

Supplemental material for “A large electronic health record-based genome-wide association study of serum lipids”

Thomas J Hoffmann^{1,2}, Elizabeth Theusch³, Tanushree Haldar², Dilrini K Ranatunga⁴, Eric Jorgenson⁴, Marisa W Medina³, Mark N Kvale², Pui-Yan Kwok², Catherine Schaefer⁴, Ronald Krauss³, Carlos Iribarren⁴, Neil Risch^{1,2,4}

¹Department of Epidemiology and Biostatistics, University of California San Francisco, San Francisco, CA 94158, USA

²Institute for Human Genetics, University of California San Francisco, San Francisco, CA, 94143 USA

³Childrens Hospital Oakland Research Institute, Oakland, CA, 94609 USA

⁴Division of Research, Kaiser Permanente, Northern California, Oakland, CA 94612, USA

List of Tables

1	GERA covariate association.	2
2	Genomic inflation factors.	3
10	Top candidate <i>ABO</i> SNPs at <i>FUT2</i> secretors	4
11	<i>ABO</i> haplotype analysis	5
13	Correlation between lipid trait GRS.	6
14	Variance explained increases with more measurements.	7
15	GERA array heritability estimates.	8
16	Time to lipidemia treatment onset.	9
17	Mendelian lipid disorders.	11

List of Figures

1	Manhattan and Q-Q plots.	12
3	Extending the GLGC summary statistics from HapMap to 1000 Genomes.	41
4	Replication p-value distribution.	43
5	Effect size estimates in RPGEH GERA vs. previously reported.	44
6	Dominance Q-Q plots	45
7	Epistasis Q-Q plots	46
8	Interaction of rs2519093 (<i>FUT2</i>) and rs601338 (<i>ABO</i>) in GERA.	47
9	Effect size estimates in RPGEH GERA	48
10	Sex Q-Q plots	49
11	Heterogeneity of GERA non-Hispanic whites vs. other groups.	49
12	Boxplots of $p(1-p)\beta^2$ minor allele frequency distributions in GERA.	56
13	Benefit of repeated measures on SNP SEs.	57
14	Lipidemia treatment time-to-onset of GRS	58

Supplementary Table 1: GERA covariate association.

(a) Mean effect size differences in Latinos (n=7,795), East Asians (n=6,855), African Americans (n=2,958), and South Asians (n=439) compared to non-Hispanic whites (n=76,627) after adjusting for age, sex, and BMI. Est, mean effect size difference from non-Hispanic whites (where each lipid trait is normalized to a standard normal distribution).

	HDL Est	HDL P	LDL Est	LDL P	TC Est	TC P	TG Est	TG P
Latinos	-0.065	1.6e-10	-0.008	0.5	0.011	0.34	0.127	1.7e-30
East Asians	-0.052	1.7e-06	0.019	0.12	0.092	5.5e-14	0.280	5.3e-125
African Americans	0.191	2.6e-33	0.025	0.17	-0.068	0.00016	-0.457	2.3e-153
South Asians	-0.330	3.9e-16	-0.025	0.59	-0.034	0.46	0.344	6.2e-15

(b) Covariate association within each group.

(i) Non-Hispanic whites (n=76,627). PC₁ represents the North-Southeast European cline. PC₂ Southwest-Northeast European.

	HDL			LDL			TG			TC		
	Sign	r ²	p	Sign	r ²	p	Sign	r ²	p	Sign	r ²	p
Age _c	+	0.0016	4e-33	+	0.02	6.2e-78	+	0.02	2.8e-210	+	0.035	3.4e-192
Age _c ²	-	0.0011	1.4e-62	-	0.035	4.3e-202	-	0.022	2.3e-104	-	0.053	0
Age _c ³	-	0.0013	1.4e-06	-	0.021	1.3e-29	-	0.014	1.4e-57	-	0.034	3.2e-63
log(BMI) _c	-	0.11	0	+	0.02	1.3e-220	+	0.12	0	+	0.012	2.2e-185
log(BMI) _c ²	+	0.00027	0.00036	-	0.0059	4.6e-103	-	6.7e-05	1.1e-11	-	0.0029	3e-78
log(BMI) _c ³	+	0.044	1.3e-32	-	0.0057	1.5e-07	-	0.041	3.4e-65	-	0.0027	7.3e-13
Female	+	0.2	0	-	0.0076	2.5e-30	-	0.014	2.2e-73	+	0.0032	1.5e-196
PC ₁	+	1.5e-05	0.96	-	0.00032	1.2e-11	+	0.00046	0.41	-	4e-05	2.1e-08
PC ₂	+	0.00045	0.38	-	0.0003	0.0087	-	7.5e-05	0.68	-	7.2e-05	0.068

(ii) Latinos (n=7,795). PC₁ is European-Native American, PC₂ African-European.

	HDL			LDL			TG			TC		
	Sign	r ²	p	Sign	r ²	p	Sign	r ²	p	Sign	r ²	p
Age _c	+	0.00078	0.069	+	0.042	0.00091	+	0.035	1.7e-16	+	0.065	5.5e-09
Age _c ²	-	0.0013	0.0015	-	0.053	1.3e-18	-	0.033	5e-09	-	0.08	4.1e-28
Age _c ³	-	0.0015	0.59	-	0.041	6.1e-06	-	0.024	3.8e-07	-	0.062	4.6e-09
log(BMI) _c	-	0.099	5.7e-102	+	0.0054	1.1e-05	+	0.085	9.4e-91	+	0.0025	0.00017
log(BMI) _c ²	+	0.0025	0.025	-	0.0055	6.8e-11	-	0.0008	0.00035	-	0.0056	2.4e-09
log(BMI) _c ³	+	0.039	0.00046	+	0.00095	0.2	-	0.031	0.00017	+	0.00014	0.56
Female	+	0.16	1.1e-294	-	0.02	2.4e-17	-	0.031	5.5e-28	+	0.0029	0.82
PC ₁	+	0.0068	1.4e-06	+	0.00056	0.027	-	0.011	2.4e-16	+	0.00017	0.46
PC ₂	-	0.0024	2.3e-05	+	0.00039	0.17	+	0.006	7.1e-09	+	0.00073	0.066

(iii) East Asians (n=6,855). PC₁ is amount of European ancestry, PC₂ Northern-Southern East Asian ancestry.

	HDL			LDL			TG			TC		
	Sign	r ²	p	Sign	r ²	p	Sign	r ²	p	Sign	r ²	p
Age _c	+	6.4e-07	0.00027	+	0.06	4.2e-07	+	0.049	9.5e-14	+	0.091	1.3e-16
Age _c ²	-	0.00017	0.21	-	0.074	5.5e-21	-	0.048	1.3e-10	-	0.1	4.5e-30
Age _c ³	-	5.2e-05	0.35	-	0.058	2.9e-07	-	0.036	5.5e-07	-	0.081	1.2e-11
log(BMI) _c	-	0.12	5.8e-84	+	0.032	2.1e-19	+	0.098	5.7e-82	+	0.018	5.7e-16
log(BMI) _c ²	+	0.059	1.5e-10	-	0.026	1.3e-06	-	0.044	6.9e-08	-	0.015	0.00013
log(BMI) _c ³	+	0.069	1.5e-07	-	0.018	0.0021	-	0.049	1.7e-08	-	0.0091	0.0013
Female	+	0.17	3.2e-228	-	0.03	7.8e-17	-	0.045	8.7e-26	-	0.0061	0.91
PC ₁	-	0.00078	0.054	+	0.0013	0.042	+	0.0005	1.7e-05	+	0.0028	0.0065
PC ₂	+	0.0099	1.2e-07	-	8.2e-07	0.26	+	0.00077	0.0098	+	0.0025	0.043

(iv) African Americans (n=2,958). PC₁ is African-European, PC₂ is amount of East Asian ancestry.

	HDL			LDL			TG			TC		
	Sign	r ²	p	Sign	r ²	p	Sign	r ²	p	Sign	r ²	p
Age _c	+	0.0059	8e-06	+	0.028	0.004	+	0.025	0.00015	+	0.047	2.8e-06
Age _c ²	-	0.00081	0.64	-	0.04	1.3e-08	-	0.034	1.2e-08	-	0.058	2.6e-12
Age _c ³	-	0.0017	0.78	-	0.027	0.0031	-	0.021	0.00018	-	0.04	0.00016
log(BMI) _c	-	0.054	3e-28	+	0.0068	1.9e-07	+	0.038	3.6e-24	+	0.00098	0.0009
log(BMI) _c ²	+	0.003	0.14	-	0.0014	0.01	+	0.0029	0.59	-	0.0016	0.21
log(BMI) _c ³	+	0.025	0.015	-	0.0011	0.1	-	0.013	4.1e-05	-	4e-05	0.055
Female	+	0.11	9e-94	-	0.013	4.6e-06	-	0.022	5.4e-15	+	0.001	0.58
PC ₁	+	0.0011	0.91	-	0.00017	0.69	-	0.0017	3.3e-05	-	0.00015	0.15
PC ₂	-	0.00041	0.033	+	2.2e-05	0.55	+	0.00025	0.14	+	1.2e-05	0.74

(v) South Asians (n=439). PC₁ is European ancestry, PC₂ is East Asian ancestry.

	HDL			LDL			TG			TC		
	Sign	r ²	p	Sign	r ²	p	Sign	r ²	p	Sign	r ²	p
Age _c	+	0.0001	0.4	-	0.016	0.059	-	0.025	0.74	-	0.03	0.14
Age _c ²	-	0.00012	0.92	-	0.034	0.13	-	0.032	0.2	-	0.052	0.088
Age _c ³	+	0.00027	0.97	-	0.032	0.79	-	0.027	0.38	-	0.049	0.64
log(BMI) _c	-	0.051	0.00012	+	0.027	0.26	+	0.099	2.3e-06	+	0.034	0.11
log(BMI) _c ²	+	0.014	0.79	-	0.022	0.21	-	0.066	0.0017	-	0.037	0.022
log(BMI) _c ³	+	0.019	0.42	-	0.021	1	-	0.052	0.059	-	0.026	0.56
Female	+	0.23	2.7e-25	-	0.033	0.00043	-	0.083	4e-07	-	0.013	0.083
PC ₁	-	0.0078	0.013	+	2.2e-05	20.81	+	0.0058	0.013	+	3e-05	0.78
PC ₂	+	0.0023	0.49	+	1.8e-05	0.84	-	2.2e-06	1	+	0.00039	0.7

Supplementary Table 2: Genomic inflation factors. GERA non-Hispanic whites, n=76,627; GERA Latinos, n=7,795; GERA East Asians, n=6,855; GERA African Americans, n=2,958; GERA South Asians, n=439; GERA, n=94,674; GLGC, n=94,674; GERA+GLGC, n=189,269. All tests were two-sided.

	LDL	HDL	TC	TG
GERA non-Hispanic White	1.10/1.10	1.15/1.15	1.15/1.10	1.15/1.15
GERA Latino	1.00/1.00	1.05/1.00	1.00/1.00	1.00/1.00
GERA East Asian	1.00/1.00	1.00/1.00	1.05/1.05	1.05/1.05
GERA African American	1.00/1.00	1.00/1.00	1.00/1.00	1.00/1.00
GERA South Asian	1.04/1.04	1.02/1.02	1.02/1.02	1.01/1.00
GERA Meta	1.07	1.09	1.07	1.09
GERA+GLGC Meta	1.07	1.10	1.07	1.09

Supplementary Table 10: Top candidate *ABO* SNPs at *FUT2* secretors. Discovery was done in the meta-analysis (n=94,674) of GERA non-Hispanic whites (n=76,627), Latinos (7,795), East Asians (n=6,855), African Americans (2,958), and South Asians (n=439), each using linear regression, two-sided test.

SNP	Chr	Pos	Allele	non-Hispanic White				Latino				East Asian				African American				Meta-analysis			
				Eff	P	Eff	P	Eff	P	Eff	P	Eff	P	Eff	P	Eff	P	I ²	Het.	P			
chr9:136138765:D	9	136138765	G/GGGCCCCACCACTA	0.127	1.2e-50	0.141	9.2e-08	0.070	0.12	0.123	0.033	0.126	5e-58	0	0.52								
chr9:13613907:D	9	13613907	G/GAAACTGCC	0.113	2.5e-48	0.189	2.2e-15	0.098	2.4e-05	0.097	0.027	0.118	9.2e-65	73	0.012								
rs2519093	9	136141870	T/C	0.131	2e-59	0.184	1.6e-13	0.109	2.9e-06	0.064	0.2	0.132	5.5e-75	59	0.061								
chr9:136145424:D	9	136145424	A/AC	0.111	2.7e-46	0.189	3.2e-15	0.080	0.00071	0.092	0.033	0.114	1.3e-60	77	0.0044								
rs9411378	9	136145425	A/C	0.112	9.1e-47	0.188	4e-15	0.080	0.00071	0.093	0.032	0.115	4.7e-61	77	0.0049								
rs550057	9	136146597	T/C	0.111	2.1e-46	0.188	2.5e-15	0.103	8e-06	0.100	0.023	0.116	2.6e-63	72	0.012								
rs507666	9	136149399	A/G	0.132	6.4e-60	0.185	1.1e-13	0.105	5.9e-06	0.068	0.17	0.132	2.6e-75	61	0.051								
chr9:136149709:D	9	136149709	A/AC	0.132	2.4e-59	0.176	8e-12	0.082	0.056	0.076	0.22	0.133	1.1e-69	43	0.16								
rs532436	9	136149830	A/G	0.132	3.6e-60	0.185	1.3e-13	0.109	2.7e-06	0.068	0.18	0.133	6.4e-76	59	0.065								
rs600038	9	136151806	C/T	0.122	6.9e-53	0.173	1.2e-12	0.109	2.7e-06	0.066	0.15	0.123	6.8e-68	52	0.099								
rs651007	9	136153875	T/C	0.120	8.8e-52	0.174	1e-12	0.108	3e-06	0.066	0.15	0.122	8.5e-67	54	0.09								
rs579459	9	136154168	C/T	0.121	9.6e-53	0.173	1.4e-12	0.113	1e-06	0.067	0.15	0.123	3.1e-68	50	0.11								
rs649129	9	136154304	T/C	0.121	9.1e-53	0.173	1.4e-12	0.110	2.2e-06	0.067	0.15	0.123	6.4e-68	51	0.11								
rs495828	9	136154867	T/G	0.121	9.1e-53	0.173	1.6e-12	0.110	2.2e-06	0.062	0.18	0.123	9.2e-68	52	0.1								
rs635634	9	136155000	T/C	0.133	7.2e-61	0.181	4e-13	0.111	1.5e-06	0.066	0.19	0.133	1.6e-76	53	0.092								

Supplementary Table 11: *ABO* haplotype analysis. Haplotype pairs with at least 50 individuals present are included, for the SNPs rs2519093 / rs507666 / chr9:136149709:D / rs532436 / rs635634. Discovery was done in the meta-analysis (n=94,674) of GERA non-Hispanic whites (n=76,627), Latinos (7,795), East Asians (n=6,855), African Americans (2,958), and South Asians (n=439), each using linear regression, two-sided test. Mean, mean residual LDL for each group; SE, standard error. All tests two-sided.

Haplotype 1	Haplotype 2	Pop	Compare to all by t-test			Compare to all by t-test		
			C/G/AC/G/C	C/G/AC/G/C	t	C/G/AC/G/C+	C/G/AC/G/C	t
C/G/AC/G/C	T/A/A/A/T	non-Hispanic white	38177	0.017	0.005	T/A/A/A/T	T/A/A/A/T	t
		Latino	4499	0.024	0.014			P
		East Asian	4264	0.035	0.014			
		African American	1775	0.116	0.025			
		All	48715	0.023	0.004			
C/G/AC/G/C	T/A/A/A/C	non-Hispanic white	17891	0.149	0.007			
		Latino	1661	0.197	0.025			
		East Asian	401	0.059	0.046			
		African American	236	0.194	0.065			
		All	20189	0.152	0.007			
C/G/AC/G/C	T/A/A/A/C	non-Hispanic white	90	-0.035	0.082	0.53	0.59	1.83
C/G/AC/G/C	C/G/AC/G/T	non-Hispanic white	100	0.103	0.091	0.93	0.35	0.067
C/G/AC/G/C	T/A/AC/A/T	non-Hispanic white	1772	0.137	0.021			
		Latino	303	0.124	0.054			
		East Asian	193	0.180	0.078			
		African American	176	0.223	0.072			
		All	2444	0.145	0.019			
T/A/A/A/T	T/A/A/A/T	non-Hispanic white	2129	0.153	0.020			
T/A/A/A/T	T/A/A/A/T	Latino	148	0.405	0.091			
T/A/A/A/T	T/A/A/A/T	All	2288	0.170	0.020			
T/A/A/A/T	T/A/AC/A/T	non-Hispanic white	87	0.307	0.099			
T/A/AC/A/T	T/G/AC/A/T	East Asian	124	0.112	0.083			
C/G/AC/G/C	T/G/AC/G/C	non-Hispanic white	92	0.024	0.099			

Supplementary Table 13: Pearson's correlation between lipid trait GRS (using all previously-reported and newly-reported lead and conditional SNPs with $R^2 < 0.3$). GERA non-Hispanic whites (n=76,627), Latinos (7,795), East Asians (n=6,855), and African Americans (2,958).

non-Hispanic white females:

	HDL	LDL	TC	TG
HDL	1.000 (1.000, 1.000)	-0.162 (-0.171, -0.153)	0.083 (0.074, 0.092)	-0.481 (-0.488, -0.473)
LDL	-0.162 (-0.171, -0.153)	1.000 (1.000, 1.000)	0.935 (0.934, 0.936)	0.259 (0.250, 0.267)
TC	0.083 (0.074, 0.092)	0.935 (0.934, 0.936)	1.000 (1.000, 1.000)	0.359 (0.351, 0.367)
TG	-0.481 (-0.488, -0.473)	0.259 (0.250, 0.267)	0.359 (0.351, 0.367)	1.000 (1.000, 1.000)

non-Hispanic white males:

	HDL	LDL	TC	TG
HDL	1.000 (1.000, 1.000)	0.021 (0.010, 0.032)	0.136 (0.125, 0.147)	-0.504 (-0.512, -0.495)
LDL	0.021 (0.010, 0.032)	1.000 (1.000, 1.000)	0.933 (0.932, 0.935)	0.107 (0.097, 0.118)
TC	0.136 (0.125, 0.147)	0.933 (0.932, 0.935)	1.000 (1.000, 1.000)	0.328 (0.319, 0.338)
TG	-0.504 (-0.512, -0.495)	0.107 (0.097, 0.118)	0.328 (0.319, 0.338)	1.000 (1.000, 1.000)

Latino females:

	HDL	LDL	TC	TG
HDL	1.000 (1.000, 1.000)	-0.120 (-0.148, -0.092)	0.127 (0.099, 0.155)	-0.471 (-0.493, -0.448)
LDL	-0.120 (-0.148, -0.092)	1.000 (1.000, 1.000)	0.930 (0.926, 0.934)	0.272 (0.245, 0.298)
TC	0.127 (0.099, 0.155)	0.930 (0.926, 0.934)	1.000 (1.000, 1.000)	0.382 (0.357, 0.406)
TG	-0.471 (-0.493, -0.448)	0.272 (0.245, 0.298)	0.382 (0.357, 0.406)	1.000 (1.000, 1.000)

Latino males:

	HDL	LDL	TC	TG
HDL	1.000 (1.000, 1.000)	0.053 (0.017, 0.088)	0.173 (0.139, 0.207)	-0.486 (-0.512, -0.458)
LDL	0.053 (0.017, 0.088)	1.000 (1.000, 1.000)	0.928 (0.923, 0.932)	0.121 (0.086, 0.156)
TC	0.173 (0.139, 0.207)	0.928 (0.923, 0.932)	1.000 (1.000, 1.000)	0.350 (0.319, 0.381)
TG	-0.486 (-0.512, -0.458)	0.121 (0.086, 0.156)	0.350 (0.319, 0.381)	1.000 (1.000, 1.000)

East Asian females:

	HDL	LDL	TC	TG
HDL	1.000 (1.000, 1.000)	-0.000 (-0.031, 0.031)	0.254 (0.225, 0.283)	-0.454 (-0.479, -0.429)
LDL	-0.000 (-0.031, 0.031)	1.000 (1.000, 1.000)	0.911 (0.905, 0.916)	0.293 (0.265, 0.321)
TC	0.254 (0.225, 0.283)	0.911 (0.905, 0.916)	1.000 (1.000, 1.000)	0.421 (0.396, 0.446)
TG	-0.454 (-0.479, -0.429)	0.293 (0.265, 0.321)	0.421 (0.396, 0.446)	1.000 (1.000, 1.000)

East Asian males:

	HDL	LDL	TC	TG
HDL	1.000 (1.000, 1.000)	0.125 (0.088, 0.161)	0.229 (0.194, 0.264)	-0.462 (-0.490, -0.433)
LDL	0.125 (0.088, 0.161)	1.000 (1.000, 1.000)	0.908 (0.901, 0.914)	0.162 (0.126, 0.198)
TC	0.229 (0.194, 0.264)	0.908 (0.901, 0.914)	1.000 (1.000, 1.000)	0.433 (0.402, 0.462)
TG	-0.462 (-0.490, -0.433)	0.162 (0.126, 0.198)	0.433 (0.402, 0.462)	1.000 (1.000, 1.000)

African American females:

	HDL	LDL	TC	TG
HDL	1.000 (1.000, 1.000)	-0.178 (-0.223, -0.132)	0.059 (0.013, 0.106)	-0.524 (-0.557, -0.489)
LDL	-0.178 (-0.223, -0.132)	1.000 (1.000, 1.000)	0.940 (0.934, 0.945)	0.239 (0.195, 0.283)
TC	0.059 (0.013, 0.106)	0.940 (0.934, 0.945)	1.000 (1.000, 1.000)	0.320 (0.277, 0.361)
TG	-0.524 (-0.557, -0.489)	0.239 (0.195, 0.283)	0.320 (0.277, 0.361)	1.000 (1.000, 1.000)

African American males:

	HDL	LDL	TC	TG
HDL	1.000 (1.000, 1.000)	-0.072 (-0.128, -0.015)	0.070 (0.013, 0.126)	-0.429 (-0.474, -0.381)
LDL	-0.072 (-0.128, -0.015)	1.000 (1.000, 1.000)	0.940 (0.933, 0.947)	0.208 (0.153, 0.261)
TC	0.070 (0.013, 0.126)	0.940 (0.933, 0.947)	1.000 (1.000, 1.000)	0.407 (0.359, 0.453)
TG	-0.429 (-0.474, -0.381)	0.208 (0.153, 0.261)	0.407 (0.359, 0.453)	1.000 (1.000, 1.000)

Supplementary Table 14: Increase in variance explained with a greater number of repeated independent measures in GERA non-Hispanic whites (for a fixed sample size of 34,936 only individuals with 5 or more measures were included). Variance explained was calculated using a risk score of the previously-described hits with previous effect sizes.

# Measurements	HDL	LDL	TG	TC
1	0.076	0.073	0.059	0.066
2	0.089	0.086	0.071	0.078
3	0.095	0.091	0.075	0.083
4	0.098	0.095	0.079	0.087
≥ 5 (all available)	0.101	0.099	0.084	0.088
Infinite (no measurement error)	0.108	0.105	0.088	0.097

Supplementary Table 15: GERA array heritability estimates. The method using GCTA required PC adjustment, whereas the REAP method does not. Adj PC, Adjusted for PCs; Y, yes; N, no; GRM, genotype relationship matrix calculated with GCTA (does not account for population structure) or PC-Relate (which accounts for population structure).

