Supplementary Online Content

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Echocardiographic Methods

Phenotypic Characterization & Harmonization:

Reproducibility Issues of Echo

High-quality phenotyping is critical for GWAS. In this context, echocardiography is the most commonly used noninvasive cardiac imaging tool. Sources of variability include inter- and intra-reader and sonographer variability, beat-to-beat and day-to-day within subject variability, temporal drift within laboratories, and biases due to missing data.[1;2] Fortunately, studies have demonstrated methods to enhance echo reproducibility: use of centralized reading stations, standardized equipment and imaging and reading protocols, trained sonographers and readers who periodically undergo reading review sessions, averaging multiple measurements, substituting 2D measurements when M-mode measurements are unreliable, and analyses of temporal drifts.[2-5] Each of the 5 participating cohorts in the EchoGen consortium has implemented several of these quality control measures. Furthermore, the analytical strategy does not involve pooling of individual participant data, but rather within-cohort analyses, and a prospective meta-analysis across the cohorts.

Cardiovascular Health Study

Participants underwent routine echocardiography at the 1989-90 and 1994-95 exams. Methods for 2-dimensional, Doppler and M-mode transthoracic echocardiography in CHS have been previously described in detail.[6] Left ventricular (LV) and left atrial chamber dimensions and aortic root size were determined by 2-dimensionally directed M-mode images according to the recommendations of the American Society of Echocardiography. Global LV ejection fraction was qualitatively assessed on 2-dimensional echocardiography as normal ($\geq$55%), mildly reduced (45% to 54%), moderately reduced (30% to 44%), or severely reduced (<30%). Left ventricular mass was estimated using M-mode echocardiography.[7] Left ventricular fractional shortening, a quantitative measure of LV systolic function, was calculated using the formula ([LV end diastolic dimension – LV end systolic dimension]/ LV end diastolic dimension x 100). Studies were evaluated by readers blinded to the participants' clinical information. Quality control measures included standardized training of echocardiography technicians and readers, observation of technicians by a trained echocardiographer, and periodic blind duplicate readings. For each trait, values were averaged over both exams.

Rotterdam Study

Transthoracic two-dimensional echocardiography was obtained by trained echocardiographers in all participants at the fourth (2002-2004) examination, using an Acuson Cypress with a 3V2c transducer. A standardized protocol was used, including two-dimensional scanning in the parasternal long axis view, parasternal short axis view, apical view and subcostal view. In addition, M-Mode scanning in the parasternal long axis view was performed (to obtain two-dimension guided M-mode measurements of the LV and aortic root), as well as pulsed wave Doppler scanning in the apical four chamber view. All studies were recorded onto videotape and assessed at the reading center by trained echocardiographers. Assessment of intra-reader and inter-reader agreement was performed during the study.

MONICA-KORA

Echocardiograms were obtained using the Sonos 1500 (Hewlett Packard Inc.) with a 2.5 or a 3.5 MHz transducer by two experienced physicians. In order to reduce inter-reader variability, all 2D-guided M-mode tracings were analyzed by a single cardiologist, blinded for all participant related data, for measurement of LV and aortic root dimensions. Measurements for M-mode-guided calculation of the left ventricular mass (LVM) were taken just below the tip of the mitral valve, using only high-quality tracings with optimal visualizations of endocardial and epicardial surfaces throughout the cardiac cycle. Bland–Altman plots were constructed from 144 duplicate readings obtained in individuals volunteering for a blinded duplicate examination. The mean relative differences in LVM were 0.6% with a 2 SD range of 14.7%.

Framingham Heart Study

All attendees underwent routine transthoracic two-dimensionally-guided M-mode echocardiography at the second (1979-1982), fourth (1987-1990), fifth (1991-1995) and sixth (1996-1998) Offspring cohort examinations. Echocardiographic equipment for image acquisition varied across these examinations: at examination cycle 2, a Hoffrel 201 ultrasound receiver (and Aerotech transducer) was used; at examinations 4 and 5, a Hewlett Packard (model 77020AC) ultrasound machine was used; at examination 6 images were acquired using a Sonos 1000 Hewlett-Packard machine. Two-dimension guided M-mode measurements of the LV and aortic root were obtained. The reproducibility of Echo measurements was systematically assessed at the sixth examination and was very good.[8]

Gutenberg Heart Study

All attendees underwent routine transthoracic two-dimensionally-guided M-mode and two-dimensional echocardiography (for LV and aortic root measurements) during baseline examination. Image acquisition was obtained by PHILIPS IE33 (Philips Ultrasound, Bothell, WA) with a 1.0 – 5.0 MHz 2D transducer. All data sets were recorded electronically for reading.

Study of Health in Pomerania

Echocardiography at baseline was conducted only in subjects 45 years or older, but without age restriction at follow-up. All examinations were performed by certified physicians using the Vingmed CFM 800A system (GE Medical Systems, Waukesha, USA). Two-dimensional guided

M-Mode images of the left ventricle (recorded at papillary level) and aortic root were obtained and digitally stored. Readings were performed according to the American Society of Echocardiography convention. All echocardiographic measurements of intra-reader, intra-observer, inter-reader and inter-observer agreements revealed a mean bias (± 2 SD) of <5% (<25%).

Austrian Stroke Prevention Study

Transthoracic two-dimensional echocardiography was performed by experienced cardiologists using a Vingmed CFM 750, CFM 800 and a System Five equipment depending on the year of imaging. A standardized protocol was used, including two-dimensional parasternal and apical views. Additionally, parasternal M-Mode imaging was performed, as well as pulsed, continuous and color Doppler imaging in the apical views. Two-dimensionally guided M-Mode measurements of LV dimensions, LV mass, left atrial size and aortic root diameter were obtained, whenever image quality allowed distinct visualization of endo- and epicardial borders. M-Mode measurements of global LV ejection fraction were substituted with estimated values obtained from 2-D echocardiography, when M-Mode measurements appeared unreliable.

Genotyping Methods:

Imputation and Controlling for Population Substructure

Cardiovascular Health Study

DNA was extracted from blood samples drawn on all participants at their baseline CHS examination in 1989-90. In 2007-2008, genotyping was performed at the General Clinical Research Center's Phenotyping/Genotyping Laboratory at Cedars-Sinai using the Illumina 370CNV BeadChip system on 3980 CHS participants who were free of CVD at baseline, consented to genetic testing, and had DNA available for genotyping. Samples were excluded for Mendelian inconsistency, or discordance with prior genotyping. Overall, genotyping was attempted in 3,980 participants and was successful in 3,865 persons. Because the other 4 cohorts in the present investigation were predominantly of European ancestry, the African American CHS participants were excluded from this analysis. Those with available echocardiographic measures from this latter sample constituted the CHS sample for the present investigation. SNPs were excluded from analysis/imputation if: the call rate was <97%; SNPs were monomorphic; the HWE p-value $<10^{-5}$. After exclusions, 306,655 autosomal SNPs were used to impute to the HapMap.

Rotterdam Study

From the 7129 participants of the Rotterdam Study who visited the research center in 1990-1993, 6680 (83.7%) had plated DNA. Of these, 6449 individuals had proper quality DNA samples and were considered for genotyping using the Illumina Infinium II HumanHap550chip v3.0 array in 2007-2008. 6239 participants had a within-person call rate of 97.5% or above. SNPs were excluded if they had a minor allele frequency (MAF) ≤1%, the HWE p-value was $<10^{-6}$, or the SNP call rate was ≤90%, resulting in data on 512,349 SNPs eligible for analyses.

MONICA-KORA

The MONICA/KORA genotyping was conducted on an Affymetrix 500K array 2 chip set (Sty I and NSP I). The mean and median call rates were 98.3% and 98.5%, respectively (details at http://epi.gsf.de/kora-gen/seiten/kora500k_e.php).

Framingham Heart Study

As part of the SNP Health Association Resource (SHARe) project, 9274 FHS participants belonging to the original, Offspring and third generation cohorts were genotyped, and of these 8508 had a within-person call rate ≥97%. Affymetrix conducted NHLBI funded genotyping on the GeneChip® Human Mapping 500K Array Set and 50K Human Gene Focused Panel, using the Bayesian Robust Linear Modeling Mahalanobis distance (BRLMM) algorithm.[9] Genotyping became available in October 2007. The average call rate was about 98%. **FHS** data cleaning was conducted simultaneously by the NCBI and FHS investigators following principles reviewed by Pompanon et al.[10] The cleaning focused on Mendelian or excessive recombination errors. SNPs were excluded if they had a call rate <95%, or a Hardy-Weinberg equilibrium (HWE) p-value $<10^{-6}$, resulting in a final number of 503,551 SNPs eligible for analyses. Individuals who were members of the Offspring cohort and who had available echocardiographic measurements were eligible for the present investigation.

Gutenberg Heart Study

Genotyping was conducted on 3341 participants (95% of 3500 attendees) of the GHS with a sample of genomic DNA available at baseline examination and written consent for genetic analysis. Genotyping was performed using the Affymetrix Genome-wide Human SNP Array 6.0 from December 2007 to April 2008. SNPs were excluded if they had a minor allele frequency (MAF) $\leq$1%, the HWE p-value was $<10^{-4}$, or the call rate was $\leq$90%. After exclusions, 643,784 SNPs remained eligible for analyses. DNA samples were excluded if they had a within-person call rate of <97%. In total, 3300 persons who met this criterion had echocardiographic data available.

Study of Health in Pomerania

The 4105 SHIP samples were genotyped using the Affymetrix Human SNP Array 6.0. Hybridization of genomic DNA was done in accordance with the manufacturer's standard recommendations. Genotypes were determined using the Birdseed2 clustering algorithm. For quality control purposes, several control samples where added. On the chip level, only subjects with a genotyping rate on QC probesets (QC call rate) of at least 86% were included. The overall genotyping efficiency of the GWA was 98.56%. The genetic data analysis workflow was created using the Software InforSense. Genetic data were stored using the database Caché (InterSystems).

Austrian Stroke Prevention Study

Genotyping was performed in 947 participants using the Illumina Human610-Quad BeadChip according to the manufacturer`s protocol. In total 882 DNA samples met QC criteria. Exclusion criteria were samples with low call rate (<98%, n=32), with excess autosomal heterozygosity (> 0.350, n=1), with sex-mismatch (n=11), or as outliers identified by the IBS clustering analysis (>3 standard deviations from population mean, n=19 or IBS probabilities > 97%, n=2).

In total 550635 markers out of 620901 passed QC. Overall, 30232 markers were excluded due to low (<98%) call rate, because they were out of HWE (P <1e-06), or had low (<1%) minor allele frequency.

Imputation and controlling for population stratification

The various GWAS used different genotyping platforms/chips, so that they do not include the same sets of SNPs. Many specific SNPs genotyped on one platform are not on another array (and *vice versa*) but they are highly correlated with a different SNP on that array. For instance, 82% of all 2.2 million HapMap CEU SNPs ≥5% MAF are captured by Affymetrix 500K and Illumina 550K arrays at $r^2 \geq 0.5$ with mean maximum r^2 to Affy SNPs of 0.91 and to Illumina of 0.95; only 3% of SNPs are not captured by either. Investigators have annotated the set of all variants on different platforms that capture at an $r^2 > 0.5$ an allele on an alternate platform. Consequently, new algorithms allow imputation of all 2.5 million HapMap SNPs using a HapMap sample as a scaffold.[11;12] FHS, Rotterdam, MONICA-KORA, GHS and ASPS used the Markov Chain Haplotyping (MACH) algorithm (http://www.sph.umich.edu/csg/abecasis/MaCH/) and the HapMap CEU sample (release 22, build 36) to impute the untyped HapMap SNPs. CHS has used the BIMBAM algorithm for imputation (available at http://stephenslab.uchicago.edu/software.html).[13] SHIP used the IMPUTE algorithm (http://www.stats.ox.ac.uk/~marchini/software/gwas/impute.html) and the HapMap CEU sample for imputation. For each imputed SNP a reliability of imputation was estimated (as the ratio of the empirically observed dosage variance to the expected binomial dosage variance). Thus, all studies have imputed the genotype "dosage," which is the expected number of minor alleles, for all SNPs. We performed meta-analysis on each imputed SNP.

All cohorts used genomic control to estimate population stratification.[14] For this purpose, we evaluated quantile-quantile (Q-Q) plots and λ estimates to ensure that the p value distributions in each of the 5 cohorts conformed to a null distribution at all but the extreme tail. The quantile-quantile (Q-Q) plot of our inverse variance meta-analysis results for each echocardiographic trait (**eFigure 1, Panels A-F** in supplementary online material) shows the distribution of the observed test statistic (negative log of p-values, on the Y-axis) plotted against the distribution of test statistic expected under the null-hypothesis (on the X-axis). For each echocardiographic trait, we note that the observed p-values conform to the null distribution across the entire range until about $p<10^{-4}$; we expect that true positive associations reside beyond this region and that population substructure is negligible for analyses of any of the echocardiographic traits.

In the FHS dataset, we evaluated the principal components (PC) approach additionally.[15] First, we applied PC analysis (calculated through Eigenstrat, http://www.broad.mit.edu/tools/software.html) to genotypic data to infer continuous axes of genetic variation (principal components – PCs) describing ancestral heterogeneity (top eigenvectors of a covariance matrix). Next, we assessed the association between the PCs and echocardiographic phenotypes. Since the FHS consists of families, the principal components were built using a subset of biologically unrelated subjects. Thus, we created 10 PC using Eigenstrat. We determined that PC scores (generated from top 10 PC identified by EIGENSTRAT in the FHS 550K genotype data) accounted for <1% of the variation in echo phenotypes; the regression coefficients analyzed in the 550K FHS age- and sex-adjusted GWAS data with and without adjusting for the PC are highly correlated (r=0.999). Thus, we do not expect population substructure to influence our results substantively.

