Supplemental Material

SUPPLEMENTAL METHODS

Selection of ECGs

In studies with multiple visits, ECG were selected from following visits: baseline visit (MESA, RS I-III), exam 20 (FHS Original cohort), exam 6 (FHS Offspring cohort), and exam 1 (FHS Gen 3).

Gene expression and eQTL analyses in left atrial tissue samples

Human left atrial tissue samples were obtained from the Cleveland Clinic Atrial Tissue Bank and Arrhythmia Biorepository, processed on the Illumina Human Hap550 v3 or Hap610 v1 chips and Illumina HumanHT-12 v3 or v4 chips to obtain genotype and RNA expression data, respectively. Human left atrial samples were obtained from 289 individuals of European American (EA) ethnicity; 266 samples were from left atrial appendage (LAA) tissue and 23 the left atrial pulmonary vein junction tissue (LA-PV). Of the 289 subjects, 80 were females, 70 had no history of AF, and 136 came from patients that were in AF at the time of tissue acquisition. Of 40 individuals of African American (AA) ethnicity, 25 were females, 16 had no history of AF, and 12 were in AF at the time of tissue acquisition; 34 samples were from LAA and 6 from LA-PV tissue; Detailed methods have been described previously.[1] SNP-gene expression association tests (eQTL analyses) were performed for all genome-wide significant genetic variants identified in analyses of P-wave duration and P-wave terminal force. False discovery rate (FDR) values were calculated from the p-values using the Benjamini and Hochberg method.[2] Cis probe-variant pairs with an FDR value less than 0.05 were deemed significant at the genome-wide level. In addition, for each variant set of interest, FDR values were calculated for that set.

In silico functional annotation and eQTL analyses

We assessed the linkage disequilibrium (LD) between the most significant variant in our study and previous studies, for all genetic loci reported in previous published GWAS of P-wave indices, using the

pairwise LD function of the SNAP software version 2.2.[3] LD was categorized as follows; strong LD, $r^2 \geq 0.8$; moderate LD, $r^2 < 0.8$ and ≥ 0.50; weak LD, $r^2 < 0.5$ and ≥ 0.2; no LD, $r^2 < 0.2$. We used the 1000 Genomes Pilot 1 SNP data set, and chose the European (CEU) population panel for variants identified in European studies and the African (YRI) population panel for variants discovered in African-American studies. We also used the SNAP software to identify proxies for the most significant SNP from each genetic locus identified in the GWAS, using the same settings as described above in addition to a distance limit of 500 kb and an LD r^2 threshold of 0.8.

All top hits and their proxies were selected for eQTL and SNP function analyses. We performed a lookup of statistically significant eQTLs in cardiac and skeletal muscle tissues, using the Genome-Tissue Expression database (GTEx),[4] which was accessed on October 21, 2015. We assessed SNP function through the NCBI dbSNP website on October 30, 2015.

SUPPLEMENTAL RESULTS

P-wave duration and P-wave terminal force are genetically associated

After LD-clumping using r^2>0.1, 96 significant SNPs remained from the P-wave duration analysis and 75 significant SNPs remained from the P-wave terminal force analysis, which were included in the respective GRS. The P-wave terminal force GRS was associated with measured P-wave duration (β=0.007; SE=0.0005; p=1.2x10^{-42}) and the P-wave duration GRS was associated with measured P-wave terminal force (β=11.2; SE=2.46, p=5.3x10^{-6}). After LD-clumping using r^2>0.05, 85 significant SNPs remained from the P-wave duration analysis and 66 significant SNPs remained from the P-wave terminal force analysis, which were included in the respective GRS. The P-wave terminal force GRS was associated with measured P-wave duration (β=0.007; SE=0.0005; p=1.2x10^{-44}) and the P-wave duration GRS was associated with measured P-wave terminal force (β=12.4; SE=2.67, p=3.3x10^{-6}). The estimated percentage of total variance of the measured P-wave terminal force explained by the P-wave duration GRS is 0.06%, for both r^2 thresholds, and conversely, the estimated fraction of the total variance of the measured P-wave duration explained by the P-wave terminal force GRS is 0.5%, for both r^2 thresholds.

SUPPLEMENTAL DISCUSSION

The sodium channel (SCN5A/SCN10A), caveolin (CAV1/CAV2), and TBX5 loci broadly contribute to atrial conduction.

A limited number of genetic loci have been associated with several atrial electrocardiographic traits, suggesting that they are important contributors in the propagation of atrial electrical activity from the sinoatrial node through the atrioventricular node.

The genetic region that stands out as most robustly associated with the overall conduction properties of the atria and the AV-node in previous GWAS is clearly the *SCN5A*/*SCN10A* region. These well-characterized genes encode the sodium channels $Na_V1.5$ and $Na_V1.8$, crucial for depolarization of cardiomyocytes and the initialization of the action potential itself. These genes have been associated with the PR interval,[5-11] P-wave duration,[5, 10, 12] and P-wave segment[5, 12] and both were associated with P-wave duration in the present study. Moreover, the *SCN5A* locus has been associated with QRS duration[13] and Brugada syndrome,[14] underscoring the relevance of this region to overall cardiac conduction.

Similarly, the *TBX3/5* and *CAV1/CAV2* loci have been associated with PR-interval, PR-segment,[6-9, 11, 12], AF,[15-18] and in the present study with P-wave duration. Both loci display convincing eQTLs in left atrial tissue in this study. *CAV1/CAV2* also has been related to AV-nodal automaticity and QRS duration.[7, 13, 19] The genes *NKX2-5* and *SOX5*, which both encode transcription factors important in the embryonic development of the atria, have been associated with both PR-interval[6] and heart rate.[20, 21]

Genetic loci unique to P-wave duration

The 5p12 locus is adjacent to *HCN1*, which encodes the hyperpolarization activated cyclic nucleotide-gated ion channel 1, a channel contributing to the pacemaker current in cardiac cells and neurons.[22] The

most abundant HCN channel in the human sinoatrial node (SAN) is HCN4; however, expression of both *HCN1* and *HCN4* has been shown in rabbit SAN and Purkinje fibers[23] and HCN1 can co-assemble with other HCN channel isoforms.[24] *HCN1* deficient mice develop severe sinoatrial deficiency, including bradycardia, sinus dysrhythmia, sinus pauses, and other properties of sick sinus syndrome.[25]

The most significant variant on chromosome 2p21 (rs11689011) was intronic to *EPAS1*, which encodes a hypoxia-inducible transcription factor expressed mainly in vascular endothelial cells,[26] but also in the carotid body and in catecholamine producing organs in mice.[27] *EPAS1* deficient mice display reduced levels of catecholamines and pronounced bradycardia, before they die mid-gestation, without morphological changes in the circulatory system.[27] Overexpression of the *EPAS1* gene leads to increased expression of adrenomedullin, implicating *EPAS1* in the adaptation of cardiac myocytes during heart failure.[28] Two variants in strong LD with rs11689011 (rs7579899, CEU r^2=1 and rs11894252, CEU r^2=0.96) were reported in a previous GWAS to be associated with renal cell carcinoma.[29, 30] A third proxy, rs1867785 (CEU r^2=0.96), has been associated with retinopathy in premature neonates and patent ductus arteriosus.[31, 32] However, the specific mechanism by which genetic variants at the *EPAS1* locus alters P-wave duration remains unclear.

The gene *SSBP3,* harboring the most significant variant at 1p32, has not previously been described in relation to any cardiac phenotype. However, AF-associated variants intronic to this gene were the strongest eQTLs identified in left atrial samples in this study. *SSBP3* encodes the single stranded DNA binding protein 3, which is expressed in heart tissue and has been suggested to be an important regulatory component of developmental programs in the cell.[33]

The locus at 4q26 surrounds *CAMK2D,* which encodes the Ca^{2+}/Calmodulin-Dependent Protein Kinase Type II Delta. This serine/threonine protein kinase is activated at increased Ca^{2+} levels and is involved in the regulation of calcium homeostasis and the excitation-contraction coupling in cardiomyocytes.

CAMK2D has a range of cardiac downstream effects, such as regulation of sarcoplasmic reticulum Ca^{2+}-release through the ryanodine receptor[34] and Ca^{2+}-uptake through phospholamban inhibition of SERCA,[35] regulation of voltage-gated L-type Ca^{2+} channels,[36, 37] and regulation of Nav1.5[38] and Kv4.3,[39] which may lead to arrhythmogenesis. All of these functions may be involved in atrial conduction and modify P-wave duration.

The *CAND2* genetic locus was associated with P wave duration in combined meta-analysis of European and African-American ancestries. *CAND2* was previously associated with AF by Sinner et al.[15] The most significant AF variant (rs4642101) is in moderate LD with the most significant variant in our study (rs1467026, CEU r^2=0.7), suggesting that the variants represent the same locus. Rs1467026 is a significant eQTL for *CAND2* ($p=7.5x10^{-27}$), *KRT18P17* ($p=9.2x10^{-11}$), and *RP11-767C1.2* ($p=1.2x10^{-9}$) expression in skeletal muscle based on GTEx data. Sinner and colleagues showed that rs4642101 increased the expression of *CAND2* in left atrial tissue samples and that knockdown in zebrafish led to prolongation of the atrial action potential. Taken together, the association with both P-wave duration and AF, and the functional evidence provided by Sinner et al., implicate *CAND2* in atrial conduction and arrhythmogenesis, although further work is needed to clarify the underlying mechanism.

Genetic loci unique to P-wave terminal force

The most significant variant at 1p13 is intronic to *KCND3,* which encodes K_v4.3, the pore-forming subunit of the transient outward K^+ current, I_{to}. The I_{to} current is instrumental in phase 1 of cardiac repolarization and affects calcium handling. Another variant in the region surrounding *KCND3* has previously been associated with P-wave duration, but does not seem to represent the same signal (CEU r^2=0.2).[12] Gain-of-function mutations in *KCND3* have been shown to be associated with early-onset AF,[40] shortening of action potential duration, and Brugada syndrome.[41] Although further studies are needed to elucidate the mechanism underlying the association between the *KCND3* locus and increased P-wave

terminal force, we speculate that the P-wave terminal force could be affected by down-regulation of Kv4.3 that leads to a prolongation of the APD, with a resulting delayed atrial repolarization.

On chromosome 15q25, the most significant variant (rs201517563) was located intronic to *ALPK3,* which encodes the protein kinase alpha-kinase 3, abundantly expressed in cardiac tissue and active in cardiomyocyte differentiation. Interestingly, among the many transcription factors that bind to the promoter region of this gene are *NKX2-5* and *MEIS1,* both of which were previously associated with PR-interval.[6] The gene Neuromedin B (*NMB),* for which there were convincing eQTL associations at the 15q25 locus, has previously been associated with ECG defined left ventricular hypertrophy (rs2292462)[42] and the same variant was associated with left ventricular hypertrophy in type 2 diabetics.[43] *NMB* has also been associated with obesity in children.[44]

In African Americans only, the variant rs10832139 was identified 44 kb upstream of *SPON1* on chromosome 11. *SPON1* encodes Spondin 1 Extracellular Matrix Protein, which was first identified as a promoter of axon growth in the spinal cord and the peripheral nervous system.[45] Later, *SPON1* was shown to be a strong growth promoting factor for vascular smooth muscle cells[46] and it has been suggested as a candidate hypertension gene.[47] Recently, an intronic variant (rs2618516) in *SPON1* was associated with brain connectivity in a GWAS by Jahanshad and colleagues, and older individuals with this variant displayed milder dementia symptoms.[48] However, there was no LD between the two variants (CEU r^2=0.01, YRI r^2=0.02), and the biologic link between *SPON1* and P-wave terminal force is unclear.