Trait	Adj PC	GRM	Method	Genotypes	h^2	N
LDL	N	GCTA	GCTA	Genotyped	23.3 (21.4, 25.2)	55163
LDL	N	GCTA	GCTA	Imputed	30.1 (27.7, 32.5)	55163
LDL	N	GCTA	GEAR	Genotyped	19.8 (17.8, 21.7)	55163
LDL	N	GCTA	GEAR	Imputed	21.1 (19.3, 22.9)	55163
LDL	N	PC-Relate	GEAR	Genotyped	17.2 (15.4, 19.0)	59327
LDL	N	PC-Relate	GEAR	Imputed	19.3 (17.6, 21.0)	59327
LDL	Y	GCTA	GCTA	Genotyped	23.3 (21.4, 25.2)	55163
LDL	Y	GCTA	GCTA	Imputed	30.1 (27.7, 32.5)	55163
LDL	Y	GCTA	GEAR	Genotyped	19.8 (17.8, 21.7)	55163
LDL	Y	GCTA	GEAR	Imputed	20.7 (18.9, 22.5)	55163
LDL	Y	PC-Relate	GEAR	Genotyped	16.9 (15.0, 18.7)	59327
LDL	Y	PC-Relate	GEAR	Imputed	18.8 (17.1, 20.4)	59327
HDL	N	GCTA	GCTA	Genotyped	33.2 (31.3, 35.1)	55163
HDL	N	GCTA	GCTA	Imputed	36.2 (33.8, 38.6)	55163
HDL	N	GCTA	GEAR	Genotyped	25.6 (23.6, 27.5)	55163
HDL	N	GCTA	GEAR	Imputed	27.6 (25.9, 29.4)	55163
HDL	N	PC-Relate	GEAR	Genotyped	27.1 (25.3, 28.9)	59327
HDL	N	PC-Relate	GEAR	Imputed	28.1 (26.5, 29.7)	59327
HDL	Y	GCTA	GCTA	Genotyped	32.8 (31.0, 34.7)	55163
HDL	Y	GCTA	GCTA	Imputed	35.8 (33.4, 38.2)	55163
HDL	Y	GCTA	GEAR	Genotyped	26.2 (24.3, 28.1)	55163
HDL	Y	GCTA	GEAR	Imputed	24.1 (22.3, 25.9)	55163
HDL	Y	PC-Relate	GEAR	Genotyped	27.8 (26.0, 29.5)	59327
HDL	Y	PC-Relate	GEAR	Imputed	24.8 (23.2, 26.5)	59327
TG	N	GCTA	GCTA	Genotyped	30.6 (28.8, 32.5)	55163
TG	N	GCTA	GCTA	Imputed	36.8 (34.4, 39.2)	55163
TG	N	GCTA	GEAR	Genotyped	26.3 (24.4, 28.1)	55163
TG	N	GCTA	GEAR	Imputed	28.4 (26.7, 30.1)	55163
TG	N	PC-Relate	GEAR	Genotyped	24.4 (22.6, 26.1)	59327
TG	N	PC-Relate	GEAR	Imputed	26.6 (25.0, 28.2)	59327
TG	Y	GCTA	GCTA	Genotyped	30.5 (28.7, 32.4)	55163
TG	Y	GCTA	GCTA	Imputed	36.7 (34.3, 39.1)	55163
TG	Y	GCTA	GEAR	Genotyped	26.3 (24.5, 28.2)	55163
TG	Y	GCTA	GEAR	Imputed	27.8 (26.1, 29.5)	55163
TG	Y	PC-Relate	GEAR	Genotyped	24.4 (22.7, 26.1)	59327
TG	Y	PC-Relate	GEAR	Imputed	26.2 (24.6, 27.8)	59327
TC	N	GCTA	GCTA	Genotyped	25.3 (23.4, 27.1)	55163
TC	N	GCTA	GCTA	Imputed	33.0 (30.6, 35.5)	55163
TC	N	GCTA	GEAR	Genotyped	23.1 (21.1, 25.0)	55163
TC	N	GCTA	GEAR	Imputed	25.6 (23.8, 27.3)	55163
TC	N	PC-Relate	GEAR	Genotyped	20.9 (19.1, 22.7)	59327
TC	N	PC-Relate	GEAR	Imputed	24.0 (22.3, 25.6)	59327
TC	Y	GCTA	GCTA	Genotyped	25.3 (23.4, 27.1)	55163
TC	Y	GCTA	GCTA	Imputed	33.0 (30.6, 35.4)	55163
TC	Y	GCTA	GEAR	Genotyped	23.2 (21.2, 25.1)	55163
TC	Y	GCTA	GEAR	Imputed	25.0 (23.2, 26.8)	55163
TC	Y	PC-Relate	GEAR	Genotyped	20.7 (18.9, 22.5)	59327
TC	Y	PC-Relate	GEAR	Imputed	23.2 (21.6, 24.9)	59327

Supplementary Table 16: Time to lipedemia treatment onset using a Cox proportional hazards model. Non-hispanic white females, n=44,856; non-Hispanic white males, n=31,771; Latino females, n=4,708; Latino males, n=3,087; East Asian females, n=4,013; East Asian males, n=2,842; African American males, n=1,761; African American females, n=1,197.

LDL GRS:

Group	Sex	HRI	GRS	LDL	SE	GRS	LDL	P	GRS	LDL	Concordance
non-Hispanic white	Female	2.504		0.018			10 ⁻³⁵⁰		0.610		
non-Hispanic white	Male	2.198		0.020			10 ⁻³⁴⁵		0.590		
Latino	Female	2.399	0.061				10 ⁻⁴⁴⁶		0.604		
Latino	Male	2.227	0.068				10 ⁻³¹		0.584		
East Asian	Female	1.848	0.095				1.3e-10		0.548		
East Asian	Male	1.967	0.091				10 ⁻¹³		0.553		
African American	Female	1.881	0.081				10 ⁻¹⁴		0.584		
African American	Male	1.841	0.088				10 ⁻¹¹		0.577		
Meta	Female	2.442	0.017				10 ⁻⁶¹²		—		
Meta	Male	2.174	0.018				10 ⁻³⁹⁷		—		

HDL GRS:

Group	Sex	HRI	GRS	LDL	SE	GRS	LDL	P	GRS	LDL	Concordance
non-Hispanic white	Female	0.717		0.021			10 ⁻³⁴		0.534		
non-Hispanic white	Male	0.787		0.024			10 ⁻²²		0.522		
Latino	Female	0.716	0.069				1.6e-06		0.536		
Latino	Male	0.823	0.078				0.013		0.517		
East Asian	Female	0.916	0.088				0.32		0.514		
East Asian	Male	0.818	0.096				0.035		0.520		
African American	Female	0.834	0.098				0.058		0.513		
African American	Male	0.870	0.119				0.24		0.512		
Meta	Female	0.730	0.019				10 ⁻⁵⁸		—		
Meta	Male	0.794	0.022				10 ⁻²⁵		—		

TG GRS:

Group	Sex	HRI	GRS	TG	SE	GRS	TG	P	GRS	TG	Concordance
non-Hispanic white	Female	1.784		0.023			10 ⁻¹³³		0.556		
non-Hispanic white	Male	1.511		0.021			10 ⁻⁸²		0.543		
Latino	Female	1.738	0.074				10 ⁻¹³		0.557		
Latino	Male	1.583	0.070				10 ⁻¹⁰		0.547		
East Asian	Female	1.563	0.090				7.1e-07		0.545		
East Asian	Male	1.533	0.077				3.2e-08		0.543		
African American	Female	1.373	0.110				0.0039		0.528		
African American	Male	1.555	0.111				6.5e-05		0.540		
Meta	Female	1.750	0.021				10 ⁻¹⁵³		—		
Meta	Male	1.519	0.019				10 ⁻¹⁰¹		—		

LDL and TG GRS:

Group	Sex	HRI	GRS	LDL	SE	GRS	LDL	HRI	GRS	TG	SE	GRS	TG	P	GRS	TG	Concordance
non-Hispanic white	Female	2.353	0.019	10 ⁻⁴⁴⁸		1.340			0.024	10 ⁻³³		0.614					
non-Hispanic white	Male	2.128	0.020	10 ⁻³¹⁷		1.396			0.022	10 ⁻⁵³		0.596					
Latino	Female	2.250	0.063	10 ⁻³⁷		1.334			0.077			0.608			0.00017		
Latino	Male	2.132	0.069	10 ⁻²⁸		1.440			0.070			0.591			2.3e-07		
East Asian	Female	1.689	0.059	1.3e-07		1.366			0.094			0.558			0.00087		
East Asian	Male	1.832	0.093	10 ⁻¹⁰		1.398			0.079			0.562			2e-05		
African American	Female	1.843	0.084	10 ⁻¹³		1.116			0.114			0.584			0.0073		
African American	Male	1.760	0.089	2.4e-10		1.352			0.112			0.579			0.0073		
Meta	Female	2.297	0.017	10 ⁻⁴⁹⁷		1.332			0.022	10 ⁻³⁸		—			—		
Meta	Male	2.099	0.018	10 ⁻³⁶⁰		1.398			0.020	10 ⁻⁶⁴		—			—		

LDL and HDL GRS:

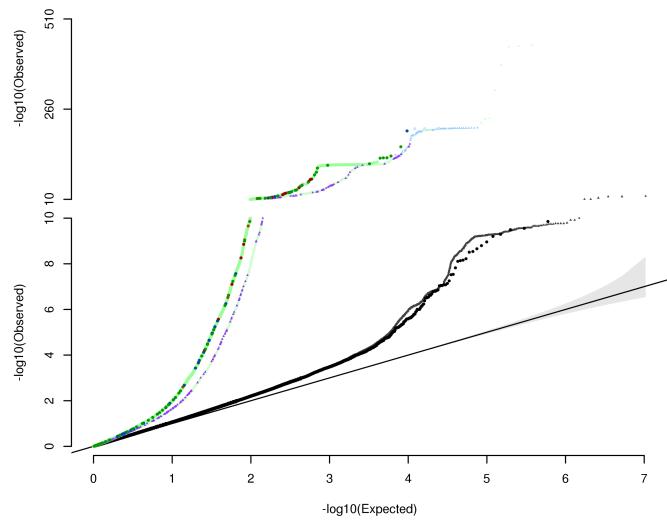
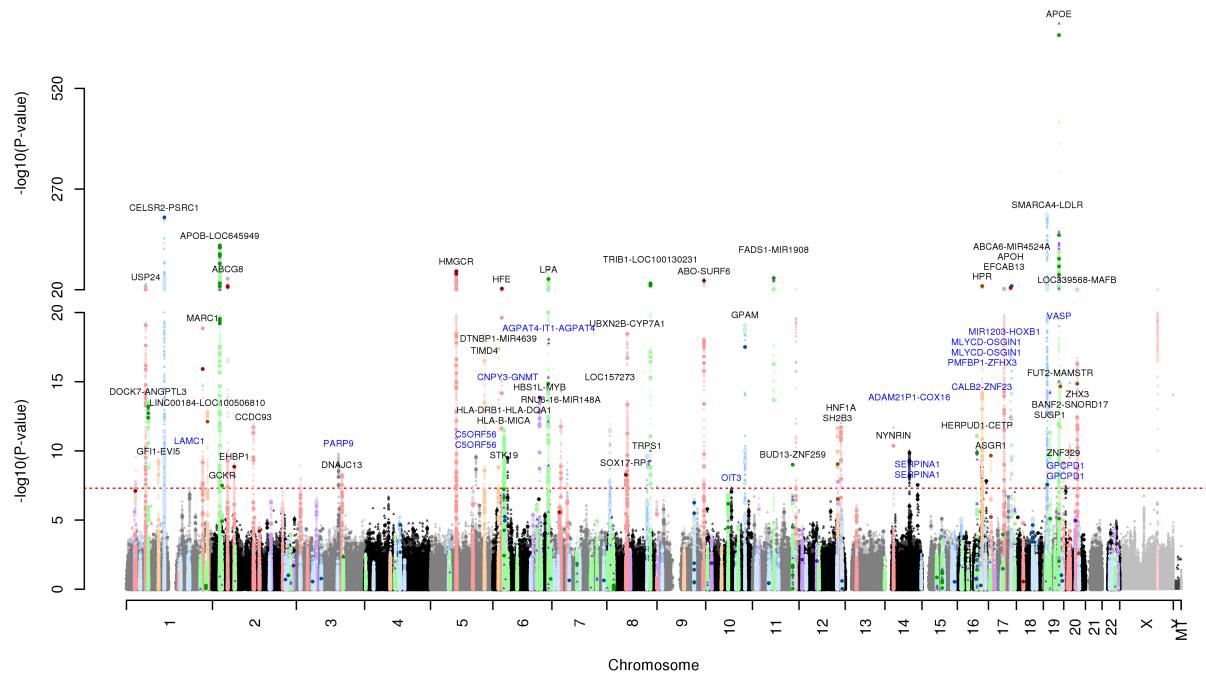
LDL, TG, and HDL GRS:

Supplementary Table 17: Mendelian lipid disorders.

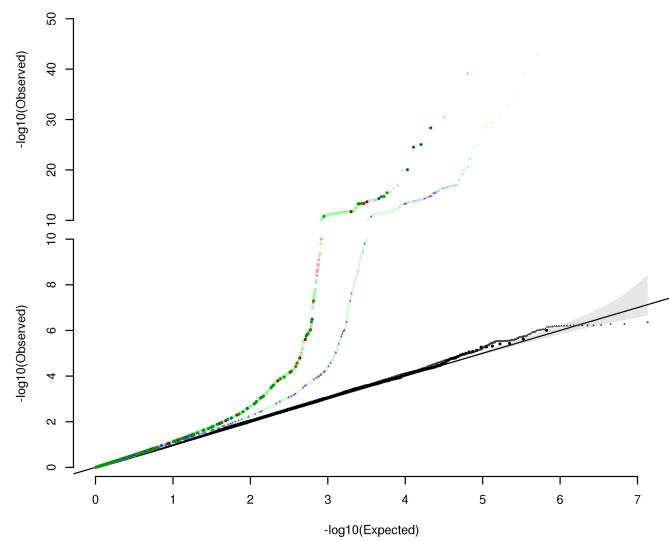
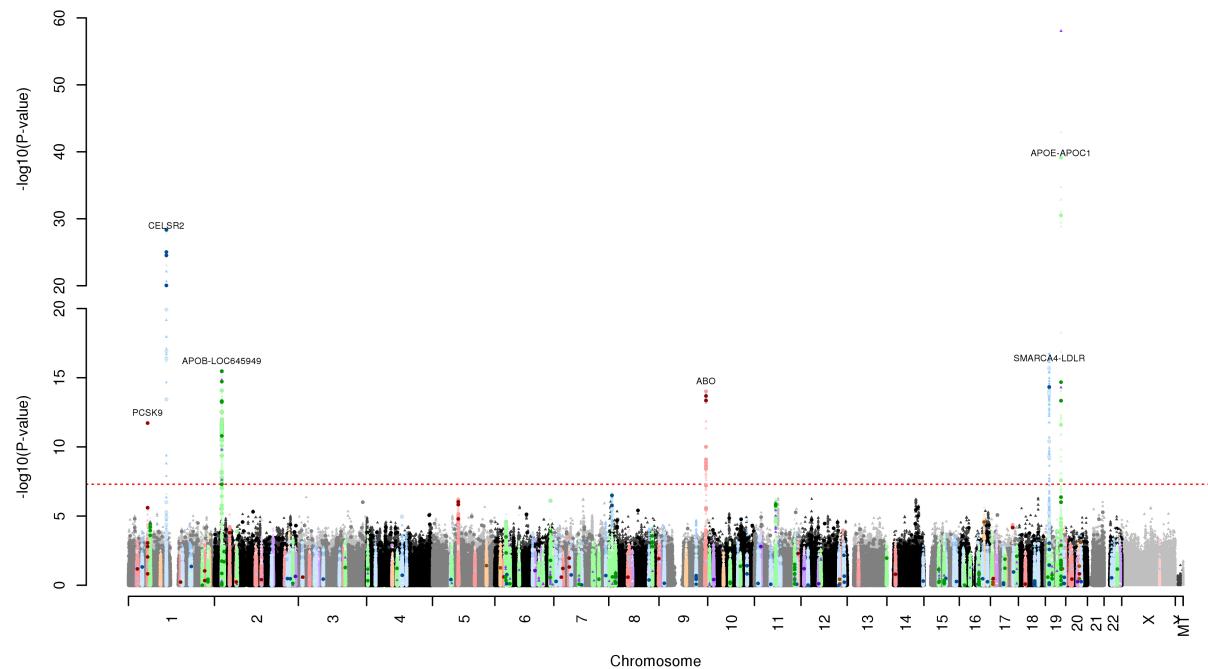
Defect	Disease	Gene	Location
Low HDL	Apo A-1 Deficiency	APOA1	11q23
	LCAT Deficiency	LCAT	16q22
	Tangier Disease	ABCA1	9q31
High HDL	CETP Deficiency	CETP	16q13
Low LDL	Abetalipoproteinemia	MTTP	4q24
	Familial hypobetalip.	APOB	2p24
	PCSK9 Deficiency	PCSK9	1p32
High LDL	AD hypercholest.	PCSK9	1p32
	AR hypercholest.	LDLRAP	1 1p36
	Fam. Defec. APOB-100	APOB	2p24
	Fam. Hypercholest.	LDLR	19p13
	Sitosterolemia	ABCG5	2p21
High TG	Sitosterolemia	ABCG8	2p21
	Combined lipase def.	LMF1	16p13
	Hypertrig. Type 1	LPL	8p21

Supplementary Figure 1: Manhattan plots and Q-Q plots of each ancestry/ethnicity, and of the meta-analysis, for each of the four lipids traits. In each plot, 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 " $<0.5\text{Mb}$ prev. known" indicates that a SNP was previously identified to be a particular lipids risk variant, and that the current SNP is within 0.5 megabases of that SNP (a 1 megabase window). Tests were done using linear regression in GERA non-Hispanic whites ($n=76,627$), GERA Latinos (7,795), GERA East Asians ($n=6,855$), GERA African Americans (2,958), and GERA South Asians ($n=439$), and a fixed effects meta-analysis.

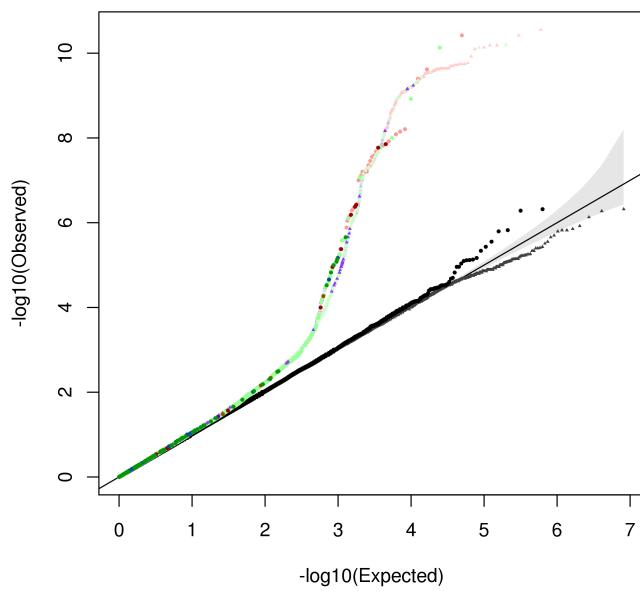
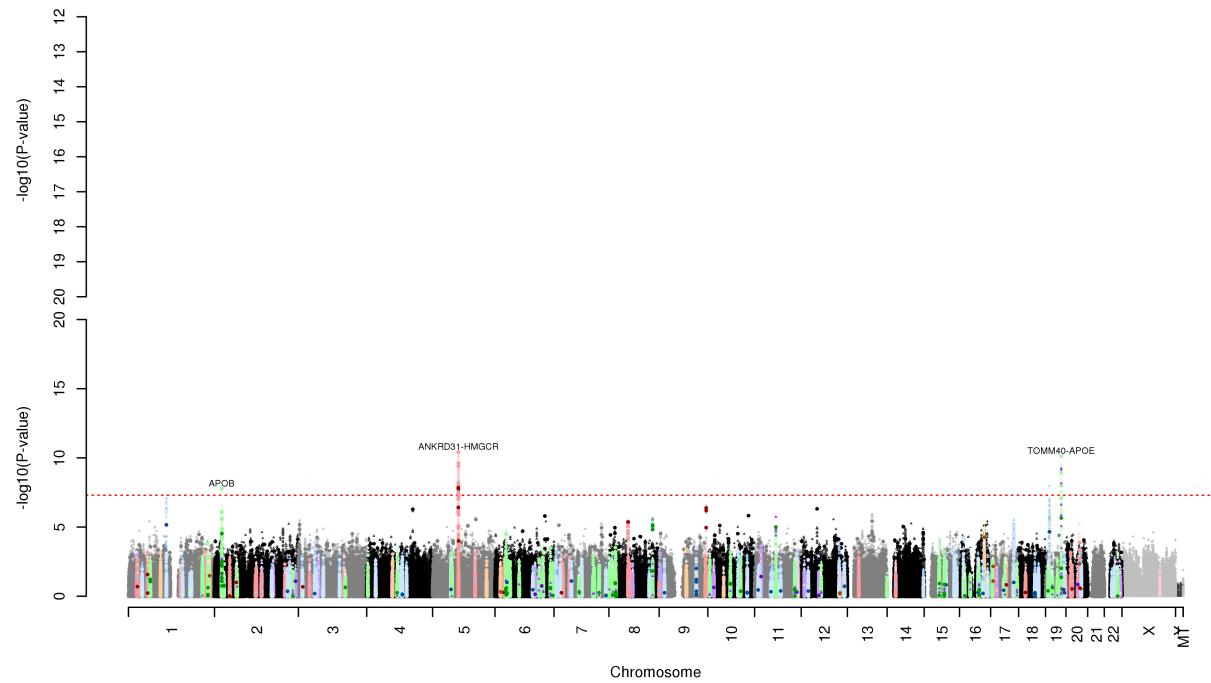
LDL non-Hispanic whites. $\lambda_{\text{typed}} = 1.10$, $\lambda_{\text{imputed}} = 1.10$.



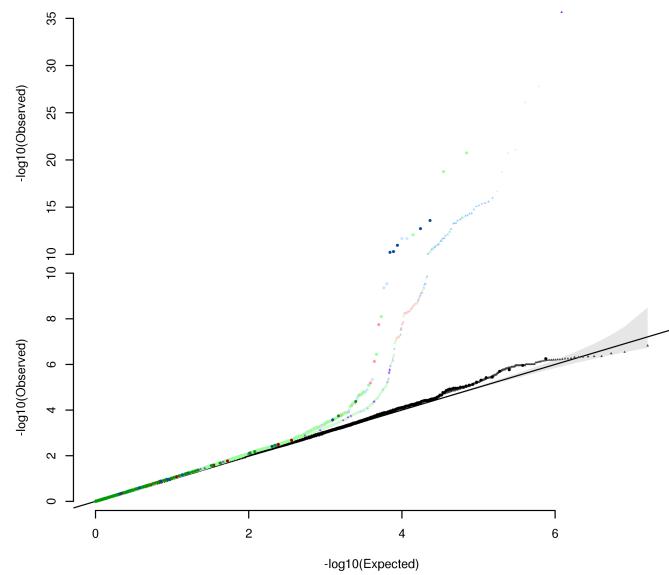
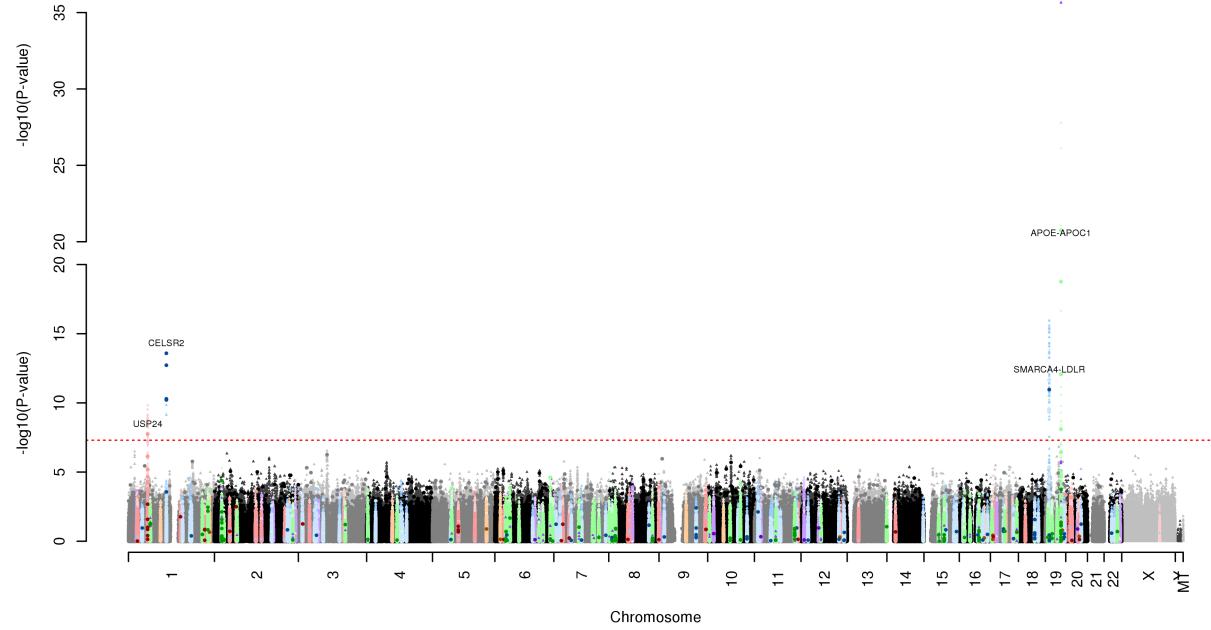
LDL Latinos. $\lambda_{\text{typed}} = 1.00$, $\lambda_{\text{imputed}} = 1.00$.



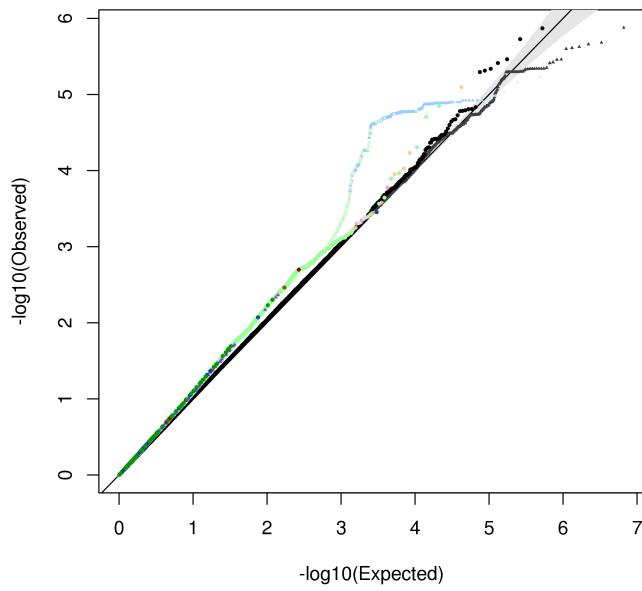
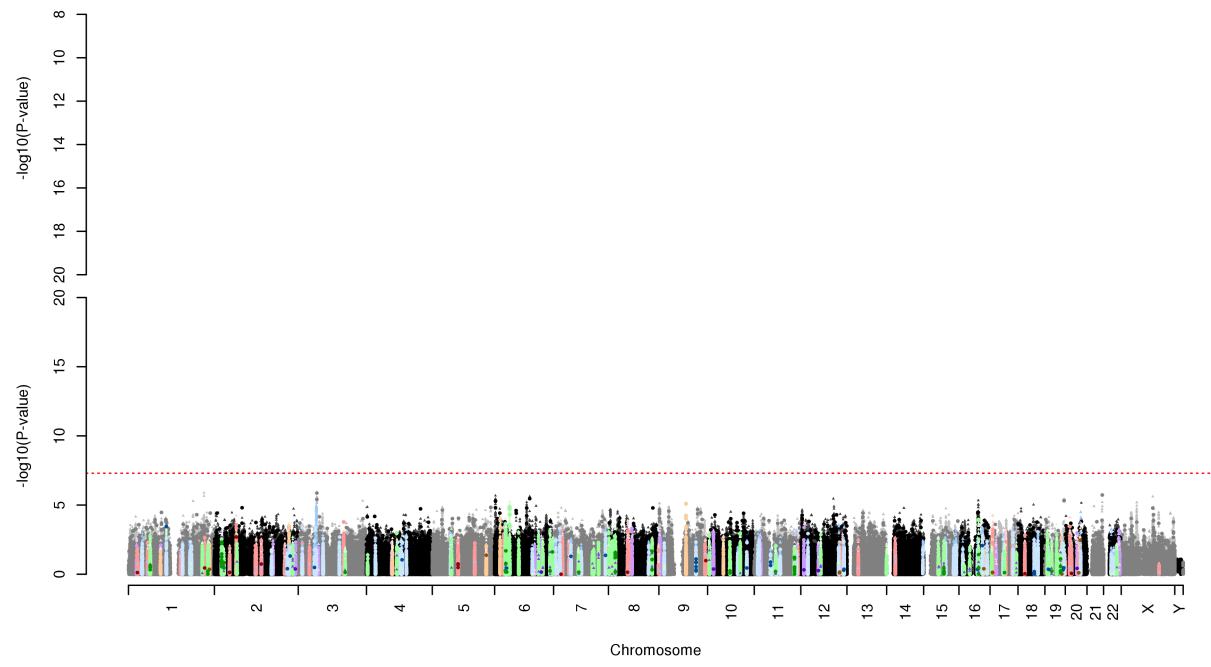
LDL East Asians. $\lambda_{\text{typed}} = 1.00$, $\lambda_{\text{imputed}} = 1.00$.