Description of Loci Associated ($p<5x10^{-7}$) With Echocardiographic Traits in Stage 1

For LVM, 3 SNPs clustered at 14 q12 exceeded the threshold of genome-wide significance (only the top SNP is listed in Table 2). This locus is intergenic, the nearest gene *NOVA1* is 270 kb distant downstream. *NOVA1* encodes neuro-oncological ventral antigen 1, a neuron-specific RNA-binding protein expressed mainly in neural tissue.[16] This protein is a member of the Nova family of paraneoplastic disease antigens (being recognized and inhibited by paraneoplastic antibodies), and is known to regulate RNA splicing in developing neurons.[16] It is expressed in cardiac tissue but has no known role in cardiac physiology in the published literature. Two other loci on chromosomes 2 and 15 are also intergenic being adjacent to *CALM2* and *MEIS2* genes (both genes being expressed in the heart). *CALM2* codes for calmodulin, which binds calcium and thereby regulates the activity of numerous protein kinases and phosphatases involved in cellular processes. Calmodulin plays a critical role in mediating cardiac hypertrophy.[17;18]*MEIS2* encodes a homeobox protein belonging to the TALE ('three amino acid loop extension') family, a group of highly conserved transcription regulators that are essential contributors to developmental programs.

For LVDD, 24 SNPs at 6q22 emerged as genome-wide significant. Several of these SNPs were in linkage disequilibrium (LD) with the most strongly associated SNP, rs89107, and with intragenic variants in the gene *SLC35F1* (solute carrier family 35, member F1). See main manuscript for discussion of this locus.

Five SNPs at 3 separate loci on chromosomes 10q23, 16q23 and 5q21were associated with LVWT. A SNP at 10q23, rs7910620, is in *GRID1* (a gene expressed in cardiac tissue).

Another SNP at 16q23, rs2059238, is in *WWOX* (WW domain containing oxidoreductase, expressed in the heart), which encodes a protein (an oxidoreductase) that contains 2 WW domains and a short-chain dehydrogenase/reductase domain (SRD).[19] Proteins with WW domains play a critical role in the regulation of protein degradation, transcription, and RNA splicing, and the presence of an SRD domain may suggest a role for *WWOX* in steroid metabolism.[19] In experimental animals this oxidoreductase is a mediator of tumor necrosis factor-alpha-induced apoptosis.[20]. The 3 SNPs at 5q21 are in perfect LD with each other, are intergenic, and located between 36.6- 80 kb from *SLC25A46*, which is a member of the solute carrier family 25 (SLC25, which transport molecules over the mitochondrial membrane). It is expressed in cardiac tissue but its exact role in disease is unclear.

A SNP in *HN1L* (hematological and neurological expressed 1-like protein) was associated with LV systolic dysfunction. *HN1L* is expressed in cardiac tissue but its function is not known.

One hundred and forty-nine SNPs in 7 loci were associated with aortic root diameter: 120 SNPs at 17p13, 1 at 17q21, 10 at 1p21, 10 at 5q23, 2 at 12p12, 5 at 12q14, and 1 at 15q24. See the text of the main manuscript for a discussion of genetic loci on chromosomes 5q23, 12p12 and 12q14, and 17p13. The SNP at locus 17q21, rs17608766, is in *GOSR2* (Golgi SNAP receptor complex member 2). *GOSR2* is expressed in aortic tissue, and encodes a membrane protein that regulates trafficking of proteins across the medial- and trans-Golgi compartments.[21] *GOSR2* has been implicated in hypertension, in part due to its chromosomal location near a genetic linkage site and its function regulating transmembrane transport.[21] rs893817 at 15q24 is in *LOXL1* (lysyl oxidase-like 1; expressed in aorta and vascular tissues), which is an extracellular copper-dependent enzyme that catalyses the formation of lysine-derived crosslinks and elastin polymers at sites of elastogenesis. Lysyl oxidase null mice die in the perinatal period and have aortic aneurysms at necropsy, possibly due to increased proteolytic degradation of elastin that has deficient crosslinks.[22] For the locus on chromosome 1, the closest gene is *PALMD* (palmdelphin; 62 kb). *PALMD* is expressed in many tissues, is most abundant in cardiac (including the aorta) and skeletal muscle, and regulates intracellular signaling and membrane-cytoskeletal interactions.[23]

Tables and Figures

eTable 1. Echocardiographic Methods

	CHS	**RS**	**KORA**	**FHS**	**GHS**	**SHIP**	**ASPS**
Year of Echo	1989-1990	2002-2004	1994	1978-1998	2007	1997-2006	1991-1994 and 1999-2003
Instrument	Toshiba	Acuson	HP sonos 1500	HP	Philips	Vingmed	Vingmed
Readers	MD/ CertifiedTechs	MD/ CertifiedTechs	MD	MD/ CertifiedTechs	MD/ CertifiedTechs	Certified Physicians	MD
M-Mode, ASE method	Yes	Yes	Yes	Yes	Yes	Yes	Yes

ASE: American Society of Echocardiography.

eTable 2. Statistical Power for Stage 2

Trait	RSID	chr	effallele	Stage 1			Stage 2 Power	
				P-value	Meta Beta	SE	replicate Stage 1 effect	80% power for beta=
LV mass	rs17568359	14	C	8.53x10^{-8}	-4.7780	0.8922	0.86	-4.3570
	rs7565161	2	A	3.19x10^{-7}	-3.0130	0.5894	0.95	-2.2960
LV diastolic dimensions	rs89107	6	G	1.14x10^{-8}	-0.0290	0.0051	0.90	-0.0247
	rs11153768	6	T	4.61x10^{-7}	0.0260	0.0051	0.83	0.0249
LV wall thickness	rs7910620	10	G	5.62x10^{-9}	0.1652	0.0284	1.0	0.0756
	rs2059238	16	A	1.89x10^{-7}	-0.0197	0.0038	0.89	-0.0171
	rs17132261	5	T	3.36x10^{-7}	0.0601	0.0118	0.80	0.0597
LVSD	rs2235487	16	G	1.98x10^{-7}	-0.3822	0.0735	1.0	-0.2070
Aortic root size	rs10852932	17	T	4.32x10^{-11}	0.0311	0.0047	0.98	0.0212
	rs4523957	17	G	1.87x10^{-10}	0.0306	0.0048	0.98	0.0209
	rs413016	17	T	3.34x10^{-7}	0.0276	0.0054	0.90	0.0233
	rs17608766	17	C	1.43x10^{-7}	0.0381	0.0072	0.93	0.0300
	rs7543130	1	A	8.08x10^{-9}	0.0258	0.0045	0.93	0.0203
	rs17470137	5	A	1.63x10^{-8}	0.0287	0.0051	0.94	0.0225
	rs4026608	12	C	7.30x10^{-8}	-0.0256	0.0048	0.92	-0.0210
	rs10770612	12	G	2.40x10^{-7}	0.0346	0.0067	0.96	0.0257
	rs893817	15	G	4.12x10^{-7}	0.0237	0.0047	0.87	0.0214

Power estimates computed using Quanto software, version 1.2.3 (http://hydra.usc.edu/GxE).

eTable 3. Imputed vs genotyped SNPs among top associations in Stages 1 and 2

Trait	SNPID	Stage 1										Stage 2			
		CHS		RS		KORA		FHS		GHS		SHIP		ASPS	
		imputed	o/e variance	imputed	o/e variance *	imputed	o/e variance	imputed	o/e variance	imputed	o/e variance	imputed	o/e variance	imputed	o/e variance
LV mass	rs17568359	1	0.775	1	0.938	0	1	1	1	0	1	0	1	1	0.985
	rs7565161	1	0.90	1	0.94	-	-	1	0.26	1	0.997	1	0.869	1	0.944
	rs8031633	-	-	1	0.68	1	0.57	1	0.84	1	0.99	-	-	-	-
LVDD	**rs89107**	1	0.92	1	0.999	1	0.99	1	0.99	1	0.71	1	0.997	**0**	1
	rs11153768	1	0.98	1	0.97	1	0.96	1	0.98	1	0.40	**0**	1	1	0.975
LVWT	rs7910620	1	<0.2	1	0.201	NA	NA	1	0.344	1	1	0	1	1	0.16
	rs2059238	1	0.784	1	0.976	1	0.351	1	0.595	1	0.436	1	0.941	1	0.96
	rs17132261	1	0.453	1	0.879	1	0.954	1	0.996	0	1	0	1	1	0.93
LV systolic dysfunction	rs2235487	0	1	0	0.997	1	0.73	1	0.84	1	0.87	1	0.997	0	1
Aortic root	**rs10852932**	1	0.967	1	0.999	NA	NA	1	1	NA	NA	1	0.921	1	0.998
	rs4523957	1	0.882	1	0.928	1	0.825	1	0.88	NA	NA	1	0.822	1	0.924
	rs413016	0	1	0	1	1	0.879	1	0.948	NA	NA	1	0.879	0	1
	rs17608766	1	0.296	0	1	1	0.854	1	0.876	NA	NA	1	0.976	0	1
	rs7543130	0	1	0	1	1	0.921	1	0.975	NA	NA	1	0.974	0	1
	rs17470137	1	0.883	1	0.996	1	0.921	1	0.975	NA	NA	1	0.935	1	0.979
	rs4026608	1	0.964	1	0.889	1	0.698	1	0.855	NA	NA	**0**	1	1	0.869
	rs10770612	**0**	1	**0**	1	1	0.433	1	0.452	NA	NA	1	0.988	**0**	1
	rs893817	0	1	0	1	1	0.879	1	0.948	NA	NA	1	0.896	0	1

NA= not available. 0= genotyped. 1= imputed. O/E= observed to expected variance binomial dosage.

SNPs that replicated in stage 2 are shown in bold. Note that **rs89107** is in strong LD (R^{2}1, D'1) with rs281868 that is genotyped in 4 studies (all except FHS) and has a meta-analytic p value of 1.37x10^{-8}. **rs11153768** is in LD (R^{2}0.59, D'0.85) with rs6911339 that was genotyped in CHS and RS and has meta-analytic p of 2.29 x10^{-7}. **rs17470137** is in LD with rs17469907 that was genotyped in CHS and RS and has a meta-analytic p of 1.23x10^{-8}. **rs4026608** is in LD with rs899844 (R^{2}0.93, D'1) that was genotyped in CHS and RS and has a meta-analytic p of 1.60x10^{-7}.

* In RS, dosage data were used for all SNPs. Therefore, imputed data is overwritten onto genotyped data for originally typed SNPs. Thus, o/e variance is available for all SNPs.

eTable 4. SNPs Associated With LV Mass With *P* Value $<10^{-5}$

SNP	chromosome	position	meta-analysis P-value	meta-analysis beta	meta-analysis SE	coded allele	allele frequency	Nearest Gene
rs17568359	14	25707714	$8.53x10^{-8}$	-4.778	0.892	C	0.072	NOVA1
rs11846075	14	25712317	$1.39x10^{-7}$	-4.702	0.893	A	0.071	NOVA1
rs17489969	14	25712480	$1.40x10^{-7}$	-4.716	0.896	C	0.071	NOVA1
rs7565161	2	47348531	$3.19x10^{-7}$	-3.013	0.589	A	0.403	CALM2
rs8031633	15	35327294	$3.71x10^{-7}$	16.617	3.269	C	0.006	Mx10IS2
rs8031514	15	35327276	$3.71x10^{-7}$	16.619	3.269	C	0.006	Mx10IS2
rs8026758	15	35327458	$3.74x10^{-7}$	16.607	3.268	T	0.006	Mx10IS2
rs12619308	2	179437515	$8.22x10^{-7}$	-4.477	0.908	T	0.068	CCDC141
rs6501252	17	74324977	$1.41x10^{-6}$	55.595	11.525	T	0.005	USP36
rs4303351	13	39258754	$1.60x10^{-6}$	2.617	0.545	A	0.231	COG6
rs6563751	13	39267347	$1.63x10^{-6}$	2.635	0.550	A	0.231	COG6
rs6752756	2	179449350	$2.72x10^{-6}$	-4.305	0.918	T	0.066	CCDC141
rs1873163	2	179461940	$2.84x10^{-6}$	-4.482	0.957	T	0.060	CCDC141
rs198285	7	24231633	$3.57x10^{-6}$	-2.361	0.509	C	0.498	NPY
rs904162	2	47363828	$3.61x10^{-6}$	-2.511	0.542	T	0.446	TACSTD1
rs4297022	8	141182923	$4.67x10^{-6}$	-2.317	0.506	A	0.430	NIBP
rs6578069	8	141182422	$4.70x10^{-6}$	-2.307	0.504	G	0.432	NIBP
rs6116929	20	574081	$5.11x10^{-6}$	2.254	0.494	G	0.495	SRXN1
rs7224628	17	61912594	$5.22x10^{-6}$	-2.094	0.460	G	0.375	PRKCA
rs3848418	17	61911986	$5.36x10^{-6}$	-2.088	0.459	T	0.376	PRKCA
rs4603426	13	39237678	$5.50x10^{-6}$	2.348	0.517	G	0.263	COG6
rs9532427	13	39219352	$5.68x10^{-6}$	2.331	0.514	G	0.265	COG6
rs7225164	17	61912613	$5.75x10^{-6}$	-2.086	0.460	A	0.375	PRKCA
rs9548923	13	39229197	$5.79x10^{-6}$	2.333	0.515	G	0.265	COG6
rs12584772	13	39201803	$5.88x10^{-6}$	2.332	0.515	G	0.266	COG6
rs9548903	13	39201773	$5.88x10^{-6}$	2.332	0.515	G	0.267	COG6
rs9548921	13	39226132	$5.89x10^{-6}$	2.328	0.514	T	0.265	COG6
rs7329513	13	39221186	$5.90x10^{-6}$	2.328	0.514	C	0.266	COG6

rs9548902	13	39201713	$5.90x10^{-6}$	2.332	0.515	T	0.267	COG6
rs6563745	13	39203591	$5.94x10^{-6}$	2.331	0.515	A	0.266	COG6
rs6504434	17	61901919	$6.12x10^{-6}$	-2.078	0.460	C	0.375	PRKCA
rs8074294	17	61902137	$6.42x10^{-6}$	-2.071	0.459	G	0.376	PRKCA
rs11934726	4	102572384	$7.33x10^{-6}$	-15.876	3.541	T	0.015	PPP3CA
rs7727791	5	56873677	$7.56x10^{-6}$	2.156	0.482	A	0.297	DKFZp686D0972
rs3848421	17	61903483	$8.68x10^{-6}$	-2.079	0.468	G	0.364	PRKCA
rs9593407	13	79113330	$9.75x10^{-6}$	2.278	0.515	C	0.250	NDFIP2
rs10769246	11	5787516	$9.84x10^{-6}$	-7.463	1.688	T	0.026	OR52N2