The two final loci associated with P-wave terminal force, *C6orf195* and *PPP5D1*, have an unclear biologic link with the electrocardiographic phenotype and have not been reported in any previous GWAS.

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Table S1. Overview of participating studies and PWI measurements

Study	Reference	ECG analysis software	P-wave duration	P-wave terminal force
Atherosclerosis Risk in Communities (ARIC) Study	49, 50	GE 12-SL software	x	x
Cardiovascular Health Study (CHS)	51	GE 12-SL software	x	x
Erasmus Rucphen Family (ERF) Study	52	Modular ECG Analysis System	x	x
Framingham Heart Study (FHS)	53, 54	GE 12-SL software	x	x
Cooperative Health Research in the Augsburg Region (KORA)	55	The Hannover ECG system	x	NA
Gutenberg Health Study I (GHS I)	56	GE Healthcare software CASE, CardioSoft, version 6	x	NA
Multi-Ethnic Study of Atherosclerosis (MESA)	57	GE 12-SL software	x	x
Rotterdam Studies I, II, III	58	Modular ECG Analysis System	x	x
Study of Health in Pomerania (SHIP)	59	Modular ECG Analysis System	x	x
Women's Health Initiative clinical trials (WHI CT):	60			
Genome-wide Association Research Network (GARNET)		GE 12-SL software	x	x
Modification of Particulate Matter-Mediated Arrhythmogenesis in Populations (MOPMAP)		GE 12-SL software	x	x
SNP Health Association Resource Project (SHARe)		GE 12-SL software	x	x

GE, General Electric; NA, not available

Table S2. Summary of participant characteristics by cohort.

Cohort	Race	Participants n	Males %	Age	HTN %	Body mass index kg/m²	RR interval, ms	PR interval, ms	Maximum P-wave duration, ms	P-wave terminal force, ms x μV[a]
ARIC	EA	8151	46	53±6	19	27±5	915±133	160±23	106±12	1490±1643
	AA	2799	37	53±6	50	29±6	920±147	171±27	112±12	2009±1974
CHS	EA	2415	36	72±5	46	26±4	948±145	166±27	110±13	2459±1917
ERF	EA	1651	42	47±14	44	27±4	972±157	152±22	111±12	1468±1545
FHS	EA	5878	45	47±14	20	27±5	971±157	158±23	105±12	1561±1600
KORA	EA	1519	49	52±9	33	27±4	935±144	162±24	109±12	NA
MESA	EA	1907	50	61±10	24	27±5	974±148	163±25	104±13	1928±1677
	AA	964	50	60±10	37	30±6	977±150	169±27	107±12	2463±1961
GHS I	EA	2204	51	54±11	41	27±4	1001±159	160±22	109±12	NA
RS I	EA	4552	40	68±9	49	26±4	865±139	167±25	119±13	2217±208
RS II	EA	1453	45	64±8	56	27±4	871±131	165±23	117±13	2175±1809
RS III	EA	2532	42	56±6	42	27±5	876±131	162±21	115±12	1170±1415
SHIP	EA	2680	49	46±16	10	27±5	853±148	152±20	110±11	788±1237
WHI CT GARNET	EA	1617	0	65±7	31	28±6	920±132	159±24	106±13	2196±1834
WHI CT MOPMAP	EA	1119	0	62±7	32	28±6	922±132	158±23	106±13	2236±1900
WHI CT SHARe	AA	3015	0	60±7	50	31±6	913±143	166±25	110±12	2671±2156

Summary statistics are reported as mean ± standard deviation unless otherwise noted. [a]P-wave terminal force equals the duration (ms) x the negative voltage deflection (μV) of the terminal part of the P-wave in lead V1. EA, European and European-American ancestry; AA, African and African-American ancestry; ARIC, Atherosclerosis Risk in Communities Study; CHS, Cardiovascular Health Study; ERF, Erasmus Rucphen Family Study; FHS, Framingham Heart Study; MESA, Multi-Ethnic Study of Atherosclerosis; RS, Rotterdam Study; SHIP, Study of Health in Pomerania; WHI CT, Women's Health Initiative Clinical Trials cohort; GARNET, Genomics and Randomized Trials Network; MOPMAP, Modification of PM-Mediated Arrhythmogenesis in Populations; SHARe, SNP Health Association Resource.

Table S3. Details regarding study samples, genotyping, and data cleaning.

	GHS I	ARIC	CHS	ERF	FHS	KORA	MESA	RS-I, II, III	SHIP	WHI CT		
Study	Gutenberg Health Study	Atherosclerosis Risk in Communities Study	Cardiovascular Health Study	Erasmus Rucphen Family Study	Framingham Heart Study	Kooperative Gesungheitsforschung in der Region Augsburg	Multi-Ethnic Study of Atherosclerosis	Rotterdam Study	The Study of Health in Pomerania	Genome-wide Association Research Network Effects of Treatment	Modification of PM-Mediated Arrhythmogenesis in Populations	SNP Health Association Resource Project
Array	Affymetrix 6.0	Affymetrix 6.0	Illumina 370 CNV + Illumina ITMAT-Broad-CARe (IBC)	Illumina 318K and 370K, Affymetrix 250K	Affymetrix Gene Chip® 500K Array Set & 50K Human Gene Focused Panel	Affymetrix 6.0	Affymetrix 6.0	Illumina Infinium HumanHap550 - chip v3.0	Affymetrix 6.0	Illumina HumanOmni 1-Quad v1-0 B	Affymetrix Gene Titan, Axiom Genome-Wide Human CEU 1	Affymetrix 6.0
Calling Algorithm	Birdseed	Birdseed	BeadStudio	BeadStudio	BRLMM	Birdseed v2	Birdseed v2	BeadStudio	Birdseed v2	BeadStudio v3.1.3.0	Affymetrix Power Tools v1.14.3	Birdseed
Per SNP Call rate	<95%	<95%	<97%	<98%	<97%	<93%	<95%	<98%	ND	98%	95%	95%
HWE p-value	$<10^{-4}$	$<10^{-5}$	$<10^{-5}$	$<10^{-6}$	$<10^{-6}$	NA	NA	$<10^{-6}$	ND	$<10^{-4}$	$<10^{-6}$	$<10^{-6}$
Mendelian errors	NA	NA	≤2	Genotypes were set to missing for problematic family sub-units.	N>100	NA	NA	NA	NA	NA	NA	NA
Excess heterozygosity	NA	NA	ND	ND	Subject hetero-zygosity >5 SD away from the mean	ND	>0.53	>0.336; n=21	ND	NA	NA	NA
MAF	<1%	EA: <0.5% AA: <1%	Excluded SNPs with 0 heterozygotes	<1%	<1%	NA	NA	<1%	ND	None	<0.5%	<1%

Selection criteria for PCs	-	Analysis committee recommendations	-	Used linear mixed effects models to account for relatedness	All PCs unassociated p>0.05	No population substructure	Analysis committee recommendations	Outliers as identified by IBS clustering were excluded	Eigenstrat, MDS with HapMap reference population	-	>6 SD from top 10 PCs	-
Number of PCs in the model	0	EA: 4 AA: 10	0	0	0	0	EA: 0 AA: 10	4	0	3	3	10
Number of SNPs used for imputation	662,405	EA: 711,589 AA: 806,416		678,524	EA: 445,149	651,596	EA: 854,755 AA: 861,124	512,849	869,224	-	535,600	829,370
Imputation software	IMPUTE v.2.1.0[61]	Pre-phasing with ShapeIt v.1.r532[62] Imputation with IMPUTE v.2.1.0[61]	MACH1, minimac[63, 64]	MACH1 v.1.0.151[63, 64]	MACH1 v.1.0.151[63, 64]	MACH1 v.1.0.15[63, 64]	IMPUTE v.2.1.0[61]	MACH1 v.1.0.151[63, 64]	IMPUTE v.0.5.0 against HapMap II CEU v.22[61]	BEAGLE v.3.3.1[65]	MACH1, minimac[63, 64]	MACH v.1.0.16[63, 64]
Imputation Backbone / NCBI Build	Build 36	1000 Genomes Phase I integrated variant set release (v.3) in NCBI build 37 (hg19)	1000 Genomes Phase I integrated variant set release (v.3) in NCBI build 37 (hg19)	Build 36	Build 37	Build 36	Build 36 / EA: HapMap I+II CEU r24 AA: HapMap I+II CEU+YRI+CHB+JPT r22	Build 36	Build 36	Build 37	Build 36	Build 36
SNP position from NCBI build	Build 36	Build 37	Build 37	Build 36	Build 37	Build 36	Build 36	Build 36	Build 36	1000G EUR	Hapmap r22 CEU	Hapmap 2 YRI/CEU 1:1
GWAS Statistical Analysis	SNPTEST[66]	FaST-LMM[67]	R[68]	GenABEL, ProbABEL, R[68]	R packages kinship, GEE, coxpH 3[68]	ProbABEL, R[68]	R package GEE[68]	Mach2QTL, [63, 64] GenABEL + PLINK,[69] R,[68] GRIMP[70]	QUICKTEST v.0.95[71]	R[68]	R[68]	R[68]
Total number of SNPs used in the analysis (MAF>0.005)	2,564,344	EA: 9,337,140 AA: 15,879,929	EA: 9,403,802 (no MAF filtering)	2,402,234 2,320,937 (0.005 < MAF < 0.995)	8,522,176 (MAF>=0.01, imputation quality>0.3)	2,543,887	EA: 2,592,133 AA: 2,975,847	RS-I 8,818,618, RS-II 8,798,976, RS-III 8,846,227 (MAF>0.01, imputation quality >0.3)	2,748,910	8,864,574	2,543,830	2,203,608

Inflation factor (λ)	NA	EA: Pmax: 1.02 PTF: 1.01 AA: Pmax: 1.01 PTF: 0.98	Pmax: 1.02 PTF: 1.01	Pmax:1.00 PTF: 1.03	Pmax: 1.01 PTF:1.02	Pmax: 1.01	EA: Pmax: 1.029 PTF: 1.036 AA: Pmax: 1.029 PTF: 1.025	Pmax: RS1: 1.025 RS2: 1.013 RS3: 1.013 PTF: RS1: 0.992 RS2: 0.958 RS3: 1.010	Pmax: 0.98 PTF: 1.01	PTF: 1.01	PTF: 1.00	PTF: 1.02

NA, not applicable; ND, not determined; PC, principal component; Pmax, maximum P-wave duration; PTF, P-wave terminal force

Table S4. Summary of genome-wide significant genetic associations for P-wave maximum duration in participants of European and African ancestry.