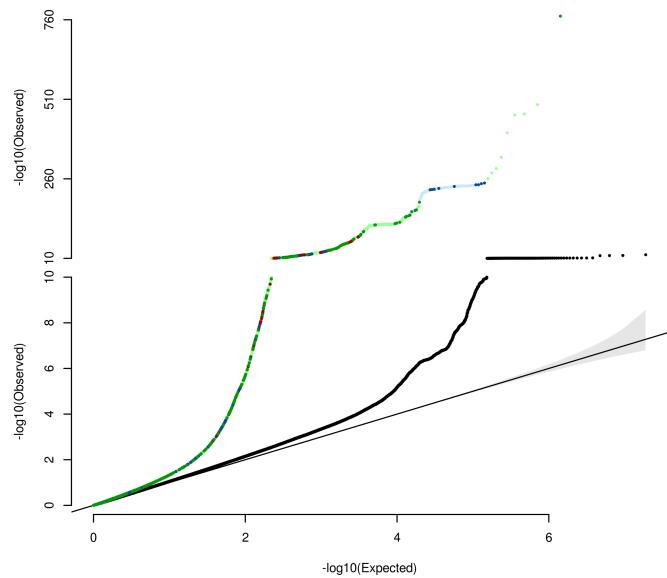
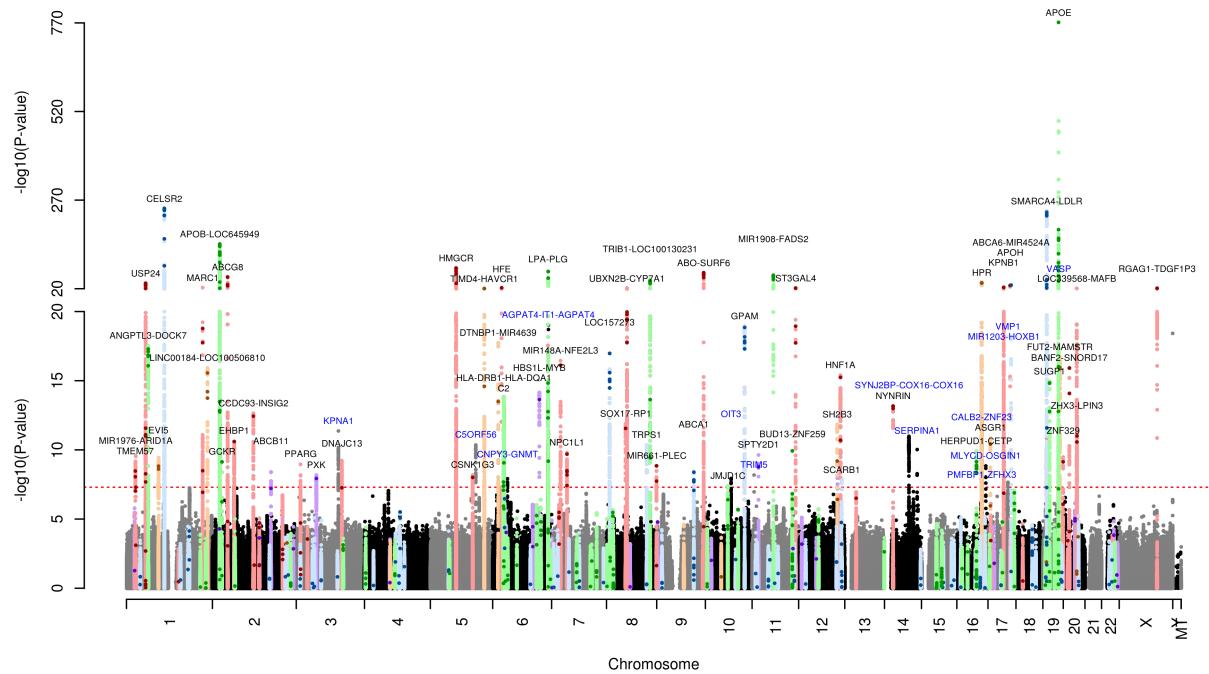
LDL African Americans. $\lambda_{\text{typed}} = 1.00$, $\lambda_{\text{imputed}} = 1.00$.



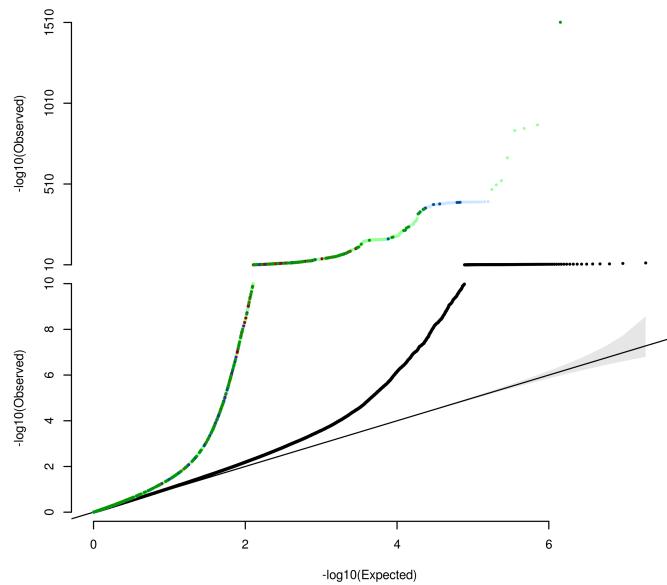
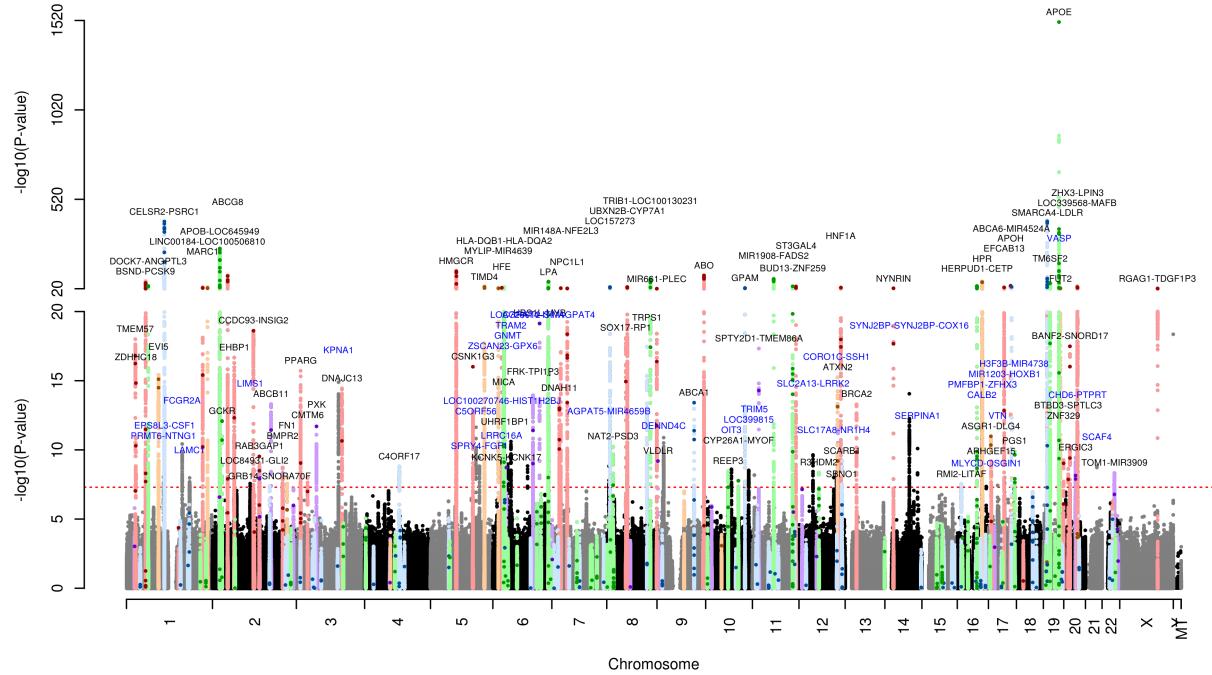
LDL South Asians. $\lambda_{\text{typed}} = 1.04$, $\lambda_{\text{imputed}} = 1.04$.



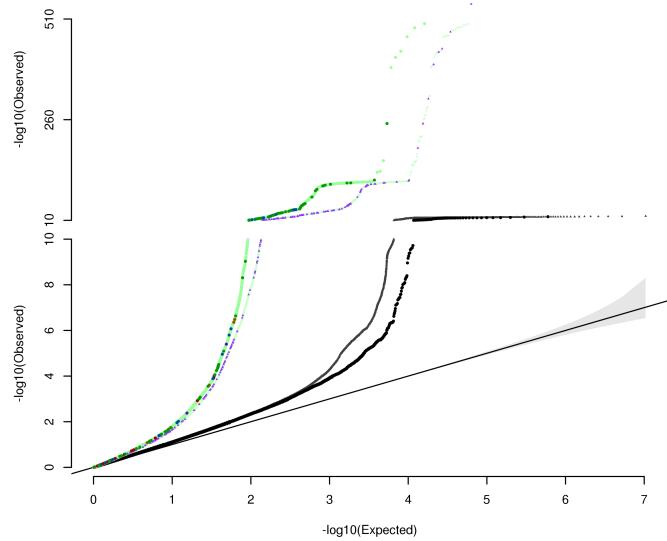
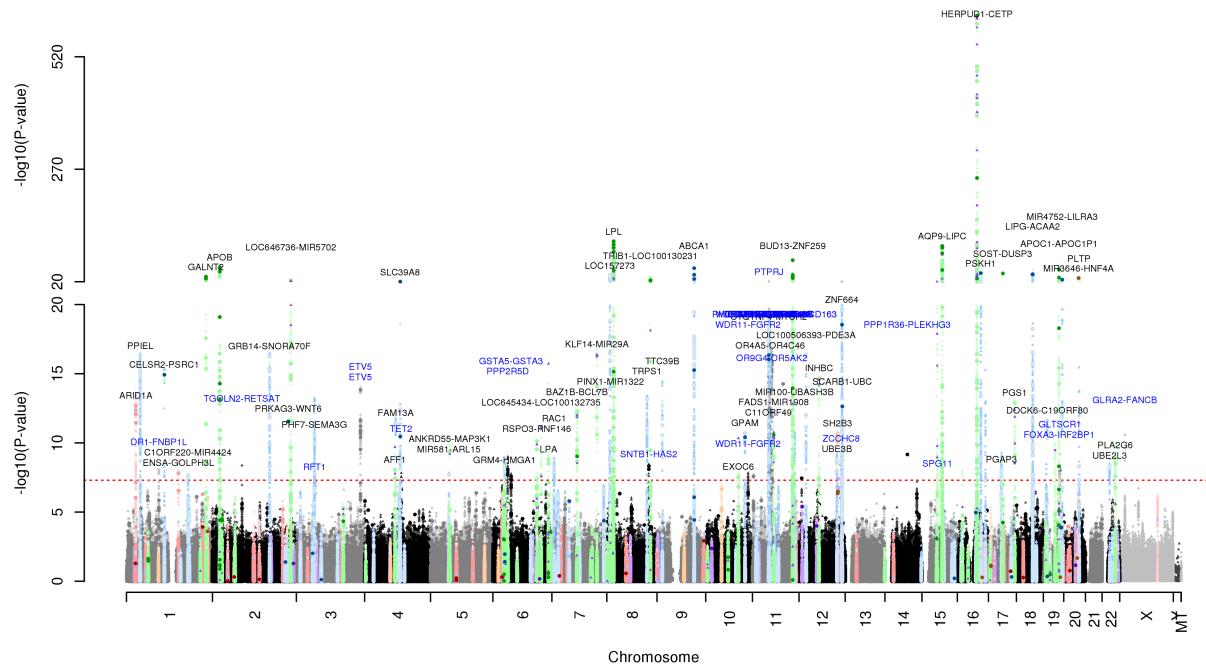
LDL GERA. $\lambda = 1.07$.



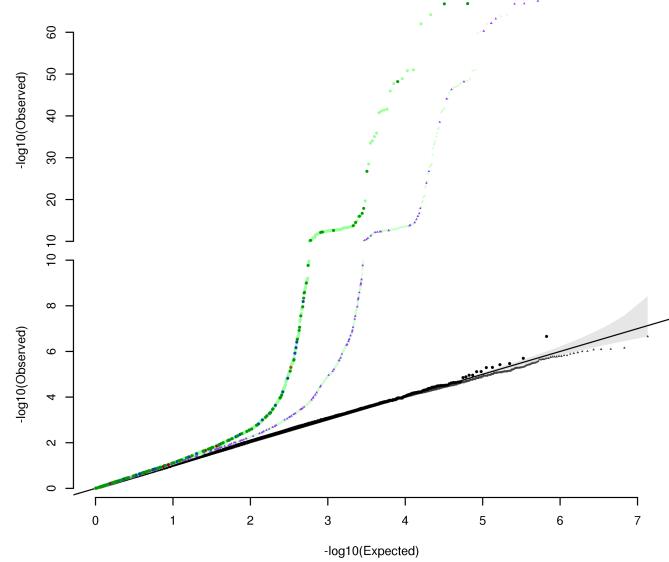
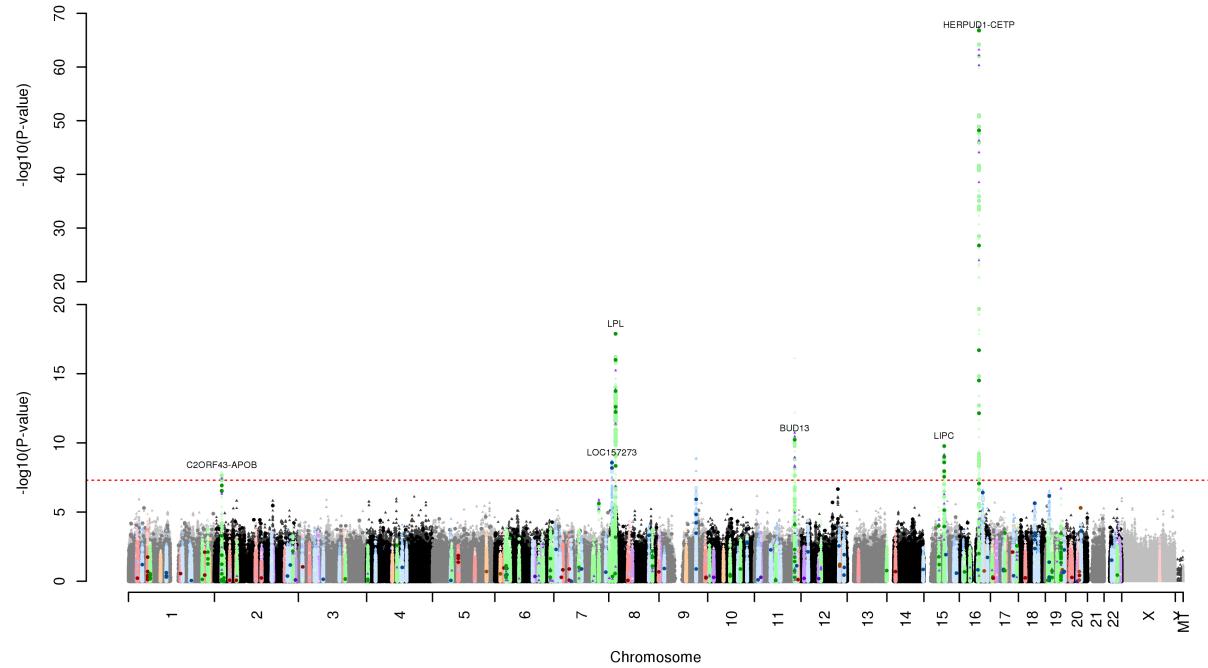
LDL GERA+GLGC. $\lambda = 1.07$.



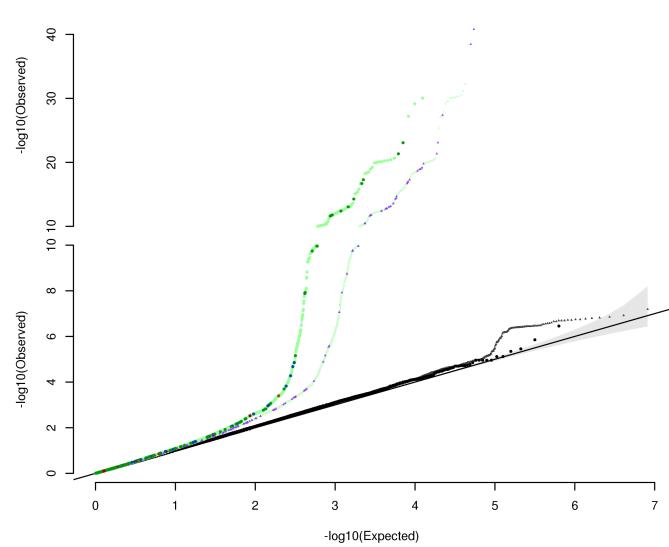
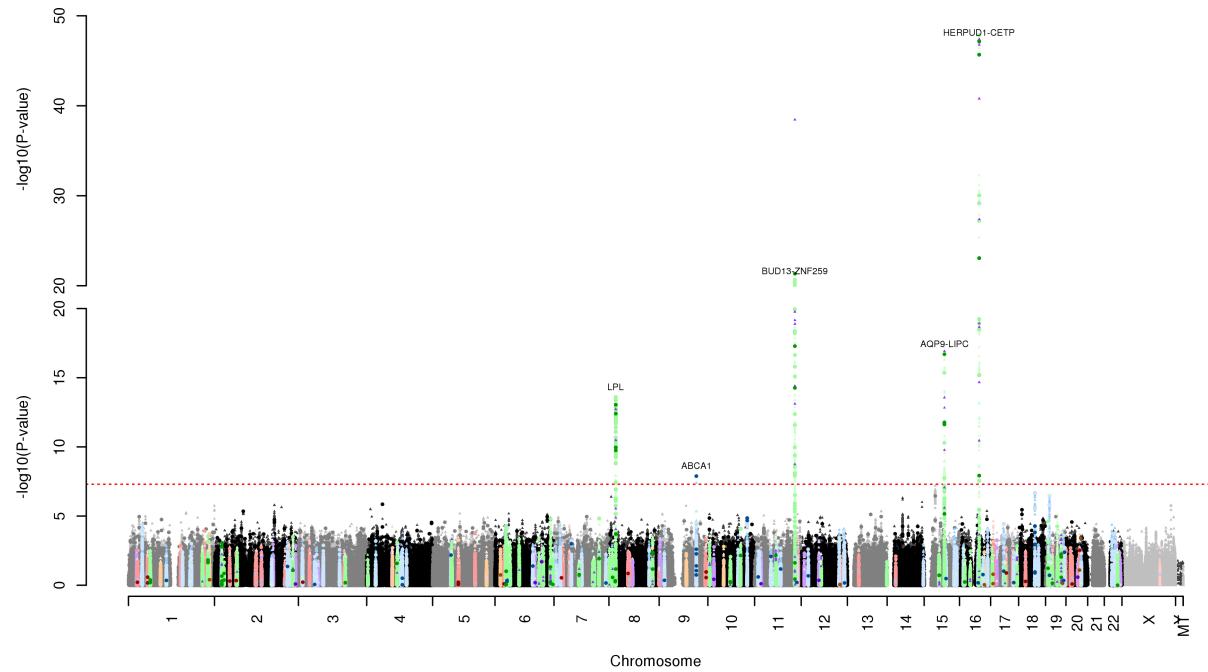
HDL non-Hispanic whites. $\lambda_{\text{typed}} = 1.15$, $\lambda_{\text{imputed}} = 1.15$.



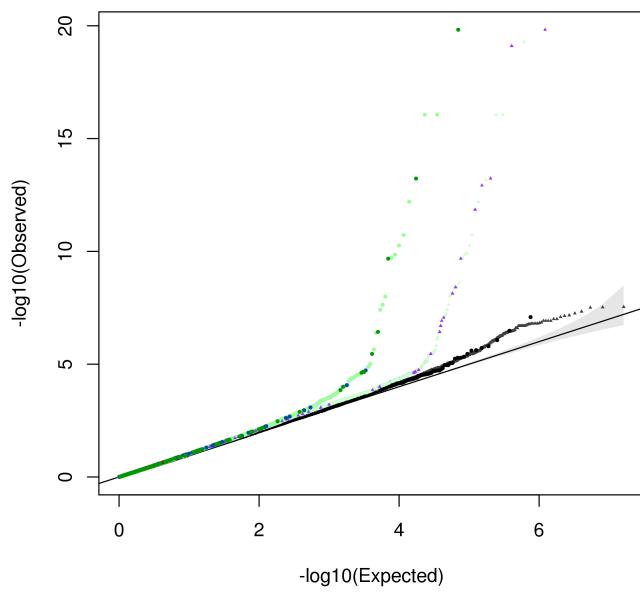
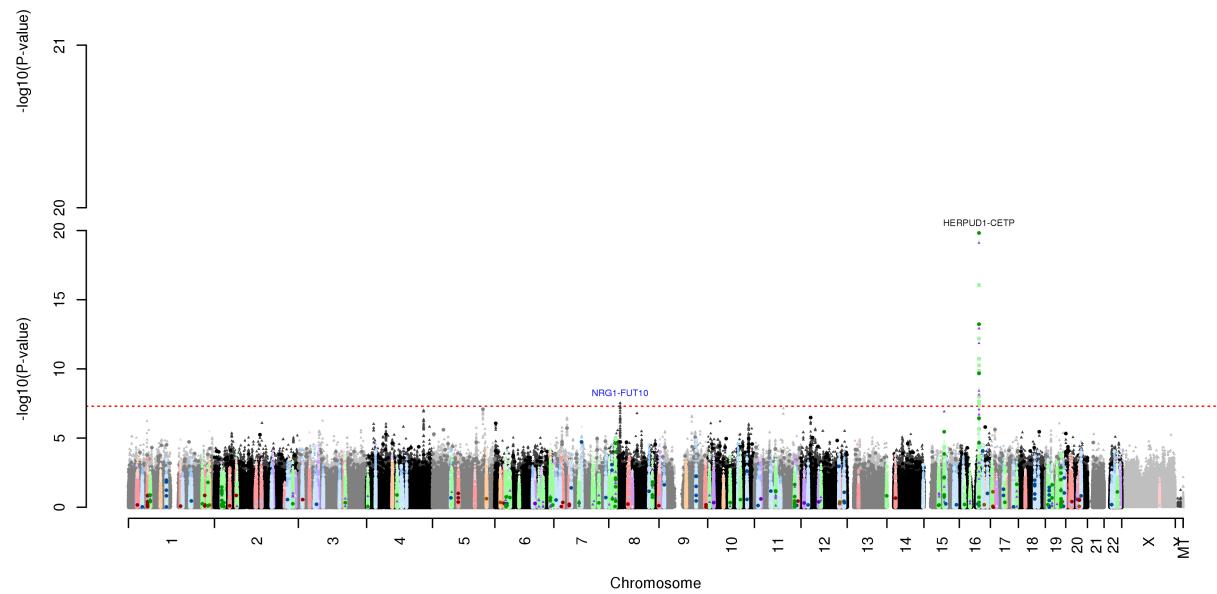
HDL Latinos. $\lambda_{\text{typed}} = 1.05$, $\lambda_{\text{imputed}} = 1.00$.



