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Roselli, Anna Carolina

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SUPPLEMENTARY TEXT AND TABLES
Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation

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1. SUPPLEMENTARY TABLES

Supplementary Table 1. Baseline characteristics for the GWAS meta-analysis

Race	Study name	Status/study	Total (n)	AF (*n*)	Males (%)	Age at DNA collection (mean±SD)	Age at DNA collection (range)	Age at AF onset (mean± SD)	HTN *n* (%)	BMI kg/m^2 (mean±SD)	DM n (%)	MI n (%)	HF n (%)
EUR							**Prevalent**						
	AFLMU/	Cases	448	–	303 (68)	51±8	29-65	–	182 (41)	28±5	35 (8)	4 (1)	8 (2)
	KORA	Referents	438	–	221 (50)	56±7	45-69	–	198 (45)	28±4	18 (4)	0	3 (1)
	AGES	Cases	199	–	128 (64)	78±5	68-95	–	184 (92)	27±5	34 (17)	51 (26)	47 (24)
		Referents	2989	–	1213 (41)	76±5	66-95	–	2387 (80)	–	332 (11)	346 (12)	50 (2)
	Beat-AF	Cases	1520	–	1090 (72)	68±12	19-94	61±13	1151 (76)	27±5	195 (13)	298 (20)	215 (14)
		Referents	1520	–	705 (46)	36±5	23-44	–	212 (14)	25±4	7 (1)	0	0 (0)
	BioMe	Cases	291	–	200 (69)	75±9	56-89	–	263 (90)	28±5	47 (18)	21 (7)	122 (42)
		Referents	860	–	474 (55)	70±9	37-89	–	614 (71)	27±6	164 (20)	29 (3)	98 (11)
	BioVU	Cases	428	–	245 (57)	72±12	24-98	–	356 (83)	29±6	117 (27)	17 (4)	--
		Referents	9757	–	4911 (50)	62±17	18-100	–	6458 (66)	29±8	2018 (21)	313 (3)	–
	CCAF	Cases	606	–	460 (76)	59±11	20-85	52±12	331 (55)	30±6	59 (10)	0	0
		Referents	2930	–	1109 (38)	29±22	0-87	–	–	–	–	–	–
	COROGENE	Cases	248	–	161 (65)	74±8	44-91	–	128 (52)	28±5	69 (28)	132 (53)	91 (37)
		Referents	1978	–	1373 (69)	65±12	24-100	–	1042 (53)	28±5	388 (20)	578 (29)	482 (24)
	FHS	Cases	270	–	160 (60)	77±10	45–97	71±11	191 (71)	27±5	43 (16)	66 (24)	59 (22)
		Referents	4134	–	1798 (44)	65±13	31–101	–	2025 (49)	28±5	327 (8)	229 (6)	53 (1)
	GS_SFHS	Cases	203	–	79 (39)	67±11	39-99	–	85 (42)	28±5	23 (11)	24 (12)	–
		Referents	6651	–	3974 (60)	54±12	18-98	–	1134 (17)	27±5	290 (4)	391 (5)	–
	LURIC	Cases	368	–	262 (71)	66±9	32-88	–	278 (74)	28±4	167 (46)	117 (32)	112 (30)
		Referents	2666	–	1861 (70)	62±11	17-92	–	1930 (72)	27±4	1050 (39)	1146 (43)	472 (18)
	MDCS	Cases	119	–	84 (71)	64±6	48-73	58±8	101 (85)	28±4	8 (7)	22 (18)	12 (10)
		Referents	5758	–	2485 (43)	58±6	45-73	–	3775 (66)	26±4	276 (5)	167 (3)	16 (0.3)
	MGH AF study	Cases	366	–	295 (81)	53±101	21-77	46±12	85.8 (23)	28±5	12 (3)	4 (1)	10 (3)
		Referents	911	–	485 (53)	48±9	18-83	–	–	–	–	–	–
	MGH CAMP	Cases	665	–	476 (72)	61±10	27-79	–	41 (6)	–	176 (26)	161 (24)	232 (35)
		Referents	2128	–	1197 (56)	60±12	30-81	–	66 (3)	–	542 (25)	359 (17)	318 (15)
	SHIP	Cases	106	–	67 (63)	65±11	21-80	–	58 (55)	30±5	24 (23)	14 (13)	29 (27)
		Referents	1815	–	859 (47)	50±15	20-80	–	437 (24)	27±5	192 (11)	54 (3)	158 (9)
	WTCCC2	Cases	330	–	168 (51)	70±12	45-92	70±12	197 (60)	–	–	–	–
	Munich	Referents	797	–	410 (51)	63±11	51-83	–	–	–	–	–	–
							Incident						
	AGES	Cohort	2694	586	303 (52)	78±5	67-95	83±6	510 (87)	27±4	83 (14)	102 (17)	41 (7)
	ARIC	Cohort	8880	1420	4457 (47)	54±6	44-66	71±8	2547 (27)	27±5	818 (9)	390 (4)	360 (4)
	CHS	Cohort	3201	1011	1240 (39)	72±5	65-98	82±6	1679 (53)	26±4	377 (12)	0	0
	FHS	Cohort	4134	610	1798 (44)	65±13	31–101	78±11	2025 (49)	28±5	327 (8)	229 (6)	53 (1)
	MDCS	Cohort	5758	1113	2485 (43)	58±6	45-73	73±7	3775 (66)	26±4	276 (5)	167 (3)	16 (0.3)
	MESA	Cohort	2527	155	1206 (48)	63±10	44-84	76±8	975 (39)	28±5	151 (6)	62 (3)	52 (2)
	PIVUS	Cohort	949	154	474 (50)	70±0.2	70-71	–	650 (69)	27±4	123 (13)	65 (7)	32 (3)
	PREVEND	Cohort	3520	113	1811 (51)	50±12	28-75	68±8	974 (28)	26±4	133 (4)	86 (2)	6 (0.2)
	PROSPER	Cohort	5244	505	2524 (48)	75±3	69-83	78±3	3257 (62)	27±4	544 (10)	708 (14)	0
	TWINGENE	Cohort	6813	403	3239 (48)	65±8	47-94	69±10	3585 (53)	26±4	664 (10)	287 (4)	78 (1)
	ULSAM	Cohort	1120	294	1120 (100)	71±1	69-74	76±8	804 (72)	26±3	121 (11)	90 (8)	13 (1)
	WGHS	Cohort	20856	959	0 (0)	54±7	43- 89	69±8	5024 (24)	26±5	503 (2)	–	–
							Combined prevalent and incident						
	ANGES	Prev + inc	779	226	496 (64)	64±10	36-88	69±10	479 (62)	28±4	232 (30)	272 (35)	100 (13)
	FINCAVAS	Prev + inc	2879	971	1737 (60)	59±11	19-85	64±12	2056 (71)	28±5	484 (17)	780 (27)	313 (11)
	RS1	Prev + inc	5947	1025	2410 (41)	69±9	55-99	78±8*	3433 (58)	26±4	674 (11)	419 (7)	210 (4)
	RS2	Prev + inc	1806	146	831 (46)	65±8	55-95	74±9*	1309 (73)	27±4	233 (13)	101 (6)	26 (1)
	RS3	Prev + inc	3030	121	1321 (44)	57±7	46-97	63±10*	1479 (49)	28±5	234 (8)	79 (3)	12 (0.4)
AA							**Prevalent**						
	BioMe	Cases	174	–	67 (39)	65±13	30-89	–	166 (95)	31±9	73 (50)	18 (10)	96 (55)
		Referents	2132	–	723 (34)	56±14	22-89	–	1591 (75)	31±8	650 (33)	70 (3)	294 (14)
							Incident						
	ARIC	Cohort	2768	278	1068 (37)	53±6	44-66	70±7	1606 (56)	30±6	547 (19)	110 (4)	189 (7)
	CHS	Cohort	801	189	296 (37)	73±6	65-93	82±7	475 (59)	29±6	198 (25)	68 (9)	50 (6)
AS							**Prevalent**						
	Biobank Japan	Cases	837	–	572 (68)	68±10	25-94	–	–	24±4	394 (47)	70 (8)	219 (26)
		Referents	3293	–	1810 (55)	52±16	3-96	–	–	22±4	220 (9)	37 (2)	18 (1)
HISP	**BioMe**	Cases	277	–	136 (49)	70±12	31-89	–	268 (97)	29±6	129 (51)	37 (13)	160 (58)
		Referents	3081	–	1114 (36)	58±15	20-89	–	2214 (72)	30±7	1035 (37)	140 (5)	372 (12)
BRAZ	**SPHFC**	Cases	197	–	131 (63)	60±12	24-84	–	130 (66)	29±6	51 (26)	51 (26)	197 (100)
		Referents	758	–	478 (67)	56±13	18-93	–	473 (62)	27±6	214 (28)	222 (29)	758 (100)

Abbreviations: AF, atrial fibrillation; AA, African American; AS, Asian; BMI, body mass index; BRAZ, Brazilian; DM, diabetes mellitus; EUR, European ancestry; HF, heart failure; HISP, Hispanic; HTN, hypertension; MI, myocardial infarction; SPHFC, Sao Paulo Heart Failure Cohort. *Incident cases only.

Supplementary Table 2. Baseline characteristics for the ExWAS meta-analysis

Race	Study name	Status /study	Total (*n*)	Males (%)	Age at DNA collection (mean±SD)	Age at DNA collection (range)	Age of AF onset (mean±SD)	HTN *n* (%)	BMI kg/m^2 (mean±SD)	DM *n* (%)	MI n (%)	HF *n* (%)
EUR	**AFLMU/**	Cases_all	2347	1760 (75)	57±11	17-93	55±12	1058 (45)	-	-	-	-
	KORA/MGH	Cases_AFNET	1645	1219 (74)	58±10	17-93	50±13	777 (47)	28±5	171 (7)	188 (13)	-
		Cases_MGH	702	541 (77)	56±12	18-86	56±10	281 (40)	29±6	35 (5)	25 (4)	43 (6)
		Referents	2844	1368 (48)	49±13	25-74	NA	993 (35)	27±5	81 (3)	52 (2)	87 (3)
	AGES	Cases incident	354	180 (51)	78±6	67-95	82±6	307 (87)	28±4	45 (13)	54 (15)	13 (4)
		Cases prevalent	280	165 (59)	78±5	67-95	-	256 (91)	27±5	44 (16)	61 (22)	28 (10)
		Referents	2341	1090 (41)	77±6	66-99	-	2142(80)	27±5	44 (16)	304 (11)	41 (2)
	ARIC	Cases	1452	837 (58)	57±5	45-65	70±7	602 (41)	28±5	204 (14)	129 (9)	115 (8)
		Referents	9215	1786 (45)	54±6	44-66	-	983 (25)	27±5	323 (8)	131 (3)	114 (3)
	BEAT-AF	Cases	1532	1098 (68)	68±12	19-94	61±13	1161 (76)	27±5	198 (13)	216 (14)	299 (20)
		Referents	1532	711 (46)	35±5	23-44	-	213 (14)	25±4	7 (1)	0	0
	BioMe	Cases	371	265 (71)	74±9	49-89	-	339 (91)	28±6	72 (22)	39 (11)	172 (46)
		Referents	1178	710 (60)	68±10	32-89	-	862 (73)	28±6	244 (22)	57 (5)	144 (12)
	BioVU	Cases	991	454 (46)	76±12	23-99	-	809 (82)	28±7	183 (19)	66 (7)	-
		Referents	21,309	11,498 (54)	64±17	16-99	-	12,711 (60)	28±7	3198 (15)	816 (4)	-
	CHS	Cases incident	1377	649 (47)	73±5	65-95	82±6	831 (60)	26±4	295 (21)	167 (12)	68 (5)
		Cases prevalent	124	74 (60)	76±6	65-94	75±6	74 (60)	26±5	29 (23)	18 (15)	32 (26)
		Referents	2631	1094 (42)	72±5	65-100	-	1404 (53)	26±4	541 (21)	217 (8)	77 (3)
	FHS	Cases incident	376	184 (49)	73±11	43-100	79±10	162 (43)	28±6	58 (15)	31 (8)	5 (1)
		Cases prevalent	161	105 (65)	76±10	50-96	70±11	52 (33)	28±5	32 (20)	25 (16)	9 (6)
		Referents	1767	719 (41)	64±12	32-97	-	488 (28)	28±5	173 (10)	57 (3)	4 (0.2)
	GS_SFHS	Cases	203	79 (39)	67±11	39-99	-	85 (42)	28±5	23 (11)	24 (12)	-
		Referents	6651	3974 (60)	54±12	18-98	-	1134 (17)	27±5	290 (4)	391 (5)	-
	MESA	Cases	136	1206 (48)	63±10	44-84	76±8	975 (39)	28±5	151 (6)	62 (3)	52 (2)
		Referents	2,362									
	MGH CAMP	Cases	668	479 (72)	61±10	27-79	-	41 (6)	-	178 (27)	162 (24)	233 (35)
		Referents	2138	1204 (56)	60±12	30-81	-	66 (3)	-	547 (26)	360 (17)	320 (15)
	RS I	Cases incident	346	170 (49)	72±8	55-93	-	226 (65)	27±4	50 (15)	26 (8)	14 (4)
		Cases prevalent	168	85 (51)	76±8	56-98	-	111(66)	26±3	28 (19)	34 (23)	-
		Referents	2370	1097 (46)	69±8	55-99	-	1259 (53)	26±4	222 (9)	143 (6)	56 (2)
	SHIP	Cases	96	63 (66)	64±12	21-80	-	72 (75)	30±5	21 (22)	14 (15)	-
		Referents	1749	841 (48)	50±15	20-80	-	901 (52)	27±5	175 (10)	53 (3)	-
		Cases - Trend	52	42 (81)	69±11	24-81	-	36 (72)	31±6	19 (37)	4 (8)	-
		Referents - Trend	3385	1636 (48)	52±15	20-82	-	1594 (47)	28±5	401 (12)	86 (3)	-
	WGHS	Cases incident	959	0	55±7	49-59	73±7	4812 (24)	25±7	485 (2)	0	0
		Referents	19307									
	WHI_OS*	Cases prevalent	786	0	66±7	50-81	73±6	2081 (34)	27±6	301 (5)	237 (4)	115 (2)
		Cases incident	587	0	-	-	-	-	-	-	-	-
		Referents	4804	0	-	-	-	-	-	-	-	-
	WHI_CT**	Cases	119	0	-	-	-	-	-	-	-	-
		Referents	10,601	0	-	-	-	-	-	-	-	-
AA	**ARIC**	Cases	330	142 (43)	56±6	45-66	70±7	231 (70)	31±7	107 (32)	20 (6)	37 (11)
		Referents	3373	382 (38)	54±6	44-66	-	543 (54)	30±6	187 (19)	41 (4)	59 (6)
	BioMe	Cases	253	109 (43)	66±13	30-89	-	244 (96)	31±9	113 (53)	30 (12)	159 (63)
		Referents	2713	927 (34)	57±14	22-89	-	2134 (79)	31±8	949 (39)	107 (4)	435 (16)
	WHI_OS*	Cases prevalent	54	0	67±6	50-79	71±6	502 (43)	29±6	135 (12)	31 (3)	23 (2)
		Cases incident	44	0	-	-	-	-	-	-	-	-
		Referents	1204	0	-	-	-	-	-	-	-	-
AS	**Biobank Japan**	Cases	8180	5713 (70)	68±10	15-99	68±10	-	24±4	1798 (22)	699 (9)	2028 (25)
		Referents	28,612	11,223 (39)	56±10	20-81	-	-	-	1025 (5)	457 (2)	19 (0.1)

Abbreviations: AF, atrial fibrillation; AA, African American; AS, Asian; BMI, body mass index; DM, diabetes mellitus; EUR, European ancestry; HF, heart failure; HTN, hypertension; MI, myocardial infarction. *Observational study. **Clinical trial.

Supplementary Table 3. Detailed description of the genes at novel atrial fibrillation loci

Chromosomal location, Sentinel variant, *Gene(s)*: Description of the genes at the locus.
GWAS loci
1q24, rs72700118, *METTL11B/KIFAP3*: The most significant variant at 1q24 lies downstream of the closest gene, *METTL11B*, which encodes an N-terminal mono-methyltransferase that regulates DNA-protein interactions.[3] It is an important cell cycle regulator and mediator of DNA repair mechanisms since *METTL11B* knockout mice either die shortly after birth or display various developmental defects.[4] Interestingly, it also has been shown that METTL11B might act as a tumor suppressor protein in breast cancer.[5] *METTL11B* is highly expressed in right atrial and left ventricular tissue in GTEx. Analyses revealed that METTL11B may potentially interact with the atrial specific myosin light chain gene (MYL4) that has been linked to atrial fibrillation.[6,7] The locus also includes the gene *KIFAP3,* for which there also was a significant eQTL in the CCAF human atrial samples (**Supplementary Table S17 and S19**). *KIFAP3* encodes the kinesin associated protein 3, which regulates small G proteins by stimulating GDP/GTP exchange reactions or inhibiting their membrane interactions.[8] The gene is expressed in right atrial and left ventricular human tissue samples in the GTEx database. It is thought that this protein serves as a linker between human chromosome-associated polypeptide (HCAP) and KIF3A/B, a kinesin superfamily protein in the nucleus, and that this motor complex mediates binding to motor proteins enabling mainly anterograde transport of vesicles along microtubules.[9,10] *KIFAP3* variants have previously been associated with increased survival in sporadic amyotrophic lateral sclerosis and a combined phenotype of obesity and endometriosis in GWAS.[11,12] Reduced expression of *KIFAP3* has been demonstrated in clear cell renal carcinomas and was correlated with tumor aggressiveness and poorer patient outcomes,[13] whereas overexpression of the gene has been shown in breast cancer tumors.[14] In addition, *KIFAP3* has been shown to be involved in control of female puberty onset.[15] No relation to cardiac phenotypes have been noted for *KIFAP3* so far.
2p13, rs3771537, ***ANXA4/GMCL1:*** At 2p13, the most significant variant was intronic to *ANXA4*, whereas there were significant eQTLs for *ANXA4, GMCL1, PCYOX1,* and *SNRNP27* in GTEx left ventricle and skeletal muscle tissue (**Supplementary Table S17-S18**). *ANXA4* encodes Annexin 4, which is a Ca^{2+} and phospholipid binding protein that modulates membrane permeability, growth, apoptosis.[16] It has been demonstrated to be overexpressed in various cancers like lung cancer, colorectal cancer or prostate cancer where it enhances tumor invasion and chemotherapy resistance.[17] It has further been shown that *ANXA4* is involved in β-adrenergic signaling since Anxa4$^{-/-}$ mice show increased cellular cAMP levels and enhanced left ventricle contraction force upon adrenergic stimulation, whereas calcium stimulation in the left atrium lead to increased contraction force relative to wildtype mice.[18] Moreover, annexin 4 has been shown to bind to adenylyl cyclase type 5; thus, it has been suggested that annexin 4 directly modulates the β-adrenoceptor cAMP-dependent signal transduction pathway by inhibiting adenylyl cyclase 5.[18] In line with this hypothesis, *ANXA4* has been shown to be upregulated in human failing hearts.[19] *GMCL1,* which encodes Germ Cell-Less protein 1, is predominantly expressed in the testis, where it is

involved in spermatogenesis.[20,21] It has been demonstrated to regulate chromatin in germ cells by interacting with GAGE12I[22] and might also have a role in oncogenesis since it is expressed in various cancers like B cell lymphoma.[23] A direct link to cardiac physiology or disease; however, is currently missing.

2p14, rs2540949, *CEP68*: The most significant variant at 2p14 was intronic to *CEP68*, which encodes the centrosomal protein 68 that is important for the cell cycle by regulating centrosome cohesion.[24] There were significant eQTLs for *CEP68* in both the CCAF human atrial samples (**Supplementary Table S17 and 19**) and GTEx atrial, left ventricle, and skeletal muscle tissue (**Supplementary Table S17-S18**). At the onset of mitosis CEP68 dissociates from the centrosomes allowing the centrosomes to separate.[25] Variants in *CEP68* has been associated with aspirin-induced asthma[26] and acute urticaria/angioedema induced by non-steroidal anti-inflammatory drugs.[27]

2p31, rs2288327, *TTN/TTN-AS1:* At 2q31 we identified six significant coding variants in the A-band and M-line of titin, which all were predicted to be benign by PolyPhen and SIFT. The *TTN* gene spans 363 exons and the encoded protein stretches through half the length of a sarcomere.[28] Titin ensures sarcomere integrity and elasticity, and binds actin and myosin, which are crucial players in the contractile machinery in striated muscle.[29,30] Truncating mutations in titin have been shown to be the most important cause of dilated cardiomyopathy;[31–35] however, the gene displays considerable variation, making interpretation of mutational findings challenging.[36] Titin has been associated with the QT-interval in previous GWAS,[37,38] but the lead variant in our study (rs2288327) was not in LD with the QT-associated *TTN* variant (rs7561149, r^2=0.004).

5q22, rs337711, *KCNN2:* The variant at 5q22 is located in an intron of the gene *KCNN2* that encodes the small-conductance calcium-activated potassium channel, subfamily N, member 2 or SK2 channel. There was a significant eQTL for *KCNN2* itself in the CCAF human atrial tissue samples (**Supplementary Table S19**). This ion channel is predominantly expressed in the atria[39] and is involved in electrical remodeling resulting in atrial fibrillation.[39,40] In chronic atrial fibrillation, SK2 expression is reduced leading to significant changes in action potential duration (APD), a finding that has been confirmed in knockout mice. Furthermore, SK2 channels have been demonstrated to be involved in ventricular repolarization and also development of ventricular arrhythmias, especially in failing hearts where SK2 channels are upregulated both in patients and animal models.[41–45] Functional analysis revealed that the activation and modulation of SK2 channels is dependent on Ryr2-mediated calcium release[46] and that amiodarone can inhibit SK2 channels in a time- and voltage-independent but calcium-dependent mechanism, partly explaining its antiarrhythmic effects in failing hearts.[47] Additionally, genome-wide association studies have identified *KCNN2* as a susceptibility gene for coronary aneurysms in Kawasaki disease.[48,49] SK2 channels have also been shown to be involved in ischemia-induced neuronal cell death,[50,51] neuronal plasticity and learning,[52–55] drug addiction,[56,57] regulation of sleep duration,[58] and maintenance of the ionic milieu of the inner ear fluid.[59] They may be therapeutic targets for Parkinson's disease, since activation of SK2 channels provides protective effects in human dopaminergic neurons.[60]

5q31, rs2967791, *PKD2L2/KLHL3/WNT8A/FAM13B*: *PKD2L2* encodes the polycystic kidney disease 2-like 2 protein that belongs to the transient receptor potential (TRP) superfamily and is highly expressed in human brain, kidney, and testis.[61,62] In rodents, it is also expressed in the heart and has been demonstrated to be involved in calcium homeostasis, proliferation, and apoptosis.[61–63]

KLHL3 encodes the gene Kelch Like Family Member 3 that is part of the E3 ubiquitin ligase complex regulating the sodium/chloride cotransporter (NCC), the epithelial sodium channel (ENaC), and the renal outer medullary potassium channel (ROMC) in the kidney.[64,65] It is an important regulator of the electrolyte homeostasis and therefore the blood pressure.[66,67] Genetic variants of *KLHL3* have been described to cause familial hyperkaliemic hypertension. [65,68,69]

WNT8A is a member of the WNT/beta catenin-signaling network that plays an essential role in development and carcinogenesis.[70] *WNT8A* has been demonstrated to regulate body axis extension[71] and neuroectodermal posteriorization.[72] *WNT8A* polymorphisms have been shown to be associated with Hirschsprung's disease and its expression is upregulated in stenotic colon segments in patients.[73] Interestingly, *in vitro* overexpression of WNT8 results in impaired calcium handling[74] and might therefore also be involved in atrial fibrillation pathophysiology.

For the 5q31 locus, we identified an eQTL for the gene *FAM13B* in eQTL enrichment analysis (**Supplemental table S17**). *FAM13B* (syn. *C5ORF5*) consists of 23 exons spanning over 27 kb; the transcript is 5.47 kb and encodes a protein of 915 amino acids.[75] It contains a putative rhoGAP domain at the N-terminus and two bipartite nuclear localization signals and is predominantly expressed in brain and male reproductive tissue[76] (Human Protein Atlas available from www.proteinatlas.org). So far, *FAM13B* has not been reported in a cardiovascular context.

8p22, rs7508, *ASAH1/PCM1*: At 8p22, the lead atrial fibrillation risk variant was associated with decreased expression of *ASAH1* (rs7508; $P = 5.1 \times 10^{-3}$) in CCAF human atrial samples and increased expression of *PCM1* (rs7508; $P = 9.6 \times 10^{-14}$) in both the CCAF samples (**Supplementary Table S17 and S19**) and GTEx left ventricle and skeletal muscle tissue (**Supplementary Table S17-S18**). *ASAH1* encodes the acid ceramidase 1 that is involved in lipid metabolism by degradation of ceramide into sphingosine and free fatty acids within lysosomes.[77,78] Overexpression of ceramidase has been reported in several cancer cell types,[79–81] resulting in increased proliferation[82] and invasiveness,[83,84] predominantly in prostate cancer, which in turn has led to studies showing promising results of ceramidase inhibitors as new cancer therapeutics.[85,86] Ceramidase has also been implicated in Farber's disease (lipogranulomatosis),[87,88] spinal muscular atrophy with myoclonic epilepsy,[89] and Alzheimer's disease.[90] *ASAH1* is highly expressed in the heart.[91] Accumulation of ceramide has been shown to result in oxidative stress, electron transport chain dysfunction, and cardiomyocyte apoptosis in rats.[92,93]

PCM1 encoding pericentriolar material 1, has been demonstrated to be an integral component of centriolar satellites in ciliogenesis.[94] It has also been shown to be involved in neurogenesis ,[95] the centrosomal actin network,[96] hematological neoplasms,[97] and associated with schizophrenia.[98]

10q24, rs35176054, *SH3PXD2A*: The variant at 10q24 is located intronic to the gene *SH3PXD2A* that encodes the SH3 and PX domain-containing protein 2A or Adapter protein TKS5 that plays an essential role in various malignancies. It interacts with Src tyrosine kinase to promote tumor growth and the formation of invadopodia resulting in degradation of extracellular matrix and invasion of cancer cells into surrounding tissue in breast, ovarian, colon, lung, prostate cancer, melanoma, and glioma.[99–103] Its expression level has been demonstrated to be negatively correlated with tumor size and patient survival in ovarian cancer.[104,105] However, it is also involved in normal embryonic development by regulating neural crest migration[106,107] and in macrophage or microglia physiology.[108,109]

11q24, rs75190942, *KCNJ5:* The genetic variant rs75190942 is located at 11q24 within the gene *KCNJ5*, that encodes the G protein-activated inward rectifier potassium channel 4 (Kir3.4/GIRK4). There was a significant eQTL for *KCNJ5* itself in CCAF human atrial tissue samples (**Supplementary Table S17 and S19**) and in GTEx left ventricle tissue (**Supplementary Table S17-S18**). GIRK4 is known to form heteromeres with Kir3.1/GIRK1/KCNJ3, constituting the I_{KAch} channel complex, which contributes to the regulation of the membrane potential in the sinoatrial node and atria – making it a therapeutic target for atrial fibrillation. This ion channel has been shown to regulate pacemaker activity and recovery of resting heart rate after sympathetic stimulation.[110] GIRK4 inactivation can also rescue arrhythmias that are induced by genetic silencing of funny currents.[111] Furthermore, it determines inducibility, dynamics and termination of atrial fibrillation by regulating action potential duration.[112] Additionally, genetic polymorphisms in *KCNJ5* are associated with early-onset lone atrial fibrillation,[113] whereas mutations in this gene have been shown to cause long QT syndrome.[114] GIRK4 is also expressed in the ventricles and contributes to ventricular repolarization[115] and has been shown to be significantly downregulated in patients with dilated cardiomyopathy.[116] Furthermore, mutations in *KCNJ5* can cause Andersen-Tawil syndrome,[117] primary aldosteronism[118] and has been detected in adrenal tumors.[119] Also, *KCNJ5* is associated with Tourette Syndrome and Attention-Deficit/Hyperactivity Disorder.[120]

ExWAS loci

3p22, rs6800541, *SCN10A:* The variant rs6800541 is located intronic to *SCN10A*, the gene that encodes the sodium channel Nav1.8. It is highly expressed in primary sensory neurons and dorsal root ganglion neurons and has been linked to nociception, painful neuropathy, and multiple sclerosis.[121] Recently, it has been shown that Nav1.8 is also expressed in the heart where it contributes to the late sodium current.[122,123] Genome-wide association studies demonstrated genetic variants in *SCN10A* as risk loci for quantitative ECG traits like PR interval,[124–128] and QRS duration,[126,129,130] as well as for atrial fibrillation[124,126,130,131] and Brugada Syndrome.[132] Also, mutations in *SCN10A* has been shown to be responsible for a large fraction of cases of Brugada Syndrome.[133] Data suggest that *SCN10A* affects cardiac conduction either directly through cardiomyocytes, indirectly through intracardiac neurons, or by modulation of *SCN5A* expression.[134,135]

12p12, rs11047543, *SOX5:* The most significant SNP at 12p12 is located downstream of the *SOX5* gene. SOX5 is a transcription factor that has been shown to be involved in limb development,[136] chondrogenesis,[137] brain development,[138] and lung development.[139] Our current study confirmed previous genome-wide association studies that showed a significant association between *SOX5* and early-onset atrial fibrillation.[124,140] Furthermore, *SOX5* has been demonstrated to be significantly associated with PR-interval,[124] left ventricular mass,[141] resting heart rate,[142] osteoporosis,[143] systemic sclerosis,[144] AIDS,[145] chronic obstructive pulmonary disease,[139] and non-obstructive azoospermia.[146] Additionally, it is involved in the development of lung cancer,[147] hepatocellular carcinoma,[148] follicular lymphoma,[149] and melanoma.[163]

Locus identified in both GWAS and EWAS:

6q22, rs4946333 (GWAS), rs89107 (EWAS), *SLC35F1/PLN:*** At 6q22 we identified a locus including the phospholamban gene (*PLN*), *SLC35F1,* and *CEP85L*. Phospholamban regulates cardiac contractility and relaxation through inhibiting the cardiac muscle sarcoplasmic reticulum calcium ATPase SERCA.[164] Mutations in this gene has been associated with hypertrophic[165,166] and dilated cardiomyopathy.[167,168]

SLC35F1 encodes a member of the solute carrier family 35. *SLC35F1* knockout mice display reduced levels of hemoglobin and lactate dehydrogenase but do not show any further phenotype. Previous GWAS have associated the locus surrounding *SLC35F1/PLN/CEP85L* with resting heart rate,[6,15] QT-interval,[12,14] and left ventricle internal diastolic diameter.[11] One of the variants associated with heart rate by den Hoed et al. also associated with atrial fibrillation in secondary analyses.[6]

Supplementary Table 4. Results from Asian ancestry SKAT gene based test

Gene	Chr	CMAF	N variants	P-value
Filter: Variants predicted to be damaging				
SH3PXD2A	10q24	0.4	6	$4.77x10^{-11}$
Filter: Nonsynonymous and splice site variants				
SH3PXD2A	10q24	0.4	11	$4.21x10^{-11}$

Chr, chromosome; CMAF, cumulative minor allele frequency per gene.

Supplementary Table 5. Single variant association results for the variants that were analyzed in the two significant gene-based tests for *SH3PDX2A* in the Asian ancestry group.

rsID	Risk/ref allele	Amino acid substitution**	RAF, %	OR	95% CI	P-value
rs149867987	A/G	p.His110Tyr	0.01	16.72	2.23-125.31	0.006
rs200938753*	G/A	p.Arg761Cys	99.89	1.45	0.74-2.84	0.27
rs202011870*	C/A	p.Leu396Arg	0.18	4.68	2.97-7.39	3.30E-11
rs201065560*	A/G	p.Arg1031Cys	0.02	2.03	0.55-7.47	0.29
rs74661743*	G/A	p.Arg1003Cys	99.93	1.02	0.42-2.47	0.97
rs79061932	G/A	p.Arg994Cys	99.99	1.13	0.07-18.44	0.93
rs201439736	C/T	p.Ala886Thr	99.97	1.44	0.46-4.52	0.54
rs201054626*	T/C	p.Arg302Gln	0.01	4.85	0.83-28.47	0.08
rs143819462	T/C	p.Arg269Gln	0.01	2.34	0.39-13.93	0.35
rs147297499	T/C	p.Asp231Asn	0.005	13.31	0.67-264.24	0.09
rs143409187*	T/C	p.Arg102Gln	0.007	2.85	0.15-55.03	0.49

The gene-based test was significant for the subset of nonsynonymous and splice site variants, which included all listed variants, and the subset of nonsynonymous possibly damaging variants, which included 6 of the listed variants (*). **NCBI Reference sequence accession and version number NP_055446.2. RAF, risk allele frequency; CI, confidence interval; OR, odds ratio.

Supplementary Table 6. Results from ancestry-specific GWAS meta-analyses

	rsID	Chr	Gene	Location relative to gene	Risk/ref allele	RAF, %	OR	95% CI	P-value
EUR	*15,993 cases, 113,719 referents*								
	Novel associations								
	rs10800507	1q24	*METTL11B/KIFAP3*	Intergenic	C/G	51	1.09	1.06-1.12	$1.87x10^{-11}$
	rs62133983	2p13	***ANXA4****/GMCL1*	Intronic	G/T	52	1.09	1.06-1.12	1.36x10-10
	rs2723064	2p14	*CEP68*	Intergenic	T/C	61	1.09	1.06-1.12	1.88x10-10
	rs6864727	5q31	***PKD2L2****/WNT8A/FAM13B*	Intronic	C/T	31	1.08	1.05-1.11	$1.12x10^{-8}$
	rs281868	6q22	***SLC35F1****/PLN*	Intronic	G/A	50	1.08	1.05-1.10	$1.03x10^{-8}$
	rs7508	8p22	***ASAH1****/PCM1*	3'UTR	A/G	73	1.10	1.06-1.13	$6.34x10^{-10}$
	rs35176054	10q24	***SH3PXD2A***	Intronic	A/T	13	1.14	1.10-1.18	$1.75x10^{-11}$
	rs75190942	11q24	***KCNJ5***	Intronic	A/C	8	1.18	1.11-1.25	$2.82x10^{-8}$
	rs2921421	15q21	*CGNL1*	Intergenic	G/C	3	1.72	1.42-2.09	$3.29x10^{-8}$
	Previously known associations								
	rs11264280	1q21	*KCNN3*	Intergenic	T/C	32	1.13	1.10-1.16	$2.77x10^{-17}$
	rs651386	1q24	*PRRX1*	Intergenic	A/T	57	1.11	1.08-1.14	$6.23x10^{-15}$
	rs2129977	4q25	*PITX2*	Intergenic	A/G	22	1.45	1.41-1.49	$7.25x10^{-136}$
	rs12664873	6q22	*GJA1*	Intergenic	T/G	69	1.08	1.05-1.12	$1.80x10^{-8}$
	rs11773845	7q31	***CAV1/2***	Intronic	A/C	60	1.10	1.07-1.13	$3.35x10^{-13}$
	rs7026071	9q22	***C9orf3***	Intronic	T/C	41	1.09	1.07-1.12	$2.86x10^{-11}$
	rs10824026	10q22	*SYNPO2L*	Intergenic	A/G	84	1.13	1.09-1.17	$8.29x10^{-11}$
	rs11598047	10q24	***NEURL1***	Intronic	G/A	17	1.18	1.14-1.22	$3.16x10^{-21}$
	rs883079	12q24	***TBX5***	3'UTR	T/C	72	1.11	1.08-1.15	$1.31x10^{-13}$
	rs7183206	15q24	*HCN4*	Intergenic	A/G	15	1.13	1.09-1.18	$7.70x10^{-12}$
	rs2106261	16q22	***ZFHX3***	Intronic	T/C	18	1.19	1.15-1.23	$4.01x10^{-24}$
AA	*641 cases, 4956 referents*								
	rs6843082	4q25	*PITX2*	Intergenic	G/A	30	1.40	1.24-1.58	$4.31x10^{-8}$
AS	*837 cases, 2456 referents*								
	Novel association								
	rs7138621	12q15	*CPSF6*	Intergenic	G/C	95	7.92	4.26-14.73	$6.48x10^{-11}$
	Previously known association								
	rs2723334	4q25	*PITX2*	Intergenic	T/C	70	1.94	1.68-2.25	$8.46x10^{-19}$

The most significant variant at each genetic locus associated with atrial fibrillation is listed. Gene names in bold font indicate that the variant is located within the gene, whereas additional gene names indicate eQTL gene or gene strongly suspected to be causal due to the function of the encoded protein. For intergenic variants, the closest gene(s) are listed. Chr, chromosome; CI, confidence interval; OR, odds

ratio; EUR, European ancestry; AA, African American ancestry; AS, Asian ancestry; RAF, risk allele frequency.

Supplementary Table 7. Results from European and Asian ancestry ExWAS meta-analysis

	rsID	Chr	Gene	Location relative to gene	Risk/ref allele	RAF, %	OR	95% CI	P-value
EUR	*13,496 cases, 96,273 referents*								
	Novel associations								
	rs6800541	3p22	***SCN10A***	Intronic	T/C	60	1.08	1.05-1.12	8.75×10^{-7}
	rs89107	6q22	***SLC35F1****/PLN*	Intronic	G/A	50	1.09	1.06-1.13	2.71×10^{-7}
	rs11047543	12p12	*SOX5*	Intergenic	G/A	85	1.13	1.08-1.18	4.65×10^{-7}
	Previously known associations								
	rs13376333	1q21	***KCNN3***	Intronic	T/C	31	1.14	1.10-1.17	1.58×10^{-13}
	rs2200733	4q25	*PITX2*	Intergenic	T/C	12	1.60	1.52-1.67	9.95×10^{-90}
	rs3807989	7q31	***CAV1***	Intronic	G/A	59	1.09	1.06-1.13	2.93×10^{-8}
	rs60632610	10q22	***SYNPO2L***	Exonic; nonsyn	C/T	85	1.13	1.08-1.18	2.53×10^{-8}
	rs2106261	16q22	***ZFHX3***	Intronic	A/G	17	1.21	1.16-1.26	3.37×10^{-18}
AS	*8180 cases, 28,612 referents*								
	Novel associations								
	rs55952639	2p14	***CEP68***	Exonic; syn	T/C	76	1.13	1.07-1.18	1.29×10^{-6}
	rs11047543	12p12	*SOX5*	Intergenic	G/A	88	1.18	1.10-1.26	1.16×10^{-6}
	Previously known associations								
	rs17042171	4q25	*PITX2*	Intergenic	A/C	48	1.69	1.62-1.76	4.04×10^{-137}

The most significant variant at each genetic locus associated with atrial fibrillation is listed. Gene names in bold font indicate that the variant is located within the gene, whereas additional gene names indicate eQTL gene or gene strongly suspected to be causal due to the function of the encoded protein. For intergenic variants the closest gene(s) are listed. Chr, chromosome; CI, confidence interval; OR, odds ratio; EUR, European ancestry; AA, African American ancestry; AS, Asian ancestry; nonsyn, nonsynonymous; syn, synonymous; RAF, risk allele frequency

Supplementary Table 8. Results from European incident atrial fibrillation GWAS meta-analysis

rsID	Chr	Gene	Location relative to gene	Risk/ref allele	RAF, %	OR	95% CI	P-value
rs11264280	1q21	*KCNN3*	Intergenic	T/C	32	1.12	1.08-1.16	$3.57x10^{-9}$
rs6843082	4q25	*PITX2*	Intergenic	G/A	21	1.38	1.33-1.44	$8.21x10^{-57}$
rs7394190	10q22	*SYNPO2L*	Intergenic	G/A	84	1.15	1.09-1.21	$3.09x10^{-8}$
rs60848348	10q24	***NEURL1***	Intronic	T/C	20	1.13	1.09-1.18	$1.69x10^{-8}$
rs4499262	16q22	***ZFHX3***	Intronic	A/C	17	1.14	1.09-1.19	$4.01x10^{-8}$

The most significant variant at each genetic locus associated with atrial fibrillation is listed. Gene names in bold font indicate that the variant is located within the gene. Chr, chromosome; CI, confidence interval; OR, odds ratio; RAF, risk allele frequency

Supplementary Table 9. Results from European prevalent atrial fibrillation GWAS meta-analysis

rsID	Chr	Gene	Location relative to gene	Risk/ref allele	RAF, %	OR	95% CI	P-value
Novel associations								
rs72700118	1q24	*METTL11B/KIFAP3*	Intergenic	A/C	11	1.24	1.17-1.31	$9.93x10^{-13}$
rs6546550	2p13	***ANXA4****/GMCL1*	Intronic	C/G	54	1.12	1.08-1.16	$1.36x10^{-8}$
rs1454934	12p11	***PKP2***	Intronic	T/C	16	1.16	1.1-1.22	$4.18x10^{-8}$
Previously known associations								
rs36004974	1q21	***KCNN3***	Intronic	G/A	32	1.14	1.1-1.19	$4.36x10^{-10}$
rs577676	1q24	*PRRX1*	Intergenic	C/T	55	1.15	1.1-1.19	$2.77x10^{-12}$
rs61303432	4q25	*PITX2*	Intergenic	T/C	14	1.71	1.62-1.8	$6.66x10^{-92}$
rs2109514	7q31	*CAV1/2*	Intergenic	A/G	51	1.15	1.11-1.19	$6.73x10^{-13}$
rs11598047	10q24	***NEURL1***	Intronic	G/A	17	1.24	1.18-1.31	$4.34x10^{-16}$
rs2106261	16q22	***ZFHX3***	Intronic	T/C	18	1.25	1.19-1.31	$9.68x10^{-20}$

The most significant variant at each genetic locus associated with atrial fibrillation is listed. Gene names in bold font indicate that the variant is located within the gene. Chr, chromosome; CI, confidence interval; OR, odds ratio; RAF, risk allele frequency

Supplementary Table 10. Comparison of results for common variant loci between the AFGen Consortium combined ancestry analysis and the Biobank Japan study.

					Discovery				Biobank Japan (8180 cases; 28,612 referents)			
Ancestry	**rsID**	**Chr**	**Gene(s)**	**Risk/ref allele**	**RAF, %**	**OR**	**95% CI**	**P-value**	**RAF, %**	**OR**	**95% CI**	**P-value**
					GWAS*							
Combined	Novel associations											
	rs72700118	1q24	*METTL11B*	A/C	12	1.14	1.10-1.23	2.60×10^{-11}	No information (rare in East Asians)			
	rs3771537	2p13	*ANXA4/GMCL1*	A/C	53	1.09	1.06-1.14	7.92×10^{-12}	32	1.06	1.01-1.11	1.39×10^{-2}
	rs2540949	**2p14**	***CEP68***	**A/T**	**61**	**1.08**	**1.06-1.13**	**2.93×10^{-10}**	**68**	**1.16**	**1.11-1.21**	**2.93×10^{-10}**
	rs2288327	2q31	*TTN/TTN-AS1*	G/A	20	1.09	1.06-1.14	2.05×10^{-8}	61	1.05	1.00-1.09	4.52×10^{-2}
	rs337711	**5q22**	***KCNN2***	**T/C**	**39**	**1.07**	**1.05-1.11**	**2.93×10^{-8}**	**14**	**1.16**	**1.10-1.23**	**4.97×10^{-7}**
	rs2967791	5q31	*.3/WNT8A/FAM*	T/C	54	1.07	1.05-1.11	2.73×10^{-8}	89	1.05	0.98-1.13	1.68×10^{-1}
	rs4946333	6q22	*SLC35F1/PLN*	G/A	50	1.08	1.05-1.12	1.89×10^{-9}	77	1.03	0.98-1.08	2.45×10^{-1}
	rs7508	8p22	*ASAH1*	A/G	72	1.09	1.06-1.14	5.16×10^{-10}	55	1.05	1.01-1.10	1.67×10^{-2}
	rs35176054	10q24	*SH3PXD2A*	A/T	13	1.14	1.10-1.22	8.63×10^{-12}	No information (monomorphic in Japanese)			
	rs75190942	11q24	*KCNJ5*	A/C	8	1.17	1.11-1.26	1.59×10^{-8}	5	1.06	0.94-1.20	3.12×10^{-1}
	Previously known associations											
	rs11264280	1q21	*KCNN3*	T/C	31	1.12	1.09-1.21	6.41×10^{-17}	9	1.11	1.03-1.20	4.25×10^{-3}
	rs520525	**1q24**	***PRRX1***	**A/G**	**71**	**1.12**	**1.09-1.20**	**6.39×10^{-16}**	**64**	**1.1**	**1.06-1.16**	**1.28×10^{-5}**
	rs11718898	3p25	*CAND2*	C/T	65	1.08	1.05-1.11	4.68×10^{-8}	30	1.04	1.00-1.09	7.58×10^{-2}
	rs6843082	**4q25**	***PITX2***	**G/A**	**25**	**1.45**	**1.41-1.99**	**3.41×10^{-155}**	**68**	**1.84**	**1.75-1.94**	**9.85×10^{-127}**
	rs12664873	**6q22**	***GJA1***	**T/G**	**70**	**1.08**	**1.05-1.12**	**1.19×10^{-8}**	**70**	**1.1**	**1.05-1.15**	**8.86×10^{-5}**
	rs1997572	**7q31**	***CAV1/2***	**G/A**	**59**	**1.1**	**1.08-1.17**	**6.64×10^{-15}**	**67**	**1.18**	**1.13-1.24**	**6.83×10^{-13}**
	rs7026071	9q22	*C9orf3*	T/C	40	1.09	1.07-1.15	1.31×10^{-12}	28	1.05	1.00-1.10	4.21×10^{-2}
	rs11598047	**10q24**	***NEURL1***	**G/A**	**16**	**1.18**	**1.14-1.31**	**1.67×10^{-22}**	**9**	**1.41**	**1.32-1.51**	**6.17×10^{-24}**
	rs7915134	10q22	*SYNPO2L*	C/T	85	1.12	1.08-1.19	1.68×10^{-10}	83	1.07	1.01-1.13	1.84×10^{-2}
	rs883079	**12q24**	***TBX5***	**T/C**	**70**	**1.11**	**1.09-1.19**	**1.80×10^{-15}**	**42**	**1.18**	**1.13-1.24**	**5.45×10^{-15}**
	rs1152591	**14q23**	***SYNE2***	**A/G**	**46**	**1.09**	**1.06-1.13**	**1.04×10^{-10}**	**36**	**1.08**	**1.04-1.13**	**4.09×10^{-4}**
	rs74022964	15q24	*HCN4*	T/C	17	1.12	1.08-1.19	2.37×10^{-11}	3	1.04	0.91-1.19	5.91×10^{-1}
	rs2106261	**16q22**	***ZFHX3***	**T/C**	**19**	**1.2**	**1.17-1.37**	**8.18×10^{-32}**	**31**	**1.33**	**1.27-1.39**	**9.63×10^{-36}**
Asian	Novel associations											
	rs7138621	12q15	*CPSF6*	G/C	95	7.92	4.26-14.73	6.48×10^{-11}	94	1.02	0.93-1.11	7.13×10^{-1}
	Previously known associations											
	rs2723334	**4q25**	***PITX2***	**T/C**	**70**	**1.94**	**1.68-2.25**	**8.46×10^{-19}**	**68**	**1.8**	**1.71-1.89**	**7.84×10^{-121}**
					ExWAS							
Combined	Novel associations											
	rs6800541	3p22	*SCN10A*	T/C	61	1.08	1.05-1.12	8.79×10^{-7}	86	1.1	1.03-1.16	3.44×10^{-3}
	rs89107	6q22	*SLC35F1*	G/A	58	1.07	1.04-1.10	9.51×10^{-7}	78	1.03	0.98-1.08	2.39×10^{-1}
	rs11047543	**12p12**	***SOX5***	**G/A**	**86**	**1.14**	**1.10-1.19**	**2.47×10^{-12}**	**88**	**1.18**	**1.10-1.26**	**1.57×10^{-6}**
	Previously known associations											
	rs13376333	1q21	*KCNN3*	T/C	12	1.13	1.09-1.16	1.46×10^{-12}	2	1.09	0.92-1.30	3.16×10^{-1}
	rs17042171	**4q25**	***PITX2***	**A/C**	**50**	**1.64**	**1.59-1.69**	**8.31×10^{-227}**	**45**	**1.71**	**1.64-1.78**	**9.69×10^{-135}**
	rs3807989	**7q31**	***CAV1***	**G/A**	**58**	**1.09**	**1.06-1.12**	**6.52×10^{-8}**	**67**	**1.18**	**1.13-1.23**	**7.95×10^{-13}**
	rs60632610	10q22	*SYNPO2L*	C/T	85	1.12	1.08-1.15	1.54×10^{-10}	84	1.08	1.02-1.14	1.15×10^{-2}
	rs10151658	14q23	*SYNE2*	C/A	6	1.07	1.04-1.09	5.16×10^{-7}	43	1.05	1.01-1.10	2.67×10^{-2}
	rs2106261	**16q22**	***ZFHX3***	**A/G**	**19**	**1.21**	**1.16-1.26**	**4.00×10^{-19}**	**31**	**1.33**	**1.27-1.39**	**9.63×10^{-36}**
	Results from AFGen exome chip gene-based test											
Asian	**rs202011870**	**10q24**	***SH3PXD2A***	**C/A**	**0.18**	**4.68**	**2.97-7.39**	**3.30E-11**	**0.2**	**4.03**	**2.63-6.19**	**1.80×10^{-10}**

For each genetic locus, we have reported the variant with the lowest *P* -value. Bold font indicates significant association with AF in Biobank Japan, when correcting for multiple testing of 33 variants ($P<1.5\times10^{-3}$). *****The GWAS analysis contained 837 cases and 3293 referents from BBJ. Chr, chromosome; RAF, risk allele frequency; OR, odds ratio; CI, confidence interval.

Supplementary Table 11. Comparison of results for common variant loci between the AFGen Consortium combined ancestry analysis and the UK Biobank study.

				Discovery				UK Biobank (3,366 cases; 139,852 referents)			
rsID	Chr	Gene(s)	Risk / ref allele	RAF, %	OR	95% CI	P-value	RAF, %	OR	95% CI	P-value
GWAS											
Novel associations											
rs72700118	**1q24**	***METTL11B/KIFAP3***	**A/C**	**12**	**1.14**	**1.10-1.23**	**$2.60x10^{-11}$**	**12**	**1.21**	**1.12-1.29**	**$2.59x10^{-7}$**
rs3771537	2p13	*ANXA4/GMCL1*	A/C	53	1.09	1.06-1.14	$7.92x10^{-12}$	54	1.05	1.00-1.10	0.064
rs2540949	**2p14**	***CEP68***	**A/T**	**61**	**1.08**	**1.06-1.13**	**$2.93x10^{-10}$**	**62**	**1.1**	**1.04-1.15**	**$3.90x10^{-4}$**
rs2288327	2q31	*TTN/TTN-AS1*	G/A	20	1.09	1.06-1.14	$2.05x10^{-8}$	16	1.08	1.01-1.16	0.016
rs337711	5q22	*KCNN2*	T/C	39	1.07	1.05-1.11	$2.93x10^{-8}$	40	1.04	0.99-1.09	0.144
rs2967791	**5q31**	***KLHL3/WNT8A/FAM13B***	**T/C**	**54**	**1.07**	**1.05-1.11**	**$2.73x10^{-8}$**	**54**	**1.09**	**1.04-1.15**	**$4.47x10^{-4}$**
rs4946333	6q22	*SLC35F1/PLN*	G/A	50	1.08	1.05-1.12	$1.89x10^{-9}$	50	1.04	0.99-1.10	0.087
rs7508	8p22	*ASAH1/PCM1*	A/G	72	1.09	1.06-1.14	$5.16x10^{-10}$	73	1.06	1.00-1.12	0.038
rs35176054	**10q24**	***SH3PXD2A***	**A/T**	**13**	**1.14**	**1.10-1.22**	**$8.63x10^{-12}$**	**11**	**1.24**	**1.15-1.33**	**$5.7x10^{-9}$**
rs75190942	11q24	*KCNJ5*	A/C	8	1.17	1.11-1.26	$1.59x10^{-8}$	9	1.12	1.03-1.22	0.005
Previously known associations											
rs11264280	**1q21**	***KCNN3***	**T/C**	**31**	**1.12**	**1.09-1.21**	**$6.41x10^{-17}$**	**32**	**1.23**	**1.17-1.30**	**$4.27x10^{-15}$**
rs520525	**1q24**	***PRRX1***	**A/G**	**71**	**1.12**	**1.09-1.20**	**$6.39x10^{-16}$**	**71**	**1.11**	**1.05-1.17**	**$4.41x10^{-4}$**
rs11718898	3p25	*CAND2*	C/T	65	1.08	1.05-1.11	$4.68x10^{-8}$	66	1.06	1.00-1.11	0.04
rs6843082	**4q25**	***PITX2***	**G/A**	**25**	**1.45**	**1.41-1.99**	**$3.41x10^{-155}$**	**20**	**1.6**	**1.51-1.69**	**$1.75x10^{-62}$**
rs12664873	6q22	*GJA1*	T/G	70	1.08	1.05-1.12	$1.19x10^{-8}$	70	1.06	1.01-1.12	0.031
rs1997572	**7q31**	***CAV1/2***	**G/A**	**59**	**1.1**	**1.08-1.17**	**$6.64x10^{-15}$**	**59**	**1.16**	**1.11-1.22**	**$5.04x10^{-9}$**
rs7026071	**9q22**	***C9orf3***	**T/C**	**40**	**1.09**	**1.07-1.15**	**$1.31x10^{-12}$**	**40**	**1.13**	**1.07-1.19**	**$1.80x10^{-6}$**
rs7915134	10q22	*SYNPO2L*	C/T	85	1.12	1.14-1.31	$1.68x10^{-10}$	86	1.09	1.01-1.17	0.02
rs11598047	**10q24**	***NEURL1***	**G/A**	**16**	**1.18**	**1.08-1.19**	**$1.67x10^{-22}$**	**15**	**1.17**	**1.10-1.25**	**$2.03x10^{-6}$**
rs883079	**12q24**	***TBX5***	**T/C**	**70**	**1.11**	**1.09-1.19**	**$1.80x10^{-15}$**	**73**	**1.11**	**1.05-1.17**	**$4.06x10^{-4}$**
rs1152591	**14q23**	***SYNE2***	**A/G**	**46**	**1.09**	**1.06-1.13**	**$1.04x10^{-10}$**	**49**	**1.11**	**1.06-1.17**	**$2.74x10^{-5}$**
rs74022964	15q24	*HCN4*	T/C	17	1.12	1.08-1.19	$2.37x10^{-11}$	15	1.08	1.01-1.15	0.029
rs2106261	**16q22**	***ZFHX3***	**T/C**	**19**	**1.2**	**1.17-1.37**	**$8.18x10^{-32}$**	**17**	**1.27**	**1.20-1.35**	**$1.36x10^{-14}$**
ExWAS											
Novel associations											
rs6800541	3p22	*SCN10A*	T/C	61	1.08	1.05-1.12	$8.79x10^{-7}$	60	1.08	1.02-1.13	0.004
rs89107	6q22	*SLC35F1/PLN*	G/A	58	1.07	1.04-1.10	$9.51x10^{-7}$	51	1.04	0.99-1.10	0.087
rs11047543	12p12	*SOX5*	G/A	86	1.14	1.10-1.19	$2.47x10^{-12}$	85	1.07	1.00-1.14	0.065
Previously known associations											
rs13376333	**1q21**	***KCNN3***	**T/C**	**23**	**1.13**	**1.09-1.16**	**$1.46x10^{-12}$**	**31**	**1.17**	**1.11-1.23**	**$1.10x10^{-9}$**
rs17042171	**4q25**	***PITX2***	**A/C**	**21**	**1.64**	**1.59-1.69**	**$8.31x10^{-227}$**	**11**	**1.75**	**1.64-1.87**	**$1.24x10^{-60}$**
rs3807989	**7q31**	***CAV1***	**G/A**	**58**	**1.09**	**1.06-1.12**	**$6.52x10^{-8}$**	**59**	**1.16**	**1.10-1.22**	**$1.22x10^{-8}$**
rs60632610	10q22	*SYNPO2L*	C/T	85	1.12	1.08-1.15	$1.54x10^{-10}$	86	1.09	1.02-1.17	0.016
rs10151658	14q23	*SYNE2*	C/A	49	1.07	1.04-1.09	$5.16x10^{-7}$	57	1.05	1.00-1.10	0.076
rs2106261	**16q22**	***ZFHX3***	**A/G**	**17**	**1.21**	**1.16-1.26**	**$4.00x10^{-19}$**	**17**	**1.27**	**1.20-1.35**	**$1.36x10^{-14}$**

For each genetic locus, we have reported the variant with the lowest P-value. Bold font indicates significant association with AF in the UK Biobank, when correcting for multiple testing of 31 variants ($P < 1.6x10^{-3}$). Chr, chromosome; RAF, risk allele frequency; OR, odds ratio; CI, confidence interval.

Supplementary Table 12. Approximate and joint conditional analysis in European ancestry GWAS meta-analysis identify 20 independent genetic loci associated with atrial fibrillation

rsID	Chr	Gene	Location relative to gene	P-value
rs11264280	1	*KCNN3*	Intergenic	2.77×10^{-17}
rs10800507	1	*METTL11B*	Intergenic	1.87×10^{-11}
rs651386	1	*PRRX1*	Intergenic	6.23×10^{-15}
rs2723065	2	*CEP68*	Intergenic	1.91×10^{-10}
rs62133983	2	***ANXA4***	Intronic	1.36×10^{-10}
rs2129977*	4	*PITX2*	Intergenic	7.25×10^{-136}
rs6864727	5	***PKD2L2***	Intronic	1.12×10^{-8}
rs281868	6	***SLC35F1***	Intronic	1.03×10^{-8}
rs7773091	6	*GJA1*	Intergenic	2.02×10^{-8}
rs11773845	7	***CAV1***	Intronic	3.35×10^{-13}
rs7508	8	***ASAH1***	3'UTR	6.34×10^{-10}
rs7026071	9	***C9orf3***	Intronic	2.86×10^{-11}
rs11598047	10	***NEURL1***	Intronic	3.16×10^{-21}
rs35176054	10	***SH3PXD2A***	Intronic	1.75×10^{-11}
rs10824026	10	*SYNPO2L*	Intergenic	8.29×10^{-11}
rs75190942	11	***KCNJ5***	Intronic	2.82×10^{-8}
rs883079	12	***TBX5***	3'UTR	1.31×10^{-13}
rs2921421	15	*CGNL1*	Intergenic	3.29×10^{-8}
rs8040533	15	*HCN4*	Intergenic	3.09×10^{-11}
rs2106261	16	***ZFHX3***	Intronic	4.01×10^{-24}

Chr, chromosome; UTR, untranslated region. Bold font indicates that the variant lies within the gene. *The 4q25/*PITX2* region was not analyzed because the complexity of this association signal is not accurately evaluated with the GCTA method (**Online Methods**).

Supplementary Table 13. Overlap with atrial fibrillation risk factor GWAS loci

rsID	Chr	Closest gene*	rsID GWAS Catalog	LD	GWAS P-Value	HR	PR-S	PR-I	QRS	QT	Echo LVIDD	Stroke
ALL ANCESTRIES												
rs6843082	4	*PITX2(dist=154788);C4orf32(dist=1348486)*	rs6843082	1	$3.41x10^{-155}$							3
rs6843082	4	*PITX2(dist=154788);C4orf32(dist=1348486)*	rs12646447	0.51	$1.12x10^{-148}$							4
rs6843082	4	*PITX2(dist=154788);C4orf32(dist=1348486)*	rs2200733	0.51	$2.32x10^{-150}$							5
rs2967791	5	*KLHL3/WNT8A*	rs7722600	0.15	$1.25x10^{-6}$	6						
rs4946333	6	*SLC35F1/PLN*	rs457162	<0.10	0.0686					7		
rs4946333	6	*SLC35F1/PLN*	rs11752626	0.43	0.0001					8		
rs4946333	6	*SLC35F1/PLN*	rs11970286	0.48	$3.29x10^{-5}$					9,10		
rs4946333	6	*SLC35F1/PLN*	rs12210810	<0.10	0.001					10		
rs4946333	6	*SLC35F1/PLN*	rs12210733	<0.10	0.001					7		
rs4946333	6	*SLC35F1/PLN*	rs89107	0.99	$4.03x10^{-9}$						11	
rs4946333	6	*SLC35F1/PLN*	rs3902035	<0.10	0.002					7		
rs4946333	6	*SLC35F1/PLN*	rs11756438	0.29	0.0008					12		
rs4946333	6	*SLC35F1/PLN*	rs6906287	0.38	$5.84x10^{-5}$				13			
rs4946333	6	*SLC35F1/PLN*	rs11153730	0.45	$2.01x10^{-5}$	6				7,14		
rs4946333	6	*SLC35F1/PLN*	rs281868	1	$2.12x10^{-9}$	15						
rs1997572	7	*CAV1*	rs3807989	0.93	$1.47x10^{-14}$		16	9,17,18	9			
rs1997572	7	*CAV1*	rs11773845	0.94	$7.53x10^{-15}$			19,20				
rs1997572	7	*CAV1*	rs9920	0.15	0.0005					7		
rs883079	12	*TBX5*	rs883079	1	$1.80x10^{-15}$				21			
rs883079	12	*TBX5*	rs7312625	0.90	$1.03x10^{-14}$			22				
rs883079	12	*TBX5*	rs1895585	0.83	$1.25x10^{-14}$			19				
rs883079	12	*TBX5*	rs7135659	0.88	$9.59x10^{-15}$			20				
rs883079	12	*TBX5*	rs3825214	0.59	$1.82x10^{-10}$			9	9	9		
rs74022964	15	*HCN4(dist=15659);C15orf60(dist=58235)*	rs4489968	0.77	$4.59x10^{-11}$	6						
rs2106261	16	*ZFHX3*	rs879324	0.91	$1.13x10^{-25}$							3

Table showing overlap of genetic associations between cardiac phenotypes, identified through interrogation of the NHGRI-EBI GWAS catalog.[2] Numbers in superscript in the phenotype columns indicate references to the literature. Chr, chromosome; LD, linkage disequilibrium r^2 with lead SNP; HR, heart rate; PR-S, PR-segment; PR-I, PR-interval; LVIDD, Left Ventricle Internal Diastolic Diameter. *For intronic variants, the gene the variant is located within is listed; for intergenic variants, the closest genes upstream and downstream are listed.