SNP	Chr	Location relative to gene	Closest gene	Minor/major allele	MAF, %	Minor allele effect, β (SE)	P value	Variance explained, %
European ancestry (n=37,678)								
rs562408	1p32	Intronic	*SSBP3*	A/G	44	-0.53 (0.09)	1.97×10^{-8}	0.09
rs11689011	2p21	Intronic	*EPAS1*	T/C	42	0.60 (0.09)	1.18×10^{-10}	0.12
rs41312411	3p22	Intronic	*SCN5A*	G/C	15	1.91 (0.15)	9.63×10^{-40}	0.43
rs6790396	3p22	Intronic	*SCN10A*	C/G	41	1.22 (0.09)	2.17×10^{-39}	0.49
rs2285703	4q26	Intronic	*CAMK2D*	G/A	26	0.56 (0.10)	3.77×10^{-8}	0.08
rs4276421	5p12	Intergenic	*HCN1*	C/T	42	0.61 (0.09)	1.47×10^{-11}	0.12
rs13242816	7q31	Intronic	*CAV1/CAV2*	T/C	8	1.21 (0.19)	8.24×10^{-11}	0.11
rs148020424	12q24	Intronic	*TBX5*	G/GGAAAGAAAGAAAAGAGAAA	27	0.85 (0.12)	5.72×10^{-13}	0.13
rs452036	14q11	Intronic	*MYH6*	A/G	36	0.59 (0.10)	6.49×10^{-10}	0.09
African ancestry (n=6778)								
rs3922844	3p21	Intronic	*SCN5A*	T/C	47	-1.66 (0.22)	3.26×10^{-14}	0.83
rs1895582	12q24	Intronic	*TBX5*	G/A	28	1.33 (0.23)	1.41×10^{-8}	0.49

Adjusted for age and sex. Chr, chromosome; MAF, Minor allele frequency; SE, standard error.

Table S5. Summary of genetic associations for P-wave maximum duration in combined ancestry analysis.

SNP	Chr	Location relative to gene	Closest gene	Minor / major allele	MAF, %	Minor allele effect, β (SE)	P value	Variance explained, %
rs562408	1p32	Intronic	*SSBP3*	A/G	43%	-0.52 (0.09)	2.78×10^{-9}	0.08
rs11894252	2p21	Intronic	*EPAS1*	T/C	43%	0.52 (0.09)	1.43×10^{-9}	0.08
rs1467026	3p25	Intergenic	*CAND2*	G/A	39%	0.51 (0.09)	1.61×10^{-8}	0.07
rs41312411	3p22	Intronic	*SCN5A*	G/C	15%	1.90 (0.14)	1.85×10^{-40}	0.41
rs4276421	5p12	Intergenic	*HCN1*	C/T	44%	0.58 (0.08)	3.52×10^{-12}	0.12
rs3801995	7q31	Intronic	*CAV1/CAV2*	T/C	26%	0.60 (0.09)	1.04×10^{-10}	0.10
rs7312625	12q24	Intronic	*TBX5*	G/A	27%	0.80 (0.09)	2.41×10^{-18}	0.18
rs452036	14q11	Intronic	*MYH6*	A/G	38%	0.64 (0.09)	3.99×10^{-13}	0.11

Adjusted for age and sex. Chr, chromosome; MAF, minor allele frequency; SD, standard error.

Table S6. Comparison of all genome-wide significant loci across P-wave duration and P-wave terminal force analyses.

SNP	Chr	Location relative to gene	Closest gene	P-wave duration analysis		P-wave terminal force analysis	
				Minor allele effect, β (SE)	P value	Minor allele effect, β (SE)	P value
Significant in P-wave duration analysis							
European ancestry (n=37,678)							
rs562408	1p32	Intronic	*SSBP3*	-0.53 (0.09)	1.97×10^{-8}	-7.29 (13.13)	0.58
rs11689011	2p21	Intronic	*EPAS1*	0.60 (0.09)	1.18×10^{-10}	-7.25 (13.11)	0.58
rs41312411	3p22	Intronic	*SCN5A*	1.91 (0.15)	9.63×10^{-40}	-0.68 (20.36)	0.97
rs6790396	3p22	Intronic	*SCN10A*	1.22 (0.09)	2.17×10^{-39}	NA	NA
rs2285703	4q26	Intronic	*CAMK2D*	0.56 (0.10)	3.77×10^{-8}	19.21 (14.55)	0.19
rs4276421	5p12	Intergenic	*HCN1*	0.61 (0.09)	1.47×10^{-11}	-2.19 (12.65)	0.86
rs13242816	7q31	Intronic	*CAV1*	1.21 (0.19)	8.24×10^{-11}	9.71 (26.00)	0.71
rs148020424	12q24	Intronic	*TBX5*	0.85 (0.12)	5.72×10^{-13}	NA	NA
rs452036	**14q11**	**Intronic**	***MYH6***	**0.59 (0.10)**	$\mathbf{6.49 \times 10^{-10}}$	**112.32 (13.37)**	$\mathbf{4.44 \times 10^{-17}}$
African ancestry (n=6778)							
rs3922844	3p21	Intronic	*SCN5A*	-1.66 (0.22)	3.26×10^{-14}	12.90 (37.29)	0.73
rs1895582	12q24	Intronic	*TBX5*	1.33 (0.23)	1.41×10^{-8}	-21.67 (39.67)	0.58
Significant in P-wave terminal force analysis							
European ancestry (n=33,955)							
rs12090194	1p13	Intronic	*KCND3*	-0.28 (0.10)	0.004	119 (13)	5.56×10^{-19}
rs11242779	6p25	Intergenic	*C6orf195*	0.37 (0.09)	6.37×10^{-5}	-71 (13)	2.10×10^{-8}
rs445754	14q11	Intronic	*MYH6*	0.54 (0.11)	5.11×10^{-7}	131 (15)	3.22×10^{-18}
rs201517563	15q25	Intergenic	*ALPK3*	NA	NA	-86 (15)	3.95×10^{-9}
rs4435363	19q13	Intronic	*PPP5D1*	0.24 (0.11)	0.039	-93 (16)	3.84×10^{-9}
African ancestry (n=6778)							
rs10832139	11p15	Intergenic	*SPON1*	-0.50 (0.22)	0.025	214 (38)	2.44×10^{-8}

Variants that reached genome-wide significance in both P-wave duration and P-wave terminal force analyses are indicated by bold font. Chr, chromosome; SE, standard error; NA, not available.

Table S7. Shared associations between the present P-wave duration GWAS and previous PWI GWAS.

rsID present study	Chr	Closest gene	Ancestry	rsID previous study	LD, r^2 CEU/YRI	PR-interval	P-wave duration	PR-segment	Heart rate
rs41312411	3p22	*SCN5A*	EUR	rs11708996	0.94/NA	EUR[6]			
				rs6599222	0.55/NA	AA[72]		EUR[12]	
				rs7638909	0.16/NA	Kosrae[5]*	Kosrae[5]*	Kosrae[5]*	
rs3922844	3p21	*SCN5A*	AA	rs3922844	1/1	AA[9, 72]		EUR[12]	
				rs11708996	0.07/NA	EUR[6]			
				rs6599222	0.001/0.24	AA[72]		EUR[12]	
				rs7638909	0.05/0.006	Kosrae[5]*	Kosrae[5]*	Kosrae[5]*	
rs6790396	3p21	*SCN10A*	EUR	rs6800541	1/NA	EUR[6], AS[11]			
				rs6795970	0.97/0.07	EUR[7], AS[11]	AS[10]		
				rs6801957	0.97/1	AA[9], AS[11]	EUR[12]	EUR[12]	
				rs6798015	0.87/0.51	AA[72]			
rs13242816	7q31	*CAV1*	EUR	rs3807989	0.11/NA	EUR[6, 7],AS[8, 11]		EUR[12]	
				rs11773845	0.11/NA	AA[9]			
rs3801995	7q31	*CAV1*	EUR+AA	rs3807989	0.56/0.17	EUR[6, 7],AS[8, 11]		EUR[12]	
				rs11773845	0.56/0.17	AA[9]			
rs148020424	12q24	TBX5	EUR	rs7312625	NA/NA	AA[72]			
				rs3825214	NA/NA				EUR[7]
				rs1895585	NA/NA	AA[9]			
rs1895582	12q24	*TBX5*	AA	rs7312625	0.80/0.81	AA[72]			
				rs3825214	0.65/0.33				EUR[7]
				rs1895585	NA/NA	AA[9]			
rs7312625	12q24	*TBX5*	EUR+AA	rs7312625	1/1	AA[72]			
				rs3825214	0.76/0.23				EUR[7]
				rs1895585	0.87/0.78	AA[9]			
rs452036	14q11	*MYH6*	EUR	rs452036	1/1				EUR[20], AA[73]
				rs365990	0.96/1				EUR[7, 20, 21], AA[73]

rsID present study	Chr	Closest gene	Ancestry	rsID previous study	LD, r^2 CEU/YRI	PR-interval	P-wave duration	PR-segment	Heart rate
				rs223116**	0.16/0.002				EUR[20]

Overview of shared genetic loci between present and previous GWAS. The variants identified in previous study are reported with rsID, LD information, previously associated electrocardiographic phenotype, and discovery ancestry group. Chr, chromosome; LD, Linkage disequilibrium; CEU, Utah residents with Northern and Western European ancestry from the 1000 Genomes; YRI, Yoruba in Ibadan, Nigeria, African ancestry group from the 1000 Genomes; NA, not available in SNAP LD search; EUR, European ancestry; AA, African American ancestry; AS, Asian ancestry. *Founder population in Micronesia, **Intronic to *MYH7*.

Table S8. Significant eQTLs in left atrial tissue samples for genetic loci associated with P-wave duration.

Index SNP	Closest gene/s*	Chr	Position	rsID	Probe ID	Gene	MA	Fold change**	TSS distance	r^2†	FDR_gw‡	FDR_dur††
Variants identified in European ethnicity GWAS analysis - eQTLs in European American atrial samples												
rs562408	***SSBP3***	1	54742618	rs562408	ILMN_1814165	*SSBP3*	A	1.112	136.534	0.062	0.007	0.003
rs562408	***SSBP3***	1	54742471	rs590041	ILMN_1814165	*SSBP3*	T	1.111	136.681	0.061	0.008	0.003
rs41312411	***SCN5A***	3	38624253	rs3922844	ILMN_1694956	*SCN5A*	T	1.080	66.911	0.040	0.075	0.034
rs13242816	***CAV1***	7	116198621	rs1997571	ILMN_1687583	*CAV1*	G	0.819	33.782	0.184	7.90×10^{-10}	5.40×10^{-10}
rs13242816	***CAV1***	7	116198828	rs1997572	ILMN_1687583	*CAV1*	A	0.819	33.989	0.184	7.90×10^{-10}	5.40×10^{-10}
rs13242816	***CAV1***	7	116186241	rs3807989	ILMN_1687583	*CAV1*	A	0.819	21.402	0.184	8.07×10^{-10}	5.40×10^{-10}
rs13242816	***CAV1***	7	116191301	rs11773845	ILMN_1687583	*CAV1*	C	0.819	26.462	0.184	8.16×10^{-10}	5.40×10^{-10}
rs13242816	***CAV1***	7	116194228	rs7804372	ILMN_1687583	*CAV1*	A	0.859	29.389	0.082	0.001	0.0005
rs13242816	***CAV1***	7	116197579	rs3807994	ILMN_1687583	*CAV1*	A	0.860	32.74	0.080	0.001	0.0005
rs13242816	***CAV1***	7	116198466	rs10953822	ILMN_1687583	*CAV1*	C	0.860	33.627	0.080	0.001	0.0005
rs13242816	***CAV1***	7	116198090	rs6466588	ILMN_1687583	*CAV1*	T	0.860	33.251	0.080	0.001	0.0005
rs13242816	***CAV1***	7	116197245	rs3807992	ILMN_1687583	*CAV1*	A	0.860	32.406	0.080	0.001	0.0005
rs13242816	***CAV1***	7	116196763	rs3807990	ILMN_1687583	*CAV1*	T	0.860	31.924	0.080	0.001	0.0005
rs13242816	***CAV1***	7	116193705	rs3757732	ILMN_1687583	*CAV1*	A	0.860	28.866	0.079	0.001	0.0005
rs13242816	***CAV1***	7	116193729	rs3757733	ILMN_1687583	*CAV1*	A	0.860	28.89	0.079	0.001	0.0005
rs13242816	***CAV1***	7	116190597	rs3801995	ILMN_1687583	*CAV1*	T	0.860	25.758	0.079	0.001	0.0005
rs13242816	***CAV1***	7	116190693	rs3815412	ILMN_1687583	*CAV1*	C	0.860	25.854	0.079	0.001	0.0005
rs13242816	***CAV1***	7	116194905	rs729949	ILMN_1687583	*CAV1*	A	0.860	30.066	0.079	0.001	0.0005
rs13242816	***CAV1***	7	116194384	rs7789117	ILMN_1687583	*CAV1*	T	0.860	29.545	0.079	0.001	0.0005
rs13242816	***CAV1***	7	116191812	rs9885998	ILMN_1687583	*CAV1*	A	0.860	26.973	0.079	0.001	0.0005
rs13242816	***CAV1***	7	116191697	rs9886216	ILMN_1687583	*CAV1*	G	0.860	26.858	0.079	0.001	0.0005
rs13242816	***CAV1***	7	116198621	rs1997571	ILMN_2149226	*CAV1*	G	1.043	33.782	0.071	0.002	0.001
rs13242816	***CAV1***	7	116198828	rs1997572	ILMN_2149226	*CAV1*	A	1.043	33.989	0.071	0.002	0.001
rs13242816	***CAV1***	7	116191301	rs11773845	ILMN_2149226	*CAV1*	C	1.043	26.462	0.071	0.003	0.001
rs13242816	***CAV1***	7	116186241	rs3807989	ILMN_2149226	*CAV1*	A	1.043	21.402	0.070	0.003	0.001
rs13242816	***CAV1***	7	116198621	rs1997571	ILMN_1735220	*CAV2*	G	1.051	271.187	0.053	0.019	0.009
rs13242816	***CAV1***	7	116198828	rs1997572	ILMN_1735220	*CAV2*	A	1.051	271.394	0.053	0.019	0.009