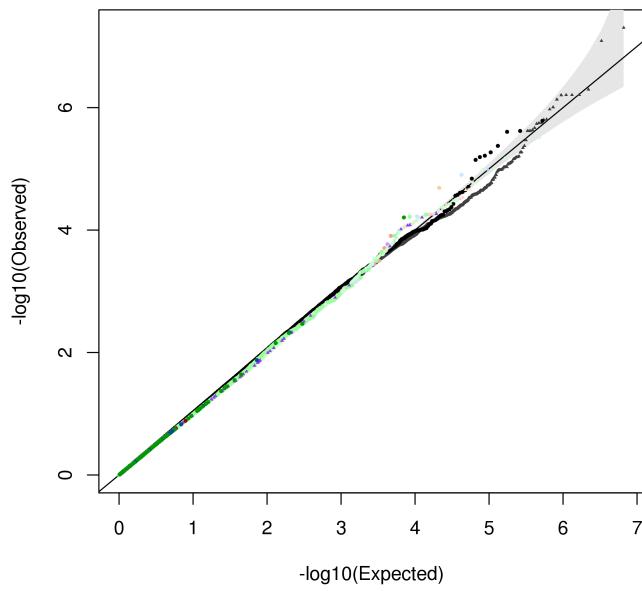
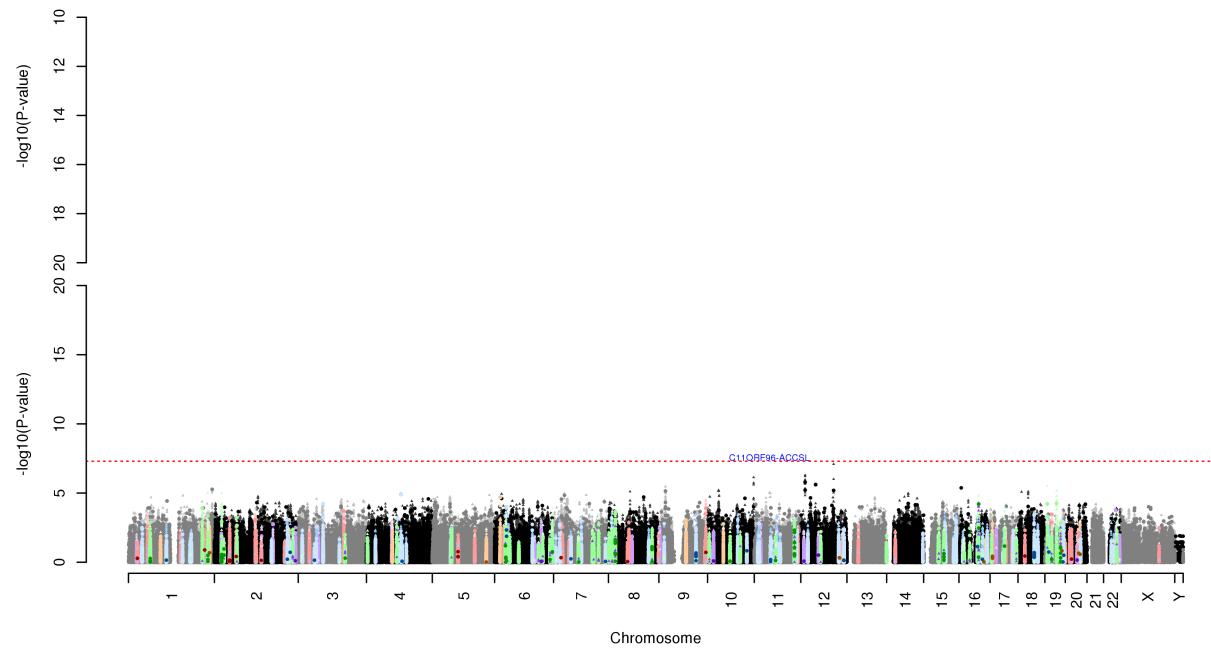
HDL East Asians. $\lambda_{\text{typed}} = 1.00$, $\lambda_{\text{imputed}} = 1.00$.



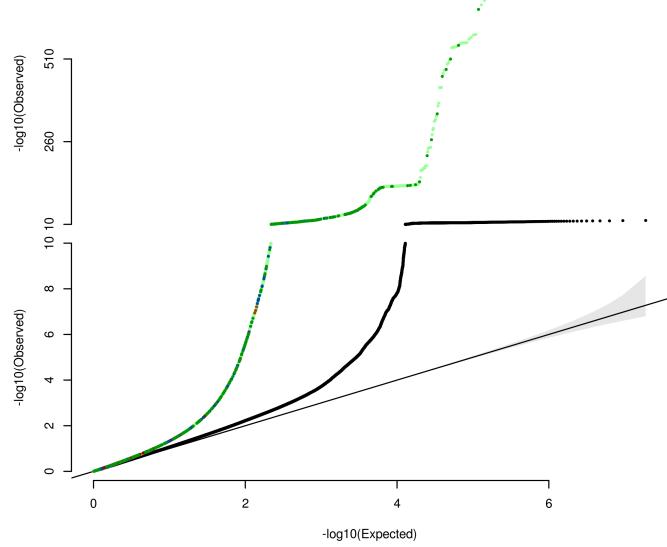
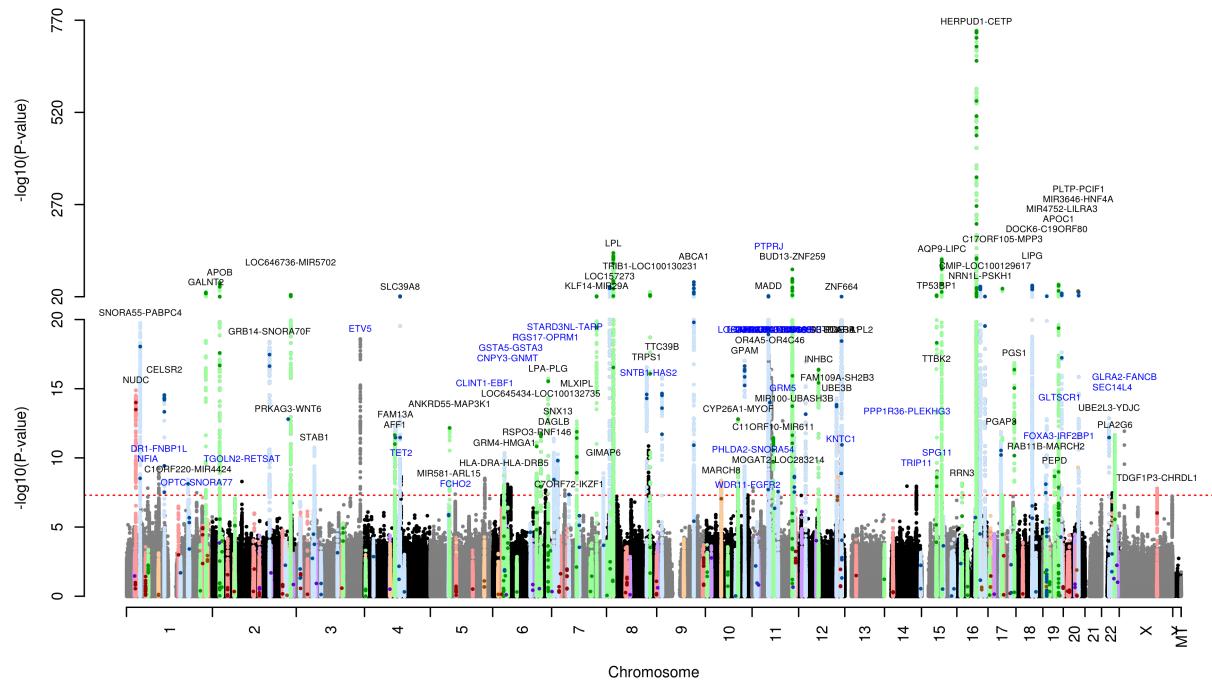
HDL African Americans. $\lambda_{\text{typed}} = 1.00$, $\lambda_{\text{imputed}} = 1.00$.



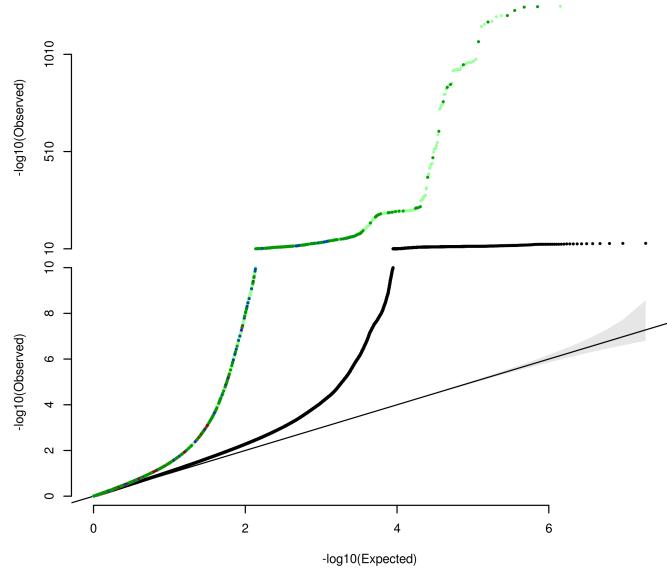
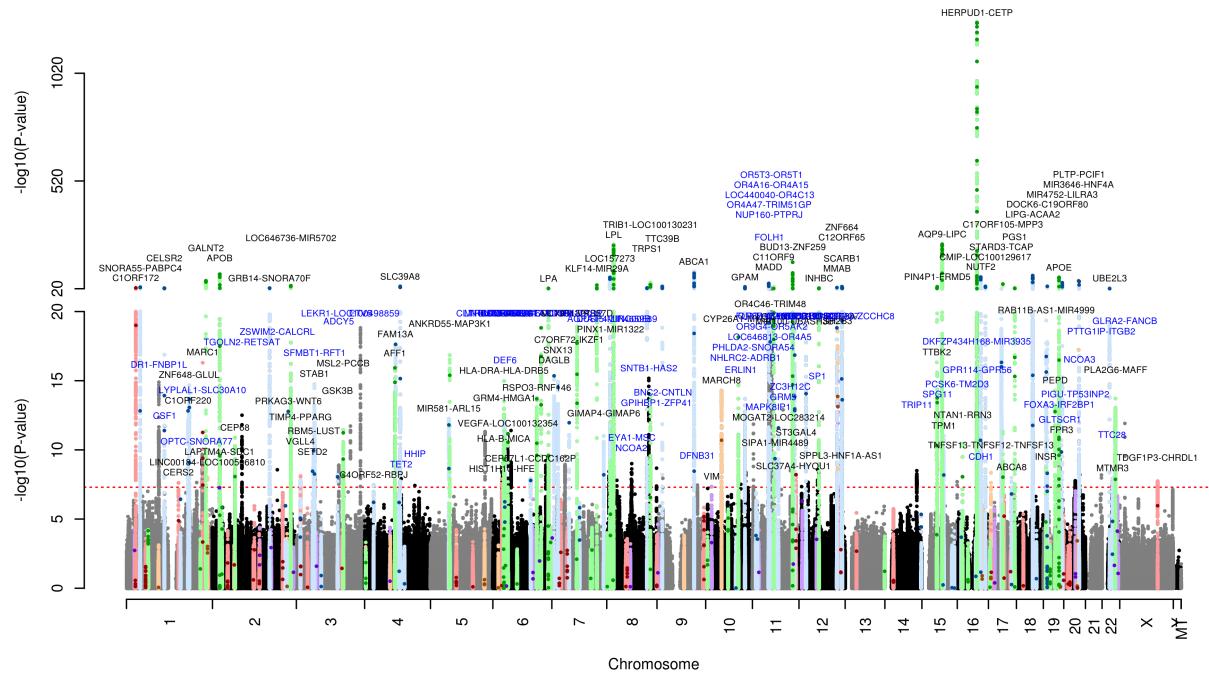
HDL South Asians. $\lambda_{\text{typed}} = 1.02$, $\lambda_{\text{imputed}} = 1.02$.



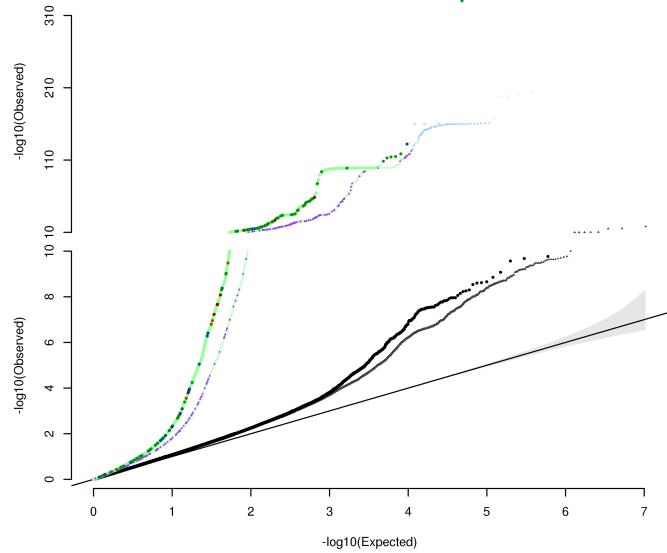
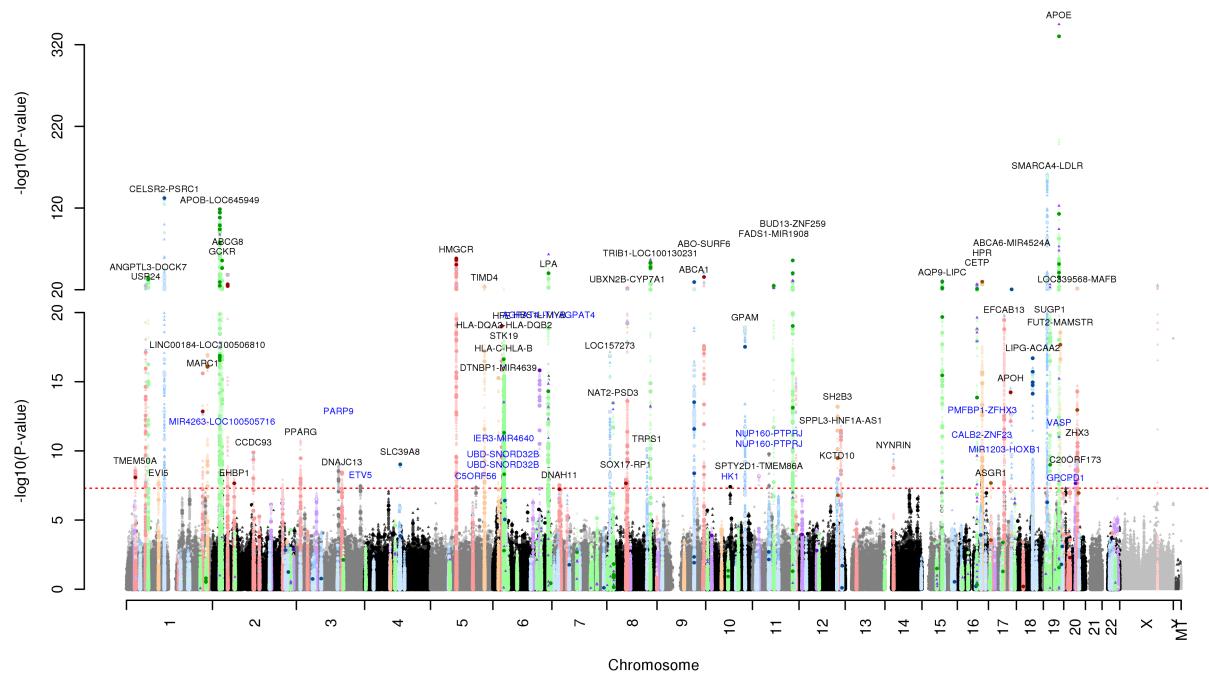
HDL GERA. $\lambda = 1.09$.



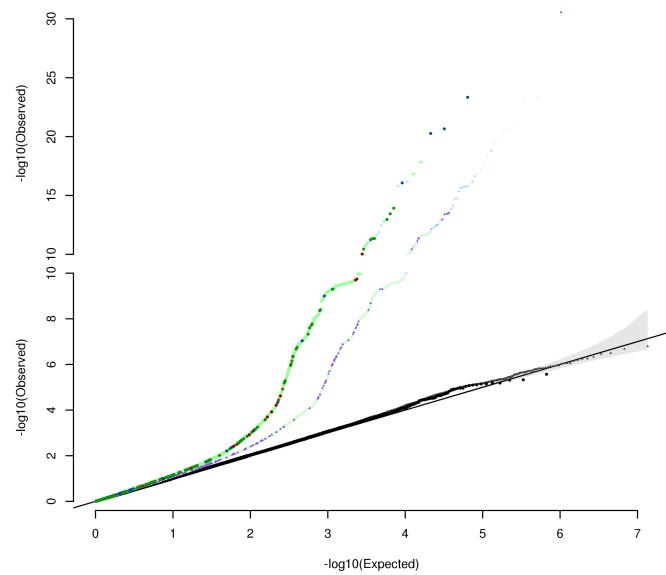
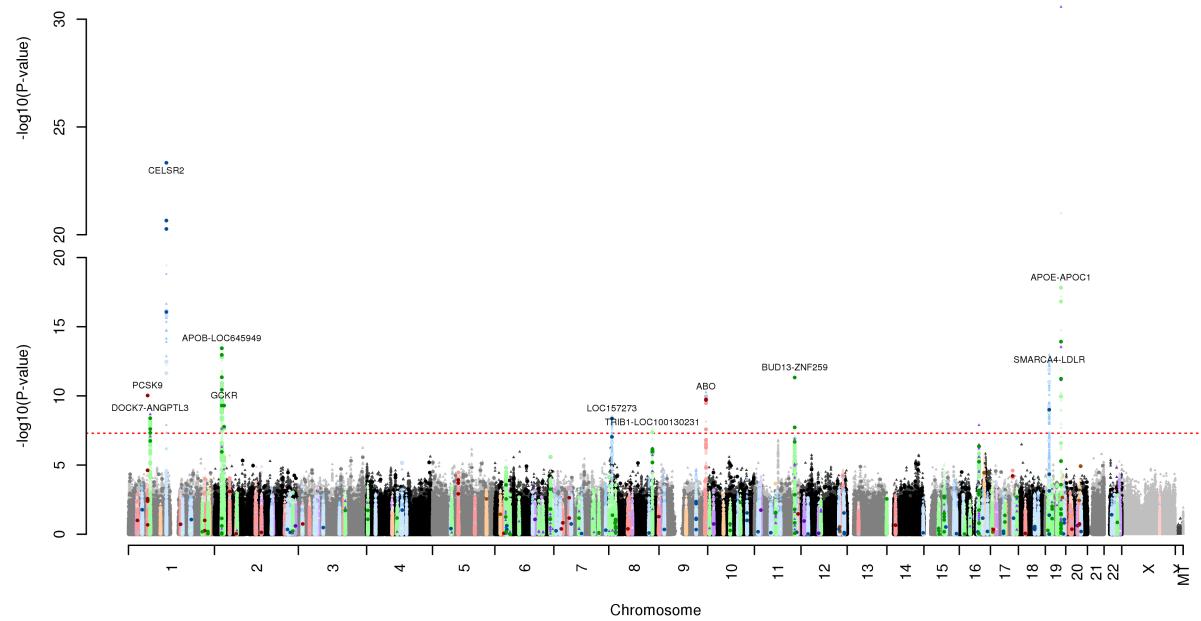
HDL GERA+GLGC. $\lambda = 1.10$.



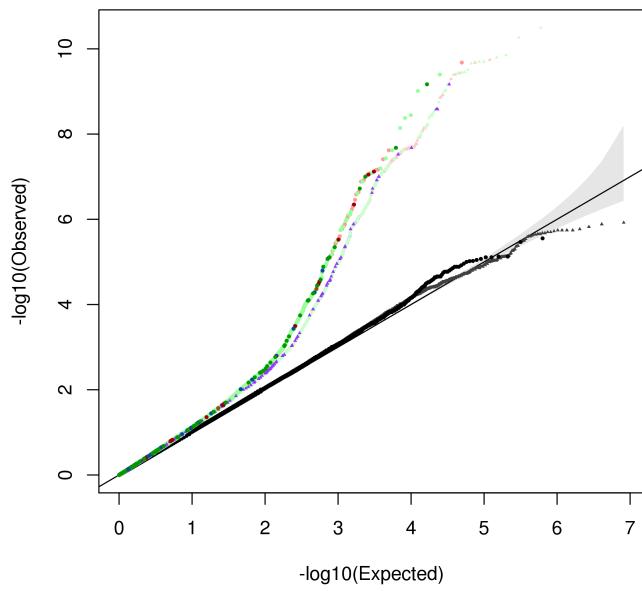
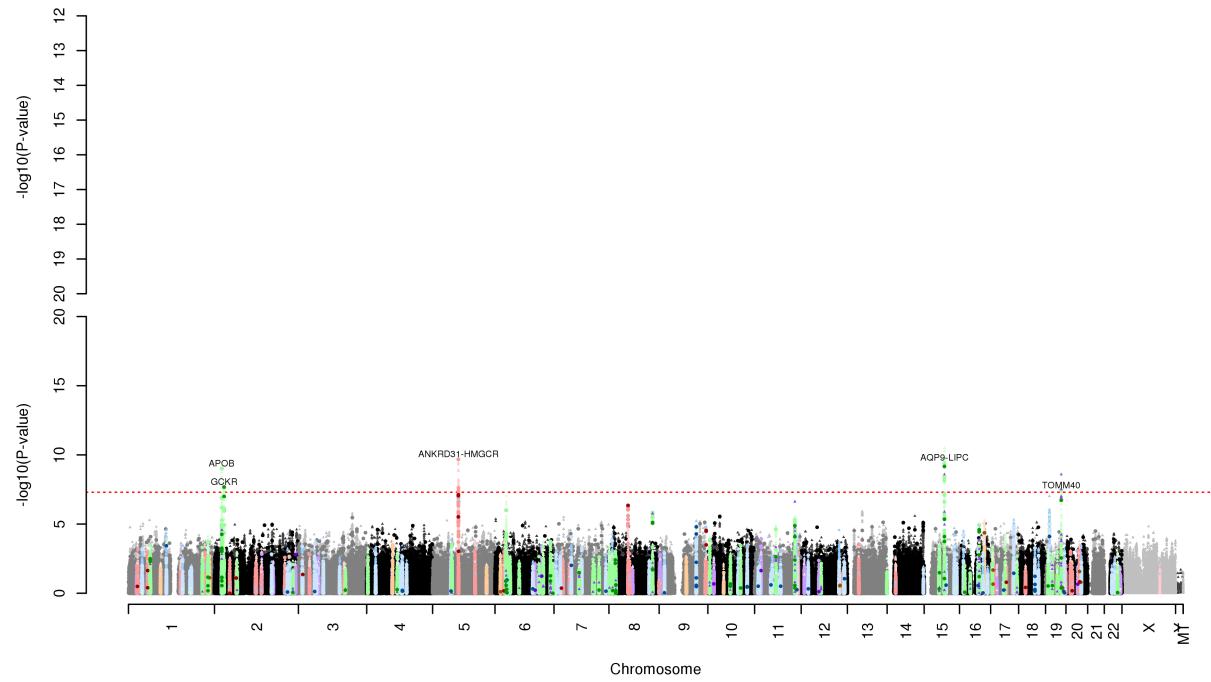
TC non-Hispanic whites. $\lambda_{\text{typed}} = 1.15$, $\lambda_{\text{imputed}} = 1.10$.



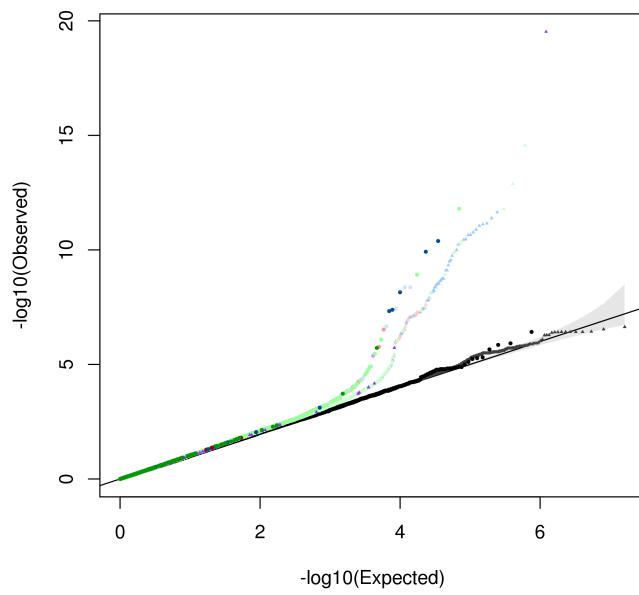
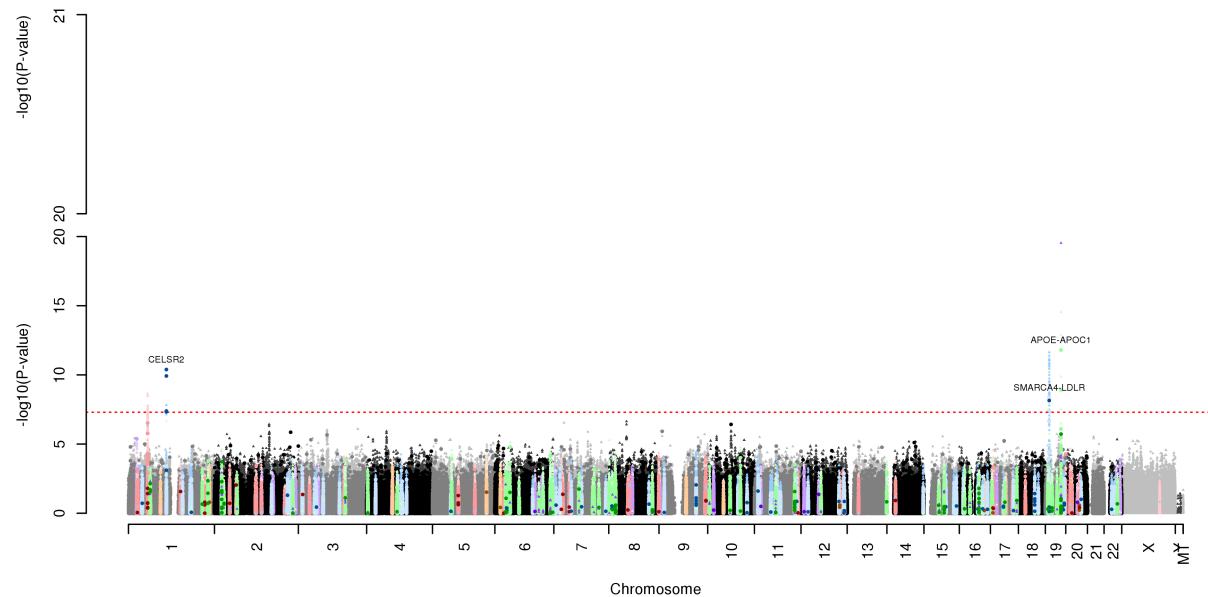
TC Latinos. $\lambda_{\text{typed}} = 1.00$, $\lambda_{\text{imputed}} = 1.00$.