Supplementary Table 14. Association between novel atrial fibrillation loci and stroke subtypes in the Neuro-CHARGE Stroke Consortium

			All stroke		Ischemic stroke		Cardioembolic stroke	
rsID	**Gene***	**Risk/ref allele**	**OR**	**P-value**	**OR**	**P-value**	**OR**	**P-value**
rs72700118	*METTL11B*	A/C	1.01	0.70	1.02	0.61	1.09	0.38
rs3771537	***ANXA4****/GMCL1*	A/C	1.00	0.85	0.99	0.75	0.99	0.88
rs2540949	***CEP68***	A/T	1.04	0.12	1.05	0.09	1.14	0.02
rs2288327	***TTN/TTN-AS1***	G/A	1.05	0.08	1.08	0.02	1.22	0.01
rs337711	***KCNN2***	T/C	0.97	0.16	0.96	0.18	0.97	0.63
rs2967791	***KLHL3****/WNT8A/FAM13B*	T/C	1.03	0.14	1.04	0.10	1.11	0.05
rs4946333	***SLC35F1****/PLN*	G/A	0.97	0.21	0.97	0.18	0.97	0.58
rs7508	***ASAH1***	A/G	1.04	0.12	1.04	0.17	1.11	0.14
rs35176054	***SH3PXD2A***	A/T	1.03	0.38	1.01	0.77	1.07	0.44
rs75190942	***KCNJ5***	A/C	1.01	0.85	1.04	0.45	-	-

OR, odds ratio. *Gene names in bold font indicate that the variant is located within the gene, whereas additional gene names indicate eQTL gene or gene strongly suspected to be causal due to the function of the encoded protein. For intergenic variants, the closest gene(s) are listed.

Supplementary Table 15. Association between novel atrial fibrillation loci and stroke subtypes in the Metastroke Consortium

			Ischemic stroke		Cardioembolic stroke		Large vessel disease		Small vessel disease	
rsID	**Gene***	**Risk/ref allele**	**OR**	**P-value**	**OR**	**P-value**	**OR**	**P-value**	**OR**	**P-value**
rs72700118	*METTL11B/ KIFAP3*	A/C	1.07	0.02	1.14	0.02	1.01	0.92	1.04	0.53
rs3771537	***ANXA4****/GMCL1*	A/C	0.99	0.52	1.02	0.57	0.94	0.08	1.00	0.95
rs2540949	***CEP68***	A/T	0.99	0.63	1.03	0.40	1.05	0.18	0.97	0.54
rs2288327	***TTN/TTN-AS1***	G/A	1.02	0.54	1.03	0.61	1.02	0.66	1.07	0.21
rs337711	***KCNN2***	T/C	1.01	0.50	1.08	0.04	1.00	0.90	0.94	0.19
rs2967791	***KLHL3****/WNT8A/FAM13B*	T/C	1.02	0.39	1.05	0.19	1.06	0.15	0.92	0.05
rs4946333	***SLC35F1****/PLN*	G/A	0.98	0.26	0.91	0.01	0.89	0.003	1.01	0.79
rs7508	***ASAH1***	A/G	0.98	0.37	1.00	1.00	1.03	0.45	0.94	0.17
rs35176054	***SH3PXD2A***	A/T	1.01	0.67	1.07	0.25	0.96	0.46	1.10	0.13
rs75190942	***KCNJ5***	A/C	1.02	0.59	1.09	0.31	1.03	0.73	0.98	0.80

OR, odds ratio. *Gene names in bold font indicate that the variant is located within the gene, whereas additional gene names indicate eQTL gene or gene strongly suspected to be causal due to the function of the encoded protein. For intergenic variants, the closest gene(s) are listed.

Supplementary Table 16. GO terms enriched in atrial fibrillation associated loci compared to GWAS catalog loci and to 1000 genomes matched loci

Gene Ontology Description	P-value	FDR Q-value
Compared to 1000 Genomes Matched Loci		
Small conductance calcium-activated potassium channel activity	9.48×10^{-5}	3.01×10^{-1}
Metal ion transport	1.62×10^{-4}	1.00
Potassium channel activity	2.52×10^{-4}	4.00×10^{-1}
Z disc	2.70×10^{-4}	3.85×10^{-1}
Monovalent inorganic cation transport	3.52×10^{-4}	1.00
Potassium ion transmembrane transport	5.08×10^{-4}	1.00
Cellular potassium ion transport	5.08×10^{-4}	1.00
Potassium ion transmembrane transporter activity	5.70×10^{-4}	6.04×10^{-1}
Regulation of cardiac muscle contraction	6.92×10^{-4}	1.00
Striated muscle tissue development	6.92×10^{-4}	1.00
Potassium ion transport	7.08×10^{-4}	1.00
Cation transport	7.34×10^{-4}	1.00
Regulation of heart rate	9.10×10^{-4}	1.00
Compared to GWAS catalog Loci		
Small conductance calcium-activated potassium channel activity	2.64×10^{-4}	7.43×10^{-1}
Z disc	2.67×10^{-4}	3.34×10^{-1}
Metal ion transport	3.17×10^{-4}	1.00
Potassium channel activity	4.14×10^{-4}	5.83×10^{-1}
Monovalent inorganic cation transport	7.01×10^{-4}	1.00

Supplementary Table 17. Summary of top eQTLS within atrial fibrillation associated loci

Index variant	Closest gene	Chr	eQTL variant	eQTL gene	Tissue	eQTL approach	*P* -value	FDR_gw*	r2**	Description of eQTL gene
rs11264280	*KCNN3*	1q21	1:154862564:C_CA	*ADAM15*	Left atrial appendage	CCAF		$8.38x10^{-4}$	-	ADAM Metallopeptidase Domain 15
rs72700118	*METTL11B*	1q24	rs72700114	*KIFAP3*	Left atrial appendage	CCAF		$1.65x10^{-2}$	-	Kinesin Associated Protein 3
rs520525	*PRRX1*	1q24	rs525489	*PRRX1*	Left atrial appendage	CCAF		$5.48x10^{-6}$	0.29	Paired related homeobox 1
rs520525	*PRRX1*	1q24	rs680084	*PRRX1*	Left ventricle	GTEx lookup	$5.2x10^{-6}$		0.35	Paired related homeobox 1
rs520525	*PRRX1*	1q24	rs651822	*PRRX1*	Skeletal muscle	GTEx lookup	$1.68x10^{-6}$		0.89	Paired related homeobox 1
rs520525	*PRRX1*	1q24	rs1234284	*RP1-79C4.4*	Left ventricle	GTEx lookup	$2.52x10^{-8}$		-	LincRNA
rs520525	*PRRX1*	1q24	rs651822	*RP1-79C4.4*	Skeletal muscle	GTEx lookup	$1.53x10^{-14}$		0.89	LincRNA
rs3771537	*ANXA4*	2p13	rs11126244	*ANXA4*	Left ventricle	GTEx lookup	$1.55x10^{-6}$		0.21	Annexin A4
rs3771537	*ANXA4*	2p13	rs12619656	*GMCL1*	Left ventricle	GTEx lookup	$1.06x10^{-6}$		0.35	Germ cell-less, spermatogenesis associated 1
rs3771537	*ANXA4*	2p13	rs56222989	*GMCL1*	Skeletal muscle	GTEx lookup	$5.52x10^{-13}$		0.36	Germ cell-less, spermatogenesis associated 1
rs3771537	*ANXA4*	2p13	rs55866046	*PCYOX1*	Left ventricle	GTEx lookup	$1.27x10^{-5}$		0.27	Prenylcysteine oxidase 1
rs3771537	*ANXA4*	2p13	rs2312555	*SNRNP27*	Skeletal muscle	GTEx lookup	$1.55x10^{-13}$		0.99	Small Nuclear Ribonucleoprotein U4/U6.U5 Subunit 27
rs2540949	*CEP68*	2p14	rs2540950	*CEP68*	Left atrial appendage	CCAF		$9.35x10^{-14}$	0.93	Centrosomal protein 68kDa
rs2540949	*CEP68*	2p14	rs2249105	*CEP68*	Atrial appendage	GTEx lookup	$6.13x10^{-13}$		0.93	Centrosomal protein 68kDa
rs2540949	*CEP68*	2p14	rs74181299	*CEP68*	Left ventricle	GTEx lookup	$9.45x10^{-8}$		1.00	Centrosomal protein 68kDa
rs2540949	*CEP68*	2p14	rs2540949	*CEP68*	Skeletal muscle	GTEx lookup	$5.02x10^{-13}$		1.00	Centrosomal protein 68kDa
rs11718898	*CAND2*	3p25	rs11718898	*CAND2*	Skeletal muscle	GTEx lookup	$2.24x10^{-20}$		1.00	Cullin-associated NEDD8-dissociated protein 2
rs11718898	*CAND2*	3p25	rs11718898	*KRT18P17*	Skeletal muscle	GTEx lookup	$2.24x10^{-9}$		1.00	Keratin 18 Pseudogene 17
rs11718898	*CAND2*	3p25	rs11718898	*RP11-767C1.2*	Skeletal muscle	GTEx lookup	$1.02x10^{-6}$		1.00	Antisense RNA gene
rs337711	*KCNN2*	5q22	rs337705	*KCNN2*	Left atrial appendage	CCAF		$9.05x10^{-3}$	0.99	Potassium Calcium-Activated Channel Subfamily N Member 2
rs2967791	*KLHL3*	5q31	rs2967793	*FAM13B*	Atrial appendage	GTEx region based analysis	$3.12x10^{-7}$		0.15	Family with sequence similarity 13, member B
rs2967791	*KLHL3*	5q31	rs11745324	*REEP2*	Left ventricle	GTEx region based analysis	$1.02x10^{-5}$		0.35	Receptor accessory protein 2
rs1997572	*CAV1*	7q31	rs1049337	*CAV1*	Left atrial appendage	CCAF		$4.96x10^{-4}$	0.26	Caveolin 1
rs1997572	*CAV2*	7q31	rs2270188	*CAV2*	Left atrial appendage	CCAF		$1.83x10^{-8}$	0.46	Caveolin 2
rs7508	*ASAH1*	8p22	rs399485	*ASAH1*	Left atrial appendage	CCAF		$2.08x10^{-3}$	0.92	N-Acylsphingosine Amidohydrolase 1
rs7508	*ASAH1*	8p22	rs7508	*PCM1*	Left atrial appendage	CCAF		$9.56x10^{-14}$	1.00	Pericentriolar material 1
rs7508	*ASAH1*	8p22	rs7508	*PCM1*	Left ventricle	GTEx lookup	$3.18x10^{-6}$		1.00	Pericentriolar material 1
rs7508	*ASAH1*	8p22	rs7508	*PCM1*	Skeletal muscle	GTEx lookup	$1.12x10^{-6}$		1.00	Pericentriolar material 1
rs7508	*ASAH1*	8p22	rs483159	*RP11-806O11.1*	Left ventricle	GTEx region based analysis	$1.93x10^{-7}$		0.74	Processed transcript
rs7915134	*SYNPO2L*	10q22	rs60212594	*MYOZ1*	Left atrial appendage	CCAF		$8.27x10^{-34}$	0.95	Myozenin 1
rs7915134	*SYNPO2L*	10q22	rs4746139	*SYNPO2L*	Left atrial appendage	CCAF		$6.32x10^{-6}$	0.92	Synaptopodin 2 Like
rs7915134	*SYNPO2L*	10q22	rs3861036	*PLAU*	Atrial appendage	GTEx region based analysis	$2.11x10^{-7}$		0.16	Plasminogen activator, urokinase
rs7915134	*SYNPO2L*	10q22	rs68170615	*USP54*	Left ventricle	GTEx region based analysis	$2.38x10^{-5}$		-	Ubiquitin specific peptidase 54
rs7915134	*SYNPO2L*	10q22	rs2177843	*MYOZ1*	Atrial appendage	GTEx lookup	$5.93x10^{-24}$		0.83	Myozenin 1
rs7915134	*SYNPO2L*	10q22	rs147790633	*FUT11*	Skeletal muscle	GTEx lookup	$3.84x10^{-6}$		0.90	Fucosyltransferase 11 (alpha (1,3) fucosyltransferase)
rs7915134	*SYNPO2L*	10q22	rs201617396	*RP11-137L10.6*	Left ventricle	GTEx region based analysis	$2.38x10^{-5}$		-	PPP3CB antisense RNA 1 (head to head)
rs11598047	*NEURL*	10q24	rs12268602	*USMG5;MIR1307*	Left atrial appendage	CCAF		$3.25x10^{-2}$	0.14	Up-regulated during skeletal muscle growth protein 5; MicroRNA 1307
rs75190942	*KCNJ5*	11q24	rs76097649	*KCNJ5*	Left atrial appendage	CCAF		$2.77x10^{-2}$	1.00	Potassium channel, inwardly rectifying subfamily J, member 5
rs75190942	*KCNJ5*	11q24	rs76097649	*KCNJ5*	Left ventricle	GTEx lookup	$3.15x10^{-6}$		1.00	Potassium channel, inwardly rectifying subfamily J, member 5
rs75190942	*KCNJ5*	11q24	rs78907918	*C11orf45*	Left ventricle	GTEx region based analysis	$4.97x10^{-7}$		0.83	Chromosome 11 open reading frame 45
rs883079	*TBX5*	12q24	rs1946295	*TBX5*	Left atrial appendage	CCAF		$1.69x10^{-3}$	0.80	T-box 5
rs883079	*TBX5*	12q24	rs2891503	*TBX5*	Left ventricle	GTEx lookup	$3.84x10^{-6}$		0.73	T-box 5
rs1152591	*SYNE2*	14q23	rs2738413	*SYNE2*	Left atrial appendage	CCAF		$7.47x10^{-12}$	1.00	Spectrin repeat containing, nuclear envelope 2
rs1152591	*SYNE2*	14q23	rs2738413	*SYNE2*	Left ventricle	GTEx lookup	$2.54x10^{-11}$		1.00	Spectrin repeat containing, nuclear envelope 2

CCAF, Cleveland Clinic Atrial Tissue Bank and Arrhythmia Biorepository; Chr, chromosome; eQTL, expression quantitative trait locus; GTEx, Genotype-Tissue Expression database. *Genome-wide false discovery rate. **LD between index variant and eQTL variant. For some variants, there were no LD information available in the 1000 Genomes reference database (-).

Supplementary Table 18. *In silico* eQTL analysis in GTEx database

Index SNP*	*Closest Gene/s***	Chr	Position	rsID†	Tissue	Gene‡	Effect Allele	Beta	TSS Distance	P-value
				GWAS						
Variants identified in combined ethnicity analysis - eQTLs from GTEx Release V6										
rs520525	*GORAB(dist=105281);PRRX1(dist=5058)*	1	170628255	rs680084	Left ventricle	PRRX1	A	0.32	-3614	5.20E-06
rs520525	*GORAB(dist=108789);PRRX1(dist=1550)*	1	170631763	rs629234	Left ventricle	PRRX1	C	0.31	-106	6.83E-06
rs520525	*GORAB(dist=37630);PRRX1(dist=72709)*	1	170560604	rs6658866	Left ventricle	RP1-79C4.4	G	-0.40	-75918	9.05E-08
rs520525	*GORAB(dist=38430);PRRX1(dist=71909)*	1	170561404	rs6659754	Left ventricle	RP1-79C4.4	T	-0.39	-75118	2.94E-07
rs520525	*GORAB(dist=40109);PRRX1(dist=70230)*	1	170563083	rs577827	Left ventricle	RP1-79C4.4	C	0.38	-73439	1.15E-07
rs520525	*GORAB(dist=40231);PRRX1(dist=70108)*	1	170563205	rs12027180	Left ventricle	RP1-79C4.4	T	0.40	-73317	1.75E-06
rs520525	*GORAB(dist=43031);PRRX1(dist=67308)*	1	170566005	rs763567	Left ventricle	RP1-79C4.4	G	-0.39	-70517	2.53E-07
rs520525	*GORAB(dist=44463);PRRX1(dist=65876)*	1	170567437	rs1928715	Left ventricle	RP1-79C4.4	T	-0.41	-69085	9.33E-08
rs520525	*GORAB(dist=45740);PRRX1(dist=64599)*	1	170568714	rs12755237	Left ventricle	RP1-79C4.4	A	-0.42	-67808	6.17E-08
rs520525	*GORAB(dist=45922);PRRX1(dist=64417)*	1	170568896	rs12742164	Left ventricle	RP1-79C4.4	G	-0.43	-67626	2.83E-08
rs520525	*GORAB(dist=46343);PRRX1(dist=63996)*	1	170569317	rs3903239	Left ventricle	RP1-79C4.4	G	-0.41	-67205	1.18E-07
rs520525	*GORAB(dist=46715);PRRX1(dist=63624)*	1	170569689	rs12760630	Left ventricle	RP1-79C4.4	A	-0.41	-66833	1.21E-07
rs520525	*GORAB(dist=47069);PRRX1(dist=63270)*	1	170570043	rs10800529	Left ventricle	RP1-79C4.4	C	0.41	-66479	1.12E-06
rs520525	*GORAB(dist=47525);PRRX1(dist=62814)*	1	170570499	rs7412231	Left ventricle	RP1-79C4.4	C	-0.41	-66023	1.29E-07
rs520525	*GORAB(dist=48869);PRRX1(dist=61470)*	1	170571843	rs1234230	Left ventricle	RP1-79C4.4	G	-0.39	-64679	9.15E-08
rs520525	*GORAB(dist=49972);PRRX1(dist=60367)*	1	170572946	rs10919437	Left ventricle	RP1-79C4.4	A	-0.40	-63576	1.58E-07
rs520525	*GORAB(dist=50284);PRRX1(dist=60055)*	1	170573258	rs61217505	Left ventricle	RP1-79C4.4	T	-0.41	-63264	9.94E-08
rs520525	*GORAB(dist=50840);PRRX1(dist=59499)*	1	170573814	rs476810	Left ventricle	RP1-79C4.4	C	-0.38	-62708	2.01E-07
rs520525	*GORAB(dist=51954);PRRX1(dist=58385)*	1	170574928	rs1234233	Left ventricle	RP1-79C4.4	T	-0.37	-61594	2.17E-07
rs520525	*GORAB(dist=53133);PRRX1(dist=57206)*	1	170576107	rs2206062	Left ventricle	RP1-79C4.4	C	-0.40	-60415	2.06E-07
rs520525	*GORAB(dist=53764);PRRX1(dist=56575)*	1	170576738	rs566850	Left ventricle	RP1-79C4.4	G	-0.37	-59784	2.47E-07
rs520525	*GORAB(dist=54081);PRRX1(dist=56258)*	1	170577055	rs722597	Left ventricle	RP1-79C4.4	A	0.41	-59467	1.12E-06
rs520525	*GORAB(dist=54261);PRRX1(dist=56078)*	1	170577235	rs647438	Left ventricle	RP1-79C4.4	T	-0.39	-59287	1.39E-07
rs520525	*GORAB(dist=54866);PRRX1(dist=55473)*	1	170577840	rs72482606	Left ventricle	RP1-79C4.4	A	0.41	-58682	1.12E-06
rs520525	*GORAB(dist=55332);PRRX1(dist=55007)*	1	170578306	rs10919440	Left ventricle	RP1-79C4.4	G	-0.40	-58216	2.27E-07
rs520525	*GORAB(dist=55613);PRRX1(dist=54726)*	1	170578587	rs494339	Left ventricle	RP1-79C4.4	A	-0.39	-57935	1.14E-07
rs520525	*GORAB(dist=56115);PRRX1(dist=54224)*	1	170579089	rs10919441	Left ventricle	RP1-79C4.4	A	0.40	-57433	1.69E-06
rs520525	*GORAB(dist=56620);PRRX1(dist=53719)*	1	170579594	rs546258	Left ventricle	RP1-79C4.4	T	-0.37	-56928	3.08E-07
rs520525	*GORAB(dist=57503);PRRX1(dist=52836)*	1	170580477	rs553905	Left ventricle	RP1-79C4.4	G	-0.37	-56045	4.37E-07
rs520525	*GORAB(dist=58560);PRRX1(dist=51779)*	1	170581534	rs2982131	Left ventricle	RP1-79C4.4	C	-0.37	-54988	3.52E-07
rs520525	*GORAB(dist=58660);PRRX1(dist=51679)*	1	170581634	rs10919444	Left ventricle	RP1-79C4.4	A	-0.40	-54888	1.81E-07
rs520525	*GORAB(dist=58713);PRRX1(dist=51626)*	1	170581687	rs34252585	Left ventricle	RP1-79C4.4	A	0.40	-54835	1.68E-06
rs520525	*GORAB(dist=59601);PRRX1(dist=50738)*	1	170582575	rs1952675	Left ventricle	RP1-79C4.4	G	-0.40	-53947	1.98E-07
rs520525	*GORAB(dist=60537);PRRX1(dist=49802)*	1	170583511	rs6677540	Left ventricle	RP1-79C4.4	A	-0.39	-53011	3.98E-07
rs520525	*GORAB(dist=60970);PRRX1(dist=49369)*	1	170583944	rs6690642	Left ventricle	RP1-79C4.4	C	-0.39	-52578	4.14E-07
rs520525	*GORAB(dist=62123);PRRX1(dist=48216)*	1	170585097	rs2206063	Left ventricle	RP1-79C4.4	C	0.40	-51425	1.58E-06
rs520525	*GORAB(dist=62858);PRRX1(dist=47481)*	1	170585832	rs619456	Left ventricle	RP1-79C4.4	C	-0.36	-50690	5.05E-07
rs520525	*GORAB(dist=63341);PRRX1(dist=46998)*	1	170586315	rs736791	Left ventricle	RP1-79C4.4	A	-0.40	-50207	2.72E-07
rs520525	*GORAB(dist=64241);PRRX1(dist=46098)*	1	170587215	rs576736	Left ventricle	RP1-79C4.4	G	0.43	-49307	2.66E-07
rs520525	*GORAB(dist=64366);PRRX1(dist=45973)*	1	170587340	rs577676	Left ventricle	RP1-79C4.4	T	0.38	-49182	6.26E-06
rs520525	*GORAB(dist=65620);PRRX1(dist=44719)*	1	170588594	rs2022373	Left ventricle	RP1-79C4.4	C	0.42	-47928	5.17E-07
rs520525	*GORAB(dist=66463);PRRX1(dist=43876)*	1	170589437	rs10489231	Left ventricle	RP1-79C4.4	A	0.42	-47085	3.68E-07
rs520525	*GORAB(dist=66936);PRRX1(dist=43403)*	1	170589910	rs2022372	Left ventricle	RP1-79C4.4	A	-0.39	-46612	2.93E-07
rs520525	*GORAB(dist=67593);PRRX1(dist=42746)*	1	170590567	rs12031871	Left ventricle	RP1-79C4.4	T	0.43	-45955	2.42E-07
rs520525	*GORAB(dist=68336);PRRX1(dist=42003)*	1	170591310	rs651386	Left ventricle	RP1-79C4.4	T	0.38	-45212	4.78E-06
rs520525	*GORAB(dist=68834);PRRX1(dist=41505)*	1	170591808	rs10753817	Left ventricle	RP1-79C4.4	G	0.43	-44714	2.41E-07
rs520525	*GORAB(dist=71095);PRRX1(dist=39244)*	1	170594069	rs12072276	Left ventricle	RP1-79C4.4	G	0.42	-42453	4.27E-07
rs520525	*GORAB(dist=71142);PRRX1(dist=39197)*	1	170594116	rs10919446	Left ventricle	RP1-79C4.4	A	0.42	-42406	3.75E-07
rs520525	*GORAB(dist=72144);PRRX1(dist=38195)*	1	170595118	rs12074059	Left ventricle	RP1-79C4.4	T	0.41	-41404	5.57E-07
rs520525	*GORAB(dist=73098);PRRX1(dist=37241)*	1	170596072	rs494521	Left ventricle	RP1-79C4.4	T	0.38	-40450	8.69E-07
rs520525	*GORAB(dist=73284);PRRX1(dist=37055)*	1	170596258	rs1234275	Left ventricle	RP1-79C4.4	G	0.38	-40264	6.32E-07
rs520525	*GORAB(dist=73399);PRRX1(dist=36940)*	1	170596373	rs1234274	Left ventricle	RP1-79C4.4	G	0.38	-40149	6.33E-07
rs520525	*GORAB(dist=73571);PRRX1(dist=36768)*	1	170596545	rs11577602	Left ventricle	RP1-79C4.4	T	0.42	-39977	6.50E-07
rs520525	*GORAB(dist=73598);PRRX1(dist=36741)*	1	170596572	rs10800530	Left ventricle	RP1-79C4.4	A	0.42	-39950	6.50E-07
rs520525	*GORAB(dist=75213);PRRX1(dist=35126)*	1	170598187	rs638704	Left ventricle	RP1-79C4.4	T	0.37	-38335	1.13E-06
rs520525	*GORAB(dist=76599);PRRX1(dist=33740)*	1	170599573	rs10919448	Left ventricle	RP1-79C4.4	C	0.42	-36949	6.37E-07
rs520525	*GORAB(dist=78034);PRRX1(dist=32305)*	1	170601008	rs189058353	Left ventricle	RP1-79C4.4	A	0.37	-35514	2.32E-06
rs520525	*GORAB(dist=78339);PRRX1(dist=32000)*	1	170601313	rs12068805	Left ventricle	RP1-79C4.4	C	0.42	-35209	5.67E-07
rs520525	*GORAB(dist=78961);PRRX1(dist=31378)*	1	170601935	rs12566725	Left ventricle	RP1-79C4.4	T	0.42	-34587	5.66E-07
rs520525	*GORAB(dist=81148);PRRX1(dist=29191)*	1	170604122	rs598993	Left ventricle	RP1-79C4.4	C	0.37	-32400	1.68E-06
rs520525	*GORAB(dist=81964);PRRX1(dist=28375)*	1	170604938	rs541557	Left ventricle	RP1-79C4.4	G	0.37	-31584	1.68E-06
rs520525	*GORAB(dist=83112);PRRX1(dist=27227)*	1	170606086	rs644784	Left ventricle	RP1-79C4.4	T	0.42	-30436	5.59E-07
rs520525	*GORAB(dist=83380);PRRX1(dist=26959)*	1	170606354	rs656539	Left ventricle	RP1-79C4.4	T	0.42	-30168	5.58E-07
rs520525	*GORAB(dist=85107);PRRX1(dist=25232)*	1	170608081	rs539045	Left ventricle	RP1-79C4.4	T	0.37	-28441	1.69E-06
rs520525	*GORAB(dist=85694);PRRX1(dist=24645)*	1	170608668	rs533603	Left ventricle	RP1-79C4.4	G	0.42	-27854	5.45E-07
rs520525	*GORAB(dist=86216);PRRX1(dist=24123)*	1	170609190	rs473832	Left ventricle	RP1-79C4.4	C	0.37	-27332	8.85E-07
rs520525	*GORAB(dist=86651);PRRX1(dist=23688)*	1	170609625	rs580487	Left ventricle	RP1-79C4.4	C	0.37	-26897	1.70E-06
rs520525	*GORAB(dist=86769);PRRX1(dist=23570)*	1	170609743	rs578928	Left ventricle	RP1-79C4.4	C	0.42	-26779	5.41E-07
rs520525	*GORAB(dist=87736);PRRX1(dist=22603)*	1	170610710	rs549449	Left ventricle	RP1-79C4.4	C	0.42	-25812	5.19E-07
rs520525	*GORAB(dist=89288);PRRX1(dist=21051)*	1	170612262	rs492804	Left ventricle	RP1-79C4.4	T	0.37	-24260	1.11E-06
rs520525	*GORAB(dist=89899);PRRX1(dist=20440)*	1	170612873	rs639652	Left ventricle	RP1-79C4.4	A	0.36	-23649	1.82E-06
rs520525	*GORAB(dist=89952);PRRX1(dist=20387)*	1	170612926	rs639720	Left ventricle	RP1-79C4.4	C	0.42	-23596	5.17E-07
rs520525	*GORAB(dist=90876);PRRX1(dist=19463)*	1	170613850	rs654461	Left ventricle	RP1-79C4.4	T	0.37	-22672	1.05E-06
rs520525	*GORAB(dist=90895);PRRX1(dist=19444)*	1	170613869	rs567328	Left ventricle	RP1-79C4.4	A	0.38	-22653	7.46E-07
rs520525	*GORAB(dist=91068);PRRX1(dist=19271)*	1	170614042	rs544478	Left ventricle	RP1-79C4.4	T	0.38	-22480	7.82E-07
rs520525	*GORAB(dist=91270);PRRX1(dist=19069)*	1	170614244	rs666419	Left ventricle	RP1-79C4.4	C	0.42	-22278	5.17E-07
rs520525	*GORAB(dist=92886);PRRX1(dist=17453)*	1	170615860	rs593173	Left ventricle	RP1-79C4.4	A	0.42	-20662	5.17E-07
rs520525	*GORAB(dist=92943);PRRX1(dist=17396)*	1	170615917	rs593560	Left ventricle	RP1-79C4.4	A	0.37	-20605	1.09E-06
rs520525	*GORAB(dist=93381);PRRX1(dist=16958)*	1	170616355	rs2988392	Left ventricle	RP1-79C4.4	C	0.36	-20167	1.69E-06
rs520525	*GORAB(dist=94332);PRRX1(dist=16007)*	1	170617306	rs608930	Left ventricle	RP1-79C4.4	T	0.37	-19216	7.89E-07
rs520525	*GORAB(dist=94405);PRRX1(dist=15934)*	1	170617379	rs619699	Left ventricle	RP1-79C4.4	A	0.45	-19143	2.63E-07
rs520525	*GORAB(dist=95317);PRRX1(dist=15022)*	1	170618291	rs623752	Left ventricle	RP1-79C4.4	G	0.37	-18231	6.72E-07

Supplementary Table 18. *continued*

rs520525	*GORAB(dist=95408);PRRX1(dist=14931)*	1	170618382	rs531007	Left ventricle	RP1-79C4.4	G	0.37	-18140	6.54E-07
rs520525	*GORAB(dist=96350);PRRX1(dist=13989)*	1	170619324	rs1234282	Left ventricle	RP1-79C4.4	T	0.47	-17198	5.41E-08
rs520525	*GORAB(dist=96633);PRRX1(dist=13706)*	1	170619607	rs575432	Left ventricle	RP1-79C4.4	G	0.36	-16915	2.23E-06
rs520525	*GORAB(dist=96956);PRRX1(dist=13383)*	1	170619930	rs651822	Left ventricle	RP1-79C4.4	T	0.41	-16592	9.51E-07
rs520525	*GORAB(dist=99994);PRRX1(dist=10345)*	1	170622968	rs1234284	Left ventricle	RP1-79C4.4	T	0.47	-13554	2.52E-08
rs520525	*GORAB(dist=100135);PRRX1(dist=10204)*	1	170623109	rs588837	Left ventricle	RP1-79C4.4	G	0.37	-13413	1.17E-06
rs520525	*GORAB(dist=100946);PRRX1(dist=9393)*	1	170623920	rs12089974	Left ventricle	RP1-79C4.4	A	0.42	-12602	2.65E-06
rs520525	*GORAB(dist=102893);PRRX1(dist=7446)*	1	170625867	rs501680	Left ventricle	RP1-79C4.4	C	0.46	-10655	9.04E-08
rs520525	*GORAB(dist=103979);PRRX1(dist=6360)*	1	170626953	rs663887	Left ventricle	RP1-79C4.4	A	0.46	-9569	9.04E-08
rs520525	*GORAB(dist=104820);PRRX1(dist=5519)*	1	170627794	rs552277	Left ventricle	RP1-79C4.4	C	0.45	-8728	1.40E-07
rs520525	*GORAB(dist=105281);PRRX1(dist=5058)*	1	170628255	rs680084	Left ventricle	RP1-79C4.4	A	0.38	-8267	5.99E-07
rs520525	*GORAB(dist=105414);PRRX1(dist=4925)*	1	170628388	rs583006	Left ventricle	RP1-79C4.4	G	0.42	-8134	1.60E-06
rs520525	*GORAB(dist=105461);PRRX1(dist=4878)*	1	170628435	rs524877	Left ventricle	RP1-79C4.4	C	0.46	-8087	9.04E-08
rs520525	*GORAB(dist=106864);PRRX1(dist=3475)*	1	170629838	rs600093	Left ventricle	RP1-79C4.4	A	0.46	-6684	1.01E-07
rs520525	*GORAB(dist=107285);PRRX1(dist=3054)*	1	170630259	rs601938	Left ventricle	RP1-79C4.4	T	0.46	-6263	9.08E-08
rs520525	*GORAB(dist=108446);PRRX1(dist=1893)*	1	170631420	rs627848	Left ventricle	RP1-79C4.4	A	0.46	-5102	9.14E-08
rs520525	*GORAB(dist=108789);PRRX1(dist=1550)*	1	170631763	rs629234	Left ventricle	RP1-79C4.4	C	0.38	-4759	4.19E-07
rs520525	*PRRX1*	1	170635002	rs525489	Left ventricle	RP1-79C4.4	G	0.34	-1520	4.44E-06
rs520525	*PRRX1*	1	170635084	rs503706	Left ventricle	RP1-79C4.4	C	0.34	-1438	4.44E-06
rs520525	*PRRX1*	1	170636079	rs473133	Left ventricle	RP1-79C4.4	T	0.34	-443	4.42E-06
rs520525	*PRRX1*	1	170638333	rs520525	Left ventricle	RP1-79C4.4	G	0.44	1811	4.05E-07
rs520525	*PRRX1*	1	170638658	rs10919449	Left ventricle	RP1-79C4.4	A	0.34	2136	1.10E-06
rs520525	*GORAB(dist=94405);PRRX1(dist=15934)*	1	170617379	rs619699	Skeletal muscle	PRRX1	A	0.22	-14490	4.96E-06
rs520525	*GORAB(dist=96350);PRRX1(dist=13989)*	1	170619324	rs1234282	Skeletal muscle	PRRX1	T	0.21	-12545	1.04E-05
rs520525	*GORAB(dist=96956);PRRX1(dist=13383)*	1	170619930	rs651822	Skeletal muscle	PRRX1	T	0.22	-11939	1.68E-06
rs520525	*GORAB(dist=99994);PRRX1(dist=10345)*	1	170622968	rs1234284	Skeletal muscle	PRRX1	T	0.21	-8901	6.56E-06
rs520525	*GORAB(dist=102893);PRRX1(dist=7446)*	1	170625867	rs501680	Skeletal muscle	PRRX1	C	0.20	-6002	1.30E-05
rs520525	*GORAB(dist=103979);PRRX1(dist=6360)*	1	170626953	rs663887	Skeletal muscle	PRRX1	A	0.20	-4916	1.30E-05
rs520525	*GORAB(dist=105461);PRRX1(dist=4878)*	1	170628435	rs524877	Skeletal muscle	PRRX1	C	0.20	-3434	1.30E-05
rs520525	*GORAB(dist=106864);PRRX1(dist=3475)*	1	170629838	rs600093	Skeletal muscle	PRRX1	A	0.21	-2031	7.09E-06
rs520525	*GORAB(dist=107285);PRRX1(dist=3054)*	1	170630259	rs601938	Skeletal muscle	PRRX1	T	0.20	-1610	1.38E-05
rs520525	*PRRX1*	1	170638333	rs520525	Skeletal muscle	PRRX1	G	0.21	6464	1.10E-05
rs520525	*GORAB(dist=37630);PRRX1(dist=72709)*	1	170560604	rs6658866	Skeletal muscle	RP1-79C4.4	G	-0.38	-75918	1.25E-09
rs520525	*GORAB(dist=38430);PRRX1(dist=71909)*	1	170561404	rs6659754	Skeletal muscle	RP1-79C4.4	T	-0.39	-75118	1.72E-10
rs520525	*GORAB(dist=40109);PRRX1(dist=70230)*	1	170563083	rs577827	Skeletal muscle	RP1-79C4.4	C	0.40	-73439	1.08E-10
rs520525	*GORAB(dist=40231);PRRX1(dist=70108)*	1	170563205	rs12027180	Skeletal muscle	RP1-79C4.4	T	0.39	-73317	1.69E-08
rs520525	*GORAB(dist=43031);PRRX1(dist=67308)*	1	170566005	rs763567	Skeletal muscle	RP1-79C4.4	G	-0.39	-70517	2.66E-10
rs520525	*GORAB(dist=44463);PRRX1(dist=65876)*	1	170567437	rs1928715	Skeletal muscle	RP1-79C4.4	T	-0.39	-69085	2.78E-10
rs520525	*GORAB(dist=45740);PRRX1(dist=64599)*	1	170568714	rs12755237	Skeletal muscle	RP1-79C4.4	A	-0.40	-67808	2.59E-10
rs520525	*GORAB(dist=45922);PRRX1(dist=64417)*	1	170568896	rs12742164	Skeletal muscle	RP1-79C4.4	G	-0.40	-67626	2.32E-10
rs520525	*GORAB(dist=46343);PRRX1(dist=63996)*	1	170569317	rs3903239	Skeletal muscle	RP1-79C4.4	G	-0.39	-67205	2.53E-10
rs520525	*GORAB(dist=46715);PRRX1(dist=63624)*	1	170569689	rs12760630	Skeletal muscle	RP1-79C4.4	A	-0.39	-66833	2.53E-10
rs520525	*GORAB(dist=47069);PRRX1(dist=63270)*	1	170570043	rs10800529	Skeletal muscle	RP1-79C4.4	C	0.38	-66479	5.17E-08
rs520525	*GORAB(dist=47525);PRRX1(dist=62814)*	1	170570499	rs7412231	Skeletal muscle	RP1-79C4.4	C	-0.39	-66023	2.55E-10
rs520525	*GORAB(dist=48869);PRRX1(dist=61470)*	1	170571843	rs1234230	Skeletal muscle	RP1-79C4.4	G	-0.37	-64679	4.16E-09
rs520525	*GORAB(dist=49972);PRRX1(dist=60367)*	1	170572946	rs10919437	Skeletal muscle	RP1-79C4.4	A	-0.39	-63576	2.60E-10
rs520525	*GORAB(dist=50284);PRRX1(dist=60055)*	1	170573258	rs61217505	Skeletal muscle	RP1-79C4.4	T	-0.40	-63264	9.87E-11
rs520525	*GORAB(dist=50840);PRRX1(dist=59499)*	1	170573814	rs476810	Skeletal muscle	RP1-79C4.4	C	-0.38	-62708	5.99E-10
rs520525	*GORAB(dist=51954);PRRX1(dist=58385)*	1	170574928	rs1234233	Skeletal muscle	RP1-79C4.4	T	-0.38	-61594	6.10E-10
rs520525	*GORAB(dist=53133);PRRX1(dist=57206)*	1	170576107	rs2206062	Skeletal muscle	RP1-79C4.4	C	-0.39	-60415	2.69E-10
rs520525	*GORAB(dist=53764);PRRX1(dist=56575)*	1	170576738	rs566850	Skeletal muscle	RP1-79C4.4	G	-0.38	-59784	6.29E-10
rs520525	*GORAB(dist=54081);PRRX1(dist=56258)*	1	170577055	rs722597	Skeletal muscle	RP1-79C4.4	A	0.38	-59467	5.21E-08
rs520525	*GORAB(dist=54261);PRRX1(dist=56078)*	1	170577235	rs647438	Skeletal muscle	RP1-79C4.4	T	-0.37	-59287	3.49E-09
rs520525	*GORAB(dist=54866);PRRX1(dist=55473)*	1	170577840	rs72482606	Skeletal muscle	RP1-79C4.4	A	0.38	-58682	5.21E-08
rs520525	*GORAB(dist=55332);PRRX1(dist=55007)*	1	170578306	rs10919440	Skeletal muscle	RP1-79C4.4	G	-0.39	-58216	2.39E-10
rs520525	*GORAB(dist=55613);PRRX1(dist=54726)*	1	170578587	rs494339	Skeletal muscle	RP1-79C4.4	A	-0.37	-57935	2.85E-09
rs520525	*GORAB(dist=56115);PRRX1(dist=54224)*	1	170579089	rs10919441	Skeletal muscle	RP1-79C4.4	A	0.40	-57433	4.65E-09
rs520525	*GORAB(dist=56620);PRRX1(dist=53719)*	1	170579594	rs546258	Skeletal muscle	RP1-79C4.4	T	-0.38	-56928	6.66E-10
rs520525	*GORAB(dist=57503);PRRX1(dist=52836)*	1	170580477	rs553905	Skeletal muscle	RP1-79C4.4	G	-0.37	-56045	1.56E-09
rs520525	*GORAB(dist=58560);PRRX1(dist=51779)*	1	170581534	rs2982131	Skeletal muscle	RP1-79C4.4	C	-0.38	-54988	9.67E-10
rs520525	*GORAB(dist=58660);PRRX1(dist=51679)*	1	170581634	rs10919444	Skeletal muscle	RP1-79C4.4	A	-0.39	-54888	2.92E-10
rs520525	*GORAB(dist=58713);PRRX1(dist=51626)*	1	170581687	rs34252585	Skeletal muscle	RP1-79C4.4	A	0.40	-54835	4.65E-09
rs520525	*GORAB(dist=59601);PRRX1(dist=50738)*	1	170582575	rs1952675	Skeletal muscle	RP1-79C4.4	G	-0.39	-53947	2.96E-10
rs520525	*GORAB(dist=60537);PRRX1(dist=49802)*	1	170583511	rs6677540	Skeletal muscle	RP1-79C4.4	A	-0.39	-53011	3.02E-10
rs520525	*GORAB(dist=60970);PRRX1(dist=49369)*	1	170583944	rs6690642	Skeletal muscle	RP1-79C4.4	C	-0.39	-52578	3.05E-10
rs520525	*GORAB(dist=62123);PRRX1(dist=48216)*	1	170585097	rs2206063	Skeletal muscle	RP1-79C4.4	C	0.40	-51425	4.53E-09
rs520525	*GORAB(dist=62858);PRRX1(dist=47481)*	1	170585832	rs619456	Skeletal muscle	RP1-79C4.4	C	-0.38	-50690	7.70E-10
rs520525	*GORAB(dist=63341);PRRX1(dist=46998)*	1	170586315	rs736791	Skeletal muscle	RP1-79C4.4	A	-0.39	-50207	3.16E-10
rs520525	*GORAB(dist=64241);PRRX1(dist=46098)*	1	170587215	rs576736	Skeletal muscle	RP1-79C4.4	G	0.38	-49307	2.00E-08
rs520525	*GORAB(dist=64366);PRRX1(dist=45973)*	1	170587340	rs577676	Skeletal muscle	RP1-79C4.4	T	0.34	-49182	1.11E-07
rs520525	*GORAB(dist=65620);PRRX1(dist=44719)*	1	170588594	rs2022373	Skeletal muscle	RP1-79C4.4	C	0.40	-47928	5.12E-09
rs520525	*GORAB(dist=66463);PRRX1(dist=43876)*	1	170589437	rs10489231	Skeletal muscle	RP1-79C4.4	A	0.42	-47085	1.53E-09
rs520525	*GORAB(dist=66936);PRRX1(dist=43403)*	1	170589910	rs2022372	Skeletal muscle	RP1-79C4.4	A	-0.40	-46612	1.45E-10
rs520525	*GORAB(dist=67593);PRRX1(dist=42746)*	1	170590567	rs12031871	Skeletal muscle	RP1-79C4.4	T	0.38	-45955	2.89E-08
rs520525	*GORAB(dist=68336);PRRX1(dist=42003)*	1	170591310	rs651386	Skeletal muscle	RP1-79C4.4	T	0.31	-45212	2.17E-06
rs520525	*GORAB(dist=68834);PRRX1(dist=41505)*	1	170591808	rs10753817	Skeletal muscle	RP1-79C4.4	G	0.39	-44714	2.23E-08
rs520525	*GORAB(dist=71095);PRRX1(dist=39244)*	1	170594069	rs12072276	Skeletal muscle	RP1-79C4.4	G	0.39	-42453	1.17E-08
rs520525	*GORAB(dist=71142);PRRX1(dist=39197)*	1	170594116	rs10919446	Skeletal muscle	RP1-79C4.4	A	0.40	-42406	1.07E-08
rs520525	*GORAB(dist=72144);PRRX1(dist=38195)*	1	170595118	rs12074059	Skeletal muscle	RP1-79C4.4	T	0.42	-41404	7.92E-10
rs520525	*GORAB(dist=73098);PRRX1(dist=37241)*	1	170596072	rs494521	Skeletal muscle	RP1-79C4.4	T	0.38	-40450	1.40E-09
rs520525	*GORAB(dist=73284);PRRX1(dist=37055)*	1	170596258	rs1234275	Skeletal muscle	RP1-79C4.4	G	0.40	-40264	1.27E-10
rs520525	*GORAB(dist=73399);PRRX1(dist=36940)*	1	170596373	rs1234274	Skeletal muscle	RP1-79C4.4	G	0.40	-40149	1.26E-10
rs520525	*GORAB(dist=73571);PRRX1(dist=36768)*	1	170596545	rs11577602	Skeletal muscle	RP1-79C4.4	T	0.39	-39977	1.54E-08
rs520525	*GORAB(dist=73598);PRRX1(dist=36741)*	1	170596572	rs10800530	Skeletal muscle	RP1-79C4.4	A	0.39	-39950	1.54E-08
rs520525	*GORAB(dist=75213);PRRX1(dist=35126)*	1	170598187	rs638704	Skeletal muscle	RP1-79C4.4	T	0.40	-38335	1.25E-10
rs520525	*GORAB(dist=76599);PRRX1(dist=33740)*	1	170599573	rs10919448	Skeletal muscle	RP1-79C4.4	C	0.40	-36949	8.05E-09
rs520525	*GORAB(dist=78034);PRRX1(dist=32305)*	1	170601008	rs189058353	Skeletal muscle	RP1-79C4.4	A	0.37	-35514	1.83E-09

Supplementary Table 18. *continued*

rs520525	*GORAB(dist=78339);PRRX1(dist=32000)*	1	170601313	rs12068805	Skeletal muscle	RP1-79C4.4	C	0.43	-35209	7.23E-10
rs520525	*GORAB(dist=78961);PRRX1(dist=31378)*	1	170601935	rs12566725	Skeletal muscle	RP1-79C4.4	T	0.43	-34587	7.23E-10
rs520525	*GORAB(dist=81148);PRRX1(dist=29191)*	1	170604122	rs598993	Skeletal muscle	RP1-79C4.4	C	0.35	-32400	2.34E-08
rs520525	*GORAB(dist=81964);PRRX1(dist=28375)*	1	170604938	rs541557	Skeletal muscle	RP1-79C4.4	G	0.35	-31584	2.34E-08
rs520525	*GORAB(dist=83112);PRRX1(dist=27227)*	1	170606086	rs644784	Skeletal muscle	RP1-79C4.4	T	0.43	-30436	7.26E-10
rs520525	*GORAB(dist=83380);PRRX1(dist=26959)*	1	170606354	rs656539	Skeletal muscle	RP1-79C4.4	T	0.43	-30168	7.26E-10
rs520525	*GORAB(dist=85107);PRRX1(dist=25232)*	1	170608081	rs539045	Skeletal muscle	RP1-79C4.4	T	0.35	-28441	2.34E-08
rs520525	*GORAB(dist=85694);PRRX1(dist=24645)*	1	170608668	rs533603	Skeletal muscle	RP1-79C4.4	G	0.43	-27854	7.36E-10
rs520525	*GORAB(dist=86216);PRRX1(dist=24123)*	1	170609190	rs473832	Skeletal muscle	RP1-79C4.4	C	0.40	-27332	1.29E-10
rs520525	*GORAB(dist=86651);PRRX1(dist=23688)*	1	170609625	rs580487	Skeletal muscle	RP1-79C4.4	C	0.36	-26897	1.46E-08
rs520525	*GORAB(dist=86769);PRRX1(dist=23570)*	1	170609743	rs578928	Skeletal muscle	RP1-79C4.4	C	0.43	-26779	7.45E-10
rs520525	*GORAB(dist=87736);PRRX1(dist=22603)*	1	170610710	rs549449	Skeletal muscle	RP1-79C4.4	C	0.43	-25812	8.88E-10
rs520525	*GORAB(dist=89288);PRRX1(dist=21051)*	1	170612262	rs492804	Skeletal muscle	RP1-79C4.4	T	0.40	-24260	5.98E-11
rs520525	*GORAB(dist=89899);PRRX1(dist=20440)*	1	170612873	rs639652	Skeletal muscle	RP1-79C4.4	A	0.35	-23649	1.34E-08
rs520525	*GORAB(dist=89952);PRRX1(dist=20387)*	1	170612926	rs639720	Skeletal muscle	RP1-79C4.4	C	0.43	-23596	9.12E-10
rs520525	*GORAB(dist=90876);PRRX1(dist=19463)*	1	170613850	rs654461	Skeletal muscle	RP1-79C4.4	T	0.40	-22672	7.33E-11
rs520525	*GORAB(dist=90895);PRRX1(dist=19444)*	1	170613869	rs567328	Skeletal muscle	RP1-79C4.4	A	0.40	-22653	1.03E-10
rs520525	*GORAB(dist=91068);PRRX1(dist=19271)*	1	170614042	rs544478	Skeletal muscle	RP1-79C4.4	T	0.40	-22480	8.78E-11
rs520525	*GORAB(dist=91270);PRRX1(dist=19069)*	1	170614244	rs666419	Skeletal muscle	RP1-79C4.4	C	0.43	-22278	9.19E-10
rs520525	*GORAB(dist=92886);PRRX1(dist=17453)*	1	170615860	rs593173	Skeletal muscle	RP1-79C4.4	A	0.43	-20662	9.19E-10
rs520525	*GORAB(dist=92943);PRRX1(dist=17396)*	1	170615917	rs593560	Skeletal muscle	RP1-79C4.4	A	0.40	-20605	5.97E-11
rs520525	*GORAB(dist=93381);PRRX1(dist=16958)*	1	170616355	rs2988392	Skeletal muscle	RP1-79C4.4	C	0.35	-20167	1.75E-08
rs520525	*GORAB(dist=94332);PRRX1(dist=16007)*	1	170617306	rs608930	Skeletal muscle	RP1-79C4.4	T	0.40	-19216	1.21E-10
rs520525	*GORAB(dist=94405);PRRX1(dist=15934)*	1	170617379	rs619699	Skeletal muscle	RP1-79C4.4	A	0.43	-19143	6.66E-10
rs520525	*GORAB(dist=95317);PRRX1(dist=15022)*	1	170618291	rs623752	Skeletal muscle	RP1-79C4.4	G	0.40	-18231	7.73E-11
rs520525	*GORAB(dist=95408);PRRX1(dist=14931)*	1	170618382	rs531007	Skeletal muscle	RP1-79C4.4	G	0.40	-18140	7.41E-11
rs520525	*GORAB(dist=95487);PRRX1(dist=14852)*	1	170618461	rs12038255	Skeletal muscle	RP1-79C4.4	A	0.36	-18061	1.93E-06
rs520525	*GORAB(dist=96350);PRRX1(dist=13989)*	1	170619324	rs1234282	Skeletal muscle	RP1-79C4.4	T	0.44	-17198	1.71E-10
rs520525	*GORAB(dist=96633);PRRX1(dist=13706)*	1	170619607	rs575432	Skeletal muscle	RP1-79C4.4	G	0.36	-16915	1.13E-08
rs520525	*GORAB(dist=96956);PRRX1(dist=13383)*	1	170619930	rs651822	Skeletal muscle	RP1-79C4.4	T	0.51	-16592	1.53E-14
rs520525	*GORAB(dist=99994);PRRX1(dist=10345)*	1	170622968	rs1234284	Skeletal muscle	RP1-79C4.4	T	0.47	-13554	5.44E-12
rs520525	*GORAB(dist=100135);PRRX1(dist=10204)*	1	170623109	rs588837	Skeletal muscle	RP1-79C4.4	G	0.41	-13413	2.28E-11
rs520525	*GORAB(dist=100946);PRRX1(dist=9393)*	1	170623920	rs12089974	Skeletal muscle	RP1-79C4.4	A	0.48	-12602	1.68E-11
rs520525	*GORAB(dist=102893);PRRX1(dist=7446)*	1	170625867	rs501680	Skeletal muscle	RP1-79C4.4	C	0.46	-10655	2.29E-11
rs520525	*GORAB(dist=103979);PRRX1(dist=6360)*	1	170626953	rs663887	Skeletal muscle	RP1-79C4.4	A	0.46	-9569	2.29E-11
rs520525	*GORAB(dist=104820);PRRX1(dist=5519)*	1	170627794	rs552277	Skeletal muscle	RP1-79C4.4	C	0.46	-8728	2.56E-11
rs520525	*GORAB(dist=105281);PRRX1(dist=5058)*	1	170628255	rs680084	Skeletal muscle	RP1-79C4.4	A	0.31	-8267	7.62E-07
rs520525	*GORAB(dist=105414);PRRX1(dist=4925)*	1	170628388	rs583006	Skeletal muscle	RP1-79C4.4	G	0.43	-8134	5.14E-10
rs520525	*GORAB(dist=105461);PRRX1(dist=4878)*	1	170628435	rs524877	Skeletal muscle	RP1-79C4.4	C	0.46	-8087	2.29E-11
rs520525	*GORAB(dist=106864);PRRX1(dist=3475)*	1	170629838	rs600093	Skeletal muscle	RP1-79C4.4	A	0.45	-6684	7.36E-11
rs520525	*GORAB(dist=107285);PRRX1(dist=3054)*	1	170630259	rs601938	Skeletal muscle	RP1-79C4.4	T	0.46	-6263	2.26E-11
rs520525	*GORAB(dist=108446);PRRX1(dist=1893)*	1	170631420	rs627848	Skeletal muscle	RP1-79C4.4	A	0.46	-5102	2.24E-11
rs520525	*GORAB(dist=108789);PRRX1(dist=1550)*	1	170631763	rs629234	Skeletal muscle	RP1-79C4.4	C	0.32	-4759	3.28E-07
rs520525	*PRRX1*	1	170635002	rs525489	Skeletal muscle	RP1-79C4.4	G	0.37	-1520	3.05E-09
rs520525	*PRRX1*	1	170635084	rs503706	Skeletal muscle	RP1-79C4.4	C	0.37	-1438	3.06E-09
rs520525	*PRRX1*	1	170635369	rs501005	Skeletal muscle	RP1-79C4.4	G	0.30	-1153	3.51E-06
rs520525	*PRRX1*	1	170636079	rs473133	Skeletal muscle	RP1-79C4.4	T	0.37	-443	3.00E-09
rs520525	*PRRX1*	1	170638333	rs520525	Skeletal muscle	RP1-79C4.4	G	0.44	1811	4.25E-10
rs520525	*PRRX1*	1	170638658	rs10919449	Skeletal muscle	RP1-79C4.4	A	0.40	2136	2.64E-11
rs11264280	*ZBTB7B*	1	154990297	rs2242194	Skeletal muscle	ZBTB7B	G	0.13	15170	6.46E-06
rs2540949	*SLC1A4(dist=25049);CEP68(dist=7446)*	2	65276049	rs1009360	Atrial appendage	CEP68	C	-0.53	-7451	2.27E-11
rs2540949	*SLC1A4(dist=25452);CEP68(dist=7043)*	2	65276452	rs1009358	Atrial appendage	CEP68	C	-0.52	-7048	1.14E-10
rs2540949	*SLC1A4(dist=25736);CEP68(dist=6759)*	2	65276736	rs2540951	Atrial appendage	CEP68	G	-0.52	-6764	1.14E-10
rs2540949	*SLC1A4(dist=28223);CEP68(dist=4272)*	2	65279223	rs2540950	Atrial appendage	CEP68	T	-0.55	-4277	7.74E-11
rs2540949	*SLC1A4(dist=28321);CEP68(dist=4174)*	2	65279321	rs2723066	Atrial appendage	CEP68	G	-0.55	-4179	7.74E-11
rs2540949	*SLC1A4(dist=28414);CEP68(dist=4081)*	2	65279414	rs2723065	Atrial appendage	CEP68	G	-0.54	-4086	4.52E-11
rs2540949	*SLC1A4(dist=28805);CEP68(dist=3690)*	2	65279805	rs2723064	Atrial appendage	CEP68	C	-0.54	-3695	4.31E-11
rs2540949	*SLC1A4(dist=29185);CEP68(dist=3310)*	2	65280185	rs2723063	Atrial appendage	CEP68	G	-0.51	-3315	2.85E-10
rs2540949	*SLC1A4(dist=29220);CEP68(dist=3275)*	2	65280220	rs2723062	Atrial appendage	CEP68	A	-0.55	-3280	7.74E-11
rs2540949	*CEP68*	2	65283972	rs74181299	Atrial appendage	CEP68	C	-0.57	472	2.93E-12
rs2540949	*CEP68*	2	65284231	rs2540949	Atrial appendage	CEP68	T	-0.55	731	3.35E-11
rs2540949	*CEP68*	2	65284623	rs2540948	Atrial appendage	CEP68	C	-0.55	1123	5.62E-11
rs2540949	*CEP68*	2	65287896	rs2249105	Atrial appendage	CEP68	G	-0.57	4396	6.13E-13
rs2540949	*CEP68*	2	65289825	rs2540945	Atrial appendage	CEP68	G	-0.57	6325	1.33E-12
rs2540949	*CEP68*	2	65290842	rs2241161	Atrial appendage	CEP68	A	-0.51	7342	4.31E-10
rs2540949	*CEP68*	2	65291546	rs2241160	Atrial appendage	CEP68	G	-0.53	8046	3.99E-11
rs2540949	*CEP68*	2	65296280	rs2252867	Atrial appendage	CEP68	C	-0.57	12780	6.13E-13
rs2540949	*RAB1A*	2	65315903	rs1420185	Atrial appendage	CEP68	A	0.54	32403	1.43E-10
rs3771537	*AAK1(dist=88028);ANXA4(dist=10122)*	2	69959005	rs2312550	Left ventricle	ANXA4	C	-0.22	87448	1.61E-06
rs3771537	*AAK1(dist=91816);ANXA4(dist=6334)*	2	69962793	rs10203645	Left ventricle	ANXA4	A	-0.21	91236	5.26E-06
rs3771537	*AAK1(dist=92069);ANXA4(dist=6081)*	2	69963046	rs2872073	Left ventricle	ANXA4	G	-0.21	91489	5.26E-06
rs3771537	*ANXA4*	2	69971317	rs4852984	Left ventricle	ANXA4	A	-0.22	99760	3.13E-06
rs3771537	*ANXA4*	2	69971429	rs4852319	Left ventricle	ANXA4	A	-0.22	99872	2.38E-06
rs3771537	*ANXA4*	2	69972704	rs13028222	Left ventricle	ANXA4	C	-0.22	101147	2.31E-06
rs3771537	*ANXA4*	2	69973737	rs6705820	Left ventricle	ANXA4	A	-0.22	102180	2.07E-06
rs3771537	*ANXA4*	2	69974873	rs11126244	Left ventricle	ANXA4	A	-0.22	103316	1.55E-06
rs3771537	*ANXA4*	2	69975000	rs11126245	Left ventricle	ANXA4	T	-0.22	103443	1.55E-06
rs3771537	*ANXA4*	2	69978290	rs4852988	Left ventricle	ANXA4	G	-0.20	106733	1.19E-05
rs3771537	*ANXA4*	2	69980427	rs7589995	Left ventricle	ANXA4	G	-0.20	108870	9.02E-06
rs2540949	*SLC1A4(dist=25049);CEP68(dist=7446)*	2	65276049	rs1009360	Left ventricle	CEP68	C	-0.32	-7451	6.82E-07
rs2540949	*SLC1A4(dist=25452);CEP68(dist=7043)*	2	65276452	rs1009358	Left ventricle	CEP68	C	-0.35	-7048	2.80E-07
rs2540949	*SLC1A4(dist=25736);CEP68(dist=6759)*	2	65276736	rs2540951	Left ventricle	CEP68	G	-0.35	-6764	2.80E-07
rs2540949	*SLC1A4(dist=28223);CEP68(dist=4272)*	2	65279223	rs2540950	Left ventricle	CEP68	T	-0.33	-4277	2.66E-06
rs2540949	*SLC1A4(dist=28321);CEP68(dist=4174)*	2	65279321	rs2723066	Left ventricle	CEP68	G	-0.33	-4179	2.66E-06
rs2540949	*SLC1A4(dist=28414);CEP68(dist=4081)*	2	65279414	rs2723065	Left ventricle	CEP68	G	-0.36	-4086	1.69E-07
rs2540949	*SLC1A4(dist=28805);CEP68(dist=3690)*	2	65279805	rs2723064	Left ventricle	CEP68	C	-0.36	-3695	1.65E-07
rs2540949	*SLC1A4(dist=29185);CEP68(dist=3310)*	2	65280185	rs2723063	Left ventricle	CEP68	G	-0.32	-3315	4.86E-07

