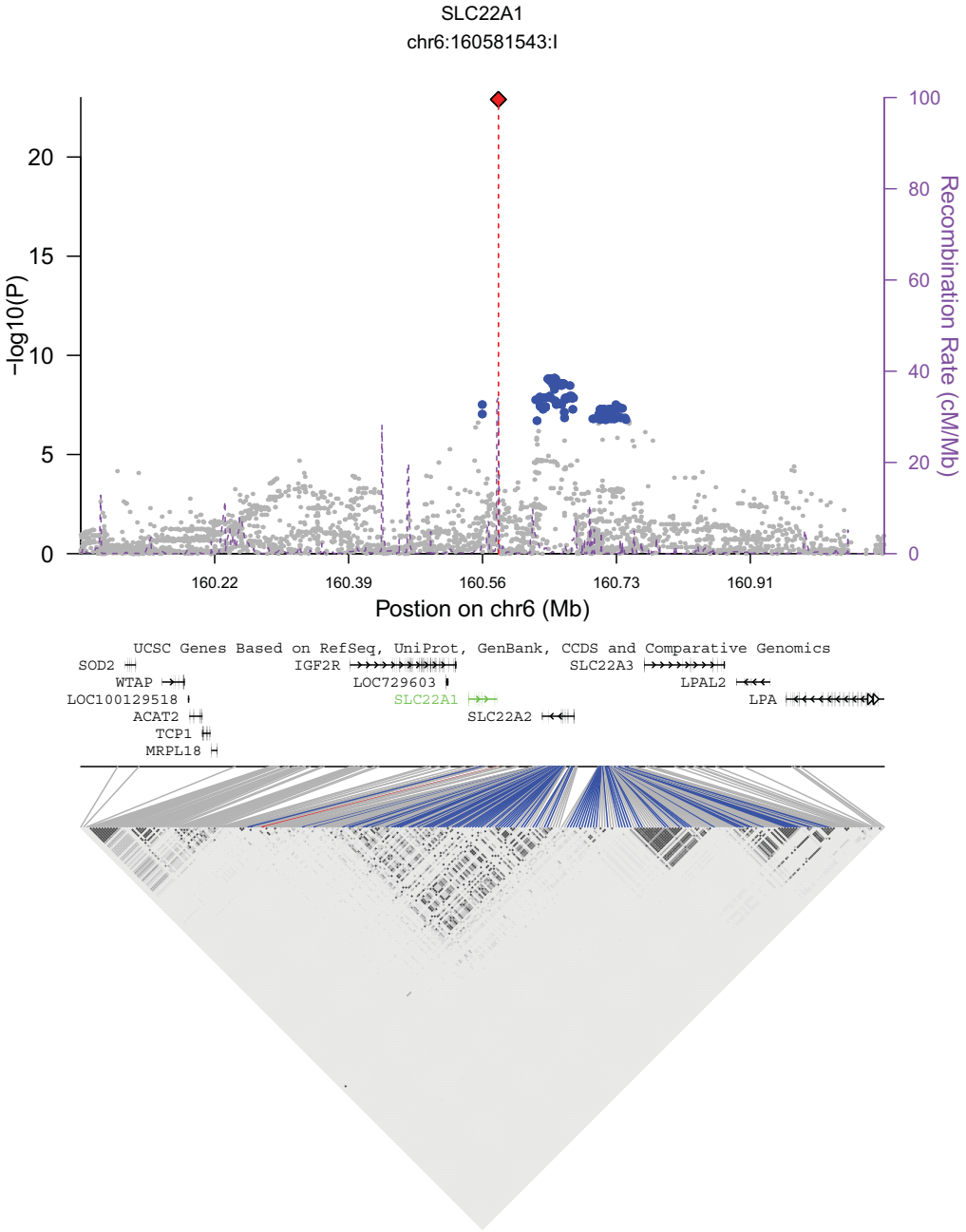


Figure S3: cis-eQTL for the two most significant genes (SLC22A1 and SLC22A3) surrounding the rs4646284 locus in the Mayo clinic dataset. The rs4646284 is the most significant locus at both genes, and is denoted in the figure by it's b37 chromosome position chr6:160581543:I.