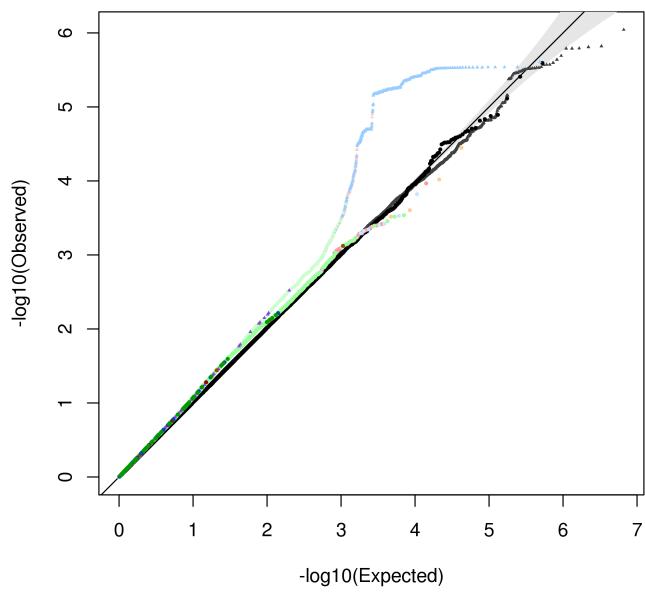
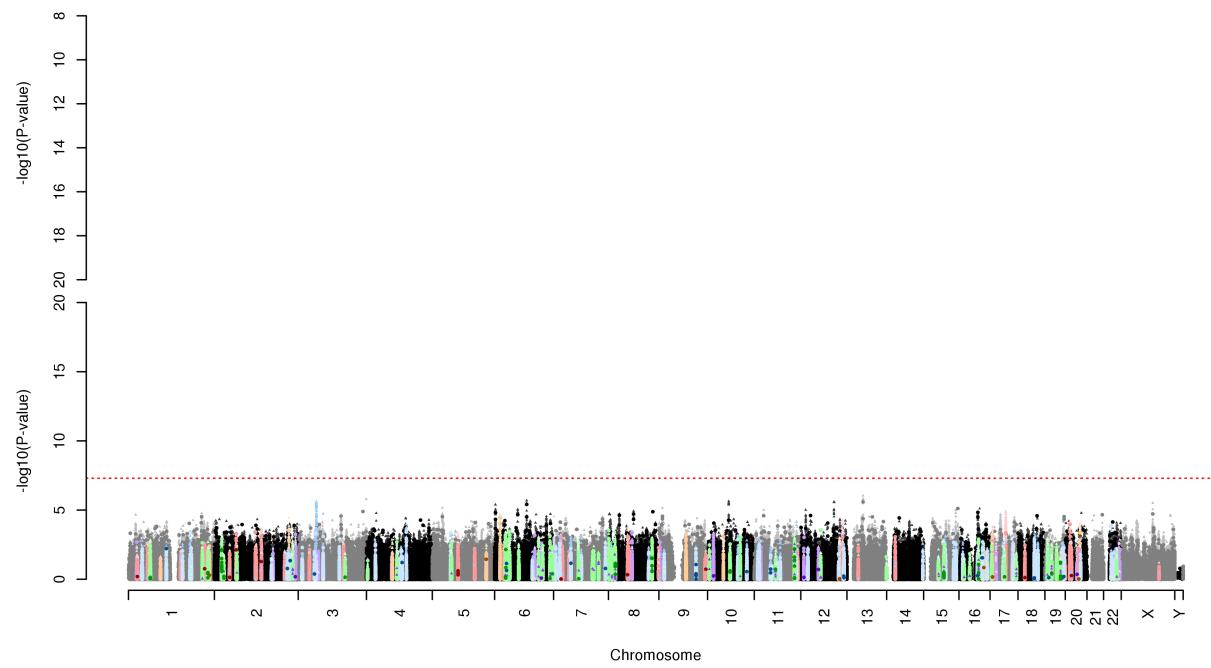
TC East Asians. $\lambda_{\text{typed}} = 1.05$, $\lambda_{\text{imputed}} = 1.05$.



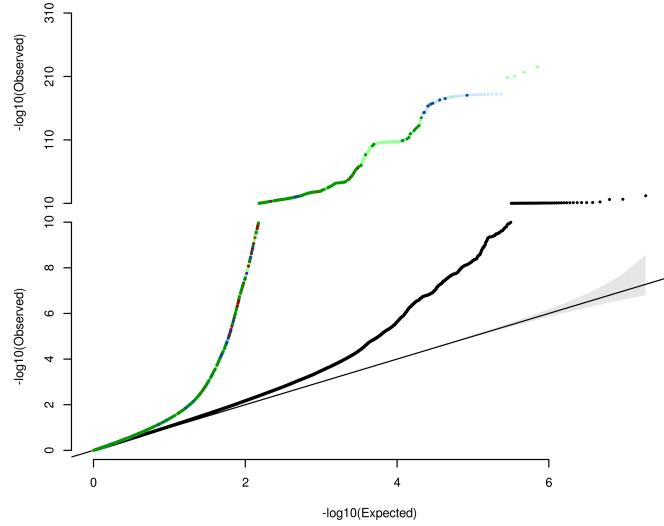
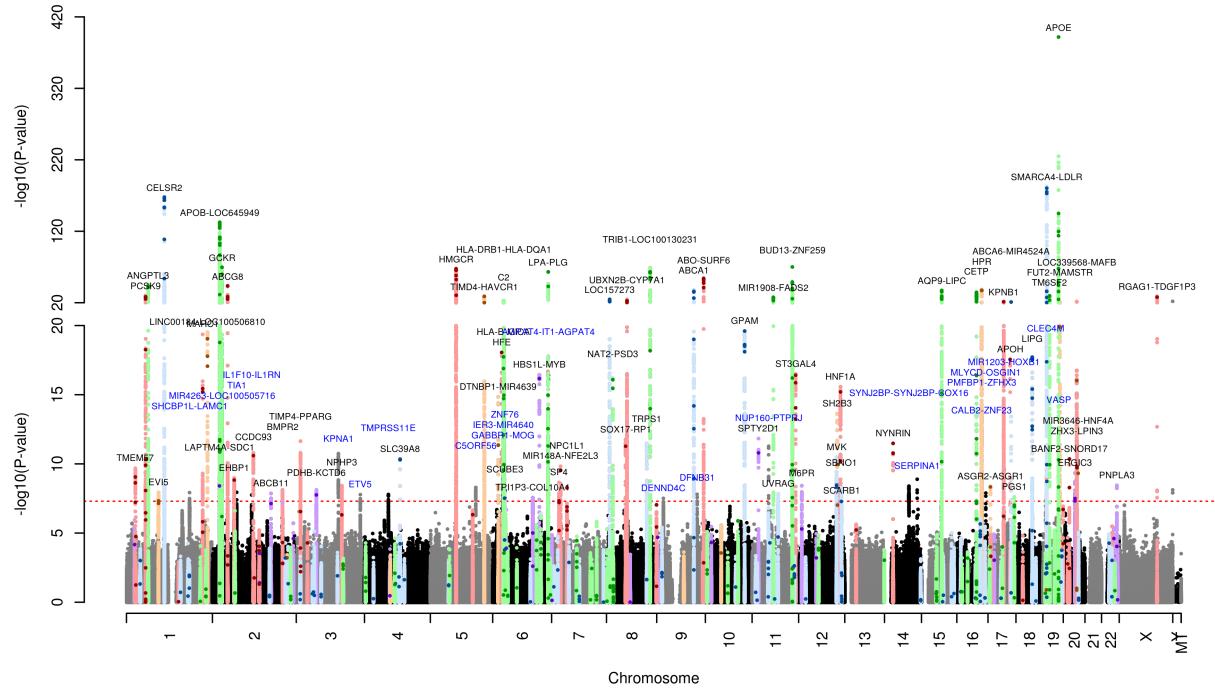
TC African Americans. $\lambda_{\text{typed}} = 1.00$, $\lambda_{\text{imputed}} = 1.00$.



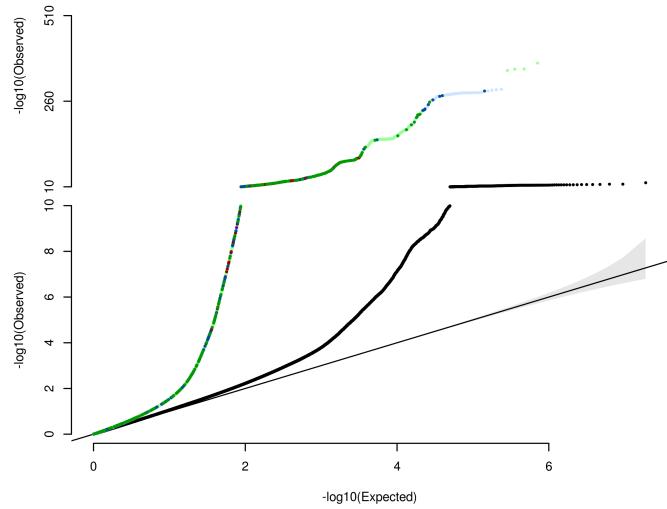
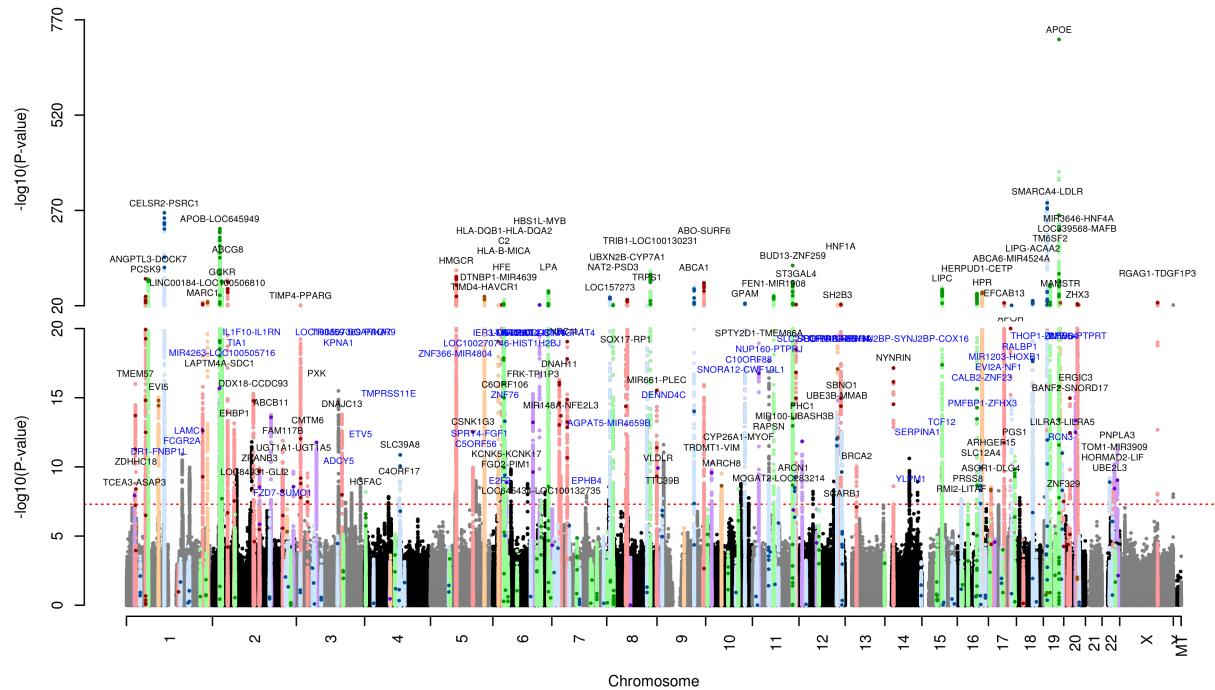
TC South Asians. $\lambda_{\text{typed}} = 1.02$, $\lambda_{\text{imputed}} = 1.02$.



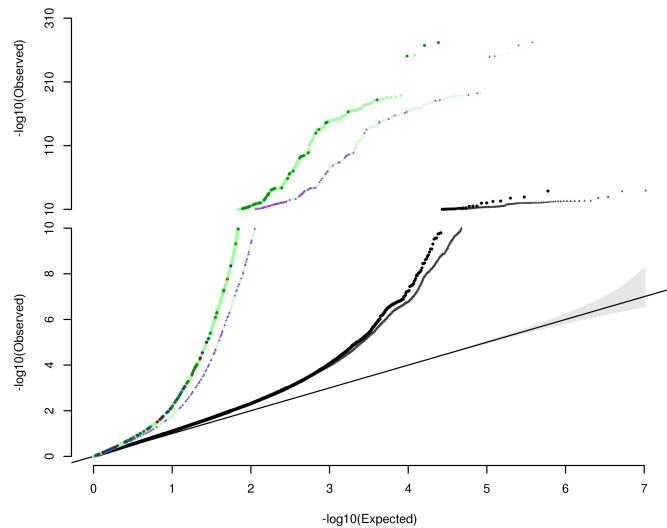
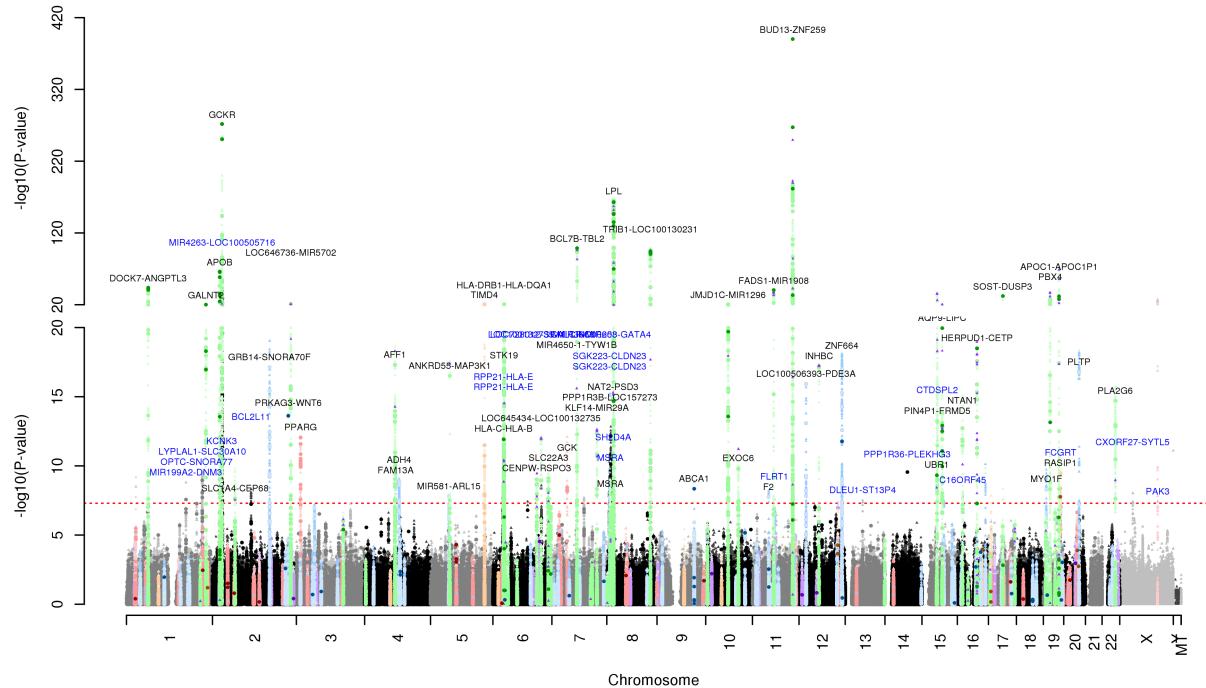
TC GERA. $\lambda = 1.07$.



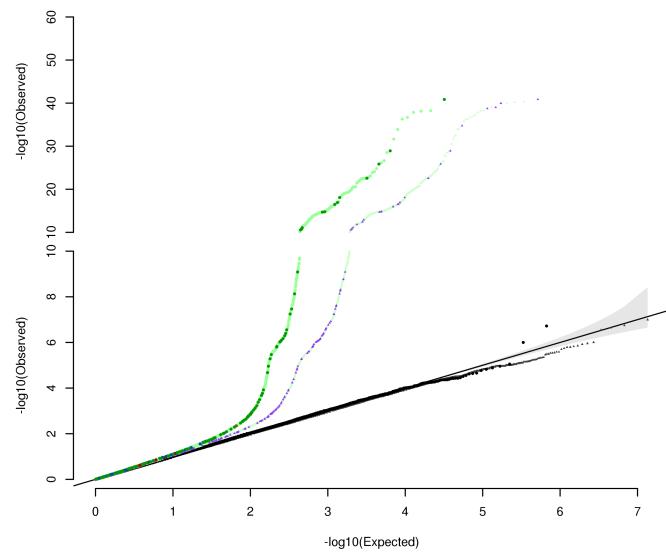
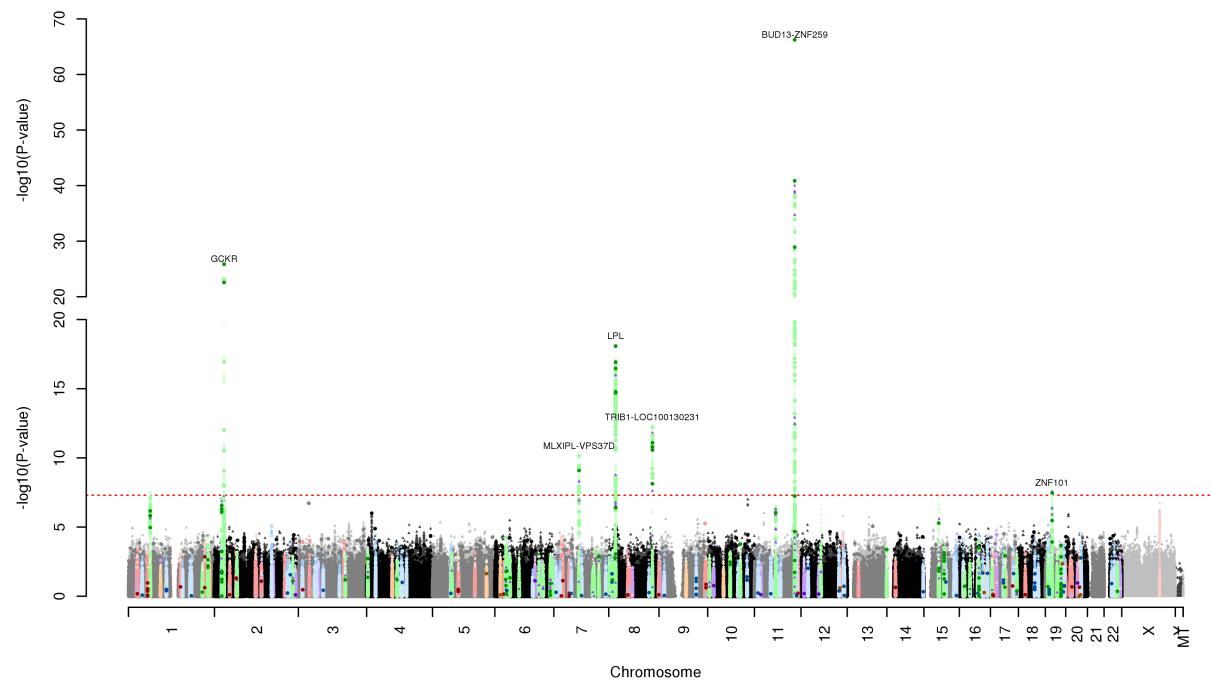
TC GERA+GLGC. $\lambda = 1.07$.



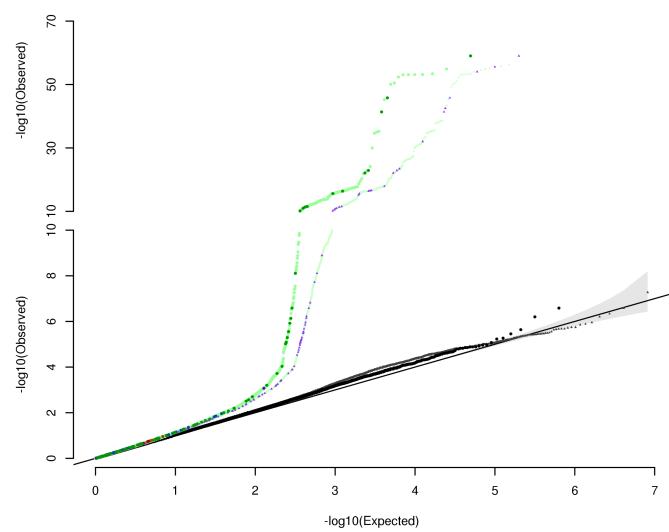
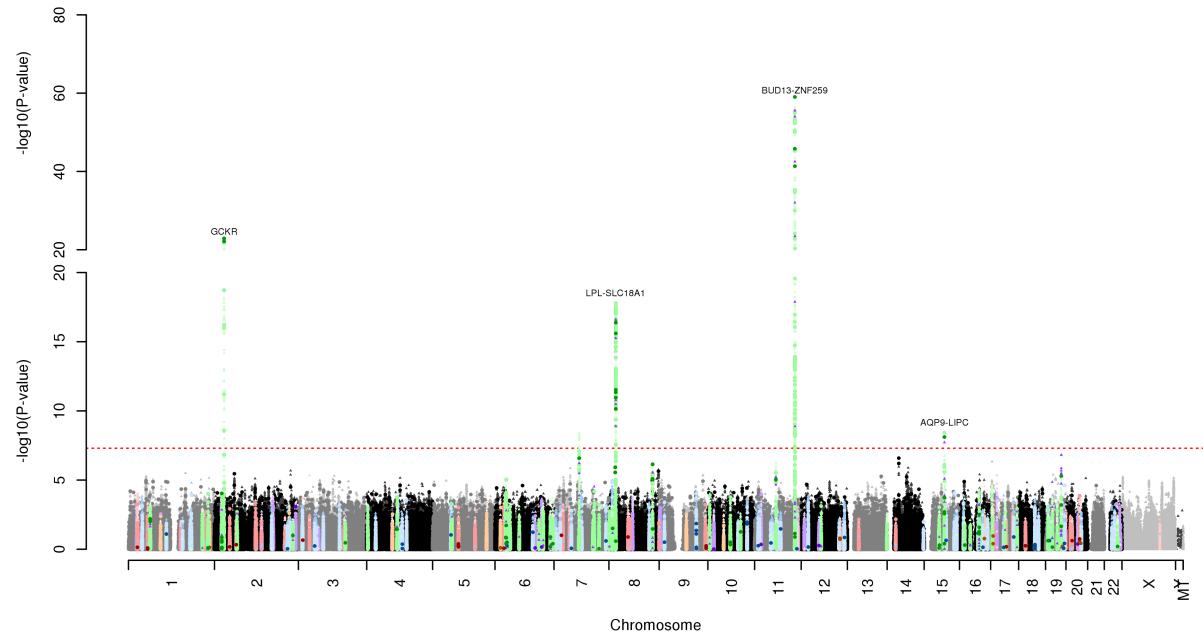
TG non-Hispanic whites. $\lambda_{\text{typed}} = 1.15$, $\lambda_{\text{imputed}} = 1.15$.