eTable 5. SNPs Associated With LV Diastolic Dimensions With *P* Value <10^{-5}

SNP	chromosome	position	meta-analysis P-value	meta-analysis beta	meta-analysis SE	coded allele	allele frequency	Nearest Gene
rs89107	6	118684736	1.14x10-8	-0.029	0.005	G	0.501	SLC35F1
rs4946333	6	118672358	1.34x10-8	-0.029	0.005	G	0.499	SLC35F1
rs281868	6	118680754	1.37x10-8	-0.029	0.005	A	0.494	SLC35F1
rs6912208	6	118673209	1.41x10-8	-0.029	0.005	G	0.499	SLC35F1
rs283077	6	118676372	2.24x10-8	-0.028	0.005	T	0.497	SLC35F1
rs9401060	6	118668041	2.60x10-8	-0.029	0.005	A	0.492	SLC35F1
rs9489327	6	118668582	2.95x10-8	-0.028	0.005	T	0.500	SLC35F1
rs11153730	6	118774215	5.06x10-8	-0.028	0.005	T	0.501	SLC35F1
rs937277	6	118779768	6.93x10-8	-0.029	0.005	G	0.353	SLC35F1
rs1761631	6	118783577	7.72x10-8	-0.029	0.005	A	0.351	SLC35F1
rs11758375	6	118710463	1.07x10-7	-0.027	0.005	T	0.501	SLC35F1
rs927348	6	118698800	1.10x10-7	-0.027	0.005	G	0.503	SLC35F1
rs6927800	6	118710815	1.12x10-7	-0.027	0.005	C	0.501	SLC35F1
rs11968293	6	118741391	1.19x10-7	-0.027	0.005	A	0.488	SLC35F1
rs7749263	6	118672943	1.22x10-7	-0.027	0.005	A	0.505	SLC35F1
rs1572226	6	118741772	1.91x10-7	-0.027	0.005	C	0.488	SLC35F1
rs731695	6	118695183	1.97x10-7	-0.027	0.005	T	0.502	SLC35F1
rs7772845	6	118752709	2.09x10-7	0.026	0.005	T	0.445	SLC35F1
rs1334489	6	118746080	2.29x10-7	0.026	0.005	A	0.445	SLC35F1
rs6911339	6	118760314	2.29x10-7	0.026	0.005	A	0.443	SLC35F1
rs7452622	6	118704990	3.02x10-7	0.027	0.005	A	0.481	SLC35F1
rs11153768	6	119094845	4.61x10-7	0.026	0.005	T	0.446	C6orf204
rs11970286	6	118787067	4.69x10-7	0.026	0.005	T	0.454	SLC35F1
rs11968176	6	119007633	6.50x10-7	0.026	0.005	A	0.462	PLN
rs6906287	6	119069433	6.72x10-7	0.025	0.005	C	0.454	C6orf204
rs4307206	6	118920013	6.81x10-7	0.025	0.005	A	0.451	C6orf204
rs12661338	6	118901383	6.87x10-7	0.025	0.005	A	0.450	C6orf204
rs17825393	6	118879276	6.90x10-7	0.025	0.005	C	0.450	C6orf204

rs9481842	6	119081491	7.03x10-7	-0.029	0.006	G	0.267	C6orf204
rs11752626	6	118895345	7.36x10-7	0.025	0.005	T	0.450	C6orf204
rs4945623	6	119087249	7.67x10-7	0.025	0.005	C	0.455	C6orf204
rs11967375	6	118930668	7.87x10-7	0.025	0.005	G	0.455	C6orf204
rs10872167	6	119095055	8.06x10-7	0.025	0.005	A	0.481	C6orf204
rs17227124	6	118848075	8.72x10-7	0.025	0.005	C	0.452	C6orf204
rs763254	6	118993308	1.14x10-6	0.025	0.005	C	0.453	PLN
rs17226667	6	118828321	1.27x10-6	0.025	0.005	G	0.452	C6orf204
rs9656375	7	128308476	1.42x10-6	-0.037	0.008	A	0.188	ATP6V1F
rs8023331	15	21218853	1.82x10-6	-0.645	0.135	T	0.006	MKRN3
rs1006932	6	118749444	1.89x10-6	-0.025	0.005	A	0.400	SLC35F1
rs2501470	6	118759441	1.95x10-6	-0.025	0.005	G	0.394	SLC35F1
rs11153725	6	118664651	2.03x10-6	-0.025	0.005	C	0.395	SLC35F1
rs2359630	4	7755695	2.19x10-6	0.027	0.006	T	0.282	SORCS2
rs6678829	1	202104183	2.36x10-6	-0.028	0.006	G	0.225	SNRPx10
rs7533264	1	202104722	2.37x10-6	-0.028	0.006	G	0.225	SNRPx10
rs9970867	1	202103619	2.37x10-6	-0.028	0.006	C	0.225	SNRPx10
rs9969998	1	202103370	2.42x10-6	-0.028	0.006	T	0.225	SNRPx10
rs7540013	1	202102461	2.47x10-6	-0.028	0.006	A	0.225	SNRPx10
rs6421775	1	202101338	2.56x10-6	-0.028	0.006	A	0.226	SNRPx10
rs6702750	1	202108915	2.59x10-6	-0.029	0.006	C	0.222	SNRPx10
rs6697629	1	202099734	2.71x10-6	-0.028	0.006	T	0.226	SNRPx10
rs4951274	1	202096164	2.71x10-6	-0.028	0.006	A	0.227	SNRPx10
rs6664617	1	202109044	2.82x10-6	-0.028	0.006	T	0.222	SNRPx10
rs4598553	1	202106660	2.82x10-6	-0.028	0.006	C	0.222	SNRPx10
rs2298870	1	202105896	2.84x10-6	-0.028	0.006	C	0.223	SNRPx10
rs7542275	1	202104832	2.86x10-6	-0.028	0.006	C	0.223	SNRPx10
rs11590770	1	202102354	2.89x10-6	-0.028	0.006	A	0.225	SNRPx10
rs4951031	1	202096179	2.94x10-6	-0.028	0.006	G	0.228	SNRPx10
rs4951275	1	202096642	2.97x10-6	-0.028	0.006	G	0.227	SNRPx10
rs12212795	6	118761001	3.48x10-6	-0.054	0.012	C	0.058	SLC35F1
rs12210810	6	118759897	3.48x10-6	-0.054	0.012	C	0.058	SLC35F1

rs4604758	1	202109147	3.60x10-6	-0.028	0.006	C	0.222	SNRPx10
rs12771324	10	96364911	3.73x10-6	0.108	0.023	T	0.021	Hx10LLS
rs1532222	7	128304181	3.90x10-6	-0.034	0.007	T	0.167	ATP6V1F
rs4749460	10	29902974	4.09x10-6	-0.046	0.010	A	0.080	SVIL
rs7786074	7	128307527	4.09x10-6	-0.034	0.007	T	0.214	ATP6V1F
rs10826661	10	29902440	4.48x10-6	-0.046	0.010	G	0.080	SVIL
rs7899653	10	29901907	4.57x10-6	-0.046	0.010	A	0.080	SVIL
rs12199837	6	119037337	4.65x10-6	-0.049	0.011	A	0.074	C6orf204
rs6702792	1	202112581	4.83x10-6	-0.028	0.006	A	0.222	SNRPx10
rs11007656	10	29897704	4.91x10-6	-0.045	0.010	G	0.080	SVIL
rs6593980	1	202110365	4.96x10-6	-0.028	0.006	A	0.223	SNRPx10
rs11606985	11	2800252	4.96x10-6	0.035	0.008	C	0.244	KCNQ1
rs11240612	1	202112172	5.07x10-6	-0.028	0.006	C	0.222	SNRPx10
rs6701012	1	202113219	5.09x10-6	-0.028	0.006	C	0.222	SNRPx10
rs16915456	9	29952701	5.21x10-6	0.033	0.007	T	0.149	LINGO2
rs2253959	4	7755718	5.83x10-6	0.026	0.006	T	0.286	SORCS2
rs12215355	6	118787245	6.09x10-6	-0.053	0.012	C	0.057	SLC35F1
rs1005256	7	15006130	6.09x10-6	0.025	0.005	C	0.382	DGKB
rs1977386	10	29892728	6.16x10-6	-0.045	0.010	A	0.077	SVIL
rs6752756	2	179449350	6.43x10-6	-0.048	0.011	T	0.066	CCDC141
rs16915458	9	29953072	6.44x10-6	0.033	0.007	G	0.146	LINGO2
rs945868	1	80945616	6.62x10-6	-0.025	0.006	C	0.365	LPHN2
rs1361098	1	80944529	6.67x10-6	-0.025	0.006	G	0.365	LPHN2
rs12255867	10	29907113	6.68x10-6	-0.045	0.010	G	0.077	SVIL
rs11576057	1	202053897	6.72x10-6	-0.029	0.006	A	0.202	ZC3H11A
rs17701520	9	29952872	6.80x10-6	0.033	0.007	A	0.146	LINGO2
rs12619308	2	179437515	6.88x10-6	-0.047	0.011	T	0.068	CCDC141
rs6675962	1	80947893	6.98x10-6	-0.025	0.006	G	0.365	LPHN2
rs4878421	9	29951233	6.99x10-6	0.033	0.007	G	0.148	LINGO2
rs17774158	9	29952398	7.25x10-6	0.033	0.007	C	0.149	LINGO2
rs11756440	6	119100335	7.45x10-6	0.023	0.005	A	0.466	C6orf204
rs7762823	6	118663228	7.50x10-6	-0.024	0.005	G	0.422	SLC35F1

rs11756438	6	119100325	7.54x10-6	0.023	0.005	A	0.465	C6orf204
rs17774136	9	29952346	7.74x10-6	0.033	0.007	A	0.148	LINGO2
rs13299889	9	29952125	7.92x10-6	0.033	0.007	C	0.148	LINGO2
rs4945348	11	78797081	8.30x10-6	-0.033	0.007	C	0.136	ODZ4
rs10457327	6	118798845	8.41x10-6	-0.052	0.012	C	0.061	SLC35F1
rs10511836	9	29950545	8.44x10-6	0.033	0.007	T	0.149	LINGO2
rs7027471	9	29954976	8.60x10-6	0.032	0.007	T	0.143	LINGO2
rs4677899	3	124897007	8.83x10-6	0.119	0.027	A	0.012	MYLK
rs1869866	3	124895938	8.97x10-6	0.119	0.027	A	0.012	MYLK
rs546929	9	29628167	9.08x10-6	0.044	0.010	T	0.082	LINGO2
rs3733989	5	167622795	9.42x10-6	-0.026	0.006	A	0.302	ODZ2
rs4403497	9	29950458	9.67x10-6	0.032	0.007	A	0.150	LINGO2

eTable 6. SNPs Associated With LV Wall Thickness With *P* Value $<10^{-5}$

SNP	chromosome	position	meta-analysis P-value	meta-analysis beta	meta-analysis SE	coded allele	allele frequency	Nearest Gene
rs7910620	10	87836939	5.62x10-9	0.165245257	0.028354833	G	0.008994159	GRID1
rs2059238	16	76816311	1.89x10-7	-0.019719424	0.003785172	A	0.224243496	WWOX
rs17132261	5	110036113	3.36x10-7	0.060132778	0.011785919	T	0.014548744	SLC25A46
rs17132250	5	110022562	3.42x10-7	0.059134182	0.011598403	A	0.014948811	SLC25A46
rs17132292	5	110065983	3.64x10-7	0.0627422	0.012333545	C	0.014385766	SLC25A46
rs13205800	6	49745560	1.10x10-6	0.017970859	0.003687574	C	0.20979031	CRISP2
rs12518142	5	109664484	1.26x10-6	0.044330417	0.009147131	T	0.039318338	MAN2A1
rs1533013	5	171950809	2.85x10-6	0.048244832	0.010306166	G	0.021801132	SH3PXD2B
rs7669852	4	77761422	2.87x10-6	-0.013495965	0.00288364	A	0.360930117	SHROOM3
rs4802577	19	54353652	3.00x10-6	-0.044009477	0.009422855	A	0.063942136	TRPM4
rs9896894	17	61944232	3.17x10-6	0.013984965	0.003001363	T	0.340114272	PRKCA
rs17132193	5	109892382	3.26x10-6	0.053079015	0.011405621	C	0.015907479	SLC25A46
rs4957904	5	109901920	3.34x10-6	0.053147091	0.011431986	T	0.016079691	SLC25A46
rs10204096	2	46737243	3.57x10-6	0.013175789	0.002842772	T	0.408079175	CRIPT
rs12515045	5	109832876	3.61x10-6	0.052626633	0.011360603	G	0.015781895	SLC25A46
rs4305421	3	134176232	4.51x10-6	0.013039938	0.002843061	A	0.399695484	TMEM108
rs11755355	6	49741713	4.57x10-6	0.014992041	0.003270795	T	0.270389587	CRISP2
rs10179861	2	46736706	5.08x10-6	0.013032462	0.002857165	T	0.407355952	CRIPT
rs12513391	5	109802271	5.15x10-6	0.053079542	0.011644156	T	0.015749429	SLC25A46
rs10203903	2	46737034	5.43x10-6	0.012994289	0.002857437	T	0.407146173	CRIPT
rs8125881	20	50077919	5.80x10-6	0.026041748	0.005744159	A	0.152184855	ZFP64
rs13205275	6	49745061	6.71x10-6	0.014084422	0.003127901	T	0.283501317	CRISP2
rs11752738	6	49744677	6.77x10-6	0.014082666	0.003128897	T	0.283641937	CRISP2
rs9305525	21	15290518	7.09x10-6	0.169193305	0.03767495	T	0.008268698	NRIP1
rs13200858	6	49744088	7.30x10-6	0.014040957	0.003130921	G	0.282827192	CRISP2
rs11653643	17	61946193	7.35x10-6	0.013146091	0.002932148	A	0.344850431	PRKCA
rs11759936	6	49741349	7.40x10-6	0.014034213	0.003131258	A	0.282389483	CRISP2
rs3733246	4	77755805	7.43x10-6	-0.013205772	0.002946981	C	0.354771441	SHROOM3