(S3.1) Cis-eQTL of SLC22A1



(S3.2) Cis-eQTL of SLC22A3

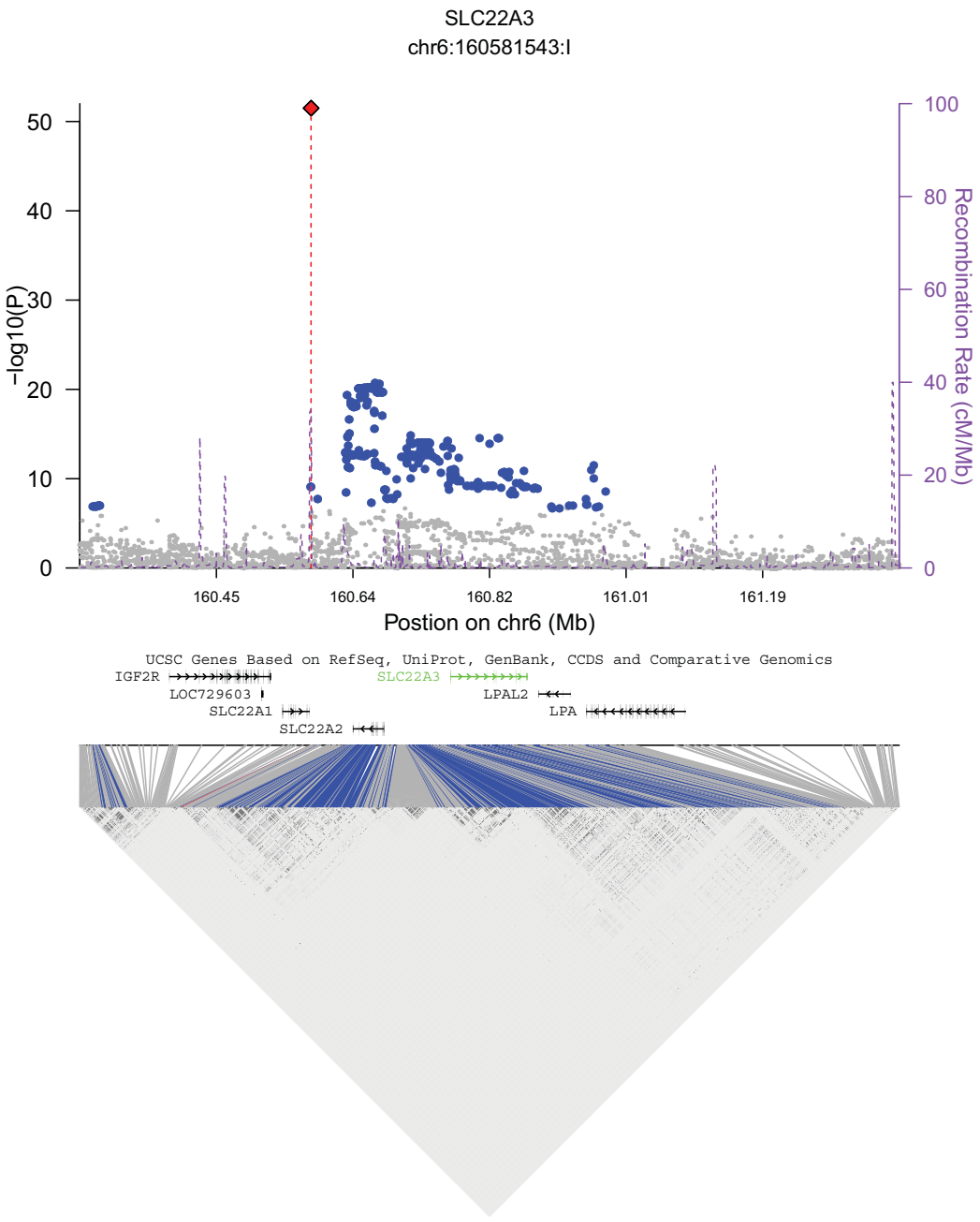


Figure S4: Comparison of variant associations from previous reports and results from each of the four major Kaiser race/ethnicity groups. Plotted values are the log odds ratios from pervious and current studies. Lines denote the 95% confidence intervals for the respective studies. The blue line is the y=x line, and the red line is the regression line (with no intercept).