Supplementary Table 18. *continued*

rs2540949	*SLC1A4(dist=29220);CEP68(dist=3275)*	2	65280220	rs2723062	Left ventricle	CEP68	A	-0.33	-3280	2.66E-06
rs2540949	*CEP68*	2	65283972	rs74181299	Left ventricle	CEP68	C	-0.36	472	9.45E-08
rs2540949	*CEP68*	2	65284231	rs2540949	Left ventricle	CEP68	T	-0.35	731	1.76E-07
rs2540949	*CEP68*	2	65284623	rs2540948	Left ventricle	CEP68	C	-0.33	1123	2.77E-06
rs2540949	*CEP68*	2	65287896	rs2249105	Left ventricle	CEP68	G	-0.33	4396	3.14E-07
rs2540949	*CEP68*	2	65289825	rs2540945	Left ventricle	CEP68	G	-0.32	6325	1.29E-06
rs2540949	*CEP68*	2	65296280	rs2252867	Left ventricle	CEP68	C	-0.33	12780	3.14E-07
rs3771537	*ANXA4*	2	70025737	rs7561890	Left ventricle	GMCL1	T	-0.42	-31037	3.08E-06
rs3771537	*ANXA4*	2	70033584	rs2228203	Left ventricle	GMCL1	T	-0.39	-23190	1.10E-05
rs3771537	*ANXA4*	2	70035482	rs17037082	Left ventricle	GMCL1	G	-0.42	-21292	3.08E-06
rs3771537	*ANXA4*	2	70047644	rs2290452	Left ventricle	GMCL1	A	-0.40	-9130	6.17E-06
rs3771537	*ANXA4*	2	70049222	rs58819073	Left ventricle	GMCL1	A	-0.40	-7552	6.21E-06
rs3771537	*ANXA4*	2	70053816	rs11900749	Left ventricle	GMCL1	C	-0.40	-2958	7.71E-06
rs3771537	*ANXA4(dist=1575);GMCL1(dist=1647)*	2	70055171	rs33992437	Left ventricle	GMCL1	C	-0.40	-1603	9.36E-06
rs3771537	*ANXA4(dist=1909);GMCL1(dist=1313)*	2	70055505	rs1531025	Left ventricle	GMCL1	A	-0.28	-1269	1.05E-05
rs3771537	*GMCL1*	2	70056116	rs2278932	Left ventricle	GMCL1	G	-0.39	-658	6.66E-06
rs3771537	*GMCL1*	2	70056365	rs2278933	Left ventricle	GMCL1	C	-0.40	-409	7.31E-06
rs3771537	*GMCL1*	2	70059607	rs72839877	Left ventricle	GMCL1	C	-0.39	2833	1.12E-05
rs3771537	*GMCL1*	2	70063315	rs60483174	Left ventricle	GMCL1	T	-0.41	6541	5.80E-06
rs3771537	*GMCL1*	2	70064435	rs3771534	Left ventricle	GMCL1	T	-0.41	7661	5.80E-06
rs3771537	*GMCL1*	2	70065997	rs12619656	Left ventricle	GMCL1	A	-0.44	9223	1.06E-06
rs3771537	*GMCL1*	2	70066102	rs12613917	Left ventricle	GMCL1	G	-0.41	9328	5.80E-06
rs3771537	*GMCL1*	2	70066891	rs11888098	Left ventricle	GMCL1	C	-0.41	10117	5.80E-06
rs3771537	*GMCL1*	2	70066922	rs11888102	Left ventricle	GMCL1	G	-0.41	10148	5.80E-06
rs3771537	*GMCL1*	2	70068057	rs3771533	Left ventricle	GMCL1	A	-0.41	11283	5.80E-06
rs3771537	*GMCL1*	2	70068755	rs2872076	Left ventricle	GMCL1	A	-0.41	11981	5.71E-06
rs3771537	*GMCL1*	2	70076650	rs6546552	Left ventricle	GMCL1	C	-0.41	19876	5.72E-06
rs3771537	*GMCL1*	2	70077422	rs7577662	Left ventricle	GMCL1	G	-0.41	20648	5.72E-06
rs3771537	*GMCL1*	2	70077433	rs7565230	Left ventricle	GMCL1	C	-0.41	20659	5.72E-06
rs3771537	*GMCL1*	2	70084977	rs921711	Left ventricle	GMCL1	G	-0.37	28203	6.53E-06
rs3771537	*GMCL1*	2	70085961	rs7596535	Left ventricle	GMCL1	A	-0.37	29187	6.51E-06
rs3771537	*GMCL1*	2	70086363	rs36081078	Left ventricle	GMCL1	G	-0.41	29589	2.55E-06
rs3771537	*GMCL1*	2	70086728	rs72839885	Left ventricle	GMCL1	T	-0.41	29954	2.70E-06
rs3771537	*GMCL1*	2	70087159	rs4852356	Left ventricle	GMCL1	G	-0.31	30385	1.88E-06
rs3771537	*GMCL1*	2	70088016	rs13412830	Left ventricle	GMCL1	C	-0.37	31242	7.51E-06
rs3771537	*GMCL1*	2	70089130	rs56222989	Left ventricle	GMCL1	G	-0.41	32356	2.70E-06
rs3771537	*GMCL1*	2	70097735	rs7568485	Left ventricle	GMCL1	C	-0.37	40961	6.51E-06
rs3771537	*GMCL1*	2	70099424	rs1013083	Left ventricle	GMCL1	G	-0.38	42650	9.27E-06
rs3771537	*GMCL1*	2	70101889	rs61138247	Left ventricle	GMCL1	C	-0.37	45115	7.49E-06
rs3771537	*MXD1(dist=2511);ASPRV1(dist=14637)*	2	70172587	rs6756513	Left ventricle	GMCL1	A	-0.33	115813	2.67E-06
rs3771537	*MXD1(dist=3954);ASPRV1(dist=13194)*	2	70174030	rs7569566	Left ventricle	GMCL1	C	-0.30	117256	4.34E-06
rs3771537	*MXD1(dist=3978);ASPRV1(dist=13170)*	2	70174054	rs7581977	Left ventricle	GMCL1	G	-0.28	117280	1.01E-05
rs3771537	*SNRNP27*	2	70120078	rs55866046	Left ventricle	PCYOX1	C	0.23	-364440	1.27E-05
rs2540949	*SLC1A4(dist=25049);CEP68(dist=7446)*	2	65276049	rs1009360	Skeletal muscle	CEP68	C	-0.21	-7451	9.51E-09
rs2540949	*SLC1A4(dist=25452);CEP68(dist=7043)*	2	65276452	rs1009358	Skeletal muscle	CEP68	C	-0.27	-7048	7.47E-13
rs2540949	*SLC1A4(dist=25736);CEP68(dist=6759)*	2	65276736	rs2540951	Skeletal muscle	CEP68	G	-0.27	-6764	7.47E-13
rs2540949	*SLC1A4(dist=28223);CEP68(dist=4272)*	2	65279223	rs2540950	Skeletal muscle	CEP68	T	-0.26	-4277	3.11E-11
rs2540949	*SLC1A4(dist=28321);CEP68(dist=4174)*	2	65279321	rs2723066	Skeletal muscle	CEP68	G	-0.26	-4179	3.11E-11
rs2540949	*SLC1A4(dist=28414);CEP68(dist=4081)*	2	65279414	rs2723065	Skeletal muscle	CEP68	G	-0.27	-4086	7.43E-13
rs2540949	*SLC1A4(dist=28805);CEP68(dist=3690)*	2	65279805	rs2723064	Skeletal muscle	CEP68	C	-0.27	-3695	7.43E-13
rs2540949	*SLC1A4(dist=29185);CEP68(dist=3310)*	2	65280185	rs2723063	Skeletal muscle	CEP68	G	-0.22	-3315	3.67E-09
rs2540949	*SLC1A4(dist=29220);CEP68(dist=3275)*	2	65280220	rs2723062	Skeletal muscle	CEP68	A	-0.26	-3280	3.11E-11
rs2540949	*CEP68*	2	65283972	rs74181299	Skeletal muscle	CEP68	C	-0.26	472	4.68E-12
rs2540949	*CEP68*	2	65284231	rs2540949	Skeletal muscle	CEP68	T	-0.27	731	5.02E-13
rs2540949	*CEP68*	2	65284623	rs2540948	Skeletal muscle	CEP68	C	-0.25	1123	1.73E-10
rs2540949	*CEP68*	2	65287896	rs2249105	Skeletal muscle	CEP68	G	-0.23	4396	1.95E-10
rs2540949	*CEP68*	2	65289825	rs2540945	Skeletal muscle	CEP68	G	-0.23	6325	4.85E-10
rs2540949	*CEP68*	2	65290842	rs2241161	Skeletal muscle	CEP68	A	-0.18	7342	1.95E-06
rs2540949	*CEP68*	2	65291546	rs2241160	Skeletal muscle	CEP68	G	-0.18	8046	3.74E-07
rs2540949	*CEP68*	2	65296280	rs2252867	Skeletal muscle	CEP68	C	-0.23	12780	1.95E-10
rs2540949	*RAB1A*	2	65315903	rs1420185	Skeletal muscle	CEP68	A	0.26	32403	9.07E-12
rs3771537	*ANXA4*	2	69975819	rs10211658	Skeletal muscle	GMCL1	A	-0.20	-80955	3.77E-06
rs3771537	*ANXA4*	2	70013733	rs721566	Skeletal muscle	GMCL1	G	-0.37	-43041	1.38E-11
rs3771537	*ANXA4*	2	70014986	rs11677629	Skeletal muscle	GMCL1	C	-0.37	-41788	1.38E-11
rs3771537	*ANXA4*	2	70015108	rs11683908	Skeletal muscle	GMCL1	G	-0.42	-41666	5.98E-09
rs3771537	*ANXA4*	2	70015781	rs57792077	Skeletal muscle	GMCL1	G	-0.35	-40993	1.12E-10
rs3771537	*ANXA4*	2	70015831	rs11695691	Skeletal muscle	GMCL1	A	-0.35	-40943	3.56E-10
rs3771537	*ANXA4*	2	70017392	rs57830265	Skeletal muscle	GMCL1	G	-0.37	-39382	1.17E-11
rs3771537	*ANXA4*	2	70018272	rs56398743	Skeletal muscle	GMCL1	C	-0.37	-38502	1.38E-11
rs3771537	*ANXA4*	2	70022446	rs1598179	Skeletal muscle	GMCL1	C	-0.39	-34328	2.53E-12
rs3771537	*ANXA4*	2	70025737	rs7561890	Skeletal muscle	GMCL1	T	-0.38	-31037	1.34E-11
rs3771537	*ANXA4*	2	70031797	rs3771541	Skeletal muscle	GMCL1	G	-0.30	-24977	2.24E-11
rs3771537	*ANXA4*	2	70031941	rs3771540	Skeletal muscle	GMCL1	G	-0.30	-24833	2.50E-11
rs3771537	*ANXA4*	2	70033584	rs2228203	Skeletal muscle	GMCL1	T	-0.40	-23190	5.27E-12
rs3771537	*ANXA4*	2	70033649	rs17037076	Skeletal muscle	GMCL1	A	-0.37	-23125	4.99E-11
rs3771537	*ANXA4*	2	70033795	rs3771538	Skeletal muscle	GMCL1	T	-0.37	-22979	4.94E-11
rs3771537	*ANXA4*	2	70034465	rs2124009	Skeletal muscle	GMCL1	C	-0.37	-22309	4.89E-11
rs3771537	*ANXA4*	2	70034793	rs2168115	Skeletal muscle	GMCL1	G	-0.30	-21981	2.62E-11
rs3771537	*ANXA4*	2	70035482	rs17037082	Skeletal muscle	GMCL1	G	-0.40	-21292	3.02E-12
rs3771537	*ANXA4*	2	70036711	rs13392884	Skeletal muscle	GMCL1	G	-0.29	-20063	1.34E-10
rs3771537	*ANXA4*	2	70038232	rs6546550	Skeletal muscle	GMCL1	G	-0.30	-18542	2.33E-11
rs3771537	*ANXA4*	2	70038792	rs3771537	Skeletal muscle	GMCL1	C	-0.27	-17982	2.40E-10
rs3771537	*ANXA4*	2	70039224	rs4853027	Skeletal muscle	GMCL1	T	-0.30	-17550	2.37E-11
rs3771537	*ANXA4*	2	70039677	rs2305523	Skeletal muscle	GMCL1	C	-0.30	-17097	2.26E-11
rs3771537	*ANXA4*	2	70040542	rs2312555	Skeletal muscle	GMCL1	A	-0.27	-16232	2.61E-10
rs3771537	*ANXA4*	2	70041004	rs11673732	Skeletal muscle	GMCL1	T	-0.39	-15770	5.65E-12
rs3771537	*ANXA4*	2	70041033	rs11673826	Skeletal muscle	GMCL1	A	-0.27	-15741	1.76E-10

Supplementary Table 18. *continued*

rs3771537	*ANXA4*	2	70041181	rs72839869	Skeletal muscle	GMCL1	T	-0.39	-15593	5.85E-12
rs3771537	*ANXA4*	2	70041440	rs4853028	Skeletal muscle	GMCL1	A	-0.38	-15334	1.08E-11
rs3771537	*ANXA4*	2	70042332	rs60168146	Skeletal muscle	GMCL1	G	-0.39	-14442	5.81E-12
rs3771537	*ANXA4*	2	70042915	rs72839870	Skeletal muscle	GMCL1	A	-0.39	-13859	5.79E-12
rs3771537	*ANXA4*	2	70043598	rs3771536	Skeletal muscle	GMCL1	A	-0.39	-13176	5.77E-12
rs3771537	*ANXA4*	2	70043775	rs3771535	Skeletal muscle	GMCL1	T	-0.40	-12999	4.70E-12
rs3771537	*ANXA4*	2	70045063	rs6744970	Skeletal muscle	GMCL1	A	-0.40	-11711	2.48E-12
rs3771537	*ANXA4*	2	70046964	rs72839874	Skeletal muscle	GMCL1	A	-0.40	-9810	1.69E-12
rs3771537	*ANXA4*	2	70047644	rs2290452	Skeletal muscle	GMCL1	A	-0.40	-9130	1.80E-12
rs3771537	*ANXA4*	2	70049222	rs58819073	Skeletal muscle	GMCL1	A	-0.40	-7552	1.78E-12
rs3771537	*ANXA4*	2	70050725	rs7563062	Skeletal muscle	GMCL1	A	-0.30	-6049	9.23E-12
rs3771537	*ANXA4*	2	70053668	rs7600468	Skeletal muscle	GMCL1	G	-0.29	-3106	4.98E-10
rs3771537	*ANXA4*	2	70053816	rs11900749	Skeletal muscle	GMCL1	C	-0.40	-2958	5.13E-12
rs3771537	*ANXA4(dist=1575);GMCL1(dist=1647)*	2	70055171	rs33992437	Skeletal muscle	GMCL1	C	-0.40	-1603	4.20E-12
rs3771537	*ANXA4(dist=1909);GMCL1(dist=1313)*	2	70055505	rs1531025	Skeletal muscle	GMCL1	A	-0.30	-1269	1.20E-11
rs3771537	*GMCL1*	2	70056116	rs2278932	Skeletal muscle	GMCL1	G	-0.40	-658	1.86E-12
rs3771537	*GMCL1*	2	70056365	rs2278933	Skeletal muscle	GMCL1	C	-0.39	-409	7.03E-12
rs3771537	*GMCL1*	2	70057448	rs3732266	Skeletal muscle	GMCL1	G	-0.30	674	6.46E-12
rs3771537	*GMCL1*	2	70059607	rs72839877	Skeletal muscle	GMCL1	C	-0.40	2833	4.56E-12
rs3771537	*GMCL1*	2	70062276	rs72839879	Skeletal muscle	GMCL1	T	-0.40	5502	4.75E-12
rs3771537	*GMCL1*	2	70062360	rs10167142	Skeletal muscle	GMCL1	C	-0.31	5586	5.31E-12
rs3771537	*GMCL1*	2	70062454	rs10202159	Skeletal muscle	GMCL1	T	-0.31	5680	5.32E-12
rs3771537	*GMCL1*	2	70063315	rs60483174	Skeletal muscle	GMCL1	T	-0.41	6541	2.31E-12
rs3771537	*GMCL1*	2	70063527	rs4420721	Skeletal muscle	GMCL1	T	-0.37	6753	3.46E-11
rs3771537	*GMCL1*	2	70063563	rs4401231	Skeletal muscle	GMCL1	C	-0.31	6789	4.38E-12
rs3771537	*GMCL1*	2	70063660	rs4241261	Skeletal muscle	GMCL1	G	-0.31	6886	4.83E-12
rs3771537	*GMCL1*	2	70064155	rs1377995	Skeletal muscle	GMCL1	G	-0.31	7381	4.45E-12
rs3771537	*GMCL1*	2	70064435	rs3771534	Skeletal muscle	GMCL1	T	-0.41	7661	2.07E-12
rs3771537	*GMCL1*	2	70064927	rs1377996	Skeletal muscle	GMCL1	A	-0.39	8153	1.41E-12
rs3771537	*GMCL1*	2	70065997	rs12619656	Skeletal muscle	GMCL1	A	-0.42	9223	1.24E-12
rs3771537	*GMCL1*	2	70066102	rs12613917	Skeletal muscle	GMCL1	G	-0.41	9328	1.77E-12
rs3771537	*GMCL1*	2	70066891	rs11888098	Skeletal muscle	GMCL1	C	-0.41	10117	1.66E-12
rs3771537	*GMCL1*	2	70066922	rs11888102	Skeletal muscle	GMCL1	G	-0.41	10148	1.65E-12
rs3771537	*GMCL1*	2	70068057	rs3771533	Skeletal muscle	GMCL1	A	-0.41	11283	1.51E-12
rs3771537	*GMCL1*	2	70068635	rs2872075	Skeletal muscle	GMCL1	T	-0.31	11861	2.29E-12
rs3771537	*GMCL1*	2	70068755	rs2872076	Skeletal muscle	GMCL1	A	-0.41	11981	1.43E-12
rs3771537	*GMCL1*	2	70071529	rs7575111	Skeletal muscle	GMCL1	G	-0.44	14755	3.33E-12
rs3771537	*GMCL1*	2	70073703	rs6546551	Skeletal muscle	GMCL1	T	-0.31	16929	1.41E-12
rs3771537	*GMCL1*	2	70076650	rs6546552	Skeletal muscle	GMCL1	C	-0.42	19876	1.07E-12
rs3771537	*GMCL1*	2	70076954	rs4852349	Skeletal muscle	GMCL1	T	-0.30	20180	1.02E-11
rs3771537	*GMCL1*	2	70077422	rs7577662	Skeletal muscle	GMCL1	G	-0.42	20648	1.07E-12
rs3771537	*GMCL1*	2	70077433	rs7565230	Skeletal muscle	GMCL1	C	-0.42	20659	1.07E-12
rs3771537	*GMCL1*	2	70079633	rs1551374	Skeletal muscle	GMCL1	T	-0.31	22859	2.58E-12
rs3771537	*GMCL1*	2	70084977	rs921711	Skeletal muscle	GMCL1	G	-0.39	28203	8.05E-13
rs3771537	*GMCL1*	2	70085961	rs7596535	Skeletal muscle	GMCL1	A	-0.39	29187	1.16E-12
rs3771537	*GMCL1*	2	70086363	rs36081078	Skeletal muscle	GMCL1	G	-0.42	29589	5.54E-13
rs3771537	*GMCL1*	2	70086728	rs72839885	Skeletal muscle	GMCL1	T	-0.42	29954	5.53E-13
rs3771537	*GMCL1*	2	70087159	rs4852356	Skeletal muscle	GMCL1	G	-0.26	30385	4.91E-09
rs3771537	*GMCL1*	2	70088016	rs13412830	Skeletal muscle	GMCL1	C	-0.38	31242	2.41E-12
rs3771537	*GMCL1*	2	70089130	rs56222989	Skeletal muscle	GMCL1	G	-0.42	32356	5.52E-13
rs3771537	*GMCL1*	2	70090579	rs13017134	Skeletal muscle	GMCL1	G	-0.29	33805	1.20E-11
rs3771537	*GMCL1*	2	70090913	rs56168154	Skeletal muscle	GMCL1	T	-0.42	34139	1.25E-12
rs3771537	*GMCL1*	2	70091246	rs10865380	Skeletal muscle	GMCL1	C	-0.28	34472	2.01E-11
rs3771537	*GMCL1*	2	70091772	rs60390734	Skeletal muscle	GMCL1	C	-0.42	34998	1.25E-12
rs3771537	*GMCL1*	2	70093647	rs57278310	Skeletal muscle	GMCL1	C	-0.28	36873	2.66E-11
rs3771537	*GMCL1*	2	70093898	rs60248458	Skeletal muscle	GMCL1	G	-0.42	37124	1.25E-12
rs3771537	*GMCL1*	2	70093910	rs60207187	Skeletal muscle	GMCL1	A	-0.29	37136	1.20E-11
rs3771537	*GMCL1*	2	70097735	rs7568485	Skeletal muscle	GMCL1	C	-0.39	40961	1.16E-12
rs3771537	*GMCL1*	2	70098808	rs3214007	Skeletal muscle	GMCL1	G	-0.31	42034	2.66E-12
rs3771537	*GMCL1*	2	70099424	rs1013083	Skeletal muscle	GMCL1	G	-0.41	42650	1.48E-12
rs3771537	*GMCL1*	2	70101889	rs61138247	Skeletal muscle	GMCL1	C	-0.38	45115	5.49E-12
rs3771537	*GMCL1*	2	70102735	rs4853109	Skeletal muscle	GMCL1	G	-0.39	45961	3.62E-12
rs3771537	*GMCL1*	2	70103504	rs17037193	Skeletal muscle	GMCL1	C	-0.42	46730	1.25E-12
rs3771537	*GMCL1*	2	70103802	rs17037194	Skeletal muscle	GMCL1	C	-0.42	47028	1.25E-12
rs3771537	*GMCL1*	2	70106832	rs6747542	Skeletal muscle	GMCL1	C	-0.29	50058	1.45E-11
rs3771537	*GMCL1*	2	70107409	rs2124007	Skeletal muscle	GMCL1	G	-0.42	50635	1.32E-12
rs3771537	*GMCL1(dist=1529);SNRNP27(dist=12819)*	2	70108256	rs1056482	Skeletal muscle	GMCL1	A	-0.28	51482	1.89E-11
rs3771537	*GMCL1(dist=4984);SNRNP27(dist=9364)*	2	70111711	rs6546553	Skeletal muscle	GMCL1	A	-0.28	54937	8.67E-11
rs3771537	*GMCL1(dist=9721);SNRNP27(dist=4627)*	2	70116448	rs60515724	Skeletal muscle	GMCL1	T	-0.38	59674	6.35E-11
rs3771537	*GMCL1(dist=10288);SNRNP27(dist=4060)*	2	70117015	rs10165883	Skeletal muscle	GMCL1	T	-0.30	60241	8.13E-12
rs3771537	*GMCL1(dist=10347);SNRNP27(dist=4001)*	2	70117074	rs2054046	Skeletal muscle	GMCL1	C	-0.39	60300	3.03E-11
rs3771537	*GMCL1(dist=10449);SNRNP27(dist=3899)*	2	70117176	rs12232914	Skeletal muscle	GMCL1	T	-0.29	60402	8.49E-11
rs3771537	*GMCL1(dist=10645);SNRNP27(dist=3703)*	2	70117372	rs12233079	Skeletal muscle	GMCL1	G	-0.28	60598	1.18E-10
rs3771537	*GMCL1(dist=10694);SNRNP27(dist=3654)*	2	70117421	rs2054047	Skeletal muscle	GMCL1	C	-0.29	60647	6.38E-11
rs3771537	*GMCL1(dist=11661);SNRNP27(dist=2687)*	2	70118388	rs13002091	Skeletal muscle	GMCL1	T	-0.28	61614	2.92E-10
rs3771537	*GMCL1(dist=11700);SNRNP27(dist=2648)*	2	70118427	rs13028508	Skeletal muscle	GMCL1	A	-0.27	61653	4.93E-10
rs3771537	*GMCL1(dist=12742);SNRNP27(dist=1606)*	2	70119469	rs3755389	Skeletal muscle	GMCL1	C	-0.28	62695	1.25E-10
rs3771537	*SNRNP27*	2	70120078	rs55866046	Skeletal muscle	GMCL1	C	-0.42	63304	3.31E-11
rs3771537	*SNRNP27*	2	70124316	rs3752781	Skeletal muscle	GMCL1	A	-0.27	67542	7.47E-10
rs3771537	*SNRNP27*	2	70124805	rs6720498	Skeletal muscle	GMCL1	C	-0.27	68031	1.76E-09
rs3771537	*SNRNP27*	2	70125763	rs13015457	Skeletal muscle	GMCL1	T	-0.28	68989	2.05E-10
rs3771537	*SNRNP27*	2	70125988	rs4852375	Skeletal muscle	GMCL1	G	-0.29	69214	1.28E-10
rs3771537	*SNRNP27*	2	70126666	rs58206747	Skeletal muscle	GMCL1	G	-0.38	69892	1.07E-10
rs3771537	*SNRNP27*	2	70127229	rs6716937	Skeletal muscle	GMCL1	A	-0.28	70455	2.07E-10
rs3771537	*SNRNP27*	2	70128717	rs7598283	Skeletal muscle	GMCL1	G	-0.27	71943	7.20E-10
rs3771537	*SNRNP27*	2	70131584	rs1048130	Skeletal muscle	GMCL1	A	-0.38	74810	1.82E-10
rs3771537	*SNRNP27*	2	70132676	rs1048266	Skeletal muscle	GMCL1	G	-0.28	75902	2.06E-10

Supplementary Table 18. *continued*

rs3771537	*SNRNP27(dist=1739);MXD1(dist=8066)*	2	70134107	rs10166011	Skeletal muscle	GMCL1	G	-0.28	77333	2.29E-10
rs3771537	*SNRNP27(dist=3338);MXD1(dist=6467)*	2	70135706	rs6546554	Skeletal muscle	GMCL1	A	-0.28	78932	2.06E-10
rs3771537	*SNRNP27(dist=3392);MXD1(dist=6413)*	2	70135760	rs6546555	Skeletal muscle	GMCL1	G	-0.28	78986	2.81E-10
rs3771537	*SNRNP27(dist=4249);MXD1(dist=5556)*	2	70136617	rs11126249	Skeletal muscle	GMCL1	G	-0.37	79843	2.74E-10
rs3771537	*SNRNP27(dist=5130);MXD1(dist=4675)*	2	70137498	rs1979214	Skeletal muscle	GMCL1	C	-0.27	80724	6.84E-10
rs3771537	*SNRNP27(dist=5406);MXD1(dist=4399)*	2	70137774	rs6736408	Skeletal muscle	GMCL1	T	-0.28	81000	2.06E-10
rs3771537	*SNRNP27(dist=5743);MXD1(dist=4062)*	2	70138111	rs6739780	Skeletal muscle	GMCL1	A	-0.28	81337	2.20E-10
rs3771537	*SNRNP27(dist=5802);MXD1(dist=4003)*	2	70138170	rs6754896	Skeletal muscle	GMCL1	C	-0.28	81396	2.06E-10
rs3771537	*SNRNP27(dist=6633);MXD1(dist=3172)*	2	70139001	rs6546556	Skeletal muscle	GMCL1	G	-0.28	82227	2.06E-10
rs3771537	*SNRNP27(dist=6766);MXD1(dist=3039)*	2	70139134	rs7592647	Skeletal muscle	GMCL1	T	-0.27	82360	6.50E-10
rs3771537	*SNRNP27(dist=7903);MXD1(dist=1902)*	2	70140271	rs897122	Skeletal muscle	GMCL1	T	-0.28	83497	2.07E-10
rs3771537	*MXD1*	2	70144596	rs11902198	Skeletal muscle	GMCL1	A	-0.28	87822	2.27E-10
rs3771537	*MXD1*	2	70145717	rs6546558	Skeletal muscle	GMCL1	T	-0.28	88943	1.87E-10
rs3771537	*MXD1*	2	70145833	rs6546559	Skeletal muscle	GMCL1	A	-0.27	89059	6.82E-10
rs3771537	*MXD1*	2	70146121	rs6721891	Skeletal muscle	GMCL1	G	-0.28	89347	2.06E-10
rs3771537	*MXD1*	2	70146125	rs6750488	Skeletal muscle	GMCL1	T	-0.28	89351	2.06E-10
rs3771537	*MXD1*	2	70146625	rs7419837	Skeletal muscle	GMCL1	C	-0.28	89851	2.63E-10
rs3771537	*MXD1*	2	70149225	rs1454498	Skeletal muscle	GMCL1	A	-0.28	92451	1.69E-10
rs3771537	*MXD1*	2	70149873	rs80352135	Skeletal muscle	GMCL1	A	-0.37	93099	3.41E-10
rs3771537	*MXD1*	2	70150215	rs6738174	Skeletal muscle	GMCL1	C	-0.28	93441	2.59E-10
rs3771537	*MXD1*	2	70150674	rs6725425	Skeletal muscle	GMCL1	C	-0.28	93900	1.69E-10
rs3771537	*MXD1*	2	70151471	rs10205487	Skeletal muscle	GMCL1	G	-0.27	94697	5.55E-10
rs3771537	*MXD1*	2	70152027	rs726920	Skeletal muscle	GMCL1	C	-0.28	95253	1.66E-10
rs3771537	*MXD1*	2	70153436	rs10496174	Skeletal muscle	GMCL1	G	-0.27	96662	5.11E-10
rs3771537	*MXD1*	2	70154037	rs7573442	Skeletal muscle	GMCL1	A	-0.27	97263	5.09E-10
rs3771537	*MXD1*	2	70154134	rs12713682	Skeletal muscle	GMCL1	A	-0.27	97360	5.84E-10
rs3771537	*MXD1*	2	70154187	rs11893500	Skeletal muscle	GMCL1	C	-0.27	97413	5.11E-10
rs3771537	*MXD1*	2	70155482	rs4144081	Skeletal muscle	GMCL1	A	-0.28	98708	1.67E-10
rs3771537	*MXD1*	2	70156540	rs6712827	Skeletal muscle	GMCL1	G	-0.27	99766	5.12E-10
rs3771537	*MXD1*	2	70156589	rs6741449	Skeletal muscle	GMCL1	G	-0.28	99815	1.71E-10
rs3771537	*MXD1*	2	70160658	rs897119	Skeletal muscle	GMCL1	C	-0.27	103884	8.16E-10
rs3771537	*MXD1*	2	70160982	rs897120	Skeletal muscle	GMCL1	G	-0.28	104208	1.79E-10
rs3771537	*MXD1*	2	70161032	rs6729760	Skeletal muscle	GMCL1	T	-0.28	104258	2.58E-10
rs3771537	*MXD1*	2	70161342	rs12613947	Skeletal muscle	GMCL1	G	-0.28	104568	1.63E-10
rs3771537	*MXD1*	2	70163316	rs34586537	Skeletal muscle	GMCL1	G	-0.28	106542	1.29E-10
rs3771537	*MXD1*	2	70163434	rs11126251	Skeletal muscle	GMCL1	G	-0.28	106660	1.07E-10
rs3771537	*MXD1*	2	70164034	rs3771531	Skeletal muscle	GMCL1	C	-0.28	107260	1.26E-10
rs3771537	*MXD1*	2	70164805	rs3771530	Skeletal muscle	GMCL1	C	-0.30	108031	6.75E-11
rs3771537	*MXD1*	2	70164840	rs3771529	Skeletal muscle	GMCL1	A	-0.37	108066	3.32E-10
rs3771537	*MXD1*	2	70165966	rs7349311	Skeletal muscle	GMCL1	A	-0.41	109192	1.47E-10
rs3771537	*MXD1*	2	70167197	rs12475412	Skeletal muscle	GMCL1	T	-0.29	110423	7.37E-11
rs3771537	*MXD1(dist=1494);ASPRV1(dist=15654)*	2	70171570	rs897121	Skeletal muscle	GMCL1	T	-0.30	114796	8.46E-11
rs3771537	*MXD1(dist=2040);ASPRV1(dist=15108)*	2	70172116	rs11686934	Skeletal muscle	GMCL1	G	-0.22	115342	5.38E-07
rs3771537	*MXD1(dist=2390);ASPRV1(dist=14758)*	2	70172466	rs12713684	Skeletal muscle	GMCL1	G	-0.24	115692	4.54E-08
rs3771537	*MXD1(dist=2511);ASPRV1(dist=14637)*	2	70172587	rs6756513	Skeletal muscle	GMCL1	A	-0.27	115813	7.70E-08
rs3771537	*MXD1(dist=3954);ASPRV1(dist=13194)*	2	70174030	rs7569566	Skeletal muscle	GMCL1	C	-0.27	117256	1.91E-09
rs3771537	*MXD1(dist=3978);ASPRV1(dist=13170)*	2	70174054	rs7581977	Skeletal muscle	GMCL1	G	-0.28	117280	9.81E-10
rs3771537	*AAK1(dist=90535);ANXA4(dist=7615)*	2	69961512	rs13420511	Skeletal muscle	SNRNP27	C	-0.19	-159180	1.57E-05
rs3771537	*AAK1(dist=91163);ANXA4(dist=6987)*	2	69962140	rs6739197	Skeletal muscle	SNRNP27	G	-0.19	-158552	1.57E-05
rs3771537	*AAK1(dist=92470);ANXA4(dist=5680)*	2	69963447	rs4852980	Skeletal muscle	SNRNP27	G	-0.19	-157245	1.53E-05
rs3771537	*AAK1(dist=95312);ANXA4(dist=2838)*	2	69966289	rs2013427	Skeletal muscle	SNRNP27	T	-0.20	-154403	5.64E-06
rs3771537	*AAK1(dist=95541);ANXA4(dist=2609)*	2	69966518	rs7424888	Skeletal muscle	SNRNP27	A	-0.19	-154174	1.44E-05
rs3771537	*ANXA4*	2	69975819	rs10211658	Skeletal muscle	SNRNP27	A	-0.20	-144873	3.58E-06
rs3771537	*ANXA4*	2	69976384	rs62133983	Skeletal muscle	SNRNP27	T	-0.20	-144308	3.17E-06
rs3771537	*ANXA4*	2	69980174	rs7577493	Skeletal muscle	SNRNP27	G	-0.18	-140518	1.71E-05
rs3771537	*ANXA4*	2	69980193	rs7563401	Skeletal muscle	SNRNP27	T	-0.18	-140499	1.71E-05
rs3771537	*ANXA4*	2	69980910	rs10181122	Skeletal muscle	SNRNP27	T	-0.18	-139782	1.71E-05
rs3771537	*ANXA4*	2	69981295	rs7567400	Skeletal muscle	SNRNP27	A	-0.18	-139397	1.71E-05
rs3771537	*ANXA4*	2	70031797	rs3771541	Skeletal muscle	SNRNP27	G	-0.27	-88895	4.90E-10
rs3771537	*ANXA4*	2	70031941	rs3771540	Skeletal muscle	SNRNP27	G	-0.28	-88751	2.71E-10
rs3771537	*ANXA4*	2	70034793	rs2168115	Skeletal muscle	SNRNP27	G	-0.27	-85899	4.63E-10
rs3771537	*ANXA4*	2	70036711	rs13392884	Skeletal muscle	SNRNP27	G	-0.28	-83981	1.07E-10
rs3771537	*ANXA4*	2	70038232	rs6546550	Skeletal muscle	SNRNP27	G	-0.28	-82460	3.45E-10
rs3771537	*ANXA4*	2	70038792	rs3771537	Skeletal muscle	SNRNP27	C	-0.28	-81900	6.61E-12
rs3771537	*ANXA4*	2	70039224	rs4853027	Skeletal muscle	SNRNP27	T	-0.28	-81468	2.53E-10
rs3771537	*ANXA4*	2	70039677	rs2305523	Skeletal muscle	SNRNP27	C	-0.28	-81015	2.27E-10
rs3771537	*ANXA4*	2	70040542	rs2312555	Skeletal muscle	SNRNP27	A	-0.30	-80150	1.55E-13
rs3771537	*ANXA4*	2	70041033	rs11673826	Skeletal muscle	SNRNP27	A	-0.30	-79659	4.81E-13
rs3771537	*ANXA4*	2	70050725	rs7563062	Skeletal muscle	SNRNP27	A	-0.27	-69967	7.39E-10
rs3771537	*ANXA4*	2	70053668	rs7600468	Skeletal muscle	SNRNP27	G	-0.27	-67024	1.47E-09
rs3771537	*ANXA4(dist=1909);GMCL1(dist=1313)*	2	70055505	rs1531025	Skeletal muscle	SNRNP27	A	-0.27	-65187	7.70E-10
rs3771537	*GMCL1*	2	70057448	rs3732266	Skeletal muscle	SNRNP27	G	-0.27	-63244	1.15E-09
rs3771537	*GMCL1*	2	70062360	rs10167142	Skeletal muscle	SNRNP27	C	-0.26	-58332	1.32E-09
rs3771537	*GMCL1*	2	70062454	rs10202159	Skeletal muscle	SNRNP27	T	-0.26	-58238	1.30E-09
rs3771537	*GMCL1*	2	70063563	rs4401231	Skeletal muscle	SNRNP27	C	-0.27	-57129	1.13E-09
rs3771537	*GMCL1*	2	70063660	rs4241261	Skeletal muscle	SNRNP27	G	-0.26	-57032	1.28E-09
rs3771537	*GMCL1*	2	70064155	rs1377995	Skeletal muscle	SNRNP27	G	-0.27	-56537	1.20E-09
rs3771537	*GMCL1*	2	70068635	rs2872075	Skeletal muscle	SNRNP27	T	-0.27	-52057	9.44E-10
rs3771537	*GMCL1*	2	70073703	rs6546551	Skeletal muscle	SNRNP27	T	-0.27	-46989	1.09E-09
rs3771537	*GMCL1*	2	70076954	rs4852349	Skeletal muscle	SNRNP27	T	-0.28	-43738	2.27E-10
rs3771537	*GMCL1*	2	70079633	rs1551374	Skeletal muscle	SNRNP27	T	-0.26	-41059	6.16E-09
rs3771537	*GMCL1*	2	70087159	rs4852356	Skeletal muscle	SNRNP27	G	-0.25	-33533	2.09E-08
rs3771537	*GMCL1*	2	70090579	rs13017134	Skeletal muscle	SNRNP27	G	-0.28	-30113	1.24E-11
rs3771537	*GMCL1*	2	70091246	rs10865380	Skeletal muscle	SNRNP27	C	-0.29	-29446	4.19E-12
rs3771537	*GMCL1*	2	70093647	rs57278310	Skeletal muscle	SNRNP27	C	-0.28	-27045	5.25E-12
rs3771537	*GMCL1*	2	70093910	rs60207187	Skeletal muscle	SNRNP27	A	-0.28	-26782	1.24E-11
rs3771537	*GMCL1*	2	70098808	rs3214007	Skeletal muscle	SNRNP27	G	-0.27	-21884	7.58E-10

Supplementary Table 18. *continued*

rs3771537	*GMCL1*	2	70106832	rs6747542	Skeletal muscle	SNRNP27	C	-0.28	-13860	1.14E-11
rs3771537	*GMCL1(dist=1529);SNRNP27(dist=12819)*	2	70108256	rs1056482	Skeletal muscle	SNRNP27	A	-0.28	-12436	9.89E-12
rs3771537	*GMCL1(dist=4984);SNRNP27(dist=9364)*	2	70111711	rs6546553	Skeletal muscle	SNRNP27	A	-0.28	-8981	1.97E-11
rs3771537	*GMCL1(dist=10288);SNRNP27(dist=4060)*	2	70117015	rs10165883	Skeletal muscle	SNRNP27	T	-0.28	-3677	1.61E-10
rs3771537	*GMCL1(dist=10449);SNRNP27(dist=3899)*	2	70117176	rs12232914	Skeletal muscle	SNRNP27	T	-0.28	-3516	8.61E-11
rs3771537	*GMCL1(dist=10645);SNRNP27(dist=3703)*	2	70117372	rs12233079	Skeletal muscle	SNRNP27	G	-0.28	-3320	1.02E-10
rs3771537	*GMCL1(dist=10694);SNRNP27(dist=3654)*	2	70117421	rs2054047	Skeletal muscle	SNRNP27	C	-0.27	-3271	3.38E-10
rs3771537	*GMCL1(dist=11661);SNRNP27(dist=2687)*	2	70118388	rs13002091	Skeletal muscle	SNRNP27	T	-0.28	-2304	9.10E-11
rs3771537	*GMCL1(dist=11700);SNRNP27(dist=2648)*	2	70118427	rs13028508	Skeletal muscle	SNRNP27	A	-0.28	-2265	9.03E-11
rs3771537	*GMCL1(dist=12742);SNRNP27(dist=1606)*	2	70119469	rs3755389	Skeletal muscle	SNRNP27	C	-0.28	-1223	9.75E-11
rs3771537	*SNRNP27*	2	70124316	rs3752781	Skeletal muscle	SNRNP27	A	-0.28	3624	6.28E-11
rs3771537	*SNRNP27*	2	70124805	rs6720498	Skeletal muscle	SNRNP27	C	-0.28	4113	9.58E-11
rs3771537	*SNRNP27*	2	70125763	rs13015457	Skeletal muscle	SNRNP27	T	-0.28	5071	4.93E-11
rs3771537	*SNRNP27*	2	70125988	rs4852375	Skeletal muscle	SNRNP27	G	-0.28	5296	5.43E-11
rs3771537	*SNRNP27*	2	70127229	rs6716937	Skeletal muscle	SNRNP27	A	-0.28	6537	4.95E-11
rs3771537	*SNRNP27*	2	70128717	rs7598283	Skeletal muscle	SNRNP27	G	-0.28	8025	6.99E-11
rs3771537	*SNRNP27*	2	70132676	rs1048266	Skeletal muscle	SNRNP27	G	-0.28	11984	4.94E-11
rs3771537	*SNRNP27(dist=1739);MXD1(dist=8066)*	2	70134107	rs10166011	Skeletal muscle	SNRNP27	G	-0.28	13415	5.98E-11
rs3771537	*SNRNP27(dist=3338);MXD1(dist=6467)*	2	70135706	rs6546554	Skeletal muscle	SNRNP27	A	-0.28	15014	4.94E-11
rs3771537	*SNRNP27(dist=3392);MXD1(dist=6413)*	2	70135760	rs6546555	Skeletal muscle	SNRNP27	G	-0.29	15068	3.97E-11
rs3771537	*SNRNP27(dist=5130);MXD1(dist=4675)*	2	70137498	rs1979214	Skeletal muscle	SNRNP27	C	-0.28	16806	5.78E-11
rs3771537	*SNRNP27(dist=5406);MXD1(dist=4399)*	2	70137774	rs6736408	Skeletal muscle	SNRNP27	T	-0.28	17082	4.94E-11
rs3771537	*SNRNP27(dist=5743);MXD1(dist=4062)*	2	70138111	rs6739780	Skeletal muscle	SNRNP27	A	-0.28	17419	6.68E-11
rs3771537	*SNRNP27(dist=5802);MXD1(dist=4003)*	2	70138170	rs6754896	Skeletal muscle	SNRNP27	C	-0.28	17478	4.94E-11
rs3771537	*SNRNP27(dist=6633);MXD1(dist=3172)*	2	70139001	rs6546556	Skeletal muscle	SNRNP27	G	-0.28	18309	4.94E-11
rs3771537	*SNRNP27(dist=6766);MXD1(dist=3039)*	2	70139134	rs7592647	Skeletal muscle	SNRNP27	T	-0.28	18442	7.87E-11
rs3771537	*SNRNP27(dist=7903);MXD1(dist=1902)*	2	70140271	rs897122	Skeletal muscle	SNRNP27	T	-0.28	19579	4.94E-11
rs3771537	*MXD1*	2	70144596	rs11902198	Skeletal muscle	SNRNP27	A	-0.29	23904	2.83E-11
rs3771537	*MXD1*	2	70145717	rs6546558	Skeletal muscle	SNRNP27	T	-0.28	25025	1.07E-10
rs3771537	*MXD1*	2	70145833	rs6546559	Skeletal muscle	SNRNP27	A	-0.28	25141	5.67E-11
rs3771537	*MXD1*	2	70146121	rs6721891	Skeletal muscle	SNRNP27	G	-0.28	25429	4.94E-11
rs3771537	*MXD1*	2	70146125	rs6750488	Skeletal muscle	SNRNP27	T	-0.28	25433	4.94E-11
rs3771537	*MXD1*	2	70146625	rs7419837	Skeletal muscle	SNRNP27	C	-0.28	25933	1.12E-10
rs3771537	*MXD1*	2	70149225	rs1454498	Skeletal muscle	SNRNP27	A	-0.29	28533	4.20E-11
rs3771537	*MXD1*	2	70150215	rs6738174	Skeletal muscle	SNRNP27	C	-0.29	29523	2.57E-11
rs3771537	*MXD1*	2	70150674	rs6725425	Skeletal muscle	SNRNP27	C	-0.29	29982	4.20E-11
rs3771537	*MXD1*	2	70151471	rs10205487	Skeletal muscle	SNRNP27	G	-0.28	30779	4.92E-11
rs3771537	*MXD1*	2	70152027	rs726920	Skeletal muscle	SNRNP27	C	-0.29	31335	4.20E-11
rs3771537	*MXD1*	2	70153436	rs10496174	Skeletal muscle	SNRNP27	G	-0.28	32744	4.99E-11
rs3771537	*MXD1*	2	70154037	rs7573442	Skeletal muscle	SNRNP27	A	-0.28	33345	4.91E-11
rs3771537	*MXD1*	2	70154134	rs12713682	Skeletal muscle	SNRNP27	A	-0.29	33442	3.82E-11
rs3771537	*MXD1*	2	70154187	rs11893500	Skeletal muscle	SNRNP27	C	-0.28	33495	4.99E-11
rs3771537	*MXD1*	2	70155482	rs4144081	Skeletal muscle	SNRNP27	A	-0.29	34790	4.08E-11
rs3771537	*MXD1*	2	70156540	rs6712827	Skeletal muscle	SNRNP27	G	-0.28	35848	4.80E-11
rs3771537	*MXD1*	2	70156589	rs6741449	Skeletal muscle	SNRNP27	G	-0.28	35897	4.08E-11
rs3771537	*MXD1*	2	70160658	rs897119	Skeletal muscle	SNRNP27	C	-0.28	39966	8.07E-11
rs3771537	*MXD1*	2	70160982	rs897120	Skeletal muscle	SNRNP27	G	-0.28	40290	3.99E-11
rs3771537	*MXD1*	2	70161032	rs6729760	Skeletal muscle	SNRNP27	T	-0.28	40340	2.18E-10
rs3771537	*MXD1*	2	70161342	rs12613947	Skeletal muscle	SNRNP27	G	-0.28	40650	4.34E-11
rs3771537	*MXD1*	2	70163316	rs34586537	Skeletal muscle	SNRNP27	G	-0.28	42624	5.99E-11
rs3771537	*MXD1*	2	70163434	rs11126251	Skeletal muscle	SNRNP27	G	-0.28	42742	1.15E-10
rs3771537	*MXD1*	2	70164034	rs3771531	Skeletal muscle	SNRNP27	C	-0.28	43342	6.17E-11
rs3771537	*MXD1*	2	70164805	rs3771530	Skeletal muscle	SNRNP27	C	-0.22	44113	5.57E-07
rs3771537	*MXD1*	2	70167197	rs12475412	Skeletal muscle	SNRNP27	T	-0.28	46505	5.54E-11
rs3771537	*MXD1(dist=1494);ASPRV1(dist=15654)*	2	70171570	rs897121	Skeletal muscle	SNRNP27	T	-0.25	50878	3.45E-08
rs3771537	*MXD1(dist=2040);ASPRV1(dist=15108)*	2	70172116	rs11686934	Skeletal muscle	SNRNP27	G	-0.27	51424	2.81E-10
rs3771537	*MXD1(dist=2390);ASPRV1(dist=14758)*	2	70172466	rs12713684	Skeletal muscle	SNRNP27	G	-0.24	51774	1.39E-08
rs3771537	*MXD1(dist=3954);ASPRV1(dist=13194)*	2	70174030	rs7569566	Skeletal muscle	SNRNP27	C	-0.21	53338	2.46E-06
rs3771537	*MXD1(dist=3978);ASPRV1(dist=13170)*	2	70174054	rs7581977	Skeletal muscle	SNRNP27	G	-0.21	53362	3.20E-06
rs11718898	*CAND2*	3	12848822	rs11718898	Skeletal muscle	CAND2	C	0.50	10851	2.24E-20
rs11718898	*CAND2*	3	12848822	rs11718898	Skeletal muscle	KRT18P17	C	0.42	-18652	2.24E-09
rs11718898	*CAND2*	3	12848822	rs11718898	Skeletal muscle	RP11-767C1.2	C	0.30	25405	1.02E-06
rs7508	*ASAH1*	8	17913970	rs7508	Left ventricle	PCM1	A	0.20	133621	3.18E-06
rs7508	*ASAH1*	8	17913970	rs7508	Skeletal muscle	PCM1	A	-0.20	133621	1.12E-06
rs7915134	*SYNPO2L*	10	75404300	rs11000728	Atrial appendage	MYOZ1	G	1.33	-2785	1.78E-21
rs7915134	*SYNPO2L*	10	75405635	rs41280404	Atrial appendage	MYOZ1	G	1.30	-4120	5.15E-21
rs7915134	*SYNPO2L*	10	75406141	rs3740293	Atrial appendage	MYOZ1	C	1.15	-4626	4.11E-18
rs7915134	*SYNPO2L*	10	75406912	rs34163229	Atrial appendage	MYOZ1	T	1.32	-5397	1.98E-21
rs7915134	*SYNPO2L*	10	75407290	rs3812629	Atrial appendage	MYOZ1	A	1.32	-5775	1.86E-21
rs7915134	*SYNPO2L*	10	75407649	rs4746139	Atrial appendage	MYOZ1	C	1.35	-6134	1.30E-20
rs7915134	*SYNPO2L*	10	75409877	rs2177843	Atrial appendage	MYOZ1	T	1.34	-8362	5.93E-24
rs7915134	*SYNPO2L*	10	75414344	rs60212594	Atrial appendage	MYOZ1	C	1.36	-12829	1.52E-23
rs7915134	*SYNPO2L*	10	75415677	rs60632610	Atrial appendage	MYOZ1	T	1.35	-14162	4.70E-23
rs7915134	*SYNPO2L*	10	75416789	rs12570126	Atrial appendage	MYOZ1	G	1.13	-15274	3.20E-16
rs7915134	*SYNPO2L(dist=1417);AGAP5(dist=16784)*	10	75417249	rs4746140	Atrial appendage	MYOZ1	C	1.12	-15734	3.98E-16
rs7915134	*SYNPO2L(dist=3831);AGAP5(dist=14370)*	10	75419663	rs11000734	Atrial appendage	MYOZ1	G	1.13	-18148	3.47E-16
rs7915134	*SYNPO2L(dist=4282);AGAP5(dist=13919)*	10	75420114	rs6480708	Atrial appendage	MYOZ1	A	1.12	-18599	3.98E-16
rs7915134	*SYNPO2L(dist=4348);AGAP5(dist=13853)*	10	75420180	rs7915134	Atrial appendage	MYOZ1	T	1.28	-18665	2.54E-20
rs7915134	*SYNPO2L(dist=4738);AGAP5(dist=13463)*	10	75420570	rs7900932	Atrial appendage	MYOZ1	C	1.28	-19055	5.55E-21
rs7915134	*SYNPO2L(dist=5376);AGAP5(dist=12825)*	10	75421208	rs10824026	Atrial appendage	MYOZ1	A	-1.12	-19693	3.98E-16
rs7915134	*SYNPO2L(dist=5614);AGAP5(dist=12587)*	10	75421446	rs7394152	Atrial appendage	MYOZ1	T	1.30	-19931	1.88E-21
rs7915134	*SYNPO2L(dist=5748);AGAP5(dist=12453)*	10	75421580	rs7394178	Atrial appendage	MYOZ1	A	1.27	-20065	5.46E-21
rs7915134	*SYNPO2L(dist=5816);AGAP5(dist=12385)*	10	75421648	rs7394190	Atrial appendage	MYOZ1	A	1.13	-20133	3.03E-16
rs7915134	*SYNPO2L(dist=6482);AGAP5(dist=11719)*	10	75422314	rs78249997	Atrial appendage	MYOZ1	T	1.32	-20799	7.49E-21
rs7915134	*SYNPO2L(dist=12464);AGAP5(dist=5737)*	10	75428296	rs148321568	Atrial appendage	MYOZ1	T	1.50	-26781	4.54E-21
rs7915134	*SYNPO2L(dist=14169);AGAP5(dist=4032)*	10	75430001	rs4745719	Atrial appendage	MYOZ1	G	-0.96	-28486	3.66E-11
rs7915134	*AGAP5*	10	75447582	rs147790633	Atrial appendage	MYOZ1	C	1.36	-46067	2.07E-20

Supplementary Table 18. *continued*

rs7915134	*AGAP5*	10	75449789	rs76443711	Atrial appendage	MYOZ1	C	1.41	-48274	3.07E-21
rs7915134	*AGAP5*	10	75450901	rs138055607	Atrial appendage	MYOZ1	G	1.41	-49386	3.04E-21
rs7915134	*BMS1P4*	10	75462510	rs76192127	Atrial appendage	MYOZ1	C	1.40	-60995	5.05E-21
rs7915134	*BMS1P4*	10	75464587	rs4745721	Atrial appendage	MYOZ1	A	1.41	-63072	6.14E-21
rs7915134	*FUT11(dist=3034);CHCHD1(dist=2798)*	10	75539010	rs11000775	Atrial appendage	MYOZ1	C	1.23	-137495	7.28E-16
rs7915134	*SYNPO2L*	10	75407649	rs4746139	Skeletal muscle	FUT11	C	-0.26	-125299	1.13E-05
rs7915134	*SYNPO2L*	10	75409877	rs2177843	Skeletal muscle	FUT11	T	-0.25	-123071	1.37E-05
rs7915134	*SYNPO2L*	10	75416789	rs12570126	Skeletal muscle	FUT11	G	-0.23	-116159	1.51E-05
rs7915134	*SYNPO2L(dist=1417);AGAP5(dist=16784)*	10	75417249	rs4746140	Skeletal muscle	FUT11	C	-0.24	-115699	7.13E-06
rs7915134	*SYNPO2L(dist=3831);AGAP5(dist=14370)*	10	75419663	rs11000734	Skeletal muscle	FUT11	G	-0.23	-113285	1.37E-05
rs7915134	*SYNPO2L(dist=4282);AGAP5(dist=13919)*	10	75420114	rs6480708	Skeletal muscle	FUT11	A	-0.23	-112834	1.43E-05
rs7915134	*SYNPO2L(dist=4738);AGAP5(dist=13463)*	10	75420570	rs7900932	Skeletal muscle	FUT11	C	-0.24	-112378	1.85E-05
rs7915134	*SYNPO2L(dist=5376);AGAP5(dist=12825)*	10	75421208	rs10824026	Skeletal muscle	FUT11	A	0.24	-111740	1.05E-05
rs7915134	*SYNPO2L(dist=5816);AGAP5(dist=12385)*	10	75421648	rs7394190	Skeletal muscle	FUT11	A	-0.25	-111300	5.90E-06
rs7915134	*SYNPO2L(dist=6482);AGAP5(dist=11719)*	10	75422314	rs78249997	Skeletal muscle	FUT11	T	-0.25	-110634	1.56E-05
rs7915134	*SYNPO2L(dist=12464);AGAP5(dist=5737)*	10	75428296	rs148321568	Skeletal muscle	FUT11	T	-0.26	-104652	1.38E-05
rs7915134	*AGAP5*	10	75447582	rs147790633	Skeletal muscle	FUT11	C	-0.27	-85366	3.84E-06
rs7915134	*AGAP5*	10	75449789	rs76443711	Skeletal muscle	FUT11	C	-0.27	-83159	1.10E-05
rs7915134	*AGAP5*	10	75450901	rs138055607	Skeletal muscle	FUT11	G	-0.27	-82047	1.12E-05
rs7915134	*BMS1P4*	10	75462510	rs76192127	Skeletal muscle	FUT11	C	-0.27	-70438	1.18E-05
rs7915134	*BMS1P4*	10	75464587	rs4745721	Skeletal muscle	FUT11	A	-0.27	-68361	1.20E-05
rs7915134	*FUT11(dist=3034);CHCHD1(dist=2798)*	10	75539010	rs11000775	Skeletal muscle	FUT11	C	-0.28	6062	5.20E-06
rs75190942	*KCNJ5*	11	128764570	rs76097649	Left ventricle	KCNJ5	A	0.58	3319	3.15E-06
rs75190942	*KCNJ5*	11	128764571	rs75190942	Left ventricle	KCNJ5	A	0.58	3320	3.15E-06
rs883079	*RBM19(dist=385634);TBX5(dist=1925)*	12	114789810	rs2891503	Left ventricle	TBX5	G	0.26	56437	3.84E-06
rs1152591	*SYNE2*	14	64649894	rs1255977	Left ventricle	SYNE2	G	0.24	330211	7.92E-08
rs1152591	*SYNE2*	14	64651663	rs1266927	Left ventricle	SYNE2	A	0.28	331980	1.53E-10
rs1152591	*SYNE2*	14	64654431	rs1255984	Left ventricle	SYNE2	G	0.27	334748	1.65E-09
rs1152591	*SYNE2*	14	64655161	rs1255986	Left ventricle	SYNE2	T	0.27	335478	1.51E-09
rs1152591	*SYNE2*	14	64657684	rs1255988	Left ventricle	SYNE2	A	0.27	338001	1.26E-09
rs1152591	*SYNE2*	14	64667337	rs1152601	Left ventricle	SYNE2	C	0.21	347654	4.04E-06
rs1152591	*SYNE2*	14	64674981	rs1152595	Left ventricle	SYNE2	C	0.21	355298	2.11E-06
rs1152591	*SYNE2*	14	64675044	rs1152594	Left ventricle	SYNE2	G	0.23	355361	5.14E-07
rs1152591	*SYNE2*	14	64675895	rs1152593	Left ventricle	SYNE2	T	0.25	356212	3.81E-08
rs1152591	*SYNE2*	14	64679960	rs2738413	Left ventricle	SYNE2	G	0.29	360277	2.54E-11
rs1152591	*SYNE2*	14	64680848	rs1152591	Left ventricle	SYNE2	G	0.29	361165	5.79E-11
rs1152591	*SYNE2*	14	64683926	rs1152589	Left ventricle	SYNE2	T	0.27	364243	2.58E-09
rs1152591	*SYNE2*	14	64690784	rs1152586	Left ventricle	SYNE2	C	0.27	371101	1.24E-09
rs1152591	*SYNE2*	14	64692630	rs1152582	Left ventricle	SYNE2	C	0.25	372947	3.37E-08
rs1152591	*ESR2*	14	64697485	rs1152577	Left ventricle	SYNE2	G	0.25	377802	2.29E-08
Variants identified in European ethnicity analysis - eQTLs from GTEx Release V6										
rs651386	*GORAB(dist=105281);PRRX1(dist=5058)*	1	170628255	rs680084	Left ventricle	PRRX1	A	0.32	-3614	5.20E-06
rs651386	*GORAB(dist=108789);PRRX1(dist=1550)*	1	170631763	rs629234	Left ventricle	PRRX1	C	0.31	-106	6.83E-06
rs651386	*GORAB(dist=37630);PRRX1(dist=72709)*	1	170560604	rs6658866	Left ventricle	RP1-79C4.4	G	-0.40	-75918	9.05E-08
rs651386	*GORAB(dist=38430);PRRX1(dist=71909)*	1	170561404	rs6659754	Left ventricle	RP1-79C4.4	T	-0.39	-75118	2.94E-07
rs651386	*GORAB(dist=40109);PRRX1(dist=70230)*	1	170563083	rs577827	Left ventricle	RP1-79C4.4	C	0.38	-73439	1.15E-07
rs651386	*GORAB(dist=40231);PRRX1(dist=70108)*	1	170563205	rs12027180	Left ventricle	RP1-79C4.4	T	0.40	-73317	1.75E-06
rs651386	*GORAB(dist=43031);PRRX1(dist=67308)*	1	170566005	rs763567	Left ventricle	RP1-79C4.4	G	-0.39	-70517	2.53E-07
rs651386	*GORAB(dist=44463);PRRX1(dist=65876)*	1	170567437	rs1928715	Left ventricle	RP1-79C4.4	T	-0.41	-69085	9.33E-08
rs651386	*GORAB(dist=45740);PRRX1(dist=64599)*	1	170568714	rs12755237	Left ventricle	RP1-79C4.4	A	-0.42	-67808	6.17E-08
rs651386	*GORAB(dist=45922);PRRX1(dist=64417)*	1	170568896	rs12742164	Left ventricle	RP1-79C4.4	G	-0.43	-67626	2.83E-08
rs651386	*GORAB(dist=46343);PRRX1(dist=63996)*	1	170569317	rs3903239	Left ventricle	RP1-79C4.4	G	-0.41	-67205	1.18E-07
rs651386	*GORAB(dist=46715);PRRX1(dist=63624)*	1	170569689	rs12760630	Left ventricle	RP1-79C4.4	A	-0.41	-66833	1.21E-07
rs651386	*GORAB(dist=47069);PRRX1(dist=63270)*	1	170570043	rs10800529	Left ventricle	RP1-79C4.4	C	0.41	-66479	1.12E-06
rs651386	*GORAB(dist=47525);PRRX1(dist=62814)*	1	170570499	rs7412231	Left ventricle	RP1-79C4.4	C	-0.41	-66023	1.29E-07
rs651386	*GORAB(dist=48869);PRRX1(dist=61470)*	1	170571843	rs1234230	Left ventricle	RP1-79C4.4	G	-0.39	-64679	9.15E-08
rs651386	*GORAB(dist=49972);PRRX1(dist=60367)*	1	170572946	rs10919437	Left ventricle	RP1-79C4.4	A	-0.40	-63576	1.58E-07
rs651386	*GORAB(dist=50284);PRRX1(dist=60055)*	1	170573258	rs61217505	Left ventricle	RP1-79C4.4	T	-0.41	-63264	9.94E-08
rs651386	*GORAB(dist=50840);PRRX1(dist=59499)*	1	170573814	rs476810	Left ventricle	RP1-79C4.4	C	-0.38	-62708	2.01E-07
rs651386	*GORAB(dist=51954);PRRX1(dist=58385)*	1	170574928	rs1234233	Left ventricle	RP1-79C4.4	T	-0.37	-61594	2.17E-07
rs651386	*GORAB(dist=53133);PRRX1(dist=57206)*	1	170576107	rs2206062	Left ventricle	RP1-79C4.4	C	-0.40	-60415	2.06E-07
rs651386	*GORAB(dist=53764);PRRX1(dist=56575)*	1	170576738	rs566850	Left ventricle	RP1-79C4.4	G	-0.37	-59784	2.47E-07
rs651386	*GORAB(dist=54081);PRRX1(dist=56258)*	1	170577055	rs722597	Left ventricle	RP1-79C4.4	A	0.41	-59467	1.12E-06
rs651386	*GORAB(dist=54261);PRRX1(dist=56078)*	1	170577235	rs647438	Left ventricle	RP1-79C4.4	T	-0.39	-59287	1.39E-07
rs651386	*GORAB(dist=54866);PRRX1(dist=55473)*	1	170577840	rs72482606	Left ventricle	RP1-79C4.4	A	0.41	-58682	1.12E-06
rs651386	*GORAB(dist=55332);PRRX1(dist=55007)*	1	170578306	rs10919440	Left ventricle	RP1-79C4.4	G	-0.40	-58216	2.27E-07
rs651386	*GORAB(dist=55613);PRRX1(dist=54726)*	1	170578587	rs494339	Left ventricle	RP1-79C4.4	A	-0.39	-57935	1.14E-07
rs651386	*GORAB(dist=56115);PRRX1(dist=54224)*	1	170579089	rs10919441	Left ventricle	RP1-79C4.4	A	0.40	-57433	1.69E-06
rs651386	*GORAB(dist=56620);PRRX1(dist=53719)*	1	170579594	rs546258	Left ventricle	RP1-79C4.4	T	-0.37	-56928	3.08E-07
rs651386	*GORAB(dist=57503);PRRX1(dist=52836)*	1	170580477	rs553905	Left ventricle	RP1-79C4.4	G	-0.37	-56045	4.37E-07
rs651386	*GORAB(dist=58560);PRRX1(dist=51779)*	1	170581534	rs2982131	Left ventricle	RP1-79C4.4	C	-0.37	-54988	3.52E-07
rs651386	*GORAB(dist=58660);PRRX1(dist=51679)*	1	170581634	rs10919444	Left ventricle	RP1-79C4.4	A	-0.40	-54888	1.81E-07
rs651386	*GORAB(dist=58713);PRRX1(dist=51626)*	1	170581687	rs34252585	Left ventricle	RP1-79C4.4	A	0.40	-54835	1.68E-06
rs651386	*GORAB(dist=59601);PRRX1(dist=50738)*	1	170582575	rs1952675	Left ventricle	RP1-79C4.4	G	-0.40	-53947	1.98E-07
rs651386	*GORAB(dist=60537);PRRX1(dist=49802)*	1	170583511	rs6677540	Left ventricle	RP1-79C4.4	A	-0.39	-53011	3.98E-07
rs651386	*GORAB(dist=60970);PRRX1(dist=49369)*	1	170583944	rs6690642	Left ventricle	RP1-79C4.4	C	-0.39	-52578	4.14E-07
rs651386	*GORAB(dist=62123);PRRX1(dist=48216)*	1	170585097	rs2206063	Left ventricle	RP1-79C4.4	C	0.40	-51425	1.58E-06
rs651386	*GORAB(dist=62858);PRRX1(dist=47481)*	1	170585832	rs619456	Left ventricle	RP1-79C4.4	C	-0.36	-50690	5.05E-07
rs651386	*GORAB(dist=63341);PRRX1(dist=46998)*	1	170586315	rs736791	Left ventricle	RP1-79C4.4	A	-0.40	-50207	2.72E-07
rs651386	*GORAB(dist=64241);PRRX1(dist=46098)*	1	170587215	rs576736	Left ventricle	RP1-79C4.4	G	0.43	-49307	2.66E-07
rs651386	*GORAB(dist=64366);PRRX1(dist=45973)*	1	170587340	rs577676	Left ventricle	RP1-79C4.4	T	0.38	-49182	6.26E-06
rs651386	*GORAB(dist=65620);PRRX1(dist=44719)*	1	170588594	rs2022373	Left ventricle	RP1-79C4.4	C	0.42	-47928	5.17E-07
rs651386	*GORAB(dist=66463);PRRX1(dist=43876)*	1	170589437	rs10489231	Left ventricle	RP1-79C4.4	A	0.42	-47085	3.68E-07
rs651386	*GORAB(dist=66936);PRRX1(dist=43403)*	1	170589910	rs2022372	Left ventricle	RP1-79C4.4	A	-0.39	-46612	2.93E-07
rs651386	*GORAB(dist=67593);PRRX1(dist=42746)*	1	170590567	rs12031871	Left ventricle	RP1-79C4.4	T	0.43	-45955	2.42E-07
rs651386	*GORAB(dist=68336);PRRX1(dist=42003)*	1	170591310	rs651386	Left ventricle	RP1-79C4.4	T	0.38	-45212	4.78E-06
rs651386	*GORAB(dist=68834);PRRX1(dist=41505)*	1	170591808	rs10753817	Left ventricle	RP1-79C4.4	G	0.43	-44714	2.41E-07