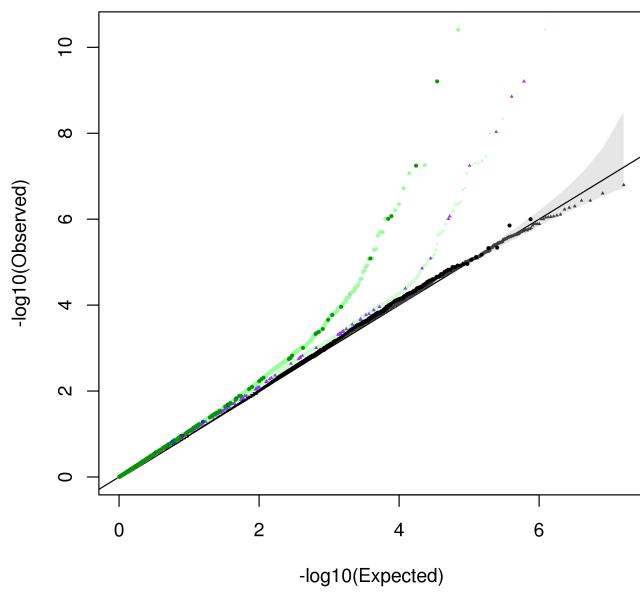
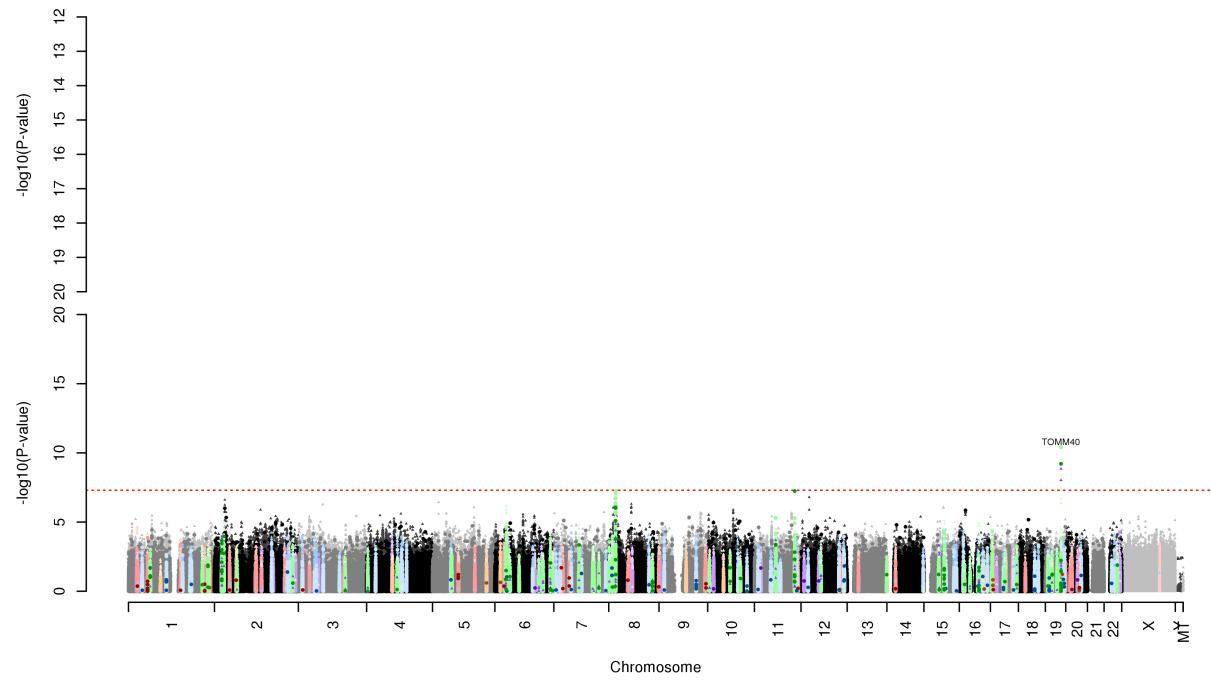
TG Latinos. $\lambda_{\text{typed}} = 1.00$, $\lambda_{\text{imputed}} = 1.00$.



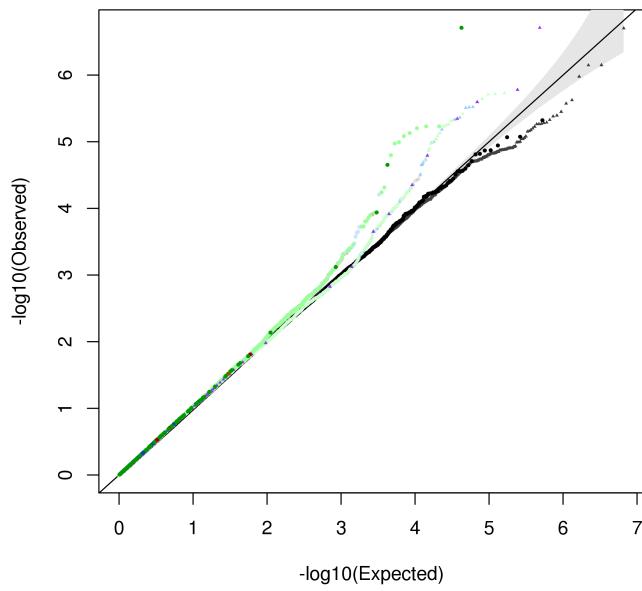
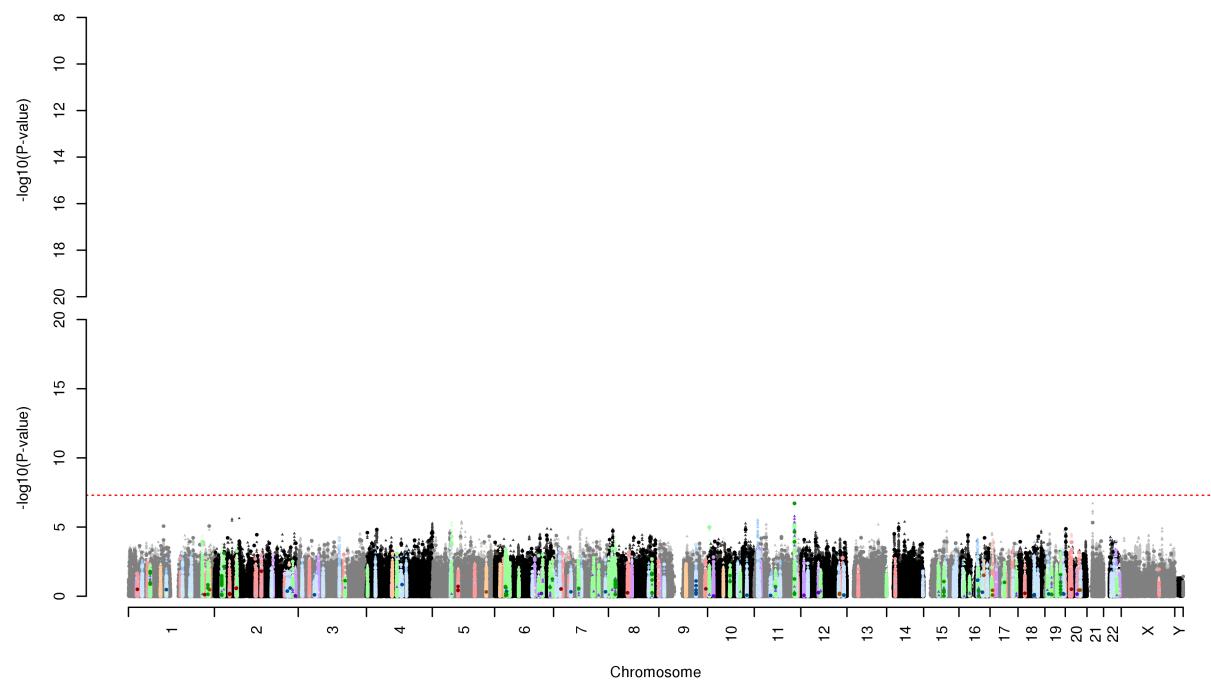
TG East Asians. $\lambda_{\text{typed}} = 1.05$, $\lambda_{\text{imputed}} = 1.05$.



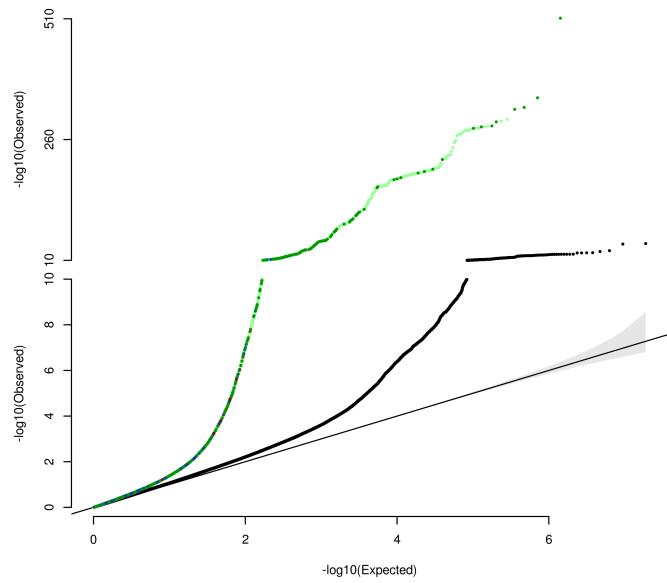
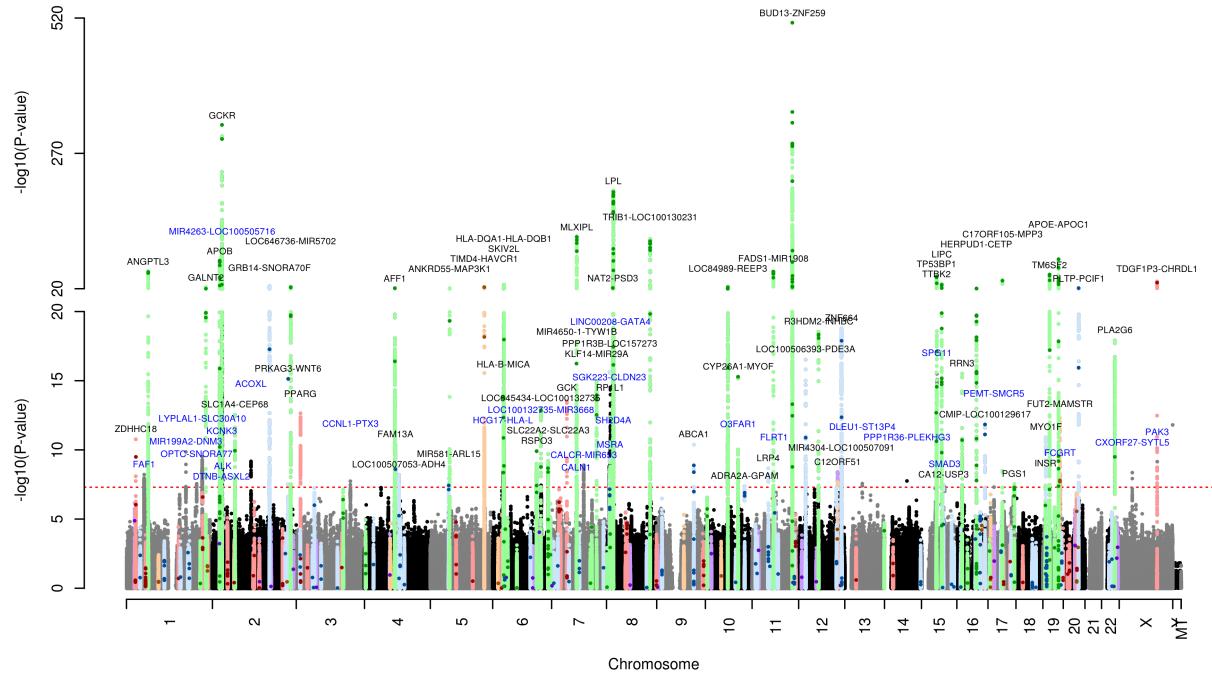
TG African Americans. $\lambda_{\text{typed}} = 1.00$, $\lambda_{\text{imputed}} = 1.00$.



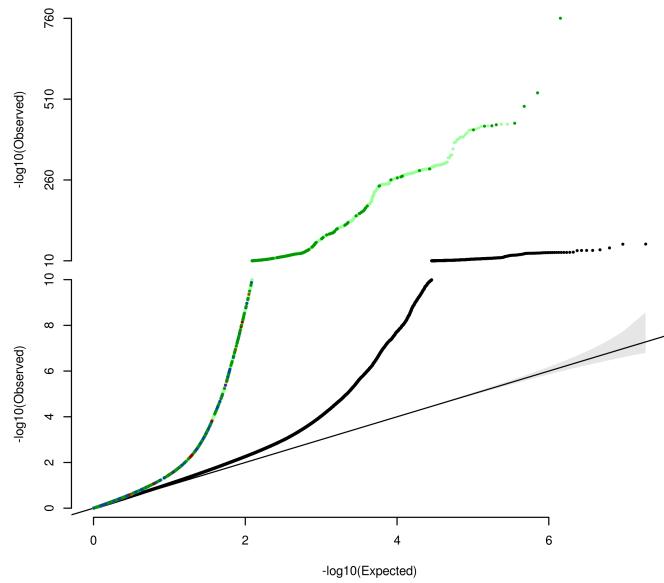
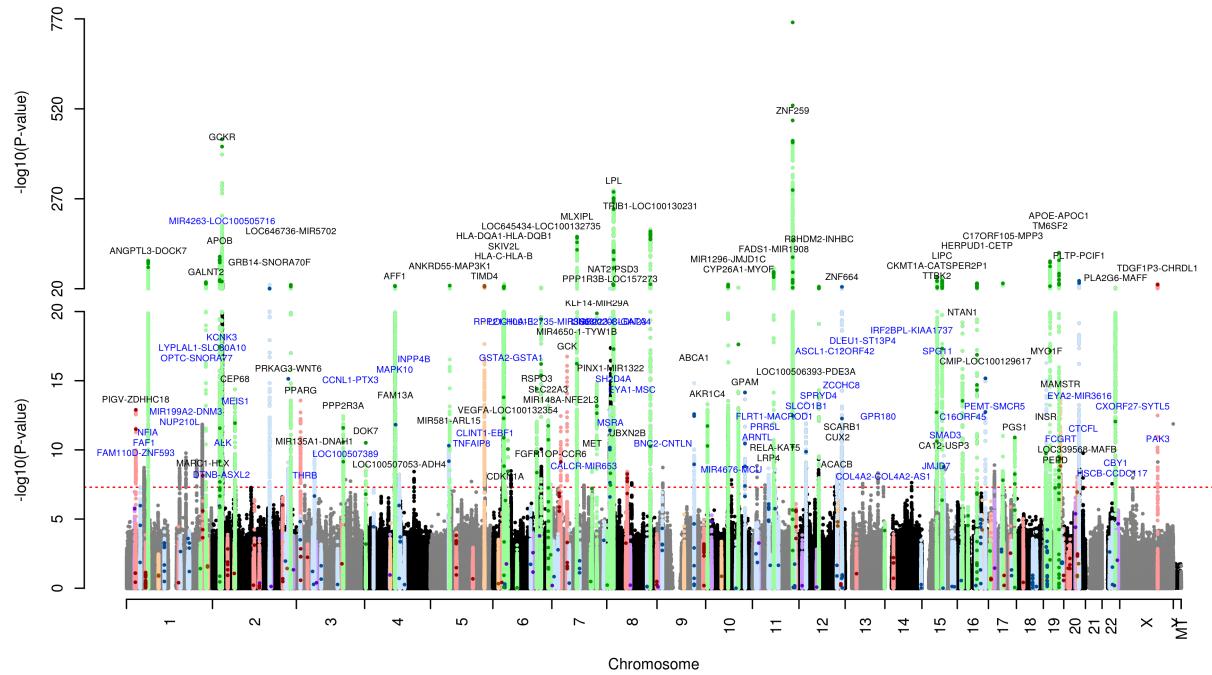
TG South Asians. $\lambda_{\text{typed}} = 1.01$, $\lambda_{\text{imputed}} = 1.00$.



TG GERA. $\lambda = 1.09$.

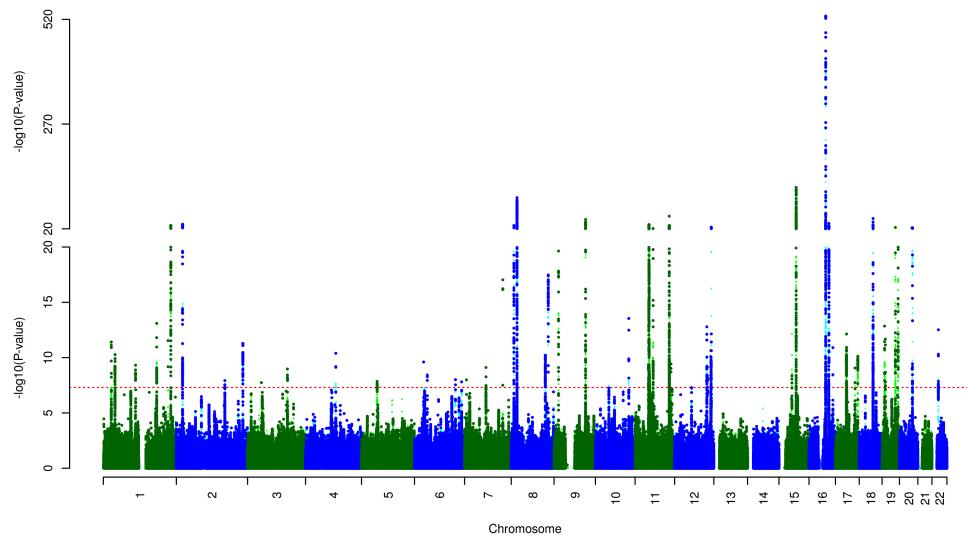


TG GERA+GLGC. $\lambda = 1.09$.

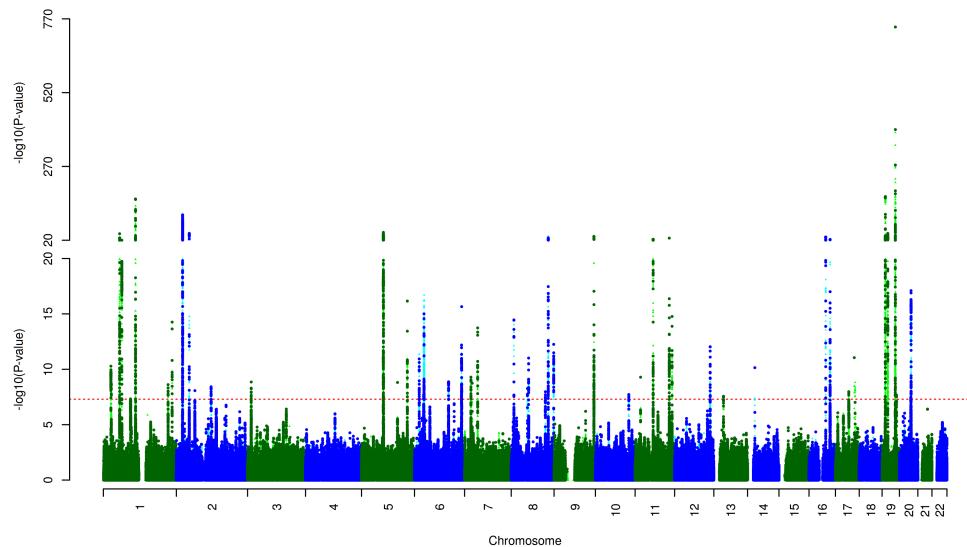


Supplementary Figure 3: Extending the GLGC ($n=94,595$) summary statistics (linear regression) from HapMap to 1000 Genomes.

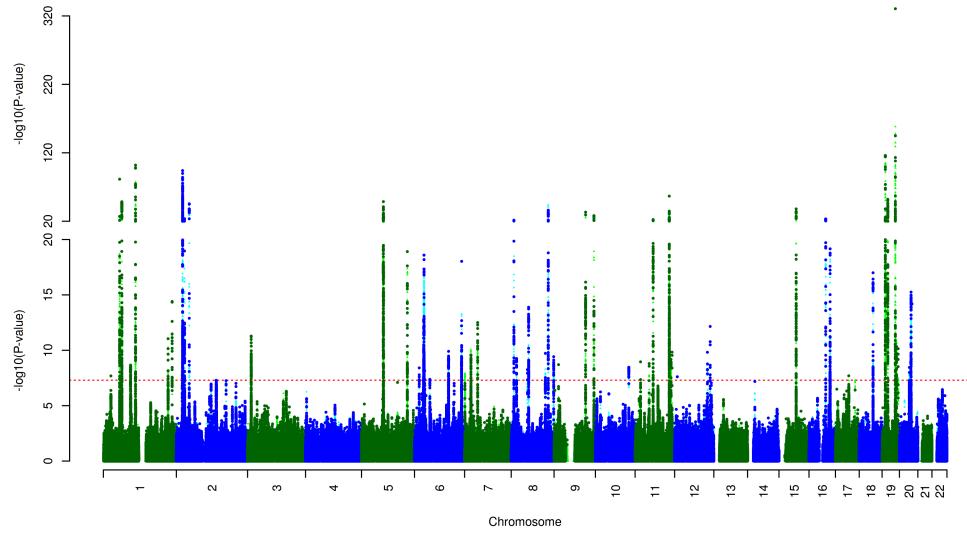
HDL.



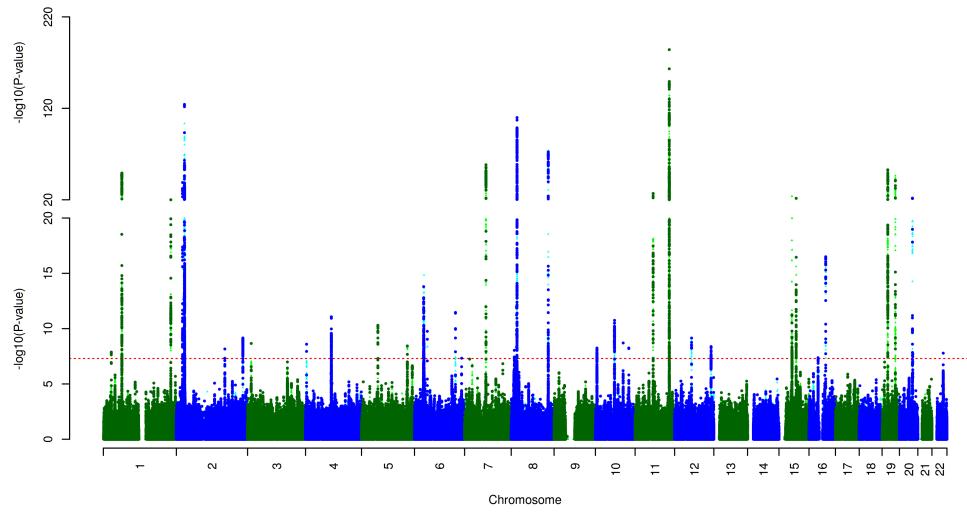
LDL.



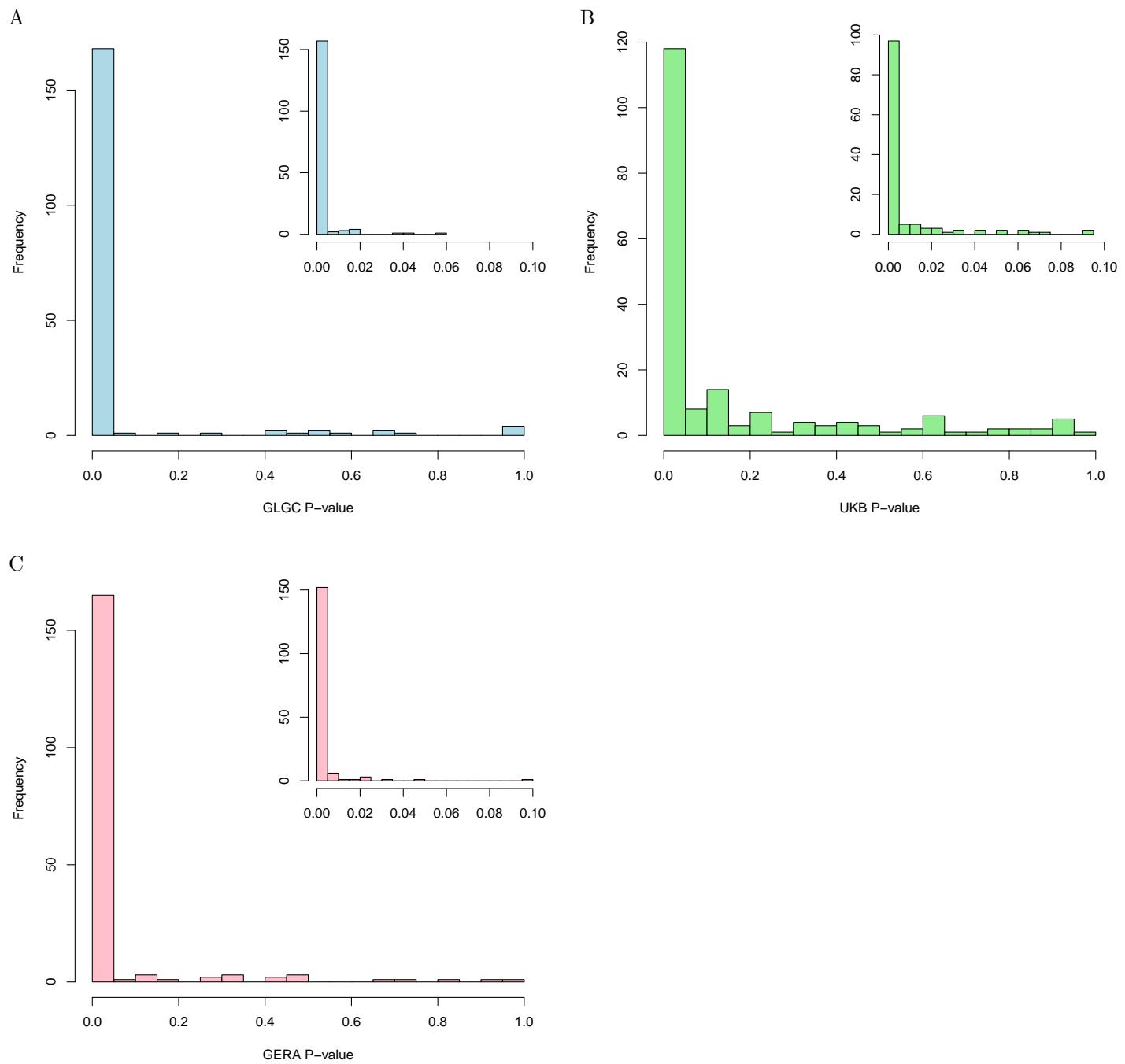
TC.