rs13193433	6	49742848	7.45x10-6	0.014030643	0.003131649	G	0.281880012	CRISP2
rs12520182	5	109797609	7.56x10-6	0.052383305	0.011700061	C	0.015609954	SLC25A46
rs751722	20	59126678	7.66x10-6	0.016434879	0.003672958	G	0.164892055	CDH4
rs12527781	6	49743411	7.68x10-6	0.014009639	0.003131359	G	0.282939686	CRISP2
rs6071498	20	59129793	7.80x10-6	0.01647222	0.003684601	C	0.167107866	CDH4
rs10948521	6	49741201	7.93x10-6	0.013990759	0.003132027	A	0.282373256	CRISP2
rs1407112	6	49749455	8.12x10-6	0.014170037	0.003175665	T	0.277872003	CRISP2
rs13213036	6	49750465	8.24x10-6	0.014161075	0.003175893	A	0.277805037	CRISP2
rs17572279	6	49727047	8.43x10-6	0.013787977	0.003095639	A	0.286274724	RHAG
rs11759109	6	49729670	8.56x10-6	0.013832084	0.003107873	T	0.284139017	RHAG
rs11752255	6	49729488	8.71x10-6	0.013752334	0.003092501	C	0.285871564	RHAG
rs12528363	6	49739130	8.86x10-6	0.013918486	0.003132436	G	0.282364607	RHAG
rs2369953	3	134169915	9.00x10-6	0.012784641	0.002879449	A	0.396040243	TMEM108
rs2104003	20	59125863	9.07x10-6	0.016342434	0.003682276	G	0.164740241	CDH4
rs12526795	6	49739053	9.15x10-6	0.013896298	0.00313231	C	0.282458888	RHAG
rs13198479	6	49738551	9.27x10-6	0.013883712	0.003131506	G	0.282388194	RHAG
rs13198350	6	49738488	9.31x10-6	0.013877452	0.003130773	G	0.282600703	RHAG
rs13198297	6	49738239	9.36x10-6	0.013869873	0.003129891	T	0.282754879	RHAG
rs13206923	6	49733210	9.43x10-6	0.013809877	0.003117438	C	0.282838591	RHAG
rs3763082	5	109751374	9.60x10-6	0.05169222	0.011679431	A	0.014481914	SLC25A46
rs13207716	6	49733694	9.78x10-6	0.013791154	0.003118799	T	0.28267577	RHAG
rs13207529	6	49733371	9.78x10-6	0.013788277	0.003118188	A	0.282756878	RHAG
rs2244497	17	61931405	9.82x10-6	0.01304065	0.002949641	C	0.345579749	PRKCA
rs4957906	5	109989362	9.82x10-6	0.051195592	0.01158008	C	0.015698344	SLC25A46

eTable 7. SNPs Associated With LV Systolic Dysfunction With *P* Value $<10^{-5}$

SNP	chromosome	position	meta-analysis P-value	meta-analysis beta	meta-analysis SE	coded allele	allele frequency	Nearest Gene
rs2235487	16	1670312	1.98x10-7	-0.382	0.073	G	0.218	HN1L
rs9305048	19	14740034	8.28x10-7	0.273	0.055	G	0.443	EMR2
rs10501569	11	83931222	1.36x10-6	0.449	0.093	T	0.088	DLG2
rs17807706	11	83931002	1.37x10-6	0.430	0.089	G	0.087	DLG2
rs17807689	11	83930695	1.47x10-6	0.450	0.093	G	0.089	DLG2
rs7998746	13	111948132	3.18x10-6	0.358	0.077	T	0.117	C13orf28
rs9549896	13	111945704	3.40x10-6	0.359	0.077	T	0.117	C13orf28
rs7319673	13	111944706	3.43x10-6	0.359	0.077	T	0.117	C13orf28
rs1178436	16	1771654	3.84x10-6	-0.356	0.077	T	0.187	SPSB3
rs12144022	1	20049195	3.87x10-6	0.620	0.134	T	0.047	OTUD3
rs12136562	1	20050255	3.90x10-6	0.620	0.134	A	0.047	OTUD3
rs16858853	1	231408843	4.37x10-6	0.360	0.078	T	0.122	PCNXL2
rs7986113	13	111948574	4.39x10-6	0.361	0.079	G	0.115	C13orf28
rs17120882	13	111951242	4.50x10-6	0.361	0.079	A	0.115	C13orf28
rs17120885	13	111951360	4.80x10-6	0.361	0.079	G	0.114	C13orf28
rs344359	16	1778641	6.07x10-6	-0.369	0.082	T	0.173	NUBP2
rs7967910	12	31978798	7.02x10-6	-0.365	0.081	C	0.202	C12orf35
rs16854429	1	177876212	7.07x10-6	0.303	0.067	T	0.221	TDRD5
rs1065663	16	1779024	8.22x10-6	-0.361	0.081	G	0.177	NUBP2
rs13278261	8	16197654	8.52x10-6	0.514	0.115	A	0.048	MSR1
rs11739138	5	28122573	8.67x10-6	0.443	0.100	G	0.071	CDH9
rs16858843	1	231405943	8.79x10-6	0.337	0.076	C	0.128	PCNXL2
rs7989236	13	111953742	9.05x10-6	0.343	0.077	T	0.126	C13orf28
rs12432019	14	55248459	9.52x10-6	0.385	0.087	C	0.094	KTN1
rs12431962	14	55248246	9.54x10-6	0.386	0.087	A	0.094	KTN1
rs11621130	14	55251053	9.79x10-6	0.384	0.087	T	0.094	KTN1

eTable 8. SNPs Associated With Aortic Root With *P* Value <10^{-5}

SNP	chromosome	position	meta-analysis P-value	meta-analysis beta	meta-analysis SE	coded allele	allele frequency	Nearest Gene
rs10852932	17	2090210	4.32E-11	0.031	0.005	T	0.355	SMG6
rs216217	17	2091840	4.56E-11	0.031	0.005	G	0.354	SMG6
rs12938295	17	2107604	5.07E-11	0.031	0.005	A	0.354	SMG6
rs216193	17	2150203	5.77E-11	0.030	0.005	A	0.377	SMG6
rs11078865	17	2055859	1.35E-10	0.030	0.005	A	0.360	SMG6
rs216219	17	2094041	1.51E-10	0.029	0.005	T	0.349	SMG6
rs12603592	17	2066568	1.53E-10	0.030	0.005	T	0.346	SMG6
rs12943566	17	2104524	1.63E-10	0.029	0.005	A	0.353	SMG6
rs1532292	17	2044233	1.65E-10	0.029	0.005	G	0.381	SMG6
rs216223	17	2102698	1.70E-10	0.029	0.005	C	0.353	SMG6
rs7213232	17	2112090	1.72E-10	0.029	0.005	G	0.353	SMG6
rs1002135	17	2044333	1.74E-10	0.029	0.005	G	0.381	SMG6
rs4523957	17	2155649	1.87E-10	0.031	0.005	G	0.381	SRR
rs170044	17	2144252	2.02E-10	0.029	0.005	G	0.351	SMG6
rs2281727	17	2064695	2.22E-10	0.029	0.005	G	0.349	SMG6
rs177567	17	2144387	2.25E-10	0.029	0.005	C	0.350	SMG6
rs216206	17	2142838	2.35E-10	0.029	0.005	C	0.350	SMG6
rs216191	17	2135389	2.58E-10	0.029	0.005	C	0.350	SMG6
rs8066372	17	2127718	2.61E-10	0.029	0.005	G	0.348	SMG6
rs8074850	17	2134681	2.63E-10	0.029	0.005	A	0.350	SMG6
rs8065650	17	2127573	2.64E-10	0.029	0.005	T	0.348	SMG6
rs9905529	17	2124482	2.71E-10	0.029	0.005	C	0.351	SMG6
rs216183	17	2120673	2.73E-10	0.029	0.005	A	0.352	SMG6
rs11657644	17	2121960	2.75E-10	0.029	0.005	C	0.352	SMG6
rs216190	17	2134207	2.78E-10	0.029	0.005	C	0.350	SMG6
rs7217687	17	2045022	2.84E-10	0.029	0.005	C	0.374	SMG6
rs216189	17	2134151	2.90E-10	0.029	0.005	G	0.350	SMG6
rs9895551	17	2062672	2.93E-10	0.029	0.005	G	0.348	SMG6

rs11651451	17	2045167	3.19E-10	0.029	0.005	T	0.373	SMG6
rs749240	17	2132850	3.25E-10	0.029	0.005	T	0.351	SMG6
rs216172	17	2073254	3.38E-10	0.030	0.005	C	0.347	SMG6
rs143499	17	2079074	3.41E-10	0.030	0.005	T	0.347	SMG6
rs11078883	17	2085578	3.62E-10	0.029	0.005	G	0.348	SMG6
rs2169357	17	2043191	3.63E-10	0.029	0.005	T	0.357	SMG6
rs9906500	17	2075960	3.94E-10	0.029	0.005	A	0.352	SMG6
rs7217226	17	2082815	4.32E-10	0.029	0.005	G	0.339	SMG6
rs7212249	17	2082730	4.66E-10	0.029	0.005	T	0.339	SMG6
rs11655813	17	2065851	4.68E-10	0.030	0.005	T	0.352	SMG6
rs4790885	17	2055328	5.15E-10	0.029	0.005	A	0.343	SMG6
rs8076939	17	2046681	5.52E-10	0.029	0.005	A	0.347	SMG6
rs6503324	17	2047262	5.52E-10	0.029	0.005	A	0.347	SMG6
rs9913504	17	2048995	5.54E-10	0.029	0.005	T	0.346	SMG6
rs1231209	17	2071722	5.69E-10	0.029	0.005	A	0.345	SMG6
rs1231206	17	2072355	5.78E-10	0.029	0.005	A	0.346	SMG6
rs12602764	17	2069950	8.15E-10	0.029	0.005	T	0.345	SMG6
rs2760736	17	1983403	1.30x10-9	0.031	0.005	G	0.280	SMG6
rs7503141	17	1991395	1.32x10-9	0.031	0.005	C	0.279	SMG6
rs9894215	17	2017448	1.44x10-9	0.030	0.005	A	0.279	SMG6
rs1565763	17	2002050	2.09x10-9	0.030	0.005	C	0.279	SMG6
rs903159	17	2001859	2.14x10-9	0.030	0.005	T	0.279	SMG6
rs9913789	17	1997195	2.21x10-9	0.030	0.005	C	0.279	SMG6
rs6503293	17	1995361	2.35x10-9	0.030	0.005	A	0.278	SMG6
rs923862	17	1978132	2.38x10-9	0.029	0.005	C	0.279	SMG6
rs2760745	17	1982341	2.41x10-9	0.030	0.005	C	0.278	SMG6
rs2641444	17	1984152	2.42x10-9	0.030	0.005	C	0.278	SMG6
rs9909515	17	1986483	2.42x10-9	0.030	0.005	C	0.278	SMG6
rs4349181	17	1987713	2.42x10-9	0.030	0.005	G	0.278	SMG6
rs923864	17	1978257	2.43x10-9	0.030	0.005	T	0.279	SMG6
rs7212589	17	1989143	2.48x10-9	0.030	0.005	G	0.278	SMG6
rs2984943	17	1976885	2.69x10-9	0.030	0.005	C	0.276	SMG6

rs2984942	17	1976905	2.72x10-9	0.030	0.005	C	0.276	SMG6
rs923863	17	1978137	2.80x10-9	0.029	0.005	G	0.279	SMG6
rs2641440	17	1973932	3.21x10-9	0.030	0.005	C	0.277	SMG6
rs2172593	17	1972294	3.28x10-9	0.030	0.005	C	0.277	SMG6
rs9894613	17	2017808	4.47x10-9	0.029	0.005	T	0.292	SMG6
rs9900587	17	2017847	4.72x10-9	0.029	0.005	A	0.272	SMG6
rs391300	17	2163008	4.77x10-9	0.029	0.005	T	0.364	SRR
rs7214741	17	2032348	5.08x10-9	0.029	0.005	A	0.290	SMG6
rs2270478	17	2036598	5.59x10-9	0.029	0.005	A	0.311	SMG6
rs7212964	17	2006069	6.11x10-9	0.029	0.005	T	0.291	SMG6
rs7219693	17	2007851	6.35x10-9	0.028	0.005	A	0.290	SMG6
rs8082485	17	2007157	6.35x10-9	0.028	0.005	G	0.290	SMG6
rs4790315	17	2017279	6.39x10-9	0.028	0.005	C	0.290	SMG6
rs7220685	17	2006135	6.45x10-9	0.028	0.005	G	0.291	SMG6
rs2131702	17	1972208	6.63x10-9	0.029	0.005	C	0.279	SMG6
rs9898819	17	2023102	7.79x10-9	0.028	0.005	A	0.289	SMG6
rs898748	17	2032225	7.87x10-9	0.028	0.005	T	0.291	SMG6
rs1994883	17	2030631	7.88x10-9	0.028	0.005	A	0.293	SMG6
rs7543130	1	99822373	8.08x10-9	0.026	0.004	A	0.488	PALMD
rs898749	17	2031935	8.20x10-9	0.028	0.005	A	0.290	SMG6
rs7212342	17	2031055	8.27x10-9	0.028	0.005	G	0.291	SMG6
rs9892754	17	2031315	8.32x10-9	0.028	0.005	T	0.290	SMG6
rs1994884	17	2030758	8.38x10-9	0.028	0.005	A	0.291	SMG6
rs903161	17	2038756	8.96x10-9	0.028	0.005	T	0.307	SMG6
rs11078856	17	2038814	9.36x10-9	0.028	0.005	A	0.308	SMG6
rs2307143	17	2036504	9.41x10-9	0.028	0.005	A	0.307	SMG6
rs1563966	17	2042704	9.88x10-9	0.028	0.005	A	0.326	SMG6
rs7219557	17	2032950	1.08x10-8	0.029	0.005	A	0.288	SMG6
rs903160	17	2038515	1.09x10-8	0.028	0.005	T	0.307	SMG6
rs903162	17	2038950	1.11x10-8	0.028	0.005	A	0.297	SMG6
rs7543039	1	99822236	1.11x10-8	-0.025	0.004	C	0.500	PALMD
rs6702619	1	99818834	1.11x10-8	-0.025	0.004	T	0.500	PALMD

