Web Figure 1. The PAGE results browser grid plot. The gridplot display shows p-values across SNPs and phenotypes. Different color palettes indicate positive and negative associations. Preliminary PAGE data were used for this plot.

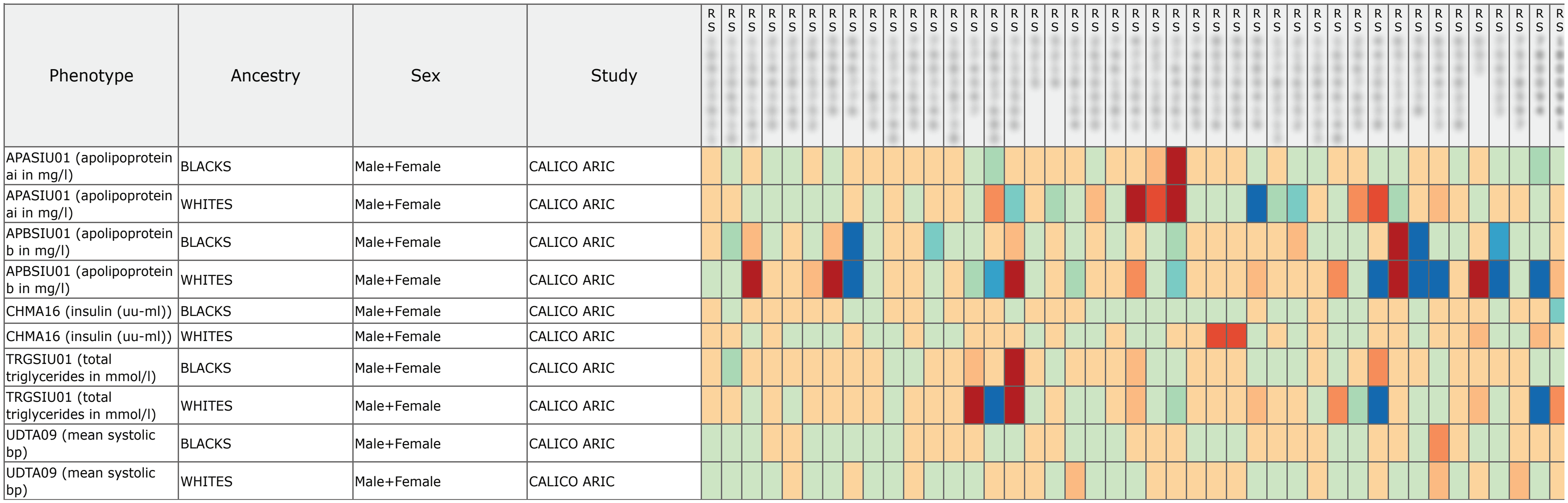
Web Figure 2. The PAGE results browser box plot. The boxplot display shows the 1st, 2nd, and 3rd quantiles by genotype for SNPs and (quantitative) phenotypes. Preliminary PAGE data were used for this plot.

Web Figure 3. The PAGE results browser forest plot. The forest plot display shows effect estimates and 95% confidence intervals across studies. Simulated data were used for this plot.