Supplementary Table 18. *continued*

rs651386	*GORAB(dist=71095);PRRX1(dist=39244)*	1	170594069	rs12072276	Left ventricle	RP1-79C4.4	G	0.42	-42453	4.27E-07
rs651386	*GORAB(dist=71142);PRRX1(dist=39197)*	1	170594116	rs10919446	Left ventricle	RP1-79C4.4	A	0.42	-42406	3.75E-07
rs651386	*GORAB(dist=72144);PRRX1(dist=38195)*	1	170595118	rs12074059	Left ventricle	RP1-79C4.4	T	0.41	-41404	5.57E-07
rs651386	*GORAB(dist=73098);PRRX1(dist=37241)*	1	170596072	rs494521	Left ventricle	RP1-79C4.4	T	0.38	-40450	8.69E-07
rs651386	*GORAB(dist=73284);PRRX1(dist=37055)*	1	170596258	rs1234275	Left ventricle	RP1-79C4.4	G	0.38	-40264	6.32E-07
rs651386	*GORAB(dist=73399);PRRX1(dist=36940)*	1	170596373	rs1234274	Left ventricle	RP1-79C4.4	G	0.38	-40149	6.33E-07
rs651386	*GORAB(dist=73571);PRRX1(dist=36768)*	1	170596545	rs11577602	Left ventricle	RP1-79C4.4	T	0.42	-39977	6.50E-07
rs651386	*GORAB(dist=73598);PRRX1(dist=36741)*	1	170596572	rs10800530	Left ventricle	RP1-79C4.4	A	0.42	-39950	6.50E-07
rs651386	*GORAB(dist=75213);PRRX1(dist=35126)*	1	170598187	rs638704	Left ventricle	RP1-79C4.4	T	0.37	-38335	1.13E-06
rs651386	*GORAB(dist=76599);PRRX1(dist=33740)*	1	170599573	rs10919448	Left ventricle	RP1-79C4.4	C	0.42	-36949	6.37E-07
rs651386	*GORAB(dist=78034);PRRX1(dist=32305)*	1	170601008	rs189058353	Left ventricle	RP1-79C4.4	A	0.37	-35514	2.32E-06
rs651386	*GORAB(dist=78339);PRRX1(dist=32000)*	1	170601313	rs12068805	Left ventricle	RP1-79C4.4	C	0.42	-35209	5.67E-07
rs651386	*GORAB(dist=78961);PRRX1(dist=31378)*	1	170601935	rs12566725	Left ventricle	RP1-79C4.4	T	0.42	-34587	5.66E-07
rs651386	*GORAB(dist=81148);PRRX1(dist=29191)*	1	170604122	rs598993	Left ventricle	RP1-79C4.4	C	0.37	-32400	1.68E-06
rs651386	*GORAB(dist=81964);PRRX1(dist=28375)*	1	170604938	rs541557	Left ventricle	RP1-79C4.4	G	0.37	-31584	1.68E-06
rs651386	*GORAB(dist=83112);PRRX1(dist=27227)*	1	170606086	rs644784	Left ventricle	RP1-79C4.4	T	0.42	-30436	5.59E-07
rs651386	*GORAB(dist=83380);PRRX1(dist=26959)*	1	170606354	rs656539	Left ventricle	RP1-79C4.4	T	0.42	-30168	5.58E-07
rs651386	*GORAB(dist=85107);PRRX1(dist=25232)*	1	170608081	rs539045	Left ventricle	RP1-79C4.4	T	0.37	-28441	1.69E-06
rs651386	*GORAB(dist=85694);PRRX1(dist=24645)*	1	170608668	rs533603	Left ventricle	RP1-79C4.4	G	0.42	-27854	5.45E-07
rs651386	*GORAB(dist=86216);PRRX1(dist=24123)*	1	170609190	rs473832	Left ventricle	RP1-79C4.4	C	0.37	-27332	8.85E-07
rs651386	*GORAB(dist=86651);PRRX1(dist=23688)*	1	170609625	rs580487	Left ventricle	RP1-79C4.4	C	0.37	-26897	1.70E-06
rs651386	*GORAB(dist=86769);PRRX1(dist=23570)*	1	170609743	rs578928	Left ventricle	RP1-79C4.4	C	0.42	-26779	5.41E-07
rs651386	*GORAB(dist=87736);PRRX1(dist=22603)*	1	170610710	rs549449	Left ventricle	RP1-79C4.4	C	0.42	-25812	5.19E-07
rs651386	*GORAB(dist=89288);PRRX1(dist=21051)*	1	170612262	rs492804	Left ventricle	RP1-79C4.4	T	0.37	-24260	1.11E-06
rs651386	*GORAB(dist=89899);PRRX1(dist=20440)*	1	170612873	rs639652	Left ventricle	RP1-79C4.4	A	0.36	-23649	1.82E-06
rs651386	*GORAB(dist=89952);PRRX1(dist=20387)*	1	170612926	rs639720	Left ventricle	RP1-79C4.4	C	0.42	-23596	5.17E-07
rs651386	*GORAB(dist=90876);PRRX1(dist=19463)*	1	170613850	rs654461	Left ventricle	RP1-79C4.4	T	0.37	-22672	1.05E-06
rs651386	*GORAB(dist=90895);PRRX1(dist=19444)*	1	170613869	rs567328	Left ventricle	RP1-79C4.4	A	0.38	-22653	7.46E-07
rs651386	*GORAB(dist=91068);PRRX1(dist=19271)*	1	170614042	rs544478	Left ventricle	RP1-79C4.4	T	0.38	-22480	7.82E-07
rs651386	*GORAB(dist=91270);PRRX1(dist=19069)*	1	170614244	rs666419	Left ventricle	RP1-79C4.4	C	0.42	-22278	5.17E-07
rs651386	*GORAB(dist=92886);PRRX1(dist=17453)*	1	170615860	rs593173	Left ventricle	RP1-79C4.4	A	0.42	-20662	5.17E-07
rs651386	*GORAB(dist=92943);PRRX1(dist=17396)*	1	170615917	rs593560	Left ventricle	RP1-79C4.4	A	0.37	-20605	1.09E-06
rs651386	*GORAB(dist=93381);PRRX1(dist=16958)*	1	170616355	rs2988392	Left ventricle	RP1-79C4.4	C	0.36	-20167	1.69E-06
rs651386	*GORAB(dist=94332);PRRX1(dist=16007)*	1	170617306	rs608930	Left ventricle	RP1-79C4.4	T	0.37	-19216	7.89E-07
rs651386	*GORAB(dist=94405);PRRX1(dist=15934)*	1	170617379	rs619699	Left ventricle	RP1-79C4.4	A	0.45	-19143	2.63E-07
rs651386	*GORAB(dist=95317);PRRX1(dist=15022)*	1	170618291	rs623752	Left ventricle	RP1-79C4.4	G	0.37	-18231	6.72E-07
rs651386	*GORAB(dist=95408);PRRX1(dist=14931)*	1	170618382	rs531007	Left ventricle	RP1-79C4.4	G	0.37	-18140	6.54E-07
rs651386	*GORAB(dist=96350);PRRX1(dist=13989)*	1	170619324	rs1234282	Left ventricle	RP1-79C4.4	T	0.47	-17198	5.41E-08
rs651386	*GORAB(dist=96633);PRRX1(dist=13706)*	1	170619607	rs575432	Left ventricle	RP1-79C4.4	G	0.36	-16915	2.23E-06
rs651386	*GORAB(dist=96956);PRRX1(dist=13383)*	1	170619930	rs651822	Left ventricle	RP1-79C4.4	T	0.41	-16592	9.51E-07
rs651386	*GORAB(dist=99994);PRRX1(dist=10345)*	1	170622968	rs1234284	Left ventricle	RP1-79C4.4	T	0.47	-13554	2.52E-08
rs651386	*GORAB(dist=100135);PRRX1(dist=10204)*	1	170623109	rs588837	Left ventricle	RP1-79C4.4	G	0.37	-13413	1.17E-06
rs651386	*GORAB(dist=100946);PRRX1(dist=9393)*	1	170623920	rs12089974	Left ventricle	RP1-79C4.4	A	0.42	-12602	2.65E-06
rs651386	*GORAB(dist=102893);PRRX1(dist=7446)*	1	170625867	rs501680	Left ventricle	RP1-79C4.4	C	0.46	-10655	9.04E-08
rs651386	*GORAB(dist=103979);PRRX1(dist=6360)*	1	170626953	rs663887	Left ventricle	RP1-79C4.4	A	0.46	-9569	9.04E-08
rs651386	*GORAB(dist=104820);PRRX1(dist=5519)*	1	170627794	rs552277	Left ventricle	RP1-79C4.4	C	0.45	-8728	1.40E-07
rs651386	*GORAB(dist=105281);PRRX1(dist=5058)*	1	170628255	rs680084	Left ventricle	RP1-79C4.4	A	0.38	-8267	5.99E-07
rs651386	*GORAB(dist=105414);PRRX1(dist=4925)*	1	170628388	rs583006	Left ventricle	RP1-79C4.4	G	0.42	-8134	1.60E-06
rs651386	*GORAB(dist=105461);PRRX1(dist=4878)*	1	170628435	rs524877	Left ventricle	RP1-79C4.4	C	0.46	-8087	9.04E-08
rs651386	*GORAB(dist=106864);PRRX1(dist=3475)*	1	170629838	rs600093	Left ventricle	RP1-79C4.4	A	0.46	-6684	1.01E-07
rs651386	*GORAB(dist=107285);PRRX1(dist=3054)*	1	170630259	rs601938	Left ventricle	RP1-79C4.4	T	0.46	-6263	9.08E-08
rs651386	*GORAB(dist=108446);PRRX1(dist=1893)*	1	170631420	rs627848	Left ventricle	RP1-79C4.4	A	0.46	-5102	9.14E-08
rs651386	*GORAB(dist=108789);PRRX1(dist=1550)*	1	170631763	rs629234	Left ventricle	RP1-79C4.4	C	0.38	-4759	4.19E-07
rs651386	*PRRX1*	1	170635002	rs525489	Left ventricle	RP1-79C4.4	G	0.34	-1520	4.44E-06
rs651386	*PRRX1*	1	170635084	rs503706	Left ventricle	RP1-79C4.4	C	0.34	-1438	4.44E-06
rs651386	*PRRX1*	1	170636079	rs473133	Left ventricle	RP1-79C4.4	T	0.34	-443	4.42E-06
rs651386	*PRRX1*	1	170638333	rs520525	Left ventricle	RP1-79C4.4	G	0.44	1811	4.05E-07
rs651386	*PRRX1*	1	170638658	rs10919449	Left ventricle	RP1-79C4.4	A	0.34	2136	1.10E-06
rs651386	*GORAB(dist=94405);PRRX1(dist=15934)*	1	170617379	rs619699	Skeletal muscle	PRRX1	A	0.22	-14490	4.96E-06
rs651386	*GORAB(dist=96350);PRRX1(dist=13989)*	1	170619324	rs1234282	Skeletal muscle	PRRX1	T	0.21	-12545	1.04E-05
rs651386	*GORAB(dist=96956);PRRX1(dist=13383)*	1	170619930	rs651822	Skeletal muscle	PRRX1	T	0.22	-11939	1.68E-06
rs651386	*GORAB(dist=99994);PRRX1(dist=10345)*	1	170622968	rs1234284	Skeletal muscle	PRRX1	T	0.21	-8901	6.56E-06
rs651386	*GORAB(dist=102893);PRRX1(dist=7446)*	1	170625867	rs501680	Skeletal muscle	PRRX1	C	0.20	-6002	1.30E-05
rs651386	*GORAB(dist=103979);PRRX1(dist=6360)*	1	170626953	rs663887	Skeletal muscle	PRRX1	A	0.20	-4916	1.30E-05
rs651386	*GORAB(dist=105461);PRRX1(dist=4878)*	1	170628435	rs524877	Skeletal muscle	PRRX1	C	0.20	-3434	1.30E-05
rs651386	*GORAB(dist=106864);PRRX1(dist=3475)*	1	170629838	rs600093	Skeletal muscle	PRRX1	A	0.21	-2031	7.09E-06
rs651386	*GORAB(dist=107285);PRRX1(dist=3054)*	1	170630259	rs601938	Skeletal muscle	PRRX1	T	0.20	-1610	1.38E-05
rs651386	*PRRX1*	1	170638333	rs520525	Skeletal muscle	PRRX1	G	0.21	6464	1.10E-05
rs651386	*GORAB(dist=37630);PRRX1(dist=72709)*	1	170560604	rs6658866	Skeletal muscle	RP1-79C4.4	G	-0.38	-75918	1.25E-09
rs651386	*GORAB(dist=38430);PRRX1(dist=71909)*	1	170561404	rs6659754	Skeletal muscle	RP1-79C4.4	T	-0.39	-75118	1.72E-10
rs651386	*GORAB(dist=40109);PRRX1(dist=70230)*	1	170563083	rs577827	Skeletal muscle	RP1-79C4.4	C	0.40	-73439	1.08E-10
rs651386	*GORAB(dist=40231);PRRX1(dist=70108)*	1	170563205	rs12027180	Skeletal muscle	RP1-79C4.4	T	0.39	-73317	1.69E-08
rs651386	*GORAB(dist=43031);PRRX1(dist=67308)*	1	170566005	rs763567	Skeletal muscle	RP1-79C4.4	G	-0.39	-70517	2.66E-10
rs651386	*GORAB(dist=44463);PRRX1(dist=65876)*	1	170567437	rs1928715	Skeletal muscle	RP1-79C4.4	T	-0.39	-69085	2.78E-10
rs651386	*GORAB(dist=45740);PRRX1(dist=64599)*	1	170568714	rs12755237	Skeletal muscle	RP1-79C4.4	A	-0.40	-67808	2.59E-10
rs651386	*GORAB(dist=45922);PRRX1(dist=64417)*	1	170568896	rs12742164	Skeletal muscle	RP1-79C4.4	G	-0.40	-67626	2.32E-10
rs651386	*GORAB(dist=46343);PRRX1(dist=63996)*	1	170569317	rs3903239	Skeletal muscle	RP1-79C4.4	G	-0.39	-67205	2.53E-10
rs651386	*GORAB(dist=46715);PRRX1(dist=63624)*	1	170569689	rs12760630	Skeletal muscle	RP1-79C4.4	A	-0.39	-66833	2.53E-10
rs651386	*GORAB(dist=47069);PRRX1(dist=63270)*	1	170570043	rs10800529	Skeletal muscle	RP1-79C4.4	C	0.38	-66479	5.17E-08
rs651386	*GORAB(dist=47525);PRRX1(dist=62814)*	1	170570499	rs7412231	Skeletal muscle	RP1-79C4.4	C	-0.39	-66023	2.55E-10
rs651386	*GORAB(dist=48869);PRRX1(dist=61470)*	1	170571843	rs1234230	Skeletal muscle	RP1-79C4.4	G	-0.37	-64679	4.16E-09
rs651386	*GORAB(dist=49972);PRRX1(dist=60367)*	1	170572946	rs10919437	Skeletal muscle	RP1-79C4.4	A	-0.39	-63576	2.60E-10
rs651386	*GORAB(dist=50284);PRRX1(dist=60055)*	1	170573258	rs61217505	Skeletal muscle	RP1-79C4.4	T	-0.40	-63264	9.87E-11
rs651386	*GORAB(dist=50840);PRRX1(dist=59499)*	1	170573814	rs476810	Skeletal muscle	RP1-79C4.4	C	-0.38	-62708	5.99E-10
rs651386	*GORAB(dist=51954);PRRX1(dist=58385)*	1	170574928	rs1234233	Skeletal muscle	RP1-79C4.4	T	-0.38	-61594	6.10E-10
rs651386	*GORAB(dist=53133);PRRX1(dist=57206)*	1	170576107	rs2206062	Skeletal muscle	RP1-79C4.4	C	-0.39	-60415	2.69E-10
rs651386	*GORAB(dist=53764);PRRX1(dist=56575)*	1	170576738	rs566850	Skeletal muscle	RP1-79C4.4	G	-0.38	-59784	6.29E-10

Supplementary Table 18. *continued*

rs651386	*GORAB(dist=54081);PRRX1(dist=56258)*	1	170577055	rs722597	Skeletal muscle	RP1-79C4.4	A	0.38	-59467	5.21E-08
rs651386	*GORAB(dist=54261);PRRX1(dist=56078)*	1	170577235	rs647438	Skeletal muscle	RP1-79C4.4	T	-0.37	-59287	3.49E-09
rs651386	*GORAB(dist=54866);PRRX1(dist=55473)*	1	170577840	rs72482606	Skeletal muscle	RP1-79C4.4	A	0.38	-58682	5.21E-08
rs651386	*GORAB(dist=55332);PRRX1(dist=55007)*	1	170578306	rs10919440	Skeletal muscle	RP1-79C4.4	G	-0.39	-58216	2.39E-10
rs651386	*GORAB(dist=55613);PRRX1(dist=54726)*	1	170578587	rs494339	Skeletal muscle	RP1-79C4.4	A	-0.37	-57935	2.85E-09
rs651386	*GORAB(dist=56115);PRRX1(dist=54224)*	1	170579089	rs10919441	Skeletal muscle	RP1-79C4.4	A	0.40	-57433	4.65E-09
rs651386	*GORAB(dist=56620);PRRX1(dist=53719)*	1	170579594	rs546258	Skeletal muscle	RP1-79C4.4	T	-0.38	-56928	6.66E-10
rs651386	*GORAB(dist=57503);PRRX1(dist=52836)*	1	170580477	rs553905	Skeletal muscle	RP1-79C4.4	G	-0.37	-56045	1.56E-09
rs651386	*GORAB(dist=58560);PRRX1(dist=51779)*	1	170581534	rs2982131	Skeletal muscle	RP1-79C4.4	C	-0.38	-54988	9.67E-10
rs651386	*GORAB(dist=58660);PRRX1(dist=51679)*	1	170581634	rs10919444	Skeletal muscle	RP1-79C4.4	A	-0.39	-54888	2.92E-10
rs651386	*GORAB(dist=58713);PRRX1(dist=51626)*	1	170581687	rs34252585	Skeletal muscle	RP1-79C4.4	A	0.40	-54835	4.65E-09
rs651386	*GORAB(dist=59601);PRRX1(dist=50738)*	1	170582575	rs1952675	Skeletal muscle	RP1-79C4.4	G	-0.39	-53947	2.96E-10
rs651386	*GORAB(dist=60537);PRRX1(dist=49802)*	1	170583511	rs6677540	Skeletal muscle	RP1-79C4.4	A	-0.39	-53011	3.02E-10
rs651386	*GORAB(dist=60970);PRRX1(dist=49369)*	1	170583944	rs6690642	Skeletal muscle	RP1-79C4.4	C	-0.39	-52578	3.05E-10
rs651386	*GORAB(dist=62123);PRRX1(dist=48216)*	1	170585097	rs2206063	Skeletal muscle	RP1-79C4.4	C	0.40	-51425	4.53E-09
rs651386	*GORAB(dist=62858);PRRX1(dist=47481)*	1	170585832	rs619456	Skeletal muscle	RP1-79C4.4	C	-0.38	-50690	7.70E-10
rs651386	*GORAB(dist=63341);PRRX1(dist=46998)*	1	170586315	rs736791	Skeletal muscle	RP1-79C4.4	A	-0.39	-50207	3.16E-10
rs651386	*GORAB(dist=64241);PRRX1(dist=46098)*	1	170587215	rs576736	Skeletal muscle	RP1-79C4.4	G	0.38	-49307	2.00E-08
rs651386	*GORAB(dist=64366);PRRX1(dist=45973)*	1	170587340	rs577676	Skeletal muscle	RP1-79C4.4	T	0.34	-49182	1.11E-07
rs651386	*GORAB(dist=65620);PRRX1(dist=44719)*	1	170588594	rs2022373	Skeletal muscle	RP1-79C4.4	C	0.40	-47928	5.12E-09
rs651386	*GORAB(dist=66463);PRRX1(dist=43876)*	1	170589437	rs10489231	Skeletal muscle	RP1-79C4.4	A	0.42	-47085	1.53E-09
rs651386	*GORAB(dist=66936);PRRX1(dist=43403)*	1	170589910	rs2022372	Skeletal muscle	RP1-79C4.4	A	-0.40	-46612	1.45E-10
rs651386	*GORAB(dist=67593);PRRX1(dist=42746)*	1	170590567	rs12031871	Skeletal muscle	RP1-79C4.4	T	0.38	-45955	2.89E-08
rs651386	*GORAB(dist=68336);PRRX1(dist=42003)*	1	170591310	rs651386	Skeletal muscle	RP1-79C4.4	T	0.31	-45212	2.17E-06
rs651386	*GORAB(dist=68834);PRRX1(dist=41505)*	1	170591808	rs10753817	Skeletal muscle	RP1-79C4.4	G	0.39	-44714	2.23E-08
rs651386	*GORAB(dist=71095);PRRX1(dist=39244)*	1	170594069	rs12072276	Skeletal muscle	RP1-79C4.4	G	0.39	-42453	1.17E-08
rs651386	*GORAB(dist=71142);PRRX1(dist=39197)*	1	170594116	rs10919446	Skeletal muscle	RP1-79C4.4	A	0.40	-42406	1.07E-08
rs651386	*GORAB(dist=72144);PRRX1(dist=38195)*	1	170595118	rs12074059	Skeletal muscle	RP1-79C4.4	T	0.42	-41404	7.92E-10
rs651386	*GORAB(dist=73098);PRRX1(dist=37241)*	1	170596072	rs494521	Skeletal muscle	RP1-79C4.4	T	0.38	-40450	1.40E-09
rs651386	*GORAB(dist=73284);PRRX1(dist=37055)*	1	170596258	rs1234275	Skeletal muscle	RP1-79C4.4	G	0.40	-40264	1.27E-10
rs651386	*GORAB(dist=73399);PRRX1(dist=36940)*	1	170596373	rs1234274	Skeletal muscle	RP1-79C4.4	G	0.40	-40149	1.26E-10
rs651386	*GORAB(dist=73571);PRRX1(dist=36768)*	1	170596545	rs11577602	Skeletal muscle	RP1-79C4.4	T	0.39	-39977	1.54E-08
rs651386	*GORAB(dist=73598);PRRX1(dist=36741)*	1	170596572	rs10800530	Skeletal muscle	RP1-79C4.4	A	0.39	-39950	1.54E-08
rs651386	*GORAB(dist=75213);PRRX1(dist=35126)*	1	170598187	rs638704	Skeletal muscle	RP1-79C4.4	T	0.40	-38335	1.25E-10
rs651386	*GORAB(dist=76599);PRRX1(dist=33740)*	1	170599573	rs10919448	Skeletal muscle	RP1-79C4.4	C	0.40	-36949	8.05E-09
rs651386	*GORAB(dist=78034);PRRX1(dist=32305)*	1	170601008	rs189058353	Skeletal muscle	RP1-79C4.4	A	0.37	-35514	1.83E-09
rs651386	*GORAB(dist=78339);PRRX1(dist=32000)*	1	170601313	rs12068805	Skeletal muscle	RP1-79C4.4	C	0.43	-35209	7.23E-10
rs651386	*GORAB(dist=78961);PRRX1(dist=31378)*	1	170601935	rs12566725	Skeletal muscle	RP1-79C4.4	T	0.43	-34587	7.23E-10
rs651386	*GORAB(dist=81148);PRRX1(dist=29191)*	1	170604122	rs598993	Skeletal muscle	RP1-79C4.4	C	0.35	-32400	2.34E-08
rs651386	*GORAB(dist=81964);PRRX1(dist=28375)*	1	170604938	rs541557	Skeletal muscle	RP1-79C4.4	G	0.35	-31584	2.34E-08
rs651386	*GORAB(dist=83112);PRRX1(dist=27227)*	1	170606086	rs644784	Skeletal muscle	RP1-79C4.4	T	0.43	-30436	7.26E-10
rs651386	*GORAB(dist=83380);PRRX1(dist=26959)*	1	170606354	rs656539	Skeletal muscle	RP1-79C4.4	T	0.43	-30168	7.26E-10
rs651386	*GORAB(dist=85107);PRRX1(dist=25232)*	1	170608081	rs539045	Skeletal muscle	RP1-79C4.4	T	0.35	-28441	2.34E-08
rs651386	*GORAB(dist=85694);PRRX1(dist=24645)*	1	170608668	rs533603	Skeletal muscle	RP1-79C4.4	G	0.43	-27854	7.36E-10
rs651386	*GORAB(dist=86216);PRRX1(dist=24123)*	1	170609190	rs473832	Skeletal muscle	RP1-79C4.4	C	0.40	-27332	1.29E-10
rs651386	*GORAB(dist=86651);PRRX1(dist=23688)*	1	170609625	rs580487	Skeletal muscle	RP1-79C4.4	C	0.36	-26897	1.46E-08
rs651386	*GORAB(dist=86769);PRRX1(dist=23570)*	1	170609743	rs578928	Skeletal muscle	RP1-79C4.4	C	0.43	-26779	7.45E-10
rs651386	*GORAB(dist=87736);PRRX1(dist=22603)*	1	170610710	rs549449	Skeletal muscle	RP1-79C4.4	C	0.43	-25812	8.88E-10
rs651386	*GORAB(dist=89288);PRRX1(dist=21051)*	1	170612262	rs492804	Skeletal muscle	RP1-79C4.4	T	0.40	-24260	5.98E-11
rs651386	*GORAB(dist=89899);PRRX1(dist=20440)*	1	170612873	rs639652	Skeletal muscle	RP1-79C4.4	A	0.35	-23649	1.34E-08
rs651386	*GORAB(dist=89952);PRRX1(dist=20387)*	1	170612926	rs639720	Skeletal muscle	RP1-79C4.4	C	0.43	-23596	9.12E-10
rs651386	*GORAB(dist=90876);PRRX1(dist=19463)*	1	170613850	rs654461	Skeletal muscle	RP1-79C4.4	T	0.40	-22672	7.33E-11
rs651386	*GORAB(dist=90895);PRRX1(dist=19444)*	1	170613869	rs567328	Skeletal muscle	RP1-79C4.4	A	0.40	-22653	1.03E-10
rs651386	*GORAB(dist=91068);PRRX1(dist=19271)*	1	170614042	rs544478	Skeletal muscle	RP1-79C4.4	T	0.40	-22480	8.78E-11
rs651386	*GORAB(dist=91270);PRRX1(dist=19069)*	1	170614244	rs666419	Skeletal muscle	RP1-79C4.4	C	0.43	-22278	9.19E-10
rs651386	*GORAB(dist=92886);PRRX1(dist=17453)*	1	170615860	rs593173	Skeletal muscle	RP1-79C4.4	A	0.43	-20662	9.19E-10
rs651386	*GORAB(dist=92943);PRRX1(dist=17396)*	1	170615917	rs593560	Skeletal muscle	RP1-79C4.4	A	0.40	-20605	5.97E-11
rs651386	*GORAB(dist=93381);PRRX1(dist=16958)*	1	170616355	rs2988392	Skeletal muscle	RP1-79C4.4	C	0.35	-20167	1.75E-08
rs651386	*GORAB(dist=94332);PRRX1(dist=16007)*	1	170617306	rs608930	Skeletal muscle	RP1-79C4.4	T	0.40	-19216	1.21E-10
rs651386	*GORAB(dist=94405);PRRX1(dist=15934)*	1	170617379	rs619699	Skeletal muscle	RP1-79C4.4	A	0.43	-19143	6.66E-10
rs651386	*GORAB(dist=95317);PRRX1(dist=15022)*	1	170618291	rs623752	Skeletal muscle	RP1-79C4.4	G	0.40	-18231	7.73E-11
rs651386	*GORAB(dist=95408);PRRX1(dist=14931)*	1	170618382	rs531007	Skeletal muscle	RP1-79C4.4	G	0.40	-18140	7.41E-11
rs651386	*GORAB(dist=95487);PRRX1(dist=14852)*	1	170618461	rs12038255	Skeletal muscle	RP1-79C4.4	A	0.36	-18061	1.93E-06
rs651386	*GORAB(dist=96350);PRRX1(dist=13989)*	1	170619324	rs1234282	Skeletal muscle	RP1-79C4.4	T	0.44	-17198	1.71E-10
rs651386	*GORAB(dist=96633);PRRX1(dist=13706)*	1	170619607	rs575432	Skeletal muscle	RP1-79C4.4	G	0.36	-16915	1.13E-08
rs651386	*GORAB(dist=96956);PRRX1(dist=13383)*	1	170619930	rs651822	Skeletal muscle	RP1-79C4.4	T	0.51	-16592	1.53E-14
rs651386	*GORAB(dist=99994);PRRX1(dist=10345)*	1	170622968	rs1234284	Skeletal muscle	RP1-79C4.4	T	0.47	-13554	5.44E-12
rs651386	*GORAB(dist=100135);PRRX1(dist=10204)*	1	170623109	rs588837	Skeletal muscle	RP1-79C4.4	G	0.41	-13413	2.28E-11
rs651386	*GORAB(dist=100946);PRRX1(dist=9393)*	1	170623920	rs12089974	Skeletal muscle	RP1-79C4.4	A	0.48	-12602	1.68E-11
rs651386	*GORAB(dist=102893);PRRX1(dist=7446)*	1	170625867	rs501680	Skeletal muscle	RP1-79C4.4	C	0.46	-10655	2.29E-11
rs651386	*GORAB(dist=103979);PRRX1(dist=6360)*	1	170626953	rs663887	Skeletal muscle	RP1-79C4.4	A	0.46	-9569	2.29E-11
rs651386	*GORAB(dist=104820);PRRX1(dist=5519)*	1	170627794	rs552277	Skeletal muscle	RP1-79C4.4	C	0.46	-8728	2.56E-11
rs651386	*GORAB(dist=105281);PRRX1(dist=5058)*	1	170628255	rs680084	Skeletal muscle	RP1-79C4.4	A	0.31	-8267	7.62E-07
rs651386	*GORAB(dist=105414);PRRX1(dist=4925)*	1	170628388	rs583006	Skeletal muscle	RP1-79C4.4	G	0.43	-8134	5.14E-10
rs651386	*GORAB(dist=105461);PRRX1(dist=4878)*	1	170628435	rs524877	Skeletal muscle	RP1-79C4.4	C	0.46	-8087	2.29E-11
rs651386	*GORAB(dist=106864);PRRX1(dist=3475)*	1	170629838	rs600093	Skeletal muscle	RP1-79C4.4	A	0.45	-6684	7.36E-11
rs651386	*GORAB(dist=107285);PRRX1(dist=3054)*	1	170630259	rs601938	Skeletal muscle	RP1-79C4.4	T	0.46	-6263	2.26E-11
rs651386	*GORAB(dist=108446);PRRX1(dist=1893)*	1	170631420	rs627848	Skeletal muscle	RP1-79C4.4	A	0.46	-5102	2.24E-11
rs651386	*GORAB(dist=108789);PRRX1(dist=1550)*	1	170631763	rs629234	Skeletal muscle	RP1-79C4.4	C	0.32	-4759	3.28E-07
rs651386	*PRRX1*	1	170635002	rs525489	Skeletal muscle	RP1-79C4.4	G	0.37	-1520	3.05E-09
rs651386	*PRRX1*	1	170635084	rs503706	Skeletal muscle	RP1-79C4.4	C	0.37	-1438	3.06E-09
rs651386	*PRRX1*	1	170635369	rs501005	Skeletal muscle	RP1-79C4.4	G	0.30	-1153	3.51E-06
rs651386	*PRRX1*	1	170636079	rs473133	Skeletal muscle	RP1-79C4.4	T	0.37	-443	3.00E-09
rs651386	*PRRX1*	1	170638333	rs520525	Skeletal muscle	RP1-79C4.4	G	0.44	1811	4.25E-10
rs651386	*PRRX1*	1	170638658	rs10919449	Skeletal muscle	RP1-79C4.4	A	0.40	2136	2.64E-11
rs11264280	*ZBTB7B*	1	154990297	rs2242194	Skeletal muscle	ZBTB7B	G	0.13	15170	6.46E-06
rs2723064	*SLC1A4(dist=25049);CEP68(dist=7446)*	2	65276049	rs1009360	Atrial appendage	CEP68	C	-0.53	-7451	2.27E-11

Supplementary Table 18. *continued*

rs2723064	*SLC1A4(dist=25452);CEP68(dist=7043)*	2	65276452	rs1009358	Atrial appendage	CEP68	C	-0.52	-7048	1.14E-10
rs2723064	*SLC1A4(dist=25736);CEP68(dist=6759)*	2	65276736	rs2540951	Atrial appendage	CEP68	G	-0.52	-6764	1.14E-10
rs2723064	*SLC1A4(dist=28223);CEP68(dist=4272)*	2	65279223	rs2540950	Atrial appendage	CEP68	T	-0.55	-4277	7.74E-11
rs2723064	*SLC1A4(dist=28321);CEP68(dist=4174)*	2	65279321	rs2723066	Atrial appendage	CEP68	G	-0.55	-4179	7.74E-11
rs2723064	*SLC1A4(dist=28414);CEP68(dist=4081)*	2	65279414	rs2723065	Atrial appendage	CEP68	G	-0.54	-4086	4.52E-11
rs2723064	*SLC1A4(dist=28805);CEP68(dist=3690)*	2	65279805	rs2723064	Atrial appendage	CEP68	C	-0.54	-3695	4.31E-11
rs2723064	*SLC1A4(dist=29185);CEP68(dist=3310)*	2	65280185	rs2723063	Atrial appendage	CEP68	G	-0.51	-3315	2.85E-10
rs2723064	*SLC1A4(dist=29220);CEP68(dist=3275)*	2	65280220	rs2723062	Atrial appendage	CEP68	A	-0.55	-3280	7.74E-11
rs2723064	*CEP68*	2	65283972	rs74181299	Atrial appendage	CEP68	C	-0.57	472	2.93E-12
rs2723064	*CEP68*	2	65284231	rs2540949	Atrial appendage	CEP68	T	-0.55	731	3.35E-11
rs2723064	*CEP68*	2	65284623	rs2540948	Atrial appendage	CEP68	C	-0.55	1123	5.62E-11
rs2723064	*CEP68*	2	65287896	rs2249105	Atrial appendage	CEP68	G	-0.57	4396	6.13E-13
rs2723064	*CEP68*	2	65289825	rs2540945	Atrial appendage	CEP68	G	-0.57	6325	1.33E-12
rs2723064	*CEP68*	2	65296280	rs2252867	Atrial appendage	CEP68	C	-0.57	12780	6.13E-13
rs62133983	*AAK1(dist=86235);ANXA4(dist=11915)*	2	69957212	rs1472950	Left ventricle	ANXA4	C	-0.21	85655	5.69E-06
rs62133983	*AAK1(dist=87967);ANXA4(dist=10183)*	2	69958944	rs2312549	Left ventricle	ANXA4	C	-0.21	87387	5.45E-06
rs62133983	*AAK1(dist=88028);ANXA4(dist=10122)*	2	69959005	rs2312550	Left ventricle	ANXA4	C	-0.22	87448	1.61E-06
rs62133983	*AAK1(dist=91816);ANXA4(dist=6334)*	2	69962793	rs10203645	Left ventricle	ANXA4	A	-0.21	91236	5.26E-06
rs62133983	*AAK1(dist=92069);ANXA4(dist=6081)*	2	69963046	rs2872073	Left ventricle	ANXA4	G	-0.21	91489	5.26E-06
rs62133983	*AAK1(dist=92678);ANXA4(dist=5472)*	2	69963655	rs4852981	Left ventricle	ANXA4	C	-0.21	92098	4.90E-06
rs62133983	*ANXA4*	2	69969918	rs7424572	Left ventricle	ANXA4	A	-0.22	98361	2.52E-06
rs62133983	*ANXA4*	2	69971317	rs4852984	Left ventricle	ANXA4	A	-0.22	99760	3.13E-06
rs62133983	*ANXA4*	2	69971429	rs4852319	Left ventricle	ANXA4	A	-0.22	99872	2.38E-06
rs62133983	*ANXA4*	2	69972704	rs13028222	Left ventricle	ANXA4	C	-0.22	101147	2.31E-06
rs62133983	*ANXA4*	2	69973737	rs6705820	Left ventricle	ANXA4	A	-0.22	102180	2.07E-06
rs62133983	*ANXA4*	2	69974873	rs11126244	Left ventricle	ANXA4	A	-0.22	103316	1.55E-06
rs62133983	*ANXA4*	2	69975000	rs11126245	Left ventricle	ANXA4	T	-0.22	103443	1.55E-06
rs62133983	*ANXA4*	2	69978290	rs4852988	Left ventricle	ANXA4	G	-0.20	106733	1.19E-05
rs62133983	*ANXA4*	2	69980427	rs7589995	Left ventricle	ANXA4	G	-0.20	108870	9.02E-06
rs2723064	*SLC1A4(dist=25049);CEP68(dist=7446)*	2	65276049	rs1009360	Left ventricle	CEP68	C	-0.32	-7451	6.82E-07
rs2723064	*SLC1A4(dist=25452);CEP68(dist=7043)*	2	65276452	rs1009358	Left ventricle	CEP68	C	-0.35	-7048	2.80E-07
rs2723064	*SLC1A4(dist=25736);CEP68(dist=6759)*	2	65276736	rs2540951	Left ventricle	CEP68	G	-0.35	-6764	2.80E-07
rs2723064	*SLC1A4(dist=28223);CEP68(dist=4272)*	2	65279223	rs2540950	Left ventricle	CEP68	T	-0.33	-4277	2.66E-06
rs2723064	*SLC1A4(dist=28321);CEP68(dist=4174)*	2	65279321	rs2723066	Left ventricle	CEP68	G	-0.33	-4179	2.66E-06
rs2723064	*SLC1A4(dist=28414);CEP68(dist=4081)*	2	65279414	rs2723065	Left ventricle	CEP68	G	-0.36	-4086	1.69E-07
rs2723064	*SLC1A4(dist=28805);CEP68(dist=3690)*	2	65279805	rs2723064	Left ventricle	CEP68	C	-0.36	-3695	1.65E-07
rs2723064	*SLC1A4(dist=29185);CEP68(dist=3310)*	2	65280185	rs2723063	Left ventricle	CEP68	G	-0.32	-3315	4.86E-07
rs2723064	*SLC1A4(dist=29220);CEP68(dist=3275)*	2	65280220	rs2723062	Left ventricle	CEP68	A	-0.33	-3280	2.66E-06
rs2723064	*CEP68*	2	65283972	rs74181299	Left ventricle	CEP68	C	-0.36	472	9.45E-08
rs2723064	*CEP68*	2	65284231	rs2540949	Left ventricle	CEP68	T	-0.35	731	1.76E-07
rs2723064	*CEP68*	2	65284623	rs2540948	Left ventricle	CEP68	C	-0.33	1123	2.77E-06
rs2723064	*CEP68*	2	65287896	rs2249105	Left ventricle	CEP68	G	-0.33	4396	3.14E-07
rs2723064	*CEP68*	2	65289825	rs2540945	Left ventricle	CEP68	G	-0.32	6325	1.29E-06
rs2723064	*CEP68*	2	65296280	rs2252867	Left ventricle	CEP68	C	-0.33	12780	3.14E-07
rs62133983	*ANXA4*	2	70025737	rs7561890	Left ventricle	GMCL1	T	-0.42	-31037	3.08E-06
rs62133983	*ANXA4*	2	70033584	rs2228203	Left ventricle	GMCL1	T	-0.39	-23190	1.10E-05
rs62133983	*ANXA4*	2	70035482	rs17037082	Left ventricle	GMCL1	G	-0.42	-21292	3.08E-06
rs62133983	*ANXA4*	2	70047644	rs2290452	Left ventricle	GMCL1	A	-0.40	-9130	6.17E-06
rs62133983	*ANXA4*	2	70049222	rs58819073	Left ventricle	GMCL1	A	-0.40	-7552	6.21E-06
rs62133983	*ANXA4*	2	70053816	rs11900749	Left ventricle	GMCL1	C	-0.40	-2958	7.71E-06
rs62133983	*ANXA4(dist=1575);GMCL1(dist=1647)*	2	70055171	rs33992437	Left ventricle	GMCL1	C	-0.40	-1603	9.36E-06
rs62133983	*ANXA4(dist=1909);GMCL1(dist=1313)*	2	70055505	rs1531025	Left ventricle	GMCL1	A	-0.28	-1269	1.05E-05
rs62133983	*GMCL1*	2	70056116	rs2278932	Left ventricle	GMCL1	G	-0.39	-658	6.66E-06
rs62133983	*GMCL1*	2	70056365	rs2278933	Left ventricle	GMCL1	C	-0.40	-409	7.31E-06
rs62133983	*GMCL1*	2	70059607	rs72839877	Left ventricle	GMCL1	C	-0.39	2833	1.12E-05
rs62133983	*GMCL1*	2	70063315	rs60483174	Left ventricle	GMCL1	T	-0.41	6541	5.80E-06
rs62133983	*GMCL1*	2	70064435	rs3771534	Left ventricle	GMCL1	T	-0.41	7661	5.80E-06
rs62133983	*GMCL1*	2	70065997	rs12619656	Left ventricle	GMCL1	A	-0.44	9223	1.06E-06
rs62133983	*GMCL1*	2	70066102	rs12613917	Left ventricle	GMCL1	G	-0.41	9328	5.80E-06
rs62133983	*GMCL1*	2	70066891	rs11888098	Left ventricle	GMCL1	C	-0.41	10117	5.80E-06
rs62133983	*GMCL1*	2	70066922	rs11888102	Left ventricle	GMCL1	G	-0.41	10148	5.80E-06
rs62133983	*GMCL1*	2	70068057	rs3771533	Left ventricle	GMCL1	A	-0.41	11283	5.80E-06
rs62133983	*GMCL1*	2	70068755	rs2872076	Left ventricle	GMCL1	A	-0.41	11981	5.71E-06
rs62133983	*GMCL1*	2	70076650	rs6546552	Left ventricle	GMCL1	C	-0.41	19876	5.72E-06
rs62133983	*GMCL1*	2	70077422	rs7577662	Left ventricle	GMCL1	G	-0.41	20648	5.72E-06
rs62133983	*GMCL1*	2	70077433	rs7565230	Left ventricle	GMCL1	C	-0.41	20659	5.72E-06
rs62133983	*GMCL1*	2	70084977	rs921711	Left ventricle	GMCL1	G	-0.37	28203	6.53E-06
rs62133983	*GMCL1*	2	70085961	rs7596535	Left ventricle	GMCL1	A	-0.37	29187	6.51E-06
rs62133983	*GMCL1*	2	70086363	rs36081078	Left ventricle	GMCL1	G	-0.41	29589	2.55E-06
rs62133983	*GMCL1*	2	70086728	rs72839885	Left ventricle	GMCL1	T	-0.41	29954	2.70E-06
rs62133983	*GMCL1*	2	70088016	rs13412830	Left ventricle	GMCL1	C	-0.37	31242	7.51E-06
rs62133983	*GMCL1*	2	70089130	rs56222989	Left ventricle	GMCL1	G	-0.41	32356	2.70E-06
rs62133983	*GMCL1*	2	70097735	rs7568485	Left ventricle	GMCL1	C	-0.37	40961	6.51E-06
rs62133983	*GMCL1*	2	70099424	rs1013083	Left ventricle	GMCL1	G	-0.38	42650	9.27E-06
rs62133983	*GMCL1*	2	70101889	rs61138247	Left ventricle	GMCL1	C	-0.37	45115	7.49E-06
rs62133983	*MXD1(dist=2511);ASPRV1(dist=14637)*	2	70172587	rs6756513	Left ventricle	GMCL1	A	-0.33	115813	2.67E-06
rs62133983	*MXD1(dist=3954);ASPRV1(dist=13194)*	2	70174030	rs7569566	Left ventricle	GMCL1	C	-0.30	117256	4.34E-06
rs62133983	*MXD1(dist=3978);ASPRV1(dist=13170)*	2	70174054	rs7581977	Left ventricle	GMCL1	G	-0.28	117280	1.01E-05
rs62133983	*SNRNP27*	2	70120078	rs55866046	Left ventricle	PCYOX1	C	0.23	-364440	1.27E-05
rs2723064	*SLC1A4(dist=25049);CEP68(dist=7446)*	2	65276049	rs1009360	Skeletal muscle	CEP68	C	-0.21	-7451	9.51E-09
rs2723064	*SLC1A4(dist=25452);CEP68(dist=7043)*	2	65276452	rs1009358	Skeletal muscle	CEP68	C	-0.27	-7048	7.47E-13
rs2723064	*SLC1A4(dist=25736);CEP68(dist=6759)*	2	65276736	rs2540951	Skeletal muscle	CEP68	G	-0.27	-6764	7.47E-13
rs2723064	*SLC1A4(dist=28223);CEP68(dist=4272)*	2	65279223	rs2540950	Skeletal muscle	CEP68	T	-0.26	-4277	3.11E-11
rs2723064	*SLC1A4(dist=28321);CEP68(dist=4174)*	2	65279321	rs2723066	Skeletal muscle	CEP68	G	-0.26	-4179	3.11E-11
rs2723064	*SLC1A4(dist=28414);CEP68(dist=4081)*	2	65279414	rs2723065	Skeletal muscle	CEP68	G	-0.27	-4086	7.43E-13
rs2723064	*SLC1A4(dist=28805);CEP68(dist=3690)*	2	65279805	rs2723064	Skeletal muscle	CEP68	C	-0.27	-3695	7.43E-13
rs2723064	*SLC1A4(dist=29185);CEP68(dist=3310)*	2	65280185	rs2723063	Skeletal muscle	CEP68	G	-0.22	-3315	3.67E-09

Supplementary Table 18. *continued*

rs2723064	*SLC1A4(dist=29220);CEP68(dist=3275)*	2	65280220	rs2723062	Skeletal muscle	CEP68	A	-0.26	-3280	3.11E-11
rs2723064	*CEP68*	2	65283972	rs74181299	Skeletal muscle	CEP68	C	-0.26	472	4.68E-12
rs2723064	*CEP68*	2	65284231	rs2540949	Skeletal muscle	CEP68	T	-0.27	731	5.02E-13
rs2723064	*CEP68*	2	65284623	rs2540948	Skeletal muscle	CEP68	C	-0.25	1123	1.73E-10
rs2723064	*CEP68*	2	65287896	rs2249105	Skeletal muscle	CEP68	G	-0.23	4396	1.95E-10
rs2723064	*CEP68*	2	65289825	rs2540945	Skeletal muscle	CEP68	G	-0.23	6325	4.85E-10
rs2723064	*CEP68*	2	65296280	rs2252867	Skeletal muscle	CEP68	C	-0.23	12780	1.95E-10
rs62133983	*ANXA4*	2	69975819	rs10211658	Skeletal muscle	GMCL1	A	-0.20	-80955	3.77E-06
rs62133983	*ANXA4*	2	70015108	rs11683908	Skeletal muscle	GMCL1	G	-0.42	-41666	5.98E-09
rs62133983	*ANXA4*	2	70015781	rs57792077	Skeletal muscle	GMCL1	G	-0.35	-40993	1.12E-10
rs62133983	*ANXA4*	2	70015831	rs11695691	Skeletal muscle	GMCL1	A	-0.35	-40943	3.56E-10
rs62133983	*ANXA4*	2	70025737	rs7561890	Skeletal muscle	GMCL1	T	-0.38	-31037	1.34E-11
rs62133983	*ANXA4*	2	70031797	rs3771541	Skeletal muscle	GMCL1	G	-0.30	-24977	2.24E-11
rs62133983	*ANXA4*	2	70031941	rs3771540	Skeletal muscle	GMCL1	G	-0.30	-24833	2.50E-11
rs62133983	*ANXA4*	2	70033584	rs2228203	Skeletal muscle	GMCL1	T	-0.40	-23190	5.27E-12
rs62133983	*ANXA4*	2	70033649	rs17037076	Skeletal muscle	GMCL1	A	-0.37	-23125	4.99E-11
rs62133983	*ANXA4*	2	70033795	rs3771538	Skeletal muscle	GMCL1	T	-0.37	-22979	4.94E-11
rs62133983	*ANXA4*	2	70034465	rs2124009	Skeletal muscle	GMCL1	C	-0.37	-22309	4.89E-11
rs62133983	*ANXA4*	2	70034793	rs2168115	Skeletal muscle	GMCL1	G	-0.30	-21981	2.62E-11
rs62133983	*ANXA4*	2	70035482	rs17037082	Skeletal muscle	GMCL1	G	-0.40	-21292	3.02E-12
rs62133983	*ANXA4*	2	70036711	rs13392884	Skeletal muscle	GMCL1	G	-0.29	-20063	1.34E-10
rs62133983	*ANXA4*	2	70038232	rs6546550	Skeletal muscle	GMCL1	G	-0.30	-18542	2.33E-11
rs62133983	*ANXA4*	2	70038792	rs3771537	Skeletal muscle	GMCL1	C	-0.27	-17982	2.40E-10
rs62133983	*ANXA4*	2	70039224	rs4853027	Skeletal muscle	GMCL1	T	-0.30	-17550	2.37E-11
rs62133983	*ANXA4*	2	70039677	rs2305523	Skeletal muscle	GMCL1	C	-0.30	-17097	2.26E-11
rs62133983	*ANXA4*	2	70040542	rs2312555	Skeletal muscle	GMCL1	A	-0.27	-16232	2.61E-10
rs62133983	*ANXA4*	2	70041004	rs11673732	Skeletal muscle	GMCL1	T	-0.39	-15770	5.65E-12
rs62133983	*ANXA4*	2	70041033	rs11673826	Skeletal muscle	GMCL1	A	-0.27	-15741	1.76E-10
rs62133983	*ANXA4*	2	70041181	rs72839869	Skeletal muscle	GMCL1	T	-0.39	-15593	5.85E-12
rs62133983	*ANXA4*	2	70041440	rs4853028	Skeletal muscle	GMCL1	A	-0.38	-15334	1.08E-11
rs62133983	*ANXA4*	2	70042332	rs60168146	Skeletal muscle	GMCL1	G	-0.39	-14442	5.81E-12
rs62133983	*ANXA4*	2	70042915	rs72839870	Skeletal muscle	GMCL1	A	-0.39	-13859	5.79E-12
rs62133983	*ANXA4*	2	70043598	rs3771536	Skeletal muscle	GMCL1	A	-0.39	-13176	5.77E-12
rs62133983	*ANXA4*	2	70043775	rs3771535	Skeletal muscle	GMCL1	T	-0.40	-12999	4.70E-12
rs62133983	*ANXA4*	2	70045063	rs6744970	Skeletal muscle	GMCL1	A	-0.40	-11711	2.48E-12
rs62133983	*ANXA4*	2	70046964	rs72839874	Skeletal muscle	GMCL1	A	-0.40	-9810	1.69E-12
rs62133983	*ANXA4*	2	70047644	rs2290452	Skeletal muscle	GMCL1	A	-0.40	-9130	1.80E-12
rs62133983	*ANXA4*	2	70049222	rs58819073	Skeletal muscle	GMCL1	A	-0.40	-7552	1.78E-12
rs62133983	*ANXA4*	2	70050725	rs7563062	Skeletal muscle	GMCL1	A	-0.30	-6049	9.23E-12
rs62133983	*ANXA4*	2	70053668	rs7600468	Skeletal muscle	GMCL1	G	-0.29	-3106	4.98E-10
rs62133983	*ANXA4*	2	70053816	rs11900749	Skeletal muscle	GMCL1	C	-0.40	-2958	5.13E-12
rs62133983	*ANXA4(dist=1575);GMCL1(dist=1647)*	2	70055171	rs33992437	Skeletal muscle	GMCL1	C	-0.40	-1603	4.20E-12
rs62133983	*ANXA4(dist=1909);GMCL1(dist=1313)*	2	70055505	rs1531025	Skeletal muscle	GMCL1	A	-0.30	-1269	1.20E-11
rs62133983	*GMCL1*	2	70056116	rs2278932	Skeletal muscle	GMCL1	G	-0.40	-658	1.86E-12
rs62133983	*GMCL1*	2	70056365	rs2278933	Skeletal muscle	GMCL1	C	-0.39	-409	7.03E-12
rs62133983	*GMCL1*	2	70057448	rs3732266	Skeletal muscle	GMCL1	G	-0.30	674	6.46E-12
rs62133983	*GMCL1*	2	70059607	rs72839877	Skeletal muscle	GMCL1	C	-0.40	2833	4.56E-12
rs62133983	*GMCL1*	2	70062276	rs72839879	Skeletal muscle	GMCL1	T	-0.40	5502	4.75E-12
rs62133983	*GMCL1*	2	70062360	rs10167142	Skeletal muscle	GMCL1	C	-0.31	5586	5.31E-12
rs62133983	*GMCL1*	2	70062454	rs10202159	Skeletal muscle	GMCL1	T	-0.31	5680	5.32E-12
rs62133983	*GMCL1*	2	70063315	rs60483174	Skeletal muscle	GMCL1	T	-0.41	6541	2.31E-12
rs62133983	*GMCL1*	2	70063527	rs4420721	Skeletal muscle	GMCL1	T	-0.37	6753	3.46E-11
rs62133983	*GMCL1*	2	70063563	rs4401231	Skeletal muscle	GMCL1	C	-0.31	6789	4.38E-12
rs62133983	*GMCL1*	2	70063660	rs4241261	Skeletal muscle	GMCL1	G	-0.31	6886	4.83E-12
rs62133983	*GMCL1*	2	70064155	rs1377995	Skeletal muscle	GMCL1	G	-0.31	7381	4.45E-12
rs62133983	*GMCL1*	2	70064435	rs3771534	Skeletal muscle	GMCL1	T	-0.41	7661	2.07E-12
rs62133983	*GMCL1*	2	70064927	rs1377996	Skeletal muscle	GMCL1	A	-0.39	8153	1.41E-12
rs62133983	*GMCL1*	2	70065997	rs12619656	Skeletal muscle	GMCL1	A	-0.42	9223	1.24E-12
rs62133983	*GMCL1*	2	70066102	rs12613917	Skeletal muscle	GMCL1	G	-0.41	9328	1.77E-12
rs62133983	*GMCL1*	2	70066891	rs11888098	Skeletal muscle	GMCL1	C	-0.41	10117	1.66E-12
rs62133983	*GMCL1*	2	70066922	rs11888102	Skeletal muscle	GMCL1	G	-0.41	10148	1.65E-12
rs62133983	*GMCL1*	2	70068057	rs3771533	Skeletal muscle	GMCL1	A	-0.41	11283	1.51E-12
rs62133983	*GMCL1*	2	70068635	rs2872075	Skeletal muscle	GMCL1	T	-0.31	11861	2.29E-12
rs62133983	*GMCL1*	2	70068755	rs2872076	Skeletal muscle	GMCL1	A	-0.41	11981	1.43E-12
rs62133983	*GMCL1*	2	70071529	rs7575111	Skeletal muscle	GMCL1	G	-0.44	14755	3.33E-12
rs62133983	*GMCL1*	2	70073703	rs6546551	Skeletal muscle	GMCL1	T	-0.31	16929	1.41E-12
rs62133983	*GMCL1*	2	70076650	rs6546552	Skeletal muscle	GMCL1	C	-0.42	19876	1.07E-12
rs62133983	*GMCL1*	2	70076954	rs4852349	Skeletal muscle	GMCL1	T	-0.30	20180	1.02E-11
rs62133983	*GMCL1*	2	70077422	rs7577662	Skeletal muscle	GMCL1	G	-0.42	20648	1.07E-12
rs62133983	*GMCL1*	2	70077433	rs7565230	Skeletal muscle	GMCL1	C	-0.42	20659	1.07E-12
rs62133983	*GMCL1*	2	70079633	rs1551374	Skeletal muscle	GMCL1	T	-0.31	22859	2.58E-12
rs62133983	*GMCL1*	2	70084977	rs921711	Skeletal muscle	GMCL1	G	-0.39	28203	8.05E-13
rs62133983	*GMCL1*	2	70085961	rs7596535	Skeletal muscle	GMCL1	A	-0.39	29187	1.16E-12
rs62133983	*GMCL1*	2	70086363	rs36081078	Skeletal muscle	GMCL1	G	-0.42	29589	5.54E-13
rs62133983	*GMCL1*	2	70086728	rs72839885	Skeletal muscle	GMCL1	T	-0.42	29954	5.53E-13
rs62133983	*GMCL1*	2	70088016	rs13412830	Skeletal muscle	GMCL1	C	-0.38	31242	2.41E-12
rs62133983	*GMCL1*	2	70089130	rs56222989	Skeletal muscle	GMCL1	G	-0.42	32356	5.52E-13
rs62133983	*GMCL1*	2	70090579	rs13017134	Skeletal muscle	GMCL1	G	-0.29	33805	1.20E-11
rs62133983	*GMCL1*	2	70090913	rs56168154	Skeletal muscle	GMCL1	T	-0.42	34139	1.25E-12
rs62133983	*GMCL1*	2	70091246	rs10865380	Skeletal muscle	GMCL1	C	-0.28	34472	2.01E-11
rs62133983	*GMCL1*	2	70091772	rs60390734	Skeletal muscle	GMCL1	C	-0.42	34998	1.25E-12
rs62133983	*GMCL1*	2	70093647	rs57278310	Skeletal muscle	GMCL1	C	-0.28	36873	2.66E-11
rs62133983	*GMCL1*	2	70093898	rs60248458	Skeletal muscle	GMCL1	G	-0.42	37124	1.25E-12
rs62133983	*GMCL1*	2	70093910	rs60207187	Skeletal muscle	GMCL1	A	-0.29	37136	1.20E-11
rs62133983	*GMCL1*	2	70097735	rs7568485	Skeletal muscle	GMCL1	C	-0.39	40961	1.16E-12
rs62133983	*GMCL1*	2	70098808	rs3214007	Skeletal muscle	GMCL1	G	-0.31	42034	2.66E-12
rs62133983	*GMCL1*	2	70099424	rs1013083	Skeletal muscle	GMCL1	G	-0.41	42650	1.48E-12