rs11166276	1	99817827	1.14x10-8	-0.025	0.004	C	0.500	PALMD
rs2760743	17	1963829	1.24x10-8	0.028	0.005	A	0.288	SMG6
rs4790070	17	2104844	1.25x10-8	0.029	0.005	C	0.254	SMG6
rs2957926	17	1970780	1.25x10-8	0.028	0.005	T	0.288	SMG6
rs2760739	17	1970967	1.25x10-8	0.028	0.005	T	0.288	SMG6
rs2760740	17	1967739	1.26x10-8	0.028	0.005	C	0.288	SMG6
rs2641438	17	1964536	1.28x10-8	0.028	0.005	G	0.289	SMG6
rs2641439	17	1964311	1.28x10-8	0.028	0.005	G	0.289	SMG6
rs11867782	17	2037257	1.33x10-8	0.028	0.005	G	0.282	SMG6
rs11078855	17	2038058	1.33x10-8	0.028	0.005	T	0.282	SMG6
rs2760741	17	1967193	1.37x10-8	0.028	0.005	T	0.288	SMG6
rs17470137	5	122559246	1.63x10-8	0.029	0.005	A	0.287	CCDC100
rs17469907	5	122556319	1.73x10-8	0.029	0.005	G	0.284	CCDC100
rs1890753	1	99812107	1.74x10-8	-0.026	0.005	G	0.490	PALMD
rs9910849	17	2122518	2.10x10-8	0.029	0.005	T	0.254	SMG6
rs170040	17	2112464	2.48x10-8	0.030	0.005	C	0.228	SMG6
rs7225168	17	1969839	2.66x10-8	0.028	0.005	G	0.293	SMG6
rs216205	17	2142900	3.10x10-8	0.028	0.005	C	0.253	SMG6
rs2273984	17	2086404	3.17x10-8	0.028	0.005	C	0.336	SMG6
rs7213756	17	2045089	4.87x10-8	0.027	0.005	A	0.312	SMG6
rs337101	5	122578545	5.05x10-8	0.028	0.005	C	0.291	CCDC100
rs6693824	1	99826185	5.21x10-8	-0.025	0.005	G	0.407	PALMD
rs2984941	17	1978293	5.38x10-8	0.027	0.005	G	0.281	SMG6
rs170043	17	2147184	5.97x10-8	0.029	0.005	A	0.226	SMG6
rs216184	17	2121020	6.13x10-8	0.029	0.005	T	0.227	SMG6
rs9899330	17	2132577	6.74x10-8	0.029	0.005	A	0.227	SMG6
rs4026608	12	64680931	7.30x10-8	-0.026	0.005	C	0.378	HMGA2
rs2641431	17	1977257	9.31x10-8	0.032	0.006	G	0.177	SMG6
rs216196	17	2149693	1.12x10-7	-0.027	0.005	C	0.269	SMG6
rs7979034	12	64695982	1.23x10-7	-0.025	0.005	A	0.362	HMGA2
rs1871675	12	64697959	1.28x10-7	-0.025	0.005	G	0.362	HMGA2
rs17608766	17	42368270	1.43x10-7	0.038	0.007	C	0.132	GOSR2

rs899844	12	64685200	1.60x10-7	-0.024	0.005	A	0.365	HMGA2
rs10878359	12	64690891	1.66x10-7	-0.024	0.005	T	0.365	HMGA2
rs2760751	17	1974856	2.14x10-7	-0.027	0.005	A	0.267	SMG6
rs337099	5	122574232	2.15x10-7	0.025	0.005	C	0.341	CCDC100
rs10770612	12	20121906	2.40x10-7	0.035	0.007	G	0.194	PDE3A
rs8077194	17	2066225	2.50x10-7	-0.026	0.005	A	0.265	SMG6
rs434775	5	122576893	2.67x10-7	0.024	0.005	T	0.339	CCDC100
rs1000792	1	99812688	2.72x10-7	-0.037	0.007	G	0.164	PALMD
rs2126202	17	2042462	3.04x10-7	0.023	0.005	C	0.466	SMG6
rs1644316	5	122559278	3.28x10-7	0.024	0.005	T	0.334	CCDC100
rs413016	17	2184211	3.34x10-7	0.028	0.005	T	0.255	TSR1
rs337086	5	122583400	3.55x10-7	0.025	0.005	A	0.336	CCDC100
rs1644317	5	122560768	3.61x10-7	0.024	0.005	A	0.334	CCDC100
rs216224	17	2103035	3.71x10-7	-0.026	0.005	C	0.268	SMG6
rs1339860	1	99827387	3.78x10-7	-0.023	0.005	A	0.405	PALMD
rs2038677	17	2124842	4.03x10-7	-0.025	0.005	C	0.272	SMG6
rs893817	15	72016118	4.12x10-7	0.024	0.005	G	0.342	LOXL1
rs9902945	17	1994420	4.14x10-7	0.031	0.006	C	0.171	SMG6
rs11959350	5	122569338	4.16x10-7	0.024	0.005	G	0.333	CCDC100
rs216215	17	2087418	4.25x10-7	-0.025	0.005	C	0.274	SMG6
rs2392041	1	99828813	4.30x10-7	-0.023	0.005	G	0.353	PALMD
rs170041	17	2116966	4.32x10-7	-0.025	0.005	T	0.267	SMG6
rs12374528	5	122569872	4.60x10-7	0.024	0.005	A	0.333	CCDC100
rs4581299	1	99808648	4.74x10-7	-0.024	0.005	A	0.352	PALMD
rs2417823	12	20079358	4.98x10-7	-0.025	0.005	C	0.276	PDE3A
rs2417822	12	20079410	5.00x10-7	-0.025	0.005	C	0.277	PDE3A
rs10770609	12	20080888	5.13x10-7	-0.024	0.005	G	0.277	PDE3A
rs2417821	12	20081535	5.26x10-7	-0.024	0.005	C	0.277	PDE3A
rs9898390	17	2124234	5.33x10-7	-0.025	0.005	C	0.271	SMG6
rs11658797	17	2035719	5.38x10-7	-0.026	0.005	T	0.270	SMG6
rs2893418	1	99824256	5.38x10-7	-0.023	0.005	G	0.351	PALMD
rs4306343	12	20081897	5.68x10-7	-0.024	0.005	A	0.276	PDE3A

rs216182	17	2119813	5.76x10-7	-0.025	0.005	G	0.271	SMG6
rs4790881	17	2015682	5.76x10-7	-0.025	0.005	C	0.295	SMG6
rs4529947	12	20082343	5.80x10-7	-0.024	0.005	G	0.276	PDE3A
rs7296393	12	95552674	5.90x10-7	-0.128	0.026	A	0.020	C12orf63
rs4409914	12	20083167	5.94x10-7	-0.024	0.005	A	0.276	PDE3A
rs7980003	12	20083537	6.08x10-7	-0.024	0.005	T	0.275	PDE3A
rs3752728	12	20084239	6.16x10-7	-0.024	0.005	G	0.275	PDE3A
rs10762771	10	53973455	6.26x10-7	-0.042	0.009	T	0.139	MBL2
rs4762921	12	20075806	6.30x10-7	-0.025	0.005	G	0.270	PDE3A
rs4762920	12	20075791	6.40x10-7	-0.025	0.005	G	0.270	PDE3A
rs893820	15	72016656	6.43x10-7	0.024	0.005	C	0.328	LOXL1
rs4762745	12	20109468	6.62x10-7	-0.024	0.005	A	0.296	PDE3A
rs893816	15	72015517	7.11x10-7	0.023	0.005	T	0.328	LOXL1
rs11657636	17	2000670	7.12x10-7	-0.024	0.005	C	0.298	SMG6
rs7209460	17	1995463	7.33x10-7	-0.024	0.005	C	0.298	SMG6
rs893818	15	72016248	7.51x10-7	0.023	0.005	A	0.328	LOXL1
rs2028387	15	72014090	7.71x10-7	0.023	0.005	C	0.328	LOXL1
rs10770608	12	20075208	7.73x10-7	-0.025	0.005	T	0.273	PDE3A
rs2760750	17	1975678	7.86x10-7	0.030	0.006	G	0.168	SMG6
rs8072532	17	1992023	8.73x10-7	-0.024	0.005	G	0.298	SMG6
rs4077284	15	72015444	8.90x10-7	0.023	0.005	A	0.348	LOXL1
rs1339862	1	99828381	9.18x10-7	-0.024	0.005	A	0.320	PALMD
rs10762788	10	54000070	9.33x10-7	-0.034	0.007	C	0.227	MBL2
rs337128	5	122469381	9.44x10-7	-0.021	0.004	A	0.454	PPIC
rs12579720	12	20065031	9.59x10-7	-0.027	0.005	C	0.239	PDE3A
rs6702910	1	99831623	9.82x10-7	-0.023	0.005	C	0.410	PALMD
rs2392040	1	99828833	1.01x10-6	-0.022	0.005	C	0.398	PALMD
rs4886776	15	72012049	1.06x10-6	0.023	0.005	A	0.328	LOXL1
rs6577383	1	99823377	1.06x10-6	-0.023	0.005	T	0.315	PALMD
rs1992314	15	72010820	1.08x10-6	0.023	0.005	G	0.328	LOXL1
rs1416889	1	99822280	1.12x10-6	-0.023	0.005	T	0.315	PALMD
rs10783114	1	99817738	1.17x10-6	-0.023	0.005	C	0.313	PALMD

rs7358616	12	20119522	1.18x10-6	-0.024	0.005	C	0.294	PDE3A
rs1339856	1	99816377	1.19x10-6	-0.023	0.005	A	0.314	PALMD
rs1339857	1	99816237	1.19x10-6	-0.023	0.005	A	0.314	PALMD
rs1339858	1	99815973	1.20x10-6	-0.023	0.005	G	0.313	PALMD
rs7973599	12	20055809	1.31x10-6	-0.029	0.006	G	0.219	PDE3A
rs7513849	1	99805424	1.39x10-6	-0.025	0.005	G	0.307	PALMD
rs2027357	1	99805115	1.41x10-6	-0.025	0.005	C	0.314	PALMD
rs7213347	17	2100007	1.52x10-6	-0.024	0.005	G	0.293	SMG6
rs6672117	1	99835005	1.55x10-6	-0.022	0.005	A	0.341	PALMD
rs2760734	17	1974394	1.59x10-6	0.029	0.006	T	0.168	SMG6
rs1556947	1	99810538	1.63x10-6	-0.023	0.005	G	0.315	PALMD
rs10770607	12	20071508	1.64x10-6	-0.024	0.005	C	0.273	PDE3A
rs6577387	1	99833137	1.67x10-6	-0.024	0.005	G	0.307	PALMD
rs7554955	1	99809622	1.69x10-6	-0.023	0.005	G	0.316	PALMD
rs1339861	1	99828206	1.69x10-6	-0.024	0.005	G	0.305	PALMD
rs4762912	12	20056731	1.97x10-6	-0.028	0.006	G	0.230	PDE3A
rs1984749	17	2196654	2.39x10-6	0.022	0.005	C	0.361	SGSM2
rs216195	17	2149917	2.39x10-6	-0.023	0.005	G	0.295	SMG6
rs11166274	1	99799123	2.47x10-6	-0.028	0.006	G	0.198	PALMD
rs4762922	12	20108916	2.59x10-6	-0.023	0.005	C	0.278	PDE3A
rs1416892	1	99833641	2.69x10-6	-0.023	0.005	C	0.313	PALMD
rs10505842	12	20059562	2.75x10-6	-0.026	0.006	A	0.227	PDE3A
rs1522778	15	36322883	3.04x10-6	0.023	0.005	A	0.397	SPRED1
rs11188500	10	82875521	3.18x10-6	-0.035	0.008	C	0.168	SH2D4B
rs6679163	1	99836966	3.22x10-6	-0.023	0.005	A	0.306	PALMD
rs6662233	1	99832322	3.23x10-6	-0.022	0.005	A	0.311	PALMD
rs1339863	1	99832047	3.25x10-6	-0.022	0.005	T	0.312	PALMD
rs7085224	10	53971746	3.30x10-6	-0.033	0.007	G	0.182	MBL2
rs7518931	1	99833976	3.31x10-6	-0.022	0.005	C	0.311	PALMD
rs1339864	1	99833117	3.34x10-6	-0.022	0.005	G	0.311	PALMD
rs6665212	1	99832285	3.43x10-6	-0.022	0.005	T	0.312	PALMD
rs10875238	1	99832188	3.51x10-6	-0.020	0.004	T	0.415	PALMD

rs7526002	1	99836609	3.67x10-6	-0.022	0.005	C	0.305	PALMD
rs335206	5	122532465	3.82x10-6	-0.020	0.004	C	0.478	PPIC
rs7900164	10	53976706	3.89x10-6	-0.033	0.007	G	0.181	MBL2
rs7952739	12	20057605	3.96x10-6	-0.026	0.006	A	0.225	PDE3A
rs335205	5	122532581	3.96x10-6	-0.020	0.004	C	0.478	PPIC
rs335201	5	122537548	4.04x10-6	-0.020	0.004	A	0.476	PPIC
rs7967625	12	20057478	4.06x10-6	-0.026	0.006	T	0.225	PDE3A
rs7530446	1	99836551	4.08x10-6	-0.022	0.005	A	0.305	PALMD
rs2392039	1	99835670	4.11x10-6	-0.022	0.005	G	0.306	PALMD
rs1881747	10	54003581	4.11x10-6	-0.033	0.007	C	0.182	MBL2
rs4445492	1	99836935	4.14x10-6	-0.022	0.005	T	0.305	PALMD
rs10770588	12	20036021	4.14x10-6	-0.025	0.005	G	0.272	PDE3A
rs10743357	12	20137595	4.17x10-6	-0.026	0.006	C	0.258	PDE3A
rs162953	5	122527547	4.19x10-6	-0.021	0.005	G	0.487	PPIC
rs3983568	12	20058482	4.27x10-6	-0.027	0.006	G	0.227	PDE3A
rs2893417	1	99835358	4.29x10-6	-0.022	0.005	A	0.306	PALMD
rs10841427	12	20046661	4.36x10-6	-0.026	0.006	T	0.236	PDE3A
rs10770599	12	20057214	4.39x10-6	-0.027	0.006	G	0.220	PDE3A
rs4762915	12	20056827	4.51x10-6	-0.026	0.006	A	0.223	PDE3A
rs10841430	12	20056134	4.52x10-6	-0.027	0.006	G	0.220	PDE3A
rs7960456	12	20056028	4.54x10-6	-0.027	0.006	T	0.220	PDE3A
rs7980458	12	20053838	4.56x10-6	-0.027	0.006	T	0.225	PDE3A
rs10219487	12	20053152	4.56x10-6	-0.027	0.006	T	0.225	PDE3A
rs7980996	12	20057377	4.62x10-6	-0.026	0.006	G	0.224	PDE3A
rs10505843	12	20059354	4.68x10-6	-0.026	0.006	T	0.234	PDE3A
rs12566247	1	43540156	4.77x10-6	0.024	0.005	T	0.336	TIE1
rs11634989	15	36320860	4.83x10-6	0.023	0.005	G	0.385	SPRED1
rs6577389	1	99837187	4.86x10-6	-0.022	0.005	A	0.304	PALMD
rs1522780	15	36323341	5.06x10-6	0.023	0.005	A	0.385	SPRED1