Web Figure 1

SNP x Phenotype x Ancestry x Sex x Study Download Data

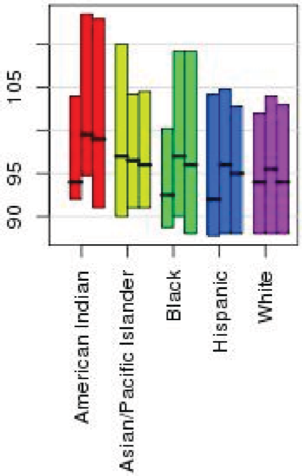
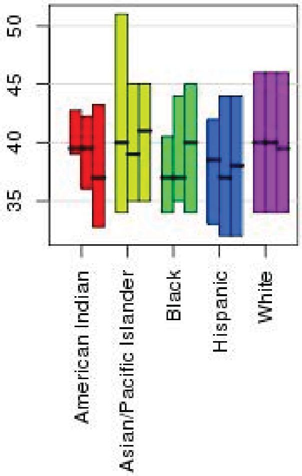
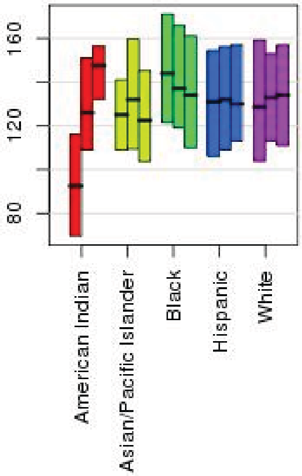
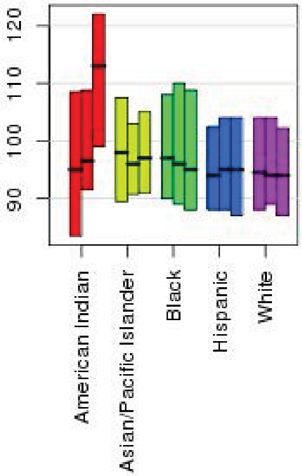
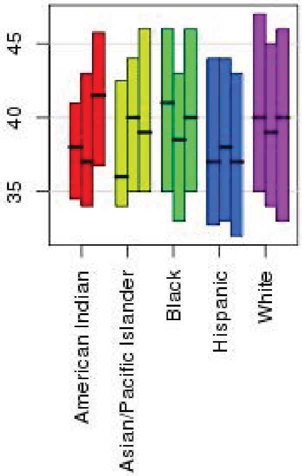
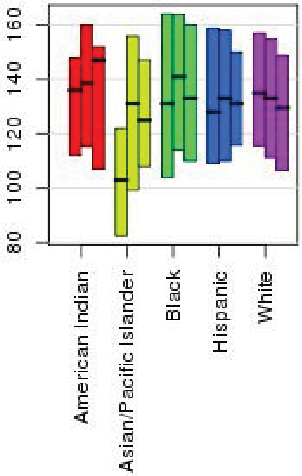
Positive Effect	.05 < *p* < 1.0	.01 < *p* < .05	.001 < *p* < .01	.0001 < *p* < .001	*p* < .0001
Negative Effect	.05 < *p* < 1.0	.01 < *p* < .05	.001 < *p* < .01	.0001 < *p* < .001	*p* < .0001



Phenotype	Ancestry	Sex	Study
APASIU01 (apolipoprotein ai in mg/l)	BLACKS	Male+Female	CALICO ARIC
APASIU01 (apolipoprotein ai in mg/l)	WHITES	Male+Female	CALICO ARIC
APBSIU01 (apolipoprotein b in mg/l)	BLACKS	Male+Female	CALICO ARIC
APBSIU01 (apolipoprotein b in mg/l)	WHITES	Male+Female	CALICO ARIC
CHMA16 (insulin (uu-ml))	BLACKS	Male+Female	CALICO ARIC
CHMA16 (insulin (uu-ml))	WHITES	Male+Female	CALICO ARIC
TRGSIU01 (total triglycerides in mmol/l)	BLACKS	Male+Female	CALICO ARIC
TRGSIU01 (total triglycerides in mmol/l)	WHITES	Male+Female	CALICO ARIC
UDTA09 (mean systolic bp)	BLACKS	Male+Female	CALICO ARIC
UDTA09 (mean systolic bp)	WHITES	Male+Female	CALICO ARIC