rs13242816	***CAV1***	7	116191301	rs11773845	ILMN_1735220	*CAV2*	C	1.051	263.867	0.052	0.020	0.010
rs13242816	***CAV1***	7	116186241	rs3807989	ILMN_1735220	*CAV2*	A	1.051	258.807	0.052	0.021	0.010
rs13242816	***CAV1***	7	116197579	rs3807994	ILMN_2149226	*CAV1*	A	1.037	32.74	0.040	0.074	0.034
rs13242816	***CAV1***	7	116196763	rs3807990	ILMN_2149226	*CAV1*	T	1.037	31.924	0.040	0.074	0.034
rs13242816	***CAV1***	7	116198466	rs10953822	ILMN_2149226	*CAV1*	C	1.037	33.627	0.040	0.075	0.034
rs13242816	***CAV1***	7	116198090	rs6466588	ILMN_2149226	*CAV1*	T	1.037	33.251	0.040	0.075	0.034
rs13242816	***CAV1***	7	116197245	rs3807992	ILMN_2149226	*CAV1*	A	1.037	32.406	0.040	0.075	0.034
rs13242816	***CAV1***	7	116193705	rs3757732	ILMN_2149226	*CAV1*	A	1.037	28.866	0.040	0.075	0.034
rs13242816	***CAV1***	7	116193729	rs3757733	ILMN_2149226	*CAV1*	A	1.037	28.89	0.040	0.075	0.034
rs13242816	***CAV1***	7	116190597	rs3801995	ILMN_2149226	*CAV1*	T	1.037	25.758	0.040	0.075	0.034
rs13242816	***CAV1***	7	116190693	rs3815412	ILMN_2149226	*CAV1*	C	1.037	25.854	0.040	0.075	0.034
rs13242816	***CAV1***	7	116194905	rs729949	ILMN_2149226	*CAV1*	A	1.037	30.066	0.040	0.075	0.034
rs13242816	***CAV1***	7	116194384	rs7789117	ILMN_2149226	*CAV1*	T	1.037	29.545	0.040	0.075	0.034
rs13242816	***CAV1***	7	116191812	rs9885998	ILMN_2149226	*CAV1*	A	1.037	26.973	0.040	0.075	0.034
rs13242816	***CAV1***	7	116191697	rs9886216	ILMN_2149226	*CAV1*	G	1.037	26.858	0.040	0.075	0.034
rs13242816	***CAV1***	7	116194228	rs7804372	ILMN_1735220	*CAV2*	A	1.051	266.794	0.039	0.082	0.037
rs148020424	***TBX5***	12	114802361	rs1946295	ILMN_1742362	*TBX5*	A	0.891	43.886	0.074	0.002	0.001
rs148020424	***TBX5***	12	114804898	rs3825215	ILMN_1742362	*TBX5*	G	0.891	41.349	0.074	0.002	0.001
rs148020424	***TBX5***	12	114802138	rs1895585	ILMN_1742362	*TBX5*	A	0.891	44.109	0.073	0.002	0.001
rs148020424	***TBX5***	12	114800813	rs4767237	ILMN_1742362	*TBX5*	A	0.891	45.434	0.073	0.002	0.001
rs148020424	***TBX5***	12	114807035	rs1895582	ILMN_1742362	*TBX5*	G	0.890	39.212	0.072	0.002	0.001
rs148020424	***TBX5***	12	114806885	rs1895583	ILMN_1742362	*TBX5*	A	0.891	39.362	0.070	0.003	0.001
rs148020424	*LOC255480;TBX5*	12	114789226	rs2384407	ILMN_1742362	*TBX5*	G	0.899	57.021	0.067	0.004	0.002
rs148020424	***TBX5***	12	114799974	rs7312625	ILMN_1742362	*TBX5*	G	0.898	46.273	0.066	0.004	0.002
rs148020424	***TBX5***	12	114805057	rs148020424	ILMN_1742362	*TBX5*	G	0.898	41.19	0.064	0.006	0.003
rs148020424	***TBX5***	12	114802760	rs1946293	ILMN_1742362	*TBX5*	G	0.902	43.487	0.060	0.008	0.004
rs148020424	***TBX5***	12	114801772	rs7135659	ILMN_1742362	*TBX5*	G	0.902	44.475	0.060	0.008	0.004
rs148020424	***TBX5***	12	114793240	rs883079	ILMN_1742362	*TBX5*	C	0.905	53.007	0.060	0.008	0.004
rs148020424	***TBX5***	12	114797306	rs7955405	ILMN_1742362	*TBX5*	A	0.908	48.941	0.054	0.017	0.008
rs148020424	***TBX5***	12	114797093	rs10507248	ILMN_1742362	*TBX5*	G	0.908	49.154	0.054	0.017	0.008
rs148020424	*LOC255480;TBX5*	12	114789350	rs2384408	ILMN_1742362	*TBX5*	A	0.899	56.897	0.048	0.032	0.016
rs148020424	*TBX5*	12	114766735	rs10850315	ILMN_1742362	*TBX5*	G	0.916	79.512	0.044	0.048	0.027

rs148020424	***TBX5***	12	114807655	rs11378406	ILMN_1742362	*TBX5*	A	0.912	38.592	0.043	0.055	0.032
rs148020424	*LOC255480;TBX5*	12	114789810	rs2891503	ILMN_1742362	*TBX5*	A	0.913	56.437	0.042	0.062	0.034
rs148020424	*LOC255480;TBX5*	12	114790884	rs1895597	ILMN_1742362	*TBX5*	T	0.912	55.363	0.042	0.063	0.034
rs148020424	*LOC255480;TBX5*	12	114790500	rs7977083	ILMN_1742362	*TBX5*	A	0.916	55.747	0.041	0.065	0.034
rs148020424	***TBX5***	12	114794057	rs2113433	ILMN_1742362	*TBX5*	T	0.909	52.19	0.041	0.066	0.034
rs148020424	*LOC255480;TBX5*	12	114791455	rs7316919	ILMN_1742362	*TBX5*	A	0.917	54.792	0.041	0.068	0.034
rs148020424	*LOC255480;TBX5*	12	114789046	rs7308120	ILMN_1742362	*TBX5*	T	0.907	57.201	0.040	0.072	0.034
Variants identified in combined ethnicity GWAS analysis - eQTLs in European American atrial samples												
rs562408	***SSBP3***	1	54742618	rs562408	ILMN_1814165	*SSBP3*	A	1.112	136.534	0.062	0.007	0.003
rs562408	***SSBP3***	1	54741767	rs603901	ILMN_1814165	*SSBP3*	C	1.110	137.385	0.060	0.008	0.003
rs562408	***SSBP3***	1	54736800	rs9662034	ILMN_1814165	*SSBP3*	C	1.106	142.352	0.056	0.014	0.006
rs562408	***SSBP3***	1	54735974	rs1537430	ILMN_1814165	*SSBP3*	C	1.106	143.178	0.055	0.015	0.006
rs562408	***SSBP3***	1	54732940	rs679200	ILMN_1814165	*SSBP3*	A	1.099	146.212	0.050	0.025	0.010
rs41312411	***SCN5A***	3	38624253	rs3922844	ILMN_1694956	*SCN5A*	T	1.080	66.911	0.040	0.075	0.030
rs3801995	***CAV2***	7	116145957	rs4730743	ILMN_1687583	*CAV1*	A	0.805	-18.882	0.237	2.93×10^{-13}	2.25×10^{-13}
rs3801995	***CAV2***	7	116145849	rs10271007	ILMN_1687583	*CAV1*	A	0.805	-18.99	0.237	2.95×10^{-13}	2.25×10^{-13}
rs3801995	***CAV1***	7	116198621	rs1997571	ILMN_1687583	*CAV1*	G	0.819	33.782	0.184	7.90×10^{-10}	4.20×10^{-10}
rs3801995	***CAV1***	7	116198828	rs1997572	ILMN_1687583	*CAV1*	A	0.819	33.989	0.184	7.90×10^{-10}	4.20×10^{-10}
rs3801995	***CAV1***	7	116186241	rs3807989	ILMN_1687583	*CAV1*	A	0.819	21.402	0.184	8.07×10^{-10}	4.20×10^{-10}
rs3801995	*CAV1;CAV2*	7	116118330	rs926197	ILMN_1687583	*CAV1*	C	0.827	-46.509	0.182	1.00×10^{-9}	4.44×10^{-10}
rs3801995	***CAV2***	7	116145849	rs10271007	ILMN_1735220	*CAV2*	A	1.088	218.415	0.161	2.09×10^{-8}	8.56×10^{-9}
rs3801995	***CAV2***	7	116145957	rs4730743	ILMN_1735220	*CAV2*	A	1.088	218.523	0.161	2.10×10^{-8}	8.56×10^{-9}
rs3801995	*CAV1;CAV2*	7	116118330	rs926197	ILMN_1735220	*CAV2*	C	1.079	190.896	0.133	9.91×10^{-7}	4.89×10^{-7}
rs3801995	***CAV1***	7	116194228	rs7804372	ILMN_1687583	*CAV1*	A	0.859	29.389	0.082	0.001	0.0004
rs3801995	***CAV1***	7	116197579	rs3807994	ILMN_1687583	*CAV1*	A	0.860	32.74	0.080	0.001	0.0004
rs3801995	***CAV1***	7	116198466	rs10953822	ILMN_1687583	*CAV1*	C	0.860	33.627	0.080	0.001	0.0004
rs3801995	***CAV1***	7	116197245	rs3807992	ILMN_1687583	*CAV1*	A	0.860	32.406	0.080	0.001	0.0004
rs3801995	***CAV1***	7	116196763	rs3807990	ILMN_1687583	*CAV1*	T	0.860	31.924	0.080	0.001	0.0004
rs3801995	***CAV1***	7	116193705	rs3757732	ILMN_1687583	*CAV1*	A	0.860	28.866	0.079	0.001	0.0004
rs3801995	***CAV1***	7	116193729	rs3757733	ILMN_1687583	*CAV1*	A	0.860	28.89	0.079	0.001	0.0004
rs3801995	***CAV1***	7	116190597	rs3801995	ILMN_1687583	*CAV1*	T	0.860	25.758	0.079	0.001	0.0004
rs3801995	***CAV1***	7	116190693	rs3815412	ILMN_1687583	*CAV1*	C	0.860	25.854	0.079	0.001	0.0004