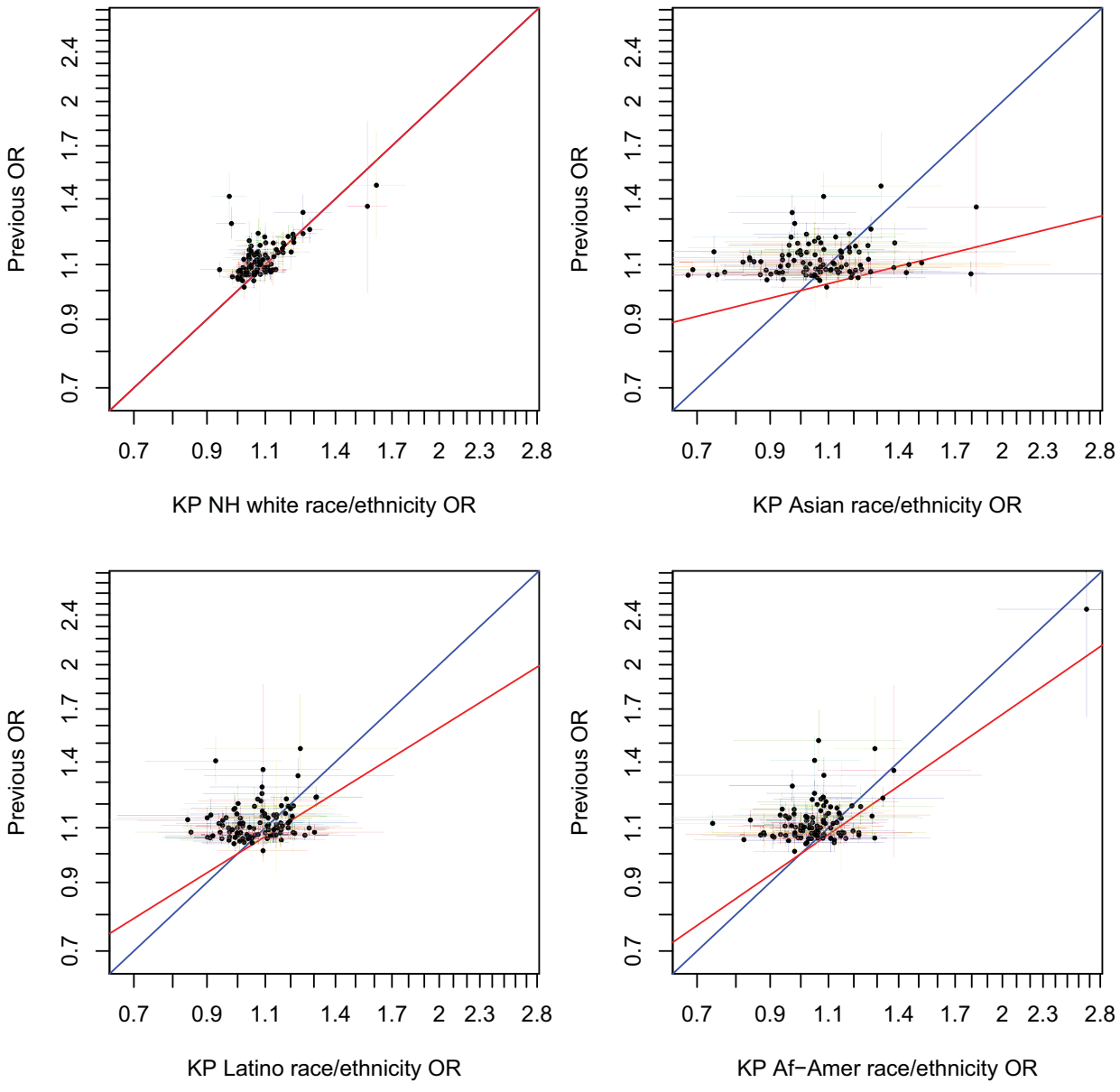


Figure S5: Prostate cancer AUC estimates for different combinations of covariates and the genetic risk score in the KP groups.