eTable 9. SNPs Associated With LA Size With *P* Value $<10^{-5}$

SNP	chromosome	position	meta-analysis P-value	meta-analysis beta	meta-analysis SE	coded allele	allele frequency	Nearest Gene
rs216196	17	2149693	9.34x10-7	-0.037	0.008	C	0.269	SMG6
rs4790312	17	1928230	2.62x10-6	0.033	0.007	T	0.482	SMG6
rs6978848	7	11213667	2.87x10-6	0.032	0.007	G	0.427	PHF14
rs216215	17	2087418	2.88x10-6	-0.033	0.007	C	0.274	SMG6
rs6949976	7	11214902	2.98x10-6	0.032	0.007	C	0.427	PHF14
rs12449600	17	1928996	3.73x10-6	0.033	0.007	A	0.580	SMG6
rs2623347	3	100620001	4.23x10-6	0.049	0.011	C	0.143	COL8A1
rs7302727	12	5030047	4.51x10-6	0.047	0.010	A	0.167	KCNA5
rs13166731	5	33659692	4.60x10-6	0.053	0.012	A	0.110	ADAMTS12
rs7715934	5	33659517	4.61x10-6	0.054	0.012	G	0.111	ADAMTS12
rs9898390	17	2124234	5.42x10-6	-0.033	0.007	C	0.271	SMG6
rs216182	17	2119813	5.44x10-6	-0.033	0.007	G	0.272	SMG6
rs216224	17	2103035	6.06x10-6	-0.033	0.007	C	0.268	SMG6
rs170041	17	2116966	6.07x10-6	-0.033	0.007	T	0.267	SMG6
rs13184524	5	33659742	6.14x10-6	0.051	0.011	T	0.101	ADAMTS12
rs2038677	17	2124842	6.25x10-6	-0.032	0.007	C	0.272	SMG6
rs10466865	12	126073052	6.30x10-6	0.055	0.012	C	0.092	TMEM132B
rs7200990	16	88364008	6.70x10-6	0.163	0.036	T	0.032	FANCA
rs6455175	6	67681986	7.57x10-6	-0.031	0.007	C	0.418	EGFL11
rs4631258	6	67647174	8.02x10-6	-0.035	0.008	T	0.261	EGFL11
rs1250586	10	80647406	9.79x10-6	-0.030	0.007	T	0.347	ZMIZ1
rs9899411	17	1929702	9.90x10-6	0.030	0.007	A	0.475	SMG6

eTable 10. Contribution of SNPs to R^2 of Traits

phenotype	R^2, no SNPs	R^2, with SNPs	Increment in R^2
CHS			
LV diastolic dimensions	0.2349	0.2366	0.0017
Aortic root	0.2616	0.2725	0.0109
GHS			
LV diastolic dimensions	0.2786	0.2824	0.0038
KORA			
LV diastolic dimensions	0.196093	0.20077	0.004677
Aortic root	0.324154	0.337167	0.013013
RS			
LV diastolic dimensions	0.20144	0.200668	0
Aortic root	0.243143	0.263241	0.020098
FHS*			
LV diastolic dimensions			0.005066
Aortic root			0.029828
*FHS used linear mixed effects models, and so data format differs in table.			

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Legend for eFigure 1

Quantile-quantile plots of the observed against expected $-\log_{10}$ (p-value) distributions relating SNPs to echocardiographic traits (**Panels A-F**) in a prospective meta-analysis. The lambdas for individual traits that are meta-analyzed are shown in the Panels.

Legend for eFigure 2

Regional plots for associations in the region centered on select SNPs that were genome-wide significant in Stage 1 and that replicated in Stage 2 (**Panels A-B**). All SNPs are plotted with their meta-analysis p-values (Stage 1) relative to their genomic position. The SNP of interest is shown in black, and the colors of the surrounding SNPs show the strength of the linkage disequilibrium (LD): white is no LD (R squared< 0.2), yellow is weak (R squared ≥0.2 but <0.5), orange is moderate (R squared ≥0.5 but < 0.8) and red is strong (R squared ≥0.8).
The light blue line represents the estimated recombination rates. Gene annotations are shown as the dark green arrows. If there are no known genes in the region, a purple arrow indicates the nearest gene.

Figure 1A, Q-Q plot for LV mass

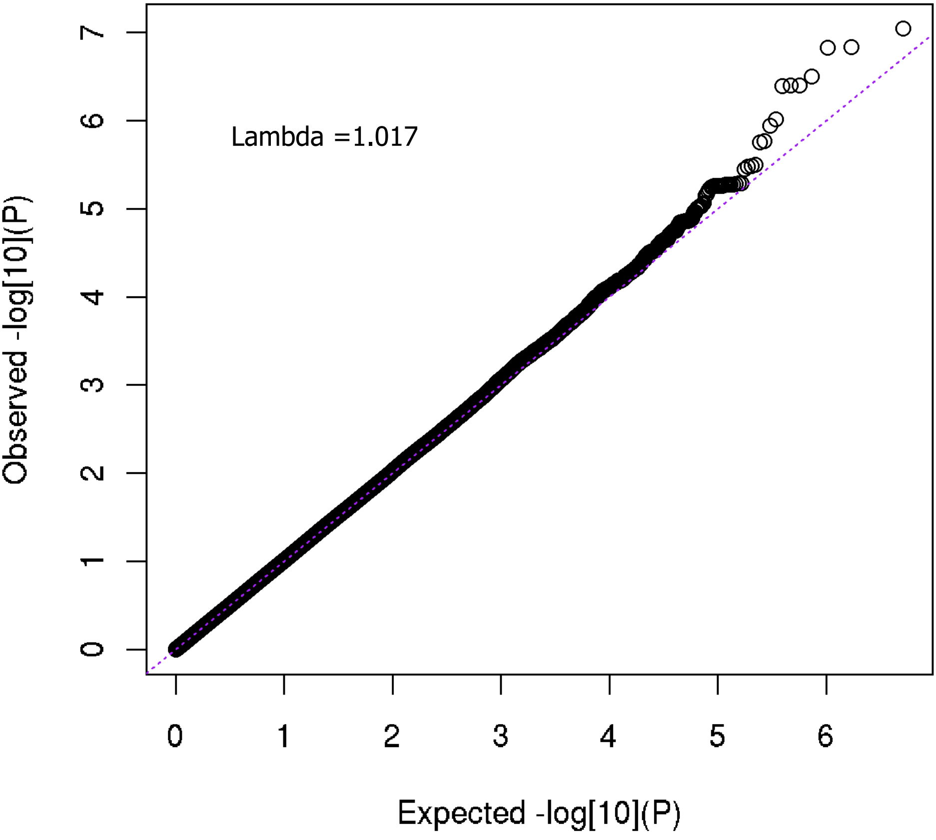


Figure 1B, Q-Q plot for LV Internal Dimensions

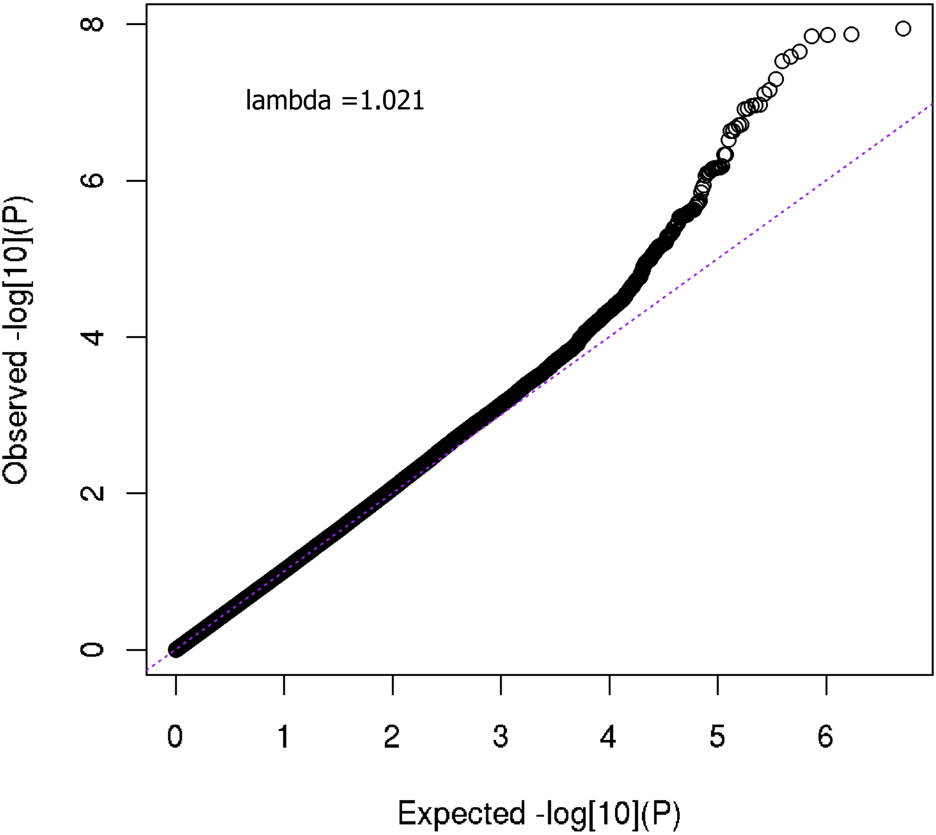
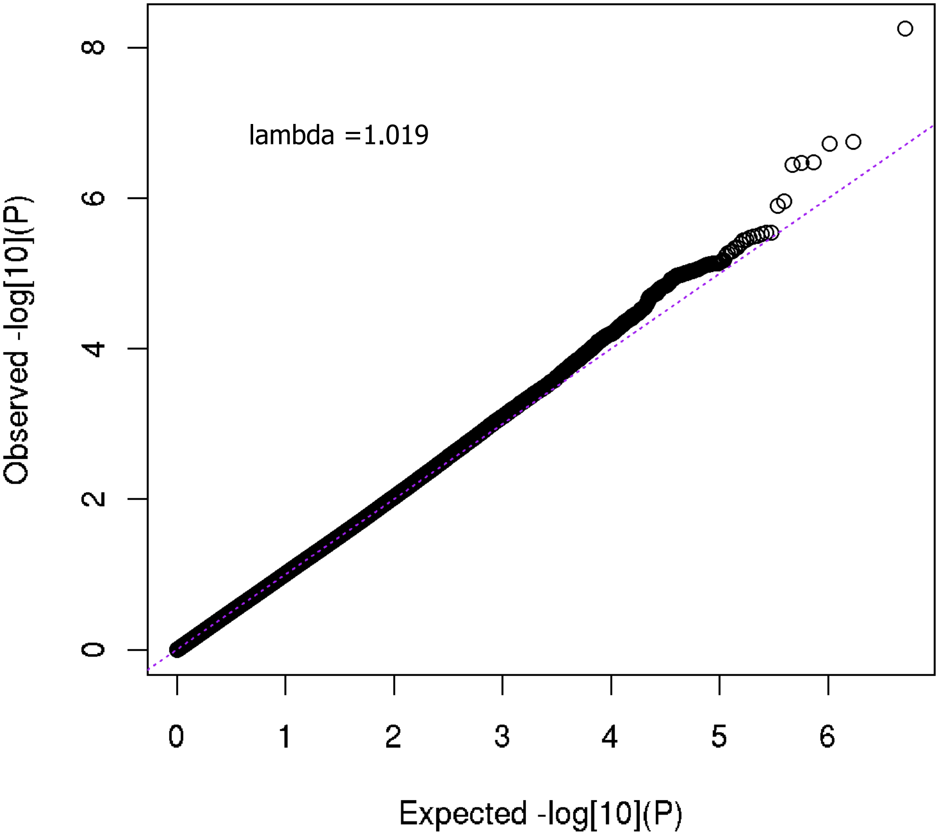
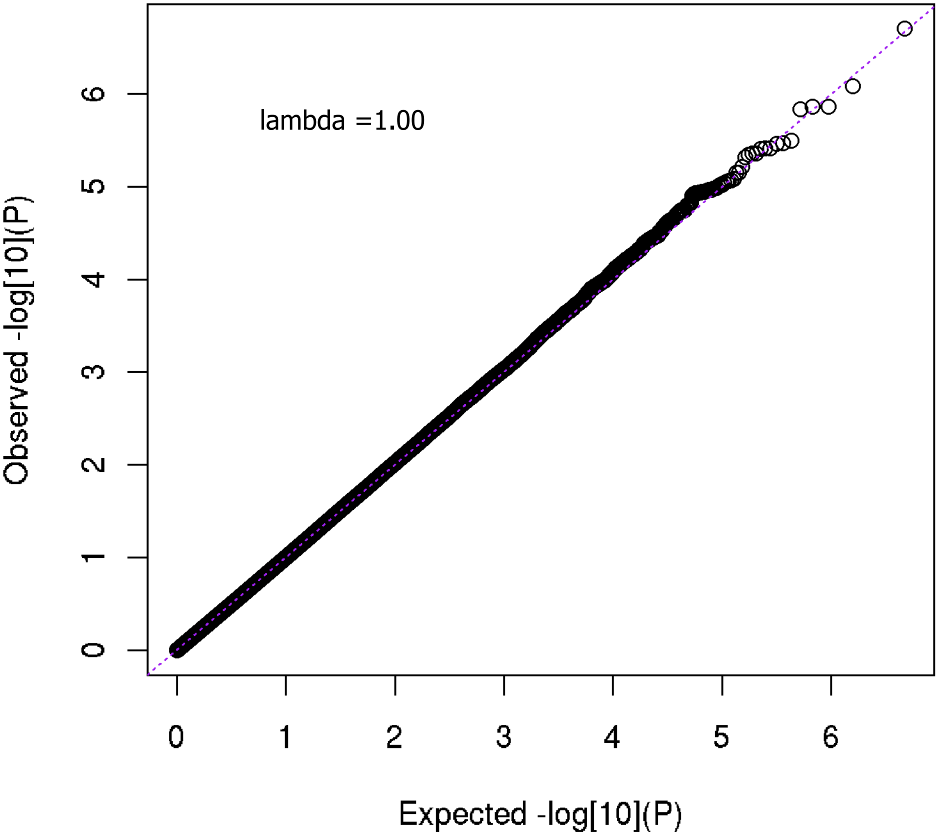