Supplementary Table 18. *continued*

rs62133983	*GMCL1*	2	70101889	rs61138247	Skeletal muscle	GMCL1	C	-0.38	45115	5.49E-12
rs62133983	*GMCL1*	2	70102735	rs4853109	Skeletal muscle	GMCL1	G	-0.39	45961	3.62E-12
rs62133983	*GMCL1*	2	70103504	rs17037193	Skeletal muscle	GMCL1	C	-0.42	46730	1.25E-12
rs62133983	*GMCL1*	2	70103802	rs17037194	Skeletal muscle	GMCL1	C	-0.42	47028	1.25E-12
rs62133983	*GMCL1*	2	70106832	rs6747542	Skeletal muscle	GMCL1	C	-0.29	50058	1.45E-11
rs62133983	*GMCL1*	2	70107409	rs2124007	Skeletal muscle	GMCL1	G	-0.42	50635	1.32E-12
rs62133983	*GMCL1(dist=1529);SNRNP27(dist=12819)*	2	70108256	rs1056482	Skeletal muscle	GMCL1	A	-0.28	51482	1.89E-11
rs62133983	*GMCL1(dist=4984);SNRNP27(dist=9364)*	2	70111711	rs6546553	Skeletal muscle	GMCL1	A	-0.28	54937	8.67E-11
rs62133983	*GMCL1(dist=9721);SNRNP27(dist=4627)*	2	70116448	rs60515724	Skeletal muscle	GMCL1	T	-0.38	59674	6.35E-11
rs62133983	*GMCL1(dist=10288);SNRNP27(dist=4060)*	2	70117015	rs10165883	Skeletal muscle	GMCL1	T	-0.30	60241	8.13E-12
rs62133983	*GMCL1(dist=10347);SNRNP27(dist=4001)*	2	70117074	rs2054046	Skeletal muscle	GMCL1	C	-0.39	60300	3.03E-11
rs62133983	*GMCL1(dist=10449);SNRNP27(dist=3899)*	2	70117176	rs12232914	Skeletal muscle	GMCL1	T	-0.29	60402	8.49E-11
rs62133983	*GMCL1(dist=10645);SNRNP27(dist=3703)*	2	70117372	rs12233079	Skeletal muscle	GMCL1	G	-0.28	60598	1.18E-10
rs62133983	*GMCL1(dist=10694);SNRNP27(dist=3654)*	2	70117421	rs2054047	Skeletal muscle	GMCL1	C	-0.29	60647	6.38E-11
rs62133983	*GMCL1(dist=11661);SNRNP27(dist=2687)*	2	70118388	rs13002091	Skeletal muscle	GMCL1	T	-0.28	61614	2.92E-10
rs62133983	*GMCL1(dist=11700);SNRNP27(dist=2648)*	2	70118427	rs13028508	Skeletal muscle	GMCL1	A	-0.27	61653	4.93E-10
rs62133983	*GMCL1(dist=12742);SNRNP27(dist=1606)*	2	70119469	rs3755389	Skeletal muscle	GMCL1	C	-0.28	62695	1.25E-10
rs62133983	*SNRNP27*	2	70120078	rs55866046	Skeletal muscle	GMCL1	C	-0.42	63304	3.31E-11
rs62133983	*SNRNP27*	2	70124316	rs3752781	Skeletal muscle	GMCL1	A	-0.27	67542	7.47E-10
rs62133983	*SNRNP27*	2	70124805	rs6720498	Skeletal muscle	GMCL1	C	-0.27	68031	1.76E-09
rs62133983	*SNRNP27*	2	70125763	rs13015457	Skeletal muscle	GMCL1	T	-0.28	68989	2.05E-10
rs62133983	*SNRNP27*	2	70125988	rs4852375	Skeletal muscle	GMCL1	G	-0.29	69214	1.28E-10
rs62133983	*SNRNP27*	2	70126666	rs58206747	Skeletal muscle	GMCL1	G	-0.38	69892	1.07E-10
rs62133983	*SNRNP27*	2	70127229	rs6716937	Skeletal muscle	GMCL1	A	-0.28	70455	2.07E-10
rs62133983	*SNRNP27*	2	70128717	rs7598283	Skeletal muscle	GMCL1	G	-0.27	71943	7.20E-10
rs62133983	*SNRNP27*	2	70131584	rs1048130	Skeletal muscle	GMCL1	A	-0.38	74810	1.82E-10
rs62133983	*SNRNP27*	2	70132676	rs1048266	Skeletal muscle	GMCL1	G	-0.28	75902	2.06E-10
rs62133983	*SNRNP27(dist=1739);MXD1(dist=8066)*	2	70134107	rs10166011	Skeletal muscle	GMCL1	G	-0.28	77333	2.29E-10
rs62133983	*SNRNP27(dist=3338);MXD1(dist=6467)*	2	70135706	rs6546554	Skeletal muscle	GMCL1	A	-0.28	78932	2.06E-10
rs62133983	*SNRNP27(dist=3392);MXD1(dist=6413)*	2	70135760	rs6546555	Skeletal muscle	GMCL1	G	-0.28	78986	2.81E-10
rs62133983	*SNRNP27(dist=4249);MXD1(dist=5556)*	2	70136617	rs11126249	Skeletal muscle	GMCL1	G	-0.37	79843	2.74E-10
rs62133983	*SNRNP27(dist=5130);MXD1(dist=4675)*	2	70137498	rs1979214	Skeletal muscle	GMCL1	C	-0.27	80724	6.84E-10
rs62133983	*SNRNP27(dist=5406);MXD1(dist=4399)*	2	70137774	rs6736408	Skeletal muscle	GMCL1	T	-0.28	81000	2.06E-10
rs62133983	*SNRNP27(dist=5743);MXD1(dist=4062)*	2	70138111	rs6739780	Skeletal muscle	GMCL1	A	-0.28	81337	2.20E-10
rs62133983	*SNRNP27(dist=5802);MXD1(dist=4003)*	2	70138170	rs6754896	Skeletal muscle	GMCL1	C	-0.28	81396	2.06E-10
rs62133983	*SNRNP27(dist=6633);MXD1(dist=3172)*	2	70139001	rs6546556	Skeletal muscle	GMCL1	G	-0.28	82227	2.06E-10
rs62133983	*SNRNP27(dist=6766);MXD1(dist=3039)*	2	70139134	rs7592647	Skeletal muscle	GMCL1	T	-0.27	82360	6.50E-10
rs62133983	*SNRNP27(dist=7903);MXD1(dist=1902)*	2	70140271	rs897122	Skeletal muscle	GMCL1	T	-0.28	83497	2.07E-10
rs62133983	*MXD1*	2	70144596	rs11902198	Skeletal muscle	GMCL1	A	-0.28	87822	2.27E-10
rs62133983	*MXD1*	2	70145717	rs6546558	Skeletal muscle	GMCL1	T	-0.28	88943	1.87E-10
rs62133983	*MXD1*	2	70145833	rs6546559	Skeletal muscle	GMCL1	A	-0.27	89059	6.82E-10
rs62133983	*MXD1*	2	70146121	rs6721891	Skeletal muscle	GMCL1	G	-0.28	89347	2.06E-10
rs62133983	*MXD1*	2	70146125	rs6750488	Skeletal muscle	GMCL1	T	-0.28	89351	2.06E-10
rs62133983	*MXD1*	2	70146625	rs7419837	Skeletal muscle	GMCL1	C	-0.28	89851	2.63E-10
rs62133983	*MXD1*	2	70149225	rs1454498	Skeletal muscle	GMCL1	A	-0.28	92451	1.69E-10
rs62133983	*MXD1*	2	70149873	rs80352135	Skeletal muscle	GMCL1	A	-0.37	93099	3.41E-10
rs62133983	*MXD1*	2	70150215	rs6738174	Skeletal muscle	GMCL1	C	-0.28	93441	2.59E-10
rs62133983	*MXD1*	2	70150674	rs6725425	Skeletal muscle	GMCL1	C	-0.28	93900	1.69E-10
rs62133983	*MXD1*	2	70151471	rs10205487	Skeletal muscle	GMCL1	G	-0.27	94697	5.55E-10
rs62133983	*MXD1*	2	70152027	rs726920	Skeletal muscle	GMCL1	C	-0.28	95253	1.66E-10
rs62133983	*MXD1*	2	70153436	rs10496174	Skeletal muscle	GMCL1	G	-0.27	96662	5.11E-10
rs62133983	*MXD1*	2	70154037	rs7573442	Skeletal muscle	GMCL1	A	-0.27	97263	5.09E-10
rs62133983	*MXD1*	2	70154134	rs12713682	Skeletal muscle	GMCL1	A	-0.27	97360	5.84E-10
rs62133983	*MXD1*	2	70154187	rs11893500	Skeletal muscle	GMCL1	C	-0.27	97413	5.11E-10
rs62133983	*MXD1*	2	70155482	rs4144081	Skeletal muscle	GMCL1	A	-0.28	98708	1.67E-10
rs62133983	*MXD1*	2	70156540	rs6712827	Skeletal muscle	GMCL1	G	-0.27	99766	5.12E-10
rs62133983	*MXD1*	2	70156589	rs6741449	Skeletal muscle	GMCL1	G	-0.28	99815	1.71E-10
rs62133983	*MXD1*	2	70160658	rs897119	Skeletal muscle	GMCL1	C	-0.27	103884	8.16E-10
rs62133983	*MXD1*	2	70160982	rs897120	Skeletal muscle	GMCL1	G	-0.28	104208	1.79E-10
rs62133983	*MXD1*	2	70161032	rs6729760	Skeletal muscle	GMCL1	T	-0.28	104258	2.58E-10
rs62133983	*MXD1*	2	70161342	rs12613947	Skeletal muscle	GMCL1	G	-0.28	104568	1.63E-10
rs62133983	*MXD1*	2	70163316	rs34586537	Skeletal muscle	GMCL1	G	-0.28	106542	1.29E-10
rs62133983	*MXD1*	2	70163434	rs11126251	Skeletal muscle	GMCL1	G	-0.28	106660	1.07E-10
rs62133983	*MXD1*	2	70164034	rs3771531	Skeletal muscle	GMCL1	C	-0.28	107260	1.26E-10
rs62133983	*MXD1*	2	70164805	rs3771530	Skeletal muscle	GMCL1	C	-0.30	108031	6.75E-11
rs62133983	*MXD1*	2	70164840	rs3771529	Skeletal muscle	GMCL1	A	-0.37	108066	3.32E-10
rs62133983	*MXD1*	2	70167197	rs12475412	Skeletal muscle	GMCL1	T	-0.29	110423	7.37E-11
rs62133983	*MXD1(dist=1494);ASPRV1(dist=15654)*	2	70171570	rs897121	Skeletal muscle	GMCL1	T	-0.30	114796	8.46E-11
rs62133983	*MXD1(dist=2390);ASPRV1(dist=14758)*	2	70172466	rs12713684	Skeletal muscle	GMCL1	G	-0.24	115692	4.54E-08
rs62133983	*MXD1(dist=2511);ASPRV1(dist=14637)*	2	70172587	rs6756513	Skeletal muscle	GMCL1	A	-0.27	115813	7.70E-08
rs62133983	*MXD1(dist=3954);ASPRV1(dist=13194)*	2	70174030	rs7569566	Skeletal muscle	GMCL1	C	-0.27	117256	1.91E-09
rs62133983	*MXD1(dist=3978);ASPRV1(dist=13170)*	2	70174054	rs7581977	Skeletal muscle	GMCL1	G	-0.28	117280	9.81E-10
rs62133983	*AAK1(dist=90535);ANXA4(dist=7615)*	2	69961512	rs13420511	Skeletal muscle	SNRNP27	C	-0.19	-159180	1.57E-05
rs62133983	*AAK1(dist=91163);ANXA4(dist=6987)*	2	69962140	rs6739197	Skeletal muscle	SNRNP27	G	-0.19	-158552	1.57E-05
rs62133983	*AAK1(dist=92470);ANXA4(dist=5680)*	2	69963447	rs4852980	Skeletal muscle	SNRNP27	G	-0.19	-157245	1.53E-05
rs62133983	*AAK1(dist=95312);ANXA4(dist=2838)*	2	69966289	rs2013427	Skeletal muscle	SNRNP27	T	-0.20	-154403	5.64E-06
rs62133983	*AAK1(dist=95541);ANXA4(dist=2609)*	2	69966518	rs7424888	Skeletal muscle	SNRNP27	A	-0.19	-154174	1.44E-05
rs62133983	*ANXA4*	2	69975819	rs10211658	Skeletal muscle	SNRNP27	A	-0.20	-144873	3.58E-06
rs62133983	*ANXA4*	2	69976384	rs62133983	Skeletal muscle	SNRNP27	T	-0.20	-144308	3.17E-06
rs62133983	*ANXA4*	2	69980174	rs7577493	Skeletal muscle	SNRNP27	G	-0.18	-140518	1.71E-05
rs62133983	*ANXA4*	2	69980193	rs7563401	Skeletal muscle	SNRNP27	T	-0.18	-140499	1.71E-05
rs62133983	*ANXA4*	2	69981295	rs7567400	Skeletal muscle	SNRNP27	A	-0.18	-139397	1.71E-05
rs62133983	*ANXA4*	2	70031797	rs3771541	Skeletal muscle	SNRNP27	G	-0.27	-88895	4.90E-10
rs62133983	*ANXA4*	2	70031941	rs3771540	Skeletal muscle	SNRNP27	G	-0.28	-88751	2.71E-10
rs62133983	*ANXA4*	2	70034793	rs2168115	Skeletal muscle	SNRNP27	G	-0.27	-85899	4.63E-10
rs62133983	*ANXA4*	2	70036711	rs13392884	Skeletal muscle	SNRNP27	G	-0.28	-83981	1.07E-10
rs62133983	*ANXA4*	2	70038232	rs6546550	Skeletal muscle	SNRNP27	G	-0.28	-82460	3.45E-10

Supplementary Table 18. *continued*

rs62133983	*ANXA4*	2	70038792	rs3771537	Skeletal muscle	SNRNP27	C	-0.28	-81900	6.61E-12
rs62133983	*ANXA4*	2	70039224	rs4853027	Skeletal muscle	SNRNP27	T	-0.28	-81468	2.53E-10
rs62133983	*ANXA4*	2	70039677	rs2305523	Skeletal muscle	SNRNP27	C	-0.28	-81015	2.27E-10
rs62133983	*ANXA4*	2	70040542	rs2312555	Skeletal muscle	SNRNP27	A	-0.30	-80150	1.55E-13
rs62133983	*ANXA4*	2	70041033	rs11673826	Skeletal muscle	SNRNP27	A	-0.30	-79659	4.81E-13
rs62133983	*ANXA4*	2	70050725	rs7563062	Skeletal muscle	SNRNP27	A	-0.27	-69967	7.39E-10
rs62133983	*ANXA4*	2	70053668	rs7600468	Skeletal muscle	SNRNP27	G	-0.27	-67024	1.47E-09
rs62133983	*ANXA4(dist=1909);GMCL1(dist=1313)*	2	70055505	rs1531025	Skeletal muscle	SNRNP27	A	-0.27	-65187	7.70E-10
rs62133983	*GMCL1*	2	70057448	rs3732266	Skeletal muscle	SNRNP27	G	-0.27	-63244	1.15E-09
rs62133983	*GMCL1*	2	70062360	rs10167142	Skeletal muscle	SNRNP27	C	-0.26	-58332	1.32E-09
rs62133983	*GMCL1*	2	70062454	rs10202159	Skeletal muscle	SNRNP27	T	-0.26	-58238	1.30E-09
rs62133983	*GMCL1*	2	70063563	rs4401231	Skeletal muscle	SNRNP27	C	-0.27	-57129	1.13E-09
rs62133983	*GMCL1*	2	70063660	rs4241261	Skeletal muscle	SNRNP27	G	-0.26	-57032	1.28E-09
rs62133983	*GMCL1*	2	70064155	rs1377995	Skeletal muscle	SNRNP27	G	-0.27	-56537	1.20E-09
rs62133983	*GMCL1*	2	70068635	rs2872075	Skeletal muscle	SNRNP27	T	-0.27	-52057	9.44E-10
rs62133983	*GMCL1*	2	70073703	rs6546551	Skeletal muscle	SNRNP27	T	-0.27	-46989	1.09E-09
rs62133983	*GMCL1*	2	70076954	rs4852349	Skeletal muscle	SNRNP27	T	-0.28	-43738	2.27E-10
rs62133983	*GMCL1*	2	70079633	rs1551374	Skeletal muscle	SNRNP27	T	-0.26	-41059	6.16E-09
rs62133983	*GMCL1*	2	70090579	rs13017134	Skeletal muscle	SNRNP27	G	-0.28	-30113	1.24E-11
rs62133983	*GMCL1*	2	70091246	rs10865380	Skeletal muscle	SNRNP27	C	-0.29	-29446	4.19E-12
rs62133983	*GMCL1*	2	70093647	rs57278310	Skeletal muscle	SNRNP27	C	-0.28	-27045	5.25E-12
rs62133983	*GMCL1*	2	70093910	rs60207187	Skeletal muscle	SNRNP27	A	-0.28	-26782	1.24E-11
rs62133983	*GMCL1*	2	70098808	rs3214007	Skeletal muscle	SNRNP27	G	-0.27	-21884	7.58E-10
rs62133983	*GMCL1*	2	70106832	rs6747542	Skeletal muscle	SNRNP27	C	-0.28	-13860	1.14E-11
rs62133983	*GMCL1(dist=1529);SNRNP27(dist=12819)*	2	70108256	rs1056482	Skeletal muscle	SNRNP27	A	-0.28	-12436	9.89E-12
rs62133983	*GMCL1(dist=4984);SNRNP27(dist=9364)*	2	70111711	rs6546553	Skeletal muscle	SNRNP27	A	-0.28	-8981	1.97E-11
rs62133983	*GMCL1(dist=10288);SNRNP27(dist=4060)*	2	70117015	rs10165883	Skeletal muscle	SNRNP27	T	-0.28	-3677	1.61E-10
rs62133983	*GMCL1(dist=10449);SNRNP27(dist=3899)*	2	70117176	rs12232914	Skeletal muscle	SNRNP27	T	-0.28	-3516	8.61E-11
rs62133983	*GMCL1(dist=10645);SNRNP27(dist=3703)*	2	70117372	rs12233079	Skeletal muscle	SNRNP27	G	-0.28	-3320	1.02E-10
rs62133983	*GMCL1(dist=10694);SNRNP27(dist=3654)*	2	70117421	rs2054047	Skeletal muscle	SNRNP27	C	-0.27	-3271	3.38E-10
rs62133983	*GMCL1(dist=11661);SNRNP27(dist=2687)*	2	70118388	rs13002091	Skeletal muscle	SNRNP27	T	-0.28	-2304	9.10E-11
rs62133983	*GMCL1(dist=11700);SNRNP27(dist=2648)*	2	70118427	rs13028508	Skeletal muscle	SNRNP27	A	-0.28	-2265	9.03E-11
rs62133983	*GMCL1(dist=12742);SNRNP27(dist=1606)*	2	70119469	rs3755389	Skeletal muscle	SNRNP27	C	-0.28	-1223	9.75E-11
rs62133983	*SNRNP27*	2	70124316	rs3752781	Skeletal muscle	SNRNP27	A	-0.28	3624	6.28E-11
rs62133983	*SNRNP27*	2	70124805	rs6720498	Skeletal muscle	SNRNP27	C	-0.28	4113	9.58E-11
rs62133983	*SNRNP27*	2	70125763	rs13015457	Skeletal muscle	SNRNP27	T	-0.28	5071	4.93E-11
rs62133983	*SNRNP27*	2	70125988	rs4852375	Skeletal muscle	SNRNP27	G	-0.28	5296	5.43E-11
rs62133983	*SNRNP27*	2	70127229	rs6716937	Skeletal muscle	SNRNP27	A	-0.28	6537	4.95E-11
rs62133983	*SNRNP27*	2	70128717	rs7598283	Skeletal muscle	SNRNP27	G	-0.28	8025	6.99E-11
rs62133983	*SNRNP27*	2	70132676	rs1048266	Skeletal muscle	SNRNP27	G	-0.28	11984	4.94E-11
rs62133983	*SNRNP27(dist=1739);MXD1(dist=8066)*	2	70134107	rs10166011	Skeletal muscle	SNRNP27	G	-0.28	13415	5.98E-11
rs62133983	*SNRNP27(dist=3338);MXD1(dist=6467)*	2	70135706	rs6546554	Skeletal muscle	SNRNP27	A	-0.28	15014	4.94E-11
rs62133983	*SNRNP27(dist=3392);MXD1(dist=6413)*	2	70135760	rs6546555	Skeletal muscle	SNRNP27	G	-0.29	15068	3.97E-11
rs62133983	*SNRNP27(dist=5130);MXD1(dist=4675)*	2	70137498	rs1979214	Skeletal muscle	SNRNP27	C	-0.28	16806	5.78E-11
rs62133983	*SNRNP27(dist=5406);MXD1(dist=4399)*	2	70137774	rs6736408	Skeletal muscle	SNRNP27	T	-0.28	17082	4.94E-11
rs62133983	*SNRNP27(dist=5743);MXD1(dist=4062)*	2	70138111	rs6739780	Skeletal muscle	SNRNP27	A	-0.28	17419	6.68E-11
rs62133983	*SNRNP27(dist=5802);MXD1(dist=4003)*	2	70138170	rs6754896	Skeletal muscle	SNRNP27	C	-0.28	17478	4.94E-11
rs62133983	*SNRNP27(dist=6633);MXD1(dist=3172)*	2	70139001	rs6546556	Skeletal muscle	SNRNP27	G	-0.28	18309	4.94E-11
rs62133983	*SNRNP27(dist=6766);MXD1(dist=3039)*	2	70139134	rs7592647	Skeletal muscle	SNRNP27	T	-0.28	18442	7.87E-11
rs62133983	*SNRNP27(dist=7903);MXD1(dist=1902)*	2	70140271	rs897122	Skeletal muscle	SNRNP27	T	-0.28	19579	4.94E-11
rs62133983	*MXD1*	2	70144596	rs11902198	Skeletal muscle	SNRNP27	A	-0.29	23904	2.83E-11
rs62133983	*MXD1*	2	70145717	rs6546558	Skeletal muscle	SNRNP27	T	-0.28	25025	1.07E-10
rs62133983	*MXD1*	2	70145833	rs6546559	Skeletal muscle	SNRNP27	A	-0.28	25141	5.67E-11
rs62133983	*MXD1*	2	70146121	rs6721891	Skeletal muscle	SNRNP27	G	-0.28	25429	4.94E-11
rs62133983	*MXD1*	2	70146125	rs6750488	Skeletal muscle	SNRNP27	T	-0.28	25433	4.94E-11
rs62133983	*MXD1*	2	70146625	rs7419837	Skeletal muscle	SNRNP27	C	-0.28	25933	1.12E-10
rs62133983	*MXD1*	2	70149225	rs1454498	Skeletal muscle	SNRNP27	A	-0.29	28533	4.20E-11
rs62133983	*MXD1*	2	70150215	rs6738174	Skeletal muscle	SNRNP27	C	-0.29	29523	2.57E-11
rs62133983	*MXD1*	2	70150674	rs6725425	Skeletal muscle	SNRNP27	C	-0.29	29982	4.20E-11
rs62133983	*MXD1*	2	70151471	rs10205487	Skeletal muscle	SNRNP27	G	-0.28	30779	4.92E-11
rs62133983	*MXD1*	2	70152027	rs726920	Skeletal muscle	SNRNP27	C	-0.29	31335	4.20E-11
rs62133983	*MXD1*	2	70153436	rs10496174	Skeletal muscle	SNRNP27	G	-0.28	32744	4.99E-11
rs62133983	*MXD1*	2	70154037	rs7573442	Skeletal muscle	SNRNP27	A	-0.28	33345	4.91E-11
rs62133983	*MXD1*	2	70154134	rs12713682	Skeletal muscle	SNRNP27	A	-0.29	33442	3.82E-11
rs62133983	*MXD1*	2	70154187	rs11893500	Skeletal muscle	SNRNP27	C	-0.28	33495	4.99E-11
rs62133983	*MXD1*	2	70155482	rs4144081	Skeletal muscle	SNRNP27	A	-0.29	34790	4.08E-11
rs62133983	*MXD1*	2	70156540	rs6712827	Skeletal muscle	SNRNP27	G	-0.28	35848	4.80E-11
rs62133983	*MXD1*	2	70156589	rs6741449	Skeletal muscle	SNRNP27	G	-0.28	35897	4.08E-11
rs62133983	*MXD1*	2	70160658	rs897119	Skeletal muscle	SNRNP27	C	-0.28	39966	8.07E-11
rs62133983	*MXD1*	2	70160982	rs897120	Skeletal muscle	SNRNP27	G	-0.28	40290	3.99E-11
rs62133983	*MXD1*	2	70161032	rs6729760	Skeletal muscle	SNRNP27	T	-0.28	40340	2.18E-10
rs62133983	*MXD1*	2	70161342	rs12613947	Skeletal muscle	SNRNP27	G	-0.28	40650	4.34E-11
rs62133983	*MXD1*	2	70163316	rs34586537	Skeletal muscle	SNRNP27	G	-0.28	42624	5.99E-11
rs62133983	*MXD1*	2	70163434	rs11126251	Skeletal muscle	SNRNP27	G	-0.28	42742	1.15E-10
rs62133983	*MXD1*	2	70164034	rs3771531	Skeletal muscle	SNRNP27	C	-0.28	43342	6.17E-11
rs62133983	*MXD1*	2	70164805	rs3771530	Skeletal muscle	SNRNP27	C	-0.22	44113	5.57E-07
rs62133983	*MXD1*	2	70167197	rs12475412	Skeletal muscle	SNRNP27	T	-0.28	46505	5.54E-11
rs62133983	*MXD1(dist=1494);ASPRV1(dist=15654)*	2	70171570	rs897121	Skeletal muscle	SNRNP27	T	-0.25	50878	3.45E-08
rs62133983	*MXD1(dist=2390);ASPRV1(dist=14758)*	2	70172466	rs12713684	Skeletal muscle	SNRNP27	G	-0.24	51774	1.39E-08
rs62133983	*MXD1(dist=3954);ASPRV1(dist=13194)*	2	70174030	rs7569566	Skeletal muscle	SNRNP27	C	-0.21	53338	2.46E-06
rs62133983	*MXD1(dist=3978);ASPRV1(dist=13170)*	2	70174054	rs7581977	Skeletal muscle	SNRNP27	G	-0.21	53362	3.20E-06
rs7508	*ASAH1*	8	17913970	rs7508	Left ventricle	PCM1	A	0.20	133621	3.18E-06
rs7508	*ASAH1*	8	17913970	rs7508	Skeletal muscle	PCM1	A	-0.20	133621	1.12E-06
rs10824026	*SYNPO2L*	10	75404300	rs11000728	Atrial appendage	MYOZ1	G	1.33	-2785	1.78E-21
rs10824026	*SYNPO2L*	10	75405635	rs41280404	Atrial appendage	MYOZ1	G	1.30	-4120	5.15E-21
rs10824026	*SYNPO2L*	10	75406141	rs3740293	Atrial appendage	MYOZ1	C	1.15	-4626	4.11E-18
rs10824026	*SYNPO2L*	10	75406912	rs34163229	Atrial appendage	MYOZ1	T	1.32	-5397	1.98E-21

Supplementary Table 18. *continued*

rs10824026	*SYNPO2L*	10	75407290	rs3812629	Atrial appendage	MYOZ1	A	1.32	-5775	1.86E-21
rs10824026	*SYNPO2L*	10	75407649	rs4746139	Atrial appendage	MYOZ1	C	1.35	-6134	1.30E-20
rs10824026	*SYNPO2L*	10	75409877	rs2177843	Atrial appendage	MYOZ1	T	1.34	-8362	5.93E-24
rs10824026	*SYNPO2L*	10	75414344	rs60212594	Atrial appendage	MYOZ1	C	1.36	-12829	1.52E-23
rs10824026	*SYNPO2L*	10	75415677	rs60632610	Atrial appendage	MYOZ1	T	1.35	-14162	4.70E-23
rs10824026	*SYNPO2L*	10	75416789	rs12570126	Atrial appendage	MYOZ1	G	1.13	-15274	3.20E-16
rs10824026	*SYNPO2L(dist=1417);AGAP5(dist=16784)*	10	75417249	rs4746140	Atrial appendage	MYOZ1	C	1.12	-15734	3.98E-16
rs10824026	*SYNPO2L(dist=3831);AGAP5(dist=14370)*	10	75419663	rs11000734	Atrial appendage	MYOZ1	G	1.13	-18148	3.47E-16
rs10824026	*SYNPO2L(dist=4282);AGAP5(dist=13919)*	10	75420114	rs6480708	Atrial appendage	MYOZ1	A	1.12	-18599	3.98E-16
rs10824026	*SYNPO2L(dist=4348);AGAP5(dist=13853)*	10	75420180	rs7915134	Atrial appendage	MYOZ1	T	1.28	-18665	2.54E-20
rs10824026	*SYNPO2L(dist=4738);AGAP5(dist=13463)*	10	75420570	rs7900932	Atrial appendage	MYOZ1	C	1.28	-19055	5.55E-21
rs10824026	*SYNPO2L(dist=5376);AGAP5(dist=12825)*	10	75421208	rs10824026	Atrial appendage	MYOZ1	A	-1.12	-19693	3.98E-16
rs10824026	*SYNPO2L(dist=5614);AGAP5(dist=12587)*	10	75421446	rs7394152	Atrial appendage	MYOZ1	T	1.30	-19931	1.88E-21
rs10824026	*SYNPO2L(dist=5748);AGAP5(dist=12453)*	10	75421580	rs7394178	Atrial appendage	MYOZ1	A	1.27	-20065	5.46E-21
rs10824026	*SYNPO2L(dist=5816);AGAP5(dist=12385)*	10	75421648	rs7394190	Atrial appendage	MYOZ1	A	1.13	-20133	3.03E-16
rs10824026	*SYNPO2L(dist=6482);AGAP5(dist=11719)*	10	75422314	rs78249997	Atrial appendage	MYOZ1	T	1.32	-20799	7.49E-21
rs10824026	*SYNPO2L(dist=12464);AGAP5(dist=5737)*	10	75428296	rs148321568	Atrial appendage	MYOZ1	T	1.50	-26781	4.54E-21
rs10824026	*SYNPO2L(dist=14169);AGAP5(dist=4032)*	10	75430001	rs4745719	Atrial appendage	MYOZ1	G	-0.96	-28486	3.66E-11
rs10824026	*SYNPO2L(dist=15246);AGAP5(dist=2955)*	10	75431078	rs3878005	Atrial appendage	MYOZ1	A	1.43	-29563	2.79E-20
rs10824026	*AGAP5*	10	75447582	rs147790633	Atrial appendage	MYOZ1	C	1.36	-46067	2.07E-20
rs10824026	*AGAP5*	10	75449789	rs76443711	Atrial appendage	MYOZ1	C	1.41	-48274	3.07E-21
rs10824026	*AGAP5*	10	75450901	rs138055607	Atrial appendage	MYOZ1	G	1.41	-49386	3.04E-21
rs10824026	*BMS1P4*	10	75462510	rs76192127	Atrial appendage	MYOZ1	C	1.40	-60995	5.05E-21
rs10824026	*BMS1P4*	10	75464587	rs4745721	Atrial appendage	MYOZ1	A	1.41	-63072	6.14E-21
rs10824026	*ZSWIM8*	10	75559077	rs11000780	Atrial appendage	MYOZ1	A	1.25	-157562	3.71E-15
rs10824026	*NDST2*	10	75562108	rs2075641	Atrial appendage	MYOZ1	A	1.17	-160593	1.67E-14
rs10824026	*CAMK2G*	10	75573778	rs2306327	Atrial appendage	MYOZ1	T	1.17	-172263	1.67E-14
rs10824026	*CAMK2G*	10	75575138	rs113799665	Atrial appendage	MYOZ1	T	1.17	-173623	1.66E-14
rs10824026	*CAMK2G*	10	75576405	rs12220394	Atrial appendage	MYOZ1	C	1.17	-174890	1.66E-14
rs10824026	*CAMK2G*	10	75576483	rs12217245	Atrial appendage	MYOZ1	C	1.17	-174968	1.67E-14
rs10824026	*CAMK2G*	10	75578720	rs4746151	Atrial appendage	MYOZ1	T	1.17	-177205	1.67E-14
rs10824026	*CAMK2G*	10	75578948	rs3843939	Atrial appendage	MYOZ1	C	1.17	-177433	1.67E-14
rs10824026	*CAMK2G*	10	75580226	rs188726810	Atrial appendage	MYOZ1	T	1.13	-178711	3.05E-13
rs10824026	*CAMK2G*	10	75583034	rs59693993	Atrial appendage	MYOZ1	T	1.22	-181519	1.78E-14
rs10824026	*CAMK2G*	10	75585307	rs2242254	Atrial appendage	MYOZ1	A	1.17	-183792	1.42E-13
rs10824026	*SYNPO2L*	10	75407649	rs4746139	Skeletal muscle	FUT11	C	-0.26	-125299	1.13E-05
rs10824026	*SYNPO2L*	10	75409877	rs2177843	Skeletal muscle	FUT11	T	-0.25	-123071	1.37E-05
rs10824026	*SYNPO2L*	10	75416789	rs12570126	Skeletal muscle	FUT11	G	-0.23	-116159	1.51E-05
rs10824026	*SYNPO2L(dist=1417);AGAP5(dist=16784)*	10	75417249	rs4746140	Skeletal muscle	FUT11	C	-0.24	-115699	7.13E-06
rs10824026	*SYNPO2L(dist=3831);AGAP5(dist=14370)*	10	75419663	rs11000734	Skeletal muscle	FUT11	G	-0.23	-113285	1.37E-05
rs10824026	*SYNPO2L(dist=4282);AGAP5(dist=13919)*	10	75420114	rs6480708	Skeletal muscle	FUT11	A	-0.23	-112834	1.43E-05
rs10824026	*SYNPO2L(dist=4738);AGAP5(dist=13463)*	10	75420570	rs7900932	Skeletal muscle	FUT11	C	-0.24	-112378	1.85E-05
rs10824026	*SYNPO2L(dist=5376);AGAP5(dist=12825)*	10	75421208	rs10824026	Skeletal muscle	FUT11	A	0.24	-111740	1.05E-05
rs10824026	*SYNPO2L(dist=5816);AGAP5(dist=12385)*	10	75421648	rs7394190	Skeletal muscle	FUT11	A	-0.25	-111300	5.90E-06
rs10824026	*SYNPO2L(dist=6482);AGAP5(dist=11719)*	10	75422314	rs78249997	Skeletal muscle	FUT11	T	-0.25	-110634	1.56E-05
rs10824026	*SYNPO2L(dist=12464);AGAP5(dist=5737)*	10	75428296	rs148321568	Skeletal muscle	FUT11	T	-0.26	-104652	1.38E-05
rs10824026	*SYNPO2L(dist=15246);AGAP5(dist=2955)*	10	75431078	rs3878005	Skeletal muscle	FUT11	A	-0.27	-101870	1.09E-05
rs10824026	*AGAP5*	10	75447582	rs147790633	Skeletal muscle	FUT11	C	-0.27	-85366	3.84E-06
rs10824026	*AGAP5*	10	75449789	rs76443711	Skeletal muscle	FUT11	C	-0.27	-83159	1.10E-05
rs10824026	*AGAP5*	10	75450901	rs138055607	Skeletal muscle	FUT11	G	-0.27	-82047	1.12E-05
rs10824026	*BMS1P4*	10	75462510	rs76192127	Skeletal muscle	FUT11	C	-0.27	-70438	1.18E-05
rs10824026	*BMS1P4*	10	75464587	rs4745721	Skeletal muscle	FUT11	A	-0.27	-68361	1.20E-05
rs10824026	*ZSWIM8*	10	75559077	rs11000780	Skeletal muscle	FUT11	A	-0.31	26129	4.62E-07
rs10824026	*NDST2*	10	75562108	rs2075641	Skeletal muscle	FUT11	A	-0.31	29160	3.50E-07
rs10824026	*CAMK2G*	10	75573778	rs2306327	Skeletal muscle	FUT11	T	-0.31	40830	3.50E-07
rs10824026	*CAMK2G*	10	75575138	rs113799665	Skeletal muscle	FUT11	T	-0.32	42190	1.90E-07
rs10824026	*CAMK2G*	10	75576405	rs12220394	Skeletal muscle	FUT11	C	-0.30	43457	6.60E-07
rs10824026	*CAMK2G*	10	75576483	rs12217245	Skeletal muscle	FUT11	C	-0.30	43535	6.43E-07
rs10824026	*CAMK2G*	10	75578720	rs4746151	Skeletal muscle	FUT11	T	-0.30	45772	6.43E-07
rs10824026	*CAMK2G*	10	75578948	rs3843939	Skeletal muscle	FUT11	C	-0.30	46000	6.43E-07
rs10824026	*CAMK2G*	10	75583034	rs59693993	Skeletal muscle	FUT11	T	-0.31	50086	5.81E-07
rs10824026	*CAMK2G*	10	75585307	rs2242254	Skeletal muscle	FUT11	A	-0.30	52359	9.77E-07
rs75190942	*KCNJ5*	11	128764570	rs76097649	Left ventricle	KCNJ5	A	0.58	3319	3.15E-06
rs75190942	*KCNJ5*	11	128764571	rs75190942	Left ventricle	KCNJ5	A	0.58	3320	3.15E-06
rs883079	*RBM19(dist=385634);TBX5(dist=1925)*	12	114789810	rs2891503	Left ventricle	TBX5	G	0.26	56437	3.84E-06
				ExWAS						
				Variants identified in combined ancestry analysis - eQTLs from GTEx Release V6						
rs60632610	*SYNPO2L*	10	75407290	rs3812629	Atrial appendage	*MYOZ1*	A	1.32	-5775	1.86E-21
rs60632610	*SYNPO2L*	10	75415677	rs60632610	Atrial appendage	*MYOZ1*	T	1.35	-14162	4.70E-23
				Variants identified in European ancestry analysis - eQTLs from GTEx Release V6						
rs60632610	*SYNPO2L*	10	75406912	rs34163229	Atrial appendage	*MYOZ1*	T	1.32	-5397	1.98E-21
rs60632610	*SYNPO2L*	10	75407290	rs3812629	Atrial appendage	*MYOZ1*	A	1.32	-5775	1.86E-21
rs60632610	*SYNPO2L*	10	75415677	rs60632610	Atrial appendage	*MYOZ1*	T	1.35	-14162	4.70E-23

At each significantly associated AF locus, we defined a region based on LD span (r2 > 0.2) with the Index SNP. All variants within this region were tested in the eQTL analyses. *The most significant variant in the region. **For intronic variants, the gene the variant is located within is listed; for intergenic variants, the closest genes upstream and downstream are listed. †Variant tested. ‡eQTL gene. This table reports the variants (rsID) that were significantly associated with altered expression of the eQTL genes. SNP, single nucleotide polymorphism; Chr, chromosome; Tissue, eQTL tissue (only results shown for Skeletal muscle, Atrial appendage and Left ventricle); Effect Allele, eQTL effect allele; Beta, eQTL effect size; TSS, Transription start site; P-value, eQTL p-value.

Supplementary Table 19. eQTL analysis of in CCAF human atrial tissue samples

Index SNP*	Closest gene/s**	Chr	Position	rsID†	Probe ID	Gene‡	MA	Fold change§	TSS distance	r2††	FDR_gw‡‡	FDR_af§§
GWAS												
Variants identified in combined ancestry analysis - eQTLs in European American samples												
rs11264280	KCNN3	1	154834183	rs1218582	ILMN_1751500	ADAM15	G	1.12973025	-188.859	0.07	0.00266	0.00057
rs11264280	KCNN3(dist=3520);PMVK(dist=50934)	1	154846274	rs883718	ILMN_1751500	ADAM15	T	1.14278728	-176.768	0.08	0.00101	0.00022
rs11264280	KCNN3(dist=6836);PMVK(dist=47618)	1	154849590	rs10908445	ILMN_1751500	ADAM15	A	1.14371567	-173.452	0.08	0.00098	0.00021
rs11264280	KCNN3(dist=19810);PMVK(dist=34644)	1	154862564	1:154862564:C_CA	ILMN_1751500	ADAM15	CA	1.14410965	-160.478	0.08	0.00084	0.00018
rs72700118	METTL11B(dist=56902);LOC284688(dist=46721)	1	170193825	rs72700114	ILMN_2119224	KIFAP3	C	0.92193558	-139.476	0.05	0.01645	0.00446
rs11264280	PBXIP1	1	154918352	rs41264253	ILMN_1756992	MUC1	A	1.21271419	244.355	0.05	0.02282	0.00659
rs520525	GORAB(dist=37630);PRRX1(dist=72709)	1	170560604	rs6658866	ILMN_1739496	PRRX1	G	0.88791122	-71.265	0.11	1.04E-05	2.05E-06
rs520525	GORAB(dist=38430);PRRX1(dist=71909)	1	170561404	rs6659754	ILMN_1739496	PRRX1	T	0.88900518	-70.465	0.11	1.32E-05	2.44E-06
rs520525	GORAB(dist=40109);PRRX1(dist=70230)	1	170563083	rs577827	ILMN_1739496	PRRX1	C	1.09741222	-68.786	0.07	0.00231	0.00051
rs520525	GORAB(dist=42175);PRRX1(dist=68164)	1	170565149	1:170565149:T_TGA	ILMN_1739496	PRRX1	TGACCAA	0.8932638	-66.72	0.10	3.89E-05	5.98E-06
rs520525	GORAB(dist=43031);PRRX1(dist=67308)	1	170566005	rs763567	ILMN_1739496	PRRX1	G	0.89327025	-65.864	0.10	3.89E-05	5.98E-06
rs520525	GORAB(dist=44463);PRRX1(dist=65876)	1	170567437	rs1928715	ILMN_1739496	PRRX1	T	0.89058846	-64.432	0.11	1.51E-05	2.74E-06
rs520525	GORAB(dist=45740);PRRX1(dist=64599)	1	170568714	rs12755237	ILMN_1739496	PRRX1	A	0.89207947	-63.155	0.11	1.85E-05	2.98E-06
rs520525	GORAB(dist=45922);PRRX1(dist=64417)	1	170568896	rs12742164	ILMN_1739496	PRRX1	G	0.88778945	-62.973	0.11	1.22E-05	2.31E-06
rs520525	GORAB(dist=46343);PRRX1(dist=63996)	1	170569317	rs3903239	ILMN_1739496	PRRX1	G	0.8920786	-62.552	0.11	1.86E-05	2.98E-06
rs520525	GORAB(dist=46715);PRRX1(dist=63624)	1	170569689	rs12760630	ILMN_1739496	PRRX1	A	0.89207947	-62.18	0.11	1.85E-05	2.98E-06
rs520525	GORAB(dist=47069);PRRX1(dist=63270)	1	170570043	rs10800529	ILMN_1739496	PRRX1	C	1.10454711	-61.826	0.06	0.00603	0.00142
rs520525	GORAB(dist=47525);PRRX1(dist=62814)	1	170570499	rs7412231	ILMN_1739496	PRRX1	C	0.89207947	-61.37	0.11	1.85E-05	2.98E-06
rs520525	GORAB(dist=48869);PRRX1(dist=61470)	1	170571843	rs1234230	ILMN_1739496	PRRX1	A	1.10515568	-60.026	0.09	0.0004	7.57E-05
rs520525	GORAB(dist=49972);PRRX1(dist=60367)	1	170572946	rs10919437	ILMN_1739496	PRRX1	A	0.8920786	-58.923	0.11	1.86E-05	2.98E-06
rs520525	GORAB(dist=50284);PRRX1(dist=60055)	1	170573258	rs61217505	ILMN_1739496	PRRX1	T	0.89207845	-58.611	0.11	1.85E-05	2.98E-06
rs520525	GORAB(dist=50840);PRRX1(dist=59499)	1	170573814	rs476810	ILMN_1739496	PRRX1	T	1.09545295	-58.055	0.07	0.00244	0.00052
rs520525	GORAB(dist=50953);PRRX1(dist=59379)	1	170573926	1:170573926:CCACT	ILMN_1739496	PRRX1	C	1.09312221	-57.943	0.05	0.02833	0.00863
rs520525	GORAB(dist=51954);PRRX1(dist=58385)	1	170574928	rs1234233	ILMN_1739496	PRRX1	C	1.09544615	-56.941	0.07	0.00244	0.00052
rs520525	GORAB(dist=52288);PRRX1(dist=58051)	1	170575261	1:170575261:CT_C	ILMN_1739496	PRRX1	C	0.89604371	-56.608	0.10	6.34E-05	1.02E-05
rs520525	GORAB(dist=53133);PRRX1(dist=57206)	1	170576107	rs2206062	ILMN_1739496	PRRX1	C	0.89207947	-55.762	0.11	1.85E-05	2.98E-06
rs520525	GORAB(dist=53764);PRRX1(dist=56575)	1	170576738	rs566850	ILMN_1739496	PRRX1	A	1.0954409	-55.131	0.07	0.00244	0.00052
rs520525	GORAB(dist=54081);PRRX1(dist=56258)	1	170577055	rs722597	ILMN_1739496	PRRX1	A	1.10371147	-54.814	0.06	0.00696	0.00167
rs520525	GORAB(dist=54261);PRRX1(dist=56078)	1	170577235	rs647438	ILMN_1739496	PRRX1	G	1.10513615	-54.634	0.09	0.0004	7.57E-05
rs520525	GORAB(dist=54866);PRRX1(dist=55473)	1	170577840	rs72482606	ILMN_1739496	PRRX1	A	1.10452045	-54.029	0.06	0.00603	0.00142
rs520525	GORAB(dist=55332);PRRX1(dist=55007)	1	170578306	rs10919440	ILMN_1739496	PRRX1	G	0.89207574	-53.563	0.11	1.85E-05	2.98E-06
rs520525	GORAB(dist=55613);PRRX1(dist=54726)	1	170578587	rs494339	ILMN_1739496	PRRX1	G	1.10346196	-53.282	0.08	0.00064	0.00013
rs520525	GORAB(dist=55641);PRRX1(dist=54698)	1	170578614	1:170578614:AT_A	ILMN_1739496	PRRX1	A	0.89069653	-53.255	0.11	1.77E-05	2.98E-06
rs520525	GORAB(dist=56115);PRRX1(dist=54224)	1	170579089	rs10919441	ILMN_1739496	PRRX1	A	1.09194487	-52.78	0.05	0.03097	0.00965
rs520525	GORAB(dist=56620);PRRX1(dist=53719)	1	170579594	rs546258	ILMN_1739496	PRRX1	C	1.0954364	-52.275	0.07	0.00245	0.00052
rs520525	GORAB(dist=57503);PRRX1(dist=52836)	1	170580477	rs553905	ILMN_1739496	PRRX1	A	1.09589929	-51.392	0.07	0.00224	0.00049
rs520525	GORAB(dist=58192);PRRX1(dist=52147)	1	170581165	1:170581165:CT_C	ILMN_1739496	PRRX1	C	0.89252445	-50.704	0.11	2.03E-05	3.19E-06
rs520525	GORAB(dist=58560);PRRX1(dist=51779)	1	170581534	rs2982131	ILMN_1739496	PRRX1	T	1.09542931	-50.335	0.07	0.00245	0.00052
rs520525	GORAB(dist=58660);PRRX1(dist=51679)	1	170581634	rs10919444	ILMN_1739496	PRRX1	A	0.89207947	-50.235	0.11	1.85E-05	2.98E-06
rs520525	GORAB(dist=58713);PRRX1(dist=51626)	1	170581687	rs34252585	ILMN_1739496	PRRX1	A	1.09051991	-50.182	0.05	0.0329	0.01033
rs520525	GORAB(dist=59601);PRRX1(dist=50738)	1	170582575	rs1952675	ILMN_1739496	PRRX1	G	0.89207947	-49.294	0.11	1.85E-05	2.98E-06
rs520525	GORAB(dist=60350);PRRX1(dist=49989)	1	170583324	rs77058424	ILMN_1739496	PRRX1	G	1.09542532	-48.545	0.07	0.00245	0.00052
rs520525	GORAB(dist=60537);PRRX1(dist=49802)	1	170583511	rs6677540	ILMN_1739496	PRRX1	A	0.89207858	-48.358	0.11	1.86E-05	2.98E-06
rs520525	GORAB(dist=60970);PRRX1(dist=49369)	1	170583944	rs6690642	ILMN_1739496	PRRX1	C	0.89207858	-47.925	0.11	1.86E-05	2.98E-06
rs520525	GORAB(dist=62123);PRRX1(dist=48216)	1	170585097	rs2206063	ILMN_1739496	PRRX1	C	1.09045	-46.772	0.05	0.03307	0.01036
rs520525	GORAB(dist=62858);PRRX1(dist=47481)	1	170585832	rs619456	ILMN_1739496	PRRX1	A	1.09542456	-46.037	0.07	0.00245	0.00052
rs520525	GORAB(dist=63341);PRRX1(dist=46998)	1	170586315	rs736791	ILMN_1739496	PRRX1	A	0.89002137	-45.554	0.11	1.39E-05	2.57E-06
rs520525	GORAB(dist=64241);PRRX1(dist=46098)	1	170587215	rs576736	ILMN_1739496	PRRX1	G	1.10266777	-44.654	0.06	0.00781	0.00191
rs520525	GORAB(dist=64366);PRRX1(dist=45973)	1	170587340	rs577676	ILMN_1739496	PRRX1	T	1.10760539	-44.529	0.07	0.00158	0.00035
rs520525	GORAB(dist=65124);PRRX1(dist=45213)	1	170588097	1:170588097:TTAG_	ILMN_1739496	PRRX1	T	0.89493375	-43.772	0.09	0.00016	2.80E-05
rs520525	GORAB(dist=65125);PRRX1(dist=45212)	1	170588098	1:170588098:TAGG_	ILMN_1739496	PRRX1	T	0.89412683	-43.771	0.10	4.46E-05	6.94E-06
rs520525	GORAB(dist=66936);PRRX1(dist=43403)	1	170589910	rs2022372	ILMN_1739496	PRRX1	A	0.89163872	-41.959	0.11	1.84E-05	2.98E-06
rs520525	GORAB(dist=67593);PRRX1(dist=42746)	1	170590567	rs12031871	ILMN_1739496	PRRX1	T	1.10048424	-41.302	0.06	0.01061	0.00272
rs520525	GORAB(dist=68336);PRRX1(dist=42003)	1	170591310	rs651386	ILMN_1739496	PRRX1	T	1.10719342	-40.559	0.07	0.00151	0.00033
rs520525	GORAB(dist=68389);PRRX1(dist=41950)	1	170591363	1:170591363:A_ATT	ILMN_1739496	PRRX1	A	0.89834049	-40.506	0.10	0.00011	1.81E-05
rs520525	GORAB(dist=68834);PRRX1(dist=41505)	1	170591808	rs10753817	ILMN_1739496	PRRX1	G	1.10044113	-40.061	0.06	0.01067	0.00273
rs520525	GORAB(dist=71095);PRRX1(dist=39244)	1	170594069	rs12072276	ILMN_1739496	PRRX1	G	1.10038628	-37.8	0.06	0.01074	0.00273
rs520525	GORAB(dist=71142);PRRX1(dist=39197)	1	170594116	rs10919446	ILMN_1739496	PRRX1	A	1.10038628	-37.753	0.06	0.01074	0.00273
rs520525	GORAB(dist=73098);PRRX1(dist=37241)	1	170596072	rs494521	ILMN_1739496	PRRX1	C	0.89489271	-35.797	0.11	3.05E-05	4.65E-06
rs520525	GORAB(dist=73284);PRRX1(dist=37055)	1	170596258	rs1234275	ILMN_1739496	PRRX1	A	0.89162938	-35.611	0.11	1.85E-05	2.98E-06
rs520525	GORAB(dist=73399);PRRX1(dist=36940)	1	170596373	rs1234274	ILMN_1739496	PRRX1	A	0.89160973	-35.496	0.11	1.84E-05	2.98E-06
rs520525	GORAB(dist=73571);PRRX1(dist=36768)	1	170596545	rs11577602	ILMN_1739496	PRRX1	T	1.10032785	-35.324	0.06	0.01082	0.00274
rs520525	GORAB(dist=73598);PRRX1(dist=36741)	1	170596572	rs10800530	ILMN_1739496	PRRX1	A	1.10032785	-35.297	0.06	0.01082	0.00274
rs520525	GORAB(dist=75213);PRRX1(dist=35126)	1	170598187	rs638704	ILMN_1739496	PRRX1	C	0.89162646	-33.682	0.11	1.85E-05	2.98E-06
rs520525	GORAB(dist=76599);PRRX1(dist=33740)	1	170599573	rs10919448	ILMN_1739496	PRRX1	C	1.10026119	-32.296	0.06	0.01091	0.00275
rs520525	GORAB(dist=78034);PRRX1(dist=32305)	1	170601008	rs189058353	ILMN_1739496	PRRX1	C	0.89785286	-30.861	0.09	0.00028	5.09E-05
rs520525	GORAB(dist=81148);PRRX1(dist=29191)	1	170604122	rs598993	ILMN_1739496	PRRX1	T	0.89394769	-27.747	0.11	2.34E-05	3.61E-06
rs520525	GORAB(dist=81964);PRRX1(dist=28375)	1	170604938	rs541557	ILMN_1739496	PRRX1	A	0.89394563	-26.931	0.11	2.34E-05	3.61E-06
rs520525	GORAB(dist=85107);PRRX1(dist=25232)	1	170608081	rs539045	ILMN_1739496	PRRX1	C	0.89393706	-23.788	0.11	2.35E-05	3.61E-06
rs520525	GORAB(dist=86216);PRRX1(dist=24123)	1	170609190	rs473832	ILMN_1739496	PRRX1	A	0.89158617	-22.679	0.11	1.87E-05	2.98E-06
rs520525	GORAB(dist=86651);PRRX1(dist=23688)	1	170609625	rs580487	ILMN_1739496	PRRX1	T	0.89393517	-22.244	0.11	2.36E-05	3.61E-06
rs520525	GORAB(dist=89288);PRRX1(dist=21051)	1	170612262	rs492804	ILMN_1739496	PRRX1	C	0.89205821	-19.607	0.11	2.16E-05	3.34E-06
rs520525	GORAB(dist=89899);PRRX1(dist=20440)	1	170612873	rs639652	ILMN_1739496	PRRX1	G	0.89398545	-18.996	0.11	2.49E-05	3.79E-06
rs520525	GORAB(dist=90876);PRRX1(dist=19463)	1	170613850	rs654461	ILMN_1739496	PRRX1	A	0.89113485	-18.019	0.11	1.75E-05	2.98E-06
rs520525	GORAB(dist=90895);PRRX1(dist=19444)	1	170613869	rs567328	ILMN_1739496	PRRX1	T	0.8911111	-18	0.11	1.71E-05	2.98E-06
rs520525	GORAB(dist=91068);PRRX1(dist=19271)	1	170614042	rs544478	ILMN_1739496	PRRX1	C	0.89158272	-17.827	0.11	1.94E-05	3.06E-06
rs520525	GORAB(dist=92943);PRRX1(dist=17396)	1	170615917	rs593560	ILMN_1739496	PRRX1	G	0.89158272	-15.952	0.11	1.94E-05	3.06E-06
rs520525	GORAB(dist=93381);PRRX1(dist=16958)	1	170616355	rs2988392	ILMN_1739496	PRRX1	G	0.89399855	-15.514	0.11	2.50E-05	3.79E-06
rs520525	GORAB(dist=94332);PRRX1(dist=16007)	1	170617306	rs608930	ILMN_1739496	PRRX1	G	0.89051509	-14.563	0.11	1.46E-05	2.69E-06
rs520525	GORAB(dist=95317);PRRX1(dist=15022)	1	170618291	rs623752	ILMN_1739496	PRRX1	A	0.88733096	-13.578	0.12	7.71E-06	1.52E-06
rs520525	GORAB(dist=95408);PRRX1(dist=14931)	1	170618382	rs531007	ILMN_1739496	PRRX1	T	0.88733785	-13.487	0.12	7.64E-06	1.52E-06
rs520525	GORAB(dist=96633);PRRX1(dist=13706)	1	170619607	rs575432	ILMN_1739496	PRRX1	A	0.89937833	-12.262	0.09	0.00033	6.24E-05
rs520525	GORAB(dist=96956);PRRX1(dist=13383)	1	170619930	rs651822	ILMN_1739496	PRRX1	T	1.08759906	-11.939	0.05	0.03847	0.01257
rs520525	GORAB(dist=100135);PRRX1(dist=10204)	1	170623109	rs588837	ILMN_1739496	PRRX1	A	0.88960365	-8.76	0.11	1.06E-05	2.08E-06
rs520525	GORAB(dist=100946);PRRX1(dist=9393)	1	170623920	rs12089974	ILMN_1739496	PRRX1	A	1.08986034	-7.949	0.05	0.04149	0.01381
rs520525	GORAB(dist=105281);PRRX1(dist=5058)	1	170628255	rs680084	ILMN_1739496	PRRX1	G	0.89330897	-3.614	0.11	2.63E-05	3.99E-06
rs520525	GORAB(dist=108789);PRRX1(dist=1550)	1	170631763	rs629234	ILMN_1739496	PRRX1	T	0.89204547	-0.106	0.11	1.94E-05	3.06E-06
rs520525	PRRX1	1	170635002	rs525489	ILMN_1739496	PRRX1	T	0.8876368	3.133	0.12	5.48E-06	1.11E-06
rs520525	PRRX1	1	170635084	rs503706	ILMN_1739496	PRRX1	T	0.88764988	3.215	0.12	5.51E-06	1.11E-06
rs520525	PRRX1	1	170635369	rs501005	ILMN_1739496	PRRX1	A	0.89498695	3.5	0.10	3.84E-05	5.97E-06