rs3801995	***CAV1***	7	116194905 rs729949	ILMN_1687583	*CAV1*	A	0.860	30.066	0.079	0.001	0.0004
rs3801995	***CAV1***	7	116194384 rs7789117	ILMN_1687583	*CAV1*	T	0.860	29.545	0.079	0.001	0.0004
rs3801995	***CAV1***	7	116191812 rs9885998	ILMN_1687583	*CAV1*	A	0.860	26.973	0.079	0.001	0.0004
rs3801995	***CAV1***	7	116191697 rs9886216	ILMN_1687583	*CAV1*	G	0.860	26.858	0.079	0.001	0.0004
rs3801995	***CAV1***	7	116198621 rs1997571	ILMN_2149226	*CAV1*	G	1.043	33.782	0.071	0.002	0.001
rs3801995	***CAV1***	7	116198828 rs1997572	ILMN_2149226	*CAV1*	A	1.043	33.989	0.071	0.002	0.001
rs3801995	***CAV1***	7	116186241 rs3807989	ILMN_2149226	*CAV1*	A	1.043	21.402	0.070	0.003	0.001
rs3801995	***CAV2***	7	116145957 rs4730743	ILMN_2149226	*CAV1*	A	1.040	-18.882	0.066	0.004	0.002
rs3801995	***CAV2***	7	116145849 rs10271007	ILMN_2149226	*CAV1*	A	1.040	-18.99	0.066	0.004	0.002
rs3801995	***CAV1***	7	116198621 rs1997571	ILMN_1735220	*CAV2*	G	1.051	271.187	0.053	0.019	0.007
rs3801995	***CAV1***	7	116198828 rs1997572	ILMN_1735220	*CAV2*	A	1.051	271.394	0.053	0.019	0.007
rs3801995	***CAV1***	7	116186241 rs3807989	ILMN_1735220	*CAV2*	A	1.051	258.807	0.052	0.021	0.009
rs3801995	***CAV1***	7	116197579 rs3807994	ILMN_2149226	*CAV1*	A	1.037	32.74	0.040	0.074	0.030
rs3801995	***CAV1***	7	116196763 rs3807990	ILMN_2149226	*CAV1*	T	1.037	31.924	0.040	0.074	0.030
rs3801995	***CAV1***	7	116198466 rs10953822	ILMN_2149226	*CAV1*	C	1.037	33.627	0.040	0.075	0.030
rs3801995	***CAV1***	7	116197245 rs3807992	ILMN_2149226	*CAV1*	A	1.037	32.406	0.040	0.075	0.030
rs3801995	***CAV1***	7	116193705 rs3757732	ILMN_2149226	*CAV1*	A	1.037	28.866	0.040	0.075	0.030
rs3801995	***CAV1***	7	116193729 rs3757733	ILMN_2149226	*CAV1*	A	1.037	28.89	0.040	0.075	0.030
rs3801995	***CAV1***	7	116190597 rs3801995	ILMN_2149226	*CAV1*	T	1.037	25.758	0.040	0.075	0.030
rs3801995	***CAV1***	7	116190693 rs3815412	ILMN_2149226	*CAV1*	C	1.037	25.854	0.040	0.075	0.030
rs3801995	***CAV1***	7	116194905 rs729949	ILMN_2149226	*CAV1*	A	1.037	30.066	0.040	0.075	0.030
rs3801995	***CAV1***	7	116194384 rs7789117	ILMN_2149226	*CAV1*	T	1.037	29.545	0.040	0.075	0.030
rs3801995	***CAV1***	7	116191812 rs9885998	ILMN_2149226	*CAV1*	A	1.037	26.973	0.040	0.075	0.030
rs3801995	***CAV1***	7	116191697 rs9886216	ILMN_2149226	*CAV1*	G	1.037	26.858	0.040	0.075	0.030
rs3801995	***CAV1***	7	116194228 rs7804372	ILMN_1735220	*CAV2*	A	1.051	266.794	0.039	0.082	0.033
rs3801995	*CAV1;CAV2*	7	116118330 rs926197	ILMN_2149226	*CAV1*	C	1.029	-46.509	0.036	0.109	0.049
rs7312625	***TBX5***	12	114802361 rs1946295	ILMN_1742362	*TBX5*	A	0.891	43.886	0.074	0.002	0.001
rs7312625	***TBX5***	12	114804898 rs3825215	ILMN_1742362	*TBX5*	G	0.891	41.349	0.074	0.002	0.001
rs7312625	***TBX5***	12	114802138 rs1895585	ILMN_1742362	*TBX5*	A	0.891	44.109	0.073	0.002	0.001
rs7312625	***TBX5***	12	114800813 rs4767237	ILMN_1742362	*TBX5*	A	0.891	45.434	0.073	0.002	0.001
rs7312625	***TBX5***	12	114807035 rs1895582	ILMN_1742362	*TBX5*	G	0.890	39.212	0.072	0.002	0.001
rs7312625	***TBX5***	12	114806885 rs1895583	ILMN_1742362	*TBX5*	A	0.891	39.362	0.070	0.003	0.001

rs7312625	*LOC255480;TBX5*	12	114789226	rs2384407	ILMN_1742362	*TBX5*	G	0.899	57.021	0.067	0.004	0.002
rs7312625	***TBX5***	12	114799974	rs7312625	ILMN_1742362	*TBX5*	G	0.898	46.273	0.066	0.004	0.002
rs7312625	***TBX5***	12	114805057	rs148020424	ILMN_1742362	*TBX5*	G	0.898	41.19	0.064	0.006	0.002
rs7312625	***TBX5***	12	114802760	rs1946293	ILMN_1742362	*TBX5*	G	0.902	43.487	0.060	0.008	0.003
rs7312625	***TBX5***	12	114801772	rs7135659	ILMN_1742362	*TBX5*	G	0.902	44.475	0.060	0.008	0.003
rs7312625	***TBX5***	12	114793240	rs883079	ILMN_1742362	*TBX5*	C	0.905	53.007	0.060	0.008	0.003
rs7312625	***TBX5***	12	114797306	rs7955405	ILMN_1742362	*TBX5*	A	0.908	48.941	0.054	0.017	0.007
rs7312625	***TBX5***	12	114797093	rs10507248	ILMN_1742362	*TBX5*	G	0.908	49.154	0.054	0.017	0.007
rs7312625	*LOC255480;TBX5*	12	114789350	rs2384408	ILMN_1742362	*TBX5*	A	0.899	56.897	0.048	0.032	0.014
rs7312625	*TBX5*	12	114766735	rs10850315	ILMN_1742362	*TBX5*	G	0.916	79.512	0.044	0.048	0.023
rs7312625	***TBX5***	12	114807655	rs11378406	ILMN_1742362	*TBX5*	A	0.912	38.592	0.043	0.055	0.027
rs7312625	*LOC255480;TBX5*	12	114789810	rs2891503	ILMN_1742362	*TBX5*	A	0.913	56.437	0.042	0.062	0.030
rs7312625	*LOC255480;TBX5*	12	114790884	rs1895597	ILMN_1742362	*TBX5*	T	0.912	55.363	0.042	0.063	0.030
rs7312625	*LOC255480;TBX5*	12	114789478	rs2384409	ILMN_1742362	*TBX5*	A	0.908	56.769	0.041	0.064	0.030
rs7312625	*LOC255480;TBX5*	12	114790500	rs7977083	ILMN_1742362	*TBX5*	A	0.916	55.747	0.041	0.065	0.030
rs7312625	***TBX5***	12	114794057	rs2113433	ILMN_1742362	*TBX5*	T	0.909	52.19	0.041	0.066	0.030
rs7312625	*LOC255480;TBX5*	12	114791455	rs7316919	ILMN_1742362	*TBX5*	A	0.917	54.792	0.041	0.068	0.030
rs7312625	*LOC255480;TBX5*	12	114789046	rs7308120	ILMN_1742362	*TBX5*	T	0.907	57.201	0.040	0.072	0.030
rs7312625	***TBX5***	12	114792236	rs6489956	ILMN_1742362	*TBX5*	T	0.912	54.011	0.039	0.085	0.035
rs7312625	***TBX5***	12	114814286	rs7964303	ILMN_1742362	*TBX5*	T	0.919	31.961	0.037	0.102	0.044
rs7312625	*LOC255480;TBX5*	12	114791528	rs1895596	ILMN_1742362	*TBX5*	A	0.905	54.719	0.036	0.110	0.049
rs452036	***MYH6***	14	23863802	rs445754	ILMN_1702105	*EFS*	T	1.091	-28.841	0.036	0.113	0.050
Variants identified in African American ethnicity GWAS analysis - eQTLs in European American atrial samples												
rs3922844	***SCN5A***	3	38624253	rs3922844	ILMN_1694956	*SCN5A*	T	1.080	66.911	0.040	0.075	0.003
rs1895582	***TBX5***	12	114807035	rs1895582	ILMN_1742362	*TBX5*	G	0.890	39.212	0.072	0.002	0.0001
rs1895582	***TBX5***	12	114799974	rs7312625	ILMN_1742362	*TBX5*	G	0.898	46.273	0.066	0.004	0.0001
rs1895582	***TBX5***	12	114807035	rs1895582	ILMN_2376958	*TBX5*	G	0.947	39.212	0.024	0.303	0.022

Filtered at FDR_dur<0.05. Grey highlighting of rows indicates eQTLs that did not reach genome-wide FDR. There were no significant eQTLs for variants identified in the African American ancestry analysis or the combined ancestry analysis in the African American atrial samples. TSS, transcription start site; SNP, single nucleotide polymorphism; Chr, chromosome. MA, minor allele in the atrial tissue biobank. *Bold text indicates variant located in gene, otherwise closest gene/s. **Fold change in expression when dosage of MA increases by 1. †Explained

(adjusted) variation in probe ID by dosage of rsID/squared adjusted Pearson correlation. ‡Genome-wide false discovery rate. ††False discovery rate specific to variant set.

Table S9. Significant eQTLs in the GTEx database.