Figure 1C. Q-Q Plot for LV Wall Thickness



N Figure 1D. Q-Q Plot for LV Systolic Dysfunction



Nc

Figure 1E. Q-Q Plot for Aortic Root Size

5

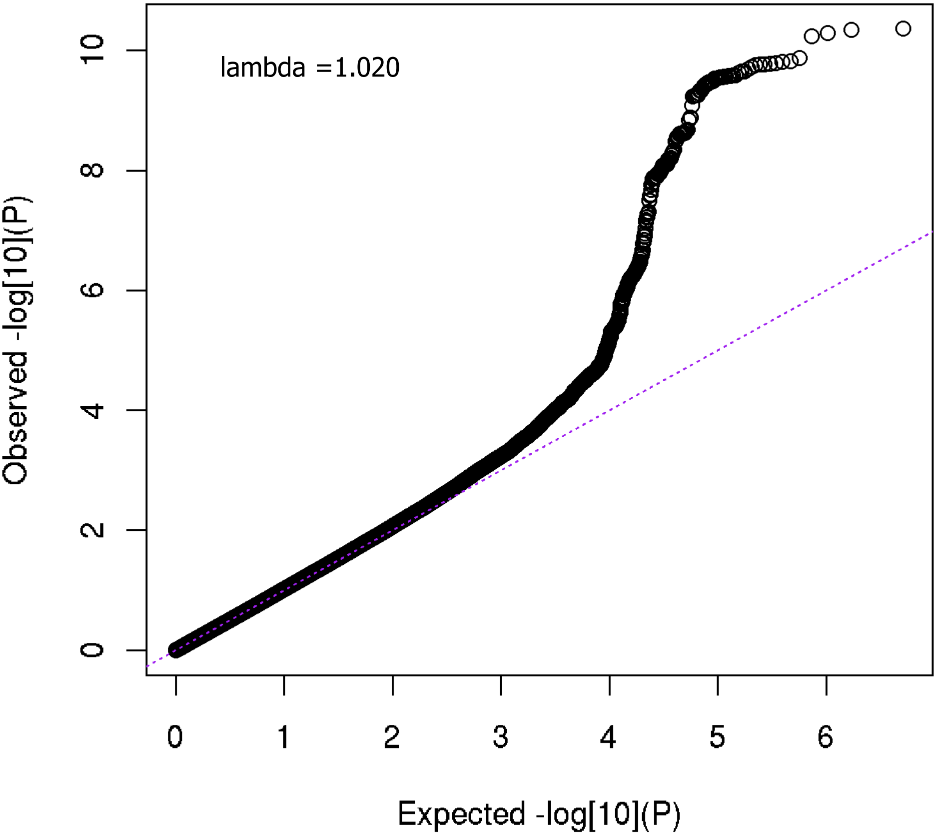


Figure 1F. Q-Q Plot for Left Atrial Size

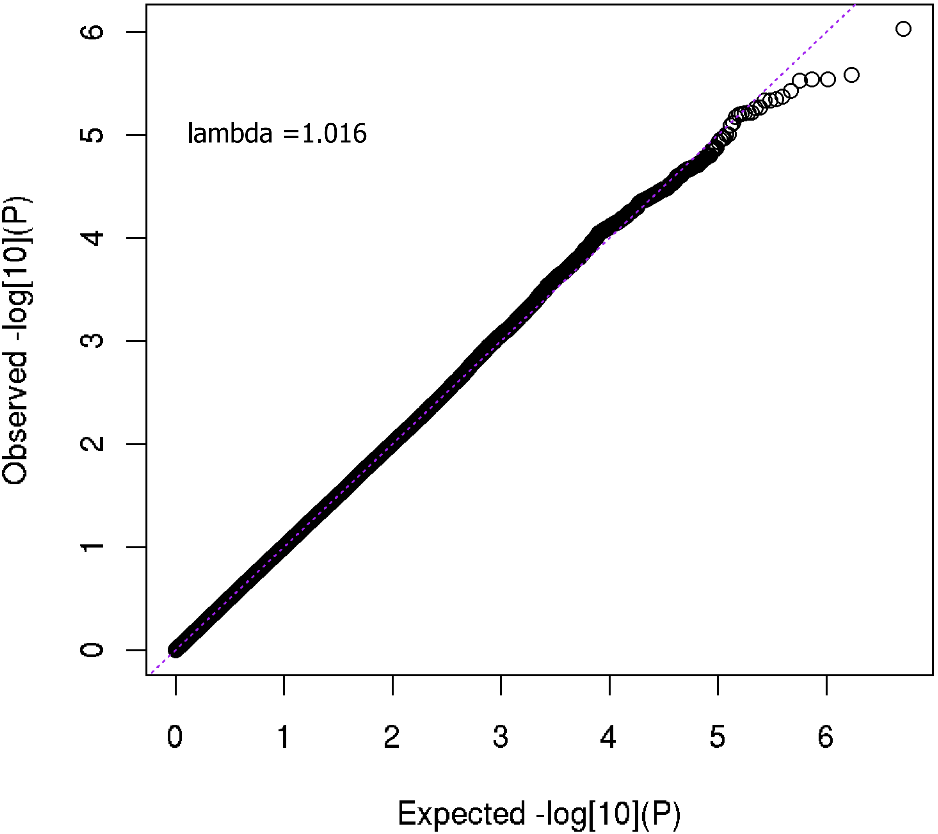


Figure 2A1. SNP Associated With LV Internal Dimensions

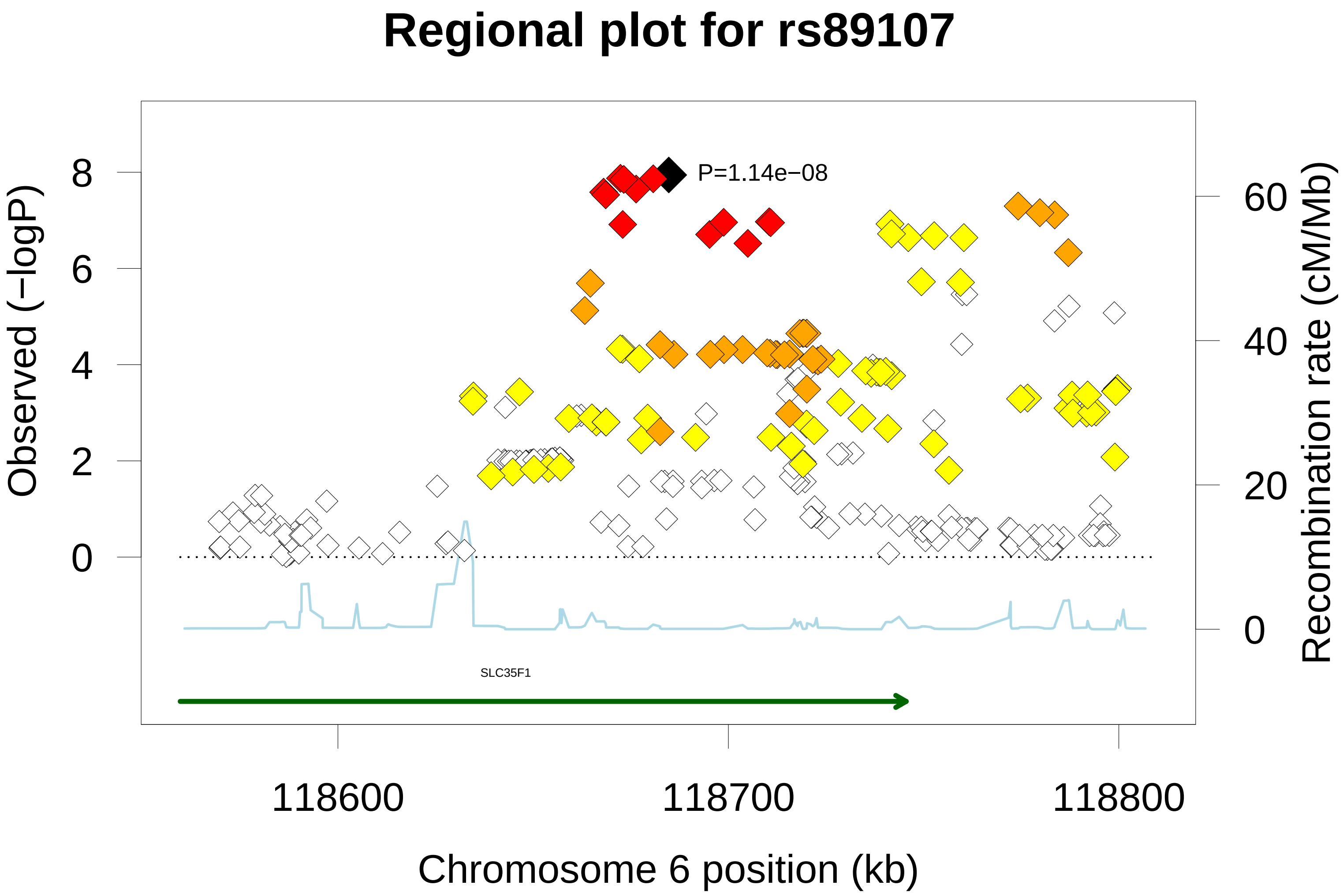


Figure 2A2. SNP Associated With LV Internal Dimensions

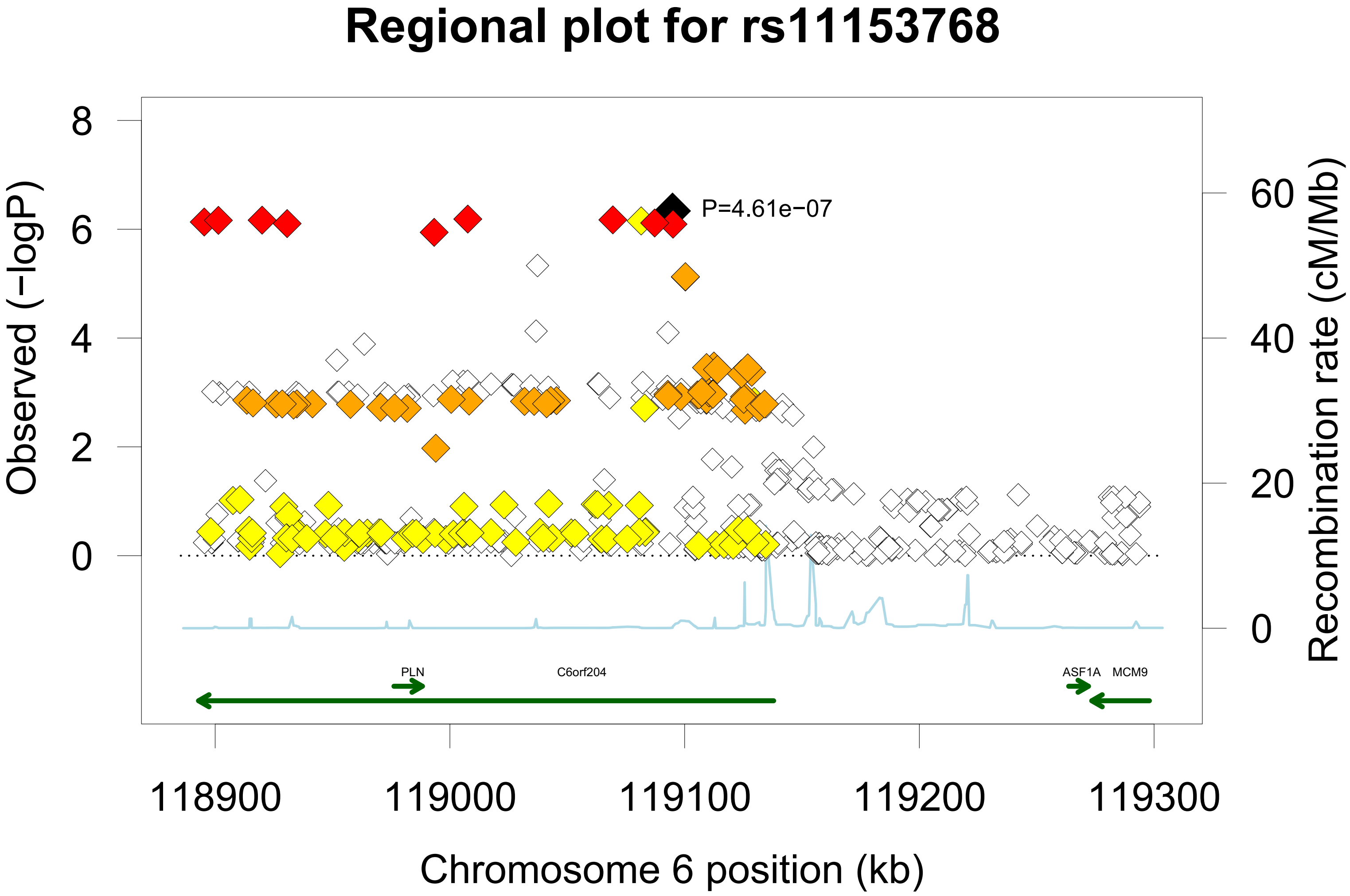