Supplementary Table 19. *continued*

rs520525	PRRX1	1	170636079	rs473133	ILMN_1739496	PRRX1	A	0.88781431	4.21	0.12	5.84E-06	1.18E-06
rs520525	PRRX1	1	170638658	rs10919449	ILMN_1739496	PRRX1	A	1.09065328	6.789	0.06	0.00599	0.00142
rs2540949	SLC1A4(dist=25049);CEP68(dist=7446)	2	65276049	rs1009360	ILMN_1808500	CEP68	C	0.84966902	-7.451	0.15	6.02E-08	1.23E-08
rs2540949	SLC1A4(dist=25452);CEP68(dist=7043)	2	65276452	rs1009358	ILMN_1808500	CEP68	C	0.81706074	-7.048	0.24	2.20E-13	4.01E-14
rs2540949	SLC1A4(dist=25736);CEP68(dist=6759)	2	65276736	rs2540951	ILMN_1808500	CEP68	G	0.8170737	-6.764	0.24	2.20E-13	4.01E-14
rs2540949	SLC1A4(dist=26367);CEP68(dist=6125)	2	65277366	2:65277366:CATTT	ILMN_1808500	CEP68	C	0.82605141	-6.134	0.22	6.64E-12	1.12E-12
rs2540949	SLC1A4(dist=28223);CEP68(dist=4272)	2	65279223	rs2540950	ILMN_1808500	CEP68	T	0.8172861	-4.277	0.24	9.35E-14	1.90E-14
rs2540949	SLC1A4(dist=28321);CEP68(dist=4174)	2	65279321	rs2723066	ILMN_1808500	CEP68	G	0.81761783	-4.179	0.24	1.06E-13	2.05E-14
rs2540949	SLC1A4(dist=28414);CEP68(dist=4081)	2	65279414	rs2723065	ILMN_1808500	CEP68	G	0.81720703	-4.086	0.24	2.26E-13	4.01E-14
rs2540949	SLC1A4(dist=28805);CEP68(dist=3690)	2	65279805	rs2723064	ILMN_1808500	CEP68	C	0.81735156	-3.695	0.24	2.51E-13	4.24E-14
rs2540949	SLC1A4(dist=29185);CEP68(dist=3310)	2	65280185	rs2723063	ILMN_1808500	CEP68	G	0.84143733	-3.315	0.18	2.24E-09	4.53E-10
rs2540949	SLC1A4(dist=29220);CEP68(dist=3275)	2	65280220	rs2723062	ILMN_1808500	CEP68	A	0.81796079	-3.28	0.24	1.36E-13	2.58E-14
rs2540949	CEP68	2	65283972	rs74181299	ILMN_1808500	CEP68	C	0.81902079	0.472	0.23	8.92E-13	1.53E-13
rs2540949	CEP68	2	65284231	rs2540949	ILMN_1808500	CEP68	T	0.82008726	0.731	0.23	9.43E-13	1.58E-13
rs2540949	CEP68	2	65284623	rs2540948	ILMN_1808500	CEP68	C	0.8205978	1.123	0.23	4.88E-13	8.32E-14
rs2540949	CEP68	2	65287896	rs2249105	ILMN_1808500	CEP68	G	0.8167069	4.396	0.23	1.72E-12	2.78E-13
rs2540949	CEP68	2	65289825	rs2540945	ILMN_1808500	CEP68	G	0.8158767	6.325	0.23	1.58E-12	2.66E-13
rs2540949	CEP68	2	65290842	rs2241161	ILMN_1808500	CEP68	A	0.83916269	7.342	0.17	5.07E-09	1.07E-09
rs2540949	CEP68	2	65291546	rs2241160	ILMN_1808500	CEP68	G	0.84153067	8.046	0.16	1.38E-08	2.97E-09
rs2540949	CEP68	2	65296280	rs2252867	ILMN_1808500	CEP68	C	0.81667979	12.78	0.23	1.73E-12	2.78E-13
rs2540949	RAB1A	2	65315903	rs1420185	ILMN_1808500	CEP68	G	0.82043683	32.403	0.19	1.93E-10	3.37E-11
rs2540949	RAB1A	2	65346974	2:65346974:A_AC	ILMN_1808500	CEP68	A	0.8152929	63.474	0.20	1.00E-10	1.68E-11
rs337711	KCNN2	5	113737062	rs337705	ILMN_1685636	KCNN2	G	0.92890985	40.42	0.06	0.00905	0.00225
rs337711	KCNN2	5	113745738	rs163210	ILMN_1685636	KCNN2	C	0.93076685	49.096	0.06	0.01181	0.003
rs337711	KCNN2	5	113746180	rs337708	ILMN_1685636	KCNN2	G	0.93076572	49.538	0.06	0.01182	0.003
rs337711	KCNN2	5	113748571	rs337711	ILMN_1685636	KCNN2	T	0.93074938	51.929	0.06	0.01183	0.003
rs337711	KCNN2	5	113757965	rs6859284	ILMN_1685636	KCNN2	G	0.93058473	61.323	0.06	0.01199	0.00304
rs1997572	CAV2	7	116140524	rs2270188	ILMN_2149226	CAV1	G	1.03895885	-24.315	0.06	0.00626	0.00147
rs1997572	CAV2	7	116140616	rs2270189	ILMN_2149226	CAV1	A	1.03897916	-24.223	0.06	0.00622	0.00147
rs1997572	CAV2	7	116145849	rs10271007	ILMN_2149226	CAV1	A	1.04007055	-18.99	0.07	0.00431	0.00096
rs1997572	CAV2	7	116145957	rs4730743	ILMN_2149226	CAV1	A	1.04009135	-18.882	0.07	0.00428	0.00096
rs1997572	CAV2	7	116147908	rs4727833	ILMN_2149226	CAV1	C	1.04046343	-16.931	0.07	0.00374	0.00083
rs1997572	CAV2	7	116148407	7:116148407:CA_C	ILMN_2149226	CAV1	CA	1.0405896	-16.432	0.07	0.00363	0.00081
rs1997572	CAV2(dist=2560);CAV1(dist=13684)	7	116151155	rs6466579	ILMN_2149226	CAV1	T	1.04061084	-13.684	0.07	0.00362	0.00081
rs1997572	CAV2(dist=3189);CAV1(dist=13055)	7	116151784	rs3919515	ILMN_2149226	CAV1	G	1.04060541	-13.055	0.07	0.00362	0.00081
rs1997572	CAV2(dist=8366);CAV1(dist=7878)	7	116156961	rs7795510	ILMN_2149226	CAV1	T	1.04054883	-7.878	0.07	0.00367	0.00082
rs1997572	CAV2(dist=11366);CAV1(dist=4878)	7	116159961	rs2109514	ILMN_2149226	CAV1	G	1.04036806	-4.878	0.07	0.00369	0.00082
rs1997572	CAV2(dist=11929);CAV1(dist=4315)	7	116160524	rs55883210	ILMN_2149226	CAV1	G	1.04036624	-4.315	0.07	0.00368	0.00082
rs1997572	CAV1	7	116169443	rs7778733	ILMN_2149226	CAV1	C	0.95302457	4.604	0.08	0.00107	0.00023
rs1997572	CAV1	7	116186241	rs3807989	ILMN_2149226	CAV1	A	1.04315421	21.402	0.07	0.00258	0.00055
rs1997572	CAV1	7	116191301	rs11773845	ILMN_2149226	CAV1	C	1.04321973	26.462	0.07	0.00251	0.00054
rs1997572	CAV1	7	116198621	rs1997571	ILMN_2149226	CAV1	G	1.04336824	33.782	0.07	0.00242	0.00052
rs1997572	CAV1	7	116198828	rs1997572	ILMN_2149226	CAV1	A	1.04336824	33.989	0.07	0.00242	0.00052
rs1997572	CAV1	7	116200587	rs1049337	ILMN_2149226	CAV1	T	0.95240712	35.748	0.08	0.0005	9.66E-05
rs1997572	TES(dist=160022);CAV2(dist=80796)	7	116058859	rs1858810	ILMN_1735220	CAV2	G	1.0604326	131.425	0.08	0.00095	0.0002
rs1997572	TES(dist=170474);CAV2(dist=70344)	7	116069311	rs1476451	ILMN_1735220	CAV2	C	1.05787546	141.877	0.07	0.00229	0.00051
rs1997572	TES(dist=171138);CAV2(dist=69680)	7	116069975	rs7781492	ILMN_1735220	CAV2	G	1.06025943	142.541	0.08	0.00111	0.00024
rs1997572	TES(dist=174730);CAV2(dist=66088)	7	116073567	rs10464649	ILMN_1735220	CAV2	C	1.05991308	146.133	0.08	0.00124	0.00027
rs1997572	TES(dist=176614);CAV2(dist=64204)	7	116075451	rs13225166	ILMN_1735220	CAV2	T	1.0592371	148.017	0.07	0.00174	0.00038
rs1997572	TES(dist=185530);CAV2(dist=55288)	7	116084367	rs12706089	ILMN_1735220	CAV2	T	1.05999009	156.933	0.08	0.00121	0.00026
rs1997572	TES(dist=189884);CAV2(dist=50934)	7	116088721	rs1011441	ILMN_1735220	CAV2	G	0.94697333	161.287	0.06	0.01091	0.00275
rs1997572	TES(dist=195146);CAV2(dist=45672)	7	116093983	rs4727831	ILMN_1735220	CAV2	A	1.05963718	166.549	0.08	0.0014	0.00031
rs1997572	TES(dist=200070);CAV2(dist=40748)	7	116098907	rs142964648	ILMN_1735220	CAV2	C	1.05765088	171.473	0.07	0.00337	0.00075
rs1997572	TES(dist=200604);CAV2(dist=40214)	7	116099441	rs115449477	ILMN_1735220	CAV2	T	1.05943805	172.007	0.08	0.00144	0.00031
rs1997572	TES(dist=202424);CAV2(dist=38394)	7	116101261	rs28494601	ILMN_1735220	CAV2	A	1.05902308	173.827	0.07	0.00196	0.00043
rs1997572	TES(dist=204941);CAV2(dist=35877)	7	116103778	rs11769417	ILMN_1735220	CAV2	A	1.05944823	176.344	0.08	0.00143	0.00031
rs1997572	TES(dist=208549);CAV2(dist=32269)	7	116107386	rs9649392	ILMN_1735220	CAV2	G	1.05908726	179.952	0.07	0.00159	0.00035
rs1997572	TES(dist=209821);CAV2(dist=30997)	7	116108658	rs768108	ILMN_1735220	CAV2	A	1.05903514	181.224	0.07	0.00161	0.00035
rs1997572	TES(dist=211218);CAV2(dist=29600)	7	116110055	rs1007751	ILMN_1735220	CAV2	A	1.08056282	182.621	0.14	5.98E-07	1.31E-07
rs1997572	TES(dist=212241);CAV2(dist=28577)	7	116111078	rs7810505	ILMN_1735220	CAV2	G	1.08055837	183.644	0.14	5.99E-07	1.31E-07
rs1997572	TES(dist=214270);CAV2(dist=26548)	7	116113107	rs717957	ILMN_1735220	CAV2	G	1.07807902	185.673	0.13	1.26E-06	2.36E-07
rs1997572	TES(dist=214907);CAV2(dist=25911)	7	116113744	rs28495552	ILMN_1735220	CAV2	C	1.07901867	186.31	0.13	1.00E-06	1.88E-07
rs1997572	TES(dist=217004);CAV2(dist=23814)	7	116115841	rs12671606	ILMN_1735220	CAV2	G	1.07907885	188.407	0.13	1.05E-06	1.94E-07
rs1997572	TES(dist=217427);CAV2(dist=23391)	7	116116264	rs28557111	ILMN_1735220	CAV2	G	1.07902595	188.83	0.13	1.02E-06	1.90E-07
rs1997572	TES(dist=219493);CAV2(dist=21325)	7	116118330	rs926197	ILMN_1735220	CAV2	C	1.07903352	190.896	0.13	9.91E-07	1.88E-07
rs1997572	TES(dist=224106);CAV2(dist=16712)	7	116122943	rs6976316	ILMN_1735220	CAV2	G	1.07905547	195.509	0.13	9.78E-07	1.87E-07
rs1997572	TES(dist=227328);CAV2(dist=13490)	7	116126165	rs6975548	ILMN_1735220	CAV2	C	1.07694334	198.731	0.13	2.26E-06	4.26E-07
rs1997572	TES(dist=228045);CAV2(dist=12773)	7	116126882	rs6980387	ILMN_1735220	CAV2	A	1.07943477	199.448	0.13	8.70E-07	1.71E-07
rs1997572	TES(dist=230168);CAV2(dist=10650)	7	116129005	rs12531767	ILMN_1735220	CAV2	A	0.92507358	201.571	0.13	1.92E-06	3.71E-07
rs1997572	TES(dist=230316);CAV2(dist=10502)	7	116129153	rs6954077	ILMN_1735220	CAV2	G	1.07954925	201.719	0.13	8.39E-07	1.68E-07
rs1997572	TES(dist=230453);CAV2(dist=10365)	7	116129290	rs6953982	ILMN_1735220	CAV2	C	1.07954945	201.856	0.13	8.38E-07	1.68E-07
rs1997572	TES(dist=232146);CAV2(dist=8672)	7	116130983	rs10282556	ILMN_1735220	CAV2	G	1.07893627	203.549	0.12	7.74E-06	1.52E-06
rs1997572	TES(dist=233374);CAV2(dist=7444)	7	116132211	rs10228178	ILMN_1735220	CAV2	G	1.07937542	204.777	0.13	8.61E-07	1.71E-07
rs1997572	TES(dist=236179);CAV2(dist=4639)	7	116135016	rs2402080	ILMN_1735220	CAV2	G	1.07901404	207.582	0.13	8.90E-07	1.72E-07
rs1997572	TES(dist=238169);CAV2(dist=2649)	7	116137006	rs13223362	ILMN_1735220	CAV2	G	1.0789877	209.572	0.13	9.03E-07	1.73E-07
rs1997572	CAV2	7	116140524	rs2270188	ILMN_1735220	CAV2	G	1.08770806	213.09	0.16	1.83E-08	3.88E-09
rs1997572	CAV2	7	116140616	rs2270189	ILMN_1735220	CAV2	A	1.0877105	213.182	0.16	1.83E-08	3.88E-09
rs1997572	CAV2	7	116141778	rs3779511	ILMN_1735220	CAV2	G	1.08631687	214.344	0.13	7.96E-07	1.68E-07
rs1997572	CAV2	7	116142460	rs11983864	ILMN_1735220	CAV2	C	1.08642077	215.026	0.13	7.90E-07	1.68E-07
rs1997572	CAV2	7	116142462	rs11983865	ILMN_1735220	CAV2	G	1.08642077	215.028	0.13	7.90E-07	1.68E-07
rs1997572	CAV2	7	116142808	rs11980719	ILMN_1735220	CAV2	A	1.08632507	215.374	0.13	8.03E-07	1.68E-07
rs1997572	CAV2	7	116143802	rs13229461	ILMN_1735220	CAV2	T	1.08667693	216.368	0.13	7.42E-07	1.63E-07
rs1997572	CAV2	7	116145639	rs12668473	ILMN_1735220	CAV2	T	1.08627456	218.205	0.13	8.32E-07	1.68E-07
rs1997572	CAV2	7	116145696	rs28587043	ILMN_1735220	CAV2	A	1.0862727	218.262	0.13	8.32E-07	1.68E-07
rs1997572	CAV2	7	116145849	rs10271007	ILMN_1735220	CAV2	A	1.08765351	218.415	0.16	2.09E-08	4.24E-09
rs1997572	CAV2	7	116145957	rs4730743	ILMN_1735220	CAV2	A	1.0876455	218.523	0.16	2.10E-08	4.24E-09
rs1997572	CAV2	7	116147908	rs4727833	ILMN_1735220	CAV2	C	1.08754212	220.474	0.16	2.25E-08	4.49E-09
rs1997572	CAV2	7	116148370	rs1052990	ILMN_1735220	CAV2	G	1.08611155	220.936	0.13	8.81E-07	1.72E-07
rs1997572	CAV2	7	116148407	7:116148407:CA_C	ILMN_1735220	CAV2	CA	1.08778351	220.973	0.16	2.11E-08	4.24E-09
rs1997572	CAV2(dist=2560);CAV1(dist=13684)	7	116151155	rs6466579	ILMN_1735220	CAV2	T	1.08622859	223.721	0.16	4.54E-08	9.38E-09
rs1997572	CAV2(dist=3189);CAV1(dist=13055)	7	116151784	rs3919515	ILMN_1735220	CAV2	G	1.08609479	224.35	0.15	4.84E-08	9.88E-09
rs1997572	CAV2(dist=5420);CAV1(dist=10824)	7	116154015	rs17588172	ILMN_1735220	CAV2	G	1.08409836	226.581	0.13	2.02E-06	3.90E-07
rs1997572	CAV2(dist=5591);CAV1(dist=10653)	7	116154186	rs17516287	ILMN_1735220	CAV2	G	1.08406276	226.752	0.13	2.10E-06	4.04E-07
rs1997572	CAV2(dist=6131);CAV1(dist=10113)	7	116154726	rs6466580	ILMN_1735220	CAV2	C	1.08393276	227.292	0.13	2.16E-06	4.13E-07
rs1997572	CAV2(dist=8136);CAV1(dist=8108)	7	116156731	rs7811851	ILMN_1735220	CAV2	T	1.0837693	229.297	0.13	2.26E-06	4.26E-07

Supplementary Table 19. *continued*

rs1997572	CAV2(dist=8366);CAV1(dist=7878)	7	116156961	rs7795510	ILMN_1735220	CAV2	T	1.08525798	229.527	0.15	7.08E-08	1.40E-08
rs1997572	CAV2(dist=11366);CAV1(dist=4878)	7	116159961	rs2109514	ILMN_1735220	CAV2	G	1.08495353	232.527	0.15	6.89E-08	1.39E-08
rs1997572	CAV2(dist=11929);CAV1(dist=4315)	7	116160524	rs55883210	ILMN_1735220	CAV2	G	1.08484023	233.09	0.15	7.23E-08	1.42E-08
rs1997572	CAV1	7	116186241	rs3807989	ILMN_1735220	CAV2	A	1.05088825	258.807	0.05	0.02129	0.00606
rs1997572	CAV1	7	116191301	rs11773845	ILMN_1735220	CAV2	C	1.05107733	263.867	0.05	0.02041	0.00576
rs1997572	CAV1	7	116198621	rs1997571	ILMN_1735220	CAV2	G	1.05147979	271.187	0.05	0.01894	0.00526
rs1997572	CAV1	7	116198828	rs1997572	ILMN_1735220	CAV2	A	1.05147979	271.394	0.05	0.01894	0.00526
rs1997572	CAV1	7	116200587	rs1049337	ILMN_1735220	CAV2	T	0.93778156	273.153	0.08	0.00105	0.00022
rs1997572	CAV1(dist=2851);MET(dist=108369)	7	116204090	rs55691296	ILMN_1735220	CAV2	G	1.05448883	276.656	0.05	0.01544	0.00414
rs7508	PCM1(dist=25295);ASAH1(dist=1173)	8	17912752	rs399485	ILMN_1684054	ASAH1	A	1.07412947	29.742	0.07	0.00208	0.00046
rs7508	ASAH1	8	17913970	rs7508	ILMN_1684054	ASAH1	G	1.07001306	28.524	0.06	0.00509	0.00117
rs7508	PCM1(dist=25295);ASAH1(dist=1173)	8	17912752	rs399485	ILMN_2042595	PCM1	A	0.8749191	132.403	0.24	2.50E-13	4.24E-14
rs7508	PCM1(dist=25295);ASAH1(dist=1173)	8	17912752	rs399485	ILMN_1690487	PCM1	A	0.92534311	132.403	0.17	9.17E-09	1.95E-09
rs7508	ASAH1	8	17913970	rs7508	ILMN_2042595	PCM1	G	0.87328956	133.621	0.24	9.56E-14	1.90E-14
rs7508	ASAH1	8	17913970	rs7508	ILMN_1690487	PCM1	G	0.92193552	133.621	0.18	9.65E-10	1.89E-10
rs7915134	SYNPO2L	10	75404300	rs11000728	ILMN_1731157	MYOZ1	G	3.00407652	-2.785	0.48	2.88E-33	3.00E-34
rs7915134	SYNPO2L	10	75405635	rs41280404	ILMN_1731157	MYOZ1	G	2.99801538	-4.12	0.48	2.86E-33	3.00E-34
rs7915134	SYNPO2L	10	75406141	rs3740293	ILMN_1731157	MYOZ1	C	2.98307123	-4.626	0.48	2.25E-33	3.00E-34
rs7915134	SYNPO2L	10	75406912	rs34163229	ILMN_1731157	MYOZ1	T	2.98936747	-5.397	0.48	1.77E-33	3.00E-34
rs7915134	SYNPO2L	10	75407290	rs3812629	ILMN_1731157	MYOZ1	A	2.98850132	-5.775	0.48	1.77E-33	3.00E-34
rs7915134	SYNPO2L	10	75407649	rs4746139	ILMN_1731157	MYOZ1	C	2.98753429	-6.134	0.48	1.77E-33	3.00E-34
rs7915134	SYNPO2L	10	75409877	rs2177843	ILMN_1731157	MYOZ1	T	2.8927014	-8.362	0.47	1.85E-32	1.28E-33
rs7915134	SYNPO2L	10	75414344	rs60212594	ILMN_1731157	MYOZ1	C	2.94847322	-12.829	0.49	8.27E-34	3.00E-34
rs7915134	SYNPO2L	10	75415677	rs60632610	ILMN_1731157	MYOZ1	T	2.9312378	-14.162	0.48	8.27E-33	7.70E-34
rs7915134	SYNPO2L	10	75416789	rs12570126	ILMN_1731157	MYOZ1	G	2.750026	-15.274	0.46	7.71E-31	3.13E-32
rs7915134	SYNPO2L(dist=1417);AGAP5(dist=16784)	10	75417249	rs4746140	ILMN_1731157	MYOZ1	C	2.7501949	-15.734	0.46	7.30E-31	3.11E-32
rs7915134	SYNPO2L(dist=3831);AGAP5(dist=14370)	10	75419663	rs11000734	ILMN_1731157	MYOZ1	G	2.75697705	-18.148	0.46	7.33E-31	3.11E-32
rs7915134	SYNPO2L(dist=4282);AGAP5(dist=13919)	10	75420114	rs6480708	ILMN_1731157	MYOZ1	A	2.75782462	-18.599	0.46	7.30E-31	3.11E-32
rs7915134	SYNPO2L(dist=4348);AGAP5(dist=13853)	10	75420180	rs7915134	ILMN_1731157	MYOZ1	T	2.90236998	-18.665	0.47	2.54E-32	1.40E-33
rs7915134	SYNPO2L(dist=4738);AGAP5(dist=13463)	10	75420570	rs7900932	ILMN_1731157	MYOZ1	C	2.77653222	-19.055	0.41	6.56E-27	3.60E-28
rs7915134	SYNPO2L(dist=5376);AGAP5(dist=12825)	10	75421208	rs10824026	ILMN_1731157	MYOZ1	G	2.75802373	-19.693	0.46	7.05E-31	3.11E-32
rs7915134	SYNPO2L(dist=5614);AGAP5(dist=12587)	10	75421446	rs7394152	ILMN_1731157	MYOZ1	T	2.90552279	-19.931	0.47	2.50E-32	1.40E-33
rs7915134	SYNPO2L(dist=5748);AGAP5(dist=12453)	10	75421580	rs7394178	ILMN_1731157	MYOZ1	A	2.90580783	-20.065	0.47	2.50E-32	1.40E-33
rs7915134	SYNPO2L(dist=5816);AGAP5(dist=12385)	10	75421648	rs7394190	ILMN_1731157	MYOZ1	A	2.62208358	-20.133	0.44	3.17E-29	1.43E-30
rs7915134	SYNPO2L(dist=6482);AGAP5(dist=11719)	10	75422314	rs78249997	ILMN_1731157	MYOZ1	T	2.90687321	-20.799	0.47	5.02E-32	2.62E-33
rs7915134	SYNPO2L(dist=12464);AGAP5(dist=5737)	10	75428296	rs148321568	ILMN_1731157	MYOZ1	T	2.99855899	-26.781	0.48	1.50E-32	1.14E-33
rs7915134	SYNPO2L(dist=14169);AGAP5(dist=4032)	10	75430001	rs4745719	ILMN_1731157	MYOZ1	A	2.32146266	-28.486	0.32	2.03E-19	2.32E-20
rs7915134	AGAP5	10	75447582	rs147790633	ILMN_1731157	MYOZ1	C	2.93673503	-46.067	0.48	1.40E-32	1.14E-33
rs7915134	AGAP5	10	75449789	rs76443711	ILMN_1731157	MYOZ1	C	2.94878683	-48.274	0.46	4.31E-31	2.30E-32
rs7915134	AGAP5	10	75450901	rs138055607	ILMN_1731157	MYOZ1	G	2.94765777	-49.386	0.46	4.58E-31	2.32E-32
rs7915134	BMS1P4	10	75462510	rs76192127	ILMN_1731157	MYOZ1	C	2.79128851	-60.995	0.40	2.44E-25	1.54E-26
rs7915134	BMS1P4	10	75464587	rs4745721	ILMN_1731157	MYOZ1	A	2.7787703	-63.072	0.39	4.95E-25	3.13E-26
rs7915134	FUT11(dist=3034);CHCHD1(dist=2798)	10	75539010	rs11000775	ILMN_1731157	MYOZ1	C	2.76986681	-137.495	0.43	1.47E-28	6.85E-30
rs7915134	SYNPO2L	10	75404300	rs11000728	ILMN_1690253	SYNPO2L	G	0.89411254	11.53	0.11	1.18E-05	2.24E-06
rs7915134	SYNPO2L	10	75405635	rs41280404	ILMN_1690253	SYNPO2L	G	0.89448298	10.195	0.11	1.24E-05	2.32E-06
rs7915134	SYNPO2L	10	75406141	rs3740293	ILMN_1690253	SYNPO2L	C	0.89405737	9.689	0.12	9.27E-06	1.83E-06
rs7915134	SYNPO2L	10	75406912	rs34163229	ILMN_1690253	SYNPO2L	T	0.89273312	8.918	0.12	6.37E-06	1.27E-06
rs7915134	SYNPO2L	10	75407290	rs3812629	ILMN_1690253	SYNPO2L	A	0.89275655	8.54	0.12	6.37E-06	1.27E-06
rs7915134	SYNPO2L	10	75407649	rs4746139	ILMN_1690253	SYNPO2L	C	0.89275743	8.181	0.12	6.32E-06	1.27E-06
rs7915134	SYNPO2L	10	75409877	rs2177843	ILMN_1690253	SYNPO2L	T	0.89689721	5.953	0.11	1.24E-05	2.32E-06
rs7915134	SYNPO2L	10	75414344	rs60212594	ILMN_1690253	SYNPO2L	C	0.89474112	1.486	0.12	7.21E-06	1.44E-06
rs7915134	SYNPO2L	10	75415677	rs60632610	ILMN_1690253	SYNPO2L	T	0.89663867	0.153	0.11	1.47E-05	2.70E-06
rs7915134	SYNPO2L	10	75416789	rs12570126	ILMN_1690253	SYNPO2L	G	0.90603327	-0.959	0.10	7.64E-05	1.22E-05
rs7915134	SYNPO2L(dist=1417);AGAP5(dist=16784)	10	75417249	rs4746140	ILMN_1690253	SYNPO2L	C	0.90612251	-1.419	0.10	7.79E-05	1.24E-05
rs7915134	SYNPO2L(dist=3831);AGAP5(dist=14370)	10	75419663	rs11000734	ILMN_1690253	SYNPO2L	G	0.90560019	-3.833	0.10	7.15E-05	1.14E-05
rs7915134	SYNPO2L(dist=4282);AGAP5(dist=13919)	10	75420114	rs6480708	ILMN_1690253	SYNPO2L	A	0.9055406	-4.284	0.10	7.08E-05	1.14E-05
rs7915134	SYNPO2L(dist=4348);AGAP5(dist=13853)	10	75420180	rs7915134	ILMN_1690253	SYNPO2L	T	0.89628608	-4.35	0.11	1.18E-05	2.24E-06
rs7915134	SYNPO2L(dist=4738);AGAP5(dist=13463)	10	75420570	rs7900932	ILMN_1690253	SYNPO2L	C	0.89508922	-4.74	0.11	1.63E-05	2.95E-06
rs7915134	SYNPO2L(dist=5376);AGAP5(dist=12825)	10	75421208	rs10824026	ILMN_1690253	SYNPO2L	G	0.90553861	-5.378	0.10	7.06E-05	1.14E-05
rs7915134	SYNPO2L(dist=5614);AGAP5(dist=12587)	10	75421446	rs7394152	ILMN_1690253	SYNPO2L	T	0.89603974	-5.616	0.11	1.12E-05	2.16E-06
rs7915134	SYNPO2L(dist=5748);AGAP5(dist=12453)	10	75421580	rs7394178	ILMN_1690253	SYNPO2L	A	0.89601777	-5.75	0.11	1.12E-05	2.16E-06
rs7915134	SYNPO2L(dist=5816);AGAP5(dist=12385)	10	75421648	rs7394190	ILMN_1690253	SYNPO2L	A	0.90751878	-5.818	0.10	5.56E-05	8.83E-06
rs7915134	SYNPO2L(dist=6482);AGAP5(dist=11719)	10	75422314	rs78249997	ILMN_1690253	SYNPO2L	T	0.89568152	-6.484	0.11	1.12E-05	2.16E-06
rs7915134	SYNPO2L(dist=12464);AGAP5(dist=5737)	10	75428296	rs148321568	ILMN_1690253	SYNPO2L	T	0.89463526	-12.466	0.11	1.62E-05	2.95E-06
rs7915134	SYNPO2L(dist=14169);AGAP5(dist=4032)	10	75430001	rs4745719	ILMN_1690253	SYNPO2L	A	0.91552183	-14.171	0.08	0.00075	0.00015
rs7915134	AGAP5	10	75447582	rs147790633	ILMN_1690253	SYNPO2L	C	0.89576648	-31.752	0.11	1.28E-05	2.38E-06
rs7915134	AGAP5	10	75449789	rs76443711	ILMN_1690253	SYNPO2L	C	0.89553338	-33.959	0.11	2.14E-05	3.34E-06
rs7915134	AGAP5	10	75450901	rs138055607	ILMN_1690253	SYNPO2L	G	0.89552033	-35.071	0.11	2.13E-05	3.34E-06
rs7915134	BMS1P4	10	75462510	rs76192127	ILMN_1690253	SYNPO2L	C	0.89437999	-46.68	0.11	2.91E-05	4.44E-06
rs7915134	BMS1P4	10	75464587	rs4745721	ILMN_1690253	SYNPO2L	A	0.89455966	-48.757	0.11	3.07E-05	4.67E-06
rs7915134	FUT11(dist=3034);CHCHD1(dist=2798)	10	75539010	rs11000775	ILMN_1690253	SYNPO2L	C	0.89596597	-123.18	0.11	1.04E-05	2.05E-06
rs11598047	NEURL	10	105293517	rs12268602	ILMN_1773313	USMG5;;MIR1307	G	1.78548794	-137.294	0.05	0.03246	0.01018
rs75190942	KCNJ5	11	128764570	rs76097649	ILMN_1772224	KCNJ5	A	1.2748893	3.319	0.05	0.02767	0.00841
rs75190942	KCNJ5	11	128764571	rs75190942	ILMN_1772224	KCNJ5	A	1.27487598	3.32	0.05	0.02768	0.00841
rs883079	RBM19(dist=362559);TBX5(dist=25000)	12	114766735	rs10850315	ILMN_1742362	TBX5	G	0.91558313	79.512	0.04	0.04775	0.01656
rs883079	RBM19(dist=385050);TBX5(dist=2509)	12	114789226	rs2384407	ILMN_1742362	TBX5	G	0.89931636	57.021	0.07	0.00399	0.00089
rs883079	RBM19(dist=385174);TBX5(dist=2385)	12	114789350	rs2384408	ILMN_1742362	TBX5	A	0.8992702	56.897	0.05	0.03162	0.00988
rs883079	TBX5	12	114793240	rs883079	ILMN_1742362	TBX5	C	0.90512761	53.007	0.06	0.00846	0.00208
rs883079	TBX5	12	114797093	rs10507248	ILMN_1742362	TBX5	G	0.90842744	49.154	0.05	0.01653	0.00446
rs883079	TBX5	12	114797306	rs7955405	ILMN_1742362	TBX5	A	0.90842321	48.941	0.05	0.01651	0.00446
rs883079	TBX5	12	114799974	rs7312625	ILMN_1742362	TBX5	G	0.89763347	46.273	0.07	0.00413	0.00092
rs883079	TBX5	12	114800813	rs4767237	ILMN_1742362	TBX5	A	0.89102324	45.434	0.07	0.00181	0.00039
rs883079	TBX5	12	114801772	rs7135659	ILMN_1742362	TBX5	G	0.90215543	44.475	0.06	0.00827	0.00203
rs883079	TBX5	12	114802138	rs1895585	ILMN_1742362	TBX5	A	0.89071384	44.109	0.07	0.0018	0.00039
rs883079	TBX5	12	114802361	rs1946295	ILMN_1742362	TBX5	A	0.89075144	43.886	0.07	0.00169	0.00037
rs883079	TBX5	12	114802760	rs1946293	ILMN_1742362	TBX5	G	0.90209148	43.487	0.06	0.00821	0.00202
rs883079	TBX5	12	114804898	rs3825215	ILMN_1742362	TBX5	G	0.89066138	41.349	0.07	0.00175	0.00038
rs883079	TBX5	12	114805057	12:114805057:G_GGA	ILMN_1742362	TBX5	G	0.89805282	41.19	0.06	0.00552	0.00129
rs883079	TBX5	12	114806885	rs1895583	ILMN_1742362	TBX5	A	0.8912239	39.362	0.07	0.00259	0.00055
rs883079	TBX5	12	114807035	rs1895582	ILMN_1742362	TBX5	G	0.89030095	39.212	0.07	0.00209	0.00046
rs1152591	SYNE2	14	64649894	rs1255977	ILMN_1754579	SYNE2	A	0.86605868	330.211	0.18	8.45E-10	1.66E-10
rs1152591	SYNE2	14	64651663	rs1266927	ILMN_1754579	SYNE2	A	1.12503791	331.98	0.14	2.79E-07	5.93E-08
rs1152591	SYNE2	14	64654431	rs1255984	ILMN_1754579	SYNE2	A	0.86459472	334.748	0.20	6.99E-11	1.21E-11
rs1152591	SYNE2	14	64655161	rs1255986	ILMN_1754579	SYNE2	C	0.86455176	335.478	0.20	6.62E-11	1.17E-11
rs1152591	SYNE2	14	64657684	rs1255988	ILMN_1754579	SYNE2	C	0.86478275	338.001	0.20	7.50E-11	1.28E-11

Supplementary Table 19. *continued*

rs1152591	SYNE2	14	64667337	rs1152601	ILMN_1754579	SYNE2	C	1.12760316	347.654	0.13	8.31E-07	1.68E-07
rs1152591	SYNE2	14	64673560	14:64673560:AT_A	ILMN_1754579	SYNE2	AT	0.85698644	353.877	0.21	1.64E-11	2.70E-12
rs1152591	SYNE2	14	64674981	rs1152595	ILMN_1754579	SYNE2	C	1.1577718	355.298	0.20	7.79E-11	1.31E-11
rs1152591	SYNE2	14	64675044	rs1152594	ILMN_1754579	SYNE2	G	1.13152027	355.361	0.15	6.91E-08	1.39E-08
rs1152591	SYNE2	14	64675895	rs1152593	ILMN_1754579	SYNE2	T	1.13386829	356.212	0.15	1.02E-07	2.03E-08
rs1152591	SYNE2	14	64679960	rs2738413	ILMN_1754579	SYNE2	A	0.85588697	360.277	0.22	7.47E-12	1.25E-12
rs1152591	SYNE2	14	64680848	rs1152591	ILMN_1754579	SYNE2	A	0.8560054	361.165	0.22	8.59E-12	1.41E-12
rs1152591	SYNE2	14	64683926	rs1152589	ILMN_1754579	SYNE2	A	0.85720621	364.243	0.21	1.46E-11	2.43E-12
rs1152591	SYNE2	14	64690784	rs1152586	ILMN_1754579	SYNE2	T	0.87198427	371.101	0.17	8.28E-09	1.78E-09
rs1152591	SYNE2	14	64692630	rs1152582	ILMN_1754579	SYNE2	G	0.87443455	372.947	0.16	2.03E-08	4.24E-09
rs1152591	ESR2	14	64697485	rs1152577	ILMN_1754579	SYNE2	T	0.88386001	377.802	0.14	4.23E-07	9.18E-08
Variants identified in European ancestry analysis - eQTLs in European American samples												
rs11264280	KCNN3	1	154834183	rs1218582	ILMN_1751500	ADAM15	G	1.12973025	-188.859	0.07	0.00266	0.00054
rs11264280	KCNN3	1	154839799	rs6656494	ILMN_1751500	ADAM15	G	1.14203699	-183.243	0.08	0.00127	0.00026
rs11264280	KCNN3	1	154840287	rs10908444	ILMN_1751500	ADAM15	A	1.14205171	-182.755	0.08	0.00126	0.00026
rs11264280	KCNN3	1	154841415	1:154841415:TCTCT	ILMN_1751500	ADAM15	T	1.15311308	-181.627	0.09	0.00033	6.09E-05
rs11264280	KCNN3(dist=1597);PMVK(dist=52857)	1	154844351	1:154844351:G_GC	ILMN_1751500	ADAM15	GC	1.15259967	-178.691	0.09	0.00026	4.62E-05
rs11264280	KCNN3(dist=2730);PMVK(dist=51724)	1	154845484	rs6669791	ILMN_1751500	ADAM15	T	1.1440583	-177.558	0.08	0.00094	0.00019
rs11264280	KCNN3(dist=3520);PMVK(dist=50934)	1	154846274	rs883718	ILMN_1751500	ADAM15	T	1.14278728	-176.768	0.08	0.00101	0.0002
rs11264280	KCNN3(dist=6507);PMVK(dist=47945)	1	154849260	1:154849260:CCAA_	ILMN_1751500	ADAM15	C	1.15463205	-173.782	0.09	0.0002	3.44E-05
rs11264280	KCNN3(dist=6725);PMVK(dist=47729)	1	154849479	rs10796934	ILMN_1751500	ADAM15	C	1.14352621	-173.563	0.08	0.00092	0.00018
rs11264280	KCNN3(dist=6836);PMVK(dist=47618)	1	154849590	rs10908445	ILMN_1751500	ADAM15	A	1.14371567	-173.452	0.08	0.00098	0.0002
rs11264280	KCNN3(dist=7017);PMVK(dist=47437)	1	154849771	rs12069356	ILMN_1751500	ADAM15	A	1.14351288	-173.271	0.08	0.00092	0.00018
rs11264280	KCNN3(dist=9553);PMVK(dist=44901)	1	154852307	rs6683557	ILMN_1751500	ADAM15	G	1.14352742	-170.735	0.08	0.0009	0.00018
rs11264280	KCNN3(dist=10541);PMVK(dist=43913)	1	154853295	rs4845678	ILMN_1751500	ADAM15	C	1.14327364	-169.747	0.08	0.00092	0.00018
rs11264280	KCNN3(dist=16284);PMVK(dist=38170)	1	154859038	rs4845398	ILMN_1751500	ADAM15	C	1.14385352	-164.004	0.08	0.00086	0.00017
rs11264280	KCNN3(dist=16827);PMVK(dist=37627)	1	154859581	rs869506	ILMN_1751500	ADAM15	C	1.14460813	-163.461	0.08	0.00078	0.00016
rs11264280	KCNN3(dist=19810);PMVK(dist=34644)	1	154862564	1:154862564:C_CA	ILMN_1751500	ADAM15	CA	1.14410965	-160.478	0.08	0.00084	0.00017
rs11264280	KCNN3(dist=20441);PMVK(dist=34013)	1	154863195	rs4845680	ILMN_1751500	ADAM15	G	1.14386829	-159.847	0.08	0.00086	0.00017
rs11264280	KCNN3(dist=22371);PMVK(dist=32083)	1	154865125	rs1580943	ILMN_1751500	ADAM15	A	1.14388084	-157.917	0.08	0.00086	0.00017
rs11264280	KCNN3(dist=34677);PMVK(dist=19777)	1	154877431	1:154877431:T_TC	ILMN_1751500	ADAM15	TC	1.13778446	-145.611	0.07	0.00187	0.00038
rs11264280	KCNN3(dist=45595);PMVK(dist=8859)	1	154888348	1:154888348:TG_T	ILMN_1751500	ADAM15	T	1.11971372	-134.694	0.05	0.01655	0.00436
rs11264280	KCNN3(dist=48716);PMVK(dist=5736)	1	154891469	1:154891469:CTGT_	ILMN_1751500	ADAM15	C	1.14885878	-131.573	0.09	0.00031	5.63E-05
rs11264280	PBXIP1	1	154918352	rs41264253	ILMN_1756992	MUC1	A	1.21271419	244.355	0.05	0.02282	0.00644
rs651386	GORAB(dist=37630);PRRX1(dist=72709)	1	170560604	rs6658866	ILMN_1739496	PRRX1	G	0.88791122	-71.265	0.11	1.04E-05	2.09E-06
rs651386	GORAB(dist=38430);PRRX1(dist=71909)	1	170561404	rs6659754	ILMN_1739496	PRRX1	T	0.88900518	-70.465	0.11	1.32E-05	2.49E-06
rs651386	GORAB(dist=40109);PRRX1(dist=70230)	1	170563083	rs577827	ILMN_1739496	PRRX1	C	1.09741222	-68.786	0.07	0.00231	0.00048
rs651386	GORAB(dist=42175);PRRX1(dist=68164)	1	170565149	1:170565149:T_TGA	ILMN_1739496	PRRX1	TGACCAA	0.8932638	-66.72	0.10	3.89E-05	6.12E-06
rs651386	GORAB(dist=43031);PRRX1(dist=67308)	1	170566005	rs763567	ILMN_1739496	PRRX1	G	0.89327025	-65.864	0.10	3.89E-05	6.12E-06
rs651386	GORAB(dist=44463);PRRX1(dist=65876)	1	170567437	rs1928715	ILMN_1739496	PRRX1	T	0.89058846	-64.432	0.11	1.51E-05	2.80E-06
rs651386	GORAB(dist=45740);PRRX1(dist=64599)	1	170568714	rs12755237	ILMN_1739496	PRRX1	A	0.89207947	-63.155	0.11	1.85E-05	3.04E-06
rs651386	GORAB(dist=45922);PRRX1(dist=64417)	1	170568896	rs12742164	ILMN_1739496	PRRX1	G	0.88778945	-62.973	0.11	1.22E-05	2.36E-06
rs651386	GORAB(dist=46343);PRRX1(dist=63996)	1	170569317	rs3903239	ILMN_1739496	PRRX1	G	0.8920786	-62.552	0.11	1.86E-05	3.04E-06
rs651386	GORAB(dist=46715);PRRX1(dist=63624)	1	170569689	rs12760630	ILMN_1739496	PRRX1	A	0.89207947	-62.18	0.11	1.85E-05	3.04E-06
rs651386	GORAB(dist=47069);PRRX1(dist=63270)	1	170570043	rs10800529	ILMN_1739496	PRRX1	C	1.10454711	-61.826	0.06	0.00603	0.00135
rs651386	GORAB(dist=47525);PRRX1(dist=62814)	1	170570499	rs7412231	ILMN_1739496	PRRX1	C	0.89207947	-61.37	0.11	1.85E-05	3.04E-06
rs651386	GORAB(dist=48869);PRRX1(dist=61470)	1	170571843	rs1234230	ILMN_1739496	PRRX1	A	1.10515568	-60.026	0.09	0.0004	7.37E-05
rs651386	GORAB(dist=49972);PRRX1(dist=60367)	1	170572946	rs10919437	ILMN_1739496	PRRX1	A	0.8920786	-58.923	0.11	1.86E-05	3.04E-06
rs651386	GORAB(dist=50284);PRRX1(dist=60055)	1	170573258	rs61217505	ILMN_1739496	PRRX1	T	0.89207845	-58.611	0.11	1.85E-05	3.04E-06
rs651386	GORAB(dist=50840);PRRX1(dist=59499)	1	170573814	rs476810	ILMN_1739496	PRRX1	T	1.09545295	-58.055	0.07	0.00244	0.00049
rs651386	GORAB(dist=50953);PRRX1(dist=59379)	1	170573926	1:170573926:CCACT	ILMN_1739496	PRRX1	C	1.09312221	-57.943	0.05	0.02833	0.00844
rs651386	GORAB(dist=51954);PRRX1(dist=58385)	1	170574928	rs1234233	ILMN_1739496	PRRX1	C	1.09544615	-56.941	0.07	0.00244	0.00049
rs651386	GORAB(dist=52288);PRRX1(dist=58051)	1	170575261	1:170575261:CT_C	ILMN_1739496	PRRX1	C	0.89604371	-56.608	0.10	6.34E-05	1.04E-05
rs651386	GORAB(dist=53133);PRRX1(dist=57206)	1	170576107	rs2206062	ILMN_1739496	PRRX1	C	0.89207947	-55.762	0.11	1.85E-05	3.04E-06
rs651386	GORAB(dist=53764);PRRX1(dist=56575)	1	170576738	rs566850	ILMN_1739496	PRRX1	A	1.0954409	-55.131	0.07	0.00244	0.00049
rs651386	GORAB(dist=54081);PRRX1(dist=56258)	1	170577055	rs722597	ILMN_1739496	PRRX1	A	1.10371147	-54.814	0.06	0.00696	0.00159
rs651386	GORAB(dist=54261);PRRX1(dist=56078)	1	170577235	rs647438	ILMN_1739496	PRRX1	G	1.10513615	-54.634	0.09	0.0004	7.37E-05
rs651386	GORAB(dist=54866);PRRX1(dist=55473)	1	170577840	rs72482606	ILMN_1739496	PRRX1	A	1.10452045	-54.029	0.06	0.00603	0.00135
rs651386	GORAB(dist=55332);PRRX1(dist=55007)	1	170578306	rs10919440	ILMN_1739496	PRRX1	G	0.89207574	-53.563	0.11	1.85E-05	3.04E-06
rs651386	GORAB(dist=55613);PRRX1(dist=54726)	1	170578587	rs494339	ILMN_1739496	PRRX1	G	1.10346196	-53.282	0.08	0.00064	0.00013
rs651386	GORAB(dist=55641);PRRX1(dist=54698)	1	170578614	1:170578614:AT_A	ILMN_1739496	PRRX1	A	0.89069653	-53.255	0.11	1.77E-05	3.04E-06
rs651386	GORAB(dist=56115);PRRX1(dist=54224)	1	170579089	rs10919441	ILMN_1739496	PRRX1	A	1.09194487	-52.78	0.05	0.03097	0.00943
rs651386	GORAB(dist=56620);PRRX1(dist=53719)	1	170579594	rs546258	ILMN_1739496	PRRX1	C	1.0954364	-52.275	0.07	0.00245	0.00049
rs651386	GORAB(dist=57503);PRRX1(dist=52836)	1	170580477	rs553905	ILMN_1739496	PRRX1	A	1.09589929	-51.392	0.07	0.00224	0.00046
rs651386	GORAB(dist=58192);PRRX1(dist=52147)	1	170581165	1:170581165:CT_C	ILMN_1739496	PRRX1	C	0.89252445	-50.704	0.11	2.03E-05	3.26E-06
rs651386	GORAB(dist=58560);PRRX1(dist=51779)	1	170581534	rs2982131	ILMN_1739496	PRRX1	T	1.09542931	-50.335	0.07	0.00245	0.00049
rs651386	GORAB(dist=58660);PRRX1(dist=51679)	1	170581634	rs10919444	ILMN_1739496	PRRX1	A	0.89207947	-50.235	0.11	1.85E-05	3.04E-06
rs651386	GORAB(dist=58713);PRRX1(dist=51626)	1	170581687	rs34252585	ILMN_1739496	PRRX1	A	1.09051991	-50.182	0.05	0.0329	0.0101
rs651386	GORAB(dist=59601);PRRX1(dist=50738)	1	170582575	rs1952675	ILMN_1739496	PRRX1	G	0.89207947	-49.294	0.11	1.85E-05	3.04E-06
rs651386	GORAB(dist=60350);PRRX1(dist=49989)	1	170583324	rs77058424	ILMN_1739496	PRRX1	G	1.09542532	-48.545	0.07	0.00245	0.00049
rs651386	GORAB(dist=60537);PRRX1(dist=49802)	1	170583511	rs6677540	ILMN_1739496	PRRX1	A	0.89207858	-48.358	0.11	1.86E-05	3.04E-06
rs651386	GORAB(dist=60970);PRRX1(dist=49369)	1	170583944	rs6690642	ILMN_1739496	PRRX1	C	0.89207858	-47.925	0.11	1.86E-05	3.04E-06
rs651386	GORAB(dist=62123);PRRX1(dist=48216)	1	170585097	rs2206063	ILMN_1739496	PRRX1	C	1.09045	-46.772	0.05	0.03307	0.01014
rs651386	GORAB(dist=62858);PRRX1(dist=47481)	1	170585832	rs619456	ILMN_1739496	PRRX1	A	1.09542456	-46.037	0.07	0.00245	0.00049
rs651386	GORAB(dist=63341);PRRX1(dist=46998)	1	170586315	rs736791	ILMN_1739496	PRRX1	A	0.89002137	-45.554	0.11	1.39E-05	2.63E-06
rs651386	GORAB(dist=64241);PRRX1(dist=46098)	1	170587215	rs576736	ILMN_1739496	PRRX1	G	1.10266777	-44.654	0.06	0.00781	0.00182
rs651386	GORAB(dist=64366);PRRX1(dist=45973)	1	170587340	rs577676	ILMN_1739496	PRRX1	T	1.10760539	-44.529	0.07	0.00158	0.00032
rs651386	GORAB(dist=65124);PRRX1(dist=45213)	1	170588097	1:170588097:TTAG_	ILMN_1739496	PRRX1	T	0.89493375	-43.772	0.09	0.00016	2.80E-05
rs651386	GORAB(dist=65125);PRRX1(dist=45212)	1	170588098	1:170588098:TAGG_	ILMN_1739496	PRRX1	T	0.89412683	-43.771	0.10	4.46E-05	7.11E-06
rs651386	GORAB(dist=66936);PRRX1(dist=43403)	1	170589910	rs2022372	ILMN_1739496	PRRX1	A	0.89163872	-41.959	0.11	1.84E-05	3.04E-06
rs651386	GORAB(dist=67593);PRRX1(dist=42746)	1	170590567	rs12031871	ILMN_1739496	PRRX1	T	1.10048424	-41.302	0.06	0.01061	0.0026
rs651386	GORAB(dist=68336);PRRX1(dist=42003)	1	170591310	rs651386	ILMN_1739496	PRRX1	T	1.10719342	-40.559	0.07	0.00151	0.00031
rs651386	GORAB(dist=68389);PRRX1(dist=41950)	1	170591363	1:170591363:A_ATT	ILMN_1739496	PRRX1	A	0.89834049	-40.506	0.10	0.00011	1.83E-05
rs651386	GORAB(dist=68834);PRRX1(dist=41505)	1	170591808	rs10753817	ILMN_1739496	PRRX1	G	1.10044113	-40.061	0.06	0.01067	0.00261
rs651386	GORAB(dist=71095);PRRX1(dist=39244)	1	170594069	rs12072276	ILMN_1739496	PRRX1	G	1.10038628	-37.8	0.06	0.01074	0.00261
rs651386	GORAB(dist=71142);PRRX1(dist=39197)	1	170594116	rs10919446	ILMN_1739496	PRRX1	A	1.10038628	-37.753	0.06	0.01074	0.00261
rs651386	GORAB(dist=73098);PRRX1(dist=37241)	1	170596072	rs494521	ILMN_1739496	PRRX1	C	0.89489271	-35.797	0.11	3.05E-05	4.76E-06
rs651386	GORAB(dist=73284);PRRX1(dist=37055)	1	170596258	rs1234275	ILMN_1739496	PRRX1	A	0.89162938	-35.611	0.11	1.85E-05	3.04E-06
rs651386	GORAB(dist=73399);PRRX1(dist=36940)	1	170596373	rs1234274	ILMN_1739496	PRRX1	A	0.89160973	-35.496	0.11	1.84E-05	3.04E-06
rs651386	GORAB(dist=73571);PRRX1(dist=36768)	1	170596545	rs11577602	ILMN_1739496	PRRX1	T	1.10032785	-35.324	0.06	0.01082	0.00262
rs651386	GORAB(dist=73598);PRRX1(dist=36741)	1	170596572	rs10800530	ILMN_1739496	PRRX1	A	1.10032785	-35.297	0.06	0.01082	0.00262
rs651386	GORAB(dist=75213);PRRX1(dist=35126)	1	170598187	rs638704	ILMN_1739496	PRRX1	C	0.89162646	-33.682	0.11	1.85E-05	3.04E-06
rs651386	GORAB(dist=76599);PRRX1(dist=33740)	1	170599573	rs10919448	ILMN_1739496	PRRX1	C	1.10026119	-32.296	0.06	0.01091	0.00263
rs651386	GORAB(dist=78034);PRRX1(dist=32305)	1	170601008	rs189058353	ILMN_1739496	PRRX1	C	0.89785286	-30.861	0.09	0.00028	5.00E-05
rs651386	GORAB(dist=81148);PRRX1(dist=29191)	1	170604122	rs598993	ILMN_1739496	PRRX1	T	0.89394769	-27.747	0.11	2.34E-05	3.69E-06