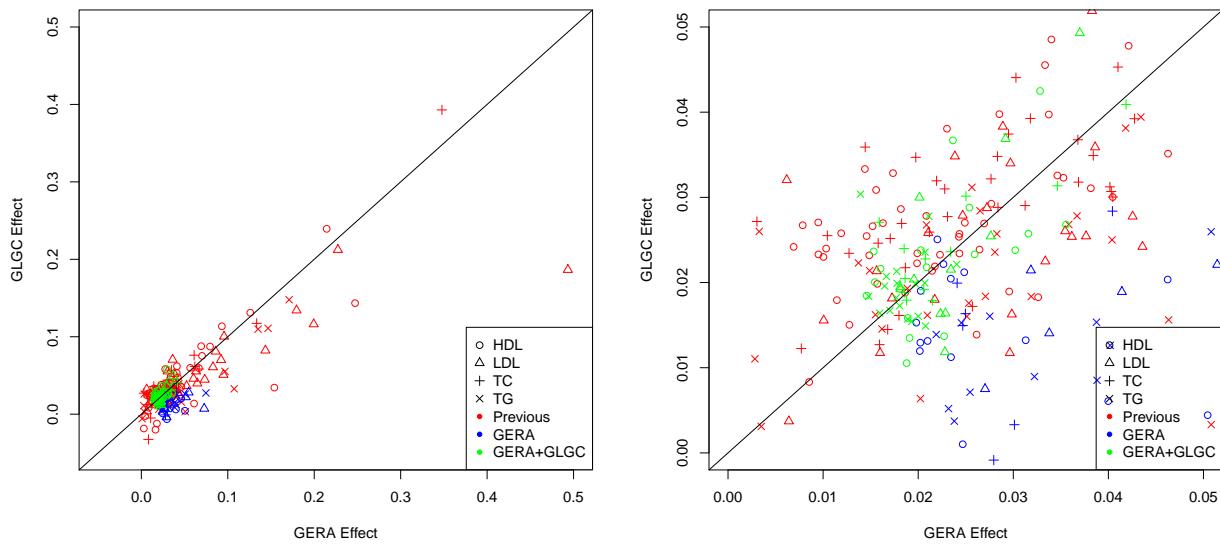
TG.



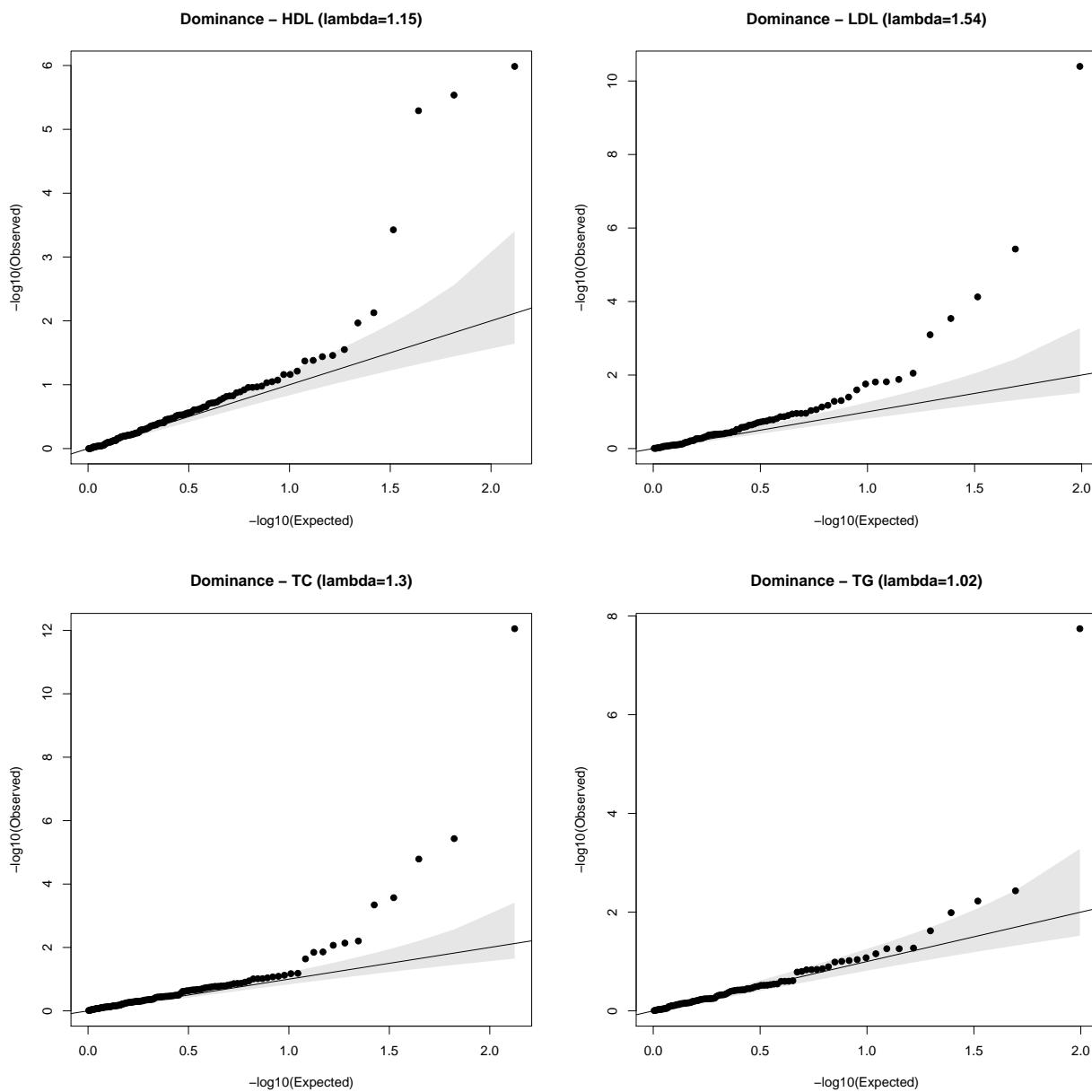
Supplementary Figure 4: Replication p-value distribution. Replication of SNPs (A) discovered in GERA (n=94,674) using GLGC (n=94,595), (B) discovered in GERA using UKB (n=460,088), and (C) all previously-identified SNPs using GERA (n=94,674). All tests two-sided via linear regression.



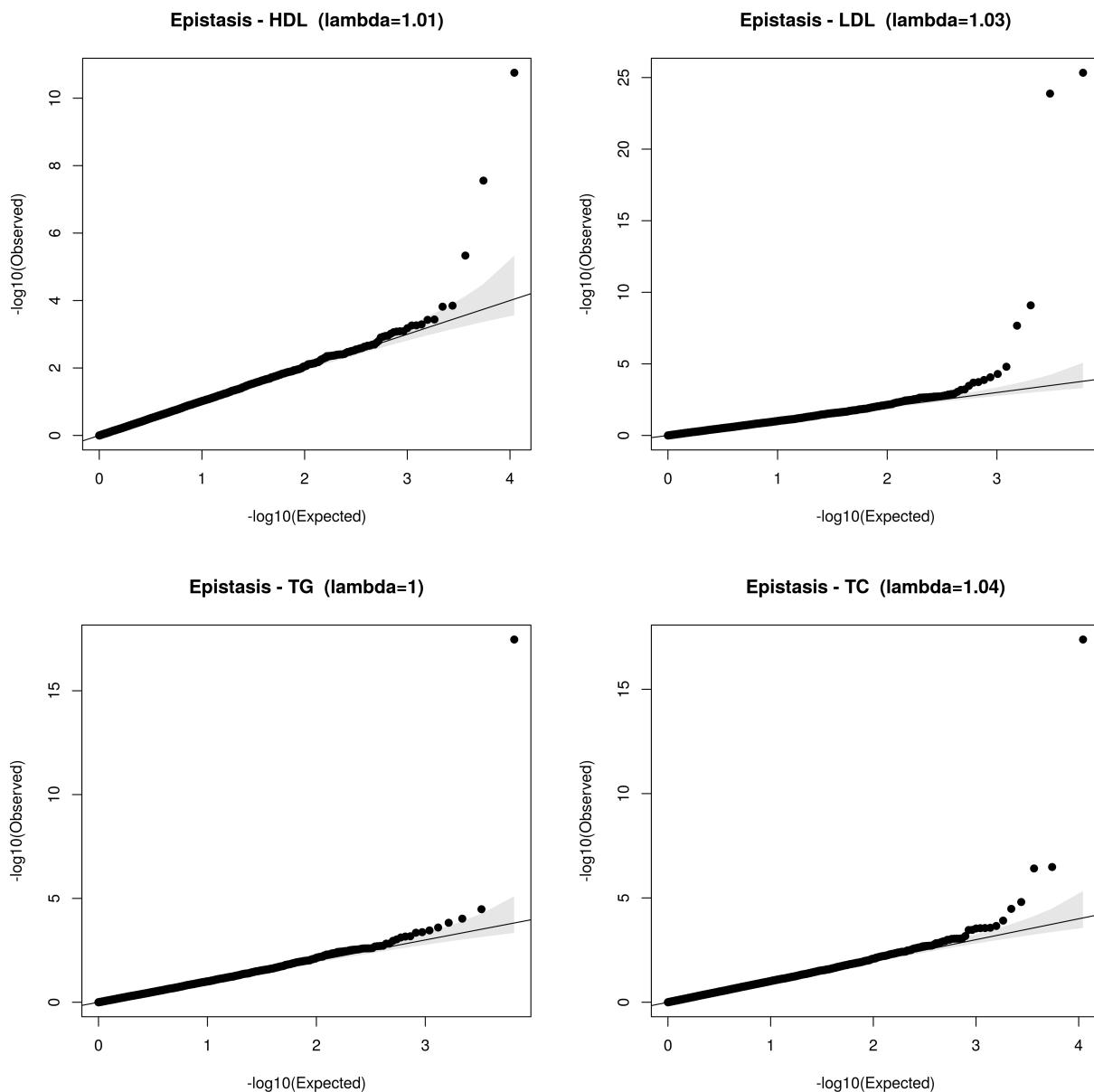
Supplementary Figure 5: Effect size estimates in the RPGEH GERA (n=94,674) cohort vs. previously-reported GLGC (n=94,595) effect size estimates. All tests two-sided via linear regression.



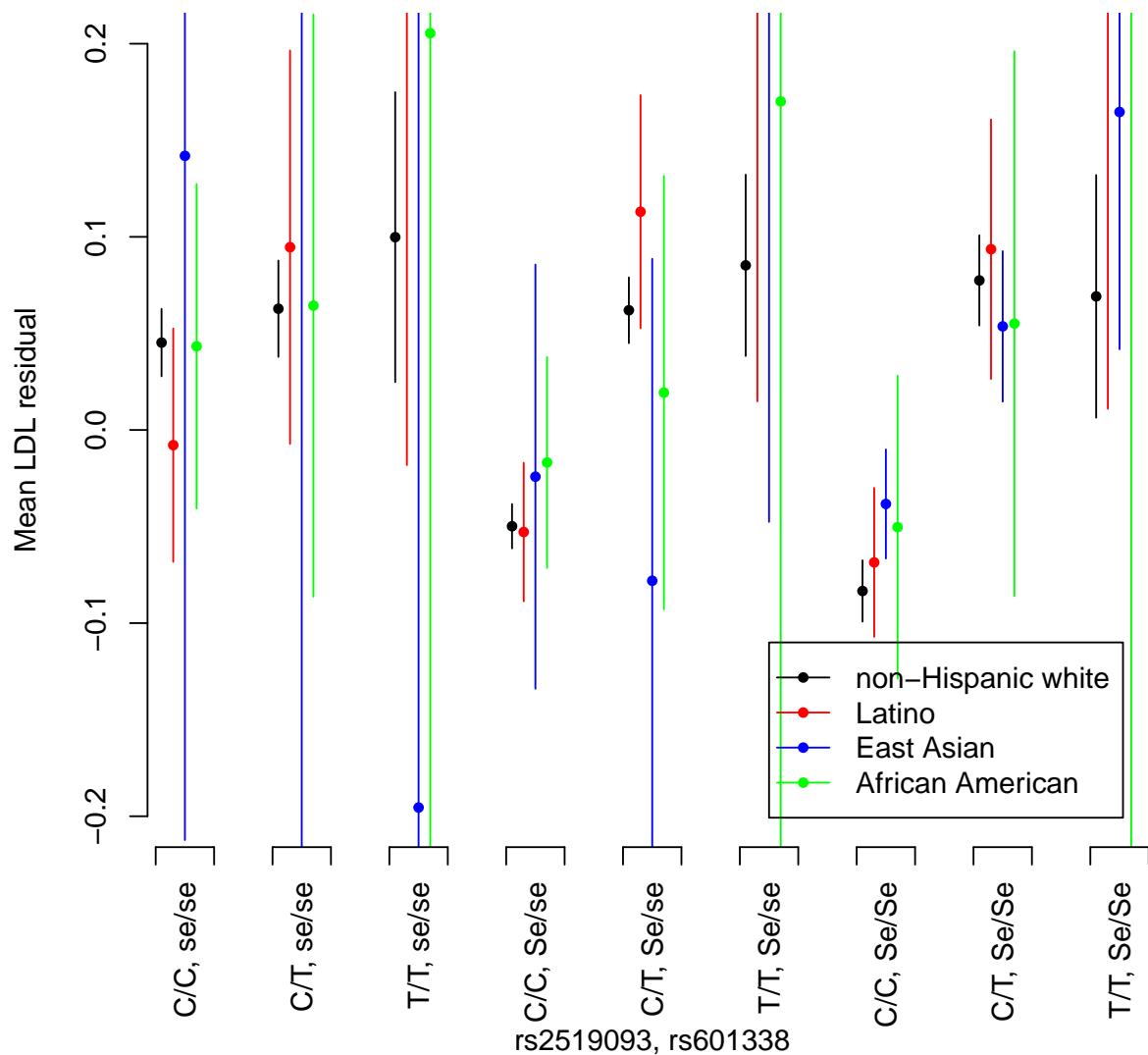
Supplementary Figure 6: Dominance Q-Q plots in RPGEH GERA (n=94,674) of all previously-, GERA-, and GERA+GLGC-identified lead SNPs. All tests two-sided via linear regression.



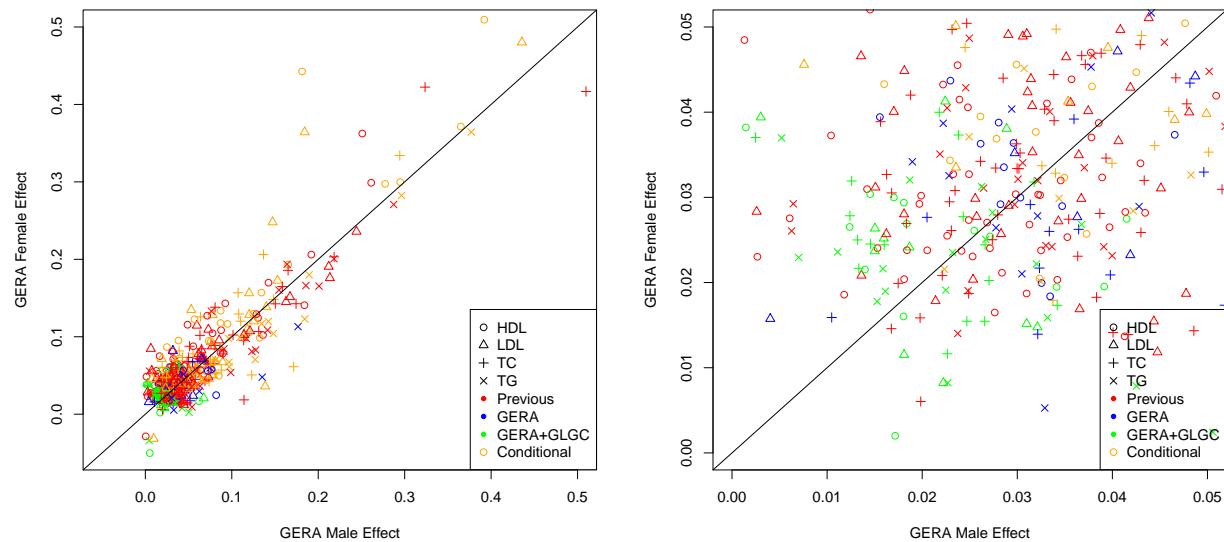
Supplementary Figure 7: Epistasis Q-Q plots in RPGEH GERA (n=94,674) of all pairwise tests of previously-, GERA-, and GERA+GLGC-identified lead SNPs. All tests two-sided via linear regression.



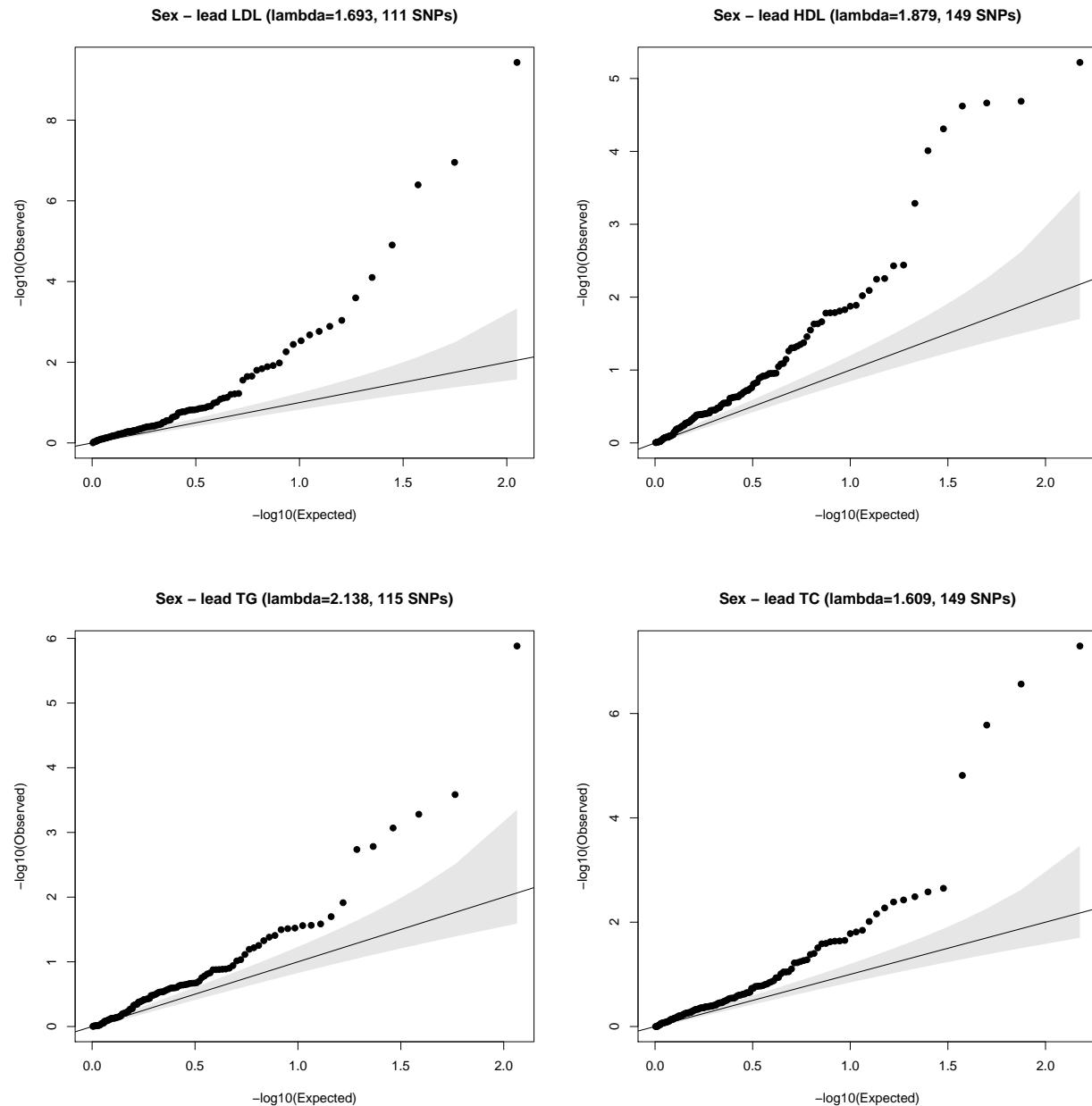
Supplementary Figure 8: Interaction of rs2519093 (*FUT2*) and rs601338 (*ABO*) in GERA (n=94,674). The rs601338 allele determines secretor status; Se/Se and Se/se are secretors (dominant) and se/se are nonsecretors. The vertical lines represents 95% confidence intervals. All tests two-sided via linear regression.



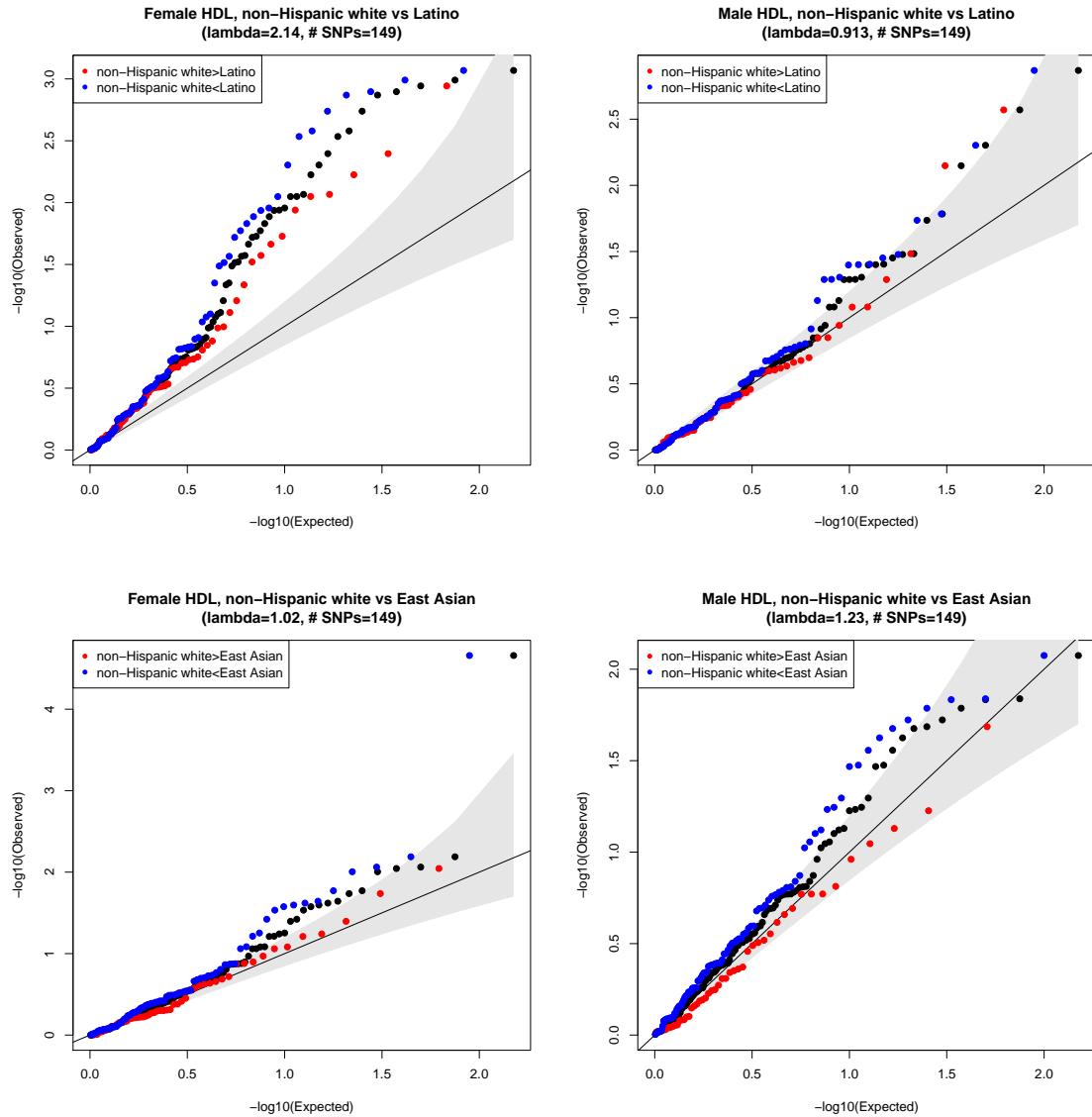
Supplementary Figure 9: Effect size estimates in RPGEH GERA (n=94,674) males (n=39,159) vs. females (n=55,515). All tests are two-sided via linear regression