SNP	Chr	Closest gene	Ancestry	eQTL gene	Smallest eQTL P-value	Tissue
P-wave duration						
rs562408	1p32	*SSBP3*	EUR	*SSBP3*	$3.47x10^{-12}$	Atrial appendage
			EUR	*SSBP3*	$3.21x10^{-6}$	Left ventricle
			EUR	*MRPL37*	$2.9x10^{-10}$	Atrial appendage
rs1895582	12q24	*TBX5*	AA	*TBX5*	$3.84x10^{-6}$	Left ventricle
rs1467026	3p25	*CAND2*	EA+AA	*CAND2*	$7.5x10^{-27}$	Skeletal muscle
				KRT18P17	$9.19x10^{-11}$	Skeletal muscle
				RP11-767C1.2	$1.2x10^{-9}$	Skeletal muscle
P-wave terminal force						
rs11073730	15q25	*ALPK3*	EUR	*RP11-182J1.16*	$1.71x10^{-7}$	Atrial appendage
			EUR	*CSPG4P11*	$1.79x10^{-7}$	Atrial appendage
			EUR	*AC103965.1*	$2.82x10^{-8}$	Atrial appendage
			EUR	*AC103965.1*	$9.04x10^{-8}$	Left ventricle
			EUR	*RP11-182J1.16*	$9.83x10^{-6}$	Left ventricle
			EUR	*WDR73*	$1.12x10^{-7}$	Left ventricle
			EUR	*AC103965.1*	$9.34x10^{-10}$	Skeletal muscle
			EUR	*ALPK3*	$1.12x10^{-17}$	Skeletal muscle
			EUR	*CSPG4P11*	$1.08x10^{-5}$	Skeletal muscle
			EUR	*WDR73*	$1.37x10^{-8}$	Skeletal muscle

Chr, chromosome; EUR, European ancestry; AA, African American ancestry

Table S10. Summary of genome-wide significant genetic associations for P-wave terminal force in participants of European and African ancestry.

SNP	Chr	Location relative to gene	Closest gene	Minor/major allele	MAF, %	Minor allele effect, β (SE)	P value	Variance explained, %
European ancestry (n=33,955)								
rs12090194	1p13	Intronic	*KCND3*	T/C	32	119 (13)	$5.56x10^{-19}$	0.25
rs11242779	6p25	Intergenic	*C6orf195*	C/T	49	-71 (13)	$2.10x10^{-8}$	0.09
rs445754	14q11	Intronic	*MYH6*	T/G	23	131 (15)	$3.22x10^{-18}$	0.22
rs201517563	15q25	Intronic	*ALPK3/NMB*	TA/T	47	-86 (15)	$3.95x10^{-9}$	0.10
rs4435363	19q13	Intronic	*PPP5D1*	G/A	20	-93 (16)	$3.84x10^{-9}$	0.10
African ancestry (n=6778)								
rs10832139	11p15	Intergenic	*SPON1*	G/A	41	214 (38)	$2.44x10^{-8}$	0.47

Adjusted for age and sex. Chr, chromosome; MAF, Minor allele frequency; SE, standard error.

Table S11. Summary of genetic associations for P-wave terminal force in combined ancestry analysis

SNP	Chr	Location relative to gene	Closest gene	Minor / major allele	MAF, %	Minor allele effect, β (SE)	P value	Variance explained, %
rs4839185	1p13	Intronic	*KCND3*	C/T	31%	117 (13)	$3.14x10^{-20}$	0.20
rs11099412	4q28	Intergenic	*PCDH18*	A/G	11%	244 (41)	$2.52x10^{-9}$	0.09
rs11242779	6p25	Intergenic	*C6orf195*	C/T	48%	-72 (12)	$7.90x10^{-9}$	0.09
rs445754	14q11	Intronic	*MYH6*	T/G	24%	136 (14)	$4.20x10^{-22}$	0.23
rs2115630	15q25	Intronic	*ALPK3/NMB*	T/C	46%	85 (14)	$6.38x10^{-10}$	0.09
rs4435363	19q13	Intronic	*PPP5D1*	G/A	20%	-96 (16)	$1.15x10^{-9}$	0.09

Adjusted for age and sex. Chr, chromosome; MAF, minor allele frequency; SD, standard error.

Table S12. Shared associations between present and previous GWAS of P-wave terminal force.

rsID present study	Chr	Closest gene	Ancestry	rsID previous study	LD, r^2 CEU/YRI	PR-interval	P-wave duration	PR-segment	Heart rate
rs12090194	1p13	*KCND3*	EUR	rs2798334	0.20/0.01		EUR[12]		
rs4839185	1p13	*KCND3*	EUR+AA	rs2798334	NA/NA		EUR[12]		
rs445754	14q11	*MYH6*	EUR	rs452036	0.65/0.26		EUR*		EUR[20], AA[73]
				rs365990	0.62/0.26				EUR[7, 21], AA[73]

Overview of shared genetic loci between present and previous GWAS. The variants identified in previous studies are reported with rsID, LD information, previously associated electrocardiographic phenotype, and ancestry group. Chr, chromosome; LD, Linkage disequilibrium; CEU, Utah residents with Northern and Western European ancestry from the 1000 Genomes; YRI, Yoruba in Ibadan, Nigeria, African ancestry group from the 1000 Genomes; NA, not available in SNAP LD search; EUR, European ancestry; AA, African American ancestry. *Variant from the present study on P-wave duration.

Table S13. Significant eQTLs in left atrial tissue samples for genetic loci associated with P-wave terminal force.

Index SNP	Closest gene/s*	Chr	Position	eQTL SNP	Probe ID	Gene	MA	Fold change**	TSS distance	r^2†	FDR_gw‡	FDR_dur††
Variants identified in European ancestry GWAS analysis - eQTLs in European American atrial samples												
rs201517563	***ALPK3***	15	85361960	rs4633690	ILMN_2347592	*NMB*	T	1.122	-160.166	0.060	0.009	0.024
rs201517563	***ALPK3***	15	85363708	rs11854291	ILMN_2347592	*NMB*	C	1.123	-161.914	0.060	0.009	0.024
rs201517563	***ALPK3***	15	85364516	rs2115630	ILMN_2347592	*NMB*	T	1.123	-162.722	0.060	0.009	0.024
rs201517563	*ALPK3*	15	85355841	rs35828350	ILMN_2347592	*NMB*	A	0.874	-154.047	0.058	0.011	0.024
rs201517563	*ZNF592*	15	85276935	rs58581703	ILMN_2347592	*NMB*	T	1.117	-75.141	0.053	0.019	0.031
rs201517563	***ZNF592***	15	85318065	rs11633377	ILMN_2347592	*NMB*	G	0.888	-116.271	0.051	0.024	0.031
rs201517563	***ZNF592***	15	85344550	rs12912388	ILMN_2347592	*NMB*	A	0.888	-142.756	0.051	0.024	0.031
rs201517563	***ZNF592***	15	85343980	rs35960805	ILMN_2347592	*NMB*	G	0.888	-142.186	0.051	0.024	0.031
rs201517563	***ZNF592***	15	85347709	rs17601029	ILMN_2347592	*NMB*	G	0.888	-145.915	0.050	0.026	0.031
rs201517563	***ALPK3***	15	85373498	rs35545192	ILMN_2347592	*NMB*	CT	0.890	-171.704	0.049	0.030	0.033
rs201517563	***ALPK3***	15	85377441	rs35808647	ILMN_2347592	*NMB*	A	0.891	-175.647	0.048	0.033	0.035
rs201517563	***ALPK3***	15	85374112	rs2340652	ILMN_2347592	*NMB*	G	0.891	-172.318	0.046	0.040	0.040
rs201517563	***SEC11A***	15	85242529	rs8029660	ILMN_2347592	*NMB*	A	1.112	-40.735	0.045	0.046	0.044
Variants identified in combined ancestry GWAS analysis - eQTLs in European American atrial samples												
rs2115630	***ALPK3***	15	85361960	rs4633690	ILMN_2347592	*NMB*	T	1.122	-160.166	0.060	0.009	0.011
rs2115630	***ALPK3***	15	85363708	rs11854291	ILMN_2347592	*NMB*	C	1.123	-161.914	0.060	0.009	0.011
rs2115630	***ALPK3***	15	85364516	rs2115630	ILMN_2347592	*NMB*	T	1.123	-162.722	0.060	0.009	0.011
rs2115630	***SEC11A***	15	85253258	rs8033459	ILMN_2347592	*NMB*	T	1.124	-51.464	0.059	0.009	0.011
rs2115630	***ALPK3***	15	85372645	rs6496452	ILMN_2347592	*NMB*	T	1.124	-170.851	0.059	0.010	0.011
rs2115630	*ALPK3*	15	85355841	rs35828350	ILMN_2347592	*NMB*	A	0.874	-154.047	0.058	0.011	0.011
rs2115630	***SEC11A***	15	85255385	rs8027779	ILMN_2347592	*NMB*	C	1.118	-53.591	0.054	0.017	0.011
rs2115630	***ZNF592***	15	85334952	rs28595395	ILMN_2347592	*NMB*	C	1.121	-133.158	0.054	0.017	0.011
rs2115630	*ALPK3*	15	85357649	rs56864281	ILMN_2347592	*NMB*	A	0.882	-155.855	0.054	0.017	0.011
rs2115630	***ZNF592***	15	85333396	rs61074241	ILMN_2347592	*NMB*	T	0.877	-131.602	0.053	0.018	0.011
rs2115630	*ZNF592*	15	85282635	rs1030863	ILMN_2347592	*NMB*	T	1.118	-80.841	0.053	0.018	0.011
rs2115630	***ZNF592***	15	85349231	rs35630683	ILMN_2347592	*NMB*	C	0.883	-147.437	0.053	0.018	0.011
rs2115630	***ZNF592***	15	85318080	rs9788687	ILMN_2347592	*NMB*	T	1.117	-116.286	0.053	0.019	0.011