Supplementary Table 19. *continued*

rs651386	GORAB(dist=81964);PRRX1(dist=28375)	1	170604938	rs541557	ILMN_1739496	PRRX1	A	0.89394563	-26.931	0.11	2.34E-05	3.69E-06
rs651386	GORAB(dist=85107);PRRX1(dist=25232)	1	170608081	rs539045	ILMN_1739496	PRRX1	C	0.89393706	-23.788	0.11	2.35E-05	3.69E-06
rs651386	GORAB(dist=86216);PRRX1(dist=24123)	1	170609190	rs473832	ILMN_1739496	PRRX1	A	0.89158617	-22.679	0.11	1.87E-05	3.05E-06
rs651386	GORAB(dist=86651);PRRX1(dist=23688)	1	170609625	rs580487	ILMN_1739496	PRRX1	T	0.89393517	-22.244	0.11	2.36E-05	3.70E-06
rs651386	GORAB(dist=89288);PRRX1(dist=21051)	1	170612262	rs492804	ILMN_1739496	PRRX1	C	0.89205821	-19.607	0.11	2.16E-05	3.41E-06
rs651386	GORAB(dist=89899);PRRX1(dist=20440)	1	170612873	rs639652	ILMN_1739496	PRRX1	G	0.89398545	-18.996	0.11	2.49E-05	3.88E-06
rs651386	GORAB(dist=90876);PRRX1(dist=19463)	1	170613850	rs654461	ILMN_1739496	PRRX1	A	0.89113485	-18.019	0.11	1.75E-05	3.04E-06
rs651386	GORAB(dist=90895);PRRX1(dist=19444)	1	170613869	rs567328	ILMN_1739496	PRRX1	T	0.8911111	-18	0.11	1.71E-05	3.04E-06
rs651386	GORAB(dist=91068);PRRX1(dist=19271)	1	170614042	rs544478	ILMN_1739496	PRRX1	C	0.89158272	-17.827	0.11	1.94E-05	3.13E-06
rs651386	GORAB(dist=92943);PRRX1(dist=17396)	1	170615917	rs593560	ILMN_1739496	PRRX1	G	0.89158272	-15.952	0.11	1.94E-05	3.13E-06
rs651386	GORAB(dist=93381);PRRX1(dist=16958)	1	170616355	rs2988392	ILMN_1739496	PRRX1	G	0.89399855	-15.514	0.11	2.50E-05	3.88E-06
rs651386	GORAB(dist=94332);PRRX1(dist=16007)	1	170617306	rs608930	ILMN_1739496	PRRX1	G	0.89051509	-14.563	0.11	1.46E-05	2.75E-06
rs651386	GORAB(dist=95317);PRRX1(dist=15022)	1	170618291	rs623752	ILMN_1739496	PRRX1	A	0.88733096	-13.578	0.12	7.71E-06	1.55E-06
rs651386	GORAB(dist=95408);PRRX1(dist=14931)	1	170618382	rs531007	ILMN_1739496	PRRX1	T	0.88733785	-13.487	0.12	7.64E-06	1.55E-06
rs651386	GORAB(dist=96633);PRRX1(dist=13706)	1	170619607	rs575432	ILMN_1739496	PRRX1	A	0.89937833	-12.262	0.09	0.00033	6.09E-05
rs651386	GORAB(dist=96956);PRRX1(dist=13383)	1	170619930	rs651822	ILMN_1739496	PRRX1	T	1.08759906	-11.939	0.05	0.03847	0.0123
rs651386	GORAB(dist=100135);PRRX1(dist=10204)	1	170623109	rs588837	ILMN_1739496	PRRX1	A	0.88960365	-8.76	0.11	1.06E-05	2.13E-06
rs651386	GORAB(dist=100946);PRRX1(dist=9393)	1	170623920	rs12089974	ILMN_1739496	PRRX1	A	1.08986034	-7.949	0.05	0.04149	0.01352
rs651386	GORAB(dist=105281);PRRX1(dist=5058)	1	170628255	rs680084	ILMN_1739496	PRRX1	G	0.89330897	-3.614	0.11	2.63E-05	4.09E-06
rs651386	GORAB(dist=108789);PRRX1(dist=1550)	1	170631763	rs629234	ILMN_1739496	PRRX1	T	0.89204547	-0.106	0.11	1.94E-05	3.13E-06
rs651386	PRRX1	1	170635002	rs525489	ILMN_1739496	PRRX1	T	0.8876368	3.133	0.12	5.48E-06	1.23E-06
rs651386	PRRX1	1	170635084	rs503706	ILMN_1739496	PRRX1	T	0.88764988	3.215	0.12	5.51E-06	1.23E-06
rs651386	PRRX1	1	170635369	rs501005	ILMN_1739496	PRRX1	A	0.89498695	3.5	0.10	3.84E-05	6.11E-06
rs651386	PRRX1	1	170636079	rs473133	ILMN_1739496	PRRX1	A	0.88781431	4.21	0.12	5.84E-06	1.26E-06
rs651386	PRRX1	1	170638658	rs10919449	ILMN_1739496	PRRX1	A	1.09065328	6.789	0.06	0.00599	0.00134
rs2723064	SLC1A4(dist=25049);CEP68(dist=7446)	2	65276049	rs1009360	ILMN_1808500	CEP68	C	0.84966902	-7.451	0.15	6.02E-08	1.34E-08
rs2723064	SLC1A4(dist=25452);CEP68(dist=7043)	2	65276452	rs1009358	ILMN_1808500	CEP68	C	0.81706074	-7.048	0.24	2.20E-13	3.12E-14
rs2723064	SLC1A4(dist=25736);CEP68(dist=6759)	2	65276736	rs2540951	ILMN_1808500	CEP68	G	0.8170737	-6.764	0.24	2.20E-13	3.12E-14
rs2723064	SLC1A4(dist=26367);CEP68(dist=6125)	2	65277366	2:65277366:CATTT	ILMN_1808500	CEP68	C	0.82605141	-6.134	0.22	6.64E-12	9.26E-13
rs2723064	SLC1A4(dist=28223);CEP68(dist=4272)	2	65279223	rs2540950	ILMN_1808500	CEP68	T	0.8172861	-4.277	0.24	9.35E-14	1.43E-14
rs2723064	SLC1A4(dist=28321);CEP68(dist=4174)	2	65279321	rs2723066	ILMN_1808500	CEP68	G	0.81761783	-4.179	0.24	1.06E-13	1.56E-14
rs2723064	SLC1A4(dist=28414);CEP68(dist=4081)	2	65279414	rs2723065	ILMN_1808500	CEP68	G	0.81720703	-4.086	0.24	2.26E-13	3.14E-14
rs2723064	SLC1A4(dist=28805);CEP68(dist=3690)	2	65279805	rs2723064	ILMN_1808500	CEP68	C	0.81735156	-3.695	0.24	2.51E-13	3.36E-14
rs2723064	SLC1A4(dist=29185);CEP68(dist=3310)	2	65280185	rs2723063	ILMN_1808500	CEP68	G	0.84143733	-3.315	0.18	2.24E-09	4.66E-10
rs2723064	SLC1A4(dist=29220);CEP68(dist=3275)	2	65280220	rs2723062	ILMN_1808500	CEP68	A	0.81796079	-3.28	0.24	1.36E-13	1.98E-14
rs2723064	CEP68	2	65283972	rs74181299	ILMN_1808500	CEP68	C	0.81902079	0.472	0.23	8.92E-13	1.23E-13
rs2723064	CEP68	2	65284231	rs2540949	ILMN_1808500	CEP68	T	0.82008726	0.731	0.23	9.43E-13	1.28E-13
rs2723064	CEP68	2	65284623	rs2540948	ILMN_1808500	CEP68	C	0.8205978	1.123	0.23	4.88E-13	6.64E-14
rs2723064	CEP68	2	65287896	rs2249105	ILMN_1808500	CEP68	G	0.8167069	4.396	0.23	1.72E-12	2.28E-13
rs2723064	CEP68	2	65289825	rs2540945	ILMN_1808500	CEP68	G	0.8158767	6.325	0.23	1.58E-12	2.16E-13
rs2723064	CEP68	2	65296280	rs2252867	ILMN_1808500	CEP68	C	0.81667979	12.78	0.23	1.73E-12	2.28E-13
rs6864727	PKD2L2	5	137245067	rs2097865	ILMN_1673478	FAM13B	T	0.92826351	142.583	0.09	0.00017	2.95E-05
rs6864727	PKD2L2	5	137247940	rs6864727	ILMN_1673478	FAM13B	C	0.92705206	139.71	0.09	0.00015	2.51E-05
rs6864727	FAM13B	5	137304877	rs6868053	ILMN_1673478	FAM13B	T	0.92717555	82.773	0.09	0.00017	2.95E-05
rs6864727	FAM13B	5	137305128	rs6882675	ILMN_1673478	FAM13B	T	0.92130238	82.522	0.10	6.85E-05	1.13E-05
rs6864727	WNT8A(dist=16287);NME5(dist=7375)	5	137443486	rs529526	ILMN_1673478	FAM13B	C	0.92496488	-55.836	0.09	0.00014	2.47E-05
rs11773845	CAV2	7	116140524	rs2270188	ILMN_2149226	CAV1	G	1.03895885	-24.315	0.06	0.00626	0.0014
rs11773845	CAV2	7	116140616	rs2270189	ILMN_2149226	CAV1	A	1.03897916	-24.223	0.06	0.00622	0.00139
rs11773845	CAV2	7	116145849	rs10271007	ILMN_2149226	CAV1	A	1.04007055	-18.99	0.07	0.00431	0.00091
rs11773845	CAV2	7	116145957	rs4730743	ILMN_2149226	CAV1	A	1.04009135	-18.882	0.07	0.00428	0.00091
rs11773845	CAV2	7	116147908	rs4727833	ILMN_2149226	CAV1	C	1.04046343	-16.931	0.07	0.00374	0.00078
rs11773845	CAV2	7	116148407	7:116148407:CA_C	ILMN_2149226	CAV1	CA	1.0405896	-16.432	0.07	0.00363	0.00077
rs11773845	CAV2(dist=2560);CAV1(dist=13684)	7	116151155	rs6466579	ILMN_2149226	CAV1	T	1.04061084	-13.684	0.07	0.00362	0.00077
rs11773845	CAV2(dist=3189);CAV1(dist=13055)	7	116151784	rs3919515	ILMN_2149226	CAV1	G	1.04060541	-13.055	0.07	0.00362	0.00077
rs11773845	CAV2(dist=8366);CAV1(dist=7878)	7	116156961	rs7795510	ILMN_2149226	CAV1	T	1.04054883	-7.878	0.07	0.00367	0.00077
rs11773845	CAV2(dist=11366);CAV1(dist=4878)	7	116159961	rs2109514	ILMN_2149226	CAV1	G	1.04036806	-4.878	0.07	0.00369	0.00077
rs11773845	CAV2(dist=11929);CAV1(dist=4315)	7	116160524	rs55883210	ILMN_2149226	CAV1	G	1.04036624	-4.315	0.07	0.00368	0.00077
rs11773845	CAV1	7	116169443	rs7778733	ILMN_2149226	CAV1	C	0.95302457	4.604	0.08	0.00107	0.00021
rs11773845	CAV1	7	116186241	rs3807989	ILMN_2149226	CAV1	A	1.04315421	21.402	0.07	0.00258	0.00052
rs11773845	CAV1	7	116191301	rs11773845	ILMN_2149226	CAV1	C	1.04321973	26.462	0.07	0.00251	0.00051
rs11773845	CAV1	7	116198621	rs1997571	ILMN_2149226	CAV1	G	1.04336824	33.782	0.07	0.00242	0.00049
rs11773845	CAV1	7	116198828	rs1997572	ILMN_2149226	CAV1	A	1.04336824	33.989	0.07	0.00242	0.00049
rs11773845	TES(dist=160022);CAV2(dist=80796)	7	116058859	rs1858810	ILMN_1735220	CAV2	G	1.0604326	131.425	0.08	0.00095	0.00019
rs11773845	TES(dist=170474);CAV2(dist=70344)	7	116069311	rs1476451	ILMN_1735220	CAV2	C	1.05787546	141.877	0.07	0.00229	0.00048
rs11773845	TES(dist=171138);CAV2(dist=69680)	7	116069975	rs7781492	ILMN_1735220	CAV2	G	1.06025943	142.541	0.08	0.00111	0.00022
rs11773845	TES(dist=174730);CAV2(dist=66088)	7	116073567	rs10464649	ILMN_1735220	CAV2	C	1.05991308	146.133	0.08	0.00124	0.00025
rs11773845	TES(dist=176614);CAV2(dist=64204)	7	116075451	rs13225166	ILMN_1735220	CAV2	T	1.0592371	148.017	0.07	0.00174	0.00036
rs11773845	TES(dist=185530);CAV2(dist=55288)	7	116084367	rs12706089	ILMN_1735220	CAV2	T	1.05999009	156.933	0.08	0.00121	0.00025
rs11773845	TES(dist=189884);CAV2(dist=50934)	7	116088721	rs1011441	ILMN_1735220	CAV2	G	0.94697333	161.287	0.06	0.01091	0.00263
rs11773845	TES(dist=195146);CAV2(dist=45672)	7	116093983	rs4727831	ILMN_1735220	CAV2	A	1.05963718	166.549	0.08	0.0014	0.00029
rs11773845	TES(dist=200070);CAV2(dist=40748)	7	116098907	rs142964648	ILMN_1735220	CAV2	C	1.05765088	171.473	0.07	0.00337	0.00071
rs11773845	TES(dist=200604);CAV2(dist=40214)	7	116099441	rs115449477	ILMN_1735220	CAV2	T	1.05943805	172.007	0.08	0.00144	0.00029
rs11773845	TES(dist=202424);CAV2(dist=38394)	7	116101261	rs28494601	ILMN_1735220	CAV2	A	1.05902308	173.827	0.07	0.00196	0.0004
rs11773845	TES(dist=204941);CAV2(dist=35877)	7	116103778	rs11769417	ILMN_1735220	CAV2	A	1.05944823	176.344	0.08	0.00143	0.00029
rs11773845	TES(dist=208549);CAV2(dist=32269)	7	116107386	rs9649392	ILMN_1735220	CAV2	G	1.05908726	179.952	0.07	0.00159	0.00032
rs11773845	TES(dist=209821);CAV2(dist=30997)	7	116108658	rs768108	ILMN_1735220	CAV2	A	1.05903514	181.224	0.07	0.00161	0.00033
rs11773845	TES(dist=211218);CAV2(dist=29600)	7	116110055	rs1007751	ILMN_1735220	CAV2	A	1.08056282	182.621	0.14	5.98E-07	1.50E-07
rs11773845	TES(dist=212241);CAV2(dist=28577)	7	116111078	rs7810505	ILMN_1735220	CAV2	G	1.08055837	183.644	0.14	5.99E-07	1.50E-07
rs11773845	TES(dist=214270);CAV2(dist=26548)	7	116113107	rs717957	ILMN_1735220	CAV2	G	1.07807902	185.673	0.13	1.26E-06	2.67E-07
rs11773845	TES(dist=214907);CAV2(dist=25911)	7	116113744	rs28495552	ILMN_1735220	CAV2	C	1.07901867	186.31	0.13	1.00E-06	2.13E-07
rs11773845	TES(dist=217004);CAV2(dist=23814)	7	116115841	rs12671606	ILMN_1735220	CAV2	G	1.07907885	188.407	0.13	1.05E-06	2.19E-07
rs11773845	TES(dist=217427);CAV2(dist=23391)	7	116116264	rs28557111	ILMN_1735220	CAV2	G	1.07902595	188.83	0.13	1.02E-06	2.15E-07
rs11773845	TES(dist=219493);CAV2(dist=21325)	7	116118330	rs926197	ILMN_1735220	CAV2	C	1.07903352	190.896	0.13	9.91E-07	2.13E-07
rs11773845	TES(dist=224106);CAV2(dist=16712)	7	116122943	rs6976316	ILMN_1735220	CAV2	G	1.07905547	195.509	0.13	9.78E-07	2.12E-07
rs11773845	TES(dist=227328);CAV2(dist=13490)	7	116126165	rs6975548	ILMN_1735220	CAV2	C	1.07694334	198.731	0.13	2.26E-06	4.79E-07
rs11773845	TES(dist=228045);CAV2(dist=12773)	7	116126882	rs6980387	ILMN_1735220	CAV2	A	1.07943477	199.448	0.13	8.70E-07	1.96E-07
rs11773845	TES(dist=230168);CAV2(dist=10650)	7	116129005	rs12531767	ILMN_1735220	CAV2	A	0.92507358	201.571	0.13	1.92E-06	4.19E-07
rs11773845	TES(dist=230316);CAV2(dist=10502)	7	116129153	rs6954077	ILMN_1735220	CAV2	G	1.07954925	201.719	0.13	8.39E-07	1.92E-07
rs11773845	TES(dist=230453);CAV2(dist=10365)	7	116129290	rs6953982	ILMN_1735220	CAV2	C	1.07954945	201.856	0.13	8.38E-07	1.92E-07
rs11773845	TES(dist=232146);CAV2(dist=8672)	7	116130983	rs10282556	ILMN_1735220	CAV2	G	1.07893627	203.549	0.12	7.74E-06	1.55E-06
rs11773845	TES(dist=233374);CAV2(dist=7444)	7	116132211	rs10228178	ILMN_1735220	CAV2	G	1.07937542	204.777	0.13	8.61E-07	1.96E-07
rs11773845	TES(dist=236179);CAV2(dist=4639)	7	116135016	rs2402080	ILMN_1735220	CAV2	G	1.07901404	207.582	0.13	8.90E-07	1.96E-07
rs11773845	TES(dist=238169);CAV2(dist=2649)	7	116137006	rs13223362	ILMN_1735220	CAV2	G	1.0789877	209.572	0.13	9.03E-07	1.97E-07
rs11773845	CAV2	7	116140524	rs2270188	ILMN_1735220	CAV2	G	1.08770806	213.09	0.16	1.83E-08	4.20E-09
rs11773845	CAV2	7	116140616	rs2270189	ILMN_1735220	CAV2	A	1.0877105	213.182	0.16	1.83E-08	4.20E-09

Supplementary Table 19. *continued*

rs11773845	CAV2	7	116141778	rs3779511	ILMN_1735220	CAV2	G	1.08631687	214.344	0.13	7.96E-07	1.92E-07
rs11773845	CAV2	7	116142460	rs11983864	ILMN_1735220	CAV2	C	1.08642077	215.026	0.13	7.90E-07	1.92E-07
rs11773845	CAV2	7	116142462	rs11983865	ILMN_1735220	CAV2	G	1.08642077	215.028	0.13	7.90E-07	1.92E-07
rs11773845	CAV2	7	116142808	rs11980719	ILMN_1735220	CAV2	A	1.08632507	215.374	0.13	8.03E-07	1.92E-07
rs11773845	CAV2	7	116143802	rs13229461	ILMN_1735220	CAV2	T	1.08667693	216.368	0.13	7.42E-07	1.86E-07
rs11773845	CAV2	7	116145639	rs12668473	ILMN_1735220	CAV2	T	1.08627456	218.205	0.13	8.32E-07	1.92E-07
rs11773845	CAV2	7	116145696	rs28587043	ILMN_1735220	CAV2	A	1.0862727	218.262	0.13	8.32E-07	1.92E-07
rs11773845	CAV2	7	116145849	rs10271007	ILMN_1735220	CAV2	A	1.08765351	218.415	0.16	2.09E-08	4.65E-09
rs11773845	CAV2	7	116145957	rs4730743	ILMN_1735220	CAV2	A	1.0876455	218.523	0.16	2.10E-08	4.65E-09
rs11773845	CAV2	7	116147908	rs4727833	ILMN_1735220	CAV2	C	1.08754212	220.474	0.16	2.25E-08	4.91E-09
rs11773845	CAV2	7	116148370	rs1052990	ILMN_1735220	CAV2	G	1.08611155	220.936	0.13	8.81E-07	1.96E-07
rs11773845	CAV2	7	116148407	7:116148407:CA_C	ILMN_1735220	CAV2	CA	1.08778351	220.973	0.16	2.11E-08	4.65E-09
rs11773845	CAV2(dist=2560);CAV1(dist=13684)	7	116151155	rs6466579	ILMN_1735220	CAV2	T	1.08622859	223.721	0.16	4.54E-08	1.02E-08
rs11773845	CAV2(dist=3189);CAV1(dist=13055)	7	116151784	rs3919515	ILMN_1735220	CAV2	G	1.08609479	224.35	0.15	4.84E-08	1.08E-08
rs11773845	CAV2(dist=5420);CAV1(dist=10824)	7	116154015	rs17588172	ILMN_1735220	CAV2	G	1.08409836	226.581	0.13	2.02E-06	4.40E-07
rs11773845	CAV2(dist=5591);CAV1(dist=10653)	7	116154186	rs17516287	ILMN_1735220	CAV2	G	1.08406276	226.752	0.13	2.10E-06	4.55E-07
rs11773845	CAV2(dist=6131);CAV1(dist=10113)	7	116154726	rs6466580	ILMN_1735220	CAV2	C	1.08393276	227.292	0.13	2.16E-06	4.65E-07
rs11773845	CAV2(dist=8136);CAV1(dist=8108)	7	116156731	rs7811851	ILMN_1735220	CAV2	T	1.0837693	229.297	0.13	2.26E-06	4.79E-07
rs11773845	CAV2(dist=8366);CAV1(dist=7878)	7	116156961	rs7795510	ILMN_1735220	CAV2	T	1.08525798	229.527	0.15	7.08E-08	1.55E-08
rs11773845	CAV2(dist=11366);CAV1(dist=4878)	7	116159961	rs2109514	ILMN_1735220	CAV2	G	1.08495353	232.527	0.15	6.89E-08	1.53E-08
rs11773845	CAV2(dist=11929);CAV1(dist=4315)	7	116160524	rs55883210	ILMN_1735220	CAV2	G	1.08484023	233.09	0.15	7.23E-08	1.56E-08
rs11773845	CAV1	7	116186241	rs3807989	ILMN_1735220	CAV2	A	1.05088825	258.807	0.05	0.02129	0.00592
rs11773845	CAV1	7	116191301	rs11773845	ILMN_1735220	CAV2	C	1.05107733	263.867	0.05	0.02041	0.00563
rs11773845	CAV1	7	116198621	rs1997571	ILMN_1735220	CAV2	G	1.05147979	271.187	0.05	0.01894	0.00513
rs11773845	CAV1	7	116198828	rs1997572	ILMN_1735220	CAV2	A	1.05147979	271.394	0.05	0.01894	0.00513
rs7508	PCM1(dist=25295);ASAH1(dist=1173)	8	17912752	rs399485	ILMN_1684054	ASAH1	A	1.07412947	29.742	0.07	0.00208	0.00043
rs7508	ASAH1	8	17913970	rs7508	ILMN_1684054	ASAH1	G	1.07001306	28.524	0.06	0.00509	0.00111
rs7508	PCM1(dist=25295);ASAH1(dist=1173)	8	17912752	rs399485	ILMN_2042595	PCM1	A	0.8749191	132.403	0.24	2.50E-13	3.36E-14
rs7508	PCM1(dist=25295);ASAH1(dist=1173)	8	17912752	rs399485	ILMN_1690487	PCM1	A	0.92534311	132.403	0.17	9.17E-09	2.08E-09
rs7508	ASAH1	8	17913970	rs7508	ILMN_2042595	PCM1	G	0.87328956	133.621	0.24	9.56E-14	1.43E-14
rs7508	ASAH1	8	17913970	rs7508	ILMN_1690487	PCM1	G	0.92193552	133.621	0.18	9.65E-10	1.94E-10
rs10824026	SYNPO2L	10	75404300	rs11000728	ILMN_1731157	MYOZ1	G	3.00407652	-2.785	0.48	2.88E-33	3.09E-34
rs10824026	SYNPO2L	10	75405635	rs41280404	ILMN_1731157	MYOZ1	G	2.99801538	-4.12	0.48	2.86E-33	3.09E-34
rs10824026	SYNPO2L	10	75406141	rs3740293	ILMN_1731157	MYOZ1	C	2.98307123	-4.626	0.48	2.25E-33	3.09E-34
rs10824026	SYNPO2L	10	75406912	rs34163229	ILMN_1731157	MYOZ1	T	2.98936747	-5.397	0.48	1.77E-33	3.09E-34
rs10824026	SYNPO2L	10	75407290	rs3812629	ILMN_1731157	MYOZ1	A	2.98850132	-5.775	0.48	1.77E-33	3.09E-34
rs10824026	SYNPO2L	10	75407649	rs4746139	ILMN_1731157	MYOZ1	C	2.98753429	-6.134	0.48	1.77E-33	3.09E-34
rs10824026	SYNPO2L	10	75409877	rs2177843	ILMN_1731157	MYOZ1	T	2.8927014	-8.362	0.47	1.85E-32	1.32E-33
rs10824026	SYNPO2L	10	75414344	rs60212594	ILMN_1731157	MYOZ1	C	2.94847322	-12.829	0.49	8.27E-34	3.09E-34
rs10824026	SYNPO2L	10	75415677	rs60632610	ILMN_1731157	MYOZ1	T	2.9312378	-14.162	0.48	8.27E-33	7.93E-34
rs10824026	SYNPO2L	10	75416789	rs12570126	ILMN_1731157	MYOZ1	G	2.750026	-15.274	0.46	7.71E-31	3.22E-32
rs10824026	SYNPO2L(dist=1417);AGAP5(dist=16784)	10	75417249	rs4746140	ILMN_1731157	MYOZ1	C	2.7501949	-15.734	0.46	7.30E-31	3.21E-32
rs10824026	SYNPO2L(dist=3831);AGAP5(dist=14370)	10	75419663	rs11000734	ILMN_1731157	MYOZ1	G	2.75697705	-18.148	0.46	7.33E-31	3.21E-32
rs10824026	SYNPO2L(dist=4282);AGAP5(dist=13919)	10	75420114	rs6480708	ILMN_1731157	MYOZ1	A	2.75782462	-18.599	0.46	7.30E-31	3.21E-32
rs10824026	SYNPO2L(dist=4348);AGAP5(dist=13853)	10	75420180	rs7915134	ILMN_1731157	MYOZ1	T	2.90236998	-18.665	0.47	2.54E-32	1.45E-33
rs10824026	SYNPO2L(dist=4738);AGAP5(dist=13463)	10	75420570	rs7900932	ILMN_1731157	MYOZ1	C	2.77653222	-19.055	0.41	6.56E-27	2.65E-28
rs10824026	SYNPO2L(dist=5376);AGAP5(dist=12825)	10	75421208	rs10824026	ILMN_1731157	MYOZ1	G	2.75802373	-19.693	0.46	7.05E-31	3.21E-32
rs10824026	SYNPO2L(dist=5614);AGAP5(dist=12587)	10	75421446	rs7394152	ILMN_1731157	MYOZ1	T	2.90552279	-19.931	0.47	2.50E-32	1.45E-33
rs10824026	SYNPO2L(dist=5748);AGAP5(dist=12453)	10	75421580	rs7394178	ILMN_1731157	MYOZ1	A	2.90580783	-20.065	0.47	2.50E-32	1.45E-33
rs10824026	SYNPO2L(dist=5816);AGAP5(dist=12385)	10	75421648	rs7394190	ILMN_1731157	MYOZ1	A	2.62208358	-20.133	0.44	3.17E-29	1.41E-30
rs10824026	SYNPO2L(dist=6482);AGAP5(dist=11719)	10	75422314	rs78249997	ILMN_1731157	MYOZ1	T	2.90687321	-20.799	0.47	5.02E-32	2.70E-33
rs10824026	SYNPO2L(dist=12464);AGAP5(dist=5737)	10	75428296	rs148321568	ILMN_1731157	MYOZ1	T	2.99855899	-26.781	0.48	1.50E-32	1.17E-33
rs10824026	SYNPO2L(dist=14169);AGAP5(dist=4032)	10	75430001	rs4745719	ILMN_1731157	MYOZ1	A	2.32146266	-28.486	0.32	2.03E-19	1.72E-20
rs10824026	SYNPO2L(dist=15246);AGAP5(dist=2955)	10	75431078	rs3878005	ILMN_1731157	MYOZ1	A	2.98365345	-29.563	0.45	4.01E-30	1.72E-31
rs10824026	AGAP5	10	75447582	rs147790633	ILMN_1731157	MYOZ1	C	2.93673503	-46.067	0.48	1.40E-32	1.17E-33
rs10824026	AGAP5	10	75449789	rs76443711	ILMN_1731157	MYOZ1	C	2.94878683	-48.274	0.46	4.31E-31	2.37E-32
rs10824026	AGAP5	10	75450901	rs138055607	ILMN_1731157	MYOZ1	G	2.94765777	-49.386	0.46	4.58E-31	2.39E-32
rs10824026	BMS1P4	10	75462510	rs76192127	ILMN_1731157	MYOZ1	C	2.79128851	-60.995	0.40	2.44E-25	1.11E-26
rs10824026	BMS1P4	10	75464587	rs4745721	ILMN_1731157	MYOZ1	A	2.7787703	-63.072	0.39	4.95E-25	2.29E-26
rs10824026	ZSWIM8	10	75559077	rs11000780	ILMN_1731157	MYOZ1	A	2.77058261	-157.562	0.43	1.42E-28	6.48E-30
rs10824026	NDST2	10	75562108	rs2075641	ILMN_1731157	MYOZ1	A	2.75009025	-160.593	0.43	2.13E-28	9.64E-30
rs10824026	CAMK2G	10	75573778	rs2306327	ILMN_1731157	MYOZ1	T	2.73975582	-172.263	0.43	2.89E-28	1.17E-29
rs10824026	CAMK2G	10	75575138	rs113799665	ILMN_1731157	MYOZ1	T	2.73963632	-173.623	0.43	2.92E-28	1.17E-29
rs10824026	CAMK2G	10	75576405	rs12220394	ILMN_1731157	MYOZ1	C	2.73947506	-174.89	0.43	2.94E-28	1.17E-29
rs10824026	CAMK2G	10	75576483	rs12217245	ILMN_1731157	MYOZ1	C	2.73947506	-174.968	0.43	2.94E-28	1.17E-29
rs10824026	CAMK2G	10	75578720	rs4746151	ILMN_1731157	MYOZ1	T	2.73860298	-177.205	0.43	4.27E-28	1.63E-29
rs10824026	CAMK2G	10	75578948	rs3843939	ILMN_1731157	MYOZ1	C	2.73851298	-177.433	0.43	4.29E-28	1.63E-29
rs10824026	CAMK2G	10	75580226	rs188726810	ILMN_1731157	MYOZ1	T	2.59219869	-178.711	0.41	1.63E-26	6.80E-28
rs10824026	CAMK2G	10	75583034	rs59693993	ILMN_1731157	MYOZ1	T	2.7314213	-181.519	0.43	4.60E-28	1.70E-29
rs10824026	CAMK2G	10	75585307	rs2242254	ILMN_1731157	MYOZ1	A	2.7377255	-183.792	0.43	5.84E-28	2.13E-29
rs10824026	SYNPO2L	10	75404300	rs11000728	ILMN_1690253	SYNPO2L	G	0.89411254	11.53	0.11	1.18E-05	2.28E-06
rs10824026	SYNPO2L	10	75405635	rs41280404	ILMN_1690253	SYNPO2L	G	0.89448298	10.195	0.11	1.24E-05	2.37E-06
rs10824026	SYNPO2L	10	75406141	rs3740293	ILMN_1690253	SYNPO2L	C	0.89405737	9.689	0.12	9.27E-06	1.87E-06
rs10824026	SYNPO2L	10	75406912	rs34163229	ILMN_1690253	SYNPO2L	T	0.89273312	8.918	0.12	6.37E-06	1.33E-06
rs10824026	SYNPO2L	10	75407290	rs3812629	ILMN_1690253	SYNPO2L	A	0.89275655	8.54	0.12	6.37E-06	1.33E-06
rs10824026	SYNPO2L	10	75407649	rs4746139	ILMN_1690253	SYNPO2L	C	0.89275743	8.181	0.12	6.32E-06	1.33E-06
rs10824026	SYNPO2L	10	75409877	rs2177843	ILMN_1690253	SYNPO2L	T	0.89689721	5.953	0.11	1.24E-05	2.37E-06
rs10824026	SYNPO2L	10	75414344	rs60212594	ILMN_1690253	SYNPO2L	C	0.89474112	1.486	0.12	7.21E-06	1.47E-06
rs10824026	SYNPO2L	10	75415677	rs60632610	ILMN_1690253	SYNPO2L	T	0.89663867	0.153	0.11	1.47E-05	2.75E-06
rs10824026	SYNPO2L	10	75416789	rs12570126	ILMN_1690253	SYNPO2L	G	0.90603327	-0.959	0.10	7.64E-05	1.24E-05
rs10824026	SYNPO2L(dist=1417);AGAP5(dist=16784)	10	75417249	rs4746140	ILMN_1690253	SYNPO2L	C	0.90612251	-1.419	0.10	7.79E-05	1.26E-05
rs10824026	SYNPO2L(dist=3831);AGAP5(dist=14370)	10	75419663	rs11000734	ILMN_1690253	SYNPO2L	G	0.90560019	-3.833	0.10	7.15E-05	1.16E-05
rs10824026	SYNPO2L(dist=4282);AGAP5(dist=13919)	10	75420114	rs6480708	ILMN_1690253	SYNPO2L	A	0.9055406	-4.284	0.10	7.08E-05	1.15E-05
rs10824026	SYNPO2L(dist=4348);AGAP5(dist=13853)	10	75420180	rs7915134	ILMN_1690253	SYNPO2L	T	0.89628608	-4.35	0.11	1.18E-05	2.28E-06
rs10824026	SYNPO2L(dist=4738);AGAP5(dist=13463)	10	75420570	rs7900932	ILMN_1690253	SYNPO2L	C	0.89508922	-4.74	0.11	1.63E-05	3.01E-06
rs10824026	SYNPO2L(dist=5376);AGAP5(dist=12825)	10	75421208	rs10824026	ILMN_1690253	SYNPO2L	G	0.90553861	-5.378	0.10	7.06E-05	1.15E-05
rs10824026	SYNPO2L(dist=5614);AGAP5(dist=12587)	10	75421446	rs7394152	ILMN_1690253	SYNPO2L	T	0.89603974	-5.616	0.11	1.12E-05	2.20E-06
rs10824026	SYNPO2L(dist=5748);AGAP5(dist=12453)	10	75421580	rs7394178	ILMN_1690253	SYNPO2L	A	0.89601777	-5.75	0.11	1.12E-05	2.20E-06
rs10824026	SYNPO2L(dist=5816);AGAP5(dist=12385)	10	75421648	rs7394190	ILMN_1690253	SYNPO2L	A	0.90751878	-5.818	0.10	5.56E-05	9.04E-06
rs10824026	SYNPO2L(dist=6482);AGAP5(dist=11719)	10	75422314	rs78249997	ILMN_1690253	SYNPO2L	T	0.89568152	-6.484	0.11	1.12E-05	2.20E-06
rs10824026	SYNPO2L(dist=12464);AGAP5(dist=5737)	10	75428296	rs148321568	ILMN_1690253	SYNPO2L	T	0.89463526	-12.466	0.11	1.62E-05	3.01E-06
rs10824026	SYNPO2L(dist=14169);AGAP5(dist=4032)	10	75430001	rs4745719	ILMN_1690253	SYNPO2L	A	0.91552183	-14.171	0.08	0.00075	0.00015
rs10824026	SYNPO2L(dist=15246);AGAP5(dist=2955)	10	75431078	rs3878005	ILMN_1690253	SYNPO2L	A	0.89765835	-15.248	0.10	6.88E-05	1.13E-05
rs10824026	AGAP5	10	75447582	rs147790633	ILMN_1690253	SYNPO2L	C	0.89576648	-31.752	0.11	1.28E-05	2.44E-06
rs10824026	AGAP5	10	75449789	rs76443711	ILMN_1690253	SYNPO2L	C	0.89553338	-33.959	0.11	2.14E-05	3.41E-06

Supplementary Table 19. *continued*

rs10824026	AGAP5	10	75450901	rs138055607	ILMN_1690253	SYNPO2L	G	0.89552033	-35.071	0.11	2.13E-05	3.41E-06
rs10824026	BMS1P4	10	75462510	rs76192127	ILMN_1690253	SYNPO2L	C	0.89437999	-46.68	0.11	2.91E-05	4.54E-06
rs10824026	BMS1P4	10	75464587	rs4745721	ILMN_1690253	SYNPO2L	A	0.89455966	-48.757	0.11	3.07E-05	4.78E-06
rs10824026	ZSWIM8	10	75559077	rs11000780	ILMN_1690253	SYNPO2L	A	0.8957955	-143.247	0.12	9.88E-06	1.99E-06
rs10824026	NDST2	10	75562108	rs2075641	ILMN_1690253	SYNPO2L	A	0.89456032	-146.278	0.12	5.81E-06	1.26E-06
rs10824026	CAMK2G	10	75573778	rs2306327	ILMN_1690253	SYNPO2L	T	0.89462393	-157.948	0.12	5.57E-06	1.23E-06
rs10824026	CAMK2G	10	75575138	rs113799665	ILMN_1690253	SYNPO2L	T	0.89464168	-159.308	0.12	5.60E-06	1.23E-06
rs10824026	CAMK2G	10	75576405	rs12220394	ILMN_1690253	SYNPO2L	C	0.8946596	-160.575	0.12	5.63E-06	1.23E-06
rs10824026	CAMK2G	10	75576483	rs12217245	ILMN_1690253	SYNPO2L	C	0.8946596	-160.653	0.12	5.63E-06	1.23E-06
rs10824026	CAMK2G	10	75578720	rs4746151	ILMN_1690253	SYNPO2L	T	0.89477294	-162.89	0.12	6.15E-06	1.31E-06
rs10824026	CAMK2G	10	75578948	rs3843939	ILMN_1690253	SYNPO2L	C	0.89478041	-163.118	0.12	6.16E-06	1.31E-06
rs10824026	CAMK2G	10	75580226	rs188726810	ILMN_1690253	SYNPO2L	T	0.89854223	-164.396	0.12	6.95E-06	1.43E-06
rs10824026	CAMK2G	10	75583034	rs59693993	ILMN_1690253	SYNPO2L	T	0.8953691	-167.204	0.12	6.92E-06	1.43E-06
rs10824026	CAMK2G	10	75585307	rs2242254	ILMN_1690253	SYNPO2L	A	0.89513094	-169.477	0.12	7.19E-06	1.47E-06
rs11598047	NEURL	10	105293517	rs12268602	ILMN_1773313	USMG5;;MIR1307	G	1.78548794	-137.294	0.05	0.03246	0.00996
rs75190942	KCNJ5	11	128764570	rs76097649	ILMN_1772224	KCNJ5	A	1.2748893	3.319	0.05	0.02767	0.00822
rs75190942	KCNJ5	11	128764571	rs75190942	ILMN_1772224	KCNJ5	A	1.27487598	3.32	0.05	0.02768	0.00822
rs883079	RBM19(dist=362559);TBX5(dist=25000)	12	114766735	rs10850315	ILMN_1742362	TBX5	G	0.91558313	79.512	0.04	0.04775	0.01621
rs883079	RBM19(dist=385050);TBX5(dist=2509)	12	114789226	rs2384407	ILMN_1742362	TBX5	G	0.89931636	57.021	0.07	0.00399	0.00084
rs883079	RBM19(dist=385174);TBX5(dist=2385)	12	114789350	rs2384408	ILMN_1742362	TBX5	A	0.8992702	56.897	0.05	0.03162	0.00966
rs883079	TBX5	12	114793240	rs883079	ILMN_1742362	TBX5	C	0.90512761	53.007	0.06	0.00846	0.00198
rs883079	TBX5	12	114797093	rs10507248	ILMN_1742362	TBX5	G	0.90842744	49.154	0.05	0.01653	0.00436
rs883079	TBX5	12	114797306	rs7955405	ILMN_1742362	TBX5	A	0.90842321	48.941	0.05	0.01651	0.00436
rs883079	TBX5	12	114799974	rs7312625	ILMN_1742362	TBX5	G	0.89763347	46.273	0.07	0.00413	0.00087
rs883079	TBX5	12	114800813	rs4767237	ILMN_1742362	TBX5	A	0.89102324	45.434	0.07	0.00181	0.00037
rs883079	TBX5	12	114801772	rs7135659	ILMN_1742362	TBX5	G	0.90215543	44.475	0.06	0.00827	0.00193
rs883079	TBX5	12	114802138	rs1895585	ILMN_1742362	TBX5	A	0.89071384	44.109	0.07	0.0018	0.00037
rs883079	TBX5	12	114802361	rs1946295	ILMN_1742362	TBX5	A	0.89075144	43.886	0.07	0.00169	0.00035
rs883079	TBX5	12	114802760	rs1946293	ILMN_1742362	TBX5	G	0.90209148	43.487	0.06	0.00821	0.00192
rs883079	TBX5	12	114804898	rs3825215	ILMN_1742362	TBX5	G	0.89066138	41.349	0.07	0.00175	0.00036
rs883079	TBX5	12	114805057	12:114805057:G_GGA	ILMN_1742362	TBX5	G	0.89805282	41.19	0.06	0.00552	0.00122
rs883079	TBX5	12	114806885	rs1895583	ILMN_1742362	TBX5	A	0.8912239	39.362	0.07	0.00259	0.00052
rs883079	TBX5	12	114807035	rs1895582	ILMN_1742362	TBX5	G	0.89030095	39.212	0.07	0.00209	0.00043
ExWAS												
Variants identified in combined ancestry analysis - eQTLs in European American samples												
rs2061690	PBXIP1	1	154919080	rs2061690	ILMN_1751500	ADAM15	T	1.13859918	-103.962	0.07731	0.00113	0.00012
rs3807989	CAV1	7	116186241	rs3807989	ILMN_2149226	CAV1	A	1.04315421	21.402	0.07033	0.00258	0.00028
rs3807989	CAV1	7	116186241	rs3807989	ILMN_1735220	CAV2	A	1.05088825	258.807	0.05177	0.02129	0.00317
rs60632610	SYNPO2L	10	75407290	rs3812629	ILMN_1731157	MYOZ1	A	2.98850132	-5.775	0.48461	1.77E-33	1.92E-35
rs60632610	SYNPO2L	10	75415677	rs60632610	ILMN_1731157	MYOZ1	T	2.9312378	-14.162	0.47802	8.27E-33	4.63E-35
rs60632610	SYNPO2L	10	75407290	rs3812629	ILMN_1690253	SYNPO2L	A	0.89275655	8.54	0.11843	6.37E-06	7.16E-07
rs60632610	SYNPO2L	10	75415677	rs60632610	ILMN_1690253	SYNPO2L	T	0.89663867	0.153	0.11197	1.47E-05	1.36E-06
rs10151658	SYNE2	14	64612858	rs10151658	ILMN_1754579	SYNE2	A	1.0997909	293.175	0.08394	0.00051	5.76E-05
Variants identified in European ancestry analysis - eQTLs in European American samples												
rs60632610	SYNPO2L	10	75406912	rs34163229	ILMN_1731157	MYOZ1	T	2.98936747	-5.397	0.48462	1.77E-33	2.67E-36
rs60632610	SYNPO2L	10	75406912	rs34163229	ILMN_1690253	SYNPO2L	T	0.89273312	8.918	0.11842	6.37E-06	1.50E-07

All variants significantly associated with AF in the combined and European ancestry GWAS and ExWAS meta-analyses were analyzed. This table reports the variants (rsID) that were significantly associated with altered expression of the eQTL genes. Filtered at FDR_gw<0.05. There were no significant eQTLs for variants identified in the African American ancestry analysis. TSS, transcription start site; SNP, single nucleotide polymorphism; Chr, chromosome. MA, minor allele in the atrial tissue biobank. *The most significant variant in the region. **For intronic variants, the gene the variant is located within is listed; for intergenic variants, the closest genes upstream and downstream are listed. †Variant tested. ‡eQTL gene. §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.

Supplementary Table 20. *In silico* functional evaluation of novel and replicated loci from GWAS and ExWAS combined ancestry analysis

rsID	Chr	Position	Gene*	Functional Annotation	eQTL CCAF	eQTL GTEx	Chromatin States	Chromatin States, Heart	DHS	DHS Heart	Protein Binding	Motifs Changed	N MC	R_DB Score
GWAS combined ancestry analysis														
rs11264280	1	154862952	*KCNN3 (dist=20198); PMVK (dist=34256)*	intergenic	*ADAM15 MUC1*	*ZBTB7B*			No	No		Mtf1_1,Zbtb3	2	7
rs520525	1	170638333	*PRRX1*	intronic	*PRRX1*	*RP1-79C4.4 PRRX1*	3_TxFlnk, 7_Enh, 1_TssA, 12_EnhBiv, 10_TssBiv, 6_EnhG, 11_BivFlnk, 2_TssAFlnk	7_Enh	Yes	Yes	SUZ12	Egr-1_disc1, Zfp740, Egr-1_known5, Gcm1, THAP1_disc2, Zfp281, YY1_disc2	7	3a
rs72700118	1	170194823	*METTL11B (dist=57900); LOC284688 (dist=45723)*	intergenic	*KIFAP3*		7_Enh	7_Enh	No	No		PLAG1, Mtf1_1, Myf_1	3	5
rs2288327	2	179411665	*TTN; TTN-AS1*	ncRNA_intronic			6_EnhG		No	No		HNF1_1, HNF1_7, Mef2_known1	3	6
rs2540949	2	65284231	*CEP68*	intronic	*CEP68*	*CEP68*	10_TssBiv, 1_TssA, 2_TssAFlnk	1_TssA	Yes	Yes	GATA2, POL24H8, TAL1, HDAC2, HMGN3, GATA1	Mrg_2	1	4
rs3771537	2	70038792	*ANXA4*	intronic		*ANXA4 SNRNP27 GMCL1 PCYOX1*	6_EnhG		No	No		RXRA_known4	1	5
rs11718898	3	12848822	*CAND2*	exonic		*KRT18P17 RP11-767C1.2 CAND2*	6_EnhG, 12_EnhBiv, 7_Enh	6_EnhG, 7_Enh	Yes	Yes	ERRA, CTCF, RAD21, CMYC	SMC3_disc1, CTCF_known1, SMC3_disc4, Rad21_disc1, TR4_disc2, CTCF_disc1, RXRA_disc2	7	2a
rs6843082	4	111718067	*PITX2 (dist=154788); C4orf32 (dist=1348486)*	intergenic			7_Enh		Yes	Yes		ZEB1_known2, Rhox11	2	6
rs2967791	5	137013106	*KLHL3*	intronic					No	No			0	7
rs337711	5	113748571	*KCNN2*	intronic	*KCNN2*		7_Enh		Yes	No	STAT3, RFX5		0	4
rs12664873	6	122463191	*GJA1 (dist=692318); HSF2 (dist=257505)*	intergenic					No	No		PLZF, Foxp1, Hoxa9	3	7
rs4946333	6	118565665	*SLC35F1*	intronic					No	No		STAT_known11, Hsf_known1, UF1H3BETA	3	7
rs1997572	7	116198828	*CAV1*	intronic	*CAV1 CAV2*		6_EnhG	6_EnhG	Yes	No		Gfi1_1, Foxp1, Pou2f2_known2, ZBRK1	4	6
rs7508	8	17913970	*ASAH1*	UTR3	*PCM1 ASAH1*	*PCM1*	6_EnhG		Yes	No		Foxj2_1	1	6
rs7026071	9	97492520	*C9orf3*	intronic					No	No		E2F_known2, E2F_known3, Zbtb3, CEBPB_known5	4	6
rs11598047	10	105342672	*NEURL*	intronic	*USMG5 MIR1307*		12_EnhBiv,7_Enh,2_TssAFlnk		Yes	No		Ets_disc5	1	4
rs35176054	10	105480387	*SH3PXD2A*	intronic			6_EnhG,7_Enh	6_EnhG,7_Enh	Yes	Yes	GATA2, P300	Nkx2_4, Pou2f2_known8, COMP1, GATA_known2	4	2b
rs7915134	10	75420180	*SYNPO2L (dist=4348); AGAP5 (dist=13853)*	intergenic	*MYOZ1 SYNPO2L*	*MYOZ1 FUT11*	7_Enh		No	No		SETDB1_disc1, NRSF_disc9, ELF1_disc3, Myc_disc10	4	7
rs75190942	11	128764571	*KCNJ5*	intronic	*KCNJ5*	*KCNJ5*	12_EnhBiv,7_Enh	7_Enh	Yes	Yes	GATA2	STAT_known8,NF-kappaB_disc2,Nkx2_4,NF-kappaB_known4,NF-kappaB_known5,Nkx3_5,Nkx2_11	7	2b
rs883079	12	114793240	*TBX5*	UTR3	*TBX5*	*TBX5*	6_EnhG,7_Enh	7_Enh	Yes	Yes		Evi-1_3	1	5
rs1152591	14	64680848	*SYNE2*	intronic	*SYNE2*	*SYNE2*	6_EnhG,3_TxFlnk,7_Enh,1_TssA,2_TssAFlnk	3_TxFlnk,1_TssA,2_TssAFlnk	Yes	Yes		GR_known6	1	5
rs74022964	15	73677264	*HCN4 (dist=15659); C15orf60 (dist=58235)*	intergenic					No	No		ERalpha-a_known4,Esr2,Pou1f1_2	3	7
rs2106261	16	73051620	*ZFHX3*	intronic			6_EnhG, 7_Enh	6_EnhG, 7_Enh	No	No		Pax-6_1,CEBPB_known5	2	7

Supplementary Table 20. *continued*

EWAS combined ancestry analysis														
rs13376333	1	154814353	*KCNN3*	intronic			12_EnhBiv, 7_Enh, 6_EnhG, 1_TssA	No	No		Hltf, CCNT2_disc1, HMGN3_disc2, BCL_disc5, GATA_known14, GATA_known1, TAL1_disc1, GATA_known2, Lmo2-complex_2, GATA_disc1, HDAC2_disc1, PU.1_known2, GATA_known10	13	1f
rs6800541	3	38774832	*SCN10A*	intronic			7_Enh	No	No			0	7
rs17042171	4	111708287	*PITX2 (dist=145008); C4orf32 (dist=1358266)*	intergenic			7_Enh	No	No		MIF-1, HMG-IY_1, NF-AT, RFX5_disc1, RFX5_known3, SREBP_disc1, RFX5_known4	7	5
rs89107	6	118578043	*SLC35F1*	intronic				No	No		AP-3	1	5
rs3807989	7	116186241	*CAV1*	intronic	*CAV1* *CAV2*		7_Enh, 6_EnhG	7_Enh,6_EnhG	Yes	Yes	CMYC, USF1, TAL1, GATA2	Myf_2, E2A_2, Myc_known1	3	3a
rs60632610	10	75415677	*SYNPO2L*	exonic; nonsynonymous	*MYOZ1* *SYNPO2L*	*MYOZ1*	12_EnhBiv, 7_Enh, 2_TssAFlnk,1_TssA	1_TssA	Yes	Yes			0	4
rs11047543	12	24788339	*LINC00477 (dist=51237); BCAT1 (dist=174619)*	intergenic			7_Enh		Yes	No		HNF4_known5, RORalpha1_1, Pax-4_2, HMG-IY_2, PLZF, RXRA_known3	6	7
rs10151658	14	64612858	*SYNE2*	exonic; nonsynonymous	*SYNE2*				No	No		NF-I_1	1	6
rs2106261	16	73051620	*ZFHX3*	intronic			7_Enh, 6_EnhG	7_Enh,6_EnhG	No	No		CEBPB_known5, Pax-6_1	2	7

Bold font indicates novel AF associated loci. Chr, chromosome; DHS, DNAse Hypersensitivity Site; N MC, number of motifs changed; R_DB, Regulome Database; TssA, Active TSS; TssAFlnk, Flanking Active TSS; TxFlnk, Transcr. at gene 5' and 3'; Tx, Strong transcription; TxWk, Weak transcription; EnhG, Genic enhancers; Enh, Enhancers; ZNF/Rpts, ZNF genes & repeats; Het, Heterochromatin; TssBiv, Bivalent/Poised TSS; BivFlnk, Flanking Bivalent TSS/Enh; EnhBiv, Bivalent Enhancer; ReprPC, Repressed PolyComb; ReprPCWk, Weak Repressed PolyComb; Quies, Quiescent/Low. *For intronic variants, the gene the variant is located within is listed; for intergenic variants, the closest genes upstream and downstream are listed.

Supplementary Table 21. Per study overlap of samples between GWAS and ExWAS analyses

Study	Overlap	
	Cases	Controls
BioVU	206	3811
WGHS	934	20,266
FHS - incident	411	1612
FHS - prevalent	181	2123
CHS - incident	922	1979
CHS -prevalent	60	2900
AGES	354	2989
RS	346	2370
CAMP	665	2128
SHIP	99	2710
AFLMU/KORA	349	415
MGH	333	0
ARIC EA	1253	3415
ARIC AA	233	742
MESA	155	2372
GS:SFHS	203	6651
BioMe EA	290	857
BioMe AA	166	2041
BioMe HA	255	2800
BEAT-AF	1520	1516
BBJ	782	0
Total	**9717**	**63,697**

Supplementary Table 22. GWAS information per study

Study	R	Array	Calling Algorithm	Per variant call rate	HWE p-value	Mendelian errors	Excess heterozygosity	MAF	Selection criteria for PCs	PCs	*N* variants for imputation	Imputation software	GWAS Statistical Analysis	*N* variants analyzed	Inflation factor, lambda
AFLMU/KORA	[169]	Illumina HumanCNV370 + Illumina Human550K	BeadStudio	≥98%	$<10^{-5}$	-	-	>1%	P<0.05	1	306,838	SHAPEIT v2.r790 + IMPUTE v.2.1.2	SNPTEST v2.5	7,540,650	1.023
AGES	[170]	Illumina HumanCNV370-Duo BeadChip	BeadStudio	≥97%	$<10^{-6}$	-	-	≥1%	P<0.05	0	329,804	MaCH v.1.0.16 + minimac	ProbABEL, R	I: 7,602,716 P: 6,085,662	I: 1.068 P: 1.006
ANGES	[171]	Illumina Metabochip	GenomeStudio	≥95%	$\geq 10^{-6}$	-	>3.18 SD from the mean removed	-	first 4 PCs	4	121,545	SHAPEIT v.2.r790 + IMPUTE2 v.2.3.0	SNPTEST v2.4.1	5,861,502	P&I: 1.011
ARIC	[172,173]	Affymetrix 6.0	Birdseed	≥95%	$<10^{-5}$	-	-	EA: >0.5% AA: >1%	Analysis committee recommendations	EA: 4 AA: 10	EA: 711,589 AA: 806,416	(1) Pre-phasing with ShapeIt (v1.r532) (2) Imputation with IMPUTE2.1.0	FAST	EA: 9,428,893 AA: 8,978,558	EA: 1.011 AA: 0.991
Beat-AF	[174]	Illumina HumanCoreExome	BeadStudio	≥95%	$>10^{-6}$	-	>3 SD from the mean removed	≥1%	First 10 PCs	10	254,488	SHAPEIT v2.r790 + IMPUTE v.2.3.2	SNPTEST v.2.5	9,309,201	1.022

Study	R	Array	Calling Algorithm	Per variant call rate	HWE p-value	Mendelian errors	Excess heterozygosity	MAF	Selection criteria for PCs	PCs	*N* variants for imputation	Imputation software	GWAS Statistical Analysis	*N* variants analyzed	Inflation factor, lambda
BBJ	[175]	Illumina Human610 Quad and Illumina Human Hap550v3 BeadChip	Beadstudio	≥99%	$>10^{-6}$	-	-	≥1%	First 2 PCs	2	432,042	MaCH + minimac	PLINK v1.07	6,429,092	1.024
BioMe	[176]	Illumina HumanOmni ExpressExome-8 v1.0	zCall (GenomeStudio)	≥90%	$p>10^{-6}$	-	-	≥1%	first 4 PCs	4	768,517	IMPUTE2	SNPTEST v.2.5	EA: 7,022,478 AA: 8,200,353 HA: 8,139,248	EA: 1.008 AA: 1.019 HA: 1.026
BioVU	[177]	Illumina Omni5 + Omni1 + 1M + 660K	GenomeStudio	≥98%	$<10^{-5}$	-	-	≥1%	First 2 PCs	2	4,167,400	IMPUTE2 v2.3.0	PLINK v1.90	660: 3,187,278 omni: 4,373,169	660: 1.003 Omni: 1.01
CCAF	[169]	Hap550 v1&v3 chip + Hap610 v1 chip	BeadStudio	≥95%	FDR>10^{-4}	-	FDR>0.01	≥1%	P<0.05	4	516,461	Shapeit v2.r727 + IMPUTE v.2.3.0	SNPtest v.2.5	8,122,372	1.026
CHS - AA	[178]	HumanOmni1-Quad_v1	GenomeStudio	≥97%	$\geq 10^{-5}$	≤1 in CEPH trios	-	>0.01 %	PCs with P<0.05 and all PCs before the associated PC	3	963,248	IMPUTE version 2.2.2	R	8,152,032	1.001
CHS - EA	[178]	Illumina 370 CNV + ITMAT-Broad-CARe (IBC) Illumina iSELECT chip	BeadStudio	≥97%	$\geq 10^{-5}$	≤2 in CEPH trios	-	>0.01 %	PCs with P<0.05 and all PCs before the associated PC	0	359,592	MaCH + minimac	R	8,278,530	1.045

Study	R	Array	Calling Algorithm	Per variant call rate	HWE p-value	Mendelian errors	Excess heterozygosity	MAF	Selection criteria for PCs	PCs	*N* variants for imputation	Imputation software	GWAS Statistical Analysis	*N* variants analyzed	Inflation factor, lambda
COROGENE	[179]	Illumina Metabochip + CoreExome	GenomeStudio	≥95%	≥10^{-5}	-	-	≥1%	-	0	553,581	IMPUTE v2.2.2	SNPTEST v2.4.1	6,956,681	1.019
FHS	[180,181]	Affymetrix, Gene Chip®, 500K Array Set & 50K Human Gene Focused Panel	BRLMM	≥97%	<10^{-6}		Subject hetero-zygosity >5 SD away from the mean	≥1%	All PCs u-ssociated, p>0.05	0	385,958	Mach1 v1.0.15	R packages kinship, GEE, COXPH	I: 7525764 P: 6556225	I: 1.019 P: 1.04
FINCAVAS	[182]	Illumina Metabochip + CoreExome	GenomeStudio	≥95%	≥10^{-6}	-	>3.23 SD from the mean removed	-	First 4 PCs	4	Metabochip: 120,689 CoreExome: 277,211	SHAPEIT v.2.r790 + IMPUTE2 v.2.3.0	SNPTEST v2.4.1	8,384,365	P&I: 1.04
GS:SFHS	[183]	Illumina Omni Express Plus Exome	BeadStudio	Omni ≥98% Exome ≥99%	<10^{-6}	-	-	Omni <1% Exome <0.01 %	PCs associated after adjustment for sex and age with p<0.05)	1	706,198 (690,759 Autosomes)	ShapeIt2 (pre-phasing), IMPUTE2 (imputation)	ProbABEL	6,563,971	0.997
HNR	[184]	Illumina: Omni Express, Omni1, CoreExomeA and CoreExomeB			<10^{-5}		Subject hetero-zygosity >5 SD away from the mean	MAF ≥0.01 and ≤99.9	First 10 PCs	10	Omni1: 682,618 OmniEx: 646,304 CoreExB: 255,584 CoreExA: 256,445	Impute v.2.3.0	SNPTEST	Excluded due to sample size	
LURIC	[185]	Affymetrix 6.0	Birdseed v.2	≥98%	0.0001	-	-	≥1%	First 3 PCs	3	686,195	IMPUTE v.2	SNPtest v.2.5	7,270,779	1.003

Study	R	Array	Calling Algorithm	Per variant call rate	HWE p-value	Mendelian errors	Excess heterozygosity	MAF	Selection criteria for PCs	PCs	*N* variants for imputation	Imputation software	GWAS Statistical Analysis	*N* variants analyzed	Inflation factor, lambda
MDCS	[186]	Illumina Human Omni Express Exome 1.0	GenomeStudio	≥95%	0.0001	-	-	≥1%	All PCs u-ssociated, p>0.05	0	816,728	IMPUTE v.2	SNPtest v.2.5	I: 8,981,701 P: 5,392,317	I: 0.99 P: 1.00
MESA	[187,188]	Affymetrix 6.0	Birdseed v1.33	≥95%	$<10^{-6}$	-	-	≥1%	First 2 PCs	2	881,666	IMPUTE2	ProbABEL	5,340,434	1.027
MGH AF study	[169]	Affymetrix 6.0	Birdseed	≥97%	$<10^{-6}$	-	-	≥1%	-	0	663,637	IMPUTE v2	PLINK v1.07	6,764,173	1.028
MGH CAMP		Infinium HumanCoreExome-24 BeadChips	zCall (GenomeStudio)	≥95%	$\geq 10^{-6}$	-	-	≥1%	PC1-PC10	10	224,343	IMPUTE2	PLINK v1.08	8,262,143	1.01
MGH Stroke	[3,189]	Affymetrix 6.0 + Illumina 610	Birdseed / GenCall	>95% MAF >5%	$<10^{-6}$	-	>±3 SD from the mean	>5%	-	2	GASROS Affymetrix: 579,083 GASROS Illumi-: 398,434 GOCHA: 521,363	IMPUTE2 v.2.3.0	SNPtest v.2.4.1	Excluded due to sample size	
WTCCC2 Munich	[3,190]	Illumina 660	GenCall	>98%	$>10^{-5}$	-	-	>1%	-	0	495,851	MACH+minimac	SNPTEST	5,891,675	1.019

Study	R	Array	Calling Algorithm	Per variant call rate	HWE p-value	Mendelian errors	Excess heterozygosity	MAF	Selection criteria for PCs	PCs	*N* variants for imputation	Imputation software	GWAS Statistical Analysis	*N* variants analyzed	Inflation factor, lambda
PIVUS	[191]	Illumina OmniExpress +Metabochip	GenCall	≥99% (MAF< 5%) or ≥95% (MAF≥ 5%)	$>10^{-6}$	-	>3 SD from the mean	≥1%	First 2 PCs	2	738,879	IMPUTE v.2.2.2	SNPTEST v.2.5	6,045,282	1.006
PREVEND	[192]	Illumina CytoSNP12 v2	GenomeStudio	>95%	$>10^{-6}$	-	-	≥1%	First 5 PCs	5	232,571	IMPUTE1	SNPTEST v.2	5,091,540	1.031
PROSPER	[193]	Illumina Beadchip 660Quad	BeadStudio	≥98%	$<10^{-6}$	-		>1%		4	557,192	IMPUTE v.2.2.2	SNPTEST	7,819,558	1.009
RS	[194]	Illumina Infinium HumanHap550 chip v3.0	BeadStudio	≥98%	$<10^{-6}$	-	>0.336	>1%	First 4 PCs	4	512,849	Mach 1 vs 1.0.151	ProbABEL	RSI: 7,695,631 RS2: 5,543,119 RS3: 5,224,770	P&I RS1: 1.022 RS2: 1.003 RS3: 1.033
SPHFC	[195]	Affymetrix Axion Brazilian Biobank Array	Birdseed v.2	≥97%	$<10^{-6}$	-	-	≥1%	First 3 PCs			IMPUTE v3	PLINK v1.08	7,104,209	1.02
SHIP	[196]	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed2	≥80%	>0.0001	-	-	≥1%	First 10 PCs	-	905,910	IMPUTE v.2.2.2	QUICKTEST v0.95	5,289,189	0.997
TWINGENE	[197]	Illumina HumanOmniExpress	GenCall	≥97%	$>10^{-7}$	-	>5 SD from the mean	≥1%	First 3 PCs	3	644,556	minimac (release 2012-10-03)	SNPTEST v.2.5	7,201,417	0.983

Study	R	Array	Calling Algorithm	Per variant call rate	HWE p-value	Mendelian errors	Excess heterozygosity	MAF	Selection criteria for PCs	PCs	*N* variants for imputation	Imputation software	GWAS Statistical Analysis	*N* variants analyzed	Inflation factor, lambda
ULSAM	[198]	Illumina Omni2.5+Metabochip	GenCall	≥99% (MAF< 5%) or ≥95% (MAF≥ 5%)	$>10^{-6}$	-	>3 SD from the mean	≥1%	First 2 PCs	2	1,587,454	IMPUTE v.2.2.2	SNPTEST v.2.5	7,297,774	0.996
WGHS	[199]	Illumina HumanHap 300 DuoPlus	BeadStudio v. 3.3	≥90%	$>10^{-6}$	-	-	≥1%	PCs 1,2, & 10	3	332,927	MaCH v.1.0.16 + minimac (release 5/29/2012)	ProbABEL	8,144,887	1.02

Supplementary Table 23. General principles for quality control and filtering

Pre-imputation:
Per marker quality control: Call rate (exclude markers if <95%) Hardy-Weinberg Equilibrium (exclude markers if marked deviation) Duplicate concordance (exclude markers with high discordance rates) Mendelian inconsistencies (exclude markers with an excess of Mendelian inconsistencies) Genotype completeness (exclude markers with relatively high missingness) Polymorphism check (exclude monomorphic markers which can represent assay failures) **Per individual quality checks typically include:** Principal Component Analysis Exclude samples with high degree of missingness Exclude samples with unusual heterozygosity Exclude monomorphic markers which can represent assay failures **Exclude related individuals for non-family studies**
Imputation:
Cases and controls imputed together **Criteria for imputation:** 1000G release used for imputation: 20110521 Phase 1 Integrated release ALL Gene reference assembly: GRCh37 SNPs oriented to forward/+ strand
Individuals study analysis:
Account for genotype uncertainty of imputed SNPs **Control for population stratification**
Meta-analysis:
Criteria for including variants (GWAS/EWAS) Imputation quality >0.3 MAF ≥0.01 (GWAS), MAF ≥0.005 (EWAS) Variant present in ≥2 studies Effect allele frequency x imputation quality (INFO) x number of cases ≥10 **Criteria for including genes (gene based tests)** Cumulative MAF per gene ≤0.005 **Quality control:** Estimate genomic inflation factor lambda for each study, and adjust if lambda >1 Check distribution of meta-analysis –log10(p-values) using QQ plots

Supplementary Table 24. ExWAS information per study

Study	R	Array	Calling Algorithm	Per variant call rate	HWE p-value	Mendelian errors	Excess heterozygosity	MAF	Selection criteria for PCs	PCs	Total *N* variants analyzed
AFLMU/ MGH AF	[169]	Illumina Infinium HumanExome BeadChip v1.0	CHARGE	-	-	-	Exclude |het|>5 SD	-	p<0.01 in association adjusted for age and sex; derived under exclusion of candidate regions	11	241,465
AGES	[170]	Illumina Exome Chip v1.0	Illumina GenomeStudio2011.1	≥95%	$<10^{-6}$	-	-	-	p<0.05	0	247,501
ARIC	[172]	Illumina HumanExome Beadchip v.1.0	Centrally at CHARGE	0.95	-	-	-	-	First 10 PCs	10	223,577
BBJ	[175]	Infinium OmniExpressExome-8 BeadChip Kit	Illumina GenCall	>0.99	$>10^{-6}$ in control	no trios in samples; QC done using IBS	Yes	Exclude monomorphic in either control or case	Eigenstrates	2	61,024
BEAT-AF	[174]	Illumina HumanCoreExome	BeadStudio	≥95%	$>10^{-6}$	-	> 3 SD from the mean removed	ALL	First 10 PCs	10	495,970
BioMe	[176]	Illumina HumanOmniExpress Exome-8 v1.0	zCall (GenomeStudio)	≥90%	$>10^{-6}$	-	-	≥1%	first 4 PCs	4	241,465
BioVU	[177]	Illumina Infinium HumanExome BeadChip	GenomeStudio	>0.95	$>10^{-6}$	>1 removed	Yes (rate >0.44)	-	first 3 PCs	3	247,039
CHS	[178]	Illumina HumanExome BeadChip v1.0	GenomeStudios	≥97%	None	Any among CEPH trio controls	None	None	5 unless others are associated with the outcome	5	247,870

Study	R	Array	Calling Algorithm	Per variant call rate	HWE p-value	Mendelian errors	Excess heterozygosity	MAF	Selection criteria for PCs	PCs	Total *N* variants analyzed
FHS	[180,181]	Illumina HumanExome BeadChip v1.0	GenomeStudio v. 2011.1 and zCall following CHARGE protocol[200]	-	-	-	-	-	p<0.01 in association adjusted for age and sex	0	247,501
GS:SFHS	[183]	Illumina HumanExome Beadchip v.1-A	GenomeStudio v. 2011.1 CHARGE protocol	0.98	-	-	-	Remove Monomorphic	First 3 PCs	1	247,870
KORA	[201,202]	Illumina Infinium HumanExome BeadChip v1.0	CHARGE	-	-	-	Exclude |het|>5 SD	-	p<0.01 in association adjusted for age and sex; derived under exclusion of candidate regions	11	241,465
LURIC	[185]										Excluded
MESA	[187,200]	Illumina Exome Chip v1.0	GenomeStudio v. 2011.1 and zCall following CHARGE protocol	0.95	$>10^{-6}$	-	-	ALL	Eigenstrates	2	247,039
MGH CAMP		Infinium HumanCoreExome-24 BeadChips	zCall (GenomeStudio)	≥95%	$\geq 10^{-7}$	-	-	≥1%	First 10 PCs	10	247,501
RS	[194]	Illumina Human Exome BeadChip v1.0	zCall following CHARGE	<0.97	-	-	Het excess >0.1 AND Het excess ≤0.9	28,471 monomorphic SNPs were excluded (MAF<1E-9)	First 5	5	247,870
SHIP/SHIP-Trend	[196]	Illumina HumanExome Beadchip v.1.0	SOP v5, zCall v3.3	-	-	-	-	-	First 10 PCs	First 10 PCs	247,039
WGHS	[199,203]	Illumina HumanExome Beadchip v.1.1A	GenomeStudio v. 2011.1 and zCall following CHARGE protocol	0.95	-	-	-	-	-	0	247,727
WHI - CT		Illumina Human	GenomeStudio	0.95	-	-	-	-	Plink	2	246,670

Study	R	Array	Calling Algorithm	Per variant call rate	HWE p-value	Mendelian errors	Excess heterozygosity	MAF	Selection criteria for PCs	PCs	Total *N* variants analyzed
		Exome BeadChip v1.0	v2010.3								
WHI - OS		Illumina Human Exome BeadChip v1.0	GenomeStudio v2010.3	0.95	-	-	-	-	Plink	2	246,670

Supplementary Table 25. Baseline characteristics of African American ancestry replication studies

	Cases	Controls	Total
N	447	442	889
Women, %	44	48	46
Age at enrollment, mean (SD)	55 (11)	61 (14)	60 (14)
Age at diagnosis, mean (SD)	58 (14)	-	-
Age range (Q1-Q3)	50-61	52-72	51-69
HTN, %	88	87	88
DM, %	37	41	39
HF, %	24	8	16
MI, %	8	3	6

SD, standard deviation; HTN, hypertension; DM, diabetes mellitus; HF, heart failure; MI, myocardial infarction.