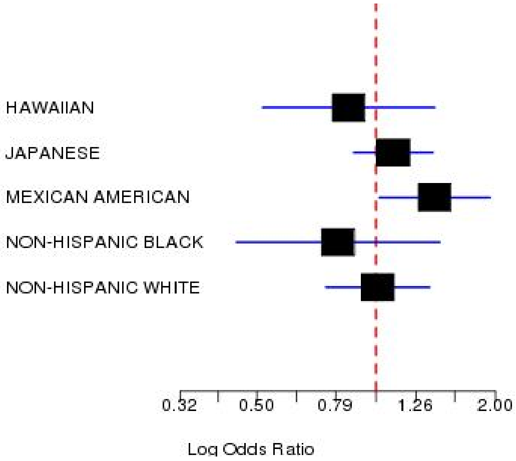
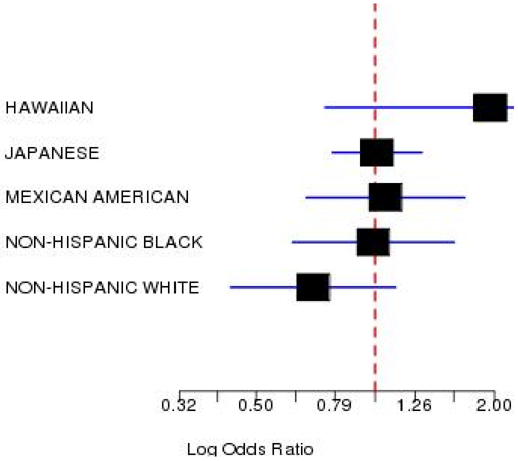
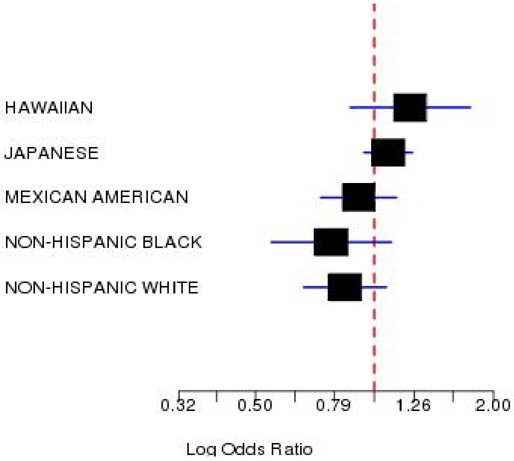
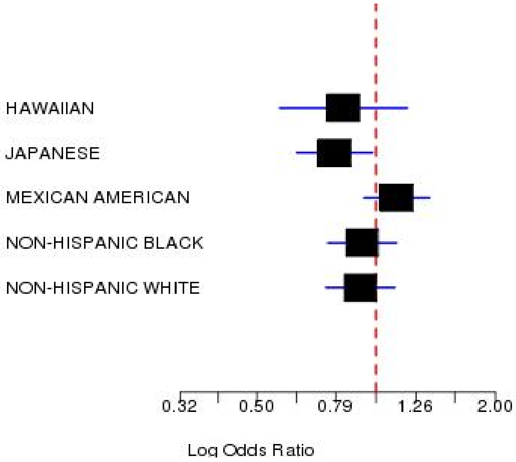
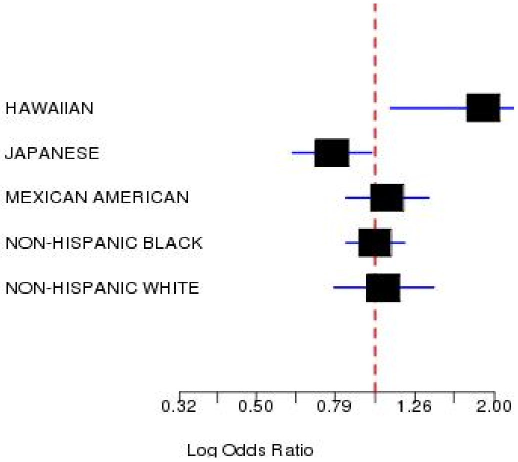
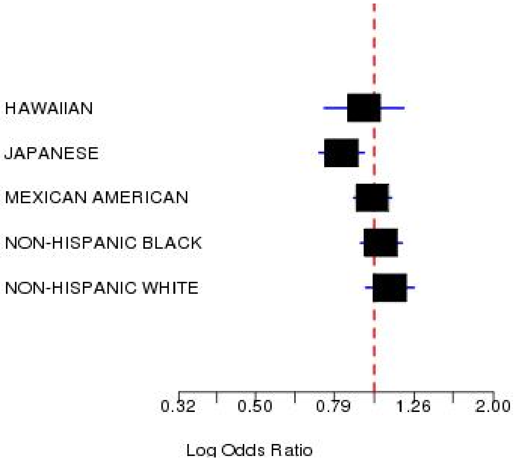
Web Figure 2

SNP x Study x Phenotype x Sex [Download Data]

	Phenotype	coregluc - Core Glucose (Mg/dl)	corehdl3 - Core High-Density Lipoprotein-3 (Mg/dl)	coreldlc - Core LDL Cholesterol (Mg/dl)
SNP	Study\Sex	Female	Female	Female
rs [redacted]	WHI			
rs[redacted]	WHI			

Web Figure 3

SNP x Study x Phenotype x Sex [Download Data]

	Phenotype	cataract - History of Cataract Surgery from Baseline Questionnaire	glaucoma - History of Glaucoma from Baseline Questionnaire	ulcer - History of Ulcer (Stomach or Duodenal) from Baseline Questionnaire
SNP	Study\Sex	Male+Female	Male+Female	Male+Female
rs [redacted]	MEC			
rs[redacted]	MEC			

Web Table 1. PAGE-wide power to replicate and generalize SNPs previously associated with LDL-C levels.

A total of 19 SNPs previously associated with LDL-C levels were genotyped by at least two PAGE study sites. Each SNP, its chromosomal and base-pair location (based on Genome Build 37), its putative function based on location, and the nearest gene are given in the first four columns of the table. The number of PAGE study sites that genotyped each SNP is denoted, with four PAGE study sites representing the maximum. The expected genetic effect size (β) is based on the literature, and the reference is indicated in the Table. For each test of association, we calculated the power to detect the expected effect size assuming a significance threshold of 0.005 and the coded allele frequency observed in the population. In the power columns, "(+)" denotes that the sample size for that test of association has sufficient power (>80%) to detect the expected effect size at $P = 0.005$.