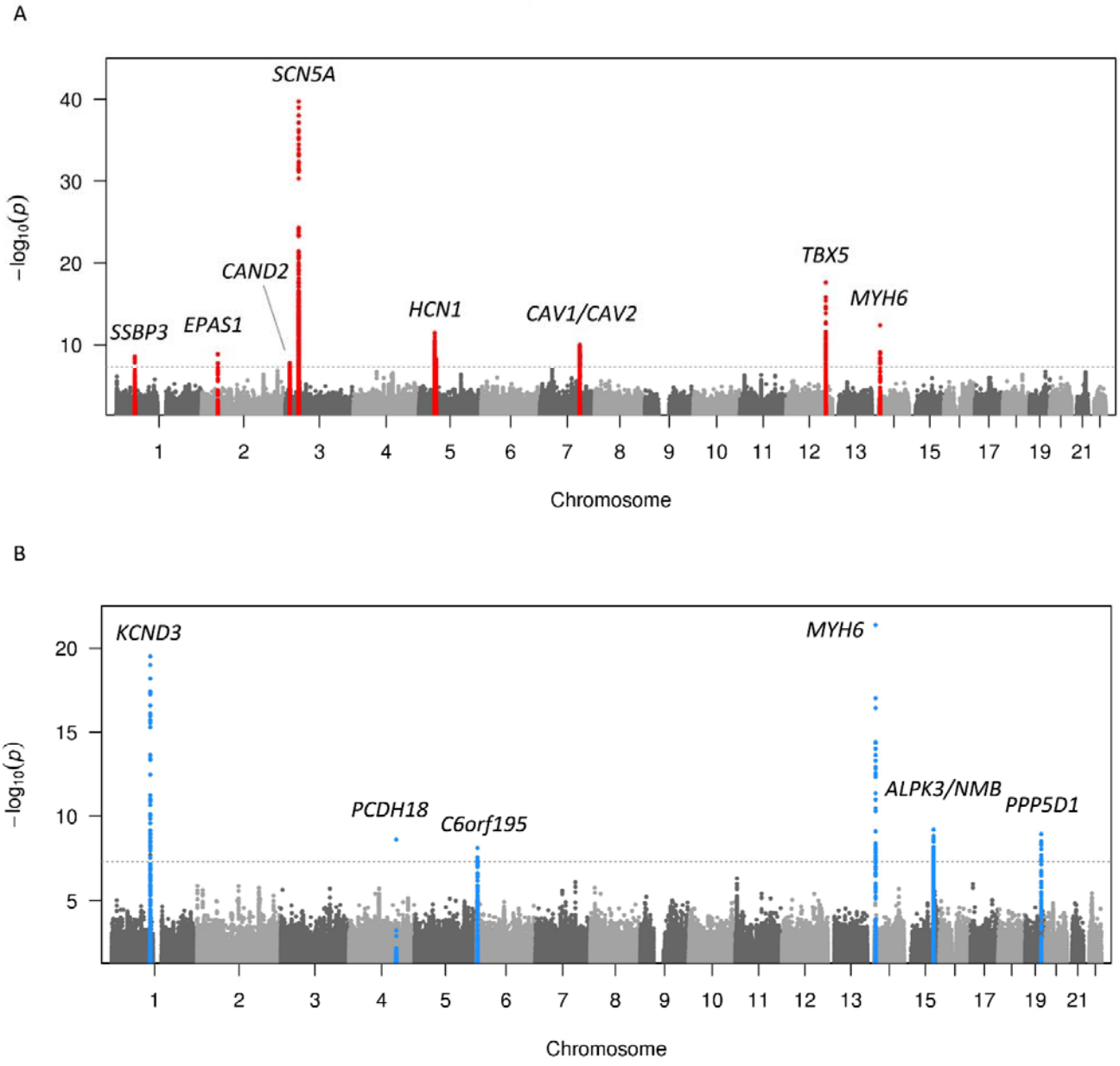
rs2115630	*ZNF592*	15	85276935	rs58581703	ILMN_2347592	*NMB*	T	1.117	-75.141	0.053	0.019	0.011
rs2115630	***ZNF592***	15	85320924	rs202221250	ILMN_2347592	*NMB*	AC	1.117	-119.13	0.053	0.019	0.011
rs2115630	***ZNF592***	15	85323568	rs55646601	ILMN_2347592	*NMB*	T	1.117	-121.774	0.052	0.020	0.011
rs2115630	*ZNF592*	15	85350081	rs11073729	ILMN_2347592	*NMB*	C	1.115	-148.287	0.052	0.020	0.011
rs2115630	***ZNF592***	15	85297793	rs6496401	ILMN_2347592	*NMB*	T	1.116	-95.999	0.052	0.020	0.011
rs2115630	*ZNF592*	15	85280212	rs34570071	ILMN_2347592	*NMB*	A	0.885	-78.418	0.052	0.022	0.011
rs2115630	*SEC11A*	15	85273880	rs12592554	ILMN_2347592	*NMB*	A	1.116	-72.086	0.052	0.022	0.011
rs2115630	*ZNF592*	15	85277888	rs8028490	ILMN_2347592	*NMB*	A	1.116	-76.094	0.051	0.023	0.011
rs2115630	***ZNF592***	15	85318065	rs11633377	ILMN_2347592	*NMB*	G	0.888	-116.271	0.051	0.024	0.011
rs2115630	***ZNF592***	15	85302373	rs12899981	ILMN_2347592	*NMB*	A	0.888	-100.579	0.051	0.024	0.011
rs2115630	***ZNF592***	15	85337699	rs12903134	ILMN_2347592	*NMB*	A	0.888	-135.905	0.051	0.024	0.011
rs2115630	***ZNF592***	15	85322351	rs12908549	ILMN_2347592	*NMB*	G	0.888	-120.557	0.051	0.024	0.011
rs2115630	***ZNF592***	15	85344550	rs12912388	ILMN_2347592	*NMB*	A	0.888	-142.756	0.051	0.024	0.011
rs2115630	***ZNF592***	15	85337800	rs35726233	ILMN_2347592	*NMB*	T	0.888	-136.006	0.051	0.024	0.011
rs2115630	***ZNF592***	15	85311382	rs35758837	ILMN_2347592	*NMB*	T	0.888	-109.588	0.051	0.024	0.011
rs2115630	***ZNF592***	15	85343980	rs35960805	ILMN_2347592	*NMB*	G	0.888	-142.186	0.051	0.024	0.011
rs2115630	***ZNF592***	15	85319692	rs36033486	ILMN_2347592	*NMB*	G	0.888	-117.898	0.051	0.024	0.011
rs2115630	***ZNF592***	15	85321220	rs62019469	ILMN_2347592	*NMB*	C	0.888	-119.426	0.051	0.024	0.011
rs2115630	*ZNF592*	15	85288087	rs62019463	ILMN_2347592	*NMB*	A	0.888	-86.293	0.051	0.024	0.011
rs2115630	*ZNF592*	15	85285536	rs17599989	ILMN_2347592	*NMB*	C	0.888	-83.742	0.051	0.024	0.011
rs2115630	*ZNF592*	15	85280210	rs35738019	ILMN_2347592	*NMB*	C	0.888	-78.416	0.051	0.024	0.011
rs2115630	*ZNF592*	15	85280792	rs60957376	ILMN_2347592	*NMB*	G	0.888	-78.998	0.051	0.024	0.011
rs2115630	***ZNF592***	15	85316465	rs12914760	ILMN_2347592	*NMB*	T	0.887	-114.671	0.051	0.024	0.011
rs2115630	***ZNF592***	15	85298662	rs12910012	ILMN_2347592	*NMB*	C	0.888	-96.868	0.051	0.024	0.011
rs2115630	*SEC11A*	15	85268036	rs62021226	ILMN_2347592	*NMB*	C	0.888	-66.242	0.050	0.025	0.011
rs2115630	***ZNF592***	15	85294469	rs62019464	ILMN_2347592	*NMB*	A	0.888	-92.675	0.050	0.025	0.011
rs2115630	*SEC11A*	15	85264461	rs58416181	ILMN_2347592	*NMB*	A	0.888	-62.667	0.050	0.025	0.011
rs2115630	***ZNF592***	15	85324467	rs11633267	ILMN_2347592	*NMB*	C	0.888	-122.673	0.050	0.025	0.011
rs2115630	***ZNF592***	15	85347709	rs17601029	ILMN_2347592	*NMB*	G	0.888	-145.915	0.050	0.026	0.011
rs2115630	***ZNF592***	15	85331271	rs34342559	ILMN_2347592	*NMB*	G	0.888	-129.477	0.049	0.028	0.011
rs2115630	***ZNF592***	15	85331629	rs35557864	ILMN_2347592	*NMB*	G	0.888	-129.835	0.049	0.028	0.011
rs2115630	***ZNF592***	15	85331493	rs62019472	ILMN_2347592	*NMB*	G	0.888	-129.699	0.049	0.028	0.011

rs2115630	***ALPK3***	15	85373498	rs35545192	ILMN_2347592	*NMB*	CT	0.890	-171.704	0.049	0.030	0.012
rs2115630	***ALPK3***	15	85377441	rs35808647	ILMN_2347592	*NMB*	A	0.891	-175.647	0.048	0.033	0.013
rs2115630	***SEC11A***	15	85258203	rs35524990	ILMN_2347592	*NMB*	C	0.890	-56.409	0.048	0.034	0.013
rs2115630	***SEC11A***	15	85257599	rs34900908	ILMN_2347592	*NMB*	A	0.890	-55.805	0.048	0.034	0.013
rs2115630	***SEC11A***	15	85256159	rs62021219	ILMN_2347592	*NMB*	T	0.890	-54.365	0.047	0.034	0.013
rs2115630	***SEC11A***	15	85256303	rs12907808	ILMN_2347592	*NMB*	C	0.890	-54.509	0.047	0.034	0.013
rs2115630	***SEC11A***	15	85250253	rs4643294	ILMN_2347592	*NMB*	T	0.890	-48.459	0.047	0.035	0.013
rs2115630	***SEC11A***	15	85248133	rs35316992	ILMN_2347592	*NMB*	G	0.891	-46.339	0.047	0.035	0.013
rs2115630	***SEC11A***	15	85240403	rs12908699	ILMN_2347592	*NMB*	T	0.891	-38.609	0.047	0.036	0.013
rs2115630	***SEC11A***	15	85231585	rs34028043	ILMN_2347592	*NMB*	A	0.892	-29.791	0.046	0.038	0.014
rs2115630	***ALPK3***	15	85374112	rs2340652	ILMN_2347592	*NMB*	G	0.891	-172.318	0.046	0.040	0.014
rs2115630	*ZNF592*	15	85354596	rs11073730	ILMN_2347592	*NMB*	T	1.104	-152.802	0.042	0.063	0.026

Filtered at FDR_ptf<0.05. Grey highlighting of rows indicates eQTLs that did not reach genome-wide FDR. There were no significant eQTLs for variants identified in the African American and combined ancestry analysis in the African American atrial samples and no significant eQTLs for variants identified in the African American ancestry analysis in the European ancestry atrial samples. TSS, transcription start site; SNP, single nucleotide polymorphism; Chr, chromosome; MA, minor allele in the atrial tissue biobank. *Bold text indicates variant located in gene, otherwise closest gene/s. **Fold change in expression when dosage of MA increases by 1. †Explained (adjusted) variation in probe ID by dosage of rsID/squared adjusted Pearson correlation. ‡Genome-wide false discovery rate. ††False discovery rate specific to variant set.