Supplementary Table 26. Results from replication in African American ancestry studies

rsID	Risk allele	RAF, %	OR	95% CI	P-value
rs115339321	T	97	1.53	0.82-2.18	0.18
rs79433233	A	3	1.36	0.75-2.47	0.31

RAF, risk allele frequency; OR, odds ratio; CI, confidence interval.

Supplementary Table 27. Results from DEPICT pathway analysis of GWAS meta-analysis results

Original gene set ID	Original gene set description	Nominal P-value
KEGG ARRHYTHMOGENIC RIGHT VENTRICULAR CARDIOMYOPATHY ARVC	KEGG ARRHYTHMOGENIC RIGHT VENTRICULAR CARDIOMYOPATHY ARVC	1.27×10^{-6}
KEGG_TIGHT_JUNCTION	KEGG TIGHT JUNCTION	1.75×10^{-6}
MP:0003157	impaired muscle relaxation	2.28×10^{-6}
GO:0016459	myosin complex	8.31×10^{-6}
GO:0060429	epithelium development	1.17×10^{-5}
MP:0000751	myopathy	1.25×10^{-5}
GO:0030855	epithelial cell differentiation	1.67×10^{-5}
KEGG HYPERTROPHIC CARDIOMYOPATHY HCM	KEGG HYPERTROPHIC CARDIOMYOPATHY HCM	3.07×10^{-5}
REACTOME MUSCLE CONTRACTION	REACTOME MUSCLE CONTRACTION	4.18×10^{-5}
GO:0031589	cell-substrate adhesion	8.50×10^{-5}

Supplementary Table 28. Top 5 enriched canonical pathways from Ingenuity Pathway Analysis of GWAS meta-analysis results

Ingenuity Canonical Pathways	P-value	Ratio	Molecules
Coagulation System	0.0088	3/35 (8.6%)	F11, KLKB1, PLAU
Clathrin-mediated Endocytosis Signaling	0.011	7/197 (3.6%)	MET, UBD, FGF17, ACTR2, AAK1, HIP1, PCYOX1
Protein Ubiquitination Pathway	0.013	8/255 (3.1%)	UBD, UBE2G2, USP18, UBE2Q1, BAG1, PSMD5, USP54, PSMD3
Superpathway of Geranylgeranyldiphosphate Biosynthesis I (via Mevalonate)	0.018	2/17 (11.8%)	FDPS, PMVK
Ephrin Receptor Signaling	0.02	6/174 (3.4%)	ACTR2, SHC1, EFNA3, CREB5, EFNA4, EFNA1

Supplementary Table 29. Enriched diseases or functions annotation from Ingenuity canonical pathway analysis of GWAS meta-analysis results

Diseases or Functions Annotation	P-value	*N* molecules	Molecules
Arrhythmia of heart ventricle	$3.0x10^{-9}$	12	CASQ2, CSF3, DSG2, HCN4, KCNG2, KCNJ5, PKP2, SCN10A, SCN5A, TBX5, THRA, TTN
Ventricular tachycardia	$1.7x10^{-8}$	10	CASQ2, CSF3, DSG2, HCN4, KCNG2, KCNJ5, PKP2, SCN5A, TBX5, THRA
Tachycardia	$2.5x10^{-8}$	11	CASQ2, CSF3, DSG2, HCN4, KCNG2, KCNJ5, PITX2, PKP2, SCN5A, TBX5, THRA
Arrhythmia	$5.0x10^{-8}$	16	CASQ2, CSF3, DSG2, HCN4, KCNG2, KCNJ5, NR3C1, PITX2,PKP2, PLN, SCN10A, SCN5A, TBX5, THRA, TTN, TUBA8
Ventricular fibrillation	$9.5x10^{-7}$	7	DSG2, KCNG2, KCNJ5, PKP2, SCN5A, THRA, TTN
Cardiomyopathy of heart ventricle	$1.2x10^{-6}$	6	CAV1, DSG2, HCN4, PKP2, SCN5A, TTN
Cardiac fibrillation	$1.6x10^{-6}$	11	DSG2, KCNG2, KCNJ5,NR3C1, PITX2,PKP2, PLN, SCN5A, THRA, TTN, TUBA8
Hypertrophy of cardiac muscle	$5.5x10^{-6}$	10	CAV1, CSF3, FBXO32, IL6R, mir-23, PLAU, RAB1A, SHC1, TBX5, TTN
Arrhythmogenic right ventricular dysplasia	$5.7x10^{-6}$	5	DSG2, HCN4, PKP2, SCN5A, TTN

2. Supplementary Note

Detailed Description of participating studies

The meta-analyses described in this manuscript included the following studies described elsewhere: The **Age, Gene/Environment Susceptibility Study (AGES) Reykjavik study**[169]**,** the **Atrial Fibrillation Biobank LMU (AFLMU)** in the context of the **Arrhythmia-Biobank-LMU** (formerly known as **AFNET**) and the **Cooperative Health Research in the Region of Augsburg (KORA)**[169]**,** the **Atherosclerosis Risk in Communities (ARIC) study**[169]**, Cleveland Clinic Lone Atrial Fibrillation GeneBank Study (CCAF)**[169]**,** the **Cardiovascular Health Study (CHS)**[169], **Framingham Heart Study (FHS)**[169], **Massachusetts General Hospital (MGH) AF study**[169], the **Rotterdam Study (RS)**[169], the **Study of Health in Pomerania (SHIP)**[169], **BioVU**[212], the **Women's Genome Health Study (WGHS)**[169], The **PROspective Study of Pravastatin in the Elderly at Risk (PROSPER)**[175], **Biobank Japan (BBJ)**[175], in addition to the studies described here:

ANGES: The Angiography and Genes Study (ANGES) population consists of 1,000 Finnish individuals participating in the ongoing ANGES study. Angiographic, genetic, and covariate data was available for 808 individuals (516 men and 292 women; mean age 62±10). The data was collected between September 2002 and July 2005. All patients underwent coronary angiography at Tampere University Hospital due to clinically suspected coronary artery disease. The study is a cross-sectional study, and after the angiography, patients were treated according to the Finnish Current Care Guidelines. Patients were also interviewed by a study nurse, and a questionnaire was used to collect general information - age, sex, body mass index, alcohol consumption, smoking, medication, as well as traditional risk factors of atherosclerosis and myocardial infarction. The study has been approved by the Ethics Committee of Pirkanmaa Hospital District and written informed consent was obtained from each patient.

BEAT-AF: The Basel Atrial Fibrillation Cohort Study (BEAT-AF) is a prospective observational, multicenter cohort study. Between 2010 and 2014, 1550 patients with documented atrial fibrillation were enrolled across 7 centers in Switzerland. Exclusion criteria were the inability to sign informed consent and the presence of short transient forms of atrial fibrillation. At baseline, patients completed detailed questionnaires about personal, medical, nutritional and lifestyle factors, current atrial fibrillation symptoms and co-morbidities. Current medications were recorded. A resting 12-lead electrocardiogram (ECG) was recorded and all patients underwent venous blood sampling at the local study center, including DNA from leukocytes. Yearly follow-ups by mailed questionnaires and phone interviews were performed in all patients in order to collect similar information as at baseline and to obtain details about adverse events.
Referents were enrolled from the 'genetic and phenotypic determinants of blood pressure and other cardiovascular risk factors' (GAPP) study, which is an ongoing prospective population-based cohort study among healthy adults in the Principality of Liechtenstein. Between 2010 and 2013, all inhabitants of the Principality of Liechtenstein aged between 25 and 41 years were invited and 2170 agreed to participate in the study. Main exclusion criteria were established cardiovascular disease, chronic kidney disease, diagnosed sleep apnea, a body mass index (BMI) > 35 kg/m2, intake of antidiabetic drugs or any other severe illness. Examinations included detailed assessment of personal, medical, lifestyle and nutritional factors, standardized assessment of weight, height and waist circumference, blood pressure measurement, electrocardiography, bioimpedance analysis, blood, urinary and genetic sampling, spirometry and sleep pulse oximetry with nasal flow measurement. Follow-up examinations are scheduled every 3-5 years. The detailed study design has previously been published.[174]

Bio*Me*: The Mount Sinai Bio*Me* Biobank is an ongoing, prospective, hospital- and outpatient- based population research program operated by The Charles Bronfman Institute for Personalized Medicine (IPM) at Mount Sinai and has enrolled over 33,000 participants since September 2007. Bio*Me* is an Electronic Medical Record (EMR)-linked biobank that integrates research data and clinical care information for consented patients at The Mount Sinai Medical Center, which serves diverse local communities of upper Manhattan with broad health disparities. Bio*Me* populations include 25% of African ancestry (AA), 36% of Hispanic Latino ancestry (HL), 30% of white European ancestry (EA), and 9% of other ancestry. The BioMe disease burden is reflective of health disparities in the local communities. Bio*Me* operations are fully integrated in clinical care processes, including direct recruitment from clinical sites waiting areas and phlebotomy stations by dedicated recruiters independent of clinical care providers, prior to or following a clinician standard of care visit. Recruitment currently occurs at a broad spectrum of over 30 clinical care sites.

Information on atrial fibrillation, age, sex, body mass index (BMI), type 2 diabetes (T2D), hypertension (HYP), heart failure (HFAIL), and myocardial infarct (MI) was derived from participants' EMRs: Age, sex and BMI were derived from the day of enrolment to the BioMe biobank. Prevalent atrial fibrillation cases were defined as Bio*Me* participants with the ICD-9 code 427.31 (atrial fibrillation) and/or 427.32 (atrial flutter) and controls as individuals who have had ECG's but did not have atrial fibrillation or flutter ICD-9 codes. HYP, HFAIL, and MI were defined using the ICD-9 codes 401.*, 428.*, and 410.*, respectively. In addition to the ICD-9 codes, also individuals taking antihypertensive drugs were considered as having HYP. T2D was defined using the eMerge T2D case and control definition algorithms.[213] The algorithms used were developed by a multidisciplinary team of scientists, clinicians and software specialists and have been validated with excellent performance statistics; 100% sensitivity and >98% positive predictive value for cases, and ≥98% sensitivity and ≥98% positive predictive value for controls.

Bio*Me* participants were genotyped with the Illumina HumanOmniExpressExome-8 v1.0 beadchip array and imputed to the 1000 Genomes Project Phase 1 (March12) reference panel using IMPUTE2. Genome-wide association studies (GWAS) were carried out using SNPTEST 2.4.1 after stratifying by self-reported ancestry (AA: 174 atrial fibrillation cases and 2130 controls; EA: 291 atrial fibrillation cases and 860 controls; HL: 277 atrial fibrillation cases and 3081 controls) and adjustment for a) age, sex and the first 4 GWAS PCs (Model1) and b) age, sex, BMI, T2D, HYP, HFAIL, MI, and the first 4 GWAS PCs (Model2). To ensure high quality of the association results, variants with imputation quality < 0.3, Hardy-Weinberg p-value < $1x10^{-5}$ or minor allele frequency < 0.01 were excluded.

BioVU*:* BioVU is the Vanderbilt University Medical Center's biorepository linked to de-identified electronic health records. BioVU operations[212] and ethical oversight[214] have been described elsewhere. Briefly, DNA is collected from discarded blood samples remaining after routine clinical testing at Vanderbilt outpatient clinics in Nashville, Tennessee and surrounding areas, and is linked to a de-identified version of the patient's electronic health record termed the "Synthetic Derivative." atrial fibrillation cases were defined as individuals who were aged >18 years, had an ICD-9 diagnosis for atrial fibrillation or flutter (ICD-9: 427.3, 427.31, and 427.32), or a cardiologist diagnosis of atrial fibrillation as identified by a natural language processing tool from the unstructured free text of the ECG impression. In all instances, patients with a history of a heart transplant were excluded (Current Procedural Terminology: 33935, 3394, and 580; ICD-9: V42.1, 996.83).[177]

Corogene: The Corogene study was designed as a large cohort to study mainly CAD, but also other related heart diseases such as heart failure and aortic valve disease. We selected the patients from the CAD point of view, and decided to include over 5000 consecutive patients assigned for coronary angiogram. In Finland, coronary angiogram is performed to practically all patients assigned for invasive

heart examination. Despite technical developments in diagnostics, coronary angiogram is still the gold standard for evaluating coronaries. The purpose of this study is to follow contemporary trends in coronary heart disease, and related heart disease risk factors, genetics and epigenetics by collecting cohorts referred to heart examination. New cohorts will be collected at 5-year intervals in order to see trends in CAD, its risk factors and epigenetics.

FINCAVAS: The purpose of the Finnish Cardiovascular Study (FINCAVAS) is to construct a risk profile - using genetic, haemodynamic and electrocardiographic (ECG) markers - of individuals at high risk of cardiovascular diseases, events and deaths. All patients scheduled for an exercise stress test at Tampere University Hospital, who gave informed consent to participate, were recruited between October 2001 and December 2007. The total number of participants was 4,567. In addition to repeated measurements of heart rate and blood pressure, digital high-resolution ECG at 500 Hz was recorded continuously during the entire exercise test, including the resting and recovery phases. About 20% of the patients were examined with coronary angiography. Genetic variations known or suspected to alter cardiovascular function or pathophysiology were analyzed to elucidate the effects and interactions of these candidate genes, exercise, and commonly used cardiovascular medications.

GS:SFHS: Generation Scotland: Scottish Family Health Study (GS:SFHS) is a family-based genetic epidemiology study of ~24,000 volunteers from ~7000 families across Scotland with the capacity for follow-up through record linkage and re-contact. Participants completed a demographic, health and lifestyle questionnaire and provided biological samples including DNA, and ~21,500 participants underwent detailed clinical assessment, including anthropometric, cardiovascular, respiratory, cognition and mental health. Genetic analysis (GWAS) is complete on 20,000 participants with full baseline data and CHI linkage, with linkage to SMR, prescriptions and dental records. A full cohort description can be found elsewhere.[183] Atrial fibrillation was ascertained as a diagnosis of atrial fibrillation by linkage to one or more inpatient visits with ICD-10 code I48 or ICD-9 427.31 in the Scottish Morbidity Record (SMR1) database before or after recruitment to GS:SFHS.

HNR: The study population of the Heinz Nixdorf Recall (HNR) study has been described in detail elsewhere.[184] Approved by the relevant institutional ethics committees, the study follows strict internal and external quality assurance protocols. Briefly, the study cohort comprises 4,814 men and women aged 45 – 75 years from the three adjacent Ruhr cities Essen, Bochum and Mülheim/Ruhr. The vast majority of the study population is of central European ancestry. The study area covers a region of approximately 600 km² with almost 1.2 million inhabitants. Subjects were randomly selected from statutory lists of residence and gave informed consent. The baseline examinations were from 2000-2003, the 5-Year follow-Up from 2006-2008 and the 10-Year follow-up from 2011-2015. A standardized digital 12-lead resting surface ECG was sampled at 250 Hz and recorded on a MAC 5000® ECG recorder (GE Healthcare, Freiburg, Germany). ECGs were interpreted automatically using the integrated 12SL-Code® [12SL ECG analysis with age & gender specific criteria. Physician's guide. PN 416791-004 Revision A. GE Medical Systems IT, 2000]. ECG findings were coded and transferred to our database. The ECG-codes #161 and #162 are for atrial fibrillation and atrial flutter, respectively and were combined for the purpose of this analysis.

LURIC: The Ludwigshafen Risk and Cardiovascular Health (LURIC) study is an ongoing prospective study of more than 3,300 individuals of German ancestry in whom cardiovascular and metabolic phenotypes (CAD, MI, dyslipidemia, hypertension, metabolic syndrome and diabetes mellitus) have been defined or ruled out using standardized methodologies in all study participants.[185] Inclusion criteria for LURIC were: German ancestry (limitation of genetic heterogeneity), clinical stability (except for acute coronary

syndromes) and availability of a coronary angiogram. Exclusion criteria were: any acute illness other than acute coronary syndromes, any chronic disease where non-cardiac disease predominated and a history of malignancy within the last five years. Genome-wide analyses using the Affymetrix 6.0 have been completed in all participants. A 10-year clinical follow-up for total and cause specific mortality has been completed.

MDCS: The Malmö Diet and Cancer study (MDCS) is a community-based prospective epidemiologic cohort of middle-aged individuals from Southern Sweden.[186] In total, 30,447 subjects attended a baseline exam in 1991-1996, when they filled out a questionnaire and underwent anthropometric and blood pressure measurements. Prevalent or incident cases of atrial fibrillation were ascertained from nation-wide hospital registers with high validity as described previously.[186] Genome-wide genotyping of single nucleotide variants was performed using the Illumina Human Omni Express Exome BeadChip kit. Genotyping was performed in a nested case-cohort design, including a random subset of 5878 subjects.

MESA: The Multi-Ethnic Study of Atherosclerosis (MESA) is a study of the characteristics of subclinical cardiovascular disease (disease detected non-invasively before it has produced clinical signs and symptoms) and the risk factors that predict progression to clinically overt cardiovascular disease or progression of the subclinical disease. The cohort is a diverse, population-based sample of 6,814 asymptomatic men and women aged 45-84. Approximately 38 percent of the recruited participants are white, 28 percent African American, 22 percent Hispanic, and 12 percent Asian (predominantly of Chinese descent). Participants were recruited during 2000-2002 from 6 field centers across the U.S. (at Wake Forest University; Columbia University; Johns Hopkins University; the University of Minnesota; Northwestern University, and the University of California – Los Angeles). All underwent anthropomorphic measurement and extensive evaluation by questionnaires at baseline, followed by 4 subsequent examinations at intervals of approximately 2-4 years. Age and sex were self-reported. Current atrial fibrillation at baseline was an exclusion criterion. Follow-up phone calls to study participants (every 9-12 months) were used to identify all hospitalizations. Medical records, including discharge diagnoses, were obtained for each hospitalization. Incident atrial fibrillation was defined by International Classification of Disease codes 427.31 or 427.32 (9th revision). In addition, new diagnoses of atrial fibrillation were identified at follow-up by the presence of atrial fibrillation or atrial flutter on a study ECG at Exam 5 (approximately 10 years after baseline). Further information can be found at http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000209.v13.p3.

MGH CAMP: The MGH Cardiology and Metabolic Patient (MGH CAMP) cohort comprises 3857 subjects recruited between 2008 and 2012. Two thirds of the subjects were drawn from patients who had appointments with a physician in the MGH Heart Center, whereas one third were recruited independent of any hospital visit. All subjects had plasma and serum samples collected, as well as blood for genomic DNA. Subjects with known diabetes had vascular reactivity measurements (FMD of brachial artery), while subjects without known diabetes had an oral glucose tolerance test. Exome Core Chip genotyping was performed on all subjects. Atrial fibrillation was defined as a self-reported history of fibrillation or flutter at study enrollment, or based on a validated medical record ascertainment algorithm (PPV 88%) that utilizes electrocardiographic and relevant diagnostic, procedure, and medication data.[215]

MGH Stroke study: The Genetics of Cerebral Hemorrhage on Anticoagulation (GOCHA) study is a multicenter study of the genetics of intracerebral hemorrhage in the USA, based at the Massachusetts General Hospital. The cases are individuals presented with acute primary hemorrhagic stroke, aged more than 55 years. The controls were recruited from ambulatory clinics in the same centers in which cases were enrolled.

The Genes Affecting Stroke Risk and Outcome Study (GASROS) is a single-center prospective cohort that enrolled cases with acute ischemic stroke, aged more than 18 years who presented to MGH from 2003 to 2011. Ischemic stroke was defined as a clinical syndrome of associated with a radiographically proven acute infarction consistent with a vascular pattern and without radiographic evidence of a demyelinating or neoplastic disease or other structural disease. In all subjects, the diagnosis was confirmed by diffusion weighted imaging (DWI) completed within 48 hours after symptom onset. Only patients of self-reported European ancestry were enrolled. Controls were matched to cases on the basis of age, sex and race/ethnicity.

In both GOCHA and GASROS, atrial fibrillation status was determined by reviewing medical records, and/or interview subjects or their families. The diagnosis of atrial fibrillation was established if the subject either had a pre-existing diagnosis or was diagnosed with atrial fibrillation in the hospital. The diagnosis was not confirmed by ECG in all cases.

PIVUS: The participants were randomly sampled from all men and women at age 70 living in Uppsala County in 2001 (www.medsci.uu.se/PIVUS). Of the 2025 individuals invited, 1016 participated. The participants underwent a medical examination including a detailed questionnaire on lifestyle and socioeconomic factors, fasting blood sampling, blood pressure measurement and anthropometric measurements, as previously described.[191] Blood and plasma samples have been frozen until analysis, and blood tests performed include a wide variety of traditional and more recent CVD risk factors, along with DNA extraction. In addition, the individuals have undergone extensive phenotyping including whole body MRI, echocardiography, endothelial function measurements, carotid ultrasound, DXA, and spirometry. The participants have been re-examined at age 75 and 80. Atrial fibrillation was defined by 12-lead ECG at the examinations, as well as diagnosis of atrial fibrillation or flutter in the Swedish National Patient Register before or after the baseline examination (inpatient and specialist outpatient care; ICD-9 code, 427.3 and ICD-10 code, I48).

PREVEND: The PREVEND cohort study was founded in 1997, and is an ongoing community-based cohort study including 8592 inhabitants of the city of Groningen, The Netherlands. PREVEND is investigating the natural course of microalbuminaria and its relation to renal and cardiovascular disease. Details of the protocol, atrial fibrillation ascertainment and covariate definitions have been described elsewhere (www.prevend.org). The baseline screening program consisted of 2 outpatient visits to assess demographic factors, anthropometric measurements, cardiovascular and metabolic risk factors, and health behavior and to collect blood samples and 2 24-h urine samples on 2 consecutive days. Participants were seen at 3-year intervals in the PREVEND outpatient clinic. Atrial fibrillation was ascertained if either atrial flutter or atrial fibrillation was present on a 12-lead ECG obtained at one of the three PREVEND follow-up visits, or at an outpatient visit or hospital admission in the two hospitals in the city of Groningen (University Medical Center Groningen and Martini Hospital). Participants without an electrocardiogram (ECG) (n=248), as well as participants with prevalent atrial fibrillation at the baseline screening (n=79) and without GWAS information (n=4632) were excluded, leaving 3633 for analysis.[216]

SPHFC: Participants for the Sao Paolo Heart Failure Cohort (SPHFC) were prospectively enrolled from the outpatient clinic at the Heart Institute, the University of Sao Paulo Medical School, Sao Paulo, Brazil. Only patients older than 18 years and with symptomatic heart failure (stage C) were enrolled. Different heart failure etiologies were included. Patients with prior myocardial infarction (<3 months), unstable angina, hypertrophic cardiomyopathy, valve heart disease candidates to surgical treatment, obstructive pulmonary disease, severe renal or hepatic dysfunction, current history of cancer, severe peripheral

arterial disease, cerebrovascular disease and active infection were excluded. Atrial fibrillation status was determined if either atrial flutter or atrial fibrillation was present on a 12-lead ECG at baseline evaluation or prior and could be confirmed by electronic medical record review.

TWINGENE: The Swedish Twin Registry contains data regarding health, health-related behaviors, physical activity, eating habits, and environmental stressors, along with other information from Swedish national registries. TWINGENE includes twins born before 1958 that were contacted to participate at the baseline examination between April 2004 and December 2008.[217] Health and medication data were collected from self-reported questionnaires, while blood sampling and in-person testing, including blood pressure measurement and anthropometrics were completed at a local health care center. Several biomarkers, including lipid profiles, fasting glucose, HbA1C and CRP, have been measured, and aliquoted serum is stored at the Karolinska Institutet Biobank. Atrial fibrillation was defined as a diagnosis of atrial fibrillation or flutter in the Swedish National Patient Register before or after the baseline examination (inpatient and specialist outpatient care; ICD-9 code, 427.3 and ICD-10 code, I48).

ULSAM: All men born between 1920 and 1924 in Uppsala, Sweden were invited to participate at age 50 in this longitudinal cohort study that was started in 1970. Participants were reinvestigated at the ages of 60, 70, 77, 82 and 88 years.[198] Blood samples for DNA extraction and main cardiovascular risk factors were available from the investigation at age 70. The participants have undergone extensive phenotyping at repeated time points, including euglycemic clamps, oral glucose tolerance tests, DXA, echocardiography, 24-h ambulatory blood pressure measurement, and a range of biomarkers. Atrial fibrillation was defined by 12-lead ECG at the examinations, as well as diagnosis of atrial fibrillation or flutter in the Swedish National Patient Register (inpatient and specialist outpatient care; ICD-9 code, 427.3 and ICD-10 code, I48).

WHI: The Women's Health Initiative (WHI) is one of the largest (n=161,808) studies of women's health ever undertaken in the United States. The WHI studies consisted of randomized CT, which assigned 68,132 women to active or placebo hormone therapy (HT), dietary modification or control, and/or calcium/vitamin D, supplementation or placebo with specific outcomes of common diseases of aging in women, and also an observational study (OS), which collected data on biological and lifestyle factors and health outcomes. A diverse population including 26,045 (17%) women from minority groups were recruited from 1993-1998 at 40 clinical centers across the U.S. Details of the study design have been previously described.[218,219] For the CT and OS participants enrolled in WHI and who had consented to genetic research, DNA was extracted by the Specimen Processing Laboratory at the Fred Hutchinson Cancer Research Center (FHCRC) using specimens that were collected at the time of enrollment in to the study (between 1993 and 1998).
Baseline atrial fibrillation was determined by an initial questionnaire, which probed for self-reported atrial fibrillation or by presence of atrial fibrillation on the baseline 12-lead electrocardiogram. Women were followed up with a medical history update questionnaire at years 3 to 8, which specifically probed for self-reported atrial fibrillation and hospitalizations.

WTCCC2-Munich: The Wellcome Trust Case Control Consortium 2 Munich (WTCCC2-Munich) study is a hospital-based study on ischemic stroke genetics. Only consecutive European Caucasians recruited from a single dedicated Stroke Unit from South-German origin were selected for this study from the Department of Neurology, Klinikum Großhadern, Ludwig-Maximilians-University, Munich. Age, sex and clinical risk factors were collected. Atrial fibrillation was identified by ECG measurement on day of admission. For the German samples controls were Caucasians of German origin participating into the

population KORAgen study (www.gsf.de/kora/en/english.html). This survey represents a gender- and age stratified random sample of all German residents of the Augsburg area and consists of individuals 25 to 74 years of age, with about 300 subjects for each 10-year increment. All controls were free of a history of stroke, atrial fibrillation or other cardiovascular diseases.

African American replication studies included:

Penn Medicine Biobank: The Penn Medicine BioBank was started in 2009 and aims to recruit patients within the University of Pennsylvania Health System to donate venous blood. All samples are linked to de-identified electronic medical records. Participation is completely voluntary and written and informed consent are obtained prior to sample collection. For this project, all samples were collected within the inpatient and outpatient sections of the cardiovascular division at the University of Pennsylvania. Atrial fibrillation cases were limited to adults >18 years of age. Atrial fibrillation was ascertained through an ICD-9 diagnosis of atrial fibrillation, atrial flutter or documentation within the medical record.

Duke Biobank: The CATHeterization GENetics (CATHGEN) biorepository collected biospecimens and clinical data on individuals age ≥18 undergoing cardiac catheterization for concern of ischemic heart disease at a single center (Duke University Medical Center) from 2000-2010; a total of N=9334 individuals were collected. Samples were matched at the individual level to clinical data collected at the time of catheterization and stored in the Duke Databank for Cardiovascular Diseases (DDCD). Clinical data included subject demographics, cardiometabolic risk factors, cardiac history including symptoms, age-of-onset of cardiovascular diseases, coronary anatomy and cardiac function at catheterization, laboratory data, and yearly follow-up for hospitalizations, vital status, medication use and lifestyle factors. Atrial fibrillation cases were defined as individuals who had ever had atrial fibrillation based on any ECG available at Duke University or ICD-9 code for atrial fibrillation used for inpatient or outpatient billing.

Members of the AFGen Consortium, Neurology working group of the CHARGE Consortium and METASTROKE Consortium

AFGen Consortium Members

Ingrid E. Christophersen, MD, PhD,[1–3] Michiel Rienstra, MD, PhD,[4] Carolina Roselli, MSc,[1,5,6] Xiaoyan Yin, PhD,[7,8] Bastiaan Geelhoed, PhD,[4] John Barnard, PhD,[9] Honghuang Lin, PhD,[7,8] Dan E. Arking, PhD,[10], Albert V. Smith, PhD,[11,12] Christine M. Albert, MD, MPH,[13] Mark Chaffin, MSc[1], Nathan R. Tucker, PhD,[1,2] Molong Li, MD,[2] Derek Klarin, MD,[1] Nathan A Bihlmeyer, BS,[14] Siew-Kee Low, PhD,[15] Peter E. Weeke, MD, PhD,[16,17] Martina Müller-Nurasyid, PhD,[5,18,19] J. Gustav Smith, MD, PhD,[1,20] Jennifer A. Brody, BA,[21] Maartje N. Niemeijer MD,[22] Marcus Dörr, MD,[23,24] Stella Trompet, PhD,[25] Jennifer Huffman, PhD,[26] Stefan Gustafsson, PhD,[27] Claudia Schurmann, PhD,[28,29] Marcus E. Kleber, PhD,[30] Leo-Pekka Lyytikäinen, MD,[31] Ilkka Seppälä, MD,[31] Rainer Malik, PhD,[32] Andrea R. V. R. Horimoto, PhD,[33] Marco Perez, MD,[34] Juha Sinisalo, MD, PhD,[35] Stefanie Aeschbacher, MSc,[36,37] Sébastien Thériault, MD, MSc,[38,39] Jie Yao, MS,[40] Farid Radmanesh, MD, MPH,[1,41] Stefan Weiss, PhD,[24,42] Alexander Teumer, PhD,[24,43] Seung Hoan Choi, PhD,[1] Lu-Chen Weng, PhD[1,2] Sebastian Clauss, MD,[2,18] Rajat Deo, MD, MTR,[44] Daniel J. Rader, MD,[44] Svati Shah, MD, MHS,[45] Albert Sun, MD,[45] Jemma C. Hopewell, PhD,[46] Stephanie Debette, MD, PhD,[47–50] Ganesh Chauhan, PhD,[47,48] Qiong Yang, PhD,[51] Bradford B. Worrall, MD, MSc,[52], Guillaume Paré, MD, MSc,[38,39] Yoichiro Kamatani, MD, PhD,[15] Yanick P. Hagemeijer, MSc,[4] Niek Verweij, PhD,[4] Joylene E. Siland, BSc,[4] Michiaki Kubo, MD, PhD,[53] Jonathan D. Smith, PhD,[9] David R. Van Wagoner, PhD,[9] Joshua C. Bis, PhD,[21] Siegfried Perz, MSc,[54] Bruce M. Psaty, MD, PhD,[21,55–57] Paul M. Ridker, MD, MPH,[13] Jared W. Magnani, MD, MSc,[7,58] Tamara B. Harris, MD, MS,[59] Lenore J. Launer, PhD,[59] M. Benjamin Shoemaker, MD, MSCI,[16] Sandosh Padmanabhan, MD,[60] Jeffrey Haessler, MS,[61] Traci M. Bartz, MS,[62] Melanie Waldenberger, PhD,[19,54,63] Peter Lichtner, PhD,[64] Marina Arendt, MSc,[65] Jose E. Krieger, MD, PhD,[33] Mika Kähönen, MD, PhD,[66] Lorenz Risch, MD, MPH,[67] Alfredo J. Mansur, MD, PhD,[68] Annette Peters, PhD,[19,54,69] Blair H. Smith, MD,[70] Lars Lind, MD, PhD,[71] Stuart A. Scott, PhD,[72] Yingchang Lu, MD, PHD,[28,29] Erwin B. Bottinger, MD,[28,73] Jussi Hernesniemi, MD, PhD,[31,74] Cecilia M. Lindgren, PhD,[75] Jorge A Wong, MD,[76] Jie Huang, MD, MPH,[77] Markku Eskola, MD, PhD,[74] Andrew P. Morris, PhD,[75,78] Ian Ford, PhD,[79] Alex P. Reiner, MD, MSc,[61,80] Graciela Delgado, Msc,[30] Lin Y. Chen, MD, MS,[81] Yii-Der Ida Chen, PhD,[40] Roopinder K. Sandhu, MD, MPH,[82] Man Li, PhD,[83,84] Eric Boerwinkle, PhD,[85] Lewin Eisele, MD,[65] Lars Lannfelt, MD, PhD,[86] Natalia Rost, MD, MPH, FAAN,[1,87] Christopher D. Anderson, MD, MMSc,[1,41] Kent D. Taylor, PhD,[40] Archie Campbell, MA,[88] Patrik K. Magnusson, PhD,[89] David Porteous, PhD,[88] Lynne J. Hocking, PhD,[90] Efthymia Vlachopoulou, PhD,[91] Nancy L. Pedersen, MA, PhD,[89] Kjell Nikus, MD, PhD,[74] Marju Orho-Melander, PhD,[92] Anders Hamsten, MD, PhD,[93] Jan Heeringa, MD, PhD,[22] Joshua C. Denny, MD,[16] Jennifer Kriebel, PhD,[54,63,69] Dawood Darbar, MD,[94] Christopher Newton-Cheh, MD, MPH,[1,2] Christian Shaffer, BS,[16] Peter W. Macfarlane, PhD, DSc,[95] Stefanie Heilmann, PhD,[96,97] Peter Almgren, MSc,[92] Paul L. Huang, MD, PhD,[2] Nona Sotoodehnia, MD, MPH,[98] Elsayed Z. Soliman, MD, MSc, MS,[99] Andre G. Uitterlinden, PhD,[100] PhD, Albert Hofman, MD, PhD,[22] Oscar H. Franco, MD, PhD,[22] Uwe Völker, PhD,[24,42] Karl-Heinz Jöckel, PhD,[65] Moritz F. Sinner, MD, MPH,[18,19] Henry J. Lin, MD,[40] Xiuqing Guo, PhD,[40] METASTROKE Consortium of the ISGC, Neurology Working Group of the CHARGE Consortium, Martin Dichgans, MD,[32,101,102], Erik Ingelsson, MD, PhD,[27,103] Charles Kooperberg, PhD,[61] Olle Melander, MD, PhD,[104] Ruth J. F. Loos, PhD,[28,29,105] Jari Laurikka, MD, PhD,[106] David Conen, MD, MPH,[36–38] Jonathan Rosand, MD, MSc,[1,41] Pim van der Harst, MD, PhD,[4] Marja-Liisa Lokki, PhD,[91] Sekar Kathiresan, MD,[1] Alexandre Pereira, MD, PhD,[107] J. Wouter Jukema, MD, PhD,[25,108,109] Caroline Hayward, PhD,[26] Jerome I. Rotter, MD,[110]

Winfried März, MD,[111] Terho Lehtimäki, MD, PhD,[31] Bruno H. Stricker, MD, PhD,[112] Mina K. Chung, MD,[9] Stephan B. Felix, MD,[23,24] Vilmundur Gudnason, MD, PhD,[11,12] Alvaro Alonso, MD, PhD,[113] Dan M. Roden, MD,[16] Stefan Kääb, MD, PhD,[18,19] Daniel I. Chasman, PhD,[1,114] Susan R. Heckbert, MD, PhD,[55,56] Emelia J. Benjamin, MD, ScM,[7,58,115] Toshihiro Tanaka, MD, PhD,[116,117] Kathryn L. Lunetta, PhD,[7,8] Steven A. Lubitz, MD, MPH,[1,2,118] Patrick T. Ellinor, MD, PhD,[1,2,118]

AFGen Consortium Member Affiliations

1. Program in Medical and Population Genetics, The Broad Institute of MIT and Harvard, Cambridge, MA, USA.
2. Cardiovascular Research Center, Massachusetts General Hospital, Boston, MA, USA.
3. Department of Medical Research, Bærum Hospital, Vestre Viken Hospital Trust, Norway.
4. Department of Cardiology, University of Groningen, University Medical Center Groningen, Groningen, The Netherlands.
5. Institute of Genetic Epidemiology, Helmholtz Zentrum München - German Research Center for Environmental Health, Neuherberg, Germany.
6. Institute of Medical Informatics, Biometry and Epidemiology, Chair of Genetic Epidemiology, Ludwig-Maximilians-Universität, Munich, Germany.
7. NHLBI and Boston University's Framingham Heart Study, Framingham, MA, USA.
8. Department of Biostatistics, Boston University School of Public Health, Boston, MA, USA.
9. Departments of Cardiovascular Medicine, Cellular and Molecular Medicine, Molecular Cardiology, and Quantitative Health Sciences, Cleveland Clinic, Cleveland, OH, USA.
10. McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, Baltimore, MD, USA.
11. Icelandic Heart Association, Kopavogur, Iceland.
12. Faculty of Medicine, University of Iceland, Reykavik, Iceland.
13. Divisions of Preventive and Cardiovascular Medicine, Brigham and Women's Hospital & Harvard Medical School, Boston, MA, USA.
14. Predoctoral Training Program in Human Genetics, McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, Baltimore, MD, USA.
15. Laboratory for Statistical Analysis, RIKEN Center for Integrative Medical Sciences, Yokohama, Japan.
16. Department of Medicine, Vanderbilt University Medical Center, Nashville, TN, USA.
17. The Heart Centre, Department of Cardiology, Copenhagen University Hospital, Rigshospitalet, Copenhagen, Denmark.
18. Department of Medicine I, University Hospital Munich, Ludwig-Maximilians-University, Munich, Germany.
19. DZHK (German Centre for Cardiovascular Research), partner site: Munich Heart Alliance, Munich, Germany.
20. Molecular Epidemiology and Cardiology, Clinical Sciences, Lund University, Lund, Sweden.
21. Cardiovascular Health Research Unit, Department of Medicine, University of Washington, Seattle, WA, USA.
22. Department of Epidemiology, Erasmus University Medical Center Rotterdam, Rotterdam, the Netherlands.
23. Department of Internal Medicine B, University Medicine Greifswald, Greifswald, Germany.

24. DZHK (German Centre for Cardiovascular Research), partner site: Greifswald, Germany.
25. Department of Cardiology, Leiden University Medical Center, The Netherlands.
26. MRC Human Genetics Unit, Institute of Genetics and Molecular Medicine, University of Edinburgh, UK.
27. Department of Medical Sciences, Molecular Epidemiology and Science for Life Laboratory, Uppsala University, Uppsala, Sweden.
28. The Charles Bronfman Institute for Personalized Medicine, Icahn School of Medicine at Mount Sinai, New York, NY, USA.
29. The Genetics of Obesity and Related Metabolic Traits Program, Icahn School of Medicine at Mount Sinai, New York, NY, USA.
30. Vth Department of Medicine, Medical Faculty Mannheim, Heidelberg University, Germany.
31. Department of Clinical Chemistry, Fimlab Laboratories and University of Tampere School of Medicine, Tampere, Finland.
32. Institute for Stroke and Dementia Research, Klinikum der Universität München, Ludwig-Maximilians University, München, Germany.
33. Laboratory of Genetics and Molecular Cardiology, Heart Institute, University of Sao Paulo, Sao Paulo, Brazil.
34. Stanford University, Stanford, CA, USA.
35. Heart and Lung Center HUS, Helsinki University Central Hospital, Helsinki, Finland.
36. University Hospital Basel, Switzerland.
37. Cardiovascular Research Institute Basel, Switzerland.
38. Population Health Research Institute, Hamilton, Canada.
39. Department of Pathology and Molecular Medicine, McMaster University, Hamilton, Canada.
40. Institute for Translational Genomics and Population Sciences, Department of Pediatrics, LABioMed at Harbor-UCLA Medical Center, Torrance, CA, USA.
41. Center for Human Genetics Research, Massachusetts General Hospital, Boston, MA, USA.
42. Interfaculty Institute for Genetics and Functional Genomics, University Medicine and Ernst-Moritz-Arndt-University Greifswald, Greifswald, Germany.
43. Institute for Community Medicine, University Medicine Greifswald, Greifswald, Germany.
44. Division of Cardiovascular Medicine, Department of Medicine, Perelman School of Medicine at the University of Pennsylvania, Philadelphia, PA, USA.
45. Division of Cardiology, Department of Medicine, Duke University School of Medicine, Durham, NC, USA.
46. CTSU - Nuffield Department of Population Health, University of Oxford, Oxford, UK.
47. Inserm Center U1219 (Bordeaux Population Health Centre), Bordeaux, France.
48. University of Bordeaux, Bordeaux, France.
49. Department of Neurology, Bordeaux University Hospital, Bordeaux, France.
50. Department of Neurology, Boston University School of Medicine, Boston, MA, USA.
51. Biostatistics Department, School of Public Health, Boston University, Boston, MA, USA.
52. University of Virginia Health System, Departments of Neurology and Public Health Science, Charlottesville, VA, USA.
53. RIKEN Center for Integrative Medical Sciences, Yokohama, Japan.
54. Institute of Epidemiology II, Helmholtz Zentrum München - German Research Center for Environmental Health, Neuherberg, Germany.

55. Department of Epidemiology and Cardiovascular Health Research Unit, University of Washington, Seattle, WA, USA.
56. Group Health Research Institute, Group Health Cooperative, Seattle, WA, USA.
57. Department of Health Services, University of Washington, Seattle, WA, USA.
58. Department of Medicine, Boston University School of Medicine, Boston, MA, USA.
59. Laboratory of Epidemiology, Demography, and Biometry, National Institute on Aging, Bethesda, MD, USA.
60. Institute of Cardiovascular and Medical Sciences, BHF Glasgow Cardiovascular Research Centre, University of Glasgow, Glasgow, UK.
61. Fred Hutchinson Cancer Research Center, University of Washington, Seattle, WA, USA.
62. Cardiovascular Health Research Unit, Departments of Medicine and Biostatistics, University of Washington, Seattle, WA, USA.
63. Research unit of Molecular Epidemiology, Helmholtz Zentrum München - German Research Center for Environmental Health, Neuherberg, Germany.
64. Institute of Human Genetics, Helmholtz Zentrum München - German Research Center for Environmental Health, Neuherberg, Germany.
65. Institute for Medical Informatics, Biometry, and Epidemiology, University Hospital, University Duisburg-Essen, Germany.
66. Department of Clinical Physiology, Tampere University Hospital and University of Tampere School of Medicine, Tampere, Finland.
67. University Institute of Clinical Chemistry, University of Bern, Switzerland and labormedizinisches zentrum Dr. Risch, Schaan, Liechtenstein.
68. Heart Institute, University of Sao Paulo, Sao Paulo, Brazil.
69. German Center for Diabetes Research, Neuherberg, Germany.
70. Division of Population Health Sciences, University of Dundee, Scotland, UK.
71. Department of Medical Sciences, Cardiovascular Epidemiology, Uppsala University, Uppsala, Sweden.
72. Department of Genetics and Genomic Sciences , Icahn School of Medicine at Mount Sinai, New York, NY, USA.
73. Department of Pharmacology and Systems Therapeutics, Icahn School of Medicine at Mount Sinai, New York, NY, USA.
74. Department of Cardiology, Heart Hospital, Tampere University Hospital and University of Tampere School of Medicine, Tampere, Finland.
75. Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, UK.
76. Division of Cardiology, Hamilton Health Sciences, McMaster University, Hamilton, Ontario, Canada.
77. Boston VA Research Institute, Inc., Boston, MA, USA.
78. Department of Biostatistics, University of Liverpool, Liverpool, UK.
79. Robertson Center for Biostatistics, University of Glasgow, Glasgow, UK.
80. Department of Epidemiology, University of Washington, Seattle, WA, USA.
81. Cardiovascular Division, Department of Medicine, University of Minnesota Medical School, Minneapolis, MN, USA.
82. Division of Cardiology, University of Alberta, Edmonton, Canada.
83. Department of Epidemiology, Johns Hopkins University, Baltimore, MD, USA.

84. Division of Nephrology & Hypertension, Internal Medicine, School of Medicine, University of Utah, UT, USA.
85. Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA.
86. Department of Public Health and Caring Sciences, Geriatrics, Uppsala University, Uppsala, Sweden.
87. Acute Stroke Services, Massachusetts General Hospital, Boston, MA, USA.
88. Generation Scotland, Centre for Genomic and Experimental Medicine, Institute of Genetics and Molecular Medicine, University of Edinburgh, UK.
89. Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden.
90. Musculoskeletal Research Programme, Division of Applied Medicine, University of Aberdeen, Aberdeen, UK.
91. Transplantation Laboratory, Medicum, University of Helsinki, Helsinki, Finland.
92. Department of Clinical Sciences, Lund University, Malmö, Sweden.
93. Cardiovascular Genetics and Genomics Group, Atherosclerosis Research Unit, Department of Medicine Solna, Karolinska Institutet, Stockholm, Sweden.
94. University of Illinois, Chicago, IL, USA.
95. Institute of Health and Wellbeing, College of Medical, Veterinary and Life Sciences, University of Glasgow, UK.
96. Institute of Human Genetics, University of Bonn, Germany.
97. Department of Genomics, Life & Brain Research Center, University of Bonn, Germany.
98. Cardiovascular Health Research Unit, University of Washington Medical Center, Seattle, WA, USA.
99. Epidemiological Cardiology Research Center (EPICARE), Wake Forest School of Medicine, Winston Salem, NC, USA.
100. Department of Epidemiology and Internal Medicine, Erasmus University Medical Center Rotterdam, the Netherlands.
101. Munich Cluster for Systems Neurology (SyNergy), München, Germany.
102. German Center for Neurodegenerative Diseases (DZNE), Munich, Germany.
103. Department of Medicine, Division of Cardiovascular Medicine, Stanford University School of Medicine, Stanford, CA, USA.
104. Department of Internal Medicine, Clinical Sciences, Lund University, Malmö, Sweden.
105. The Mindich Child Health and Development Institute, Icahn School of Medicine at Mount Sinai, New York, NY, USA.
106. Department of Cardio-Thoracic Surgery, Heart Hospital, Tampere University Hospital and University of Tampere School of Medicine, Tampere, Finland.
107. Laboratory of Genetics and Molecular Biology, Heart Institute, University of Sao Paulo, Sao Paulo, Brazil and Department of Genetics, Harvard Medical School, Boston, MA, USA.
108. Durrer Center for Cardiogenetic Research, Amsterdam, The Netherlands.
109. Interuniversity Cardiology Institute of the Netherlands, Utrecht, The Netherlands.
110. Institute for Translational Genomics and Population Sciences, Departments of Pediatrics and Medicine, LABioMed at Harbor-UCLA Medical Center, Torrance, CA, USA.
111. Clinical Institute of Medical and Chemical Laboratory Diagnostics, Medical University of Graz, Graz, Austria and Synlab Academy, Synlab Services GmbH, Mannheim, Germany.

112. Department of Epidemiology and Internal Medicine, Erasmus University Medical Center Rotterdam, the Netherlands and Inspectorate of Health Care, Utrecht, the Netherlands.
113. Department of Epidemiology, Rollins School of Public Health, Emory University, Atlanta, GA, USA.
114. Divisions of Preventive Medicine and Genetics, Brigham and Women's Hospital & Harvard Medical School, Boston, MA, USA.
115. Department of Epidemiology, Boston University School of Public Health, Boston, MA, USA.
116. Laboratory for Cardiovascular Diseases, RIKEN Center for Integrative Medical Sciences, Yokohama, Japan.
117. Department of Human Genetics and Disease Diversity, Tokyo Medical and Dental University Graduate School of Medical and Dental Sciences, Tokyo, Japan.
118. Cardiac Arrhythmia Service, Massachusetts General Hospital, Boston, MA, USA.

Neurology Working Group of the CHARGE Consortium Members

Ganesh Chauhan, PhD; Corey R Arnold, BSc; Audrey Y Chu, PhD; Myriam Fornage, PhD; Azadeh Reyahi, MSc; Joshua C Bis, PhD; Aki S Havulinna, DSc; Muralidharan Sargurupremraj, PhD; Albert V Smith, PhD; Hieab H H Adams, MSc; Seung Hoan Choi, MA; Stella Trompet, PhD; Melissa E Garcia, MPH; Alexander Teumer, PhD; Céline Bellenguez, PhD; Xueqiu Jian, PhD; Claudia L Satizabal, PhD; Yongmei Liu, PhD; Susan R Heckbert, MD; Kenneth Rice, PhD; Nicholas L Smith, PhD; Reinhold Schmidt, MD; Hugo J Aparicio, MD; Didier Leys, MD; Claudine Berr, MD; Jean-François Dartigues, MD; Cecilia M Lindgren, PhD; Albert Hofman, MD; Peter J Koudstaal, MD; André G Uitterlinden, PhD; Anton J M de Craen, PhD; Andrew D Johnson, PhD; Hans Jörgen Grabe, MD; Yoichiro Kamatani, MD; Oscar L Lopez, MD; Jerome I Rotter, MD; Rebecca F Gottesman, MD; David S Knopman, MD; B Gwen Windham, MD; Alexa Beiser, PhD; Curtis R French, PhD; Mark Lathrop, PhD; Vilmundur Gudnason, MD; Tobias Kurth, MD; Bruce M Psaty, MD; Tamara B Harris, MD; Stephen S Rich, PhD; Anita L deStefano, PhD; Carsten O Schmidt, PhD; Veikko Salomaa, MD; Thomas H Mosley, PhD; Erik Ingelsson, MD; Cornelia M van Duijn, PhD; Ordan J Lehmann, MD; Christophe Tzourio, MD; Lenore J Launer, PhD; M Arfan Ikram, MD; Peter Carlsson, PhD; Daniel I Chasman, PhD; Sarah J Childs, PhD; William T Longstreth, Jr, MD; Sudha Seshadri, MD; Stéphanie Debette, MD

Neurology Working Group of the CHARGE Consortium member affiliations

University Medicine Greifswald, Institute for Community Medicine, SHIP-KEF, Greifswald, Germany (AT, COS); University Medicine Greifswald, Department of Psychiatry and Psychotherapy, Greifswald, Germany (HJG); Division of Preventive Medicine, Brigham and Women's Hospital, Boston, MA, USA (DIC, AYC, TK); Harvard Medical School, Boston, MA, USA (DIC); Inserm Research Center for Epidemiology and Biostatistics (U897) - Team
Neuroepidemiology, Bordeaux, France (TK, MS, CT, JFD, GC, SD); University of Bordeaux, College of Health Sciences, Bordeaux, France (TK); University of Virginia, Charlottesville, VA USA (SSR); National institute for Health and Welfare, Helsinki, Finland (ASH, VS); Department of Epidemiology, Erasmus MC, Rotterdam, The Netherlands (HHHA, AH, CMvD, MAI); Department of Neurology, Erasmus MC, Rotterdam, The Netherlands (PJK); Department of Internal Medicine, Erasmus MC, Rotterdam, The Netherlands (AGU); Cardiovascular Health Research Unit, Department of Medicine, University of Washington, Seattle, WA, USA (JCB, BMP);
Department of Epidemiology, University of Washington, Seattle, WA, USA (BMP, WTL, NLS, SRH); Department of Health Services, University of Washington, Seattle, WA, USA (BMP); Group Health Research Institute, Group Health Cooperative, Seattle, WA, USA (BMP); Institute

for Translational Genomics and Population Sciences, Los Angeles Biomedical Research Institute at Harbor-UCLA Medical Center, Torrance, California, USA (JIR); Division of Genomic Outcomes, Department of Pediatrics, Harbor-UCLA Medical Center, California, USA (JIR); UCLA, California, USA (JIR); Department of Biostatistics, University of Washington, Seattle, WA, USA (KR); Department of Neurology; University of Washington, Seattle, WA, USA (WTL); Seattle Epidemiologic Research and Information Center of the Department of Veterans Affairs Office of Research and Development, Seattle, WA, USA (NLS); Department of Cardiology, Leiden University Medical Center, Leiden The Netherlands (ST); Department of Gerontology and Geriatrics, Leiden University Medical Center, Leiden, The Netherlands (ST, AJMdC); Center for Human Genetics, Division of Public Health Sciences, Wake Forest School of Medicine, Winston Salem, NC, USA (YL); Laboratory of Epidemiology and Population Sciences, National Institute on Aging, Bethesda, MD, USA (TBH, MEG); Department of Medical Sciences, Molecular Epidemiology and Science for Life Laboratory, Uppsala University, Uppsala, Sweden (EI); Genetic and Genomic Epidemiology Unit, Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, UK (CML); University of Bordeaux, Bordeaux, France (MS, CT, JFD, GC, SD, TK); Université of Montpellier, France (CeB); Institut Pasteur de Lille, Lille, France (CeB); Université Lille Nord de France, Lille, France (DL); Department of Neurology, Lille University Hospital, Lille, France (DL); INSERM U1171, Lille, France (DL); INSERM U1061, Montpellier, France (ClB); University Montpellier 1, Montpellier, France (ClB); Department of Neurology, Bordeaux University Hospital, Bordeaux, France (SD, JFD); Boston University School of Medicine, Boston, MA, USA (SD); IRP/NIA/NIH, Bethesda, MD, USA (LJL); Department of Neurology, University of Pittsburgh, PA, USA (OLL); Icelandic Heart Association, Kópavogur, Iceland (VG, AVS); University of Iceland, Faculty of Medicine, Reykjavik, Iceland (VG); Institute of Molecular Medicine and Human Genetics Center; University of Texas Health Science Center at Houston, Houston, TX, USA (MF, XJ); Department of Neurology; Johns Hopkins University, Baltimore, MD, USA (RFG); Department of Neurology; Mayo Clinic, Rochester, MN, USA (DSK); Department of Medicine, Division of Geriatrics; University of Mississippi Medical Center, Jackson, MS, USA (THM, BGW); McGill University and Genome Quebec Innovation Center (ML); Department of Neurology, Clinical Division of Neurogeriatrics, Medical University Graz, Austria (RS); National Heart, Lung, and Blood Institute's Framingham Heart Study Cardiovascular Epidemiology and Human Genomics Branch, Framingham, Massachusetts, USA (ADJ); Fondation Jean Dausset, Centre d'Etude du Polymorphisme Humain (CEPH), Paris, France (YK); Center for Integrative Medical Sciences, RIKEN, Yokohama, Japan (YK); Department of Neurology, Boston University School of Medicine, Boston, Massachusetts, USA (AB, ALD, HJA, SS, CLS, SHC); Department of Biostatistics, Boston University School of Public Health, Boston, Massachusetts, USA (AB, ALD, SS, SHC); The National Heart, Lung, and Blood Institute's Framingham Heart Study, Framingham, Massachusetts, USA (AB, ADJ, ALD, AYC, HJA, SS, CLS, SHC); Department of Ophthalmology, University of Alberta, Edmonton, Alberta, Canada (CRF, OJL); Alberta Children's Hospital Research Institute and Department of Biochemistry and Molecular Biology, University of Calgary, Calgary, Alberta, Canada (CRA, SJC); Department of Medical Genetics, University of Alberta, Edmonton, Alberta, Canada (OJL); Department of Chemistry and Molecular Biology, University of Gothenburg, Gothenburg, Sweden (AR, PC).

METASTROKE Consortium Contributors

Study	**Investigator**
ASGC	Elizabeth Holliday
	Chris Levi
BRAINS	Pankaj Sharma
	Iona Cotlarciuc

GASROS	Jonathan Rosand
GEOS	Steven Kittner
	John Cole
HPS	Jemma Hopewell
	Robert Clarke
ISGS/SWISS	James Meschia
	Mike Nalls
MILANO	Giorgio Boncoraglio
VISP	Bradford B. Worrall
	Michéle Sale
	Wei-Min Chen
WHI	Alex Reiner
WTCCC2-D	Martin Dichgans
	Rainer Malik
WTCCC2-UK	Hugh Markus
	Steve Bevan
CADISP	Stephanie Debette
	Ganesh Chauhan
Krakow	Agnieszka Slowik
	Joanna Pera
Leuven	Vincent Thijs
	Robin Lemmens
Lund	Arne Lindgren
Münster	E Bernd Ringelstein
	Klaus Berger
SIGN	Brackie Mitchell
Portugal	Sofia A Oliveira
	Jose M Ferro
	Astrid M Vicente
RACE	Danish Salaheen
USA	Dan Woo

Other METASTROKE participants

ARIC	Myriam Fornage
CHS	Bruce Psaty
	Josh Bis
deCODE	Solveig Gretarsdottir
FHS	Sudha Seshadri
	Qiong Yang
	Claudia L. Satizabal Barrera
HVH	Bruce Psaty
Rotterdam	Arfan Ikram
Barcelona	Israel Fernandez
BSS	Massimo Pandolfo

	Sherine Abboud
Copenhagen	Marianne Benn
	Børge G Nordestgaard
ESS	Cathie Sudlow
	Kristina Rannikmae
Glasgow	Matthew Walters
	Peter Higgins
GoDarts	Colin N A Palmer
	Alexander S F Doney
Graz	Reinhold Schmidt
INTERSTROKE	Guillame Pare
Karolinska	Konstantinos Kostulas
SMART	Paul de Bakker
	Ale Algra
Athero-Express	Sander van der Laan
	Gerald Pasterkamp
Sifap	Anne-Katrin Giese

Ancestry-specific GWAS meta-analyses

Separate GWAS in 15,993 cases and 113,719 referents of European ancestry revealed one additional association on chromosome 15q21 (rs2921421, OR 1.72, 95% CI 1.42-2.09, P=3.29x10^{-8}, **Supplementary Table 6**); however, there was only one significant variant at this locus and the variant was imputed with low quality across all studies reducing our confidence in this finding. Additional replication in another European ancestry study is needed to clarify the relevance of rs2921421. In meta-analysis of 837 cases and 2456 referents of Asian ancestry we identified an association on chromosome 12q15 (rs7138621, OR 7.92, 95% CI 4.26-14.73, P=6.48x10^{-11}), which was not significant in *in silico* replication in 8180 cases and 28,612 referents in the Biobank Japan (**Supplementary Table 10**). Separate meta-analyses in individuals of Brazilian and Hispanic descent did not identify additional loci; however, our power was limited in each of these sub-groups.

GWAS meta-analyses of incident and prevalent atrial fibrillation in Europeans

Separate GWAS meta-analyses of incident (7232 cases) and prevalent (8656 cases) atrial fibrillation in Europeans showed similar results to the European ancestry analysis (**Supplementary Tables 8-9, Supplementary Figs. 7-8**); however, we did reveal a novel atrial fibrillation locus associated with prevalent atrial fibrillation at chromosome 12p11 (rs1454934, OR 1.16, 95% CI 1.1-1.22, P=4.18x10^{-8}). The most significant variant at this locus was intronic to the gene plakophilin-2 (*PKP2*), which encodes an important component of the desmosome and is known to be associated with arrhythmogenic right ventricular cardiomyopathy[220] and Brugada syndrome.[221,222]

Replication of genetic variants specific to African American ancestry GWAS meta-analysis

The variants rs115339321 (OR 1.53, 95% CI 0.82-2.18, P=0.18) and rs79433233 (OR 1.36, 95% CI 0.75-2.47, P=0.31) were not significantly associated with atrial fibrillation in 447 atrial fibrillation cases and 442 referents of African American ancestry (**Supplementary Table 25-26**). The lack of replication may be caused by the small sample size of the replication study. Further replication in a larger sample of African American ancestry is needed to clarify the role of the variants rs115339321 and rs79433233.

Pathway analyses

1. DEPICT

The most significant pathway identified using the DEPICT software was the arrhythmogenic right ventricular cardiomyopathy (ARVC) pathway (P=1.3x10^{-6}, **Supplementary Table 27**). None of the pathways analyzed reached an FDR <5%.

2. IPA

The most significantly enriched biological pathway was the coagulation system (P=0.0088). In addition, many genes were involved in the clathrin-mediated endocytosis signaling pathway (P=0.011) and the protein ubiquitination pathway (P=0.013). The most significant pathways are listed in **Supplementary Table 28** None of the pathways reached the significance threshold (FDR<5%). In addition, many of the genes investigated were involved in arrhythmia mechanisms (**Supplementary Table 29**).

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