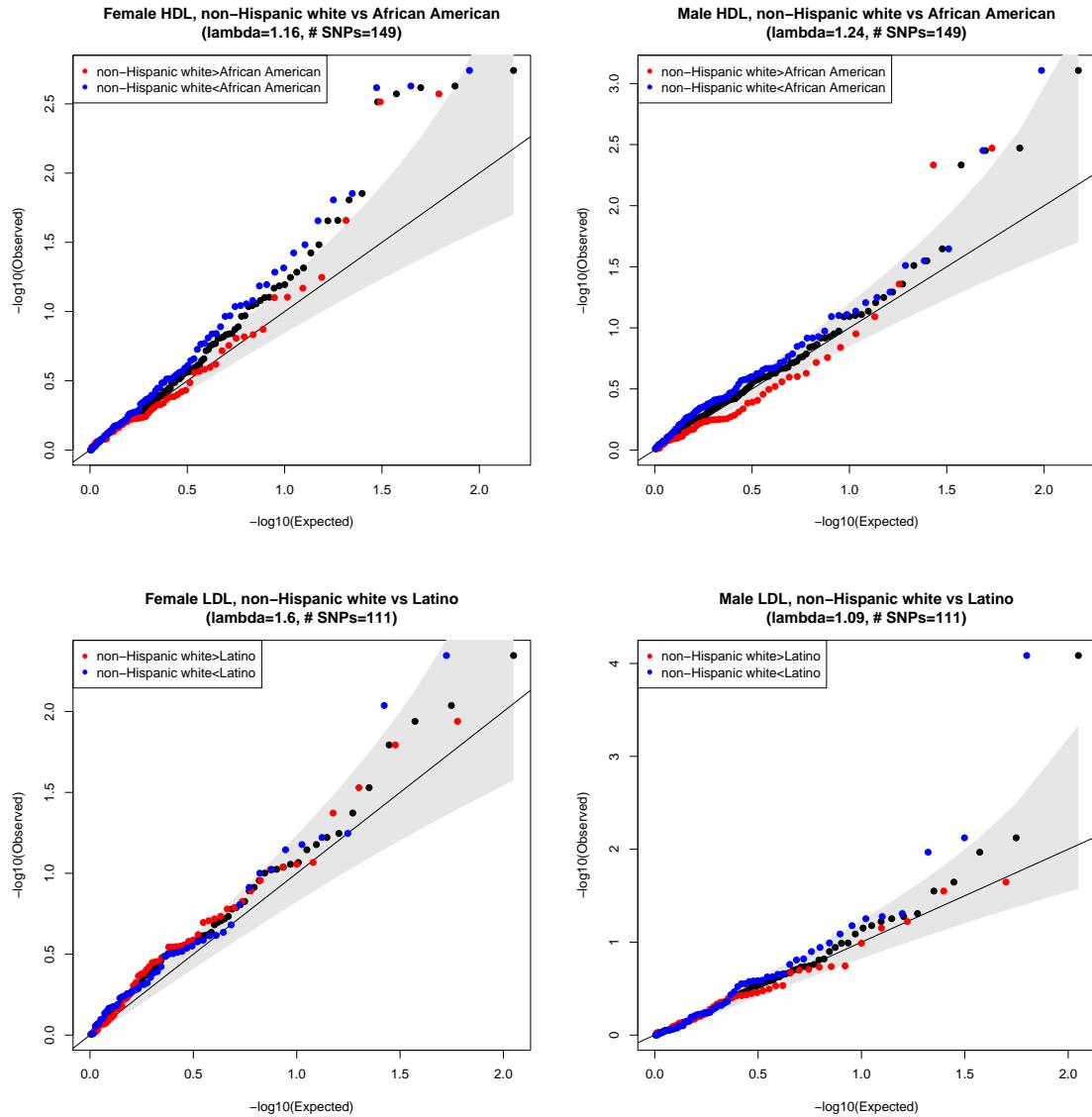


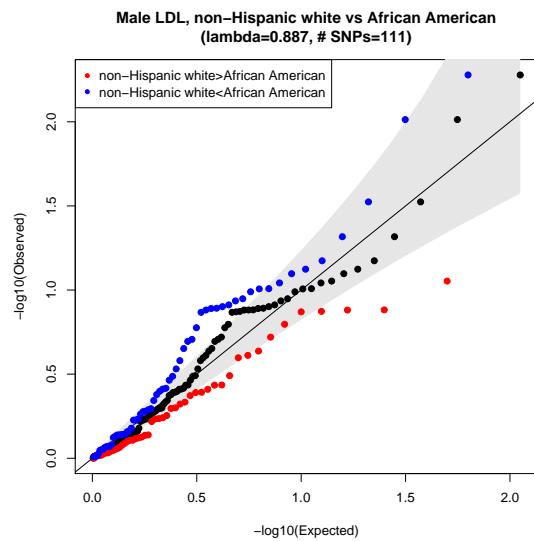
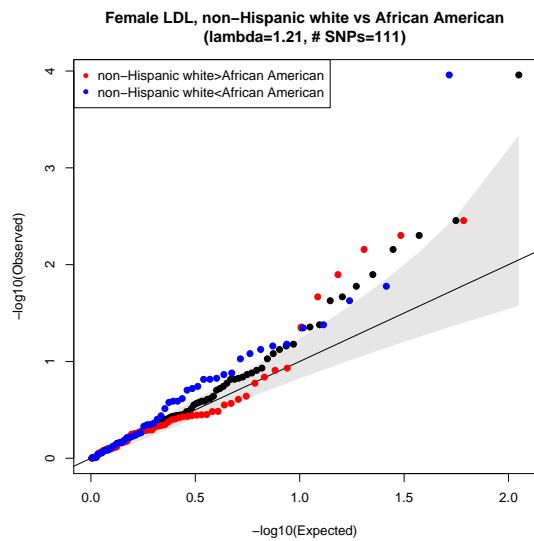
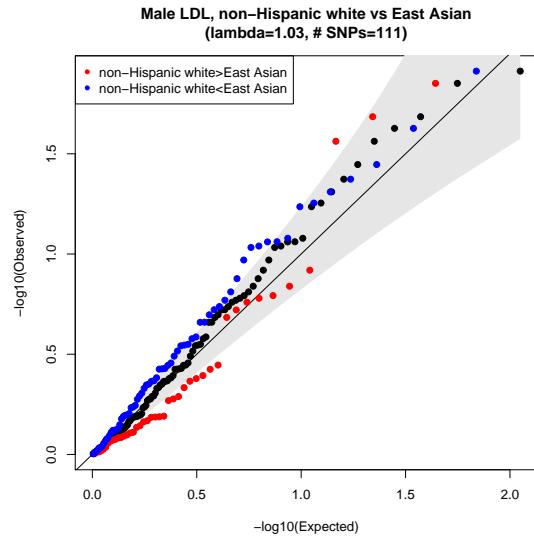
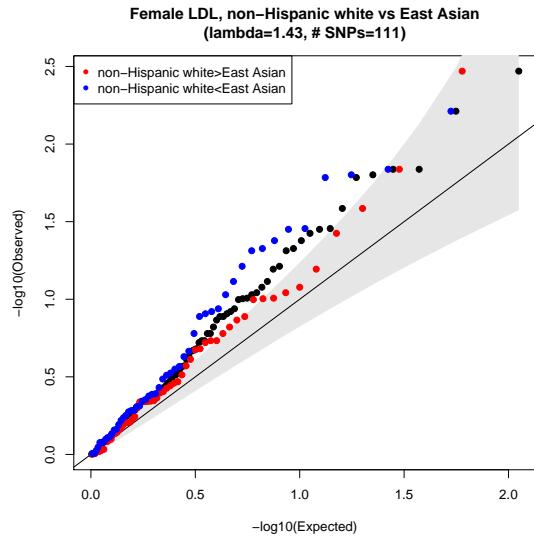
Supplementary Figure 10: Sex Q-Q plots in RPGEH GERA (n=94,674) of all previously-, GERA-, and GERA+GLGC-identified lead SNPs, comparing the effect sizes of females (n=55,515) to males (n=39,159). All tests are two-sided via linear regression.

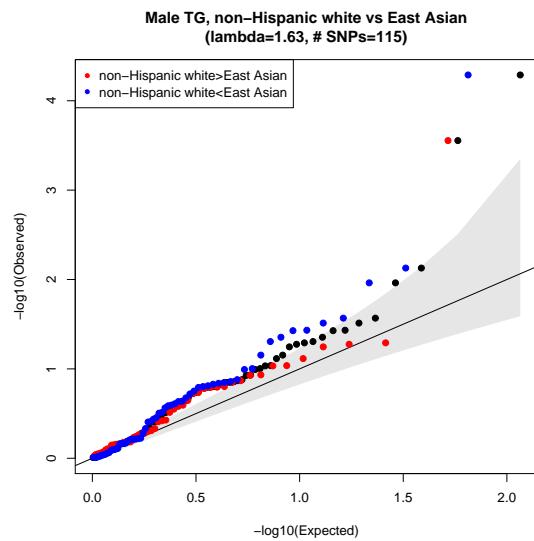
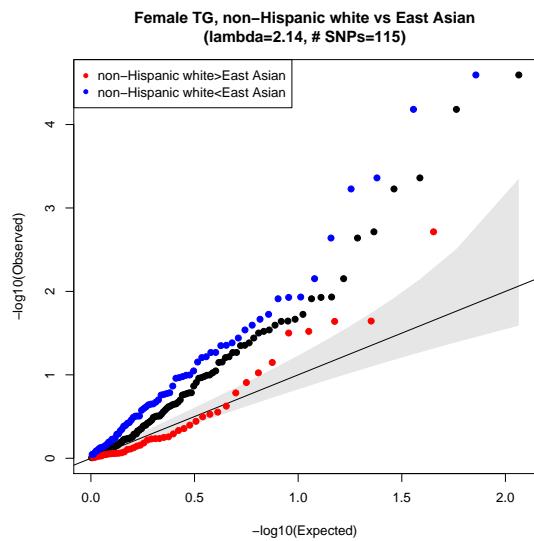
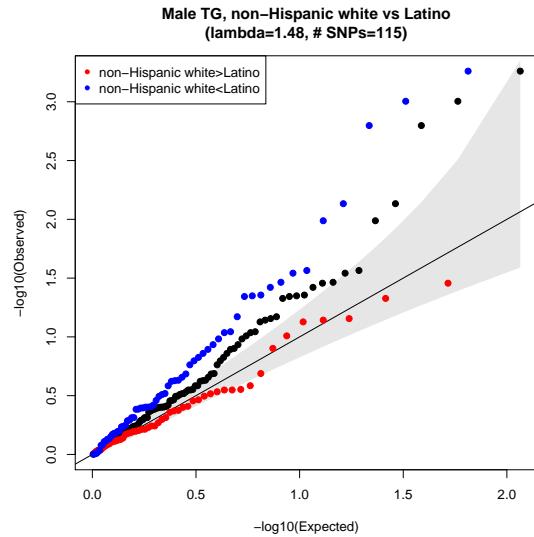
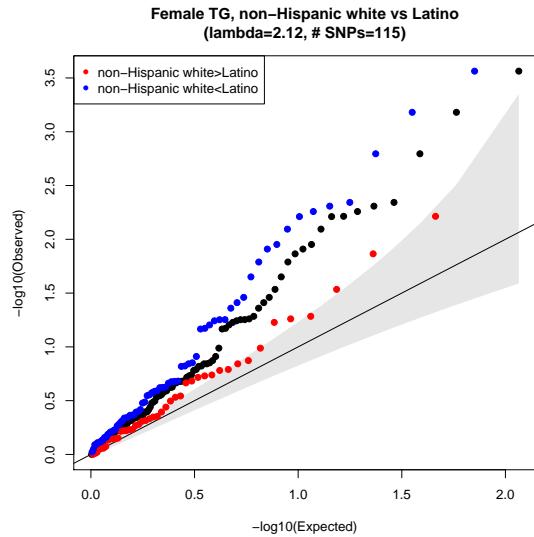


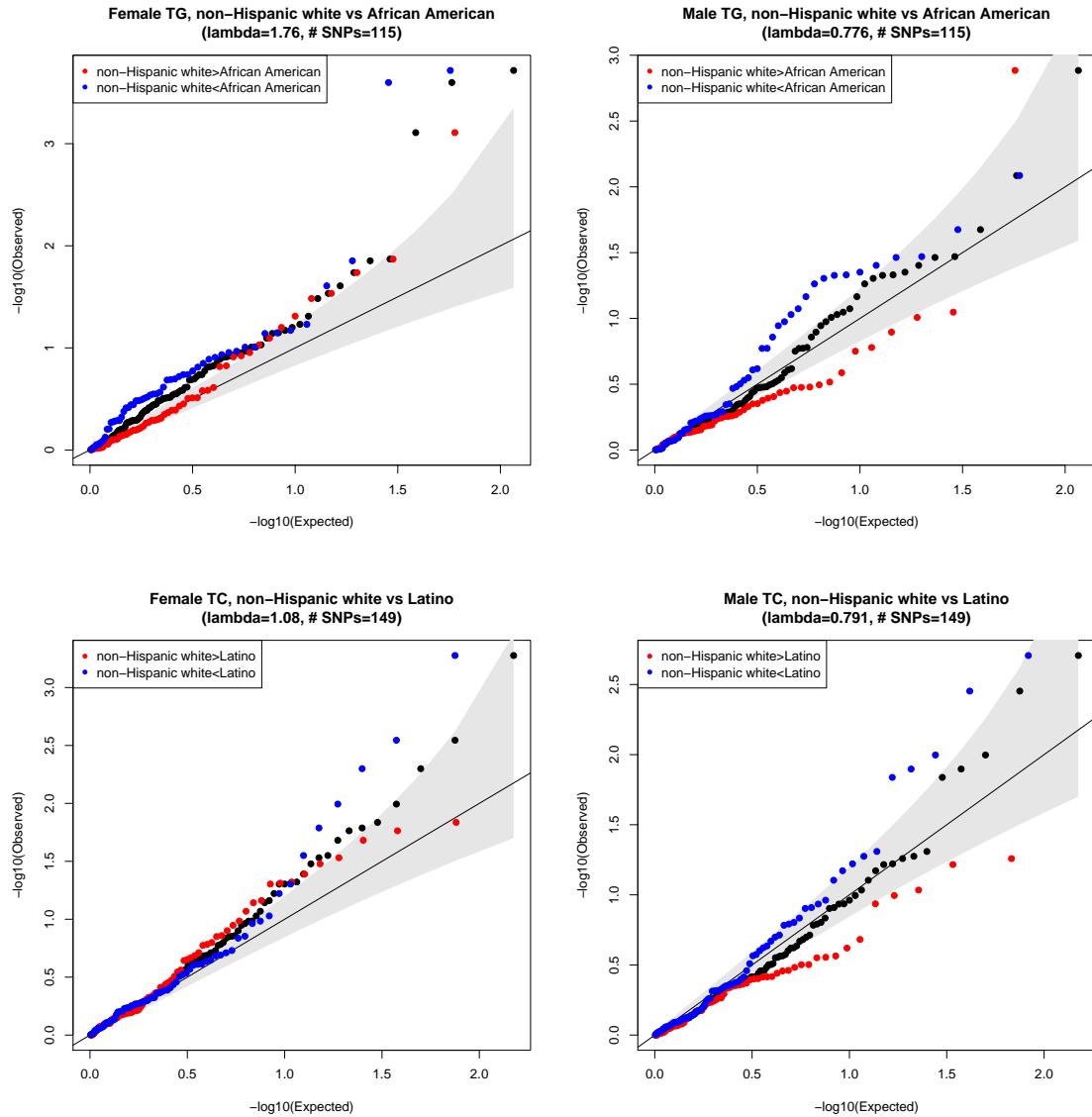
Supplementary Figure 11: Heterogeneity of GERA non-Hispanic whites (n=76,627) vs. other groups (Latinos, n=7,795; East Asians, n=6,855; African Americans, n=2,958; South Asians, n=439).

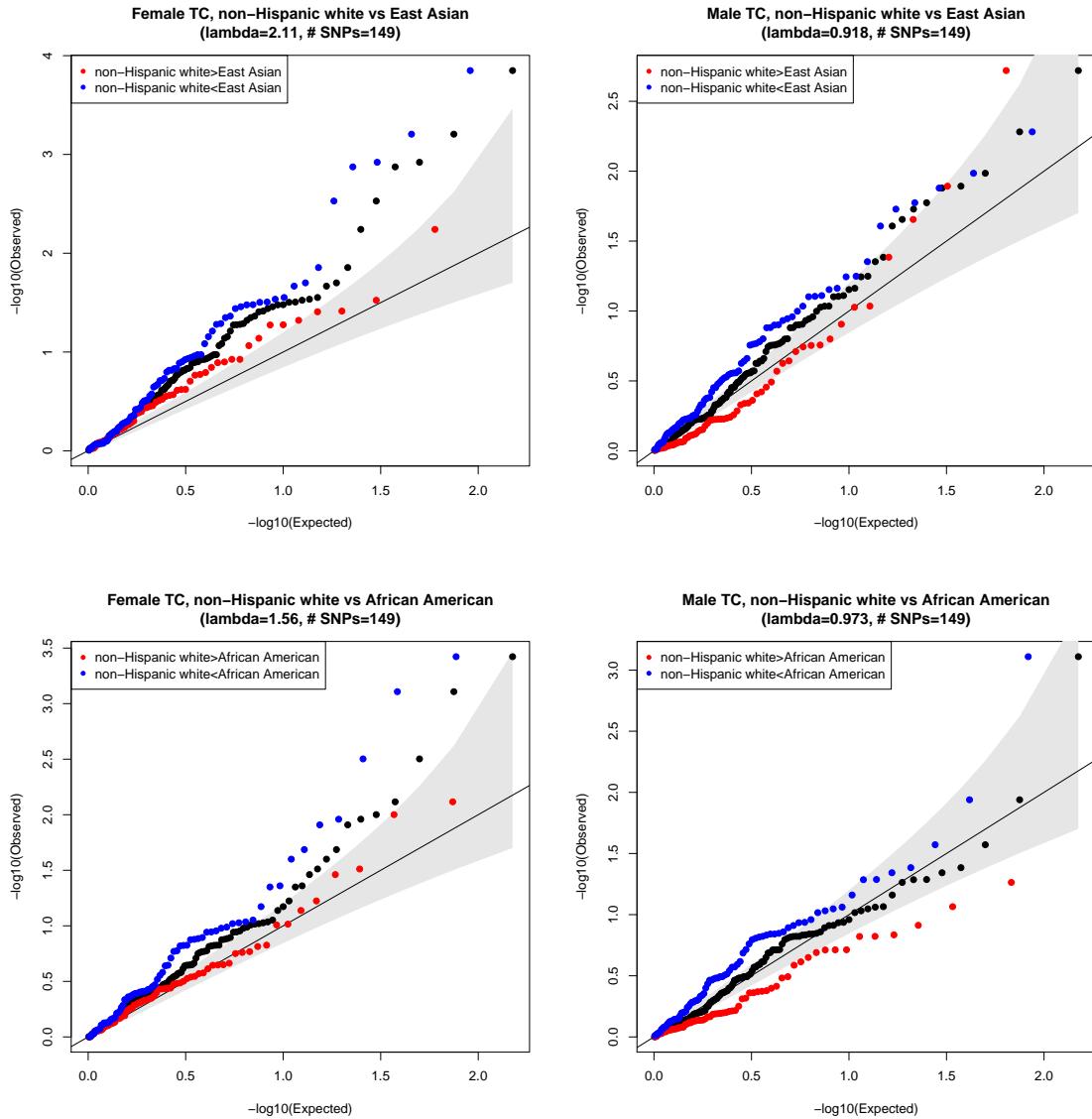




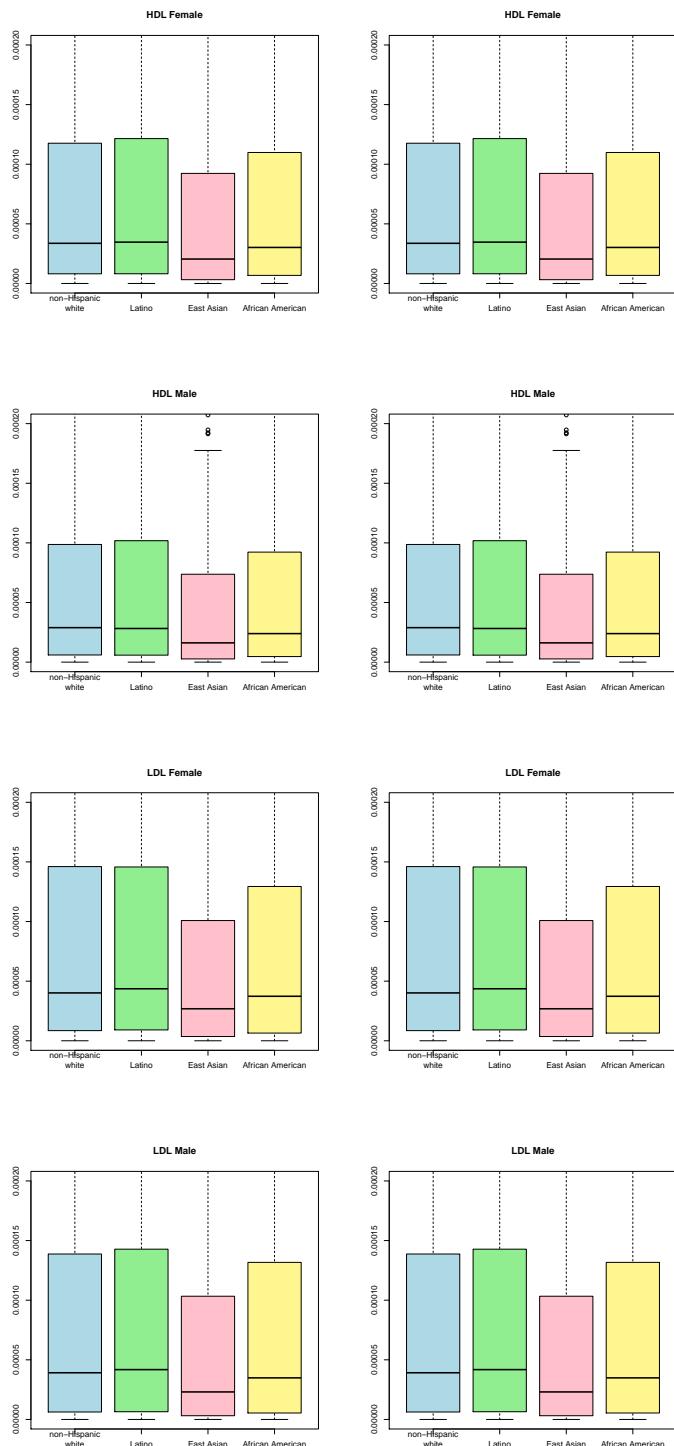




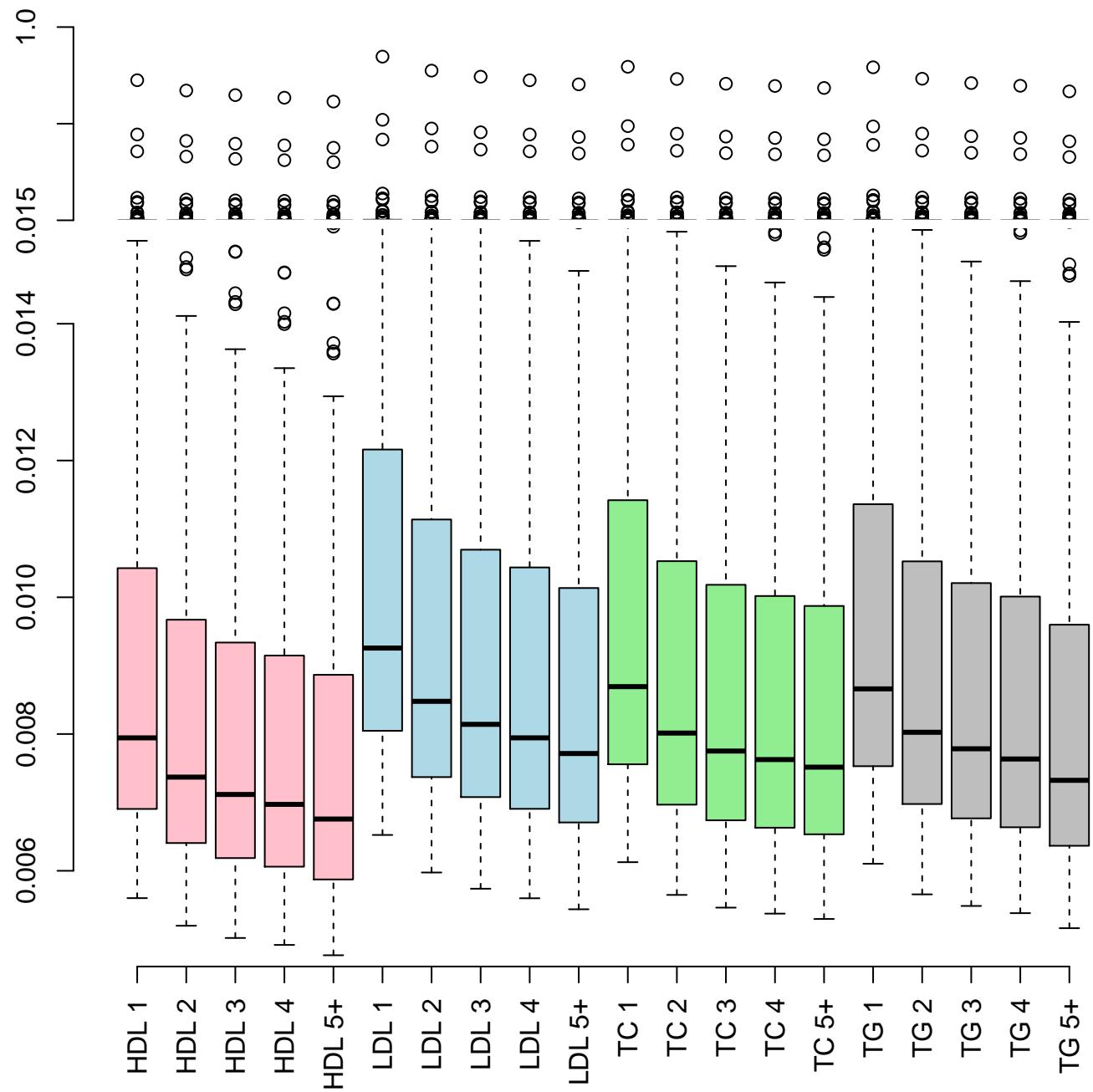




Supplementary Figure 12: Boxplots of $p(1 - p)\beta^2$ minor allele frequency distributions in GERA (non-Hispanic whites, n=76,627; Latinos, 7,795; East Asians, n=6,855; African Americans, n=2,958; South Asians, n=439). In the boxplot, each box represents the interquartile range, split by the median, with the whiskers extending to the upper and lower extremes, excluding outliers. The y-axis range was in order to view the interquartile range better.



Supplementary Figure 13: Benefit of repeated measures on SNP SEs. Boxplots of the previously-identified SNPs SEs using increasing numbers of measurements per individual (for a fixed sample size; only individuals with five or more measurements were included; n=34,936 non-Hispanic whites). The x-axis indicates the number of measurements for each of the three phenotypes. In the boxplot, each box represents the interquartile range, split by the median, with the whiskers extending to the upper and lower extremes, excluding outliers.



Supplementary Figure 14: Lipidemia treatment time-to-onset Kaplan Meier curves by LDL quintiles (lower, middle, and upper only for clarity) and TG GRS upper/lower halves. (A) Latino females (n=4,708), (B) Latino males (n=3,087), (C) East Asian females (n=4,013), (D) East Asian males (n=2,842), (E) African American females (n=1,761), (F) African American males (n=1,197). The shaded areas represent the 95% confidence intervals around the estimated curves. All tests are two-sided.