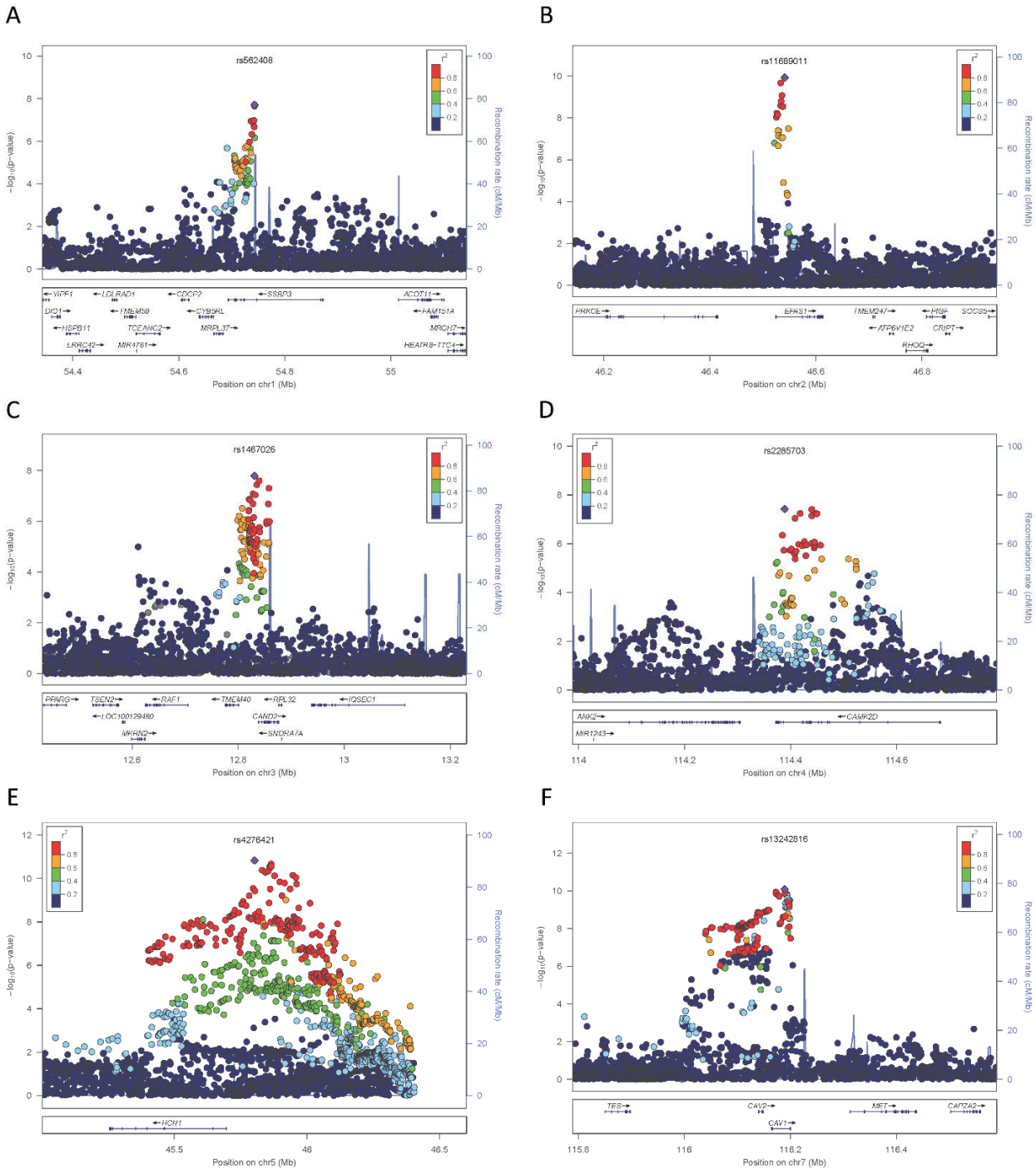
Supplemental Figures

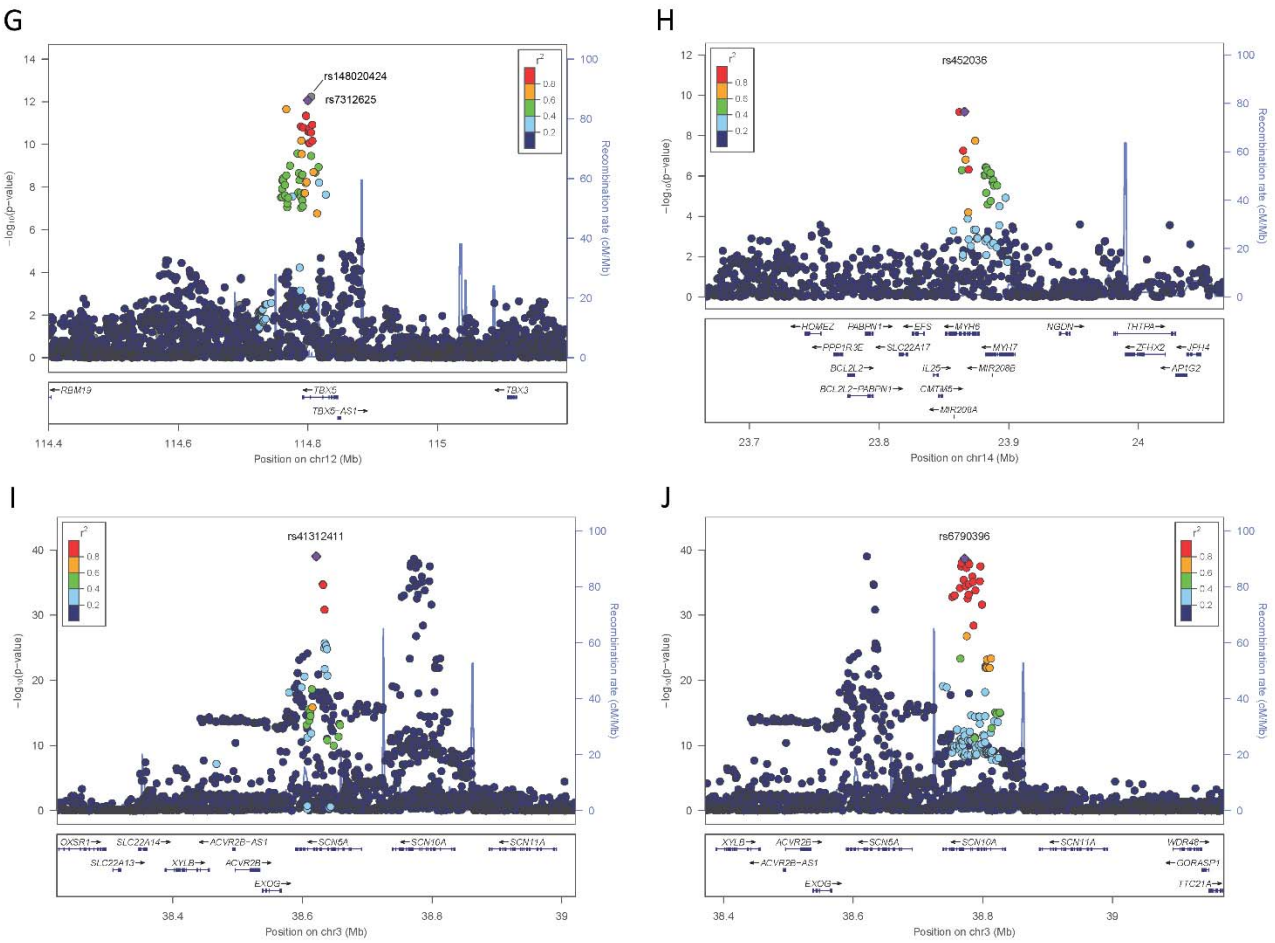
Figure S1. Manhattan plots of meta-analyses results for combined ancestry genome-wide association studies of maximum P-wave duration and P-wave terminal force



A. P-wave duration; significant genetic loci are highlighted in red**. B.** P-wave terminal force; significant genetic loci are highlighted in blue. Dashed lines represent the genome-wide significance threshold (p=5x10^{-8}).

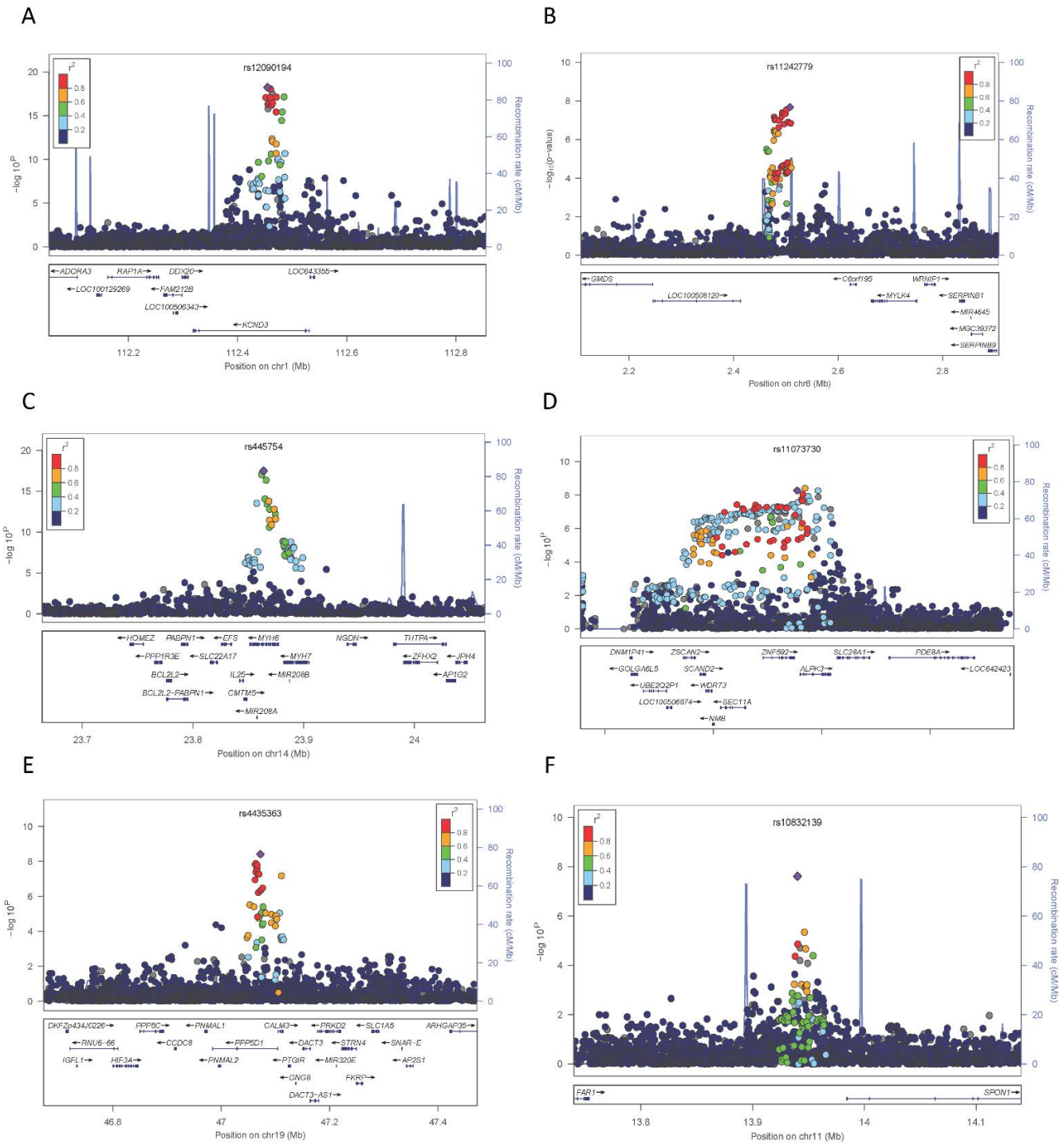
Figure S2. Regional plots of genetic loci significantly associated with P-wave maximum duration in Europeans.





At each novel locus, all SNPs in a limited region are plotted by chromosomal location and p-value (left vertical axis) from the meta-analysis. The most significant SNP is plotted as a diamond-shape, and all other SNPs are colored according to their linkage disequilibrium (LD) with the top SNP. For the *TBX5* locus (G), this is true for the second most significant variant, due to missing LD data for the most significant variant (grey). Red depicts the highest LD while blue depicts the lowest, as shown in the legend in each plot. Estimated recombination rate is displayed for each region (right vertical axis). Gene annotation is presented below the plot. LD and recombination information is based on the 1000 Genomes November 2014 EUR release. All plots were made using LocusZoom.[74] **A-H** shows novel loci, whereas **I-J** shows replicated loci. **A**, *SSBP3*; **B**, *EPAS1*; **C**, *CAND2*; **D**, *CAMK2D*; **E**, *HCN1*; **F**, *CAV1/2*; **G**, *TBX5*; **H**, *MYH6*; **I**, *SCN5A*; **J**, *SCN10A*.

Figure S3. Regional plots of genetic loci significantly associated with P-wave terminal force.



At each novel locus, all SNPs in a limited region are plotted by chromosomal location and p-value (left vertical axis) from the meta-analysis. The most significant SNP is plotted as a diamond-shape, and all

other SNPs are colored according to their linkage disequilibrium (LD) with the top SNP. Red depicts the highest LD while blue depicts the lowest, as shown in the legend in each plot. Estimated recombination rate is displayed for each region (right vertical axis). Gene annotation is presented below the plot. LD and recombination information is based on the 1000 Genomes November 2014 EUR release. All plots were made using LocusZoom.[74] **A**, *KCND3*; **B**, *C6orf195*; **C**, *MYH6*; **D**, *ALPK3/NMB*; **E**, *PPP5D1*; **F**, *SPON1*.

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