SNP	Chr. (Location)	Function	Nearest Gene	# PAGE Studies[a]	Effect Size‡ (mg/dl)	Reference	EA CAF (Power)	AA CAF (Power)	AI CAF (Power)	MA/H CAF (Power)
rs11206510	1 (55495789)	Intergenic	*PCSK9*	4	3.04	Willer et al 2008[1]	0.81 (+)	0.86 (-)	0.93 (-)	0.88 (-)
rs11591147	1 (55505397)	Non-synonymous	*PCSK9*	3	-17.1	Kathiresan et al 2009[2]	0.02 (+)	4.10E-03 (-)	0.01 (+)	001 (-)
rs646776	1 (109818280)	Downstream	*CELSR2*/*PSRC*/*SORT*	4	6.18	Kathiresan et al 2008[3]	0.78 (+)	0.65 (+)	N/a	0.81 (+)
rs599839	1 (109821916)	Downstream	*CELSR2*/*PSRC*/*SORT*	3	5.48	Willer et al 2008[1]	0.77 (+)	0.28 (+)	0.78 (+)	0.78 (-)
rs693	2 (21231945)	Synonymous	*APOB*	4	2.44	Willer et al 2008[1]	0.50 (+)	0.24 (-)	0.34 (+)	0.38 (-)
rs562338	2 (21288071)	Intergenic	*APOB*	4	-4.89	Willer et al 2008[1]	0.19 (+)	0.59 (+)	0.09 (+)	0.16 (+)
rs754523	2 (21311441)	Intergenic	*APOB*	4	-2.78	Willer et al 2008[1]	0.68 (+)	0.78 (-)	0.66 (+)	0.72 (-)
rs6544713	2	Intronic	*ABCG8*	4	5.1	Kathiresan	0.31	0.17	0.11	0.18

	(44073631)					et al 2009[2]	(+)	(+)	(+)	(+)
rs12654264	5 (74648353)	Intronic	*HMGCR*	4	-3.86	Kathiresan et al 2008[3]	0.62 (+)	0.67 (+)	0.58 (+)	0.62 (+)
rs1501908	5 (156397919)	Intergenic	*TIMD4*	3	2.38	Kathiresan et al 2009[2]	0.64 (+)	0.37 (-)	0.85 (-)	0.76 (-)
rs2650000	12 (121388712)	Intergenic	*HNF1A*	3	2.38	Kathiresan et al 2009[2]	0.35 (+)	0.12 (-)	0.41 (+)	0.37 (-)
rs6511720	19 (11202056)	Intronic	*LDLR*	4	-6.99	Teslovich et al 2010[4]	0.12 (+)	0.13 (+)	0.07 (+)	0.08 (+)
rs2228671	19 (11210662)	Synonymous	*LDLR*	2	-0.14‡	Aulchenko et al 2009[5]	0.12 (+)	0.04 (-)	N/a	0.08 (-)
rs16996148	19 (19658222)	Downstream	*CILP2/PBX4/NCAN*	4	-3.32	Willer et al 2008[1]	0.08 (+)	0.15 (+)	0.04 (-)	0.06 (-)
rs4803750	19 (45247627)	Upstream	*BCL3*	2	10.92†	Sandhu et al 2008[6]	0.93 (+)	0.92 (+)	N/a	0.86 (-)
rs10402271	19 (45329214)	Downstream	*APOE/C1/C4* gene cluster	2	-2.62	Willer et al 2008[1]	0.67 (+)	0.84 (-)	N/a	0.61 (-)
rs4420638	19 (45422696)	Downstream	*APOE/C1/C4* gene cluster	4	-7.14	Teslovich et al 2010[4]	0.82 (+)	0.79 (+)	0.90 (+)	0.90 (+)
rs2075650	19 (50087459)	Intronic	*TOMM40*	2	-0.16‡	Aulchenko et al 2009[5]	0.88 (+)	0.87 (-)	N/a	0.90 (-)
rs6102059	20 (39228784)	Intergenic	*MAFB*	3	-2.04	Kathiresan et al 2009[2]	0.30 (+)	0.43 (-)	N/a	0.29 (-)

Abbreviations: Base(-)pair (bp), untranslated region (UTR); coded allele frequency (CAF); European American (EA); African American (AA); American Indian (AI); Mexican American /Hispanic (MA/H)

[a]Number of PAGE studies that genotyped the SNP. PAGE studies include CALiCo, EAGLE, MEC, and WHI.

‡Effect size (β) is reported in s.d. (standard deviation) units

†Effect size originally expressed in mmol/L

Maximum sample sizes: EA = 21,986; AA = 9,328; AI = 6,144; MA/H = 2,532

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