Figure 2B1. SNP Associated With Aortic Root Diameter

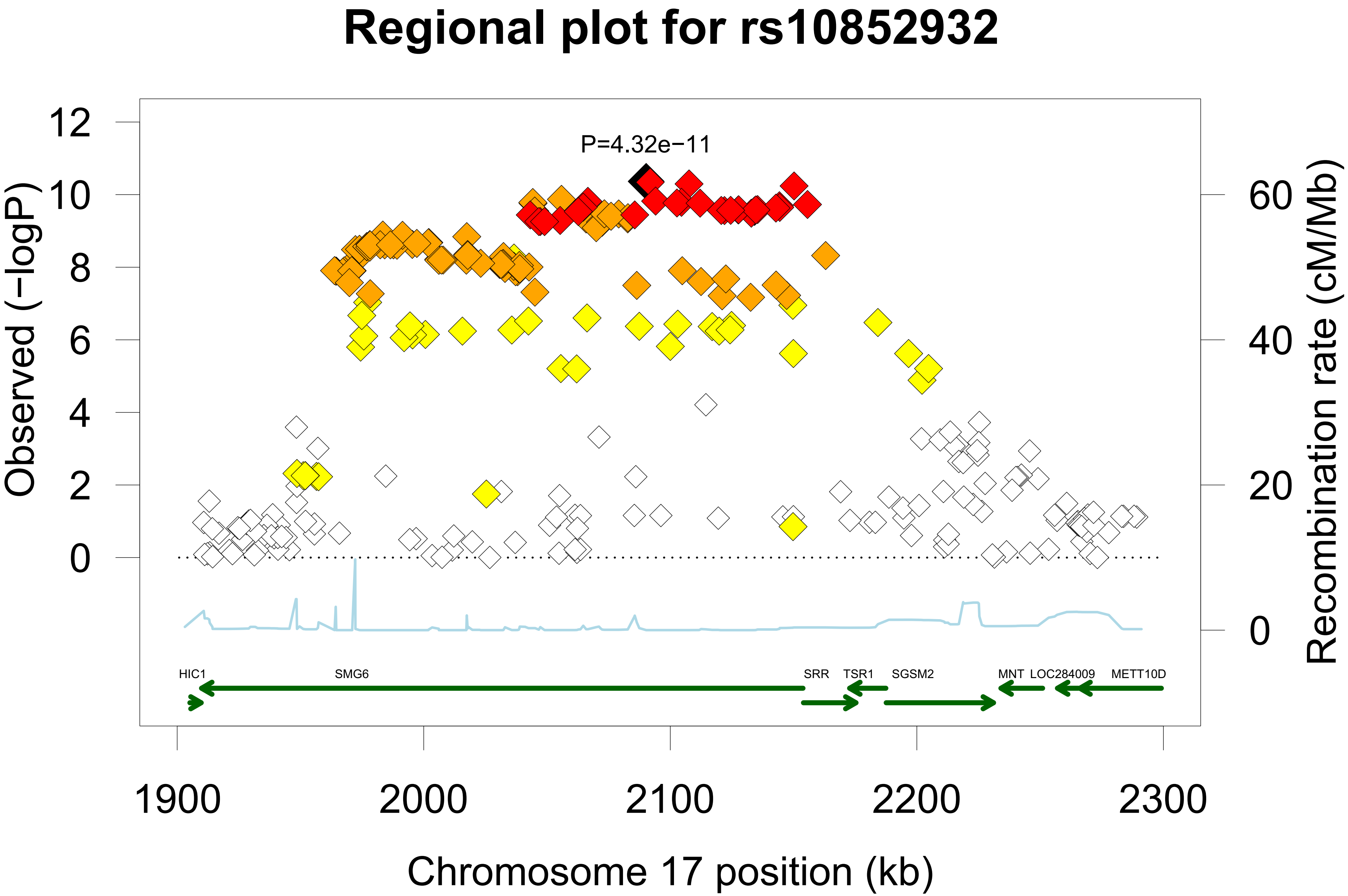


Figure 2B2. SNP Associated With Aortic Root Diameter

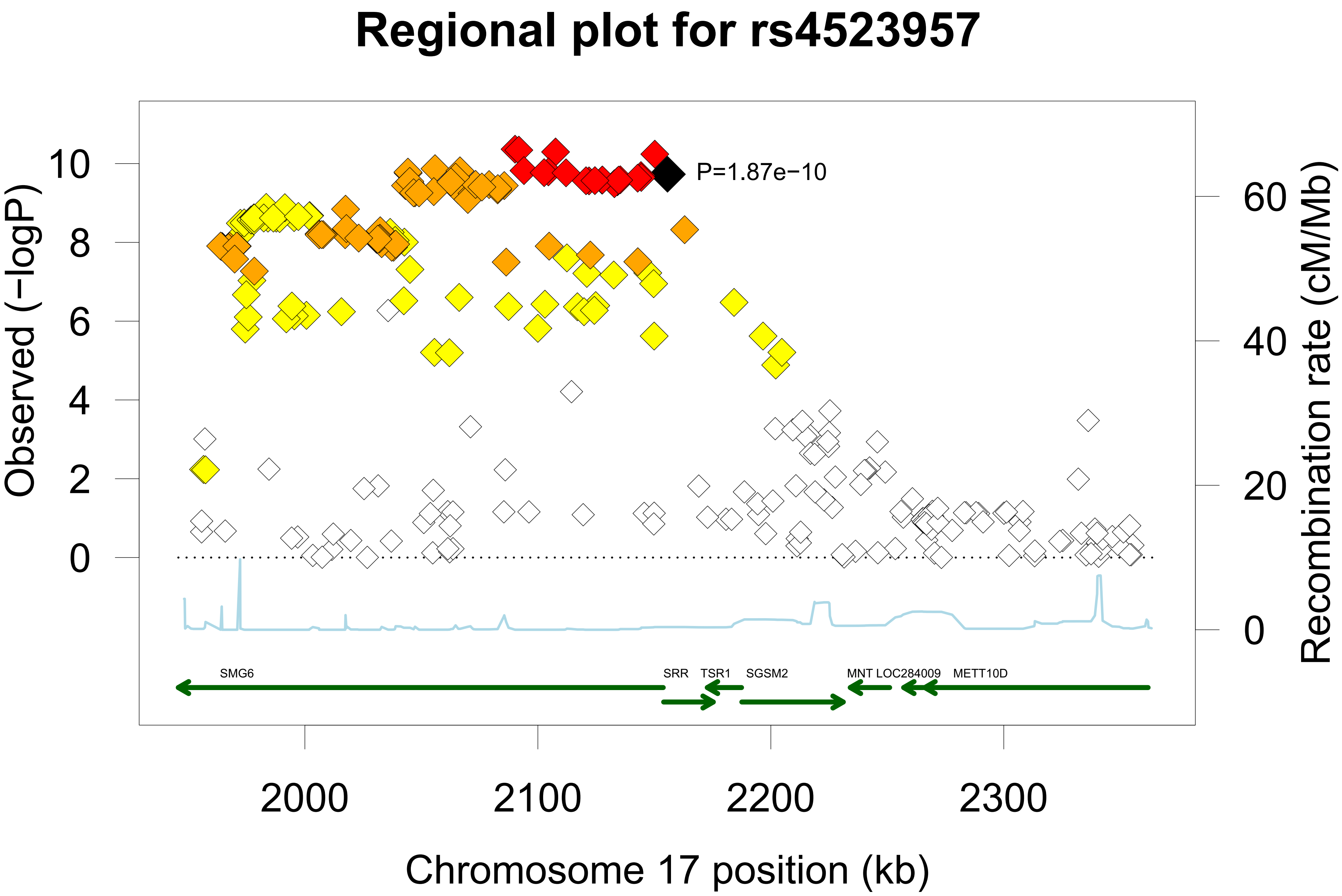


Figure 2B3. SNP Associated With Aortic Root Diameter

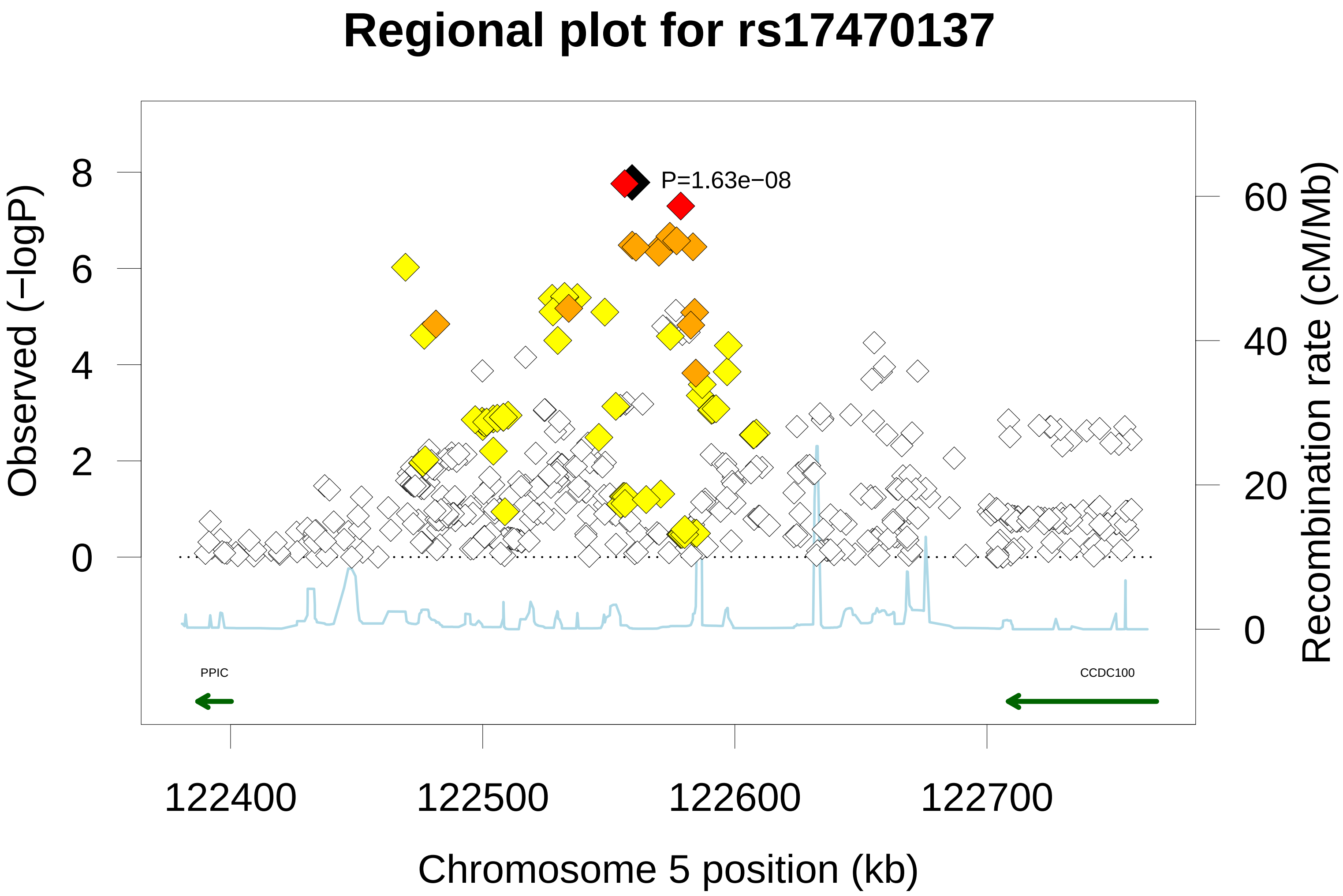


Figure 2B4. SNP Associated With Aortic Root Diameter

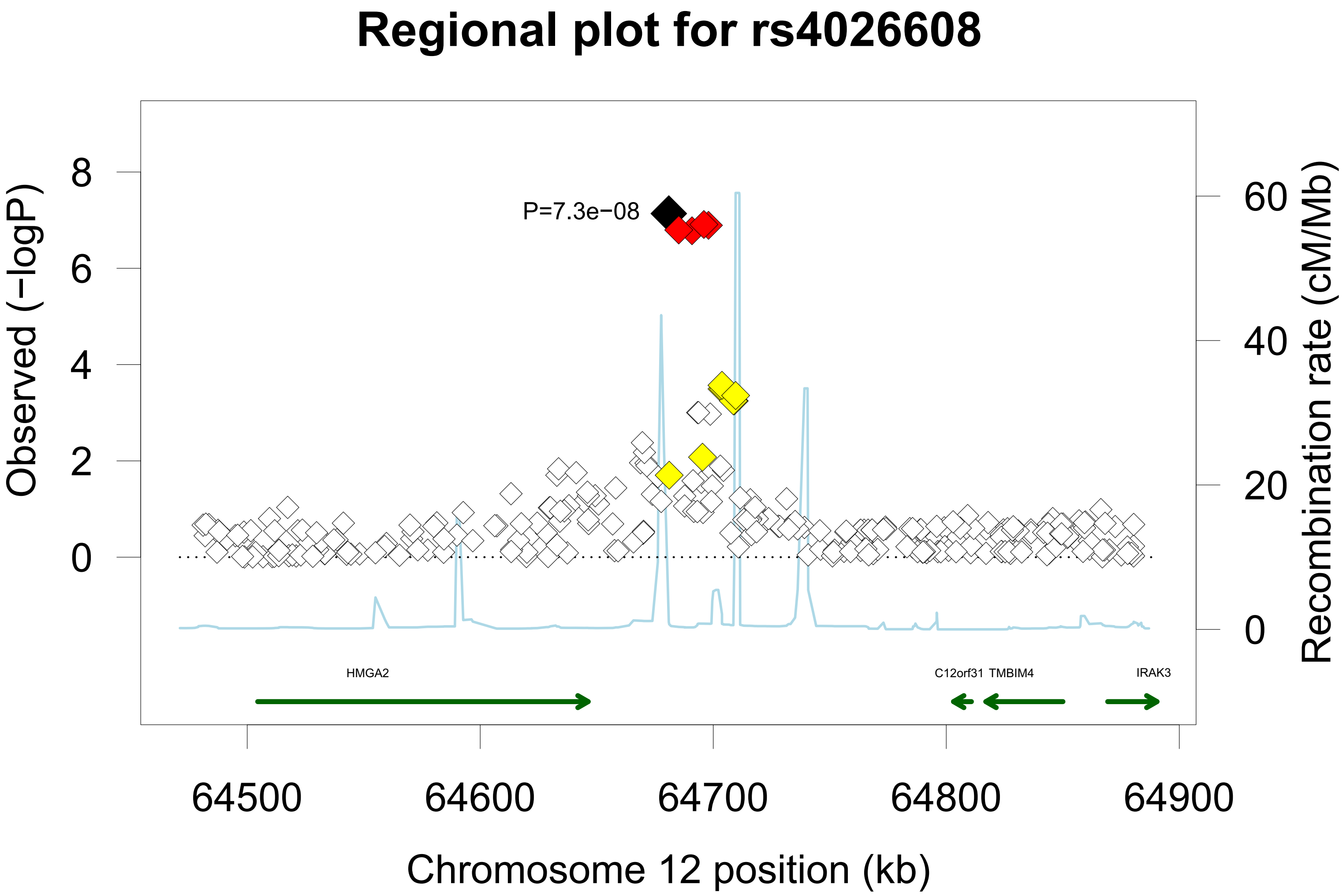


Figure 2B5. SNP Associated With Aortic Root Diameter